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Information Resources on Avian Influenza

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Avian Influenza Weblog

XML RSS Feed for the Avian Influenza

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Photo by Stephen Ausmus.
USDA, ARS Image Gallery. Online: http://www.ars.usda.gov/is/graphics/photos/
Introduction

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http://agnr.umd.edu/directory/Bio.cfm?ID=dperez1

This excellent Web resource provides a unique tool for either the general public or the avid researcher to access important sources of information about avian influenza. You will find general information about the disease as well as a number of links to national and international organizations, which provide additional resources about the disease and its implications for animal and human health. The site also provides several chapters that highlight the most up-to-date information available in each area. Described as early as 1878 as “fowl plague” by Perroncito in Italy, avian influenza has come to haunt us every now and then.

Avian influenza is a disease of poultry, whose disease symptoms vary from completely mild or unnoticeable to a catastrophic disease with a mortality rate that can reach up to 100% in some avian species. The natural hosts of the virus are ducks, shorebirds, and other species of wild aquatic birds. In the natural hosts, influenza infections cause almost no disease signs and the infection is established mostly in the intestinal tract. The virus is excreted with the feces into the water promoting a cycle of fecal-oral transmission. Occasionally, the virus “jumps” from wild birds to domestic birds causing disease outbreaks (sometimes sub clinical for awhile, and then become more obvious because they increase their virulence). Most avian influenza viruses do not infect humans. Avian influenza viruses from wild birds are so adapted to them that the chances of humans becoming infected with one of those viruses are very small. However, infections with non life-threatening avian influenza viruses have occurred in humans, mostly associated to conjunctivitis (pink eye). Avian influenza viruses that become adapted to domestic flocks are also not likely to “jump” to humans. However, the H5N1 virus experience in Asia has taught us that letting influenza viruses circulate in domestic bird species for extended periods can lead to strains that become more and more efficient at making the “jump” to humans and other animal species. Being vigilant, identifying potential disease signs, learning more about the disease and its interactions with the host, and practicing strict biosecurity measures, will do a great deal toward protecting poultry and ourselves. As the world prepares for the inevitable, poultry farmers around the world can be at the forefront in the control of the disease and thus prevent the emergence of pandemic influenza strains at the amplification stage: poultry species. On the research arena, novel vaccine strategies and faster and more sensitive diagnostic tools will soon provide a number of alternatives to the poultry sector to combat the disease. In the future, researchers will be able to predict which viruses are more likely to be a pandemic threat. However, it is only going to be through the combined effort of poultry farmers, poultry veterinarians, government agencies, diagnosticians and researchers that the inevitable can be made preventable.

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ISSN: 1473-3099.

Descriptors: influenza, avian prevention and control, international cooperation, southeastern Asia, birds, influenza, avian mortality.


NAL Call Number: SF601.P7

Abstract: Thirty blood samples were collected randomly from each of the 38 breeder-broiler farms in Jordan. Serum samples were examined using indirect ELISA for specific antibodies to avian influenza virus. The overall true flock-level sero-prevalence of avian influenza was 71% (95% CI: 55,83). Positive flocks had 2-30 sero-positive chickens and half of flocks had >20 sero-positive birds. The number of sero-positive flocks varied in the studied localities with more sero-positives in farms located within the migratory route of migratory wild fowl. The examined broiler-breeder flocks had no clinical signs, or noticeable decrease in egg production; mortalities were within the normal range (0.1-1%). The number of positive sera/flock correlated with flock size. There were a no significant (Pearsons r = 0.21, p = 0.21) correlation between positive flocks and age. A non-pathogenic AI virus infects broiler-breeder farms in Jordan. Wild local and migrating birds might promote the further spread of this virus in Jordan and other countries.

Descriptors: avian influenza, poultry, viral diseases, broiler-breeder, ELISA, age influence, Jordan.


Descriptors: fishes, fish diseases, avian influenza virus, etiology, salmoidei, animal diseases, bony fishes, influenza virus, orthomyxoviridae, viruses, salmonidae.


NAL Call Number: 41.8 T752

Descriptors: recent developments, avian influenza virus, turkeys, ducks.


NAL Call Number: aSF995.6.1615 1981a

Descriptors: avian influenza virus, poultry, ducks, turkeys, Great Britain.


NAL Call Number: SF481.M54

Descriptors: avian influenza virus, poultry, Gallus gallus, outbreaks, disease transmission, history.


NAL Call Number: 41.8 V641

Descriptors: birds microbiology, fowl plague epidemiology, influenza A virus avian isolation and purification, England, fowl plague microbiology, quarantine.


NAL Call Number: 241.71 B75

Descriptors: aviary birds, avian influenza virus, epidemiology, etiology, viroses, animal diseases, pathogenicity, disease transmission, zoonoses, human diseases, wild animals, chickens, turkeys, ducks,

NAL Call Number: 41.8 V641

Abstract: During 1980 and 1981 influenza A viruses of subtypes H3N2, H3N8, H4N1, H4N6, H6N2, H6N8, H7N7, H11N8 and H11N9 were isolated from birds in Great Britain, usually as a result of investigations of disease or death. However, all viruses were shown to be of low virulence for chickens in pathogenicity index tests. There was one occurrence of influenza virus infection of turkeys (H6N8) but viruses were frequently obtained from domestic ducks. Other viruses were isolated from exotic birds in zoos or bird collections.

Descriptors: birds microbiology, influenza A virus avian isolation and purification, animals, zoo microbiology, antibodies, viral analysis, chickens, Great Britain, hemagglutination inhibition tests veterinary, immunodiffusion veterinary, avian immunology, avian pathogenicity, poultry microbiology.


NAL Call Number: aSF995.6.I6I5 1981a

Descriptors: avian influenza virus, isolation of influenza A virus, aviary birds, exotic birds, Great Britain.

Alexander, D.J. (1980). **Isolation of influenza viruses from avian species in Great Britain.** *Comparative Immunology, Microbiology and Infectious Diseases* 3(1-2): 165-70. ISSN: 0147-9571.

NAL Call Number: QR180.C62

Descriptors: birds microbiology, influenza A virus avian isolation and purification, influenza A virus isolation and purification, turkeys microbiology, Great Britain, avian classification, influenza A virus classification, serotyping.


NAL Call Number: 41.8 R312

Descriptors: infection, Newcastle disease, viral disease, influenza virus A infection, viral disease, influenza virus B infection, viral disease, influenza virus C infection, viral disease, mortality, virulence, meeting abstract.


NAL Call Number: SF601.S8

Descriptors: avian influenza virus, transmission, poultry, wild birds, Great Britain, laws.


NAL Call Number: SF995.P65 1996

Descriptors: avian influenza virus, epidemiology, diagnosis, control, immunization, poultry diseases.


NAL Call Number: SF601.V44

Abstract: Only type A influenza viruses are known to cause natural infections in birds, but viruses of all 15 hemagglutinin and all nine neuraminidase influenza A subtypes in the majority of possible combinations have been isolated from avian species. Influenza A viruses infecting poultry can be divided into two distinct groups on the basis of their ability to cause disease. The very virulent viruses cause highly pathogenic avian influenza (HPAI), in which mortality may be as high as 100%. These viruses have been restricted to...
subtypes H5 and H7, although not all viruses of these subtypes cause HPAI. All other viruses cause a much milder, primarily respiratory disease, which may be exacerbated by other infections or environmental conditions. Since 1959, primary outbreaks of HPAI in poultry have been reported 17 times (eight since 1990), five in turkeys and 12 in chickens. HPAI viruses are rarely isolated from wild birds, but extremely high isolation rates of viruses of low virulence for poultry have been recorded in surveillance studies, giving overall figures of about 15% for ducks and geese and around 2% for all other species. Influenza viruses have been shown to affect all types of domestic or captive birds in all areas of the world, but the frequency with which primary infections occur in any type of bird depends on the degree of contact there is with feral birds. Secondary spread is usually associated with human involvement, probably by transferring infective faeces from infected to susceptible birds.

Descriptors: influenza A virus avian isolation and purification, amino acid sequence, ducks virology, Great Britain, avian pathogenicity, molecular sequence data, turkeys virology.

NAL Call Number: SF481.M54
Descriptors: international reference laboratory, diagnosis, avian influenza virus, poultry.

NAL Call Number: 41.8 Av5
Abstract: The current definitions of high-pathogenicity avian influenza (HPAI), formulated over 10 years ago, were aimed at including viruses that were overtly virulent in in vivo tests and those that had the potential to become virulent. At that time the only virus known to have mutated to virulence was the one responsible for the 1983-84 Pennsylvania epizootic. The mechanism involved has not been seen in other viruses, but the definition set a precedent for statutory control of potentially pathogenic as well as overtly virulent viruses. The accumulating evidence is that HPAI viruses arise from low-pathogenicity avian influenza (LPAI) H5 or H7 viruses infecting chickens and turkeys after spread from free-living birds. At present it can only be assumed that all H5 and H7 viruses have this potential and mutation to virulence is a random event. Therefore, the longer the presence and greater the spread in poultry the more likely it is that HPAI virus will emerge. The outbreaks in Pennsylvania, Mexico, and Italy are demonstrations of the consequences of failing to control the spread of LPAI viruses of H5 and H7 subtypes. It therefore seems desirable to control LPAI viruses of H5 and H7 subtype in poultry to limit the probability of a mutation to HPAI occurring. This in turn may require redefining statutory AI. There appear to be three options: 1) retain the current definition with a recommendation that countries impose restrictions to limit the spread of LPAI of H5 and H7 subtypes; 2) define statutory AI as an infection of birds/poultry with any AI virus of H5 or H7 subtype; 3) define statutory AI as any infection with AI virus of H5 or H7 subtype, but modify the control measures imposed for different categories of virus and/or different types of host.
Descriptors: epidemiology, infection, avian influenza, infectious disease, prevention and control, respiratory system disease, viral disease, disease eradication, epizootics, viral virulence.

NAL Call Number: 41.8 V643
Descriptors: fowl plague epidemiology, poultry diseases epidemiology, turkeys, England, influenza A virus avian isolation and purification.

NAL Call Number: 41.8 V641
Descriptors: birds microbiology, feces microbiology, influenza A virus avian isolation and purification, water supply, antigens, viral analysis, avian immunology, London, water pollution.


Abstract: A survey was conducted at two wildlife management areas of Pennsylvania (USA) to evaluate an antigen capture enzyme-linked immunosorbent assay (AC-ELISA) for the detection of avian influenza viruses (AIV) in cloacal swabs from waterfowl and to determine the influenza A virus subtypes and the distribution of these viruses among waterfowl. We collected 330 cloacal swabs from hunter-killed waterfowl in the fall of 1990 and from cage-captured waterfowl in the summer of 1991. Thirty-one hemagglutinating agents were isolated by chicken embryo inoculation (CEI) of which 27 were influenza A viruses and four Newcastle disease viruses (NDV). The prevalence of AIV infection was 8.2%. Compared to CEI, AC-ELISA was only 15% sensitive and 61% specific. Based on the distribution of AIV by species of waterfowl, mallards (Anas platyrhynchos) and American wigeons (Anas americana) were at equal risk of AIV infection even though most of the AIV isolates came from mallards. Although significant crude effects of sampling site and season on AIV recovery could be established, juvenile age was identified as the primary risk factor of AIV recovery. Twelve AIV subtypes were identified by hemagglutination inhibition (HI) and neuraminidase inhibition (NI) tests. The most prevalent subtypes were H4N8 and H6N8. We concluded that AC-ELISA was not useful for the detection of AIV in cloacal swabs from waterfowl and that CEI, HI, and NI tests remain as the method of choice for AIV screening in waterfowl. Based on the results AIV infected preferentially the young which represent the high risk group in waterfowl populations. The results from the AIV subtyping in our waterfowl survey are consistent with the results from numerous longitudinal studies of waterfowl in North America.

Descriptors: ecology, enzymology, immune system, infection, pathology, veterinary medicine, wildlife management, ELISA, epidemiology.
Egypt. *Comparative Immunology, Microbiology and Infectious Diseases* 3(1-2): 241-6. ISSN: 0147-9571.  
NAL Call Number: QR180.C62  
Descriptors: birds microbiology, influenza A virus avian isolation and purification, antigens, viral analysis, Egypt, avian classification, avian immunology, serotyping.

NAL Call Number: 286.81 F322  
Descriptors: economic impact, avian influenza virus, disease control, international trade, domestic fowl.

NAL Call Number: 41.8 Av5  
Abstract: During the summer of 1981, a respiratory disease epidemic occurred in turkeys in Brittany, France. Since this initial epizootic, which lasted through fall, epizootic waves similar to the initial one have occurred at approximately 6-month intervals, with smaller peaks at 2-month intervals. The epidemiology, clinical signs, and postmortem findings were highly suggestive of an epizootic of chlamydiosis. Serological tests for chlamydia, paramyxoviruses, avian influenza, adenovirus 127, *Mycoplasma*, and *Alcaligenes faecalis* were conducted. The chlamydia tests were the only ones consistently positive.  
Descriptors: disease outbreaks veterinary, poultry diseases epidemiology, respiratory tract infections veterinary, rhinitis veterinary, tracheitis veterinary, turkeys, antibodies, bacterial analysis, chlamydia immunology, complement fixation tests veterinary, France, poultry diseases immunology, respiratory tract infections epidemiology, respiratory tract infections immunology, rhinitis epidemiology, rhinitis immunology, seasons, tracheitis epidemiology, tracheitis immunology.

NAL Call Number: R11.C3  

Descriptors: avian influenza virology, Asia, birds virology, influenza A virus, avian physiology, avian influenza prevention and control, avian influenza transmission.

NAL Call Number: 448.8 L22  

NAL Call Number: 41.8 Am3  
Descriptors: disease outbreaks, fowl plague transmission, influenza prevention and control, influenza A virus avian, zoonoses, Hong Kong epidemiology, influenza epidemiology.

Descriptors: antiviral agents therapeutic use, bird diseases epidemiology, disease outbreaks veterinary, influenza veterinary, influenza vaccines therapeutic use, acetamides therapeutic use, amantadine therapeutic use, southeastern Asia epidemiology, Far East epidemiology, influenza drug therapy, influenza...
epidemiology, influenza prevention and control, international cooperation, neuraminidase antagonists and inhibitors, rimantadine therapeutic use, sialic acids therapeutic use, World Health Organization.


NAL Call Number: 448.8 L22  
Descriptors: fowl plague transmission, influenza A virus avian isolation and purification, Asia epidemiology, communicable diseases, emerging epidemiology, communicable diseases, emerging prevention and control, communicable diseases, emerging virology, disease outbreaks prevention and control, disease outbreaks statistics and numerical data, disease outbreaks veterinary, fowl plague epidemiology, fowl plague virology, Hong Kong epidemiology, avian pathogenicity, influenza vaccine supply and distribution, poultry virology, zoonoses transmission, zoonoses virology.

NAL Call Number: aSF601.U5  
Descriptors: United States, emus, rheas, avian influenza virus, epidemiology, birds, ratites, North America, viruses, FAD report.

NAL Call Number: 448.8 L22  
Descriptors: public health practice standards, social change, China epidemiology, communicable disease control standards, communicable disease control trends, disease outbreaks prevention and control, disease outbreaks statistics and numerical data, influenza, avian epidemiology, avian influenza prevention and control, population surveillance methods, poultry, severe acute respiratory syndrome epidemiology, severe acute respiratory syndrome prevention and control, world health.

Descriptors: chickens virology, influenza epidemiology, influenza virology, influenza A virus, avian immunology, influenza vaccines, influenza prevention and control, influenza, avian epidemiology, zoonoses epidemiology.

Descriptors: disease outbreaks prevention and control, avian influenza transmission, poultry diseases transmission, vaccination, animals, domestic animals, wild birds, disease notification, avian influenza epidemiology, avian influenza prevention and control, poultry, poultry diseases epidemiology, poultry diseases prevention and control, zoonoses.

Descriptors: fowl plague transmission, influenza epidemiology, influenza A virus avian classification, adolescent, bacterial typing techniques, chickens, child, preschool, fowl plague epidemiology, Hong Kong epidemiology, incidence, avian isolation and purification, middle aged, survival rate.

NAL Call Number: aSF601.U5  
Descriptors: avian influenza, commercial chickens, report, outbreaks.

Descriptors: hemagglutinin glycoproteins, influenza virus ultrastructure, influenza A virus avian genetics, avian pathogenicity, hydrogen-ion concentration, influenza genetics, influenza mortality, influenza virology, avian physiology, models, molecular, protein conformation, protein precursors ultrastructure.

NAL Call Number: 449.9 Un3r
Descriptors: bird diseases immunology, bird diseases microbiology, fowl plague immunology, fowl plague microbiology, antibodies, viral analysis, birds, ducks, geese, influenza A virus avian immunology, avian isolation and purification, pigeons, poultry diseases immunology, poultry diseases microbiology, quail, turkeys.

NAL Call Number: 151.65 P96
Descriptors: influenza virology, influenza A virus avian isolation and purification, population surveillance, chickens virology, China, fowl plague virology, World Health Organization.

NAL Call Number: RA407.3.M56
Abstract: As of January 6, 1998, a total of 16 confirmed and three suspected cases of human infection with avian influenza A (H5N1) viruses have been identified in Hong Kong. Confirmed cases are those from which an influenza A (H5N1) virus was isolated or in which a seroconversion to influenza A (H5N1) virus was detected by a neutralization assay. Suspected cases are those with influenza-like illness (ILI) and preliminary laboratory evidence of influenza A (H5N1) infection. This report summarizes interim findings from the ongoing epidemiologic and laboratory investigation of influenza A (H5N1) cases by health officials in Hong Kong and by CDC.
Descriptors: influenza epidemiology, influenza virology, influenza A virus avian isolation and purification, Hong Kong epidemiology, seroepidemiologic studies.

NAL Call Number: 449.9 W892B

NAL Call Number: RC960.R48
Descriptors: avian influenza, wild birds, diseases, serological survey, birds.

NAL Call Number: RC960.R48
Descriptors: outbreaks, detection, gel diffusion tests, avian influenza virus, wild birds, Brazil.

**NAL Call Number:** SF604.P27

**Descriptors:** avian influenza infection, diagnosis, transmission, chickens, *Gallus gallus*.


**NAL Call Number:** RA648.5.E46

**Abstract:** We report the first case of avian influenza in a patient with fever and diarrhea but no respiratory symptoms. Avian influenza should be included in the differential diagnosis for patients with predominantly gastrointestinal symptoms, particularly if they have a history of exposure to poultry.

**Descriptors:** gastrointestinal diseases physiopathology, influenza physiopathology, influenza A virus, avian pathogenicity, adult, chickens virology, fatal outcome, gastrointestinal diseases virology, health personnel, influenza virology, influenza, avian transmission, influenza, avian virology, poultry diseases transmission, poultry diseases virology.


**NAL Call Number:** 41.9 W64B

**Abstract:** Inland great cormorants (*Phalacrocorax carbo*) culled in France were examined in the winter of 1997-98 and 1998-99 for antibodies to Newcastle disease (ND) and influenza A strains H5 and H7 by the hemagglutination inhibition test. Antibodies to influenza A group antigen were tested by agar gel precipitin test. Ten of 53 adult individuals were seropositive for ND virus. All sera were negative for influenza A antibodies. It is speculated that ND occurred in the sampled population.

**Descriptors:** antibodies, viral blood, fowl plague epidemiology, influenza A virus avian immunology, Newcastle disease epidemiology, Newcastle disease virus immunology, birds, fowl plague blood, fowl plague immunology, France epidemiology, hemagglutination inhibition tests veterinary, avian isolation and purification, Newcastle disease blood, Newcastle disease immunology, Newcastle disease virus isolation and purification, seroepidemiologic studies.


**NAL Call Number:** 41.8 V6426

**Descriptors:** influenza A virus avian cytology, chick embryo, microscopy, electron.


**NAL Call Number:** aSF995.6.I6I5 1981a

**Descriptors:** avian influenza virus, regulatory problems, disease control.


**NAL Call Number:** 442.8 Au7

**Abstract:** Tracheal and cloacal swabs from apparently healthy ducks, gulls, shearwaters and terns in New Zealand were tested for myxoviruses by inoculation into embryonated eggs. Seven influenza A viruses belonging to three antigenic subtypes (H4N6; H1N3; H11N3) and nine paramyxoviruses of two antigenic subtypes (PMV-1; PMV-4) were isolated from feral ducks. The occurrence of the same virus subtypes in birds, including ducks, in other countries suggests that they were introduced into New Zealand by the importation of infected poultry or game birds. Ducks experimentally infected with two of the influenza A virus
isolates excreted virus in their faeces for 12 days. Infection with H4N6 subtype prevented reinfection with the same subtype but not with a different one (H1N3).

Descriptors: ducks microbiology, influenza A virus avian isolation and purification, paramyxoviridae isolation and purification, immunity, avian immunology, New Zealand, virus replication.

NAL Call Number: 41.9 W64B
Abstract: Serum antibodies to influenza A viruses and paramyxoviruses were detected in Adelie penguin (Pygoscelis adeliae) and Antarctic skua (Stercorarius skua maccormicki) sera in the Ross Sea Dependency. An avian paramyxovirus was isolated from a penguin cloacal swab.
Descriptors: avulavirus immunology, bird diseases epidemiology, fowl plague epidemiology, influenza A virus avian immunology, respirovirus infections veterinary, antarctic regions epidemiology, antibodies, viral blood, avulavirus isolation and purification, birds, cloaca microbiology, hemagglutination inhibition tests, immunoenzyme techniques, respirovirus infections epidemiology, seals.

NAL Call Number: 41.8 Am3
Descriptors: avian influenza, epidemiology, field observations, Minnesota.

NAL Call Number: 41.8 Am3
Descriptors: Mycoplasmosis synoviae, infection, avian influenza, turkeys.

NAL Call Number: 41.8 Am3
Abstract: Twenty-seven chicken red blood cell agglutinating agents were isolated from 187 tracheal swablings of apparently healthy migratory mallard ducks (Anas platyrhynchos) in the Mississippi flyway. Twenty-four of the isolants were type A influenza virus; 3 lentogenic Newcastle disease viruses were isolated. Isolations were not made from either 65 giant Canada geese (Branta canadensis) or 60 Franklins' gulls (Larus pipixcan).
Descriptors: birds microbiology, influenza A virus avian isolation and purification, Newcastle disease virus isolation and purification, ducks microbiology, geese microbiology, avian immunology, Mississippi, trachea microbiology.

NAL Call Number: 41.8 V641
Descriptors: antibodies, viral blood, bird diseases diagnosis, birds blood, coronavirus infections diagnosis, fowl plague immunology, infectious bronchitis virus immunology, influenza A virus avian immunology, respirovirus immunology, respirovirus infections diagnosis, antibodies, viral immunology, bird diseases blood, bird diseases epidemiology, birds immunology, birds virology, coronavirus infections blood, coronavirus infections epidemiology, data collection, respirovirus infections blood, respirovirus infections epidemiology, United Arab Emirates epidemiology.


**Descriptors:** orthomyxoviridae infections veterinary, poultry diseases diagnosis, respiratory tract infections veterinary, turkeys, hemagglutination inhibition tests, influenza diagnosis, influenza veterinary, Newcastle disease diagnosis, orthomyxoviridae infections diagnosis, respiratory tract infections diagnosis.


**Descriptors:** avian influenza virus, turkeys, control, prevention.


**Abstract:** A 945 nucleotide region (bases 76-1020) of the HA1 part of the HA gene was obtained for 31 influenza viruses of H7 subtype isolated primarily from Europe, Asia and Australia over the last 20 years. These were analysed phylogenetically and compared with sequences of the same region from 23 H7 subtype viruses available in Genbank. The overall results showed two geographically distinct lineages of North American and Eurasian viruses with major sublineages of Australian, historical European and equine viruses. Genetically related sublineages and clades within these major groups appeared to reflect geographical and temporal parameters rather than being defined by host avian species. Viruses of high and low virulence shared the same phylogenetic branches, supporting the theory that virulent viruses are not maintained as a separate entity in waterfowl.

**Descriptors:** hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian classification, avian genetics, amino acid sequence, fowl plague virology, genes viral, avian isolation and purification, phylogeny, poultry, sequence homology, amino acid.


**Descriptors:** disease outbreaks, fowl plague epidemiology, influenza epidemiology, Asia, Southeastern epidemiology, birds, chickens, influenza A virus avian, human.


**Abstract:** An account of an outbreak on a farm near Bendigo in 1985, where 120,000 birds were housed in 12 sheds. The virus, highly virulent, was subtype H7N7. The outbreak occurred in birds already affected with complex respiratory disease.

**Descriptors:** chickens, avian influenza virus, Victoria, Australia, birds, domestic animals, domesticated birds, Galliformes, influenza virus, livestock, Oceania, poultry, useful animals, viruses, chickens viruses.


**Descriptors:** human diseases, influenza virus A, epidemics, clinical aspects, diagnosis, reviews, Hong Kong.


**Descriptors:** avian influenza virus, poultry diseases, reviews.

NAL Call Number: SF995.W4
Descriptors: avian influenza virus, lessons, history.

NAL Call Number: SF600.Z6
Descriptors: avian influenza virus, disease control, lessons, history, vaccination, strains, reservoir hosts, geographical distribution.

NAL Call Number: 41.8 V641
Descriptors: fowl plague prevention and control, turkeys, vaccination veterinary, influenza A virus avian immunology, viral vaccines.

NAL Call Number: 449.9 Un3r
Descriptors: avian influenza virus, laboratory diagnosis, survival, feces, chickens.

NAL Call Number: SF995.I86
Descriptors: virus identification, detection, laboratory diagnosis, influenza, ducks, quails.

NAL Call Number: 41.8 Am3
Descriptors: animal husbandry, infection, respiratory system, veterinary medicine, influenza, infectious disease, prevention and control, respiratory system disease, viral disease, biosecurity, disease eradication, pathogenic outbreaks.

NAL Call Number: 448.3 Ar23
Abstract: Volunteers inoculated with avian influenza viruses belonging to subtypes currently circulating in humans (H1N1 and H3N2) were largely refractory to infection. However 11 out of 40 volunteers inoculated with the avian subtypes, H4N8, H6N1, and H10N7, shed virus and had mild clinical symptoms: they did not produce a detectable antibody response. This was presumably because virus multiplication was limited and insufficient to stimulate a detectable primary immune response. Avian influenza viruses comprise hemagglutinin (HA) subtypes 1-14 and it is possible that HA genes not so far seen in humans could enter the human influenza virus gene pool through reassortment between avian and circulating human viruses.
Descriptors: influenza A virus avian pathogenicity, adult, antibodies, viral blood, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral immunology, avian isolation and purification, avian physiology, middle aged, species specificity, virus replication.

Abstract: The current outbreak of avian influenza in South East Asia has resulted in a small number of human deaths. Avian flu can pass from birds to humans, although the number of humans infected is low. The fear is that the avian flu virus could mutate in a human who was also infected with a common flu virus, creating a new strain that could pass from human to human. Nurses, especially those working in travel
health, should keep themselves informed of the latest developments.

Descriptors: avian flu, outbreak, symptoms, South East Asia, human deaths, birds.


NAL Call Number: TP248.13.B565

Descriptors: avian influenza virus, mutants, disease transmission, zoonoses.


NAL Call Number: 448.8 L22

Descriptors: disease outbreaks, fowl plague transmission, influenza transmission, influenza virology, influenza A virus avian, zoonoses, Asia epidemiology, chickens virology, Hong Kong epidemiology, influenza epidemiology.


Descriptors: genetic engineering methods, influenza A virus human genetics, influenza B virus genetics, influenza vaccine genetics, adult, infant, avian immunology, human immunology, human pathogenicity, influenza B virus immunology, influenza B virus pathogenicity, influenza vaccine immunology, vaccines, attenuated genetics, vaccines, attenuated immunology, vaccines, combined genetics, vaccines, combined immunology.


NAL Call Number: aSF995.6.I6I5 1981a

Descriptors: avian influenza virus, disease control, international regulation, symposium.


Abstract: Current WHO reports on the Asian avian influenza virus outbreaks are poignant reminders of the potential for the emergence of highly virulent strains of influenza A virus (IAV) and the fact that it remains a scourge on human health. As IAV drifts and shifts its genetic and antigenic composition, it presents an ever-changing challenge for vaccines and antiviral medications. Short-interfering RNAs (siRNAs) are the latest class of potential antiviral therapeutics to be developed. Recent reports using siRNAs in mice suggest that they hold great promise for the prevention and treatment of IAV infections.

Descriptors: antiviral agents therapeutic use, influenza drug therapy, influenza A virus genetics, small interfering RNA therapeutic use, mice, RNA interference physiology, short-interfering RNA.


NAL Call Number: 470 Sci2

Descriptors: crime, influenza A virus, avian, microbiology legislation and jurisprudence, chickens, commerce legislation and jurisprudence, licensure, Saudi Arabia, United States.


NAL Call Number: SF604.C485

Descriptors: chickens, avian influenza virus, pathogenicity, symptoms, immunodiagnosis, Guangdong, Asia, biological properties, birds, China, diagnosis, domestic animals, domesticated birds, East Asia, Galliformes, immunological techniques, influenza virus, livestock, microbial properties, poultry, useful animals, viruses.

Abstract: There are ten avian herpesviruses, which have been isolated from eight orders. Six of these are of veterinary importance: Pacheco's parrot disease virus, pigeon herpesvirus, duck plague virus, infectious laryngotraechitis virus, herpesvirus of turkeys and Marek's disease virus. The knowledge on the epidemiology of each virus and the disease it causes is discussed. Features in common to infections with most avian herpesviruses are: infection is persistent in individuals and ubiquitous in populations; virus is shed for long periods of time after infection although in some cases erratically; infection does not necessarily result in disease and at least in some avian herpesvirus infections the incidence of disease is affected by the pathogenicity of the virus; the genetic constitution of the host and stress factors affecting the host. It is concluded that man's interference with the natural history of host species often increases the threat and incidence of disease unless preventive action is taken.

Descriptors: birds microbiology, herpesviridae isolation and purification, herpesviridae infections veterinary, ducks microbiology, herpesvirus 1, gallid isolation and purification, herpesvirus 2, gallid isolation and purification, influenza A virus avian isolation and purification, pigeons microbiology, turkeys microbiology.


Abstract: Two antigenically distinct H1N1 influenza A viruses were isolated during an outbreak of respiratory disease in Quebec swine in 1990/91. Analysis of haemagglutinin and partial nucleoprotein sequences indicated that one was a variant of the swine H1N1 influenza virus circulating in the American Midwest whereas the other was very similar to virus isolated from swine in 1930. The existence of this latter isolate supports the concept that influenza viruses can be maintained for long periods in swine, perhaps in geographically limited pockets. Serological evidence indicates that these distinct strains continued to circulate widely in south-central Quebec until at least 1993.

Descriptors: influenza A virus, porcine genetics, influenza A virus, porcine immunology, orthomyxoviridae infections veterinary, swine diseases virology, amino acid sequence, antigenic variation, antigens, viral analysis, base sequence, capsid genetics, disease outbreaks, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral analysis, hemagglutinins viral genetics, avian genetics, human genetics, molecular sequence data, orthomyxoviridae infections epidemiology, orthomyxoviridae infections virology, quebec epidemiology, sequence analysis, DNA, sequence homology, amino acid, swine, swine diseases epidemiology, viral core proteins genetics.


Abstract: The highly intensive conditions, that economic necessity has forced upon the poultry industry, have resulted in strongly changed environmental conditions and management which combined with the use of a constantly increasing number of live vaccines has highly complicated clearing up the etiology in diseased flocks. This is true not least as far as respiratory diseases concerns, which thereby often run an atypical course. A review, however, not complete, is given of the occurrence and diagnostic procedures in respiratory diseases caused by viruses, the greatest importance attached to infections caused by adenovirus and infectious bronchitis virus.

Descriptors: poultry diseases diagnosis, poultry diseases epidemiology, respiratory tract infections veterinary, virus diseases veterinary, herpesvirus 1, gallid isolation and purification, infectious bronchitis virus isolation and purification, influenza A virus avian isolation and purification, paramyxoviridae isolation and purification, poultry, reoviridae isolation and purification, respiratory tract infections diagnosis, respiratory tract infections epidemiology, virus diseases diagnosis, virus diseases epidemiology.

**Descriptors:** influenza A virus avian immunology, orthomyxoviridae infections veterinary, poultry diseases immunology, antibody formation, chickens, lactones, orthomyxoviridae infections immunology, vaccination, vaccines.


**NAL Call Number:** 41.8 AC84

**Descriptors:** avian influenza, reviews.


**Descriptors:** ducks virology, avian influenza transmission, poultry diseases transmission, zoonoses, Asia epidemiology, food contamination, avian influenza epidemiology, poultry diseases epidemiology, public health.


**NAL Call Number:** 442.8 R325

**Abstract:** A total of 145 influenza A viruses were isolated from ducks, geese and passerine birds in Ontario, Quebec and the Maritimes in July-August 1977. Antigenic characterization of these isolates included five hemagglutinin (Hsw1, Hav4, Hav5, Hav6, Hav7) and five neuraminidase subtypes (N1, N2, Neq1, Neq2, Nav1) in nine different combinations; one combination Hav7 Neq1 had not been previously reported. The majority of these viruses were Hsw1 N1, antigenically related to influenza viruses in pigs and humans. This large reservoir of influenza A viruses circulating in ducks may well be involved in the appearance of new viruses in other species, including humans.

**Descriptors:** animal population groups microbiology, animals, wild microbiology, birds microbiology, influenza A virus avian isolation and purification, Canada, disease reservoirs, ducks microbiology, hemagglutinins viral analysis, avian immunology, neuraminidase analysis, viral proteins analysis.


**NAL Call Number:** SF995.6.N4N48 1984

**Descriptors:** avian influenza virus, seminar, Sydney, review, disease control, viral diseases, poultry, Newcastle disease.


**Descriptors:** disease outbreaks, influenza A virus, avian influenza, avian influenza epidemiology, avian influenza transmission, zoonoses, human, porcine, avian influenza prevention and control, poultry, risk factors, swine.


**NAL Call Number:** 448.8 L22

**Descriptors:** disease transmission, horizontal statistics and numerical data, fowl plague transmission, Asia epidemiology, fowl plague epidemiology, fowl plague prevention and control, influenza A virus avian, poultry, World Health Organization, zoonoses epidemiology, zoonoses transmission.


**NAL Call Number:** QR360.A1J6
Abstract: Novel H1N2 influenza A viruses which were first detected in pigs in Great Britain in 1994 were examined antigenically and genetically to determine their origins and establish the potential mechanisms for genetic reassortment. The haemagglutinin (HA) of all swine H1N2 viruses examined was most closely related to, but clearly distinguishable both antigenically and genetically from, the HA of human H1N1 viruses which circulated in the human population during the early 1980s. Phylogenetic analysis of the HA gene revealed that the swine H1N2 viruses formed a distinct branch on the human lineage and were probably introduced to pigs shortly after 1980. Following apparent transfer to pigs the HA gene underwent genetic variation resulting in the establishment and cocirculation of genetically and antigenically heterogeneous virus populations. Genetic analyses of the other RNA segments of all swine H1N2 viruses indicated that the neuraminidase gene was most closely related to those of early 'human-like' swine H3N2 viruses, whilst the RNA segments encoding PB2, PB1, PA, NP, M and NS were related most closely to those of avian viruses, which have been circulating recently in pigs in Northern Europe. The potential mechanisms and probable progenitor strains for genetic reassortment are discussed, but we propose that the swine H1N2 viruses examined originated following multiple genetic reassortment, initially involving human H1N1 and 'human-like' swine H3N2 viruses, followed by reassortment with 'avian-like' swine H1N1 virus. These findings suggest multiple reassortment and replication of influenza viruses may occur in pigs many years before their detection as clinical entities.

Descriptors: influenza A virus avian genetics, human genetics, recombination, genetic, antigens, viral immunology, base sequence, DNA, viral, Europe, genes viral, genotype, hemagglutination inhibition tests, hemagglutinin glycoproteins, influenza virus genetics, avian immunology, human immunology, molecular sequence data, phylogeny, sequence analysis, DNA, swine.


NAL Call Number: QR360.A1J6

Abstract: H1N1 influenza A viruses isolated from pigs in Europe since 1981 were examined both antigenically and genetically and compared with H1N1 viruses from other sources. H1N1 viruses from pigs and birds could be divided into three groups: avian, classical swine and 'avian-like' swine viruses. Low or no reactivity of 'avian-like' swine viruses in HI tests with monoclonal antibodies raised against classical swine viruses was associated with amino acid substitutions within antigenic sites of the haemagglutinin (HA). Phylogenetic analysis of the HA gene revealed that classical swine viruses from European pigs are most similar to each other and are closely related to North American swine strains, whilst the 'avian-like' swine viruses cluster with avian viruses. 'Avian-like' viruses introduced into pigs in the UK in 1992 apparently originated directly from strains in pigs in continental Europe at that time. The HA genes of the swine viruses examined had undergone limited variation in antigenic sites and also contained fewer potential glycosylation sites compared to human H1N1 viruses. The HA exhibited antigenic drift which was more marked in 'avian-like' swine viruses than in classical swine strains. Genetic analyses of two recent 'avian-like' swine viruses indicated that all the RNA segments are related most closely to those of avian influenza A viruses.

Descriptors: influenza virus A, viral hemagglutinins, nucleotide sequences, phylogenetics, viral antigens, hemagglutination inhibition test, molecular sequence data, GENBANK u72666, GENBANK u72667, GENBANK u72668, GENBANK u72669, GENBANK z46436, GENBANK z46441.


NAL Call Number: 41.8 Av5

Abstract: A combination of in vitro and in vivo selection procedures was used to examine the possibility that certain mildly pathogenic field isolates of avian influenza (AI) virus may contain minority subpopulations of highly pathogenic virus. Two mildly pathogenic H5N2 isolates, A/chicken/New Jersey/12508/86 (NJ12508) and A/chicken/Florida/27716/86 (FL27716), recovered from chickens epidemiologically associated with urban live-bird markets, were cloned in trypsin-free chicken embryo fibroblast cultures. Selected clones were inoculated intranasally and intratracheally (IN/IT) into specific-pathogen-free laying hens, and virus reisolated from the hens that died was serially passed in hens by IN/IT inoculation. Several highly pathogenic reisolates were recovered from hens infected with the cloned NJ12508 or FL27716 virus. A
highly pathogenic NJ12508 reisolate killed 19 of 24 IN/IT-inoculated hens, and a FL27716 reisolate killed all 24 inoculated hens; signs and lesions were typical of fowl plague. In contrast, uncloned NJ12508 stock virus killed 1 of 24 hens and FL27716 stock virus killed 4 of 24 hens, and neither produced the complete spectrum of lesions associated with fowl plague. Recovery of highly pathogenic viruses from these isolates demonstrates the coexistence of pathogenically distinct subpopulations of virus. Competition for dominance among such subpopulations could explain the variable pathogenicity of some AI viruses.

Descriptors: chickens microbiology, influenza A virus avian pathogenicity, cultured cells, cytopathogenic effect, viral, fowl plague microbiology, fowl plague mortality, avian isolation and purification, serial passage, species specificity, trypsin diagnostic use.

NAL Call Number: 41.8 Av5

Abstract: The effect of calcium stress was studied in an attempt to reproduce lethal infections in laying chickens with A/Chicken/Alabama/75 (H4N8) influenza virus and with two nonpathogenic H5N2 influenza viruses from the 1983-84 outbreak in the eastern United States. Hens were fed calcium-deficient or standard diets for 7 to 14 days; then the calcium-deficient feed was replaced with standard feed supplemented with ad libitum oyster shell, and both groups of hens were inoculated with virus. When hens were infected with the H4N8 virus, respective mortalities of those on the calcium-deficient and standard diets were 19% (27/141) and 5% (7/143). The H5N2 viruses did not kill hens fed either diet. In standard pathogenicity tests, Alabama H4N8 viruses reisolated from the hens that died generally were more lethal for 4-week-old chickens than the stock virus. These results argue for characterization of the Alabama H4N8 virus as pathogenic rather than nonpathogenic as originally determined.

Descriptors: calcium deficiency, calcium, dietary metabolism, chickens metabolism, influenza A virus avian pathogenicity, orthomyxoviridae infections veterinary, poultry diseases microbiology, stress veterinary, orthomyxoviridae infections metabolism, poultry diseases metabolism, stress metabolism, stress microbiology.

NAL Call Number: SF995.W4

Descriptors: turkeys, avian influenza virus, Utah, America, birds, Galliformes, influenza virus, mountain states United States, North America, orthomyxoviridae, United States, viruses, western states United States.

NAL Call Number: SF995.W4

Descriptors: avian influenza, fowl plague, poultry.

NAL Call Number: 41.8 Am3A

Abstract: Influenza A/turkey/Oregon/71 virus has antigenic characteristics of fowl plague virus but is avirulent for chickens. The virus was inoculated intratracheally in chickens at several dosage levels and resulted in the formation of antibody and immunity against fowl plague. The avirulent virus replicated in chickens and was recoverable by tracheal swab specimens up to 4 days after inoculation. Although the virus was transmitted to contact controls at the time when their cagemates were inoculated, it was not transmitted to contact controls placed with chickens inoculated 24 hours earlier. After 10 passages in chickens, the virus remained avirulent for chickens and turkeys.

Descriptors: chickens, fowl plague prevention and control, vaccination veterinary, antibodies, viral analysis, influenza A virus avian growth and development, avian immunology, avian isolation and purification, trachea microbiology, viral vaccines, virulence.

NAL Call Number: 448.8 V81

Descriptors: disease outbreaks veterinary, influenza veterinary, influenza A virus avian classification, human classification, poultry diseases virology, antigens, viral genetics, antigens, viral immunology, cloning, molecular, genome, viral, hemagglutination inhibition tests, hemagglutinins viral genetics, Hong Kong epidemiology, influenza epidemiology, avian genetics, avian immunology, human genetics, human immunology, molecular sequence data, Pakistan epidemiology, phylogeny, poultry diseases epidemiology, sequence analysis, protein, viral proteins genetics, viral proteins immunology.


NAL Call Number: 448.8 J821

Descriptors: influenza A virus avian isolation and purification, antigens analysis, chick embryo, chickens, cross reactions, hemagglutination inhibition tests, immune sera analysis, avian classification, avian immunology, avian pathogenicity, microscopy, electron, neuraminidase analysis, neutralization tests, poultry diseases immunology, vaccination, viral vaccines administration and dosage.


NAL Call Number: QR360.A1J6

Abstract: In Italy, multiple H3N2 influenza viruses were isolated from chickens with mild respiratory disease and were shown to replicate in the respiratory tracts of experimentally infected chickens; this finding is the first to show that H3N2 influenza viruses can replicate and cause disease in chickens. H3N2 influenza viruses in pigs on nearby farms seemed a likely source of the virus; however, antigenic and molecular analyses revealed that the gene segments of the viruses in chickens were mainly of Eurasian avian origin and were distinguishable from those isolated from pigs and wild aquatic birds in Italy. Thus, several different H3 influenza viruses were circulating in Italy, but we failed to identify the source of the chicken H3N2 influenza viruses that have disappeared subsequently from Italian poultry. Until recently, the transmission of influenza viruses (other than the H5 and H7 subtypes) from their reservoir in aquatic birds to chickens was rarely detected and highly pathogenic and non-pathogenic viruses were considered to be restricted to poultry species. However, the recent reports of the transmission of H9N2 and H5N1 influenza viruses to chickens in Hong Kong and, subsequently, to humans and our findings of the transmission of H3N2 influenza viruses to domestic chickens in Italy suggest an increased role for chickens as an intermediate host in the ecology of influenza.

Descriptors: chickens, fowl plague virology, influenza veterinary, influenza A virus avian pathogenicity, poultry diseases virology, hemagglutination inhibition tests, hemagglutinin glycoproteins, influenza virus genetics, influenza virology, avian isolation and purification, avian physiolgy, porcine isolation and purification, porcine pathogenicity, Italy, molecular sequence data, sequence analysis, DNA, swine diseases virology, viral proteins genetics, virus replication.


NAL Call Number: 7 C16Pu no. 1794

Descriptors: avian influenza, outbreak alert, Canada.


NAL Call Number: 500 N484

Abstract: As a result of the Argentine experience with foot-and-mouth disease (FMD) in 2001, a need was postulated for the establishment of efficient supranational schemes for continuous surveillance of the interrelations between tropical extractives livestock systems and the prairies that are optimal for the feeding
of livestock in the southern region of South America. FMD in Argentina and in other countries, new or re-emerging risks from avian influenza with potential risks for public health, the spongiform encephalopathies, porcine reproductive and respiratory syndrome, and classical swine fever, among other animal diseases, have generated a strong reaction and evolution within the veterinary services of the country. These present lessons will influence decision-making within countries and should be accepted by the technical and scientific community. From the perspective of the official animal health sector and with the FMD eradication plan as a basis within the national territory, we have worked not only to achieve international recognition and credibility within animal health systems, but also to realize the formation of a regional block of countries that can be recognized internationally as an area with equivalent animal health status. We emphasize not only that this lesson is useful in FMD, but also that it is possible to apply the valuable conclusions reached for other emerging or re-emerging diseases.

Descriptors: animal husbandry, commerce, communicable diseases, emerging prevention and control, emerging transmission, foot and mouth disease prevention and control, foot and mouth disease transmission, domestic animals, Argentina, decision making, international cooperation, population surveillance, risk assessment.


NAL Call Number: 41.8 Av5

Abstract: Avian influenza virus (A/Chicken/Pennsylvania/83; H5N2) was recovered from the yolk, albumen, and shell surface of eggs obtained from naturally infected chicken flocks in Pennsylvania and Virginia. These findings represent the first reported isolation of avian influenza virus from the internal contents of eggs from naturally infected flocks. The need for adequate safeguards to prevent spread of the virus during commercial movement of table and hatching eggs, cracked and "checked" eggs, and egg flats and other materials is emphasized.

Descriptors: eggs, food microbiology, fowl plague transmission, influenza A virus avian isolation and purification, chickens, fowl plague epidemiology, Pennsylvania, Virginia.


Abstract: Among avian influenza viruses and avian paramyxoviruses are the aetiological agents of two of the most devastating diseases of the animal kingdom: (i). the highly pathogenic form of avian influenza, caused by some viruses of the H5 and H7 subtypes, and (ii). Newcastle disease, caused by virulent strains of APMV type 1. Mortality rates due to these agents can exceed 50% in naive bird populations, and, for some strains of AI, nearly 100%. These viruses may also be responsible for clinical conditions in humans. The virus responsible for Newcastle disease has been known to cause conjunctivitis in humans since the 1940s. The conjunctivitis is self-limiting and does not have any permanent consequences. Until 1997, reports of human infection with avian influenza viruses were sporadic and frequently associated with conjunctivitis. Recently, however, avian influenza virus infections have been associated with fatalities in human beings. These casualties have highlighted the potential risk that this type of infection poses to public health. In particular, the pathogenetic mechanisms of highly pathogenic avian influenza viruses in birds and the possibility of reassortment between avian and human viruses in the human host represent serious threats to human health. For this reason, any suspected case should be investigated thoroughly.

Descriptors: avulavirus isolation and purification, communicable disease control, disease outbreaks, fowl plague epidemiology, influenza A virus avian isolation and purification, Newcastle disease epidemiology, birds, fowl plague prevention and control, Italy epidemiology, Newcastle disease prevention and control, prognosis, risk assessment, survival analysis.


NAL Call Number: 41.8 V641

Descriptors: fowl plague epidemiology, influenza A virus avian isolation and purification, wild animals,
NAL Call Number: SF481.M54
Descriptors: disease control, avian influenza virus, turkeys, Italy.

NAL Call Number: 41.8 V641
Descriptors: disease outbreaks veterinary, fowl plague epidemiology, fowl plague prevention and control, influenza veterinary, influenza A virus avian immunology, vaccination veterinary, influenza epidemiology, influenza prevention and control, Italy epidemiology, poultry.

Capua, I., F. Mutinelli, C. Terregino, G. Cattoli, R.J. Manvell, and F. Burlini (2000). Highly pathogenic avian influenza (H7N1) in ostriches farmed in Italy. Veterinary Record 146(12): 356. ISSN: 0042-4900.
NAL Call Number: 41.8 V641
Descriptors: disease outbreaks veterinary, fowl plague, influenza A virus avian pathogenicity, ostriches virology, animal husbandry, digestive system pathology, Italy, necrosis.

NAL Call Number: SF995.6.I6 C37 2001
Descriptors: avian influenza, color atlas, text.

Capua, I., and F. Mutinelli (2000). Mortality in Muscovy ducks (Cairina moschata) and domestic geese (Anser anser var. domestica) associated with natural infection with a highly pathogenic avian influenza virus of H7N1 subtype. Avian Pathology 30(2): 179-183. ISSN: 0307-9457.
NAL Call Number: SF995.A1A9
Abstract: Among the 413 outbreaks of highly pathogenic avian influenza (HPAI) caused by a virus of the H7N1 subtype, which occurred in Italy during 1999 and 2000, an outbreak diagnosed in a backyard flock was characterized by mortality and nervous signs in ducks and geese. Dead geese (Anser anser var. domestica) and Muscovy ducks (Cairina moschata) were submitted to the laboratory for bacteriological, virological, histological and immunohistochemical investigations. Routine bacteriological tests resulted negative, while a HPAI virus of the H7N1 subtype was isolated from the geese. Pancreatic damage was observed in both the geese and the ducks, and the pancreas was also positive by immunohistochemistry for avian influenza in the geese. Histopathological lesions were observed in the central nervous system of both species, and this result was supported by positive immunohistochemical findings for the presence of the virus.
Descriptors: infection, veterinary medicine, highly pathogenic avian influenza, viral disease, immunohistochemistry, immunohistochemical, immunocytochemical techniques, diagnostic method, histology, mortality, case study.

NAL Call Number: SF995.A1A9
Abstract: From the end of March to the beginning of December 1999, an epidemic of low pathogenicity avian influenza (LPAI) affected the industrial poultry population of northern Italy. The virus responsible for the epidemic was subtyped as H7N1 with an intravenous pathogenicity index (IVPI) of 0.0, and a deduced amino acid sequence of the region coding for the cleavage site of the haemagglutinin molecule typical of low pathogenicity viruses. The circulation of the virus in a susceptible population for several months caused the emergence of a highly pathogenic virus with an IVPI of 3.0 and the presence of multiple basic amino acids in the deduced amino acid sequence for the cleavage site of the haemagglutinin molecule. Over 13 million
birds were affected by the epidemic and, in the present paper, we report the results of the clinical, virological and histopathological investigations performed on affected chickens and turkeys. Clinical, gross and microscopic lesions caused by LPAI were more severe in turkeys than in chickens, while highly pathogenicity avian influenza (HPAI) caused similar mortality rates in both species. Current European legislation considers LPAI and HPAI as two completely distinct diseases, not requiring any compulsory eradication policy for LPAI but enforcing eradication for HPAI. In the Italian 1999 to 2000 epidemic, LPAI mutated to HPAI in a densely populated area, causing great economic losses. A reconsideration of the current European Union legislation on avian influenza, including LPAI of the H5 and H7 subtypes, could possibly be an aid to avoiding devastating epidemics for the poultry industry.  

Descriptors: animal husbandry, infection, epidemiology, respiratory system, avian influenza (LPAI), high pathogenicity (HPAI), low pathogenicity, respiratory system disease, viral disease, clinical analysis analytical method, histopathological analysis analytical method, virological analysis analytical method, European Union legislation, economic losses, industrial poultry population, intravenous pathogenicity index, mortality rates.


NAL Call Number: 241.71 B75 
Descriptors: avian influenza virus, Escherichia coli, Salmonella enteritidis, health, pigeons, ducks, geese, pheasants, quails, ostriches, Italy.


NAL Call Number: 41.8 V643 
Abstract: Selected, recent research on the following avian diseases, and their causative viruses, has been reviewed: chicken anaemia, infectious bursal disease, turkey rhinotracheitis, avian nephritis, fowlpox, influenza, infectious bronchitis and turkey enteritis. 
Descriptors: bird diseases microbiology, virus diseases veterinary, birds, coronaviridae, DNA viruses, fowlpox virus, infectious bursal disease virus, influenza A virus avian, paramyxoviridae, picornaviridae, virus diseases microbiology.


NAL Call Number: 41.9 C333 
Descriptors: avian influenza virus, disease transmission, pathogenesis, disease resistance, disease control, influenza virus, orthomyxoviridae, pathogenesis, resistance to injurious factors, viruses.


NAL Call Number: 41.9 C333 
Abstract: 447 blood-serum samples of racing and free living pigeons collected in 11 districts of Czechoslovakia from August 1983 till March 1984 were examined by the haemagglutination inhibition test to the Newcastle disease virus, strain Roakin, to the pigeon PMV-1 and to the PMV-3; 121 of the samples were tested to other serotypes, PMV-2--PMV-9, and to the avian influenza A virus. 58.4% of samples were positive (greater than or equal to 2 log2) to the Roakin strain with the mean titre 3.6 log2 and 65.1% to the pigeon PMV-1 with the mean titre 4.5 log2. All samples tested were negative to other serotypes except two samples of one group positive to PMV-8 with the mean titre 4.3 log2. The titres of HI antibodies to the Roakin strain and to the pigeon PMV-1 were compared. The risk of the transmission and of the readaptation of pigeon virus to poultry was discussed. 
Descriptors: bird diseases diagnosis, pigeons, respirovirus infections veterinary, antibodies, viral analysis, bird diseases epidemiology, Czechoslovakia, hemagglutination inhibition tests veterinary, paramyxoviridae immunology, respirovirus infections diagnosis, respirovirus infections epidemiology.

**NAL Call Number:** 49 J822

**Descriptors:** avian influenza virus, disease surveys, epidemiology, ducks, turkeys, quail, geese, mallards, Taiwan.


**NAL Call Number:** 41.9 W64B

**Abstract:** Wild turkeys (*Meleagris gallopavo*) trapped within California (n = 715) or imported into California from other states (n = 381) from 1986 to 1996 were tested for exposure to certain disease agents. Prevalence of antibody to *Mycoplasma gallisepticum*, *Mycoplasma meleagridis*, *Salmonella pullorum*, *Salmonella typhimurium*, Newcastle disease virus, and avian influenza virus was low (0-4%) for wild turkeys trapped within California. With the exception of antibody prevalence to *M. meleagridis* of 33%, the same was true for wild turkeys imported into California from other states. Antibody prevalence to *Mycoplasma synoviae* was 8-10% for both groups.


**NAL Call Number:** SF604.C485

**Descriptors:** chickens, influenza virus, immunology, isolation techniques, birds, domestic animals, domesticated birds, Galliformes, livestock, poultry, useful animals, viruses.


**NAL Call Number:** 500 N21P

**Abstract:** The pathogenicity of avian H5N1 influenza viruses to mammals has been evolving since the mid-1980s. Here, we demonstrate that H5N1 influenza viruses, isolated from apparently healthy domestic ducks in mainland China from 1999 through 2002, were becoming progressively more pathogenic for mammals, and we present a hypothesis explaining the mechanism of this evolutionary direction. Twenty-one viruses isolated from apparently healthy ducks in southern China from 1999 through 2002 were confirmed to be H5N1 subtype influenza A viruses. These isolates are antigenically similar to A/Goose/Guangdong/1/96 (H5N1) virus, which was the source of the 1997 Hong Kong "bird flu" hemagglutinin gene, and all are highly pathogenic in chickens. The viruses form four pathotypes on the basis of their replication and lethality in mice. There is a clear temporal pattern in the progressively increasing pathogenicity of these isolates in the mammalian model. Five of six H5N1 isolates tested replicated in inoculated ducks and were shed from trachea or cloaca, but none caused disease signs or death. Phylogenetic analysis of the full genome indicated that most of the viruses are reassortants containing the A/Goose/Guangdong/1/96-like hemagglutinin gene and the other genes from unknown Eurasian avian influenza viruses. This study is a characterization of the H5N1 avian influenza viruses recently circulating in ducks in mainland China. Our findings suggest that immediate action is needed to prevent the transmission of highly pathogenic avian influenza viruses from the apparently healthy ducks into chickens or mammalian hosts.

**Descriptors:** ducks virology, evolution, molecular, influenza A virus, avian genetics, avian pathogenicity, influenza, avian virology, chickens, China, genes, viral genetics, genotype, avian transmission, mice, molecular sequence data, phylogeny, virulence.

NAL Call Number: 448.8 P942

Abstract: Influenza A virus with the antigenic formulae Hav4Neq2 has been isolated from Chlidonias nigra in the region of mass moultng in the territory of the Kazakh SSR. Anti-hemagglutinins for the newly isolated virus were detected in the sera of some specimens of the sea gull order. The data obtained suggest an active circulation of the virus in this region during the summer of 1977.

Descriptors: animal population groups microbiology, animals, wild microbiology, birds microbiology, influenza A virus avian isolation and purification, antibodies, viral analysis, hemagglutination inhibition tests, influenza A virus avian classification, Kazakhstan, microscopy, electron, neutralization tests, orthomyxoviridae infections epidemiology, orthomyxoviridae infections veterinary, serotyping.


Abstract: Human infections with avian influenza viruses can be severe and may be harbingers of the evolution of a pandemic strain. We present a patient in Thailand who was infected with influenza A (H5N1) virus. Prominent features included the progression from fever and dyspnea to the acute respiratory distress syndrome in a short period, lymphopenia and thrombocytopenia. Establishing the diagnosis for this patient increased public awareness of the virus and was soon followed by a halting of poultry-to-human transmission. On the basis of available data, any child with suspected avian influenza infection should be treated with oseltamivir.

Descriptors: infection, pediatrics, human medicine, pharmacology, avian influenza A virus, orthomyxoviridae, child, Thailand.


NAL Call Number: QR189.V32

Abstract: Introduction of influenza viruses with gene segments of avian origin into the human population may result in the emergence of new pathogenic human influenza viruses. The recent infection of a 3-year-old boy with an influenza A (H5N1) virus of avian origin can be considered as an example of such an event. However, this virus, influenza A/Hong Kong/156/97 (H5N1) and the 17 additional H5N1 viruses isolated from humans by the end of 1997 lack the ability to spread efficiently amongst humans and therefore have limited pandemic potential. However, the possibility of reassortment of these viruses with currently circulating human viruses illustrates the need for pandemic preparedness.


Descriptors: communicable disease control organization and administration, influenza A virus, avian isolation and purification, virus diseases epidemiology, birds, communicable diseases epidemiology, incidence, influenza epidemiology, influenza prevention and control, avian influenza epidemiology, avian influenza prevention and control, risk assessment, severe acute respiratory syndrome epidemiology, severe acute respiratory syndrome prevention and control, virus diseases prevention and control, world health.

Cohen, J. (1997). The flu pandemic that might have been. Science 277(5332): 1600-1. ISSN: 0036-8075.

NAL Call Number: 470 Sci2

Descriptors: influenza transmission, influenza virology, influenza A virus avian isolation and purification, human isolation and purification, chickens virology, child preschool, China epidemiology, disease outbreaks,

**NAL Call Number:** 448.8 V81

**Abstract:** The receptor specificity of 56 H2 and H3 influenza virus isolates from various animal species has been determined to test the relevance of receptor specificity to the ecology of influenza virus. The results show that the receptor specificity of both H2 and H3 isolates evaluated for sialic acid linkage specificity and inhibition of hemagglutination by horse serum correlates with the species of origin, as postulated earlier for H3 strains based on a limited survey of five human, three avian, and one equine strain. Elucidation of the amino acid sequence of several human H2 receptor variants and analysis of known sequences of H2 and H3 isolates revealed that receptor specificity varies in association with an amino acid change at residues 228 in addition to the change at residue 226 previously documented to affect receptor specificity of H3 but not H1 isolates. Residues 226 and 228 are leucine and serine in human isolates, which preferentially bind sialic acid alpha 2,6-galactose beta 1,4-N-acetyl glucosamine (SA alpha 2,6Gal), and glutamine and glycine in avian and equine isolates, which exhibit specificity for sialic acid alpha-2,3-galactose beta-1,3-N-acetyl galactosamine (SA alpha 2,3Gal). The results demonstrate that the correlation of receptor specificity and species of origin is maintained across both H2 and H3 influenza virus serotypes and provide compelling evidence that influenza virus hosts exert selective pressure to maintain the receptor specificity characteristics of strains isolated from that species.

**Descriptors:** influenza A virus avian metabolism, human metabolism, metabolism, receptors, virus metabolism, amino acid sequence, amino acids genetics, carbohydrate sequence, chick embryo, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral genetics, molecular sequence data, species specificity, viral envelope proteins genetics.


**NAL Call Number:** SF1.A542

**Descriptors:** Crimea Congo hemorrhagic fever, Newcastle disease, avian influenza, avipoxvirus, Borna disease, disease prevention, disease control, disease transmission methods, ostrich, *Struthio camelus*, livestock.


**Descriptors:** fowl plague microbiology, influenza A virus avian isolation and purification, birds, Brazil, feces microbiology, fowl plague epidemiology, hemagglutination inhibition tests, serotyping.


**NAL Call Number:** QR1.R4

**Descriptors:** carrier state, survey, avian influenza virus, ornamental birds, aviary birds, sparrows, doves, waxbills, Rio de Janeiro.


**Descriptors:** Newcastle disease, avian influenza virus, symptoms, diagnosis, disease control.


**Descriptors:** influenza virology, influenza A virus, avian pathogenicity, zoonoses virology, chickens virology, influenza epidemiology, influenza prevention and control, influenza transmission, isolation and purification, Japan epidemiology, respiratory protective devices, zoonoses epidemiology, zoonoses transmission.
**NAL Call Number:** 472 N21
**Descriptors:** biomedical research, birds virology, influenza veterinary, influenza A virus, avian isolation and purification, language, periodicals, swine virology, southeastern Asia epidemiology, China epidemiology, communicable disease control, communication barriers, influenza epidemiology, influenza transmission, influenza virology, avian classification, publishing, time factors, zoonoses transmission, zoonoses virology.

**NAL Call Number:** 472 N21
**Descriptors:** disease outbreaks, fowl plague epidemiology, poultry diseases epidemiology, chickens, Hong Kong epidemiology, influenza A virus avian, poultry diseases virology.

**Descriptors:** chickens, disease outbreaks veterinary, influenza A virus, avian growth and development, avian influenza epidemiology, poultry diseases epidemiology, West Nile fever epidemiology, West Nile virus growth and development, Arizona epidemiology, California epidemiology, China epidemiology, influenza, avian virology, middle aged, poultry diseases virology, Vietnam epidemiology, West Nile fever virology.

**NAL Call Number:** 500 N484
**Abstract:** The last three decades have seen an alarming number of high-profile outbreaks of new viruses and other pathogens, many of them emerging from wildlife. Recent outbreaks of SARS, avian influenza, and others highlight emerging zoonotic diseases as one of the key threats to global health. Similar emerging diseases have been reported in wildlife populations, resulting in mass mortalities, population declines, and even extinctions. In this paper, we highlight three examples of emerging pathogens: Nipah and Hendra virus, which emerged in Malaysia and Australia in the 1990s respectively, with recent outbreaks caused by similar viruses in India in 2000 and Bangladesh in 2004; West Nile virus, which emerged in the New World in 1999; and amphibian chytridiomycosis, which has emerged globally as a threat to amphibian populations and a major cause of amphibian population declines. We discuss a new, conservation medicine approach to emerging diseases that integrates veterinary, medical, ecologic, and other sciences in interdisciplinary teams. These teams investigate the causes of emergence, analyze the underlying drivers, and attempt to define common rules governing emergence for human, wildlife, and plant EIDs. The ultimate goal is a risk analysis that allows us to predict future emergence of known and unknown pathogens.
**Descriptors:** clinical medicine trends, communicable diseases, emerging therapy, conservation of natural resources, disease outbreaks, ecology, interprofessional relations, zoonoses, amphibia microbiology, Chytridiomycota pathogenicity, emerging diagnosis, emerging epidemiology, forecasting, Hendra virus pathogenicity, public health, risk assessment, veterinary medicine trends, West Nile virus pathogenicity.

**NAL Call Number:** 41.9 W64B
**Abstract:** From 1981 through 1986, plasma or serum samples were obtained from 322 wild turkeys (*Meleagris gallopavo*) from Georgia (n = 111), Kentucky (n = 21), Louisiana (n = 22), North Carolina (n = 118), Tennessee (n = 19), Missouri (n = 24) and Iowa (n = 7). These samples were tested for antibodies to *Mycoplasma gallisepticum* (MG) and in most instances, *M. synoviae* (MS), *M. meleagridis* (MM), and avian influenza (AI) virus. All 322 turkeys were seronegative for MG by the rapid plate agglutination (RPA) test. All of a subsample (n = 147) also were negative (titer less than or equal to 1:40) for MG by the hemagglutination inhibition (HI) test. Five of 253 turkeys (2%) were seropositive (+4 reaction) for MS by the RPA test; however, HI tests for MS on these five turkeys were negative as attempts to isolate MS from trachea and homogenized lung tissue. Three of 253 turkeys (1%) were seropositive (+1 to +3 reactions) for MM by the RPA test. None of 210 turkeys had antibodies to AI by the agar gel precipitation test. These data suggest
that populations of native eastern wild turkeys are not important in the epizootiology of MG, MS, MM, or AI.

Descriptors: antibodies, bacterial analysis, antibodies, viral analysis, influenza A virus avian immunology, Mycoplasma immunology, turkeys microbiology, animals, wild immunology, turkeys immunology.

NAL Call Number: 41.8 Am3
Descriptors: economic losses, economic analysis, outbreaks, disease control, avian influenza virus, turkeys, United States, Pennsylvania.

NAL Call Number: 448.3 Ar23
Abstract: A double antibody sandwich blocking ELISA, using a monoclonal antibody (MAb) against influenza A nucleoprotein (NP) was developed to detect antibodies against influenza. Collections of serum samples were obtained from human and various animal species. All influenza A subtypes induced antibodies against hemagglutinins and NP. A close correlation between titers of the hemagglutination inhibition (HI) test and the NP-ELISA was seen. Antibodies against influenza NP were demonstrated in serum samples from humans, ferrets, swine, horses, chickens, ducks, guinea pigs, mice, and seals. The serum samples were collected at intervals during prospective epidemiological studies, from experimental and natural infections, and vaccination studies. The decline of maternal antibodies was studied in swine and horses. The NP-ELISA enables rapid serological diagnosis and is suited for influenza A antibody screening, especially in species which harbor several influenza subtypes. The HI and neuraminidase inhibition tests, however, must still be used for subtyping.
Descriptors: antibodies, viral analysis, enzyme linked immunosorbent assay, influenza A virus immunology, nucleoproteins immunology, orthomyxoviridae infections immunology, viral core proteins immunology, ferrets, hemagglutination inhibition tests, horses, avian immunology, human immunology, porcine immunology, orthomyxoviridae infections veterinary, poultry, prospective studies, Rodentia, seals, species specificity, specific pathogen free organisms, swine, vaccination.

NAL Call Number: 41.8 T431
Abstract: Wild waterfowl are currently considered the largest reservoir of the various haemagglutinin (H) and neuraminidase (N) subtypes of influenza virus. Until now thirteen different H-types and nine different N-types have been detected in these populations. In the first instance, virus transmission from fowl to other animal species and to man is not causing disease problems. However, small changes at the molecular level of a given HN-subtype recently caused a dramatic increase in virulence for chickens. Genes fragments coding for haemagglutinin or neuraminidase can be exchanged between viruses which propagate in the same individual. This phenomenon-'genetic reassortment'-is of major epidemiological significance when it occurs in pigs. New influenza epidemics in the human population consistently originate in areas where waterfowl, pigs and human beings live close together. At the moment, the virological and serological diagnosis of influenza A infections is based ELISAs for antigen and antibody detection. Both ELISAs employ a monoclonal antibody directed against a conserved antigenic determinant of the influenza A nucleoprotein. The use of these tests can simplify the diagnosis of and screening for influenza A infections, particularly in those species which harbour several H- and N-subtypes.
Descriptors: fowl plague microbiology, orthomyxoviridae infections veterinary, birds microbiology, chickens microbiology, enzyme linked immunosorbent assay veterinary, influenza A virus avian genetics, avian isolation and purification, avian pathogenicity, orthomyxoviridae infections microbiology, orthomyxoviridae infections transmission, virulence.

Abstract: During the recent devastating epidemics of foot-and-mouth disease (FMD), bluetongue (BT), the highly pathogenic avian influenza (HPAI) and New Castle disease, more than 115 million animals were culled. The mass slaughter of animals raised serious ethical questions. These epidemics showed that the use of emergency vaccination is an essential element in disease control. During the last decade the FMD antigen banks have proved to be effective and this module should be extended. An international vaccine stock should be considered for classical swine fever and HPAI. Agreements with vaccine producers should be made easily available, with instant access to a vaccine reserve for rinderpest, peste des petits ruminants, BT, African horse sickness and Rift valley fever. These vaccines should meet international standards and should allow distinction between vaccinated and infected animals. Information should be gathered proactively on the use of vaccines for lumpy skin disease, sheep and goat pox and contagious bovine pleuropneumonia.

Descriptors: animals, Australia, communicable disease control methods, disease outbreaks prevention and control, veterinary disease outbreaks, drug storage, emergency treatment methods, veterinary emergency treatment, animal euthanasia, foot-and-mouth disease prevention and control, international cooperation, viral vaccines immunology, viral vaccines supply and distribution.


Abstract: Novel influenza viruses continuously emerge in the human population. Three times during the present century, an avian influenza virus subtype crossed the species barrier, starting a pandemic, and establishing itself for one to several decades in man. As the 1997 H5N1 event in Hong Kong indicated, the occurrence of another pandemic in the near future cannot be excluded. Sufficient vaccine may not be available to ameliorate the consequences of such an event, because of a shortage of time. During interpandemic periods, important antigenic drift variants sometimes arise at a point of time when, with the current state of the technique, production of a correspondingly adapted vaccine is also impossible. We may be able to solve these problems by increasing influenza surveillance and by adopting new ways of vaccine composition, production, formulation, presentation, and delivery. The recently developed anti-neuraminidase antivirals should only be considered as (valuable) adjuncts to vaccines.

Descriptors: antigenic variation, influenza epidemiology, orthomyxoviridae genetics, disease outbreaks, hn protein genetics, hemagglutinin glycoproteins, influenza virus genetics, influenza mortality, influenza prevention and control, influenza vaccine therapeutic use, orthomyxoviridae enzymology, orthomyxoviridae pathogenicity, reassortant viruses genetics, reassortant viruses pathogenicity, virulence.


NAL Call Number: 448.8 N442


NAL Call Number: 241.71 B75

Descriptors: birds, disease surveys, wild animals, monitoring, animal diseases, Italy, immunological techniques, antibiotics, biopsy, avian influenza virus, epidemiology, laboratory diagnosis, identification, etiology, biological analysis, diagnosis, Europe, histocytological analysis, influenza virus, orthomyxoviridae, surveys, viruses, Western Europe, wildlife.

NAL Call Number: 41.8 R3224
Descriptors: animals, domestic, orthomyxoviridae infections microbiology, orthomyxoviridae infections veterinary, antigens, viral analysis, chickens, epitopes, fowl plague microbiology, horse diseases microbiology, horses, influenza microbiology, influenza A virus avian immunology, human immunology, porcine immunology, mutation, recombination, genetic, swine, swine diseases microbiology.

NAL Call Number: 41.8 Av5
Abstract: From 1977 to 1983, waterfowl migrating along the Atlantic flyway were annually monitored for orthomyxoviruses and paramyxoviruses in an area in central New York State. A total of 168 influenza isolates were obtained from 1,430 waterfowl. Twenty-four combinations of hemagglutinin and neuraminidase subtypes were detected, with as many as 12 found in a single year. One combination, an H5N2 isolate in 1982, was closely related to the virulent chicken virus that appeared in Pennsylvania in 1983. The prevalence of influenza varied greatly among the common waterfowl species: mallards 42%, black ducks 30%, blue-winged teal 11%, wood ducks 2%, and Canada geese 0%. A total of 89 paramyxoviruses were also from these waterfowl. In contrast to findings with influenza virus, the prevalence of paramyxoviruses did not differ significantly among the duck species. Serotype 1 (Newcastle disease virus) was predominant; three other serotypes were also identified. These findings indicated that ducks in the Atlantic flyway continually harbor influenza viruses and paramyxoviruses. The viruses may be a source of infection for other species.
Descriptors: ducks microbiology, influenza A virus avian isolation and purification, orthomyxoviridae isolation and purification, paramyxoviridae isolation and purification, antigens, viral analysis, demography, New York, species specificity.

NAL Call Number: 151.65 P96
Descriptors: influenza A virus avian immunology, orthomyxoviridae infections immunology, viruses immunology, chick embryo, haplorhini, hemagglutination inhibition tests, hemagglutination tests, neutralization tests, Newcastle disease immunology, Newcastle disease virus immunology, poultry, virus diseases immunology, virus diseases pathology.

NAL Call Number: SF780.4.I56 1984
Descriptors: wild birds, avian influenza, Newcastle disease, viral diseases, threat, Australia, Korea, Malaysia, conference papers.

NAL Call Number: 448.8 V81
Abstract: To understand the determinants of influenza virus evolution, phylogenetic relationships were determined for nine hemagglutinin (HA) genes of the H4 subtype. These genes belong to a set of viruses isolated from several avian and mammalian species from various geographic locations around the world.
between 1956 and 1985. We found that the HA gene of the H4 subtype is 1738 nucleotides in length and is predicted to encode a polypeptide of 564 amino acids. The connecting peptide, which is removed from the precursor polypeptide by peptidases to yield the mature HA1 and HA2 polypeptides, contains only one basic amino acid. This type of connecting peptide is a feature of all avian avirulent HAs. On the basis of pairwise nucleotide sequence homology comparisons the genes can be segregated into two groups: influenza virus genes isolated in North America and those isolated from other parts of the world. A high degree of homology exists between pairs of genes from viruses of similar geographic origin. The nucleotide sequences within a group differ by 1.5 to 10.6%; in contrast, between groups the differences range from 15.8 to 19.4%. An evolutionary tree for the nine sequences suggests that North American isolates have diverged extensively from those circulating in other parts of the world. Geographic barriers which determine flyway outlay may prevent the gene pools from extensive mixing. The lack of correlation between date of isolation and evolutionary distance suggests that different H4 HA genes cocirculate in a fashion similar to avian H3 HA genes (H. Kida et al., 1987, Virology 159, 109-119) and influenza C genes (D. Buonagurio et al., 1985, Virology 146, 221-232) implying the absence of selective pressure by antibody that would give a significant advantage to antigenic variants. In contrast to avian influenza virus genes, human influenza virus genes evolve rapidly under the selective pressure of antibody.

Descriptors: hemagglutinins viral genetics, influenza A virus genetics, amino acid sequence, base sequence, cloning, molecular, geography, molecular sequence data, sequence homology, nucleic acid.


NAL Call Number: 448.8 P942

Descriptors: Newcastle disease virus, viral interference, adenoviridae, arboviruses, cattle, cervix neoplasms, chick embryo, chikungunya virus, encephalomyocarditis virus, HeLa cells, influenza A virus avian, interferons antagonists and inhibitors, l cells cell line, lactones pharmacology, mice, orthomyxoviridae, parainfluenza virus 1, human drug effects, polioviruses, rabies virus, rats, respirovirus, swine, tissue culture, vesicular stomatitis Indiana virus, virus cultivation, virus replication.


NAL Call Number: 442.8 Au7

Abstract: Three different type A influenza viruses have been isolated from pelagic birds nesting on islands of the Great Barrier Reef. One of these, isolated in 1972, was of subtype Hav6Nav5. The other two, which are described in this paper, were isolated in 1975 and belonged to subtypes Hav5Nav2 and Hav3Nav6. Of eight isolates of the latter virus, seven were recovered from cloacal swabs and only one from the trachea.

Descriptors: birds microbiology, influenza A virus avian isolation and purification, antibodies, viral analysis, antigens, viral immunology, Australia, cloaca microbiology, hemagglutinins viral analysis, influenza A virus avian immunology, neuraminidase immunology, trachea microbiology.


NAL Call Number: 448.8 V81


NAL Call Number: 47.8 N219

Descriptors: avian influenza, poultry.


NAL Call Number: 41.8 Am3

Descriptors: avian influenza, global, birds, ducks.

NAL Call Number: SF995.B5 1984
Descriptors: avian influenza virus, reviews, poultry diseases.


NAL Call Number: 472 N21


NAL Call Number: 448.3 AC85
Descriptors: bird diseases etiology, influenza veterinary, orthomyxoviridae classification, orthomyxoviridae immunology, antigens, viral, bird diseases drug therapy, bird diseases prevention and control, birds, chickens, ducks, ecology, influenza drug therapy, influenza immunology, influenza pathology, influenza prevention and control, influenza A virus avian classification, avian immunology, poultry diseases, turkeys.


NAL Call Number: SF995.I86
Descriptors: avian influenza, poultry, diseases.


NAL Call Number: SF995.B5 1972
Descriptors: reviews, birds, avian influenza virus, diseases.


Descriptors: influenza epidemiology, influenza, avian epidemiology, Asia epidemiology, birds, influenza virology.


Abstract: Severe acute respiratory syndrome (SARS) is a new disease that caused large outbreaks in several countries in the first half of 2003, resulting in infection in more than 8,000 people and more than 900 deaths. The disease originated in southern China and a novel coronavirus (SARS CoV) has been implicated as the causative organism. We present an overview of the etiology, clinical presentation and diagnosis, based on the current state of knowledge derived from published studies and our experience in the National Microbiology Centre. Influenza is a zoonosis. This appreciation of influenza ecology facilitated recognition of the H5N1 ‘bird flu’ incident in Hong Kong in 1997 in what was considered to be an incipient pandemic situation, the chicken being the source of virus for humans and. The current outbreak of avian influenza in South East Asia has resulted in a small number of human deaths. These findings highlight the importance of systematic virus surveillance of domestic poultry in recognizing changes in virus occurrence, host range and pathogenicity as signals at the avian level that could presage a pandemic.

Descriptors: disease outbreaks, avian influenza epidemiology, severe acute respiratory syndrome diagnosis, severe acute respiratory syndrome etiology, severe acute respiratory syndrome virology, southeastern Asia epidemiology, China epidemiology, diagnosis, avian influenza mortality, avian influenza...
virology, middle aged adult.

NAL Call Number: 41.8 F49
Descriptors: avian influenza virus, poultry, disease prevalence, symptoms, diagnosis, control, vaccines.

Descriptors: disease outbreaks, fowl plague epidemiology, influenza epidemiology, influenza A virus avian genetics, avian pathogenicity, world health, birds, fowl plague transmission, influenza transmission, influenza virology, risk factors.

NAL Call Number: 470 Sci2

NAL Call Number: 470 Sci2
Descriptors: genes, viral, orthomyxoviridae genetics, orthomyxoviridae isolation and purification, orthomyxoviridae infections veterinary, swine virology, swine diseases virology, databases, nucleic acid, influenza A virus, avian genetics, human genetics, Korea, orthomyxoviridae infections virology, RNA, viral genetics, World Health Organization.

NAL Call Number: 470 Sci2
Descriptors: disease outbreaks, influenza epidemiology, world health, cost of illness, influenza transmission, influenza virology, avian pathogenicity, influenza A virus, avian physiology, influenza vaccines administration and dosage, influenza vaccines supply and distribution, models, biological, orthomyxoviridae pathogenicity, orthomyxoviridae physiology, public health, reassortant viruses.

NAL Call Number: 470 Sci2

NAL Call Number: 47.8 So89
Descriptors: chickens, avian influenza virus, pathogenicity, vaccination, immunization, disinfection, South Africa, Africa, Africa South of Sahara, biological properties, birds, domestic animals, Galliformes, immunization, immunostimulation, immunotherapy, livestock, microbial properties, poultry, Southern Africa, therapy, useful animals.


NAL Call Number: SF771.A53a

Descriptors: Newcastle disease virus, avian influenza virus, shipping, culture media, preservation, specimen handling.


NAL Call Number: 41.8 N813

Abstract: A Finnish material of 455 cloacal specimens from 24 species of small migratory birds and of 54 cloacal specimens from 10 species of waterfowl was investigated for the occurrence of A type influenza virus. Influenza A virus was isolated in only one specimen, originating from a mallard (Anas platyrhynchos). Parallely, yolk material from 109 waterfowl representing 9 species was investigated for the occurrence of influenza A antibodies by complement fixation and immunodiffusion tests. In three yolk specimens, one from a widgeon (Anas penelope), one from a common gull (Larus canus) and one from a lesser blackbacked gull (Larus fuscus), positive reactions with low titres of 1:2--1:4 were obtained. The study shows that waterfowl can carry influenza A virus, but the role of small migratory birds in this respect seems to be negligible in Finland.

Descriptors: antibodies, viral analysis, birds microbiology, influenza A virus avian immunology, birds immunology, cloaca microbiology, Finland, influenza A virus avian isolation and purification.

Estudillo, L.J. (1996). Consideraciones sobre el instinto migratorio de las aves silvestres y analisis de las posibilidades reales que estas hayan sido el vector del brote de influenza aviar en Mexico. [Considerations on the migratory instinct of wild birds and analysis of the actual possibilities for these birds to have served as vectors for the avian influenza outbreak in Mexico]. Proceedings of the Western Poultry Diseases Conference 45: 22-20.

NAL Call Number: SF995.W4

Descriptors: birds, vectors, avian influenza virus, Mexico, America, disease transmission, influenza virus, Latin America, North America, orthomyxoviridae, pathogenesis, viruses.


NAL Call Number: 41.9 J275

Descriptors: influenza A virus, Newcastle disease, avian influenza virus, imported products, chicken meat, pathogenicity, China


NAL Call Number: RA648.5.E46

Descriptors: infection, public health, avian H5N1 influenza, outbreak response, respiratory system disease, viral disease, infectious diseases, infectious disease, new, reemerging, malaria, National Institute of Health initiatives, parasitic disease, blood and lymphatic disease, biomedical research importance, cross sector collaboration, vaccine development.


NAL Call Number: 470 Sci2

Descriptors: disease outbreaks veterinary, influenza epidemiology, influenza transmission, influenza A virus, avian genetics, avian pathogenicity, population surveillance, public health, animals, domestic, cluster analysis, influenza virology, human genetics, human pathogenicity, avian influenza epidemiology, avian influenza prevention and control, avian influenza transmission, avian influenza virology, mathematics, reassortant viruses genetics, reassortant viruses pathogenicity, recombination, genetic, risk assessment,

**Abstract:** Present data on influenza virus isolated from ducks and chickens, and influenza virus C. Anti-influenza drugs. Within the broad field of Glycopathology and Glycotherapeutics, research on influenza virus types A, B and C from humans and several bird species (particularly migratory birds such as ducks, since they are reservoirs for viruses), as well as the search for improved drugs designed for the prevention or treatment of epidemics/pandemics produced by most of those viruses are issues of relevant interest not only from a scientific point of view but also for repercussions on health and the important economical consequences. The research work begun by the author and collaborators at the Department of Biochemistry and Molecular Biology of the University of Salamanca (Spain) in the middle of the 1970's, developed later in close cooperation with the "(Unite d'Ecologie Virale" of the Pasteur Institute of Paris (Prof. Claude Hannoun and collaborators), has been published in about twenty papers that mainly focus on the theoretic-experimental study of: The sialidase (neuraminidase) activity of human influenza viruses types A and B. The acetyesterase activity of type C virus from humans and dogs. The sialidase activity of type A virus from ducks and pigs, in comparison with that of humans. Certain sialidase inhibitors as useful anti-influenza drugs, especially in the case of possible future influenza pandemics of avian origin.

**Descriptors:** antiviral agents therapeutic use, chickens microbiology, ducks microbiology, influenza drug therapy, avian influenza drug therapy, neuraminidase antagonists and inhibitors, orthomyxoviridae isolation and purification, acetyesterase analysis, adolescent, aged adult, aged 80 and over, child, preschool child, disease reservoirs, dogs, influenza prevention and control, influenza vaccines administration and dosage, influenza virus A enzymology, influenza virus A isolation and purification, influenza virus B enzymology, influenza virus B isolation and purification, influenza virus C enzymology, influenza virus C isolation and purification, middle aged, neuraminidase analysis, research.


**NAL Call Number:** 241.71 B75

**Descriptors:** avian influenza virus, history, symptoms, postmortem examination, vaccination, mortality, diagnosis, disease surveillance, chickens, Italy.


**NAL Call Number:** QR355.A44

**Abstract:** The study of biological properties of influenza virus strains belonging to the same subtype A(H1N1) and closely antigenically related, but isolated from different animal species (man, pig and duck), demonstrated that avian strains were more resistant than those isolated from mammals to high temperature and low pH, as shown by titration of residual infectivity in cell cultures (MDCK) and by sialidase assay. The difference in behaviour could be correlated to biological adaptation of the virus to its host. Avian body temperature is 40 degrees C and influenza virus, in ducks, is enterotropic and therefore capable of passing through the low pH values in the upper digestive tract of the animal. These results do not contradict the hypothesis of a possible filiation between avian and mammalian orthomyxoviruses.

**Descriptors:** influenza A virus physiology, body temperature, cell line, ducks, hemagglutination tests, hydrogen-ion concentration, influenza A virus avian enzymology, avian growth and development, avian physiology, human enzymology, human growth and development, human physiology, porcine enzymology, porcine growth and development, porcine physiology, influenza A virus enzymology, influenza A virus growth and development, neuraminidase analysis, plaque assay, swine, temperature, virus replication.

Fleck, F. (2004). **Avian flu virus could evolve into dangerous human pathogen, experts fear.** *Bulletin of the*

Descriptors: ducks microbiology, fowl plague complications, herpesviridae isolation and purification, herpesviridae infections veterinary, influenza A virus avian isolation and purification, fowl plague microbiology, herpesviridae infections complications, herpesviridae infections microbiology, poultry diseases microbiology.


Descriptors: disease outbreaks prevention and control, influenza epidemiology, influenza A virus classification, influenza A virus genetics, influenza A virus pathogenicity, zoonoses virology, birds, communicable disease control, influenza prevention and control, influenza transmission, avian influenza transmission, poultry, world health, zoonoses transmission.


Descriptors: avian influenza virus, review, birds, mammals.


Abstract: From the Revised Nomenclature of WHO, the fowl influenza virus A/Duck/Ukraine/63 (Hav7 Neq2) has the same neuraminidase as the equine virus A/equi 2/Miami/63 (Heq2 Neq2); the A/Chicken Germany "N"/49 virus has the same neuraminidase as the equine virus A/equi 1/Prague/56. A comparative study of the antigenic specificities confirms that the Neq2 neuraminidases are closely connected, whatever their animal origin, and that the fowl strain Hav7 Neq2 can be used for the titration of anti Neq2 antibodies in the sera of animals immunized with the equine virus Heq2 Neq2. The Neq1 neuraminidases of various animal origins are connected, but the neuraminidase of the fowl strain Hav2 Neqi is slightly inhibited by the anti Neq1 antibodies of animals immunized with the Heq1 Neq1 virus: to titrate the anti Neq1 antibodies of equine origin, the H72 Neq1 recombinant should therefore be used. The antigenic characterization of the different equine influenza strains isolated since 1967 by the study of their neuraminidase has been completed: The various neuraminidases, like the hemagglutinins of the various strains belonging to the subtype A equi2 are closely connected; a minor antigenic variation, concerning the two surface antigens, seems to exist between the strain A equi 1/Prague/56 and the strain of the same subtype isolated in 1973.

Descriptors: antigens, viral, neuraminidase immunology, orthomyxoviridae immunology, cross reactions, epitopes, hemagglutination inhibition tests, horse diseases immunology, horses, influenza immunology, influenza veterinary, influenza A virus avian immunology.


Abstract: PURPOSE OF REVIEW: Recently, several previously unrecognized respiratory viral pathogens have been identified and several influenza A virus subtypes, previously known to infect poultry and wild birds, were transmitted to humans. Here we review the recent literature on these respiratory viruses.

RECENT FINDINGS: Human metapneumovirus has now been detected worldwide, causing severe
respiratory tract illnesses primarily in very young, elderly and immunocompromised individuals. Animal models and reverse genetic techniques were designed for human metapneumovirus, and the first vaccine candidates have been developed. Considerable genetic and antigenic diversity was observed for human metapneumovirus, but the implication of this diversity for vaccine development and virus epidemiology requires further study. Two previously unrecognized human coronaviruses were discovered in 2004 in The Netherlands and Hong Kong. Their clinical impact and epidemiology are largely unknown and warrant further investigation. Several influenza A virus subtypes were transmitted from birds to humans, and these viruses continue to constitute a pandemic threat. The clinical symptoms associated with these zoonotic transmissions range from mild respiratory illnesses and conjunctivitis to pneumonia and acute respiratory distress syndrome, sometimes resulting in death. More basic research into virus ecology and evolution and development of effective vaccines and antiviral strategies are required to limit the impact of influenza A virus zoonoses and the threat of an influenza pandemic. SUMMARY: Previously unknown and emerging respiratory viruses are an important threat to human health. Development of virus diagnostic tests, antiviral strategies, and vaccines for each of these pathogens is crucial to limit their impact.


NAL Call Number: QR180.3.D4

Abstract: We have previously reported that some species of migrating ducks (pintail, mallard, widgeon and falcated teal) possess in their sera antibodies against H antigens of human or avian influenza viruses. Such findings have also been reported from other workers, and the appearance of new types of influenza viruses accompanied by outbreaks of new influenza pandemics, or circulation of influenza virus antigens in animals, birds and humans have been discussed on the basis of such findings. Recently a number of orthomyxoviruses have been isolated from wild birds such as myna, banded parakeets, etc. imported from India and some areas of South-East Asia. Some of them have H antigens not recognized previously, and some are found to have more or less common reactions with human H3 antigen, and consequently antigens Hav 7 and Heq 2, which are known to show cross-reaction with H3. The significance of such a fact in connection with the appearance of a new influenza pandemic is discussed.

Descriptors: antibodies, viral, birds microbiology, influenza A virus avian immunology, Asia, Southeastern, ducks, hemagglutinins viral, influenza A virus avian isolation and purification, Japan, neuraminidase immunology.


NAL Call Number: aSF601.U5

Descriptors: avian influenza virus, poultry, depopulation, Pennsylvania.


NAL Call Number: aSF601.U5

Descriptors: avian influenza virus, outbreaks, turkeys, Virginia, Pennsylvania.


NAL Call Number: QR375.V6

Abstract: The phylogenetic relationships of the hemagglutinin (HA) and non-structural (NS) genes from avian influenza (AI) H5 subtype viruses of North American origin are presented. Analysis of the HA genes of several previously uncharacterized isolates from waterfowl and turkeys provided clear evidence of significant sequence variation and existence of multiple virus clades or sub-lineages, maintained in migratory waterfowl. Phylogenetic analysis of NS gene sequences further demonstrated multiple sub-lineages and
also demonstrated re-assortment of two NS alleles in wild duck populations. Based on currently available HA1 gene sequences, at least four clades exist with waterfowl isolates included in three of the four groups. The most genetically unstable of these sub-lineages is composed of recent poultry isolates from the outbreak of AI in Central Mexico. This group of viruses, which replicated unabated in chickens for at least 16 months, exhibited an increased rate of mutation in both the HA and NS gene. Comparison of the HA1 sequence data for all available North American H5 subtype viruses demonstrated minimal variation both in and around the amino acids predicted to be involved in the HA receptor binding site. The sequences also revealed that migratory waterfowl, live poultry market chicken, and turkey isolates uniformly lack a glycosylation site at amino acid 236 in the HA protein which is present in commercial chicken isolates.

Descriptors: evolution, molecular, hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian genetics, viral nonstructural proteins genetics, base sequence, DNA, viral, influenza A virus avian classification, molecular sequence data, North America, phylogeny.


NAL Call Number: RC111.R4

Abstract: An analysis was made of 149 influenza A viruses isolated from ducks in Hong Kong during the period of November 1975 through October 1977. The viruses were isolated five times more frequently from ducks raised in the People's Republic of China than from those raised in Hong Kong. The isolation rate for viruses was higher from the cloaca than it was from the trachea, but this pattern varied over the two years of investigation. The large number of different combinations (30) of hemagglutinin and neuraminidase genes suggests that recombination of viruses was taking place. Analysis of these combinations showed that their distribution was not random and that certain combinations occurred more frequently, and others less frequently, than was expected. The recombination of influenza viruses and the excess or restriction of certain combinations may have implications for the evolution of pandemic strains of influenza virus in humans.

Descriptors: ducks microbiology, influenza A virus avian genetics, recombination, genetic, China, cloaca microbiology, evolution, gene frequency, genotype, hemagglutinins viral genetics, Hong Kong, influenza A virus avian isolation and purification, neuraminidase genetics, paramyxoviridae isolation and purification, seasons, trachea microbiology.


NAL Call Number: 448.3 Ar23

Descriptors: influenza A virus avian drug effects, influenza A virus avian radiation effects, mutation, centrifugation, density gradient, chick embryo, chromatography, DEAE-cellulose, fibroblasts, mutagens, protamines pharmacology, radiation effects, sodium chloride, temperature, tissue culture, ultraviolet rays, virus replication.


NAL Call Number: 41.8 Av5

Abstract: An avian influenza virus with surface antigens similar to those of fowl plague virus (Hav 1 Nav 2) was isolated in 1979 from 2 commercial turkey flocks in Central Texas. Two flocks in contact with these infected flocks developed clinical signs, gross lesions, and seroconversion but yielded no virus. This was the first recorded incidence of clinical avian influenza in Texas turkeys and only the second time that an agent with these surface antigens was isolated from turkeys in U.S.

Descriptors: fowl plague epidemiology, influenza A virus avian isolation and purification, turkeys, antibodies, viral analysis, fowl plague immunology, hemagglutination tests veterinary, immunodiffusion veterinary, influenza A virus avian immunology, Texas.


NAL Call Number: 448.8 J8295
Descriptors: host parasite relations physiology, influenza A virus, avian metabolism, RNA virus infections epidemiology, Asia epidemiology, RNA virus infections metabolism, zoonoses.

Descriptors: communicable disease control organization and administration, influenza epidemiology, influenza A virus, avian isolation and purification, avian influenza epidemiology, birds, influenza prevention and control, avian influenza prevention and control, primary prevention organization and administration, risk assessment, vaccination methods, world health.

NAL Call Number: 41.8 V641
Descriptors: antibodies, viral blood, birds immunology, coronaviridae immunology, herpesvirus 1, gallid immunology, infectious bronchitis virus immunology, infectious bursal disease virus immunology, influenza A virus avian immunology, Newcastle disease virus immunology, rotavirus immunology.

NAL Call Number: 41.8 V641
Descriptors: duck hepatitis virus, mallard ducks, avian influenza virus, Anas platyrhynchos.

NAL Call Number: 23 Au792
Descriptors: viral evolution, viral replication, infection, geographic location.

NAL Call Number: 448.3 Ar23
Abstract: Samples collected in 1987 and 1988 in Brittany from influenza-infected swine made it possible to isolate and antigenically characterize two H1N2 recombinant viruses (Sw/France/5027/87 and Sw/France/5550/88). The former virus was cloned and reinoculated to swine to allow reproduction of the disease and reisolation of a strain similar to the original one. The serodiagnostic tests carried out on both the original sera and those from the experimentally infected animals confirmed that the virus was actually type Sw/H1N2.

NAL Call Number: 41.8 Av5
Abstract: Isolation of type A influenza viruses from the feces of 5013 birds of 16 species was attempted during a 33-month study (1977-79). Seventy viruses were isolated from the feces of 3403 ring-billed gulls in Baltimore, Md., during 16 months of sampling. Six hemagglutinin (HA) subtypes and seven neuraminidase (NA) subtypes in 15 combinations were found. The H13N6 virus was the only subtype found each year and accounted for 40% of the isolates. The rate of isolation from gulls was 0.26% in the cold months and 3.0% in the warm months. Hemagglutination-inhibition (HI) and elution-inhibition antibody profiles reflected the presence of some but not all of the viruses isolated. In mute swans, the rates of seroconversions were 16% for HA antibody and 14% for NA antibody, whereas the viral isolation rate was 0.4% over a 3-year period. Both the H5 and the N2 subtypes, which were responsible for the lethal chicken outbreaks in 1983 in
Pennsylvania, were isolated from gulls in 1978 in association with subtypes not found in the chicken virus. Also, seroconversions for the H5 HA occurred in mute swans in 1978.

Descriptors: antibodies, viral blood, feces microbiology, fowl plague epidemiology, influenza A virus avian isolation and purification, age factors, Baltimore epidemiology, birds, hemagglutination inhibition tests, influenza A virus avian classification, influenza A virus avian immunology, mid-Atlantic region epidemiology, prevalence, seasons.


NAL Call Number: 448.3 AC85

Abstract: Avian influenza virus A/Larus 36/77 (Hav7Nav1) was isolated in 1977 from a trinket (Larus ridibundus) embryo. This result suggests the possibility of vertical transmission of influenza A virus.

Descriptors: birds microbiology, influenza A virus avian isolation and purification, antigens, viral analysis, birds embryology, Czechoslovakia, ecology, epitopes, influenza A virus avian immunology.


NAL Call Number: aSF601.U5

Descriptors: pheasants, waterfowl, avian influenza virus, disease control, birds, Galliformes, influenza virus, viruses, outbreaks.


NAL Call Number: 500 N21P

Abstract: Infection with avian influenza A virus of the H5N1 subtype (isolates A/HK/212/03 and A/HK/213/03) was fatal to one of two members of a family in southern China in 2003. This incident was preceded by lethal outbreaks of H5N1 influenza in waterfowl, which are the natural hosts of these viruses and, therefore, normally have asymptomatic infection. The hemagglutinin genes of the A/HK/212/03-like viruses isolated from humans and waterfowl share the lineage of the H5N1 viruses that caused the first known cases of human disease in Hong Kong in 1997, but their internal protein genes originated elsewhere. The hemagglutinin of the recent human isolates has undergone significant antigenic drift. Like the 1997 human H5N1 isolates, the 2003 human H5N1 isolates induced the overproduction of proinflammatory cytokines by primary human macrophages in vitro, whereas the precursor H5N1 viruses and other H5N1 reassortants isolated in 2001 did not. The acquisition by the viruses of characteristics that enhance virulence in humans and waterfowl and their potential for wider distribution by infected migrating birds are causes for renewed pandemic concern.

Descriptors: influenza epidemiology, influenza virology, birds virology, cytokines biosynthesis, cytokines immunology, hemagglutination inhibition tests, Hong Kong, inflammation mediators immunology, influenza transmission, influenza veterinary, influenza A virus, avian classification, avian genetics, avian immunology, avian pathogenicity, macrophages immunology, macrophages metabolism, mice, molecular sequence data, organ specificity, phylogeny, reassortant viruses immunology, reassortant viruses pathogenicity, time factors, virulence.


NAL Call Number: QR360.J6

Abstract: The transmission of H9N2 influenza viruses to humans and the realization that the A/Hong Kong/156/97-like (H5N1) (abbreviated HK/156/97) genome complex may be present in H9N2 viruses in southeastern China necessitated a study of the distribution and characterization of H9N2 viruses in poultry in the Hong Kong SAR in 1999. Serological studies indicated that H9N2 influenza viruses had infected a high proportion of chickens and other land-based birds (pigeon, pheasant, quail, guinea fowl, and chukka) from
southeastern China. Two lineages of H9N2 influenza viruses present in the live-poultry markets were represented by A/Quail/Hong Kong/G1/97 (Qa/HK/G1/97)-like and A/Duck/Hong Kong/Y280/97 (Dk/HK/Y280/97)-like viruses. Up to 16% of cages of quail in the poultry markets contained Qa/HK/G1/97-like viruses, while about 5% of cages of other land-based birds were infected with Dk/HK/Y280/97-like viruses. No reassortant between the two H9N2 virus lineages was detected despite their cocirculation in the poultry markets. Reassortant viruses represented by A/Chicken/Hong Kong/G9/97 (H9N2) were the major H9N2 influenza viruses circulating in the Hong Kong markets in 1997 but have not been detected since the chicken slaughter in 1997. The Qa/HK/G1/97-like viruses were frequently isolated from quail, while Dk/HK/Y280/97-like viruses were predominately associated with chickens. The Qa/HK/G1/97-like viruses were evolving relatively rapidly, especially in their PB2, HA, NP, and NA genes, suggesting that they are in the process of adapting to a new host. Experimental studies showed that both H9N2 lineages were primarily spread by the aerosol route and that neither quail nor chickens showed evidence of disease. The high prevalence of quail infected with Qa/HK/G1/97-like virus that contains six gene segments genetically highly related to HK/156/97 (H5N1) virus emphasizes the need for surveillance of mammals including humans.

Descriptors: genome, viral, influenza A virus avian isolation and purification, poultry virology, China, hemagglutination inhibition tests, influenza A virus avian genetics, phylogeny, temperature, virus replication.


NAL Call Number: 500 N21P

Abstract: The origin of the H5N1 influenza viruses that killed six of eighteen infected humans in 1997 and were highly pathogenic in chickens has not been resolved. These H5N1 viruses transmitted directly to humans from infected poultry. In the poultry markets in Hong Kong, both H5N1 and H9N2 influenza viruses were cocirculating, raising the possibility of genetic reassortment. Here we analyze the antigenic and genetic features of H9N2 influenza viruses with different epidemiological backgrounds. The results suggest that the H9N2 influenza viruses of domestic ducks have become established in the domestic poultry of Asia. Phylogenetic and antigenic analyses of the H9N2 viruses isolated from Hong Kong markets suggest three distinct sublineages. Among the chicken H9N2 viruses, six of the gene segments were apparently derived from an earlier chicken H9N2 virus isolated in China, whereas the PB1 and PB2 genes are closely related to those of the H5N1 viruses and a quail H9N2 virus-A/quail/Hong Kong/G1/97 (Qa/HK/G1/97)-suggesting that many of the 1997 chicken H9 isolates in the markets were reassortants. The similarity of the internal genes of Qa/HK/G1/97 virus to those of the H5N1 influenza viruses suggests that the quail virus may have been the internal gene donor. Our findings indicate that the human and poultry H5N1 influenza viruses in Hong Kong in 1997 were reassortants that obtained internal gene segments from Qa/HK/G1/97. However, we cannot be certain whether the replicate complex of H5N1 originated from Qa/HK/G1/97 or whether the reverse transfer occurred; the available evidence supports the former proposal.

Descriptors: genes viral, influenza epidemiology, influenza veterinary, influenza A virus avian classification, influenza A virus avian genetics, influenza A virus human classification, influenza A virus human genetics, poultry diseases epidemiology, chick embryo, chickens, coturnix, ducks, feces virology, Hong Kong epidemiology, influenza virology, influenza A virus avian pathogenicity, molecular sequence data, phylogeny, pigeons, poultry diseases virology.


Descriptors: disease outbreaks prevention and control, influenza epidemiology, world health, antiviral agents therapeutic use, influenza drug therapy, influenza prevention and control, influenza virology, influenza vaccine administration and dosage, orthomyxoviridae genetics, orthomyxoviridae immunology, practice guidelines, vaccination, World Health Organization.


NAL Call Number: 41.8 V6463
Descriptors: avian influenza virus, genomes, antigens, hemagglutination tests, immunological techniques, nucleic acids.


Abstract: Some emerging infectious diseases have recently become endemic in Germany. Others remain confined to specific regions in the world. Physicians notice them only when travelers after infection in endemic areas present themselves with symptoms. Several of these emerging infections will be explained. HIV is an example for an imported pathogen which has become endemic in Germany. SARS and avian influenza are zoonoses with the potential to spread from person to person. Avian influenza in humans provides a possibility for the reassortment of a potential new pandemic strain. Outbreaks of dengue fever in endemic areas are reflected in increased infections in travelers returning from these areas. Currently, West-Nile-virus infections are only imported into Germany. The timely implementation of diagnostic, therapeutic and infection control measures requires physicians to include these diseases in their differential diagnosis. To achieve this goal, good cooperation between physicians, laboratories and the public health service is essential.


NAL Call Number: 41.8 T445

Descriptors: avian influenza virus, fowl plague virus, disease control, European Union, poultry, zoonoses.


NAL Call Number: 47.8 Ar2

Abstract: In the present investigation 315 commercial meat turkey flocks slaughtered in southern part of Germany in year 2001 were serologically examined for antibodies to avian influenza A viruses. Ten blood samples per flock were collected at the time of slaughter and examined using commercial ELISAs. Samples that reacted positively in ELISA were re-examined in haemagglutination inhibition test (HI) using subtype specific antigens. From the 3150 examined samples only 26 samples obtained from 7 flocks reacted positively in ELISA. Examination of these samples in HI revealed negative results to H1, H5, H7 and H9. On the other hand, all samples reacted positive in HI using H6 antigen. In all flocks neither clinical signs nor unusual increased mortalities were observed. End of December 2001 to January 2002 outbreaks of avian influenza were observed in three turkey flocks reared in the central-west region of Germany. In all cases sudden onset of depression, decrease in feed and water intake, respiratory signs accompanied with high mortality were observed. On necropsy pericarditis, petechial haemorrhages in pericardial fat, fibrinous airsacculitis, lung congestion and pneumonia were found. In addition, enlargement of the spleen and inflammation of pancreas were detected. Virological examinations resulted in isolation of an avian influenza A virus in embryonated chicken eggs. All isolates were identified as subtype H6N2 with an intravenous pathogenicity index (IVPI) of 0.0. The current observations indicate that low pathogenic avian influenza A of subtype 6 still circulated in German turkey flocks and in most of cases accompanied with high economic losses.

Descriptors: animal husbandry, epidemiology, immune system, infection, avian influenza, epidemiology, respiratory system disease, viral disease, ELISA immunologic techniques, laboratory techniques, serology
NAL Call Number: SF481.M54
Descriptors: avian influenza virus, influenza virus A and B, clinical aspects, disease control, transmission, mortality, quarantine, vaccines, zoonoses, turkeys.

NAL Call Number: 41.8 Av5
Abstract: Isolation-reared mallards (Anas platyrhynchos) were placed on ponds in turkey-rearing areas in Minnesota, and their cloacae were periodically swabbed to attempt isolating virus from embryonated chicken eggs. Nearby turkeys were sampled by taking cloacal and tracheal swabs as well as blood samples. Hemagglutinating viruses were identified at the National Veterinary Services Laboratory, U.S. Department of Agriculture, Ames, Iowa. During this two-year study, the weekly influenza virus-isolation rate from ducks varied from 0 to 24.4%. A total of 213 influenza viruses were isolated from the ducks. Twenty-six influenza virus subtypes were detected. Ninety-seven flocks of turkeys were diagnosed as having influenza by virus isolation and/or serology. Eight influenza virus subtypes were involved in the turkey outbreaks, and seven of these were also detected in the ducks and/or other avian species. The weekly infection rate of the sentinel ducks correlated directly with observations of wild ducks at the monitoring sites. Influenza virus was isolated from water samples collected near the sentinel duck sites during the study.
Descriptors: disease outbreaks veterinary, ducks, fowl plague epidemiology, turkeys, blood microbiology, cloaca microbiology, influenza A virus avian classification, avian isolation and purification, Minnesota, serotyping veterinary, trachea microbiology.

NAL Call Number: SF481.M54
Descriptors: avian influenza virus, disease control, prevention, transmission, biosecurity.

NAL Call Number: SF601.V484
Descriptors: fowl plague prevention and control, influenza A virus avian immunology, avian physiology, influenza vaccine immunology, poultry virology, poultry diseases prevention and control, veterinary medicine, biomedical research, fowl plague immunology, poultry immunology, poultry diseases immunology.

NAL Call Number: 41.8 Av5
Descriptors: avian influenza virus, case reports, United States, Minnesota, chickens.

NAL Call Number: 448.3 Ap5
Abstract: Sentinel ducks and domestic turkey flocks were monitored for influenza infection during a 4-year period. The onset of infection among ducks was similar each year, occurring in late July or early August. Influenza in turkeys was also shown to be seasonal, but the usual onset was 6 to 8 weeks after the detection of influenza in sentinel ducks. Possible explanations for the delayed infection in turkeys are (i) increased waterfowl activity associated with fledging and congregating in late summer and early fall; (ii) vectors transmitting virus from the waterfowl habitat to poultry farms; (iii) cooler environmental temperature, allowing prolonged virus viability; (iv) cooler surface water temperature, allowing prolonged virus viability; (v) groundwater contamination from contaminated surface water; and (vi) virus adaptation in domestic turkeys.
before infection is detected. We conclude that ducks are not only a natural reservoir of influenza but also have a seasonal infection that appears to be related to seasonal influenza outbreaks in domestic turkeys in Minnesota. However, only some influenza A virus isolates circulating among waterfowl at any given time appear capable of causing detectable infection in turkeys. It is speculated that the seasonal infection in migratory waterfowl may also be related to seasonal influenza infections in other species including humans.

Descriptors: influenza veterinary, poultry diseases transmission, turkeys microbiology, antigens, viral analysis, disease reservoirs, ducks microbiology, influenza immunology, influenza transmission, influenza A virus avian growth and development, Minnesota, poultry diseases epidemiology, temperature, water microbiology.


NAL Call Number: 41.8 Av5

Abstract: Influenza was detected in a flock of broiler breeders during routine serological monitoring. Although there were no clinical signs, egg production may have been affected in hens on one story of a two-story breeder house. Intensive measures were taken to avoid transmission to other farms. Two months after the flock was found to be serologically positive, sentinel hens were placed in the flock, and they became serologically positive 1 month later. In spite of this evidence for virus being present in the flock, no detectable transmission to any other farm occurred.

Descriptors: antibodies, viral blood, chickens, fowl plague diagnosis, influenza A virus avian immunology, fowl plague prevention and control, precipitin tests.


NAL Call Number: 448.9 Am37

Descriptors: hemagglutinins, viral genetics, influenza history, influenza A virus, avian genetics, DNA, viral analysis, disease outbreaks history, history, 20th century, influenza epidemiology, influenza virology.


NAL Call Number: QR180.3.D4

Abstract: Attempts at virus isolation from cloacal swabs resulted in the recovery of 10 strains of hemagglutinating viruses from a total of 349 ducks, mainly shelducks (Tadorna tadorna) captured in the north of France. Four of these isolates were identified as influenza strains corresponding to the following antigenic composition: Hav6-N2, Hav6-Nav4 and Hav1-N2 (2 strains). Shelduck is known to be a partially migratory species, wintering in western Europe, some of them migrating northward to Scandinavia during the summer. The captures were made between November 1976 and February 1977: one of the birds was caught four times and was found to be negative for virus in November, positive in December (isolation of a strain Hav6-Nav4), negative again in January and February. Blood taken in February did not show the presence of HI antibodies to the homologous virus.

Descriptors: antigens, viral, ducks microbiology, influenza A virus avian isolation and purification, neuraminidase immunology, antibodies, viral, cloaca microbiology, France, hemagglutination inhibition tests, hemagglutinins viral, avian enzymology, avian immunology, human enzymology, seasons.


NAL Call Number: QR180.C62


Although wild ducks are known to be a major reservoir for avian influenza viruses (AIV), there are few recent published reports of surveillance directed at this group. Predominant AIV hemagglutinin (HA) subtypes reported in previous studies of ducks in North America include H3, H4, and H6, with the H5, H7, and H9 subtypes not well represented in these host populations. The objective of this study was to determine whether these subtype patterns have persisted. Each September from 1998 to 2000, cloacal swabs were collected from wild ducks banded in Roseau and Marshall counties, MN. Mallards (Anas platyrhynchos) were sampled all years, and northern pintails (A. acuta) were sampled only in 1999. Influenza viruses were isolated from 11%, 14%, and 8% of birds during 1998, 1999, and 2000, respectively. Prevalence, as expected, was highest in juveniles, ranging from 11% to 23% in mallards. Viruses representative of the HA subtypes 2, 3, 4, 5, 6, 7, 9, 10, 11, and 12 were isolated. Viruses in the H5, H7, and H9 subtypes, which are associated with high-pathogenicity influenza in poultry or recent infections in humans, were not uncommon, and each of these subtypes was isolated in 2 out of the 3 years of surveillance. 

Descriptors: epidemiology, infection, avian influenza, infectious disease, respiratory system disease, viral disease, virus reservoir.


**Abstract:** Hasta la fecha, no existian estudios en donde haya sido evaluada la persistencia del virus de influenza aviar (IA) en la carne proveniente de aves infectadas, que son enviadas al rastro para su procesamiento y venta. Tampoco, se ha evaluado si la carne de pollo de importacion, puede ser un factor de riesgo para la introduccion al pais de nuevos subtipos de virus de IA. El objetivo de la presente investigacion, fue estudiar si la carne y visceras de pollos infectados con IA, mantienen al virus, cuando son conservadas en congelacion o en hielo. Se formaron dos grupos de 100 pollos de engorda de cuatro semanas de edad libres de IA. Uno de los grupos fue inoculado con 1 x 10^3 DLEP50 del virus A/Chicken/CPA-238/94 (H5N2) de baja patogenicidad (BP), por via intranasal. El segundo grupo, se inoculo con 1 x 10^3 DLEP50 del virus A/Chicken/Queretaro/14588-19/95 (H5N2) de alta patogenicidad (AP), por la misma via. Tres dias despues de la inoculacion, ambos grupos fueron sacrificados, simulando condiciones de rastro. A la mitad de las canales de ambos grupos, se les retiraron la totalidad de las visceras, incluyendo los pulmones y rinones (canales limpias). La mitad restante, conservo los pulmones y rinones dentro de la canal (canales completas). Posteriormente, las canales fueron conservadas bajo dos condiciones de almacenamiento, -20 C y en hielo. De una forma aleatoria, a las 0 horas, 48 horas, 7, 14, 21 y 28 dias post-sacrificio (PS), se procedio a la toma de muestras para el aislamiento viral. El aislamiento se intento a partir de una mezcla de carne de la pechuga, pierna y muslo, en las canales limpias. En las canales completas, adicionalmente, el aislamiento viral se intento de una mezcla de los pulmones y rinones. De un total de 108 muestras procesadas para el aislamiento del virus de BP, 65 fueron positivas (60.18%). En el caso del virus de AP, de 108 muestras solo se pudieron realizar 32 aislamientos (29.62%). En ambos casos el virus pudo ser aislado de la carne y de las visceras, independientemente del tipo de conservacion de las canales. El virus de BP, pudo ser aislado hasta los 28 dias PS; mientras que el aislamiento del virus de AP, fue consistente solo hasta los 14 dias PS. Los resultados obtenidos en la presente investigacion preliminar, muestran que la carne y visceras provenientes de pollos infectados con el virus de IA, tanto de BP como de AP, pueden ser un factor importante para la transmision e introduccion de la enfermedad, ya fue posible recuperar al virus, independientemente del tipo de conservacion de las canales hasta por 28 dias PS. Trabajo realizado con apoyo economico de la Direccion General de Salud Animal.

**Descriptors:** chicken meat, avian influenza virus, diagnosis, animal products, influenza virus, meat, orthomyxoviridae, poultry meat, viruses.


**Abstract:**
During the latter stages of the lethal H5N2 influenza eradication program in domestic poultry in Pennsylvania in 1983-84, surveillance of waterfowl was done to determine if these birds harbored influenza viruses that might subsequently appear in poultry. From late June to November 1984, 182 hemagglutinating viruses were isolated from 2043 wild birds, primarily ducks, in the same geographical area as the earlier lethal H5N2 avian influenza outbreak. The virus isolates from waterfowl included paramyxoviruses (PMV-1, -4, and -6) and influenza viruses of 13 antigenic combinations. There was only one H5N2 isolate from a duck. Although this virus was antigenically related to the lethal H5N2 virus, genetic and antigenic analysis indicated that it could be discriminated from the virulent family of H5N2 viruses, and it did not originate from chickens. Many of the influenza viruses obtained from wild ducks were capable of replicating in chickens after experimental inoculation but did not cause disease. These studies show that many influenza A virus strains circulating in waterfowl in the vicinity of domestic poultry in Pennsylvania did not originate from domestic poultry. These influenza viruses from wild ducks were capable of infecting poultry; however, transmission of these viruses to poultry apparently was avoided by good husbandry and control measures.

**Descriptors:**
animal population groups microbiology, animals, wild microbiology, ducks microbiology, geese microbiology, orthomyxoviridae isolation and purification, paramyxoviridae isolation and purification, respirovirus isolation and purification, antigens, viral analysis, chickens, orthomyxoviridae immunology, paramyxoviridae immunology, Pennsylvania, respirovirus immunology.


**Descriptors:**
avian influenza virus, epidemiology, feral avian species, domestic avian species.


**Descriptors:**
antigens, viral analysis, ducks microbiology, influenza A virus avian isolation and purification, influenza A virus isolation and purification, Canada, ecology, epitopes, avian growth and development, avian immunology, influenza A virus immunology, recombination, genetic, swine microbiology.


**Descriptors:**
antigens, viral classification, hemagglutinins viral classification, influenza A virus classification, neuraminidase immunology, birds microbiology, epitopes, horses microbiology, avian classification, human classification, influenza A virus immunology, swine microbiology, terminology.


**Descriptors:**
ducks microbiology, influenza A virus avian isolation and purification, paramyxoviridae
isolation and purification, Alberta, antigens, viral, ducks classification, avian classification, avian immunology, paramyxoviridae classification, paramyxoviridae immunology.


Abstract: Globalisation and its effect on human development has rendered an environment that is conducive for the rapid international spread of severe acute respiratory syndrome (SARS), and other new infectious diseases yet to emerge. After the unprecedented multi-country outbreak of avian influenza with human cases in the winter of 2003-2004, an influenza pandemic is a current threat. A critical review of problems and solutions encountered during the 2003-2004 SARS epidemics will serve as the basis for considering national preparedness steps that can be taken to facilitate the early detection of avian influenza, and a rapid response to an influenza pandemic should it occur.

Descriptors: communicable disease control methods, disease outbreaks prevention and control, severe acute respiratory syndrome epidemiology, severe acute respiratory syndrome prevention and control, China epidemiology, influenza epidemiology, influenza prevention and control.


NAL Call Number: R11.C3

Descriptors: disease outbreaks, fowl plague transmission, influenza epidemiology, influenza A virus avian immunology, avian isolation and purification, avian pathogenicity, pneumonia, viral transmission, zoonoses, adolescent, adult, chickens virology, child, child, preschool, fowl plague epidemiology, fowl plague prevention and control, Hong Kong epidemiology, incidence, influenza prevention and control, middle aged, pneumonia, viral epidemiology, pneumonia, viral prevention and control, trachea virology.


NAL Call Number: SF601.J6

Descriptors: peafowl, Pavo cristatus, Bordetella avium infection, Capillaria sp. infection, Clostridium perfringens type A infection, Escherichia coli infection, Goniodes gigas infestation, Mycoplasma meleagridis infection, Mycoplasma synoviae infection, diagnostic techniques, serum plate agglutination test, antibody titer, zoo, Michigan.


NAL Call Number: 470 Sci2

Descriptors: hemagglutinin glycoproteins, influenza virus chemistry, hemagglutinin glycoproteins, influenza virus metabolism, influenza history, influenza virology, influenza A virus, human immunology, binding sites, birds, carbohydrate conformation, crystallography, x-ray, disease outbreaks history, history, 20th century, influenza epidemiology, avian immunology, avian metabolism, human metabolism, human pathogenicity, membrane glycoproteins chemistry, membrane glycoproteins metabolism, protein conformation, RNA, viral chemistry, viral genetics, viral isolation and purification, receptors, virus chemistry, receptors, virus metabolism, sialic acids metabolism, virulence.


NAL Call Number: 41.8 Av5

Descriptors: antibodies analysis, influenza veterinary, orthomyxoviridae immunology, turkeys, aerosols, cold, hemagglutination inhibition tests, hemagglutination tests, poultry diseases immunology, Wisconsin.


NAL Call Number: 41.8 Av5

Descriptors: orthomyxoviridae growth and development, orthomyxoviridae pathogenicity, chick embryo,
hemagglutinins viral analysis, orthomyxoviridae infections, poultry diseases, temperature, tissue culture, turkeys, virus cultivation.


NAL Call Number: 41.8 Av5
Descriptors: ducks, geese, influenza veterinary, orthomyxoviridae isolation and purification, poultry diseases microbiology, aerosols, antibodies analysis, disease outbreaks veterinary, hemagglutination inhibition tests, orthomyxoviridae immunology, orthomyxoviridae pathogenicity, turkeys.


ISSN: 0005-2086.

NAL Call Number: 41.8 Av5
Descriptors: influenza veterinary, orthomyxoviridae isolation and purification, poultry diseases microbiology, turkeys, disease outbreaks veterinary, hemagglutination inhibition tests, influenza epidemiology, influenza immunology, influenza pathology, orthomyxoviridae pathogenicity, Wisconsin.


NAL Call Number: 41.8 Av5
Abstract: Comparative histological and immunocytochemical studies were conducted on formalin-fixed tissues from chickens infected with avian influenza viruses of varying virulence. Results showed a distinct pattern of disease that depended on the virulence of the virus and the susceptibility of the birds. At 3 days post-intranasal inoculation with a highly virulent H7N7 virus, all 6-to-8-week-old specific-pathogen-free (SPF) birds were affected, and all developed pancreatic necrosis and encephalitis associated with specific immunoperoxidase staining. Other same-aged SPF birds were only occasionally affected 6 to 8 days after intravenous inoculation with almost avirulent H4N4, H6N2, or H3N8 virus. Specific lesions and immunoperoxidase staining were noted in the kidneys only. The H7N7 virus in older commercial birds and an H7N3 virus in young SPF and older commercial birds caused intermediate mortality rates at 4 to 11 days postinoculation, and there was a broad range of lesions and specific immunoperoxidase staining in the pancreas, brain, kidney, heart, and skeletal muscle. Two exceptional birds had immunostaining of small blood vessels throughout their bodies with or without lesions or staining in the tissues, which may have represented a transitory pre-localizing phase occurring in many birds. There was necrosis without virus antigen detection in the bursae, thymuses, and cecal tonsils, possibly secondary to stress or only transitory infection of virus. These data indicate that rapid, retrospective diagnosis of avian influenza in fixed tissues is possible by using an immunoperoxidase test on pancreas, brain, and kidney.
Descriptors: chickens, avian influenza virus, pathogenicity, disease resistance, body parts, animal tissues, antigens, histopathology, immunology, biological properties, birds, body parts, domestic animals, domesticated birds, Galliformes, immunological factors, influenza virus, livestock, microbial properties, orthomyxoviridae, pathology, poultry, resistance to injurious factors, useful animals, viruses, susceptibility, viral antigens, immunocytochemistry.


NAL Call Number: 41.9 W64B
Abstract: Wild turkeys (Meleagris gallopavo silvestris) trapped as part of a relocation program by the Arkansas Game and Fish Commission were tested for selected infectious diseases and parasites. The 45 birds were trapped at four locations in Pope, Scott, and Montgomery counties (Arkansas, USA). Forty-four blood samples for serology, 27 blood smears and 12 fecal samples were collected. Of the serum samples tested, 20 of 44 (45%) were positive for Pasteurella multocida by enzyme-linked immunosorbent assay
(ELISA), 42 of 44 (95%) were positive for *Bordetella avium* by ELISA, and 15 of 44 (34%) were positive for Newcastle disease virus antibody by the hemagglutination inhibition test. All serum samples were negative for *Mycoplasma gallisepticum*, *Mycoplasma synoviae*, avian paramyxovirus 3, avian influenza, hemorrhagic enteritis, Marek's disease, avian encephalomyelitis, laryngotracheitis, *Salmonella pullorum* and *Salmonella gallinarum*. *Haemoproteus meleagridis* was found in eight of 27 (30%) and *Leucocytozoon smithi* in nine of 27 (33%) blood smears; all smears were negative for *Plasmodium hermani*. Enteric parasites included *Ascaridia dissimilis*, *Heterakis gallinarum*, *Eimeria dispersa* and *Raillietina* spp. This study was an attempt to document the health status and disease exposure of wild turkeys in Arkansas to aid in managing and preventing the spread of disease agents to wild turkeys and other species of birds.

**Descriptors:** bird diseases epidemiology, communicable diseases veterinary, turkeys, animals, wild, antibodies, bacterial blood, antibodies, viral blood, Arkansas epidemiology, communicable disease control, communicable diseases epidemiology, disease outbreaks veterinary, feces parasitology, prevalence, protozoa isolation and purification.


**NAL Call Number:** QR67.C54

**Abstract:** Influenza pandemics, defined as global outbreaks of the disease due to viruses with new antigenic subtypes, have exacted high death tolls from human populations. The last two pandemics were caused by hybrid viruses, or reassortants, that harbored a combination of avian and human viral genes. Avian influenza viruses are therefore key contributors to the emergence of human influenza pandemics. In 1997, an H5N1 influenza virus was directly transmitted from birds in live poultry markets in Hong Kong to humans. Eighteen people were infected in this outbreak, six of whom died. This avian virus exhibited high virulence in both avian and mammalian species, causing systemic infection in both chickens and mice. Subsequently, another avian virus with the H9N2 subtype was directly transmitted from birds to humans in Hong Kong. Interestingly, the genes encoding the internal proteins of the H9N2 virus are genetically highly related to those of the H5N1 virus, suggesting a unique property of these gene products. The identification of avian viruses in humans underscores the potential of these and similar strains to produce devastating influenza outbreaks in major population centers. Although highly pathogenic avian influenza viruses had been identified before the 1997 outbreak in Hong Kong, their devastating effects had been confined to poultry. With the Hong Kong outbreak, it became clear that the virulence potential of these viruses extended to humans.

**Descriptors:** disease outbreaks prevention and control, disease outbreaks veterinary, fowl plague epidemiology, influenza epidemiology, influenza A virus avian pathogenicity, adaptation, physiological, disease vectors, fowl plague transmission, Hong Kong epidemiology, influenza virology, avian classification, Mexico epidemiology, Pennsylvania epidemiology, poultry, viral proteins, virulence.


**NAL Call Number:** SF781.R4

**Abstract:** Five diseases recorded in ostriches are regarded as posing a potential animal health threat to meat-importing countries. Newcastle disease causes an atypically low mortality in ostriches: infected birds display typical nervous symptoms but no pathognomonic lesions which could be detected during post-mortem inspection. The vaccination of feedlot birds and a thorough ante-mortem examination are regarded as necessary precautions to ensure virus carriers are not among those animals destined for slaughter and subsequent export. Avian influenza produces clinical depression and lesions can be detected at post-mortem examination. Borna disease appears to affect mainly younger birds, and the virus is probably not present in the meat of affected birds. Finally, there is little evidence to suggest that ostriches could play a role in the epidemiology of transmissible spongiform encephalopathies. Cases of anthrax are extremely rare. The importation of deboned ostrich meat reduces the risk of infected scraps being fed to susceptible animals.

**Descriptors:** bird diseases transmission, anthrax epidemiology, anthrax prevention and control, anthrax veterinary, bird diseases epidemiology, bird diseases prevention and control, birds, Borna disease epidemiology, Borna disease prevention and control, Borna disease transmission, eggs adverse effects,

**NAL Call Number:** 448.8 P942

**Abstract:** The results of seven-year ecologo-virological studies (1979-1985) of Laridae colonies on the island Zhemchuzhnyi, northern Kaspian Sea, showed annual isolation of influenza A viruses. Altogether, 95 hemagglutinating agent have been isolated. Strains with 4 different combinations of surface antigens were identified: H5N2, H13N2, H13N3, H13N6. The possibility of transovarial transmission is confirmed by the fact of isolation of an influenza virus strain A/black-headed herring gull/Astrakhan/458/85 (H13N6) from a nestling having no contacts with the environment. Simultaneous circulation of influenza A viruses (in 1983-1985: H13N2 and H13N6, in 1985: H13N3 and H13N6) and the presence in the virion of neuraminidase of human influenza virus (N2) allow to consider the isolates to be natural recombinants.

**Descriptors:** birds microbiology, fowl plague epidemiology, influenza A virus avian isolation and purification, hemagglutinins viral isolation and purification, Russia.


**NAL Call Number:** 41.8 V6426

**Descriptors:** avian influenza, review, ducks, birds.


**NAL Call Number:** 41.8 V6426

**Descriptors:** influenza veterinary, poultry diseases microbiology, antigens, viral classification, fowl plague physiopathology, immunization veterinary, influenza pathology, influenza A virus avian immunology, orthomyxoviridae immunology, orthomyxoviridae infections pathology, orthomyxoviridae infections veterinary, virulence.


**NAL Call Number:** 448.3 R323

**Descriptors:** birds microbiology, influenza A virus avian isolation and purification, disease vectors, influenza transmission, Romania.


**NAL Call Number:** 448.8 P942

**Descriptors:** birds microbiology, fowl plague epidemiology, fowl plague microbiology, influenza A virus avian isolation and purification, influenza B virus isolation and purification, serologic tests, Ukraine.


**NAL Call Number:** 41.9 T5750

**Descriptors:** fowl plague microbiology, influenza A virus avian isolation and purification, parakeets, Psittacines, antigens, viral analysis, avian immunology.

**NAL Call Number:** 41.8 V6446

**Abstract:** The hemagglutinin (HA) of six H5 influenza virus strains isolated from ducks in Japan and China in 1976 to 1996 were analyzed antigenically and genetically. Antigenic analysis using a panel of monoclonal antibodies revealed that the HA of H5 influenza viruses isolated from ducks are antigenically closely related to each other. Phylogenetic analysis indicates that the isolates from ducks in Hokkaido were derived from an ancestor common with the highly pathogenic isolates from chickens and humans in Hong Kong in 1997.

**Descriptors:** ducks virology, hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian classification, avian genetics, phylogeny, antibodies, monoclonal, antigens, viral genetics, viral immunology, chickens virology, China, genes viral, hemagglutinin glycoproteins, influenza virus immunology, Hong Kong, avian isolation and purification, Japan, RNA viral genetics, viral isolation and purification.


**Descriptors:** communicable disease control organization and administration, communicable diseases, emerging prevention and control, disease outbreaks prevention and control, influenza epidemiology, influenza A virus, avian, avian influenza prevention and control, antiviral agents therapeutic use, Australia epidemiology, birds, emerging epidemiology, immunization programs organization and administration, influenza diagnosis, influenza drug therapy.


**Descriptors:** birds, avian influenza virus, pathogenicity, host pathogen relations, biological properties, influenza virus, microbial properties, orthomyxoviridae, pathology, viruses.


**NAL Call Number:** 448.3 Ar23

**Abstract:** To provide information on the mechanism of perpetuation of influenza viruses among waterfowl reservoirs in nature, virological surveillance was carried out in Alaska during their breeding season in summer from 1991 to 1994. Influenza viruses were isolated mainly from fecal samples of dabbling ducks in their nesting places in central Alaska. The numbers of subtypes of 108 influenza virus isolates were 1 H2N3, 37 H3N8, 55 H4N6, 1 H7N3, 1 H8N2, 1 H10N2, 11 H10N7, and H10 N9. Influenza viruses were also isolated from water samples of the lakes where they nest. Even in September of 1994 when the most ducks had left for migration to south, viruses were still isolated from the lake water. Phylogenetic analysis of the NP genes of the representative isolates showed that they belong to the North American lineage of avian influenza viruses, suggesting that the majority of the waterfowls breeding in central Alaska migrate to North America and not to Asia. The present results support the notion that influenza viruses have been maintained in waterfowl population by water-borne transmission and revealed the mechanism of year-by-year perpetuation of the viruses in the lakes where they breed.

**Descriptors:** ecology, freshwater ecology, infection, methods and techniques, microbiology, wildlife management, Central Alaska fecal sample, H10N2, H10N7, H2N3, H3N8, H4N6, H7N3, H8N2, lake water, water borne transmission.


**NAL Call Number:** 41.8 Sch9

**Abstract:** The risk of zoonotic disease transmission when handling livestock or animal products is substantial. In industrialized countries, the classical zoonotic diseases such as tuberculosis or brucellosis are no longer in the foreground. Latent zoonoses such as salmonellosis and campylobacteriosis can cause serious disease in humans and have become a major public health problem during the past years. Since animals infected with these pathogens show only mild transient disease or no clinical signs at all, new...
concepts in the entire production line ("stable to table") are necessary in order to avoid human infection. Two emerging viruses with zoonotic potential--avian influenza virus and Nipah virus--have been found in Asia in 1997 and 1999. Both diseases had a major impact on disease control and public health in the countries of origin. In order to cope threats from infectious diseases, in particular those of public health relevance, a combined effort among all institutions involved will be necessary. The proposed "European Center for Infectious Diseases" and the "Swiss Center for Zoonotic Diseases" could be a potential approach in order to achieve this goal.

Descriptors: public health, infection, veterinary medicine, Campylobacteriosis, bacterial disease, Salmonellosis, animal product handling, livestock handling, meat inspection, foodborne zoonosis, food contamination prevention and control, food microbiology, meat microbiology, meat products microbiology, zoonoses transmission, animal husbandry, European Union, food handling, risk factors.


Descriptors: government agencies organization and administration, health, influenza, avian influenza prevention and control, chickens, developing countries, disease outbreaks prevention and control, influenza, avian epidemiology, information dissemination methods, Japan epidemiology.


Descriptors: avian influenza virus, diagnosis, disease control, virology, influenza virus, microbiology, orthomyxoviridae, viruses.


Descriptors: birds virology, disease outbreaks prevention and control, influenza A virus, avian genetics, avian influenza transmission, India, avian influenza pathogenicity, avian influenza diagnosis.


Descriptors: chickens, fowl plague epidemiology, Alabama, fowl plague microbiology, fowl plague pathology, influenza A virus avian isolation and purification.


Abstract: A total of 146 of 506 ostriches (\textit{Struthio camelus}) introduced into a quarantine in Denmark died within the first 23 days. The majority of deaths were in young birds up to 10 kg body weight. Avian influenza A viruses (AIVs) were isolated from 14 pools of organ tissues representing seven groups each of three or four ostriches, which died over the first 3 weeks. The AIVs were detected in respiratory tissues, kidneys and intestines. All were subtype H5N2. The intravenous pathogenicity index of each isolate for chickens was 0.0 and the four isolates examined each had the amino acid sequence -P-Q-R-E-T-R*G-L-F- at the cleavage site of the haemagglutinin protein, typical of non-pathogenic AIVs. In addition, an avirulent avian paramyxovirus type 1 virus was isolated from one pool of kidney tissues. Bacteriological examination gave no significant results. The most characteristic pathological findings were impaction of the proventriculus and...
gizzard, enteritis with stasis and multi-focal necrotic hepatitis.

Descriptors: ostriches, influenza virus A, avian paramyxovirus, flocks, quarantine, mortality, isolation, animal tissues, organs, pathogenicity, amino acid sequences, pathology, epidemiology, age differences, European Union countries, Denmark.

NAL Call Number: 41.9 D23
Descriptors: epidemiology, infection, veterinary medicine, avian influenza, diagnosis, transmission, viral disease, global epidemic.

NAL Call Number: 470 Sci2
Descriptors: antiviral agents therapeutic use, disease outbreaks prevention and control, influenza prevention and control, influenza vaccines supply and distribution, world health, adjuvants, immunologic, antiviral agents supply and distribution, clinical trials, developed countries, developing countries, influenza epidemiology, influenza A virus, avian immunology, avian pathogenicity, orthomyxoviridae immunology, orthomyxoviridae pathogenicity, patents, United States, vaccines, synthetic.

NAL Call Number: 41.8 AC83
Abstract: A large number of diseases occur in domestic, farm-raised poultry. Only two of the many different diseases are notifiable and subject to governmental control: highly pathogenic avian influenza and Newcastle disease. Diagnosis and treatment or prevention of all other conditions are left to the skills of farmers and their veterinarians. Poultry production is aimed at providing more and tastier food for the ever growing human community. Infectious diseases and technical errors during production and processing need to be minimised. The concept of hazard analysis critical control point (HACCP) has already been introduced into food processing and quality assessment. The regulations laid down in ISO 9000 will soon become a powerful and practical tool for monitoring and improving the productivity of live poultry. Approved epidemiological concepts and tools will enable the poultry industry to achieve constant and safe production. Certification on the basis of ISO 9000 of all areas of poultry production is a new approach for maintaining the health of poultry, for tracing and subsequently eliminating breaks in productivity, and securing production without health hazards for the consumer.
Descriptors: chickens, communicable diseases veterinary, poultry diseases epidemiology, turkeys, communicable diseases epidemiology, consumer product safety standards, disease outbreaks, food handling standards, guidelines, incidence, meat standards, poultry diseases diagnosis, poultry diseases etiology, poultry products standards, proportional hazards models.

NAL Call Number: SF603.V43
Abstract: The most important virus-induced diseases associated with heavy losses in the domestic goose are Derzsy's disease which is caused by a goose parvovirus and duck plague (duck viral enteritis) which is caused by an avian herpesvirus. Both diseases still occur but can be prevented by timely vaccinations. Antibodies against Influenza A viruses of the subtypes H1, H5, and H7 as well as against avian paramyxoviruses of the serogroups 4, 6, and 8, respectively, were not detected in any of the examined sera. However, antibodies against paramyxovirus type 1 were detected in sera of one source. Haemagglutination inhibition or neutralizing antibodies against avian adenoviruses (EDS76 virus and goose adenovirus of the serotypes 1, 2, and 3) were quite often detected. Based on the present knowledge their pathogenic potential is minor. Neutralizing antibodies against a reovirus originating from Muscovy ducks and against a chicken reovirus (strain U Con S 1133) were quite frequently detected. In 35 of 564 examined geese sera hepatitis B
virus was found.

Descriptors: antibodies, viral blood, geese, poultry diseases diagnosis, virus diseases veterinary, aviadenovirus immunology, avulavirus immunology, hepatitis B virus, duck immunology, hepatitis virus, duck immunology, influenza A virus avian immunology, parvovirus immunology, poultry diseases prevention and control, reoviridae immunology, virus diseases diagnosis, virus diseases prevention and control.


NAL Call Number: 448.3 Ar23

Abstract: The nucleotide sequences of the HA1 domain of the H1 hemagglutinin genes of A/duck/Hong Kong/36/76, A/duck/Hong Kong/196/77, A/sw/North Ireland/38, A/sw/Cambridge/39 and A/Yamagata/120/86 viruses were determined, and their evolutionary relationships were compared with those of previously sequenced hemagglutinin (H1) genes from avian, swine and human influenza viruses. A pairwise comparison of the nucleotide sequences revealed that the genes can be segregated into three groups, the avian, swine and human virus groups. With the exception of two swine strains isolated in the 1930s, a high degree of nucleotide sequence homology exists within the group. Two phylogenetic trees constructed from the substitutions at the synonymous site and the third codon position showed that the H1 hemagglutinin genes can be divided into three host-specific lineages. Examination of 21 hemagglutinin genes from the human and swine viruses revealed that two distinct lineages are present in the swine population. The swine strains, sw/North Ireland/38 and sw/Cambridge/39, are clearly on the human lineage, suggesting that they originate from a human A/WSN/33-like variant. However, the classic swine strain, sw/Iowa/15/30, and the contemporary human viruses are not direct descendants of the 1918 human pandemic strain, but did diverge from a common ancestral virus around 1905. Furthermore, previous to this the above mammalian viruses diverged from the lineage containing the avian viruses at about 1880.

Descriptors: evolution, hemagglutinins viral genetics, influenza A virus avian genetics, human genetics, porcine genetics, amino acid sequence, chick embryo, genes viral, hemagglutinin glycoproteins, influenza virus, avian classification, human classification, porcine classification, molecular sequence data, phylogeny, sequence homology, amino acid.


NAL Call Number: QR180.C62

Descriptors: disease reservoirs, influenza microbiology, influenza A virus genetics, orthomyxoviridae infections veterinary, genes viral, horses microbiology, influenza A virus avian, influenza A virus, porcine, orthomyxoviridae infections microbiology, orthomyxoviridae infections transmission, recombination, genetic.


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NAL Call Number: 41.8 R3224

Descriptors: influenza A virus avian isolation and purification, swine diseases virology, antigens, viral analysis, enzyme linked immunosorbent assay veterinary, incidence, avian immunology, Ontario epidemiology, swine, swine diseases epidemiology, swine diseases immunology.


NAL Call Number: SF601.J6

Abstract: As part of ongoing ecological studies and reproduction enhancement efforts for macaws in southwestern Peru, a health survey of parent- and hand-reared scarlet macaws (Ara macao) and blue and gold macaws (Ara ararauna) was conducted in 1994. Thirty-three birds were examined during handling procedures, and blood samples were collected from 27 (9 parent reared, 18 hand reared) for laboratory

NAL Call Number: SF601.J6

Abstract: As part of annual colony counts in Santa Cruz Province, Argentina, a health survey of rockhopper penguins (Eudyptes chrysocomes) was conducted in 1994. Forty-five birds were examined during handling procedures, and blood and fecal samples were collected for laboratory analysis. All birds appeared to be in good condition. No ecto- or endoparasites were found. Hematology, plasma chemistry, and plasma mineral levels were measured and correlated with the results of bacterial and viral serology. Antibodies against Chlamydia sp., avian adenovirus, avian encephalomyelitis virus, infectious bronchitis virus, avian reovirus, and paramyxovirus-1, -2, and -3 were found. Mean plasma chemistry and mineral values differed between individuals testing positive and negative on serologic tests. There was no serologic evidence of exposure to avian influenza virus, duck viral enteritis, infectious bursal disease, infectious laryngotracheitis, Aspergillus sp., or Salmonella pullorum. Trace amounts of endrin were found in the plasma of one bird, but all other chlorinated pesticide and polychlorinated biphenyl levels were below detectable limits.

Descriptors: infection, wildlife management, aspergillosis, fungal disease, avian encephalomyelitis, nervous system disease, viral disease, avian influenza, viral disease, chlamydiiosis, bacterial disease, duck viral enteritis, digestive system disease, viral disease, infectious bronchitis, respiratory system disease, viral disease, infectious bursal disease, viral disease, infectious laryngotracheitis, respiratory system disease, viral disease, bacterial serology, health evaluation, hematology, plasma chemistry, plasma mineral levels, viral serology.


NAL Call Number: 41.8 Av5

Abstract: Avian influenza outbreaks in Minnesota involving the H10N7 subtype occurred on two turkey farms in 1979 and on a third in 1980. The H10N7 (Hav2 Neq1) subtype had not previously been detected in turkeys in Minnesota or reported in the United States. The clinical signs ranged from severe, with a mortality rate as high as 31%, to subclinical. Antigenically indistinguishable viruses were isolated from healthy mallards on a pond adjacent to the turkey farms, suggesting that the virus responsible for the outbreak may have been introduced by feral ducks.

Descriptors: fowl plague epidemiology, turkeys, disease outbreaks, ducks, fowl plague etiology, fowl plague transmission, influenza A virus avian isolation and purification, Minnesota, time factors.


NAL Call Number: 41.8 Av5

Abstract: The potency and efficacy of an inactivated oil-emulsion influenza vaccine against infection,
illness, and virus shed was studied in market turkeys. No undesirable local or systemic reactions occurred following vaccination. The vaccine induced measurable antibody to nucleocapsid and hemagglutinin antigens of the virus. Challenged unvaccinated controls experienced airsacculitis, but none of the vaccinates were affected. The percent of the birds shedding virus following intranasal challenge was lower in the vaccinated groups than in the controls, and the quantity of virus shed was also smaller in vaccinated groups than in the controls.

Descriptors: antibodies, viral biosynthesis, fowl plague immunology, influenza A virus avian immunology, turkeys, viral vaccines immunology, antigens, viral immunology, capsid immunology, fowl plague prevention and control, hemagglutination inhibition tests veterinary, hemagglutinins viral immunology, immunodiffusion veterinary, vaccination veterinary, viral core proteins immunology.


NAL Call Number: 448.3 C33 (1)

Descriptors: influenza A virus avian growth and development, parrots microbiology, Psittacines microbiology, virus replication, hemagglutination inhibition tests, avian isolation and purification, organ specificity, respiratory system microbiology.


NAL Call Number: 448.8 V81

Abstract: Evidence is presented for a second major gene pool of influenza A viruses in nature. Shorebirds and gulls harbor influenza viruses when sampled in the spring and fall. Approximately half of the viruses isolated have the potential to infect ducks but the remainder do not. The hemagglutinin subtypes that are prevalent in wild ducks were rare or absent in shorebirds and gulls.

Descriptors: birds microbiology, ducks microbiology, fowl plague microbiology, genes viral, influenza A virus avian genetics, animals, wild microbiology, fowl plaque transmission, avian classification, avian isolation and purification, species specificity.


NAL Call Number: 448.8 V81

Abstract: The epidemiological features of the H5N2 outbreak of influenza in poultry were studied by sequencing the HA genes of several viruses isolated during the epidemic. Comparison of the nucleotide sequences of the HA genes indicated there was a single introduction of virulent virus. The variation rate (silent mutations) in the HA gene of the virulent Ck/Penn virus was 9.0 or 14.4% per 10 years depending on the viruses compared and was similar to that in H3 HA gene of human influenza A virus. The virulent and
Avirulent viruses isolated after October 1983 were derived from a common ancestral virus and the virulent virus did not supersede the avirulent virus, instead, the virulent and avirulent viruses coexisted and evolved separately during the course of the epidemic. The evolutionary changes in the HA of H5N2 viruses that occurred during the epidemic permitted us to establish that a virus (A/Chick/Washington/84) that was isolated 8 months after the last H5N2 virus had been isolated from poultry in Pennsylvania belonged to the family of potentially dangerous H5N2 viruses and was a direct descendent of the virus that spread to Maryland and Virginia. All of the virulent Ck/Penn viruses retained the amino acid changes at residues 13 and 69 in the HA.

Descriptors: fowl plague microbiology, hemagglutinins viral genetics, influenza A virus avian genetics, amino acid sequence, base sequence, disease outbreaks veterinary, District of Columbia, evolution, fowl plague epidemiology, genes viral, hemagglutinins viral analysis, avian isolation and purification, avian pathogenicity, Maryland, mutation, Pennsylvania, poultry, virulence.

NAL Call Number: RC111.R4
Abstract: Widespread outbreaks of avian influenza in domestic fowl throughout eastern Asia have reawakened concern that avian influenza viruses may again cross species barriers to infect the human population and thereby initiate a new influenza pandemic. Simultaneous infection of humans (or swine) by avian influenza viruses in the presence of human influenza viruses could theoretically generate novel influenza viruses with pandemic potential as a result of reassortment of genome subunits between avian and mammalian influenza viruses. These hybrid viruses would have the potential to express surface antigens from avian viruses to which the human population has no preexisting immunity. This article reviews current knowledge of the routes of transmission of avian influenza A viruses to humans, places the risk of appearance of a new pandemic influenza virus in perspective, and describes the recently observed epidemiology and clinical syndromes of avian influenza in humans.
Descriptors: influenza A virus, viral diseases, zoonoses, birds, human, avian influenza virus.

NAL Call Number: RA648.5.E46
Abstract: Influenza virus is not known to affect wild felids. We demonstrate that avian influenza A (H5N1) virus caused severe pneumonia in tigers and leopards that fed on infected poultry carcasses. This finding extends the host range of influenza virus and has implications for influenza virus epidemiology and wildlife conservation.
Descriptors: zoo animals virology, influenza veterinary, influenza A virus, avian pathogenicity, Panthera virology, chickens virology, food microbiology, influenza virology, avian genetics, lung virology, meat virology, phylogeny, tigers virology, variation genetics.

NAL Call Number: SF995.W4
Descriptors: disease surveys, water microbiology, epizootiology, monitoring, turkeys, sentinel birds, avian influenza virus.

NAL Call Number: QR360.A1J6
Descriptors: antiviral agents pharmacology, camptothecin pharmacology, influenza A virus avian growth and development, virus replication drug effects, antigens, viral analysis, autoradiography, cell line, dose response relationship, drug, hamsters, hemagglutination inhibition tests, hemagglutinins viral analysis, avian

Abstract: In February 2003, the highly pathogenic avian influenza-A virus, subtype H7N7, was the causative agent of a large outbreak of fowl plague in the Netherlands. Two days after visiting a poultry farm that was infected by fowl plague, a 57-year-old male veterinarian developed malaise, headache and fever. After 8 days he was admitted to hospital with signs of pneumonia. Five days later, his condition deteriorated alarmingly. Despite extensive pharmacotherapy he died 4 days later of acute pneumonia. Influenza-A virus, subtype H7N7, was identified by means of reverse transcriptase/PCR in broncho-alveolar washings that had been obtained earlier; routine virus culture yielded the isolate A/Nederland/219/03, which differs by 14 amino-acid substitutions from the first isolate in a chicken (A/kip/Nederland/1/03). Partly as a result of this case, the preventive measures were then adjusted; people who came into contact with infected poultry were given increased possibilities for vaccination and the administration of oseltamivir.


NAL Call Number: QR360.A1J6

Descriptors: antigens analysis, influenza A virus avian classification, turkeys, antigens, viral analysis, chickens, cross reactions, England, epitopes, hemagglutination inhibition tests, hemagglutinins viral analysis, immune sera, avian enzymology, avian immunology, avian isolation and purification, neuraminidase analysis, serotyping.


NAL Call Number: SF604.V473

Descriptors: avian influenza virus, epidemiology, pathogenicity, biological differences, ELISA, immunofluorescence, biological properties, immunoenzyme techniques, immunological techniques, influenza virus, microbial properties, viruses.


Abstract: Recent outbreaks of highly pathogenic avian influenza in chickens and ducks that occurred in 9 Asian countries including Japan alarmed to realize that there is no border for infections and gave a rise to great concern for human health as well as for agriculture. This H5N1 virus jumped the species barrier and caused severe disease with high mortality in humans in Viet Nam and Thailand; 15 deaths of 22 cases and 8 of 12, respectively. A second concern was the possibility that the situation could give rise to another influenza pandemic in humans since genetic reassortment may occur between avian and human influenza viruses when a person is concurrently infected with viruses from both species. This process of gene swapping inside the human body can give rise to a new subtype of the influenza virus to which humans would not have immunity. The outbreaks also emphasized the need to continue active surveillance on avian influenza throughout the year to undertake aggressive emergency control measures as soon as an infection is detected.

Descriptors: influenza A virus, avian genetics, avian pathogenicity, Asia epidemiology, disease outbreaks, Europe epidemiology, influenza epidemiology, influenza virology, avian influenza epidemiology, avian
Descriptors: influenza A virus avian pathogenicity, animals, domestic microbiology, animals, wild microbiology, birds microbiology, fowl plague microbiology, fowl plague transmission, hemagglutinins viral immunology, avian genetics, avian immunology.

Abstract: Ecological studies on influenza viruses revealed that the hemagglutinin genes are introduced into new pandemic strains from viruses circulating in migratory ducks through domestic ducks and pigs in southern China. Experimental infection of pigs with 38 avian influenza virus strains with H1-H13 hemagglutinins showed that at least one strain of each HA subtype replicated in the upper respiratory tract of pigs. Co-infection of pigs with a swine virus and with an avian virus generated reassortant viruses. The results indicate that avian viruses of any subtype can contribute genes in the generation of reassortants. Virological surveillance revealed that influenza viruses in waterfowl reservoir are perpetuated year-by-year in the frozen lake water while ducks are absent.
Descriptors: influenza veterinary, bird diseases transmission, birds, horse diseases transmission, horses, influenza transmission, swine, swine diseases transmission, zoonoses.

NAL Call Number: 448.8 V81
Abstract: Influenza viruses of the H3N2 subtype similar to Aichi/2/68 and Victoria/3/75 persist in pigs many years after their antigenic counterparts have disappeared from humans (Shortridge et al. (1977). Science 19, 1454-1455). To provide information on the mechanism of conservation of these influenza viruses in pigs, the hemagglutinin (HA) of four isolates from swine derived from Taiwan and Southern China were analyzed antigenically and genetically. The reactivity pattern of these viruses with a panel of monoclonal antibodies indicates that the HAs of these swine viruses were antigenically closely related to duck H3 and early human H3 viruses. Sequence analysis of the H3 genes from three swine viruses revealed that the swine H3 genes are more closely related to the duck genes than to early human H3 virus (A/Aichi/2/68). The degree of sequence homology of these genes is extremely high (more than 96.5%). Furthermore, the deduced amino acid sequence of the three swine HAs at residues 226 to 228 in the proposed receptor-binding site is Gln-Ser-Gly and is common with the majority of avian influenza viruses. These findings indicate that these H3 viruses may have been introduced into pigs from ducks. The HA gene of the fourth swine influenza virus from Southern China was genetically equally related to avian and early human H3 strains although the sequence through the receptor-binding pocket (226-228) was typical of a human H3 virus, suggesting that either this swine HA gene was derived from ducks or an early human H3 virus was introduced into the pig population where the virus accumulated substantial mutations. The present strains revealed genetic heterogeneity of swine H3 influenza viruses in nature.
Descriptors: hemagglutinins viral genetics, influenza A virus, porcine genetics, influenza A virus genetics, amino acid sequence, antibodies, monoclonal diagnostic use, base sequence, China, genes viral, avian genetics, porcine immunology, molecular sequence data, sequence homology, nucleic acid.

NAL Call Number: QR1.I57
Abstract: Influenza viruses A/duck/Hokkaido/5/77 (Hav7N2), A/budgerigar/Hokkaido/1/77 (Hav4Nav1), A/Kumamoto/22/76 (H3N2), A/Aichi/2/68 (H3N2), and A/New Jersey/8/76 (Hsw1N1) were experimentally inoculated into Pekin ducks. Of these, the influenza viruses of duck and budgerigar origin replicated in the intestinal tract of the ducks. The infected ducks shed the virus in the feces to high titers, but did not show clinical signs of disease and scarcely produced detectable serum antibodies. Using immunofluorescent staining, we demonstrated that the target cells of the duck virus in ducks were the simple columnar epithelial cells which form crypts in the large intestines, especially in the colon. After primary infection, the birds...
resisted reinfection with the duck virus at least for 28 days, but from 46 days onward they were susceptible to reinfection. These infections were quickly restricted by a brisk secondary immune response, reflected in the rapid appearance of high titers of antibody after reinoculation. In contrast to the avian influenza viruses, the remaining three influenza viruses of human origin did not replicate in the intestinal tract but did cause a serum antibody response.

**Descriptors:** ducks microbiology, influenza veterinary, influenza A virus avian growth and development, antibody formation, digestive system microbiology, feces microbiology, influenza immunology, human growth and development, parakeets microbiology, virus replication.

**Descriptors:** acquired immune deficiency syndrome, disease transmission, human immunodeficiency virus infections, international trade, travel, avian influenza virus.

**NAL Call Number:** 41.8 R312  
**Abstract:** Experimental infection of domestic fowl, ducks and geese with an influenza A virus (H7N2) isolated from a domestic duck showed that this virus was apathogenic for these poultry. A second virus (H6N2), also apathogenic and more 'non-avid' than any such isolates previously recognised in surveillance of domestic poultry in Hong Kong, was isolated from one goose after H7N2 shedding had ceased. This goose, in effect, acted as a selective isolation system for the H6N2 virus whose presence in the field isolate could not be detected in spite of multiple passage in embryonated eggs.  
**Descriptors:** chickens microbiology, ducks microbiology, fowl plague microbiology, geese microbiology, influenza A virus avian pathogenicity, poultry diseases microbiology.

**NAL Call Number:** SF602.M8  
**Descriptors:** Newcastle disease, avian influenza, classical swine fever, foot and mouth disease, vaccination, clinical techniques, slaughtered, transmission, outbreaks.

**NAL Call Number:** 448.8 N442  
**Descriptors:** disease outbreaks history, influenza transmission, severe acute respiratory syndrome transmission, zoonoses transmission, fowl plague transmission, history of medicine, 20th century, influenza epidemiology, influenza history, influenza A virus avian, poultry, severe acute respiratory syndrome epidemiology.

**NAL Call Number:** 41.8 Av5  
**Descriptors:** orthomyxoviridae infections epidemiology, orthomyxoviridae infections veterinary, poultry diseases epidemiology, agglutination tests, breeding, complement fixation tests, eggs, fertility, hemagglutination inhibition tests, Minnesota, mycoplasma, neutralization tests, ornithosis veterinary, orthomyxoviridae isolation and purification, turkeys.

**Descriptors:** disease transmission, epidemiology, outbreaks, pathology, reviews, avian influenza virus, ostriches.

Abstract: Nine type A influenza viruses were isolated from migrating and wintering ducks in Oklahoma in 1976-77. Antigenic classification of the viruses isolated revealed three different subtypes: Hav1 Nav2, Hws N1, and Hav6 N2. Transmission of influenza viruses from the wild ducks to sentinel birds (McGraw mallards) on the same lakes was not detected.

Descriptors: ducks microbiology, influenza A virus avian isolation and purification, antigens, viral analysis, avian immunology, Oklahoma.


Descriptors: avian influenza A virus, transmission, humans, outbreak, poultry farms, sub type H7N7.


Descriptors: zoonoses, influenza, wild birds, chickens, Ukraine.


Abstract: PURPOSE OF REVIEW: New emerging infections over the last few years demonstrate the potential for the introduction of epidemic illness through global migration. The increasing number of children adopted internationally (>20,000 in 2003, from the United States State Department) provides a unique situation for the spread of emerging infections through the combination of international travel by parents through areas where such infections may be contracted and the nature of the living conditions for many of the orphans being placed by this process. RECENT FINDINGS: The recent literature on three emerging infections--avian influenza, severe acute respiratory syndrome (SARS) and measles--describes clinical aspects of the illnesses and their epidemiology. For avian influenza aspects of the agrarian economy in southeast Asia enabled the virus to reach the human population. The potential for further adaptation to people could set the stage for a new pandemic. SARS evolved in rural China and spread worldwide in one season with an approximate 10% mortality. Attention to public-health measures led to control of this new illness. Most recently, outbreaks of measles in Chinese orphanages have been documented. These findings demonstrate the potential of such infections to be transmitted during the process of international adoption, and in the case of measles the realization of this potential in recent reported cases from Chinese orphanages brought to the United States on commercial airlines. SUMMARY: Clinicians involved in international adoption and public-health officials assessing emerging infections need to work together in monitoring these issues.

Descriptors: adoption, communicable diseases, emerging epidemiology, emigration and immigration, severe acute respiratory syndrome epidemiology, adolescent, adult, child, preschool child, communicable disease control, communicable diseases, emerging transmission, infant, influenza epidemiology, influenza transmission, influenza A virus, avian, SARS virus, severe acute respiratory syndrome transmission.


Abstract: Throughout Eastern Asia, there is currently an epidemic of fowl plague or highly pathogenic avian influenza, on an unprecedented scale. The prospects for rapid containment are poor. The causative virus, influenza A of the H5N1 subtype, is of limited infectivity for humans. If infection occurs, however, then the consequences are serious and even fatal in a majority of cases. In view of the receptor specificity of avian influenza viruses, this may be related to individually increased susceptibility, which does not lead to further spread. However, it is known that influenza A viruses can readily adapt to replication in the human host by the acquisition of specific gene segments or even by mutations of the avian virus. The extreme scale of human contact with influenza virus of the H5N1 subtype at present engenders fear that there is a high risk of such adaptation and a subsequent pandemic spread. Adequate precautions are necessary, not only in terms of an acceleration of vaccine production but primarily in arranging for sufficient availability of the new antiviral drugs.

Descriptors: disease outbreaks, influenza A virus, avian pathogenicity, human pathogenicity, avian influenza transmission, zoonoses, chickens, avian genetics, human genetics.


NAL Call Number: SF994.2.A1K76 1978

Descriptors: protozoal infections, aviary birds, helminths, symptoms, control, management.

**NAL Call Number:** 448.8 P942

**Abstract:** Recombination of a human influenza virus with an avian influenza virus produced a H2Nav2 recombinant with the antigenic properties analogous to those of avian influenza virus (H2Nav2) isolated from wild ducks in the Far East, USSR. Recombination of two avian influenza viruses yielded a recombinant H2N2, an antigenic analogues of influenza A/Singapore/1/57 (H2N2) virus which had started an epidemic of influenza in 1957.

**Descriptors:** antigens, viral genetics, influenza A virus genetics, recombination, genetic, animals, wild, crosses, genetic, ducks microbiology, hemagglutination inhibition tests, influenza A virus human genetics, neuraminidase antagonists and inhibitors.


**NAL Call Number:** 448.8 P942

**Abstract:** Three influenza A virus strains were isolated from shorebirds in October, 1977, in southern Turkmenia, in the vicinities of Tedzhen water reservoir. From a common tern, *A/Sterna hirundo*/Turkmenia/45/77 strain was isolated with the antigenic formula Hav6Neq2, from a teal and a black-headed gull influenza A/Anas crecca/Turkmenia/4/77 and A/Larus ridibundus/Turkmenia/13/77 strains with previously unknown combination of surface antigens Hsw(H0)Nav2 were recovered. By the molecular weight of the heavy (HA1 59,000 d) and light (HA2 24,000 d) chains of hemagglutinin, the Turkmenian viruses A/Larus ridibundus/Turkmenia/13/77 and A/Anas crecca/Turkmenia/4/77 are similar to each other and to the strains having H0 hemagglutinin: A/PR8/34 (H0N1) and A/Whale/PO/19/76 (H0Nav2). The Turkmenian viruses are characterized by a low content of the light hemagglutinin chain (HA2) which is typical of the viruses with Hsw1 hemagglutinin: A/New Jersey/8/76 (Hsw1N1) and A/SW/Wisk/68 (Hsw1N1).

**Descriptors:** birds microbiology, influenza A virus avian isolation and purification, antigens, viral isolation and purification, chick embryo, avian classification, serotyping, Turkmenistan, viral proteins analysis.


**NAL Call Number:** 448.8 P942

**Abstract:** Influenza virus A (H5N1) was isolated from the tracheal swab of a 3-year-old boy who died from influenza with the Raye syndrome in Hong Kong in May, 1997. Up to the present time, influenza viruses with hemagglutinin H5 were known to circulate only among birds. They caused a variety of diseases: from asymptomatic to epizootic with 100% mortality, particularly among chickens. The main difference between virulent and avirulent strains is as follows: virulent viruses are isolated from all tissues of an infected bird. A (H5) virus hemagglutinin, transformed into a virulent variant, becomes sensitive to cleavage by proteases of mammalian and avian cells. Intensive epidemiological surveillance of influenza in Hong Kong started by the WHO and Department of Public Health of Hong Kong in August-September, 1997, resulted in detection of 17 more cases with Influenza A (H5N1) in November-December 1997. all of the occurred before December 28, 1997 and were detected in hospitals and health centers of Hong Kong. Nine patients were children aged under 5 years. Six patients died as a result of complications (pneumonia) and exacerbations of concomitantly chronic diseases. Virological and logical studies showed that the main route of infection transmission was from birds to humans. Human to human transmission is probable. Study of 7 influenza A (H5N1) viruses isolated from patients showed that they contained all 8 RNA gene segments of avian virus. There are no reports about new cases of influenza A (H5N1) in humans in January 1998, and we can hope that the outbreak of Influenza A (H5N1) in Hong Kong caused by avian virus will not develop into a new influenza pandemic, although an unfavorable course of events is probable.

**Descriptors:** influenza virology, influenza A virus avian pathogenicity, chickens virology, Hong Kong
epidemiology, influenza epidemiology, influenza physiopathology, avian genetics, RNA, viral, virulence.


**NAL Call Number:** 47.8 P95

**Descriptors:** avian influenza virus, strains, diagnosis, control, vaccination.


**Abstract:** Aquatic birds are the natural hosts for influenza virus. It is established that avian influenza viruses provide the gene pool for the generation of new strains of human influenza virus, which can cause pandemic infections. The recent outbreak of an avian influenza virus (H5N1) in Hong Kong not only produced high mortality in chickens, but also resulted in six human fatalities. This outbreak indicates that avian influenza virus can be pathogenic for humans. We surveyed local waterfowl habitats by taking water and fecal samples for virus isolation and identification. We isolated avian influenza viruses from ponds and small lakes in Bartlesville, Lawton, Stillwater, and Tulsa. The density of birds in these sites is small. However, our virus isolation rate is comparable to that found in higher density habitats. The risk of human infection remains to be determined. We encourage primary care physicians to submit samples for virus surveillance.

**Descriptors:** birds virology, influenza A virus avian isolation and purification, influenza transmission, Oklahoma.


**NAL Call Number:** 41.8 T431

**Descriptors:** antibodies, viral blood, chickens, fowl plague epidemiology, influenza A virus avian pathogenicity, chick embryo, avian immunology, Netherlands epidemiology.


**NAL Call Number:** 41.8 T431

**Descriptors:** antibodies, viral blood, chickens, enzyme linked immunosorbent assay veterinary, fowl plague epidemiology, influenza A virus avian immunology, abattoirs, antibodies, viral immunology, chick embryo, enzyme linked immunosorbent assay methods, avian isolation and purification, Netherlands epidemiology.


**NAL Call Number:** aSF995.6.I6I5 1981a

**Descriptors:** avian influenza virus, disease control, international trade, responsibility.


**NAL Call Number:** 41.8 T431

**Descriptors:** fowl plague virology, influenza A virus avian isolation and purification, fowl plague epidemiology, fowl plague prevention and control, Netherlands epidemiology, poultry.


**NAL Call Number:** 41.8 T431

**Descriptors:** poultry, influenza virus, domestic animals, livestock, orthomyxoviridae, useful animals, viruses.

**NAL Call Number:** 41.8 T431

**Descriptors:** epidemiology, infection, pathology, veterinary medicine, avian influenza, avian influenza virus type A, epidemiology, host, infection, treatment, viral disease, zoo animal.


**NAL Call Number:** 41.8 T431

**Descriptors:** avian influenza, diagnosis, mortality, transmission, eradication, airborne transmission, outbreak rate, poultry farming, poultry industry.

Lang, G., A. Gagnon, and J.R. Geraci (1981). **Isolation of an influenza A virus from seals.** *Archives of Virology* 68(3-4): 189-95. ISSN: 0304-8608.

**NAL Call Number:** 448.3 Ar23

**Abstract:** Influenza A virus of serotype Hav1 Neq1 (H7N7 by the 1980 revised influenza typing system proposed by WHO experts) was repeatedly isolated from lung and brain tissues taken from harbor seals (*Phoca vitulina*) found suffering from pneumonia on Cape Cod Peninsula (U.S.A.) in the winter of 1979-1980. The seal isolates, although of a serotype identical to some fowl plaque virus strains, were harmless to chickens and turkeys in transmission experiments. An earlier human infection by a Hav1 Neq1 influenza virus and the serologic relatedness of this avian serotype with the equine 1 serotype are cited in support of the view that influenza viruses with these antigenic characteristics seem to have a facility to pass from birds to mammals.

**Descriptors:** influenza microbiology, influenza A virus avian isolation and purification, Pinnipedia microbiology, pneumonia, viral microbiology, seals microbiology, antigens, viral immunology, brain microbiology, epitopes, avian immunology, lung microbiology.


**NAL Call Number:** 41.8 R3224

**Descriptors:** ducks, influenza A virus avian isolation and purification, turkeys, Canada, fowl plague epidemiology, fowl plague microbiology, avian classification.


**NAL Call Number:** 280.8 T48

**Descriptors:** diagnosis, zoonoses, strains, disease transmission, outbreaks, avian influenza virus, Hong Kong.


**Abstract:** We live in an ever more connected global village linked through international travel, politics, economics, culture and human-human and human-animal interactions. The realization that the concept of globalization includes global exposure to disease-causing agents that were formerly confined to small, remote areas and that infectious disease outbreaks can have political, economic and social roots and effects is becoming more apparent. Novel infectious disease microbes continue to be discovered because they are new or newly recognized, have expanded their geographic range, have been shown to cause a new disease spectrum, have jumped the species barrier from animals to humans, have become resistant to antimicrobial agents, have increased in incidence or have become more virulent. These emerging infectious disease microbes may have the potential for use as agents of bioterrorism. Factors involved in the emergence of infectious diseases are complex and interrelated and involve all classifications of organisms transmitted in a variety of ways. In 2003, outbreaks of interest included severe acute respiratory syndrome, monkeypox and avian influenza. Information from the human genome project applied to microbial organisms and their hosts
will provide new opportunities for detection, diagnosis, treatment, prevention, control and prognosis. New technology related not only to genetics but also to satellite and monitoring systems will play a role in weather, climate and the approach to environmental manipulations that influence factors contributing to infectious disease emergence and control. Approaches to combating emerging infectious diseases include many disciplines, such as animal studies, epidemiology, immunology, ecology, environmental studies, microbiology, pharmacology, other sciences, health, medicine, public health, nursing, cultural, political and social studies, all of which must work together. Appropriate financial support of the public health infrastructure including surveillance, prevention, communication, adherence techniques and the like will be needed to support efforts to address emerging infectious disease threats.

Descriptors: communicable diseases, emerging economics, prevention and control, emerging transmission, climate, demography, disease susceptibility, disease transmission prevention and control, industry, politics, social conditions, economics, technology, travel, weather.


NAL Call Number: 41.9 W64B

Abstract: An avian influenza virus isolate, A/Mallard/Ohio/184/86 (H5N1), was evaluated for its effects on reproduction in isolation-reared adult mallard ducks (*Anas platyrhynchos*) and growth rate in juvenile mallards after intravenous inoculation. There was a significant decrease in egg production in the experimental group during the first week after inoculation, but it returned to the normal production level during the second week. No effect was seen on egg weight, shape, or fertility. Ducklings receiving this influenza virus isolate did not differ from controls in their rate of growth.

Descriptors: body weight, ducks physiology, fowl plague physiopathology, influenza A virus avian pathogenicity, reproduction, antibodies, viral blood, ducks growth and development, fertility, influenza A virus avian immunology, oviposition, random allocation.


NAL Call Number: QR180.M53

Abstract: A "new" influenza virus will appear at some time in the future. This virus will arise by natural processes, which we do not fully understand, or it might be created by some bioterrorist. The world's population will have no immunity to the new virus, which will spread like wild-fire, causing much misery, economic disruption and many deaths. Vaccines will take time to develop and the only means of control, at least in the early stages of the epidemic, are anti-viral drugs, of which the neuraminidase inhibitors currently seem the most effective.

Descriptors: disease outbreaks prevention and control, influenza epidemiology, influenza prevention and control, antiviral agents therapeutic use, birds, chickens, China epidemiology, drug resistance, viral, influenza drug therapy, influenza virology, influenza A virus avian classification, avian physiology, models, molecular, neuraminidase physiology, orthomyxoviridae genetics, orthomyxoviridae immunology.


NAL Call Number: 470 Sci2

Descriptors: chickens virology, influenza epidemiology, influenza prevention and control, influenza A virus enzymology, influenza A virus pathogenicity, antiviral agents therapeutic use, drug industry methods, drug resistance, microbial, enzyme inhibitors therapeutic use, hn protein chemistry, hn protein genetics, hn protein metabolism, Hong Kong epidemiology, influenza diagnosis, influenza drug therapy, influenza A virus avian enzymology, avian genetics, avian immunology, avian pathogenicity, human enzymology, human genetics, human immunology, human pathogenicity, influenza A virus genetics, influenza A virus immunology, influenza vaccine biosynthesis, influenza vaccine economics, influenza vaccine immunology, models, molecular, mutation genetics, neuraminidase antagonists and inhibitors, neuraminidase chemistry, neuraminidase genetics, neuraminidase metabolism, protein conformation, RNA viral analysis, viral genetics, reassortant viruses enzymology, reassortant viruses genetics, reassortant viruses immunology,
reassortant viruses pathogenicity, sialic acids therapeutic use.

NAL Call Number: 442.8 P43
Descriptors: infection, prevention and control, sea birds, drug development.

NAL Call Number: 448.8 J821
Abstract: Influenza type A virus periodically undergoes major antigenic shifts in which the hemagglutinin (HAG) and sometimes the neuraminidase (NA) antigens are replaced by HAG and NA antigens of another subtype. Three such shifts have taken place since the virus was first isolated, and all appear to have occurred in China. The way in which these "new" influenza type A viruses suddenly appear (or reappear) in the human population is not known. At a meeting held in Beijing, China, on November 10-12, 1982, participants discussed the latest findings on the molecular biology of influenza viruses and on aspects of their ecology that may offer insight into the factors responsible for the origin of pandemic influenza viruses. Information obtained in earlier studies has provided some clues about how the antigenic shifts may occur. For example, the H3N2 virus has been found to be a recombinant deriving seven of its eight genes from an H2N2 strain and gene 4 (which encodes for the HAG) from some other virus, possibly an avian influenza virus of the H3 subtype [1-3]. In addition, studies of the genome of the H1N1 virus that appeared in Anshan, China, in 1977 have shown that this virus almost certainly underwent no replication for 27 years. This finding suggests that the virus existed in an animal reservoir during this period [4, 5].
Descriptors: influenza microbiology, influenza A virus human physiology, orthomyxoviridae physiology, antigens, viral immunology, China, disease reservoirs, ecology, epitopes immunology, genes viral, hemagglutins viral immunology, influenza therapy, human genetics, influenza A virus physiology, influenza vaccine immunology, macromolecular systems, neuraminidase genetics, neuraminidase immunology, orthomyxoviridae genetics, orthomyxoviridae immunology, recombination, genetic, T lymphocytes, cytotoxic immunology, virus replication.

NAL Call Number: 41.8 Au72
Descriptors: animal welfare, chickens, avian influenza, epidemiology, cats, China epidemiology, dogs, influenza A virus, Korea.

NAL Call Number: 449.9 W892B

NAL Call Number: 47.8 So89


**Abstract:** SARS and avian influenza have many common features. They both arose in Asia and originated from animal viruses. They both have the potential to become pandemics because human beings lack antibodies to the animal-derived antigens present on the viral surface and rapid dissemination can occur from the relative ease and availability of high speed and far-reaching transportation methods. Pediatricians, in particular, should remain alert about the possibility of pandemic illnesses in their patients. Annual rates of influenza in children may be 1.5 to 3 times those in the adult population, and infection rates during a community epidemic may exceed 40% in preschool-aged children and 30% in school-aged children. Infected children also play a central role in disseminating influenza, as they are the major point of entry for the virus into the household, from which adults spread disease into the community. Of course, children younger than 24 months also are at high risk for complications from influenza. A 1999 Centers for Disease Control and Prevention projection of an influenza pandemic in the US paints a grim picture: 89,000 to 207,000 deaths, 314,000 to 734,000 hospitalizations, 18 million to 42 million outpatient visits, and 20 million to 47 million additional illnesses, at a cost to society of at least dollars 71.3 billion to dollars 166.5 billion. High-risk patients (15% of the population) would account for approximately 84% of all deaths. Although SARS has been kind to the pediatric population so far, there are no guarantees that future outbreaks would be as sparing. To aid readers in remaining up-to-date with SARS and avian influenza, some useful websites are listed in the Sidebar. Two masters of suspense, Alfred Hitchcock and Stephen King, may have been closer to the truth than they ever would have believed. Both birds and a super flu could bring about the end of civilization as we know it. But all is not lost—to paraphrase Thomas Jefferson, the price of health is eternal vigilance. Although we may not be able to prevent future pandemics, mankind has the ability to recognize new diseases and outbreaks as they occur, to study these infections and find ways to contain and treat them, and to implement the necessary measures to defeat them.

**Descriptors:** avian influenza prevention and control, severe acute respiratory syndrome prevention and control, adult, child, antiviral agents therapeutic use, disease outbreaks prevention and control, disease vectors, avian influenza diagnosis, avian influenza epidemiology, avian influenza transmission, pediatrics methods, population surveillance methods, severe acute respiratory syndrome diagnosis, severe acute respiratory syndrome epidemiology, severe acute respiratory syndrome transmission, world health, SARS.

**NAL Call Number:** 41.8 Av5

**Abstract:** Serum samples from 163 slaughter-age ostriches (*Struthio camelus*) in Ohio and Indiana were tested for antibodies to avian influenza virus (AIV), Newcastle disease virus (NDV), paramyxovirus (PMV) 2, PMV3, PMV7, infectious bursal disease virus (IBDV), *Bordetella avium, Mycoplasma synoviae, Mycoplasma gallisepticum, Ornithobacterium rhinotracheale, Salmonella pullorum, Salmonella gallinarum, and Salmonella typhimurium*. One ostrich had antibodies to AIV H5N9. 57% of the ostriches had antibodies to NDV, four ostriches had antibodies to both NDV and PMV2, and one ostrich had antibodies to NDV, PMV2, PMV3, and PMV7. None of the ostriches had antibodies to IBDV, *B. avium, M. synoviae, M. gallisepticum, O. rhinotracheale, S. pullorum, S. gallinarum, and S. typhimurium*. This is the first report of antibodies to avian influenza and PMV7 in ostriches in the United States.

**Descriptors:** antibodies, bacterial analysis, antibodies, viral analysis, ostriches immunology, aging, bird diseases immunology, bird diseases microbiology, bird diseases virology, Indiana, Ohio, ostriches microbiology, ostriches virology, seroepidemiologic studies.


**NAL Call Number:** RA648.5.E46

**Abstract:** To establish whether human-to-human transmission of influenza A H5N1 occurred in the healthcare setting in Vietnam, we conducted a cross-sectional seroprevalence survey among hospital employees exposed to 4 confirmed and 1 probable H5N1 case-patients or their clinical specimens. Eighty-three (95.4%) of 87 eligible employees completed a questionnaire and provided a serum sample, which was tested for antibodies to influenza A H5N1. Ninety-five percent reported exposure to >1 H5N1 case-patients; 59 (72.0%) reported symptoms, and 2 (2.4%) fulfilled the definition for a possible H5N1 secondary case-patient. No study participants had detectable antibodies to influenza A H5N1. The data suggest that the H5N1 viruses responsible for human cases in Vietnam in January 2004 are not readily transmitted from person to person. However, influenza viruses are genetically variable, and transmissibility is difficult to predict. Therefore, persons providing care for H5N1 patients should continue to take measures to protect themselves.

**Descriptors:** patient to professional disease transmission, health personnel, influenza transmission, avian influenza A virus growth and development, Western blotting, child, preschool child, adolescent, adult, viral blood antibodies, cross sectional studies, influenza immunology, influenza virology, avian influenza A virus immunology, middle-aged, neutralization tests, questionnaires, seroepidemiologic studies, Vietnam epidemiology.


**Descriptors:** influenza, avian influenza diagnosis, avian influenza drug therapy, acetamides therapeutic use, antiviral agents therapeutic use, birds virology, avian influenza A virus drug effects, avian influenza virology, sialic acids therapeutic use.


**Descriptors:** influenza, avian epidemiology, influenza, avian transmission.

Avian influenza A virus with H2 hemagglutinin has been adapted to mice for the first time. Alterations in the hemagglutinin of adapted variants of the virus as a result of adaptation to a new host are described. Hemagglutinin of a highly virulent adapted variant differed from the parental avirulent strain by antigenic structure, electrophoretic mobility, and receptor activity during interactions with murine red cells.

Descriptors: adaptation, physiological, hemagglutinins viral metabolism, influenza A virus avian physiology, cultured cells, chick embryo, dogs, erythrocytes virology, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral chemistry, avian metabolism, avian pathogenicity, lethal dose 50, mice.


**NAL Call Number**: QH434.V57

**Abstract**: H2 influenza virus caused a pandemic in 1957 and has the possibility to cause outbreaks in the future. To assess the evolutionary characteristics of H2 influenza viruses isolated from migratory ducks that congregate in Hokkaido, Japan, on their flyway of migration from Siberia in 2001, we investigated the phylogenetic relationships among these viruses and avian and human viruses described previously.

Phylogenetic analysis showed that the PB2 gene of Dk/Hokkaido/107/01 (H2N3) and the PA gene of Dk/Hokkaido/95/01 (H2N2) belonged to the American lineage of avian virus and that the other genes of the isolates belonged to the Eurasian lineage. These results indicate that the internal protein genes might be transmitted from American to Eurasian avian host. Thus, it is further confirmed that interregional transmission of influenza viruses occurred between the North American and Eurasian birds. The fact that reassortants could be generated in the migratory ducks between North American and Eurasian avian virus lineage further stresses the importance of global surveillance among the migratory ducks.

**Descriptors**: ducks virology, emigration and immigration, influenza A virus, avian genetics, influenza, avian virology, viral proteins genetics, Asia, Europe, avian influenza A virus classification, molecular sequence data, North America, phylogeny, sequence analysis, DNA.


**NAL Call Number**: QH434.V57

**Abstract**: Genetic analysis indicated that the pandemic influenza strains derived from wild aquatic birds harbor viruses of 15 hemagglutinin (HA) and 9 neuraminidase (NA) antigenic subtypes. Surveillance studies have shown that H9N2 subtype viruses are worldwide in domestic poultry and could infect mammalian species, including humans. Here, we genetically analyzed the HA and NA genes of five H9N2 viruses isolated from the migratory ducks in Hokkaido, Japan, the flyway of migration from Siberia during 1997-2000. The results showed that HA and NA genes of these viruses belong to the same lineages, respectively. Compared with those of A/quail/Hong Kong/G1/97-like and A/duck/Hong Kong/Y280/97-like viruses, HA and NA of the migratory duck isolates had a close relationship with those of H9N2 viruses isolated from the chicken in Korea, indicating that the Korea H9N2 viruses might be derived from the migratory ducks. The NA genes of the five isolates were located in the same cluster as those of N2 viruses, which had caused a human pandemic in 1968, indicating that the NA genes of the previous pandemic strains are still circulating in waterfowl reservoirs. The present results further emphasize the importance of carrying out molecular epidemiological surveillance of H9N2 viruses in wild ducks to obtain more information for the future human influenza pandemics preparedness.

**Descriptors**: ducks virology, influenza A virus avian genetics, amino acid sequence, base sequence, binding sites genetics, DNA, viral genetics, disease reservoirs, epidemiology, molecular, genes viral, hemagglutinins viral genetics, avian enzymology, avian immunology, avian isolation and purification, Japan, neuraminidase genetics, phylogeny.


**Descriptors**: disaster planning, disease outbreaks, health facilities, severe acute respiratory syndrome prevention and control, severe acute respiratory syndrome therapy, cross infection, avian influenza prevention and control, avian influenza therapy, organizational policy, patient isolation, severe acute respiratory syndrome epidemiology.
The redox properties of some myxoviruses [Fowl plaque virus strain Rostock (FPV), New Castle Disease virus strain Italy (NDV), B/Hong Kong, A/Port Chalmers, A/Victoria, A/Scotland, and A/Fort Del] and electron microscopic studies as well as by the determination of the hemagglutination (HA) titer (antigen efficiency). The results have shown that viruses decrease the spin concentration of Cu2+ by acting as a reducing species (electron donor) which will result in the inactivation (oxidation) of the virus. Addition of an oxidizing substance, such as H2O2, to a virus suspension also leads to an oxidation of the viruses, and, thus, to their inability to reduce Cu2+. This result is confirmed by the decrease of the HA titer of viruses with increasing Cu2+ concentrations. H2O2 could not be applied for the HA titer test since it interacts with the erythrocytes of the chicken blood used for this determination. Therefore, another oxidizing substance (oxidized glutathione, GSS) was selected which exhibited a slightly less pronounced effect than Cu2+. Since reduced glutathione (GSH) exerts a similar but less pronounced effect than GSS, it might be concluded that viruses have a redox system of their own and act as reducing or oxidizing substance depending on the biological receptor system. Electron microscopic studies confirm this hypothesis. As can be seen by the electron micrographs, increasing concentrations of either Cu2+, GSS, H2O2, KMnO4, or GSH will, finally, result in a complete destruction of the virus. Because of structural similarities it might be assumed that other types of viruses behave very similarly.

Descriptors: influenza A virus metabolism, Newcastle disease virus metabolism, copper, electron spin resonance spectroscopy, glutathione, hemagglutination, viral, avian metabolism, avian ultrastructure, human metabolism, human ultrastructure, Newcastle disease virus ultrastructure, oxidation reduction, peroxides, potassium permanganate, time factors.


Descriptors: disease prevalence, epidemiology, evolution, pathogenicity, Newcastle disease, avian influenza virus.


Descriptors: broiler chickens, pathogenicity, avian influenza virus, biological properties, birds, chickens, domestic animals, domesticated birds, Galliformes, influenza virus, livestock, meat animals, microbial properties, orthomyxoviridae, poultry, useful animals, viruses.


Descriptors: infection, viral clearance, viral infectivity, viral survival.


Makarova, K.S., Y.U.I. Wulf, E.P. Tereza, and V.A. Ratner (1998). Razlichie rezhimov molekuliarnoi evoliutsii virusov grippa A v populiatsiiakh ptits i cheloveka. [Different patterns of molecular evolution of influenza A viruses in avian and human population]. Genetika 34(7): 890-6. ISSN: 0016-6758. NAL Call Number: QH431.A1G4 Abstract: Patterns of molecular evolution of the influenza virus proteins and genes are discussed. The subsets of all viral genes corresponding to statistically significant clusters on dendrogram were shown to fall into two distinct groups. The first group was characterized by the presence of an exact linear relationship between the year of the strain isolation and the evolutionary distance. The subsets of human influenza virus genes belong to this group. A method for eliminating the "frozen" strains from the subsets and for calculating the evolutionary rates without construction of phylogenetic trees has been elaborated. The substitution rates calculated according to this technique agreed with the data obtained previously. A linear relationship was not observed in the second group. This group was predominantly composed of avian influenza virus genes. The lack of linear correlation pointed to the cocirculation of a large amount of different influenza virus genomic segments in the avian population. An approach for an examination of the role of intragenic recombination in the development of the antigenic subtypes of hemagglutinin is suggested. Our results suggest that recombination did not play a considerable role in this process, and that all modern subtypes of this protein were probably formed before the introduction of the influenza viruses into the human population. These findings are consistent with the hypothesis that influenza viruses penetrated into human population from their pools in avian populations. Descriptors: birds genetics, evolution, molecular, genes viral, influenza A virus avian genetics, human genetics, viral proteins genetics.

North America and derived a phylogenetic tree to establish their interrelationships. This analysis confirmed the divergence of H2 HA into two geographical lineages, American and Eurasian. One group of viruses isolated from shorebirds in North America had HA belonging to the Eurasian lineage, indicating an interregional transmission of the H2 gene. Characterization of HA with a monoclonal antibody panel revealed that the antigenicity of the Delaware strains differed from the other avian strains analysed. The data emphasizes the importance of avian influenza surveillance.

Descriptors: fowl plague transmission, fowl plague virology, hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian genetics, Asia, birds virology, Europe, genes viral, hemagglutination inhibition tests, avian isolation and purification, North America, phylogeny, poultry virology.


**NAL Call Number:** 448.8 V81

**Abstract:** Quail have emerged as a potential intermediate host in the spread of avian influenza A viruses in poultry in Hong Kong. To better understand this possible role, we tested the replication and transmission in quail of influenza A viruses of all 15 HA subtypes. Quail supported the replication of at least 14 subtypes. Influenza A viruses replicated predominantly in the respiratory tract. Transmission experiments suggested that perpetuation of avian influenza viruses in quail requires adaptation. Swine influenza viruses were isolated from the respiratory tract of quail at low levels. There was no evidence of human influenza A or B virus replication. Interestingly, a human-avian recombinant containing the surface glycoprotein genes of a quail virus and the internal genes of a human virus replicated and transmitted readily in quail; therefore, quail could function as amplifiers of influenza virus reassortants that have the potential to infect humans and/or other mammalian species.

Descriptors: infection, molecular genetics, respiratory system, adaptation.


Descriptors: antibodies, disease surveys, serum samples, infectious bronchitis virus serotypes, viral diseases, poultry, Ukraine.


**NAL Call Number:** SF995.A1A9

**Abstract:** Virus excretion, immune response, and, for chickens, deaths were recorded in 3-week-old ostriches and chickens inoculated by either the intramuscular or intranasal route with one of two influenza A viruses of subtype H5. One of the viruses, A/turkey/England/50-92/91 (H5N1) (50/92), was highly pathogenic for chickens causing 5/5 deaths by each route of inoculation. The other virus, A/ostrich/Denmark-Q/72420/96 (H5N2) (72420/96), isolated from ostriches in quarantine in Denmark during 1996, was of low pathogenicity for chickens, causing no clinical signs by either route of inoculation. No significant clinical signs were seen in any of the ostriches infected with either of the viruses by either route of infection. Both viruses were recoverable from both species up to 12 days post-infection, and low serological responses were detected in surviving infected ostriches and chickens at 21 days after inoculation.

Descriptors: ostriches, chickens, chicks, avian influenza virus, susceptibility, experimental infections, pathogenicity, clinical aspects, antibody formation, mortality, application methods, intramuscular injection, virus shedding, intranasal administration.


Descriptors: broilers, chickens, eggs, epidemiology, outbreaks, pathogenicity, poultry, avian influenza virus, Iran.

outbreaks in densely populated poultry areas. Developmental Biology (Basel) 119: 155-64. ISSN: 1424-6074.

Abstract: From 1997 to 2003, Italy has been affected by two epidemics of highly pathogenic avian influenza (HPAI) and by several outbreaks of low pathogenic avian influenza (LPAI). In 1999-2000 a severe HPAI epidemic affected the country, causing 413 outbreaks: a total of about 16 million birds died or were stamped out. From August 2000 to March 2001, a H7N1 LPAI strain infected 78 poultry farms. The last affected flock was stamped out on the 26th of March 2001. In October 2002, another LPAI virus of the H7N3 subtype emerged and infected a total of 388 poultry holdings. Eradication measures were based on stamping out or controlled marketing of slaughtered birds on infected farms and on the prohibition of restocking. Restriction measures on the movement of live poultry, vehicles and staff were also imposed. To supplement these disease control measures, two emergency vaccination programmes, based on the "DIVA" (Differentiating Infected from Vaccinated Animals) strategy were implemented. The two vaccination campaigns (2000-2002 and 2002-2003) both resulted in the eradication of infection. However, the first campaign appeared to be more successful that the second and possible explanations are discussed.

Descriptors: animals, disease outbreaks prevention and control, veterinary disease outbreaks, avian influenza A virus immunology, avian influenza epidemiology, avian influenza prevention and control, Italy epidemiology, population density, poultry, veterinary vaccination, viral vaccines.


NAL Call Number: 41.8 C162
Descriptors: Carnivora, influenza veterinary, monkey diseases microbiology, nose microbiology, orthomyxoviridae pathogenicity, respiratory tract infections microbiology, antigen antibody reactions, birds, cross reactions, haporhini, hemagglutination inhibition tests, horses, immune sera, influenza immunology, orthomyxoviridae isolation and purification, respiratory tract infections immunology, turkeys, virus replication.


NAL Call Number: 448.9 Am37
Descriptors: birds virology, influenza virology, influenza A virus avian, disease outbreaks prevention and control, Hong Kong epidemiology, influenza epidemiology, influenza prevention and control, influenza transmission.


NAL Call Number: QR360.J6
Abstract: In 1997 and 1998, H9N2 influenza A viruses were isolated from the respiratory organs of Indian ring-necked parakeets (Psittacula Krameri manillensis) that had been imported from Pakistan to Japan. The two isolates were closely related to each other (>99% as determined by nucleotide analysis of eight RNA segments), indicating that H9N2 viruses of the same lineage were maintained in these birds for at least 1 year. The hemagglutinins and neuraminidases of both isolates showed >97% nucleotide identity with those of H9N2 viruses isolated from humans in Hong Kong in 1999, while the six genes encoding internal proteins were >99% identical to the corresponding genes of H5N1 viruses recovered during the 1997 outbreak in Hong Kong. These results suggest that the H9N2 parakeet viruses originating in Pakistan share an immediate ancestor with the H9N2 human viruses. Thus, influenza A viruses with the potential to be transmitted directly to humans may be circulating in captive birds worldwide.

Descriptors: influenza transmission, influenza A virus avian classification, nucleoproteins, parakeets virology, amino acid sequence, Hong Kong, avian genetics, mice, inbred BALB c, molecular sequence data, phylogeny, RNA viral analysis, viral core proteins genetics.

Pathology 41(2): 101-7. ISSN: 0300-9858.

NAL Call Number: 41.8 P27

Abstract: Intranasally inoculated neurotropic influenza viruses in mice infect not only the respiratory tract but also the central nervous system (CNS), mainly the brain stem. Previous studies suggested that the route of invasion of virus into the CNS was via the peripheral nervous system, especially the vagus nerve. To evaluate the transvagal transmission of the virus, we intranasally inoculated unilaterally vagectomized mice with a virulent influenza virus (strain 24a5b) and examined the distribution of the viral protein and genome by immunohistochemistry and in situ hybridization over time. An asymmetric distribution of viral antigens was observed between vagal (nodose) ganglia: viral antigen was detected in the vagal ganglion of the vagectomized side 2 days later than in the vagal ganglion of the intact side. The virus was apparently transported from the respiratory mucosa to the CNS directly and decussately via the vagus nerve and centrifugally to the vagal ganglion of the vagectomized side. The results of this study, thus, demonstrate that neurotropic influenza virus travels to the CNS mainly via the vagus nerve.

Descriptors: brain stem virology, influenza A virus, avian, orthomyxoviridae infections virology, vagus nerve virology, immunohistochemistry, in situ hybridization, lung virology, mice, nodose ganglion virology, respiratory mucosa virology.


NAL Call Number: 448.3 Ar23

Abstract: Mink were found to be susceptible to the intranasal inoculation of human, swine, equine and avian influenza A viruses. The viruses were recovered until the 7th post inoculation (p.i.) day from the respiratory tract. The inoculated mink showed antibody response against these viruses. Contact infection in mink with A/Kumamoto/22/77 (H3N2) was possible.

Descriptors: influenza A virus pathogenicity, orthomyxoviridae infections microbiology, antibodies, viral biosynthesis, disease models, animal, hemagglutination inhibition tests, influenza A virus immunology, influenza A virus isolation and purification, orthomyxoviridae infections immunology, orthomyxoviridae infections transmission, respiratory system microbiology.


NAL Call Number: 41.8 V641

Descriptors: bird diseases microbiology, influenza veterinary, orthomyxoviridae isolation and purification, parrots, Psittacines, hemagglutinins viral, influenza microbiology, influenza A virus avian isolation and purification, lung microbiology, orthomyxoviridae immunology, orthomyxoviridae pathogenicity, trachea microbiology, virulence.


Descriptors: poultry, viral diseases, seminar, Brussels.


NAL Call Number: SF780.9.S63

Descriptors: disease control, viral diseases, bacterial diseases, infectious diseases, broilers, poultry, epidemiology, United Kingdom.


NAL Call Number: 41.8 Au72

Descriptors: chickens, disease outbreaks veterinary, avian influenza, prevention and control, southeastern Asia, epidemiology, disease outbreaks prevention and control, influenza A virus.
Descriptors: disease outbreaks prevention and control, avian influenza epidemiology, avian influenza prevention and control, zoonoses epidemiology, animal husbandry methods, southeastern Asia epidemiology, chickens, ducks.

NAL Call Number: 449.8 H343
Abstract: Two avian influenza viruses were employed; a virulent wild-type (WT) parent and the cold variant (CV) which was an attenuated virus derived by genetic recombination at 25 C. The attenuated virus grows in embryonated eggs and chicken tracheal organ cultures. Infectious virus could be recovered from lung and turbinate. Infection with attenuated virus provided protection against infection with wild virus.
Descriptors: influenza A virus avian, chick embryo, hemagglutination inhibition tests, hemagglutination, viral, recombination, genetic, virulence.

NAL Call Number: QR180.C62
Descriptors: chickens microbiology, influenza A virus avian isolation and purification, leukocytosis veterinary, poultry diseases microbiology, feces microbiology, avian classification, avian pathogenicity, lung microbiology, monocytes.

NAL Call Number: 448.3 Ar23
Abstract: A total of 18 hemagglutinating agents were isolated from 14 of 278 migrating feral ducks In Hokkaido during the surveillance studies conducted from 1978 to 1981. Seven of the 18 isolates belonged to paramyxovirus and the rest to influenza A virus. Five isolates of paramyxovirus reacted specifically with antiserum to duck/HK/199/77 and 7 isolates of influenza A virus possessed the antigenic configuration of H10N3. Three of the isolates possessed an hemagglutinin that has no antigenic relation to any of the 26 known strains of avain, swine, equine and human influenza A viruses.
Descriptors: ducks microbiology, influenza A virus avian isolation and purification, influenza A virus isolation and purification, paramyxoviridae isolation and purification, animals, wild microbiology, hemagglutinins viral immunology, avian immunology, influenza A virus immunology, Japan, orthomyxoviridae classification, paramyxoviridae classification, paramyxoviridae immunology.

NAL Call Number: 41.8 V641
Descriptors: ducks microbiology, influenza A virus avian isolation and purification, paramyxoviridae isolation and purification, chick embryo, cloaca microbiology, Japan.

NAL Call Number: 448.9 Am37
Descriptors: influenza prevention and control, influenza vaccines supply and distribution, influenza epidemiology, influenza A virus, avian, influenza vaccines administration and dosage, seasons, United States epidemiology.
NAL Call Number: SF481.M54 
Descriptors: disease control, disease prevention, disease surveys, disease transmission, epidemiology, clinical aspects, diagnostic techniques, outbreaks, pathogenicity, poultry industry, public health, World Health Organization, zoonoses, human diseases, avian influenza virus.

NAL Call Number: 41.8 Av5 
Descriptors: influenza veterinary, influenza A virus, porcine immunology, influenza A virus immunology, poultry diseases epidemiology, turkeys, antibodies, viral analysis, hemagglutination tests veterinary, immunodiffusion veterinary, influenza epidemiology, avian influenza disease, poultry diseases diagnosis.

NAL Call Number: 448.8 P942 
Abstract: Antineuraminidase antibody was determined in the subjects who had suffered influenza during the epidemics of 1970-1975 in the GDR. As early as 1970 the highest titers of antibody (greater than or equal to 1:60) were found not only to the prototype A/Hong Kong/1/68 strain but also to its subsequent drift variants A/England/42/72, A/Port Chalmers/1/73. Some subjects had antineuraminidase antibody to avian influenza virus. 
Descriptors: antibodies, viral analysis, influenza immunology, influenza A virus human immunology, neuraminidase immunology, adult, child, child, preschool, convalescence, disease outbreaks epidemiology, Germany, East, influenza epidemiology, human enzymology, neuraminidase antagonists and inhibitors.

NAL Call Number: 41.8 Am3 
Descriptors: influenza prevention and control, influenza A virus avian physiology, influenza vaccine, avian immunology, poultry, swine.

NAL Call Number: 448.8 N442 

Abstract: In reviewing recent advances in upper respiratory tract infections, we focus on five key topics. 
First, the use of ribavirin in the treatment of respiratory syncytial virus infection has been limited to the immunosuppressed. Prophylaxis in high-risk patients with specific immunoglobulin is effective and a new monoclonal antibody shows promise. Second, the efficacy of neuraminidase inhibitors in the treatment of influenza has become established. There are unresolved concerns about early implementation of therapy without a firm diagnosis; resource implications are enormous. Third, an outbreak of influenza due to avian influenza virus (H5N1) raised the possibility of a new pandemic. However, there was minimal person-to-
person spread although much was learned about pathogenesis of infection. Fourth, evidence favoring the use of ciprofloxacin rather than rifampicin for meningococcal chemoprophylaxis is reviewed. Efficacy in eradicating nasopharyngeal carriage is excellent. Finally, the management of sore throat has been considered. This remains controversial but evidence supporting antibiotic therapy in adults is lacking. If treatment is indicated in childhood, shorter courses of antibiotics may be effective.

**Descriptors:** bacterial infections drug therapy, respiratory tract infections drug therapy, respiratory tract infections microbiology, virus diseases drug therapy, adult, bacterial infections epidemiology, bacterial infections microbiology, child, preschool, clinical trials, Great Britain epidemiology, incidence, respiratory tract infections prevention and control, risk factors, virus diseases epidemiology, virus diseases virology.


**NAL Call Number:** 41.8 Av5

**Abstract:** Serum antibodies to influenza virus hemagglutinin 7, Newcastle disease virus (NDV), and avian paramyxoviruses were detected in Adelie penguin colonies in Antarctica. Infection with NDV and avian influenza virus was confined to particular colonies, whereas antibodies to the paramyxoviruses were detected in all seven colonies samples. Two avian paramyxoviruses were also isolated from cloacal swabs. Results of serological tests must be interpreted with caution, as little as known about the persistence of specific antibodies in Adelie penguins.

**Descriptors:** birds microbiology, antarctic regions, antibodies, viral analysis, birds immunology, cloaca microbiology, fluorescent antibody technique, hemagglutination inhibition tests veterinary, hemagglutination tests veterinary, influenza A virus avian immunology, Newcastle disease virus immunology, paramyxoviridae immunology, paramyxoviridae isolation and purification.


**NAL Call Number:** 41.8 Av5

**Abstract:** To determine the disease prevalence of free-living passerines, 1709 passerines were sampled from 38 different field sites in Ohio. Choanal and cloacal swabs were collected from each bird and cultured for the presence of *Pasteurella multocida*, *Salmonella* spp., and *Escherichia coli* by standard microbiologic techniques. In addition, the serum from each bird was analyzed for the presence of antibodies to *Mycoplasma gallisepticum*, *Mycoplasma synoviae*, Newcastle disease virus, and avian influenza virus. A blood smear was also made to examine for the presence of blood parasites. Results indicated that the isolation of *E. coli* varied with bird species, with the European starling having a higher (21.4%) isolation of *E. coli*. *Salmonella* spp. were also isolated from these free-living passerines. *Pasteurella multocida* was not isolated from any of the sampled passerines. These birds did not have antibodies to *M. gallisepticum*, *M. synoviae*, Newcastle disease virus, or avian influenza virus. Blood parasites were not detected in any of the birds sampled.

**Descriptors:** songbirds microbiology, animals, wild, anus microbiology, anus virology, birds microbiology, cloaca microbiology, fluorescent antibody technique, hemagglutination inhibition tests veterinary, influenza A virus avian isolation and purification, *Mycoplasma* isolation and purification, *Pasteurella multocida* isolation and purification, salmonella isolation and purification, songbirds blood.


**NAL Call Number:** SF601.J6

**Abstract:** Serum samples from 34 free-living nestling prairie falcons (*Falco mexicanus*) in southwestern Idaho were negative for antibodies to avian influenza virus, Newcastle disease virus, and three *Aspergillus* species. Serum from a single bird had hemagglutinating inhibition activity in response to *Mycoplasma synoviae*, and another bird’s serum had slight activity in response to *M. gallisepticum*.

**Descriptors:** antibodies, bacterial blood, antibodies, fungal blood, antibodies, viral blood, bird diseases epidemiology, aspergillosis epidemiology, aspergillosis immunology, aspergillosis veterinary, *Aspergillus* immunology, bird diseases immunology, birds, fowl plague epidemiology, fowl plague immunology,
hemagglutination inhibition tests veterinary, immunodiffusion veterinary, influenza A virus avian immunology, Mycoplasma immunology, Mycoplasma infections epidemiology, Mycoplasma infections immunology, Mycoplasma infections veterinary, Newcastle disease epidemiology, Newcastle disease immunology, Newcastle disease virus immunology, precipitin tests veterinary, prevalence.

NAL Call Number: SF605.A4
Descriptors: ecology, infection, veterinary medicine, wildlife management, avian influenza, duck plague, meeting abstract.

NAL Call Number: SF781.R4
Abstract: Emerging infectious diseases can be defined as infections that have newly appeared in a population or are rapidly increasing in incidence or geographic range. Many of these diseases are zoonoses, including such recent examples as avian influenza, severe acute respiratory syndrome, haemolytic uraemic syndrome (a food-borne infection caused by certain strains of Escherichia coli) and probably human immunodeficiency virus/acquired immune deficiency syndrome. Specific factors precipitating the emergence of a disease can often be identified. These include ecological, environmental or demographic factors that place people in increased contact with the natural host for a previously unfamiliar zoonotic agent or that promote the spread of the pathogen. These factors are becoming increasingly prevalent, suggesting that infections will continue to emerge and probably increase. Strategies for dealing with the problem include focusing special attention on situations that promote disease emergence, especially those in which animals and humans come into contact, and implementing effective disease surveillance and control.
Descriptors: epidemiology, infection, public health, vector biology, veterinary medicine, SARS, severe acute respiratory syndrome, haemolytic uraemic syndrome, Escherichia coli, control, demographic factors, disease emergence, disease surveillance, ecological factors, environmental factors, geographic range, zoonosis.

Descriptors: avian influenza virus, United States, Virginia, Pennsylvania, disease prevalence, outbreaks.

NAL Call Number: SF604.P32
Descriptors: isolation, characterization, outbreaks, diagnosis, diseases, avian influenza virus, poultry, mortality, Pakistan.

Descriptors: disease control, disinfectants, formaldehyde, pH, phenol, evaluation, chemical treatment, ultraviolet radiation, efficacy, avian influenza virus, poultry.

NAL Call Number: SF604.P32
Descriptors: broilers, poultry farms, isolation, clinical aspects, mortality, outbreaks, avian influenza virus, characterization, Pakistan.

**NAL Call Number:** 41.8 Av5

**Abstract:** Zanamivir has been shown to inhibit both human and avian influenza viral neuraminidases (NAs) and has been approved in several countries for the treatment and prophylaxis of influenza infection. Reliable monitoring of drug resistance is important for assessment of the impact of drug therapy on circulating virus populations. This study compares the current fluorometric (FL) method for evaluating zanamivir susceptibility with a recently developed chemiluminescent (CL) NA activity assay using viruses representative of all nine NA subtypes. The CL assay displayed signal/noise ratios that are 50-100 times greater than those associated with the FL assay. Human H3N2 strains appeared to exhibit greater NA activity relative to avian subtypes with the FL substrate but not with the CL substrate. Additionally, the CL assay remained linear over three orders of magnitude compared to only one order of magnitude for the FL assay. Four of the nine NA subtypes tested in this study displayed slightly higher inhibitor concentration that inhibits 50% of neuraminidase activity values by CL than by FL, while four displayed the opposite effect. Implications for the routine determination of resistance to NA inhibitors are discussed.

**Descriptors:** infection, avian influenza, infectious disease, respiratory system disease, viral disease, chemiluminescent neuraminidase assay bioassay techniques, clinical techniques, diagnostic techniques, laboratory techniques, antiviral susceptibility, drug resistance.

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Mutinelli, F., I. Capua, C. Terregino, and G. Cattoli (2003). **Clinical, gross, and microscopic findings in different avian species naturally infected during the H7N1 low- and high-pathogenicity avian influenza epidemics in Italy during 1999 and 2000.** *Avian Diseases* 47(Special issue): 844-848. ISSN: 0005-2086.

**NAL Call Number:** 41.8 Av5

**Descriptors:** chicken, turkey, guinea fowl, quail, ostrich, water fowl, pheasant, poultry, avian influenza epidemic, clinical aspects, diagnostic techniques, epidemiology, histopathology, immunohistochemistry, pathogenicity, postmortem examinations, Italy.

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**NAL Call Number:** SF995.A1A9

**Descriptors:** antibody testing, disease prevalence, disease surveys, seroprevalence, ELISA, egg production, poultry, mortality, avian influenza virus, Pakistan.

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**NAL Call Number:** 41.8 V641

**Descriptors:** disease outbreaks veterinary, fowl plague epidemiology, influenza A virus avian isolation and purification, poultry diseases epidemiology, avian classification, Pakistan, epidemiology, poultry.

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**Descriptors:** influenza A virus, avian pathogenicity, virulence, Asia epidemiology, disease outbreaks prevention and control, influenza epidemiology, influenza prevention and control, influenza transmission, influenza virology, avian influenza A virus classification, avian influenza A virus genetics, avian influenza A virus immunology, avian influenza epidemiology, avian influenza prevention and control, avian influenza transmission, avian influenza virology, poultry, receptors, virus physiology, viral vaccines, zoonoses epidemiology, zoonoses transmission, zoonoses virology.

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**Descriptors:** influenza A virus human genetics, viral proteins genetics, base sequence, evolution, genes,

**NAL Call Number:** 41.8 Av5

**Abstract:** Marked proliferation of macrophages engulfing yellow pigments and fragmented erythrocytes were seen in the air capillaries and blood capillaries of the lungs of chickens affected with acute fatal viral hydropericardium syndrome, highly pathogenic infectious bursal disease, and highly pathogenic avian influenza. Proliferation of lung macrophages was associated with systemic proliferation of macrophages. Acute destruction of erythrocytes in these infections may have induced systemic hyperplasia of macrophages. The acute and severe proliferation of lung macrophages may cause acute respiratory dysfunction and be one of the factors inducing mortality in infected chickens. This syndrome may be categorized as "virus-associated hemophagocytic syndrome."

**Descriptors:** immune system, infection, respiratory system, veterinary medicine, acute fatal viral hydropericardium syndrome, heart disease, viral disease, highly pathogenic avian influenza, viral disease, highly pathogenic infectious bursal disease, viral disease, virus associated hemophagocytic syndrome, blood and lymphatic disease, immune system disease, viral disease.


**NAL Call Number:** 448.3 Ar23

**Abstract:** The characteristics of an avian influenza virus were compared in detail with those of human Asian (H2N2) influenza viruses. Antigenic analysis by different antisera against H2N2 viruses and monoclonal antibodies to both the hemagglutinin and neuraminidase antigens showed that an avian isolate, A/duck/Munchen/9/79 contained hemagglutinin and neuraminidase subunits closely related to those of the early human H2N2 viruses which had been prevalent in 1957. However, this avian virus gave low HI titers with absorbed and non-absorbed antisera to different human H2N2 viruses isolated in 1957. Like human Q phase variant, such as A/RI/5-/57 (H2N2), hemagglutination of the above avian strain was not inhibited by the purified non-specific gamma-inhibitor from guinea pig serum. Growth behavior at restrictive temperature (42 degrees C) clearly differentiate the avian H2N2 virus from human influenza viruses, showing that the former virus grew well in MDCK cells at 42 degrees C but not the latters. Genomic analysis of these viruses revealed that the oligonucleotide map of H2N2 virus isolated from a duck was quite different from those of human H2N2 viruses from 1957 to 1967. The oligonucleotide mapping also indicated that different H2N2 influenza virus variants had co-circulated in humans in 1957.

**Descriptors:** influenza A virus avian immunology, influenza A virus human immunology, hemagglutinins viral immunology, influenza A virus avian genetics, influenza A virus human genetics, influenza A virus growth and development, neuraminidase immunology, RNA viral genetics.


**NAL Call Number:** 448.8 V81

**Abstract:** In 1985 a fowl plague-like disease occurred in chickens in Lockwood, Victoria, Australia and caused high mortality. An H7N7 influenza virus was isolated from the chickens (A/Chicken/Victoria/1/85); additionally, an antigenically similar virus was isolated from starlings (A/Starling/Victoria/5156/85) and serological evidence of H7N7 virus infection was found in sparrows. Antigenic analysis with monoclonal antibodies to H7, oligonucleotide mapping of total vRNA, and sequence analysis of the HA genes established that the chicken and starling influenza viruses were closely related and probably came from the same source. There was high nucleotide sequence homology (95.3%) between the HA genes of A/Chick/Vic/85 and a fowl plague-like virus isolated from chickens in Victoria 9 years earlier [A/Fowl/Vic/76 (H7N7)]. The sequence homologies indicated that the A/Chick/Vic/85 and A/Fowl/Vic/76 were derived from a common recent ancestor, while another recent H7N7 virus, Seal/Mass/1/80 originated from a different
evolutionary lineage. Experimental infection of chickens and starlings with A/Chick/Vic/1/85 (H7N7) was associated with high mortality (100%), transmission to contact birds of the same species, and virus in all organs. In sparrows one-third of the birds died after infection and virus was isolated from most organs; transmission to contact sparrows did not occur. In contrast, the H7N7 virus replicated in ducks and spread to contact ducks but caused no mortality. These studies establish that the host species plays a role in determining the virulence of avian influenza viruses, and provide the first evidence for transmission of virulent influenza viruses between domestic poultry and passerine birds. They support the hypothesis that potentially virulent H7N7 influenza viruses could be maintained in ducks where they cause no apparent disease and may sometimes spread to other wild birds and domestic poultry.

Descriptors: birds microbiology, hemagglutinins viral genetics, influenza A virus avian genetics, amino acid sequence, animals, wild microbiology, Australia, base sequence, chickens microbiology, disease reservoirs, genes viral, molecular sequence data, nucleotide mapping, RNA viral genetics, species specificity, virus replication.

NAL Call Number: aSF601.U5
Descriptors: epidemiological surveys, wildlife, avian influenza virus, wild ducks, domestic ducks, geese, seagulls, poultry, mice, rats, chuckar, pheasants, Chesapeake Bay, serological survey, Pennsylvania.

NAL Call Number: 41.8 Av5
Abstract: Wildlife surveillance was conducted for influenza viruses in conjunction with the 1983-84 lethal H5N2 avian influenza epizootic in domestic poultry in Pennsylvania, New Jersey, Maryland, and Virginia. Virus-isolation attempts made on cloacal and tracheal swabs from 4,466 birds and small rodents within the quarantined areas and 1,511 waterfowl in nearby Maryland yielded only a single H5N2 isolate from a pen-raised chukar in Pennsylvania. Antibodies against hemagglutinin type 5 and/or neuraminidase type 2 were found in 33% of the aquatic birds tested; however, this finding could not be used to confirm previous H5N2 avian influenza virus activity because of the possibility of prior infections with multiple influenza subtypes. The low prevalence of lethal H5N2 avian influenza virus in wild birds and small rodents strongly indicated that these animals were not responsible for dissemination of the disease among poultry farms during the outbreak.
Descriptors: birds microbiology, disease outbreaks veterinary, fowl plague transmission, disease reservoirs microbiology, hemagglutinins viral analysis, neuraminidase analysis, orthomyxoviridae isolation and purification, paramyxoviridae isolation and purification, Pennsylvania.

NAL Call Number: aSF995.6.I6I5 1981a

NAL Call Number: 448.8 L22
Descriptors: epidemiology, humans, infection, influenza, vaccination, clinical techniques, pandemic prevention.

NAL Call Number: 448.3 Ar22
Descriptors: influenza epidemiology, orthomyxoviridae immunology, birds, cross reactions, influenza A virus avian immunology, influenza A virus human immunology, influenza A virus, porcine immunology,
Romania, swine.


NAL Call Number: 41.8 Am3

Descriptors: chickens, disease outbreaks veterinary, fowl plague epidemiology, influenza A virus avian pathogenicity, turkeys, influenza A virus avian isolation and purification, Virginia epidemiology.


NAL Call Number: 470 Sci2

Descriptors: agricultural workers' diseases virology, antibodies, viral blood, influenza virology, influenza A virus, avian immunology, acetamides therapeutic use, agricultural workers' diseases immunology, agricultural workers' diseases prevention and control, antiviral agents therapeutic use, disease outbreaks, influenza epidemiology, influenza immunology, influenza prevention and control, Japan epidemiology, protective clothing.


NAL Call Number: 470 Sci2


NAL Call Number: 470 Sci2


NAL Call Number: 470 Sci2


NAL Call Number: 41.8 V6426

Descriptors: chemoprophylaxis, antiviral agents, amantadine, avian influenza, mortality rate, drinking water, chicks, poultry.


NAL Call Number: 448.8 V81

Descriptors: genes viral, influenza A virus genetics, brain, chick embryo, chickens, electrophoresis, genotype, influenza A virus growth and development, influenza A virus pathogenicity, RNA viral genetics, recombination, genetic.

**NAL Call Number:** QR375.V6

**Abstract:** Since 1997, novel viruses of three different subtypes and five different genotypes have emerged as agents of influenza among pigs in North America. The appearance of these viruses is remarkable because there were no substantial changes in the overall epidemiology of swine influenza in the United States and Canada for over 60 years prior to this time. Viruses of the classical H1N1 lineage were virtually the exclusive cause of swine influenza from the time of their initial isolation in 1930 through 1998. Antigenic drift variants of these H1N1 viruses were isolated in 1991-1998, but a much more dramatic antigenic shift occurred with the emergence of H3N2 viruses in 1997-1998. In particular, H3N2 viruses with genes derived from human, swine and avian viruses have become a major cause of swine influenza in North America. In addition, H1N2 viruses that resulted from reassortment between the triple reassortant H3N2 viruses and classical H1N1 swine viruses have been isolated subsequently from pigs in at least six states. Finally, avian H4N6 viruses crossed the species barrier to infect pigs in Canada in 1999. Fortunately, these H4N6 viruses have not been isolated beyond their initial farm of origin. If these viruses spread more widely, they will represent another antigenic shift for our swine population, and could pose a threat to the world's human population. Research on these novel viruses may offer important clues to the genetic basis for interspecies transmission of influenza viruses.

**Descriptors:** influenza virology, influenza A virus, porcine physiology, Canada epidemiology, fowl plague transmission, influenza A virus avian, influenza A virus, porcine classification, influenza A virus, porcine genetics, influenza A virus, porcine immunology, North America epidemiology, species specificity, swine, United States, variation genetics.


**NAL Call Number:** 448.3 Ar23

**Abstract:** Influenza virus infection in pigs is both an animal health problem and a public health concern. As such, surveillance and characterization of influenza viruses in swine is important to the veterinary community and should be a part of human pandemic preparedness planning. Studies in 1976/1977 and 1988/1989 demonstrated that pigs in the U.S. were commonly infected with classical swine H1N1 viruses, whereas human H3 and avian influenza virus infections were very rare. In contrast, human H3 and avian H1 viruses have been isolated frequently from pigs in Europe and Asia over the last two decades. From September 1997 through August 1998, we isolated 26 influenza viruses from pigs in the north central United States at the point of slaughter. All 26 isolates were H1N1 viruses, and phylogenetic analyses of the hemagglutinin and nucleoprotein genes from 11 representative viruses demonstrated that these were classical swine H1 viruses. However, monoclonal antibody analyses revealed antigenic heterogeneity among the HA proteins of the 26 viruses. Serologically, 27.7% of 2,375 pigs tested had hemagglutination-inhibiting antibodies against classical swine H1 influenza virus. Of particular significance, however, the rates of seropositivity to avian H1 (7.6%) and human H3 (8.0%) viruses were substantially higher than in previous studies.

**Descriptors:** influenza veterinary, influenza virology, influenza A virus avian isolation and purification, influenza A virus human isolation and purification, influenza A virus, porcine isolation and purification, swine diseases virology, amino acid sequence, influenza epidemiology, molecular sequence data, seroepidemiologic studies, swine, swine diseases epidemiology, United States epidemiology.


**NAL Call Number:** aSF601.U5

**Descriptors:** poultry, disease prevalence, epidemiological surveys, avian influenza virus, Pennsylvania, New Jersey, Massachusetts, New York, Florida, United States, live poultry markets.


**Descriptors:** avian influenza virus, maternal immunity, immune response, inactivated vaccines, results, acquired antibody, chicks.

Descriptors: chickens microbiology, fowl plague microbiology, influenza A virus, isolation and purification, serotyping.


Descriptors: chickens, influenza veterinary, poultry diseases diagnosis, influenza diagnosis, influenza microbiology, orthomyxoviridae isolation and purification, poultry diseases microbiology.


Descriptors: avian influenza, epidemiology, diagnosis, problems, poultry.


Abstract: Proof that a newly identified coronavirus, severe acute respiratory syndrome coronavirus (SARS-CoV) is the primary cause of severe acute respiratory syndrome (SARS) came from a series of studies on experimentally infected cynomolgus macaques (*Macaca fascicularis*). SARS-CoV-infected macaques developed a disease comparable to SARS in humans; the virus was re-isolated from these animals and they developed SARS-CoV-specific antibodies. This completed the fulfilment of Koch's postulates, as modified by Rivers for viral diseases, for SARS-CoV as the aetiological agent of SARS. Besides the macaque model, a ferret and a cat model for SARS-CoV were also developed. These animal models allow comparative pathogenesis studies for SARS-CoV infections and testing of different intervention strategies. The first of these studies has shown that pegylated interferon-alpha, a drug approved for human use, limits SARS-CoV replication and lung damage in experimentally infected macaques. Finally, we argue that, given the worldwide nature of the socio-economic changes that have predisposed the emergence of SARS and avian influenza in Southeast Asia, such changes herald the beginning of a global trend for which we are ill prepared.

Descriptors: disease models, animal, ferrets, *Macaca fascicularis*, SARS virus, severe acute respiratory syndrome etiology, zoonoses transmission, cats, severe acute respiratory syndrome physiopathology, severe acute respiratory syndrome transmission.


Descriptors: avian influenza virus, poultry.


Descriptors: animals, wild microbiology, birds microbiology, influenza A virus avian isolation and purification, Japan.

In the two winters of 1980-1982, we surveyed migratory waterfowl of some species staying in San-in District, Western Japan for influenza virus at a few stations. From November 1980 to April 1981, only two strains of influenza virus, H13N1 and H11N6 subtypes, were isolated from 465 fecal samples from pintails but none from 255 samples from whistling swans nor from 625 black-tailed gulls. From November 1981 to March 1982, 17 viruses were isolated from 1156 fecal samples. Fourteen viruses, 10 H7N3, 2 H1N6 and 2 H3N8, were isolated from 459 feces samples from whistling swans. Two viruses, H13N3 and H13N6 subtypes, were isolated from 425 fecal samples from black-tailed gulls. A strain belonging to H1N3 subtype was isolated from 30 feces samples from mallards but no virus was isolated from 242 samples from pintails.

Descriptors: birds microbiology, ducks microbiology, fowl plague epidemiology, influenza A virus avian isolation and purification, influenza A virus isolation and purification, feces microbiology, fowl plague microbiology, influenza A virus avian classification, influenza A virus classification, Japan, seasons, serotyping.


From November 1982 to March 1983, winter migratory waterfowls of some species staying in San-in District, Western Japan, were surveyed for influenza virus at five stations. A total of eight influenza A viruses were isolated from 354 faeces samples of whistling swans; in contrast, no virus was isolated from any sample of 261 black-tailed gulls, of 113 pintails and of 10 mallards. Five of eight isolates belonged to human pandemic subtype H2N2, two isolates belonged to fowl plague subtype H7N7, and the remaining one to subtype H4N6.

Descriptors: animals, wild microbiology, birds microbiology, disease reservoirs, influenza A virus avian isolation and purification, influenza A virus human isolation and purification, feces microbiology, influenza A virus human classification, Japan, mice, species specificity.


Certain species of winter migratory waterfowl in San-in District, western Japan, were surveyed for influenza virus from November 1983 to March 1984. Faeces of the waterfowl were collected regularly at five stations. Eleven influenza A viruses including H5N3 and H10N4 subtypes were isolated from 450 faecal samples from whistling swans; in contrast, no virus was isolated from any sample of 261 black-tailed gulls, of 113 pintails and of 10 mallards. Eleven isolates belonged to human pandemic subtype H2N2, two isolates belonged to fowl plague subtype H7N7, and the remaining one to subtype H4N6.

Descriptors: birds microbiology, feces microbiology, influenza A virus avian isolation and purification, Japan.


A serological surveillance was carried out to detect antibody against influenza A virus in chicken sera. A total of 8,850 field samples were collected from 47 prefectures in Japan. Initially, all the sera were screened by agar gel immunodiffusion and those sera showing positive reaction were investigated for haemagglutination-inhibition (HI) and neuraminidase-inhibition antibodies against influenza viruses. Only 6
samples had antibodies; 4 sera had antibodies against human subtype H1N1 virus; with HI activity against strain A/PR/34; three sera had strong HI activity to strain A/Tottori/4/87, which by haemagglutination test is closely related to A/Yamagata/120/86. The remaining two chicken sera had antibodies against avian subtypes H10N4 and H3N6 viruses respectively.

Descriptors: antibodies, viral blood, chickens immunology, fowl plague epidemiology, fowl plague immunology, influenza A virus avian immunology, chickens virology, demography, fowl plague blood, influenza A virus avian classification, Japan epidemiology, precipitin tests.


NAL Call Number: 41.8 Z52
Descriptors: wild birds, epidemiological surveys, avian influenza virus, avian paramyxovirus, poultry, Germany, Netherlands, Kenya.


NAL Call Number: aSF995.6.I6I5 1981a
Descriptors: avian influenza A virus, wild birds, ducks, isolation of strains, Germany, symposium.


NAL Call Number: 286.81 F322
Descriptors: avian influenza A virus, isolation, ducks, coots, Germany.


NAL Call Number: SF724.T72
Abstract: One hundred sera samples from chicken flocks showing respiratory distress but failed to respond to treatment against chronic respiratory disease (CRD) were tested for avian influenza virus antibodies. The sera samples were collected from 5, 32, and 21 weeks old broilers, broiler breeders and pullets respectively. All the 100 sera samples from the three flocks were positive for influenza virus serotype H1N1 antibodies. In addition 35.3%, 57.14% and 93.42% were positive for H5N1 serotype in the broilers, broiler breeder and point of lay pullets respectively. The clinical and public health implications of the presence of antibodies to these influenza A virus serotypes in chicken flocks are discussed.
Descriptors: animal husbandry, infection, public health, respiratory system, chronic respiratory disease, respiratory system disease, respiratory distress, respiratory system disease, clinical implications public health implications serological evidence.


NAL Call Number: QR189.V32
Abstract: The Great Influenza Pandemic of 1918-1919 was a cataclysmic outbreak of infection wherein over 50 million people died worldwide within 18 months. The question of the origin is important because most influenza surveillance at present is focussed on S.E. Asia. Two later pandemic viruses in 1957 and 1968 arose in this region. However we present evidence that early outbreaks of a new disease with rapid onset and spreadability, high mortality in young soldiers in the British base camp at Etaples in Northern France in the winter of 1917 is, at least to date, the most likely focus of origin of the pandemic. Pathologists working at Etaples and Aldershot barracks later agreed that these early outbreaks in army camps were the same disease as the infection wave of influenza in 1918. The Etaples camp had the necessary mixture of factors for emergence of pandemic influenza including overcrowding (with 100,000 soldiers daily changing), live pigs, and nearby live geese, duck and chicken markets, horses and an additional factor 24 gases (some
of them mutagenic) used in large 100 ton quantities to contaminate soldiers and the landscape. The final trigger for the ensuing pandemic was the return of millions of soldiers to their homelands around the entire world in the autumn of 1918.

Descriptors: communicable diseases, emerging history, disease outbreaks, influenza history, military personnel history, world war I, ducks, France, geese, history, 20th century, horses, influenza A virus, avian pathogenicity, swine.


NAL Call Number: SF601.J6

Descriptors: Phoebastria irrorata, Punta cevallos, biochemistry, blood, hematological parameters, records, prevalence, Galapagos Islands.


NAL Call Number: aSF601.U5

Descriptors: poultry, Mexico, avian influenza virus, disease surveys, America, domestic animals, domesticated birds, influenza virus, Latin America, livestock, North America, orthomyxoviridae, surveys, useful animals, viruses, incidence.


NAL Call Number: 41.8 Av5

Abstract: Avian influenza virus (AIV) subtypes H5N2 and H7N1 were isolated from emus (Dromaius novaehollandiae) and rheas (Rhea americana) in Texas and North Carolina. All the rheas and emus had a history of respiratory disease except one emus which was clinically normal. The isolates were not pathogenic for chickens and turkeys under the conditions of the experiment. Humoral antibodies to all known hemagglutinin (H) subtypes except H10, H13, and H14 and to all nine neuraminidase (N) subtypes were found in emus and rheas in 11 states. Therefore, emus and rheas are susceptible to infection with several AIV subtypes.

Descriptors: Texas, North Carolina, emus, rheas, avian influenza virus, pathogenicity, antibodies, America, appalachian states United States, biological properties, birds, casuariiformes, immunological factors, influenza virus, microbial properties, North America, orthomyxoviridae, rheiformes, southern plains states United States, southern states United States, United States, viruses, susceptibility.


NAL Call Number: 41.8 Av5

Abstract: Susceptibility to infection with avian influenza virus (AIV) was studied in pigeons inoculated via oculonasal (Experiment 1) or intravenous (Experiment 2) route. Chickens were included as susceptible hosts in both experiments. Two subtypes each of the highly pathogenic AIV (HPAIV; HP CK/PA H5N2 and HP CK/Australia H7N7) and nonpathogenic AIV (NPAIV; NP CK/PA H5N2 and NP emu/TX H7N1) at a dose of 10(5) embryo infective dose per bird were used as inoculum. The pigeons inoculated with HP CK/PA H5N2 or HP CK/Australia H7N7 remained apparently healthy throughout the 21-day observation period, did not shed viruses on 3, 7, 14, and 21 days postinoculation (DPI), and had no demonstrable levels of antibodies on 21 DPI. On the other hand, 9 of 12 chickens inoculated with the HPAIV died of highly pathogenic avian influenza; the viruses were recovered from their respiratory and intestinal tissues, and the surviving chickens had antibodies to AIV. Regarding responses of pigeons to inoculation with NP CK/PA H5N2 or NP emu/TX H7N1, the pigeons remained clinically healthy throughout the 21-day observation period and did not have detectable levels of antibodies on 21 DPI; only one pigeon yielded the NP emu/TX H7N1 on 3 DPI. The virus was isolated from a tracheal swab and was believed to be the residual inoculum
Based on the responses of pigeons to NPAIV and HPAIV, it was concluded that the pigeons were resistant or minimally susceptible to infection with HPAIV or NPAIV.

Descriptors: pigeons, avian influenza virus, disease resistance, experimental infection, injection, application methods, disease transmission, chickens, application methods, birds, Columbiformes, disease transmission, domestic animals, domesticated birds, Galliformes, infection, influenza virus, livestock, orthomyxoviridae, pathogenesis, poultry, resistance to injurious factors, useful animals, viruses, oculanasal inoculation, susceptibility, intravenous injection.


Descriptors: zoonoses, public health, humans, Newcastle disease virus, avian influenza virus.


Abstract: One-hundred thirty-seven BALB/c mice were intranasally inoculated with neurotropic avian influenza A virus (H5N3). Thirty-nine of these mice died within 16 days post-inoculation (PID) and 98 of the mice recovered from the infection. To investigate whether viral antigens and genomes persist in the central nervous system (CNS) of recovered mice, immunohistochemistry and reverse transcription-polymerase chain reaction (RT-PCR) methods were performed. Histopathologically, mild interstitial pneumonia and non-suppurative encephalomyelitis restricted to the basal part of the frontal lobe of the cerebrum, brain stem and thoracic spinal cord were observed in BALB/c mice until 40 PID. Small amounts of viral antigens were detected in the brain and spinal cord and some viral RNA segments (NA, NP, M, PA, HA, NS, PB1) were intermittently detected in the CNS until 48 PID. Immunosuppression of these mice by dexamethazone (DEX) treatment did not increase the frequency of detection of the lesions, viral antigens or genomes. These findings suggest that viral genomes of neurovirulent influenza virus persist with restricted transcriptive activity in the CNS of the mice even after clinical recovery from the infection.

Descriptors: central nervous system virology, fowl plague virology, influenza A virus avian isolation and purification, RNA viral analysis, brain pathology, brain virology, central nervous system pathology, disease models, animal, fowl plague mortality, fowl plague pathology, immunohistochemistry veterinary, influenza A virus avian genetics, mice, mice inbred BALB c, random allocation, reverse transcriptase polymerase chain reaction veterinary, specific pathogen free organisms.


Descriptors: disease outbreaks, fowl plague virology, influenza mortality, Asia, southeastern epidemiology, birds, influenza A virus avian, influenza A virus human.


Descriptors: influenza, avian transmission, zoonoses transmission, influenza, avian epidemiology, poultry, Vietnam epidemiology.


Descriptors: influenza, avian epidemiology, birds, Carnivora, cat diseases epidemiology, cats, poultry, world health, World Health Organization.


Online: www.ADSA.org/jds

Abstract: The Office International des Epizooties (OIE) has developed international standards to reduce the risk of the spread of high-pathogenicity avian influenza though international trade. These standards include providing a definition of high-pathogenicity avian influenza (HPAI), procedures for prompt reporting of HPAI outbreaks, requirements that must be met for a country or zone to be defined as free of HPAI, requirements that should be met to import live birds and avian products into a HPAI-free country or zone, and the general provisions that countries should meet to reduce the risk of spread of HPAI through trade. The goal of these standards is to facilitate trade while minimizing the risk of the introduction of HPAI.

Descriptors: epidemiology, infection, avian influenza, epidemiology, infectious disease, prevention and control, respiratory system disease, viral disease, disease spread international, influenza control standards.


Abstract: This investigation detailed the clinical disease, gross and histologic lesions, and distribution of viral antigen in juvenile laughing gulls (Larus atricilla) intranasally inoculated with either the A/tern/South Africa/61 (H5N3) (tern/SA) influenza virus or the A/chicken/Hong Kong/220/97 (H5N1) (chicken/HK) influenza virus, which are both highly pathogenic for chickens. Neither morbidity nor mortality was observed in gulls inoculated with either virus within the 14-day investigative period. Gross lesions resultant from infection with either virus were only mild, with the tern/SA virus causing decreased lucency of the air sacs (2/6), splenomegaly (2/6), and pancreatic mottling (1/6) and the chicken/HK virus causing only decreased lucency of the air sacs (2/8) and conjunctival edema (2/8). Histologic lesions in the tern/SA-inoculated gulls included a mild to moderate heterophilic to lymphoplasmacytic airsacculitis (6/6), mild to moderate interstitial pneumonia (3/6), and moderate necrotizing pancreatitis and hepatitis at 14 days postinoculation (DPI) (2/6). Immunohistochemical demonstration of viral antigen occurred only in association with lesions in the liver and pancreas. In contrast, viral antigen was not demonstrated in any tissues from the chicken/HK-inoculated gulls, and inflammatory lesions were confined to the air sac (3/8) and lungs (3/8). Both viruses were isolated at low titers (<101.68 mean embryo lethal dose) from oropharyngeal and cloacal swabs up to 7 days postinoculation (DPI), from the lung and kidney of one of two tern/SA-inoculated gulls at 14 DPI, and from the lung of one of two chicken/HK-inoculated gulls at 7 DPI. Antibodies to influenza viruses as determined with the agar gel precipitin test at 14 DPI were detected only in the two tern/SA-inoculated gulls and not in the two chicken/HK-inoculated gulls.

Descriptors: infection, pharmacology, veterinary medicine, avian influenza virus infection, infectious disease, respiratory system disease, viral disease, agar gel precipitin test, immunologic techniques, laboratory techniques, cloacal swab, diagnostic techniques, immunohistochemistry, intranasal influenza virus inoculation, oropharyngeal swab.

**NAL Call Number:** 41.9 D23  
**Descriptors:** avian influenza virus, pigs, poultry.


**NAL Call Number:** 41.8 Au72  
**Descriptors:** Australia, avian paramyxoviruses, avian influenza viruses, isolation and characterization, Aves, wild birds, wild duck, pigeon, quail.


**NAL Call Number:** 41.9 W64B  
**Abstract:** State wildlife agencies have translocated thousands of wild turkeys (*Meleagris gallopavo*) since the 1930s to reestablish this species. Because of threats to the domestic poultry industry and wild birds, screening for selected infectious agents has become routine since the early 1980s. One of the principal sources for Rio Grande wild turkeys (*M. gallopavo intermedia*) for translocation purposes was the Edwards Plateau of Texas (USA). Unfortunately, turkey abundance has declined in the southern Edwards Plateau since the late 1970s. Surprisingly few studies have addressed wild turkeys in this region, perhaps reflecting its status as the heart of Rio Grande turkey range. We surveyed 70 free-living Rio Grande wild turkeys from Bandera and Kerr counties, Texas, for evidence of exposure to *Salmonella typhimurium*, *S. pullorum*, *Mycoplasma gallisepticum*, *M. meleagridis*, *M. synoviae*, *Chlamydophila psittaci*, and the avian influenza, Newcastle disease, turkey corona, and reticuloendotheliosis viruses. Of these, 80% (56) were seropositive for both *M. gallisepticum* and *M. synoviae* on the serum plate antigen test. Ten of these individuals (14% of total) were positive for *M. synoviae* by hemagglutination inhibition testing. All other serologic tests were negative. Two adult females sampled in Kerr County, whose body mass was significantly less than that of other adult females trapped in the area, tested positive for reticuloendotheliosis virus (REV) proviral DNA on polymerase chain reaction. Reticuloendotheliosis virus was isolated from one of these individuals. The pathogenesis, transmission, and/or population-level influences of *M. gallisepticum*, *M. synoviae*, and REV in Rio Grande wild turkeys deserves further study.  
**Descriptors:** epidemiology, infection, veterinary medicine, wildlife management, avian influenza virus infection, epidemiology, viral disease, *Chlamydophila psittaci* infection, bacterial disease, epidemiology, *Mycoplasma gallisepticum* infection, bacterial disease, epidemiology, *Mycoplasma meleagridis* infection, bacterial disease, epidemiology, *Mycoplasma synoviae* infection, bacterial disease, epidemiology, Newcastle disease virus infection, epidemiology, viral disease, reticuloendotheliosis virus infection, epidemiology, viral disease, *Salmonella pullorum* infection, bacterial disease, *Salmonella typhimurium* infection, bacterial disease, turkey coronavirus infection, epidemiology, viral disease, hemagglutination inhibition testing clinical techniques, diagnostic techniques, polymerase chain reaction clinical techniques, diagnostic techniques, genetic techniques, laboratory techniques, serology clinical techniques, diagnostic techniques, serum plate antigen test clinical techniques, diagnostic techniques, species translocation applied and field techniques, abundance population decline.


**NAL Call Number:** 41.9 W64B  
**Abstract:** Lesser prairie chicken (*Tympanuchus pallidicinctus*) abundance, like that of most grassland birds, has declined rangewide for decades. Although habitat loss and degradation are likely ultimate causes for this decline, infectious agents, particularly microparasites, could be proximate contributors. No surveys of pathogenic bacteria or viruses have been published for this species. We surveyed 24 free-living lesser prairie chickens from Hemphill County, Texas (USA), for evidence of exposure to *Salmonella typhimurium*, *S. pullorum*, *Mycoplasma gallisepticum*, *M. synoviae*, *Chlamydophila psittaci*, and the avian influenza,
Newcastle disease, infectious bronchitis, and reticuloendotheliosis viruses. Two of 18, and eight of 17 samples were seropositive for the Massachusetts and Arkansas serotypes of infectious bronchitis virus, respectively. Five of the eight positive individuals were juveniles, two of which were seropositive for both serotypes. All other serologic and genetic tests were negative. Because the ecological significance of these results is unknown, the pathogenesis, transmission, and/or population-level influences of infectious bronchitis and related avian coronaviruses for lesser prairie chickens deserves further study.

Descriptors: epidemiology, infection, veterinary medicine, wildlife management, avian influenza virus infection, epidemiology, viral disease, Chlamydophila psittaci infection, bacterial disease, epidemiology, infectious bronchitis virus infection, epidemiology, viral disease, Mycoplasma infection, bacterial disease, epidemiology, Newcastle disease virus infection, epidemiology, viral disease, reticuloendotheliosis virus infection, epidemiology, viral disease, salmonellosis, bacterial disease, epidemiology, serology clinical techniques, diagnostic techniques, abundance habitat degradation, habitat loss, population decline.

NAL Call Number: 41.8 Av5

Abstract: In an intensive ostrich farming area in South Africa with a history of ostrich influenza outbreaks, we conducted a survey of avian influenza virus (AIV) and Newcastle disease virus (NDV) in wild aquatic birds. During late autumn and winter 1998, the time of year when outbreaks in ostriches typically start to occur, 262 aquatic birds comprising 14 species were sampled and tested for both virus infections. From eight samples, AIV, serotype H10N9, could be isolated. All isolates were apathogenic as determined by the intravenous pathogenicity index (0.00). Conversely, none of 33 sera of these wild birds showed antibodies against H10. However, one bird was found serologically positive for H6 AIV. This AIV serotype was later isolated from ostriches during an avian influenza outbreak in this area. No NDV was isolated although 34 of 46 serum samples contained NDV-specific antibodies. This is the first H10N9 isolate to be reported from Africa. In addition, our data support the notion that wild aquatic birds may function as a reservoir for AIV and NDV in South Africa.

Descriptors: infection, virology, Newcastle disease, viral disease, avian influenza A infection, viral disease, ostrich influenza infection, viral disease, intravenous pathogenicity index.

NAL Call Number: 41.8 Av5

Abstract: New Zealand has never experienced an outbreak of avian influenza, and the Ministry of Agriculture and Forestry has long been wary of the possibility of introducing high-pathogenicity avian influenza (HPAI) viruses in imported goods. Besides the potential threat posed to poultry, there are concerns that introduced viruses might have negative effects on already endangered native avian species. Under the framework of the World Trade Organization, the sanitary and phytosanitary (SPS) agreement requires member countries to base their sanitary measures for imported animal products on the Office International des Epizooties (OIE) standard or on a scientific assessment of risk. This paper presents the New Zealand experience with assessing the risk of avian influenza viruses in imported chicken meat and considers how the assessment of risk has changed in recent years as a result of the advances in understanding of the disease. The currently accepted view that low-pathogenicity avian influenza (LPAI) viruses are widespread and that they mutate to virulence after introduction into poultry has important implications concerning the appropriate definition for avian influenza viruses of regulatory concern and has possible implications concerning the significance of viruses present in this country.

Descriptors: epidemiology, foods, infection, disease risk analysis, clinical techniques, imported poultry meat, poultry product, viral contamination phytosanitary agreement, SPS agreement, viral introduction.

To evaluate the replication of a highly virulent avian influenza A virus in a potential reservoir host, mallard ducks (*Anas platyrhynchos*) were inoculated with the virulent strain A/Ty/Ont/7732/66 (H5N9). Viruses recovered from the ducks were analyzed by hemagglutination inhibition (HI) and enzyme-linked immunosorbent assay (ELISA) and found to possess antigenically altered viral hemagglutinins. Plaque formation on the Madin-Darby Canine Kidney (MDCK) cell line and on primary chicken embryo cells was investigated, and isolates recovered from the ducks differed from the wild type by being unable to form plaques on MDCK cells without trypsin. This phenotype did not appear to be due to inefficient cleavage of the hemagglutinin by host cell proteases since hemagglutinin immunoprecipitated from cell lysates was cleaved. Although the plaquing phenotype suggested attenuation of the isolates from the ducks, they were not significantly altered in their virulence for chickens shown by infectivity studies in vivo. These results indicate that replication of influenza A/Ty/Ont/7732/66 virus in ducks can produce antigenic and phenotypic variants which are still highly virulent for domestic poultry.

Descriptors: ducks microbiology, fowl plague microbiology, influenza A virus avian pathogenicity, antibodies, monoclonal immunology, antigenic variation, cell line, chickens, enzyme linked immunosorbent assay, fowl plague mortality, hemagglutination inhibition tests, hemagglutinin viral analysis, hemagglutinins viral metabolism, influenza A virus avian growth and development, influenza A virus avian immunology, influenza A virus avian physiology, phenotype, plaque assay, virulence, virus replication.


Descriptors: epidemiology, disease surveys, avian influenza virus, Italy, game birds, pheasants.

Pilet, C. (1980). *Proceedings of an International Symposium, held on September 13 and 14, 1979 at the Ecole Nationale Veterinaire d'Alfort, France*. Comparative Immunology, Microbiology and Infectious Diseases. Special Issue on Animal and Human Influenzas 3(1/2): xvi + 246. ISSN: 0147-9571.

Descriptors: influenza virus, humans, zoonoses, equine, porcine, avian, symposium.


Abstract: The last major human epidemics of infectious diseases have arisen from animals. Some of them are especially threatening. The authors call attention to the danger of spread of avian influenza, either directly or indirectly through genetic rearrangements. They underline the role of animals in the epidemiology of SARS, West Nile virus, hepatitis E, NIPA and Hendra virus, ehrlichiosis and Lyme disease. The authors recommend health surveillance not only in humans but also in animals; the teaching of zoonoses, and research on animal diseases transmissible to humans.

Descriptors: virus diseases transmission, zoonoses.


Descriptors: influenza infection, solid state NMR, laboratory techniques, antiviral drug action targets, immune system, membranes, immune surveillance, ion transport models, proton transfer reaction model, viral life cycle.


Descriptors: influenza virus, birds, gulls, Astrakhan, virus properties.
Abstract: Investigation of a number of properties of influenza viruses isolated from Laridae birds in the Astrakhan region showed that in one epizootic focus avian influenza viruses with different hemagglutinins and identical neuraminidase may circulate among Laridae birds. Among viruses with the antigenic formula Hav5Nav2 clear-cut differences in virulence and plaque-forming capacity were demonstrated.

Descriptors: birds microbiology, influenza A virus isolation and purification, antigens, viral analysis, chick embryo, chickens, cytopathogenic effect, viral, hemagglutination, viral, hemagglutinins viral analysis, influenza A virus immunology, influenza A virus pathogenicity, mice, neuraminidase analysis, plaque assay, Russia, virulence, virus replication.


NAL Call Number: 281.8 In32
Descriptors: avian influenza virus, disease prevention, disease transmission, hygiene, occupational transmission, poultry, poultry farming.

Descriptors: disease outbreaks, influenza transmission, influenza virology, influenza A virus human, poultry diseases transmission, poultry diseases virology, adolescent, adult, case control studies, chickens, child, child, preschool, ducks, Hong Kong epidemiology, infant, influenza epidemiology, influenza veterinary, middle aged, neutralization tests, population surveillance, poultry diseases epidemiology.


NAL Call Number: QR180.C4
Descriptors: bird diseases immunology, bursa of fabricius immunology, influenza immunology, thymus gland immunology, antigens, bursa of fabricius drug effects, chickens, erythrocytes immunology, hemagglutination tests, immunoelectrophoresis, lectins pharmacology, lymphocyte activation, orthomyxoviridae immunology, radiation chimera, sheep immunology, testosterone pharmacology, thymectomy.


NAL Call Number: 286.81 F322
Descriptors: avian influenza virus, economics, disease control, poultry, impact, United States.


NAL Call Number: aSF995.6.l6l5 1981a
Descriptors: avian influenza virus, Minnesota, economic impact, chickens, turkeys, outbreaks, symposium.


NAL Call Number: RA648.5.E46
Descriptors: AIDS, acquired immunodeficiency syndrome, Ebola virus disease, SARS, severe acute respiratory syndrome, West Nile fever, avian influenza, bovine spongiform encephalopathy, prion disease, Edward Hicks artist, zoonosis, biography, history, epidemiology.


NAL Call Number: QR189.A73
Descriptors: avian influenza virus, antibodies, epidemiology, identification, immune response, virulence, Iran.

Descriptors: disease control, legislation, mutations, outbreaks, policy, amino acids, poultry, sentinel surveillance, waterfowl, zoonoses, avian influenza virus, fowl.


NAL Call Number: 448.3 Ar23

Abstract: Two hundred ninety-four subjects from Milan were tested for serum hemagglutination-inhibiting (HI) and neuraminidase-inhibiting (NI) antibodies to five avian influenza viruses. No HI antibodies were found in all the serum samples. On the contrary, NI antibodies to each strain were detected depending on the year of birth of the subjects.

Descriptors: influenza immunology, influenza A virus avian immunology, hemagglutination inhibition tests, hemagglutinins viral immunology, influenza microbiology, influenza A virus avian pathogenicity, neuraminidase antagonists and inhibitors, neuraminidase immunology.


NAL Call Number: 448.8 P942


Descriptors: influenza prevention and control, influenza A virus, avian immunology, influenza vaccines supply and distribution, drug industry, United States, vaccination.


NAL Call Number: 41.8 Ir4

Descriptors: avian influenza virus, diagnosis, disease control, disease prevention, disease transmission, fowl diseases, lesions, poultry, viral replication, zoonoses, fowl, reviews.


NAL Call Number: 41.8 Av5

Descriptors: Mycoplasma infections pathology, orthomyxoviridae infections pathology, poultry diseases, antibody formation, hemagglutination inhibition tests, immune sera analysis, lung diseases pathology, lung diseases veterinary, mycoplasma pathogenicity, Mycoplasma infections immunology, orthomyxoviridae pathogenicity, orthomyxoviridae infections immunology, pulmonary alveoli immunology, pulmonary alveoli microbiology, pulmonary alveoli pathology, turkeys.


Descriptors: ducks, fowl plague microbiology, influenza A virus avian isolation and purification, antigens, viral isolation and purification, fowl plague immunology, hemagglutination tests, India.


NAL Call Number: SF481.P622
Descriptors: avian influenza virus, poultry, chickens.

Descriptors: disease outbreaks prevention and control, influenza A virus, avian influenza prevention and control, avian influenza transmission, international cooperation, zoonoses transmission.

Descriptors: influenza prevention and control, influenza A virus, avian immunology, influenza vaccines, chickens, clinical trials, influenza virology.

Reeves, K. (1998). New strain of influenza type A in Hong Kong. *Infection Control and Hospital Epidemiology the Official Journal of the Society of Hospital Epidemiologists of America* 19(2): 141. ISSN: 0899-823X.
Descriptors: influenza epidemiology, influenza virology, influenza A virus avian, Hong Kong epidemiology, influenza prevention and control, population surveillance.

NAL Call Number: 41.8 Av5
Abstract: Wild waterfowl that were captured between 1915 and 1919 and preserved in 70% ethyl alcohol were tested for influenza A virus RNA. Most of the HA1 domain of the hemagglutinin (HA) gene segment was sequenced from one bird, captured in 1917, that was infected with a virus of the same HA subtype as the 1918 human pandemic virus. The 1917 HA sequence is closely related to modern avian HA sequences, suggesting little drift in avian sequences in 80 years and that the 1918 pandemic virus probably did not acquire its hemagglutinin directly from a bird. A 151-bp fragment of the nucleoprotein gene segment was sequenced from two pre-1918 birds and compared to avian and mammalian influenza strains. The 1917 avian NP sequences are also closely related to modern avian sequences and distinct from the mammalian clade in which the 1918 NP sequence is found.
Descriptors: epidemiology, infection, molecular genetics, pandemic.

NAL Call Number: SF780.9.S63
Descriptors: epidemiology, antibiotics, diagnosis, disease control, disease prevalence, disease transmission, domestic animals, drug resistance, milk production, milk quality, models, risk factors, animal trade, zoonoses, cattle, dogs, horses, pigs, sheep, poultry, proceedings.

NAL Call Number: R21.M43
Descriptors: avian influenza, humans, continual threat, birds, pigs.

NAL Call Number: 410.9 P94
Abstract: Studies of the pathogenesis of influenza infection have involved the extensive use of animal models. The development of the current concepts of immunity to influenza and of the contribution the secretory immune system makes toward the protection of mucosal surfaces against influenza infection would have been impossible without this use of animals. The pathology and clinical signs of influenza infection in both natural and experimental hosts, the advantages and disadvantages of the most common experimental influenza infection models, and the contribution of animal models to the understanding of local and systemic immunity to influenza infection are discussed.

**Descriptors:** poultry, epidemiology, clinical aspects, diagnosis, treatment, avian influenza virus.


**Descriptors:** disease outbreaks, influenza epidemiology, influenza, avian transmission, zoonoses epidemiology, communicable diseases, emerging epidemiology, communicable diseases, emerging prevention and control, influenza prevention and control.


**NAL Call Number:** QR189.V32

**Abstract:** Direct DNA inoculations have been used to demonstrate that in vivo transfections can be used to elicit protective immune responses. The direct inoculation of an H7 haemagglutinin-expressing DNA protected chickens against lethal challenge with an H7N7 influenza virus. Three-week-old chickens were vaccinated by inoculating 100 micrograms of plasma DNA by each of three routes (intravenous, intraperitoneal, and subcutaneous). One month later, chickens were boosted with 100 micrograms of DNA by each of the three routes. At 1-2 weeks postboost, chickens were challenged via the nares with 100 lethal doses of an H7N7 virus. Low to undetectable levels of H7-specific antibodies were present postvaccination and boost. High titres of H7-specific antibodies appeared within 1 week of challenge. In a series of four experiments, 50% (28/56) of the DNA-vaccinated and < 2% (1/67) of the control chickens survived the challenge. This exceptionally simple method of immunization holds high promise for the development of subunit vaccines.

**Descriptors:** DNA, viral genetics, defective viruses immunology, genetic vectors, hemagglutinins viral immunology, influenza immunology, influenza prevention and control, influenza A virus avian immunology, influenza vaccine immunology, leukosis virus, avian genetics, plasmids, recombinant fusion proteins immunology, amantadine pharmacology, chickens immunology, defective viruses drug effects, defective viruses genetics, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral biosynthesis, hemagglutinins viral genetics, immunity, active, immunization, influenza A virus avian drug effects, influenza A virus avian genetics, recombinant fusion proteins biosynthesis, recombinant fusion proteins genetics, specific pathogen free organisms, transfection.


**NAL Call Number:** 41.8 Am3A

**Descriptors:** immunosuppression, orthomyxoviridae infections veterinary, poultry diseases immunology, turkeys immunology, bursa of fabricius immunology, bursa of fabricius surgery, hemagglutination inhibition tests, hemagglutinins viral immunology, immunity, cellular, orthomyxoviridae immunology, orthomyxoviridae infections immunology.


**NAL Call Number:** 41.8 Av5

**Descriptors:** avian influenza virus, environmental stress, environmental temperature, heat, cold, transportation, food deprivation, carrier state, poultry, turkeys.

Abstract: It has been previously reported that several human H1 influenza viruses isolated prior to 1956, in contrast to human H3 isolates which are quite specific for SA α2,6Gal sequences, apparently recognize both SA α2,3Gal and SA α2,6Gal sequences (Rogers, G.N., and Paulson, J.C., Virology 127, 361-373, 1983). In this report human H1 isolates representative of two epidemic periods, from 1934 to 1957 and from 1977 to 1986, and H1 influenza isolated from pigs, ducks, and turkeys were compared for their ability to utilize sialyloligosaccharide structures containing terminal SA α2,3Gal or SA α2,6Gal sequences as receptor determinants. Five of the eight human isolates from the first epidemic period recognize both SA α2,3Gal and SA α2,6Gal linkages, in agreement with our previous results. Of the remaining three strains, all isolated towards the end of the first epidemic, two appear to prefer SA α2,6Gal sequences while the third preferentially binds SA α2,3Gal sequences. In contrast to the early isolates, 11 of 13 human strains isolated during the second epidemic period preferentially bind SA α2,6Gal containing oligosaccharides. On the basis of changes in receptor binding associated with continued passage in the laboratory for some of these later strains, it seems likely that human H1 isolates preferentially bind SA α2,6Gal sequences in nature, and that acquisition of SA α2,3Gal-binding is associated with laboratory passage. Influenza H1 viruses isolated from pigs were predominantly SA α2,6Gal-specific while those isolated from ducks were primarily SA α2,3Gal-specific. Thus, as has been previously reported for H3 influenza isolates, receptor specificity for influenza H1 viruses appears to be influenced by the species from which they were isolated, human isolates binding preferentially to SA α2,6Gal-containing oligosaccharides while those isolated from ducks prefer SA α2,3Gal-containing oligosaccharides. However, unlike the SA α2,6Gal-specific H3 isolates, binding to cell surface receptors by the H1 influenza viruses is not sensitive to inhibition by horse serum glycoproteins, regardless of their receptor specificity. These results suggest that, while the H1 and H3 hemagglutinins appear to be subject to similar host-derived selective pressures, there appear to be certain fundamental differences in the detailed molecular interaction of the two hemagglutinins with their sialyloligosaccharide receptor determinants.

Descriptors: influenza A virus avian metabolism, influenza A virus human metabolism, influenza A virus, porcine metabolism, influenza A virus metabolism, orthomyxoviridae metabolism, receptors, virus metabolism, ducks, hemagglutination inhibition tests, hemagglutination tests, species specificity, swine, turkeys.


Descriptors: avian influenza virus, Hav 5, epidemiology, Anseriformes, Europe.

NAL Call Number: 448.3 M583
Descriptors: influenza A virus avian, viral vaccines, virus cultivation, chick embryo, chickens, HeLa cells, orthomyxoviridae infections immunology, tissue culture, vaccination.

NAL Call Number: 448.8 P942
Abstract: Two strains of influenza A viruses were isolated in 1978 from tracheal washings of 18 nestlings of black-headed gulls examined for influenza. Three strains of influenza A viruses were isolated in 1979 from 55 gull embryos collected in the same colony, the isolates being similar in their antigenic characteristics with the influenza virus isolated from a gull nestling in 1978. This confirms the possibility of simultaneous circulation of antigenically different variants of influenza A virus among birds in the same colony and transoviral transmission of virus to the offsprings.
Descriptors: bird diseases epidemiology, fowl plague epidemiology, bird diseases microbiology, bird diseases transmission, birds, cloaca microbiology, embryo, nonmammalian microbiology, fowl plague microbiology, fowl plaque transmission, influenza A virus avian isolation and purification, Siberia, trachea microbiology.

Descriptors: pharmacology, pathology, prevention, control, African horse sickness, Newcastle disease, bluetongue, contagious bovine pleuropneumonia, foot and mouth disease, goat pox, highly pathogenic avian influenza, lumpy skin disease, peste des petits ruminants, Rift Valley fever, rinderpest, sheep pox, swine fever, vesicular stomatitis, Office International des Epizooties, OIE, List A diseases, member countries, symposium.

NAL Call Number: 41.8 B45
Abstract: Findings based on molecular genetics and phylogeny indicate that avian species represent an important reservoir for influenza viruses and that virus strains of man and different mammals originated from avian influenza virus ancestors. In contrast to infectious agents causing classical zoonoses, influenza viruses have to alter their genetic make up in order to change their host range. The special, segmented structure of the viral RNA allows an exchange of gene(s) between two different influenza viruses (reassortment) resulting in viruses with different combinations of genome segments and thereby creating new biological properties. Under the selective pressure of the new host the most adapted virus variants will succeed which arose from a genetically heterogeneous virus population with additional mutations. In particular mutations of the genes encoding the polymerase complex (mutator mutations) would be advantageous for rapid adaptation in a hostile environment. The generation of influenza viruses capable of overcoming the species barrier is a rare event since only virus variants will succeed which are genetically stable and transmissible and which replicate efficiently in the new host. It is considered likely that pigs act as intermediate hosts for adaptation of avian viruses to man.
Descriptors: influenza transmission, influenza veterinary, orthomyxoviridae genetics, zoonoses, birds, mammals, mutation, orthomyxoviridae pathogenicity, species specificity, swine, variation genetics.

Descriptors: avian influenza virus, epidemiology.


NAL Call Number: QR360.A1J6

Descriptors: antibody formation, antigens, viral, fowl plague immunity, influenza A virus avian immunology, neuraminidase analysis, orthomyxoviridae immunology, chickens immunology, hemagglutination inhibition tests, hemagglutinins viral analysis, immune sera, immunization, influenza veterinary, avian enzymology, neutralization tests, orthomyxoviridae enzymology, rabbits immunology, swine, swine diseases microbiology.


Abstract: Proteolytic cleavage of the influenza virus hemagglutinin glycoprotein (HA) by cellular proteases is a prerequisite for virus infectivity, spread of the virus in the infected organism, tissue tropism, and viral pathogenicity. Production of infectious virus depends upon the structure at the HA cleavage site as well as the substrate specificity and the distribution of appropriate enzymes. Differences exist in the specificities of the endoproteases that recognize the different sequence motifs at the cleavage site. With avian influenza viruses that cause lethal systemic infections, the cleavage site consists of multibasic amino acids. Furin, which activates this type of HA, is a member of the subtilisin family and represents the prototype of ubiquitously occurring membrane-bound proteases. On the other hand, serine proteases secreted from a restricted number of cell types and some bacterial enzymes recognize a monobasic cleavage signal at HA of the mammalian and the apathogenic avian influenza viruses. The limited occurrence of these proteases results in only localized infection. Implementation of these defined conditions for virus activation may represent a novel type of disease control.

Descriptors: hemagglutinins viral physiology, orthomyxoviridae enzymology, orthomyxoviridae pathogenicity, serine endopeptidases physiology, subtilisins physiology, furin, hemagglutinins viral chemistry, substrate specificity.


NAL Call Number: QH316.5.E9

Abstract: A total of 267 passerine birds distributed among 37 species were netted during spring 1980 and summer 1981 in the Laurentian and Montreal areas. All the cloacal swabs collected at that time were free of influenza viruses. Three and five days after oral administration of avian or human influenza A virus strains, 108 isolates were obtained from 42 of 134 passerine birds. Positive samples were recovered mainly from the respiratory and the digestive tract and also from liver. Spleen and kidneys. Viral replication is cells from trachea, lungs, gizzard and caecum was detected by indirect immunofluorescence using a monoclonal antibody to influenza A virus nucleoprotein. Viral transmission from inoculated to non inoculated birds placed in the same cages was not observed. On the other hand a similar experimental inoculation of young mallard ducks showed that extensive viral transmission occurred from inoculated to non inoculated ducklings and that infection was found exclusively in the digestive tract. Furthermore viruses were detected in samples of drinking water from all cages containing infected ducks. Passerine birds do not represent an important reservoir of influenza viruses but might contribute to the formation and spreading of recombinants potentially pathogenic for man and animals.

Descriptors: birds microbiology, ecology, fowl plague microbiology, influenza microbiology, influenza A virus avian pathogenicity, human pathogenicity, fowl plague transmission, influenza transmission, Quebec.

NAL Call Number: 448.8 P942
Abstract: Ninety-eight hemagglutinating agents were isolated from washings of cloaca and organs of 750 birds collected in southern and southeastern regions of the Kazakh SSR. Determinations of their type appurtenance allowed 36 agents to be classified into influenza A virus. Among them 4 strains had H1N1 surface antigens, 29 strains were Hav2 Nav5 and 3 strains had unidentified neuraminidase and Hav2. The data on the biological properties of influenza virus strains of both subtypes are presented.

Descriptors: birds microbiology, influenza A virus avian isolation and purification, animals, wild, antigens, viral analysis, hemagglutination inhibition tests, hemagglutination, viral, avian classification, Kazakhstan, neuraminidase analysis.


NAL Call Number: 448.8 V81
Abstract: Highly pathogenic influenza A viruses periodically infect both humans and nonhuman animals, including chickens. To gain insight into the origin of influenza outbreaks in poultry, we investigated two H5N2 viruses, A/chicken/Pennsylvania/13609/93 (Ck/PA/93) and A/chicken/Florida/25717/93 (Ck/FLA/93), that had been isolated in live-bird markets in Pennsylvania and Florida during surveillance studies in 1993. Phylogenetic analysis of the HA genes of these isolates, as well as H5N2 viruses isolated from ruddy turnstone surfbirds in 1991 (A/ruddy turnstone/Delaware/244/91 [RT/DE/91]) and other known H5 strains, indicated that Ck/PA/93 and Ck/FLA/93 share a common ancestor with RT/DE/91 and did not originate from A/chicken/Pennsylvania/1370/83 (Ck/PA/1370/83), which devastated chicken populations in 1983-1984. Both isolates were nonpathogenic in chickens by experimental infection and their HA protein (HA0) could not be cleaved into HA1 and HA2 without trypsin. The sequences at the HA cleavage sites of Ck/PA/93 and Ck/FLA/93 (R-K-T-R) appear to be intermediate between those of virulent and avirulent viruses, raising the possibility that a single mutation could promote virulence in chickens. We therefore recommend eradication of such viruses as soon as they appear.

Descriptors: chickens microbiology, fowl plague microbiology, influenza A virus avian pathogenicity, amino acid sequence, antibodies, monoclonal immunology, antigens, viral immunology, base sequence, birds microbiology, DNA, viral, ducks microbiology, avian genetics, avian immunology, avian isolation and purification, molecular sequence data, phylogeny, virulence.


NAL Call Number: 448.8 V81
Abstract: Phylogenetic analysis of the N8 neuraminidase (NA) genes from 18 influenza A viruses, representing equine and avian hosts in different geographic locations, revealed three major lineages: (i) currently circulating equine 2 viruses; (ii) avian viruses isolated in the Eurasian region, including A/Equine/Jilin/1/89, a recent avian-like N8 isolate found in horses in China; and (iii) avian viruses isolated in North America. Comparison of mutation rates indicated that avian N8 genes have evolved more slowly than their equine counterparts. That is, in both avian lineages, 72% of the nucleotide changes were silent in the terminal branches of the phylogenetic tree, whereas in equine 2 viruses, 59% of the nucleotide changes were silent. This suggests greater selective pressure on the NA gene from the mammalian immune system, leading to progressive evolution. Alternatively, the slower mutation rate for avian N8 genes could reflect a selective advantage gained from a longer, continuous span of evolution. The shape of the phylogenetic tree, the evolutionary rate, and the calculated date of origin for the N8 equine 2 virus lineage were comparable to findings for the equine 2 virus hemagglutinin (HA) gene (Bean et al., J. Virol. 66, 1129-1138, 1992). This suggests that both viral membrane glycoproteins of equine 2 viruses have evolved together and have been subjected to similar levels of selective pressure. Several amino acid residues were found to differ among the three host-specific lineages, but they may not be involved in host restriction of the NA, as they are shared by EQ/Jilin/1/89 and viruses of avian origin. The present findings complement detailed structural information on the N2 and N9 subtypes and should prove valuable in understanding future X-ray diffraction studies of N8 crystals.

Descriptors: genes, structural, viral, influenza A virus genetics, neuraminidase genetics, phylogeny, amino acid sequence, base sequence, cloning, molecular, ducks, Escherichia coli genetics, horses, influenza A

**NAL Call Number:** RA648.5.E46

**Abstract:** We describe the enhanced rumor surveillance during the avian influenza H5N1 outbreak in 2004. The World Health Organization's Western Pacific Regional Office identified 40 rumors; 9 were verified to be true. Rumor surveillance informed immediate public health action and prevented unnecessary and costly responses.

**Descriptors:** influenza prevention and control, avian influenza A virus, population surveillance methods, communication, disease outbreaks, influenza epidemiology, avian influenza epidemiology, World Health Organization.


**NAL Call Number:** Z5055.U49D53

**Descriptors:** avian influenza A virus, diagnosis, pathogenicity, transmissibility, turkeys.


**NAL Call Number:** 41.8 Av5

**Descriptors:** eggs, fertility, influenza veterinary, poultry diseases physiopathology, turkeys, antibodies analysis, hemagglutination inhibition tests, influenza physiopathology, insemination, artificial, orthomyxoviridae, semen microbiology.


**NAL Call Number:** 41.8 Am3A

**Descriptors:** bird diseases microbiology, influenza veterinary, orthomyxoviridae pathogenicity, poultry diseases microbiology, turkeys, antibodies analysis, bird diseases immunology, birds, carrier state veterinary, chick embryo immunology, hemagglutination inhibition tests, immune sera analysis, influenza immunology, infections, intramuscular, injections, intravenous, nose microbiology, ovum immunology, poultry diseases immunology, trachea microbiology.


**Descriptors:** avian influenza virus, diagnosis, prevention, losses, poultry.


**NAL Call Number:** 448.8 V81

**Abstract:** H2N2 influenza A viruses caused the Asian pandemic of 1957 and then disappeared from the human population 10 years later. To assess the potential for similar outbreaks in the future, we determined the antigenicity of H2 hemagglutinins (HAs) from representative human and avian H2 viruses and then analyzed the nucleotide and amino acid sequences to determine their evolutionary characteristics in different hosts. The results of longitudinal virus surveillance studies were also examined to estimate the prevalence of avian H2 isolates among samples collected from wild ducks and domestic poultry. Reactivity patterns obtained with a large panel of monoclonal antibodies indicated antigenic drift in the HA of human H2 influenza viruses, beginning in 1962. Amino acid changes were clustered in two regions of HA1 that correspond to antigenic sites A and D of the H3 HA. By contrast, the antigenic profiles of the majority of
avian H2 HAs were remarkably conserved through 1991, resembling the prototype Japan 57 (H2N2) strain. Amino acid changes were distributed throughout HA1, indicating that antibodies do not play a major role in the selection of avian H2 viruses. Phylogenetic analysis revealed two geographic site-specific lineages of avian H2 HAs: North American and Eurasian. Evidence is presented to support interregion transmission of gull H2 viruses. The human H2 HAs that circulated in 1957-1968 form a separate phylogenetic lineage, most closely related to the Eurasian avian H2 HAs. There was an increased prevalence of H2 influenza viruses among wild ducks in 1988 in North America, preceding the appearance of H2N2 viruses in domestic fowl. As the prevalence of avian H2N2 influenza viruses increased on turkey farms and in live bird markets in New York City and elsewhere, greater numbers of these viruses have come into direct contact with susceptible humans. We conclude that antigenically conserved counterparts of the human Asian pandemic strain of 1957 continue to circulate in the avian reservoir and are coming into closer proximity to susceptible human populations.

Descriptors: disease outbreaks, disease reservoirs, hemagglutinins viral genetics, influenza epidemiology, influenza A virus genetics, orthomyxoviridae infections epidemiology, Americas epidemiology, antibodies, monoclonal, antibodies, viral immunology, Asia epidemiology, birds microbiology, Europe epidemiology, evolution, fowl plague epidemiology, fowl plague genetics, genes viral genetics, hemagglutinin glycoproteins, influenza virus, influenza genetics, influenza A virus avian genetics, avian immunology, human genetics, human immunology, influenza A virus immunology, molecular sequence data, orthomyxoviridae infections genetics, phylogeny, population surveillance, time factors.


Descriptors: antigens, surface analysis, antigens, viral analysis, hemagglutinins viral analysis, influenza A virus immunology, antigens, viral classification, hemagglutinin viral classification, influenza A virus avian immunology, human immunology, porcine immunology, neuraminidase immunology, terminology.


Descriptors: pharmacology, prevention, control, foot and mouth disease, Newcastle disease, avian influenza, Office International des Epizooties, OIE, World Trade Organization, WTO, international standards, international animal health code, List A diseases.


Descriptors: infection, occupational health, avian influenza A virus, viral pneumonia, veterinarian, human death, Netherlands.


NAL Call Number: 475 Ex7

Abstract: With regard to molecular epidemiology, influenza A viruses belong to the best-studied virus systems. At least two large reservoirs of influenza A viruses have been built up in nature, one in humans and another one in water fowls. The latter one is very heterogenous, consisting of viruses belonging to 13 hemagglutinin (HA) and 9 neuraminidase (NA) subtypes in almost all possible combinations. The segmented
structure of the influenza virus genome allows the creation of new influenza strains by reassortment. By replacement of the HA gene of human strains new pandemic viruses can be generated (antigenic shift). The particular structure of the HA enables the human influenza A-viruses to create variants which can escape the immune response of the host (antigenic drift). The nucleoprotein is responsible for keeping those two large reservoirs apart. Mixing of genes of viruses from these two reservoirs seems to happen predominantly by double infection of pigs, which apparently are tolerant for infection by either human or avian influenza viruses. The molecular mechanisms described for influenza viruses can be explained by the particular structure of their genome and their components and cannot be generalized. Each virus has developed its own strategy to multiply and to spread.

Descriptors: influenza A virus genetics, orthomyxoviridae infections epidemiology, antigens, viral genetics, antigens, viral immunology, birds microbiology, capsid genetics, capsid immunology, disease reservoirs, genes viral, hemagglutinins genetics, hemagglutinins immunology, influenza A virus immunology, influenza A virus pathogenicity, orthomyxoviridae infections immunology, variation genetics, viral core proteins genetics, viral core proteins immunology.

NAL Call Number: RA648.5.E97

Abstract: There are three ways how influenza A viruses can escape the immune response in the human population: (1) By antigenic drift. This means by mutation and selection of variants under the selection pressure of the immune system. These variants have amino acid replacements mainly in the epitopes of the hemagglutinin. (2) By antigenic shift. This means replacement of at least the hemagglutinin gene of the prevailing human strain by the allelic gene of an avian influenza virus by reassortment. (3) As a rare event, direct or indirect introduction of an avian influenza virus in toto into the human population. A prior introduction of an avian virus into pigs and an adaptation to the new host might be a presupposition for its final passage to humans. In this sense the nowadays situation is reminiscent to that of about 100 years ago, when an avian virus was presumably first introduced into pigs, and from there into humans. Immediately or some time thereafter the disastrous Spanish Flu in 1918/19 had killed at least 20,000,000 people in one winter. Pandemic strains can be created by all three means, however the most common way is by reassortment. In order to recognize a pandemic strain as soon as possible a worldwide surveillance system and collaborating laboratories equipped with corresponding modern technologies are required.

Descriptors: disease outbreaks, influenza epidemiology, influenza virology, orthomyxoviridae genetics, antigenic variation genetics, antigens, viral genetics, birds, genes viral genetics, influenza A virus avian genetics, avian immunology, porcine genetics, porcine immunology, orthomyxoviridae immunology, swine.

NAL Call Number: 448.8 V81

Abstract: There is evidence that the nucleoprotein (NP) gene of the classical swine virus (A/Swine/1976/31) clusters with the early human strains at the nucleotide sequence level, while at the level of the amino acid sequence, as defined by consensus amino acids and in functional tests, its NP is clearly "avian like." Therefore it was suggested that the Sw/31 NP had been recently under strong selection pressure, possibly caused by reassortment with other avian influenza genes, whose gene products have to cooperate intimately with NP (Gammelin et al., 1989. Virology 170, 71-80). This suggestion has been investigated by sequencing the genes of internal and nonstructural proteins of Sw/31. The data on these sequences and on the phylogenetic trees are not in accordance with that suggestion: all these genes cluster with the early human strains at the nucleotide level while, at the level of the amino acid sequence, most of them are more closely related to the avian strains, thus resembling NP in this respect. This indicates that these genes rather evolved concomitantly with the NP gene. Our data are in agreement with the suggestion that, at about the time of the Spanish Flu (1918/19), a human influenza A (H1N1) virus entered the pig population. Furthermore, it is known that the NP of the human influenza A viruses—in contrast to that of the avian and swine strains—has been under strong selection pressure to change (Gammelin et al., 1990. Mol. Biol. Evol. 7, 194-200. Gorman et al., 1990a. J. Virol. 64, 1487-1497). Thus, after transfer of a human strain into pigs, the selection pressure might be released, enabling the NP and the other genes of the swine virus to evolve...
back to the optimal avian sequences, especially at the functionally important consensus positions. The swine influenza viruses circulating since 1979 in Northern Europe—represented by A/Swine/Germany/2/81 (H1N1)—have all genes, so far examined, derived from an avian influenza virus pool and are different from the classical swine viruses.

Descriptors: influenza A virus, porcine genetics, phylogeny, RNA replicase, viral proteins genetics, chick embryo, consensus sequence, genes viral, nucleoproteins genetics, swine, viral core proteins genetics.

NAL Call Number: 41.8 Av5

Abstract: Eight-week-old chickens were inoculated with one of two exotic viruses to determine the effect of composting on virus survival. Group 1 chickens were inoculated with highly pathogenic avian influenza (HPAI) virus via the caudal thoracic air sac. Group 2 chickens were inoculated with the adenovirus that causes egg drop syndrome-76 (EDS-76) by the oral route. Five days after inoculation, lung, trachea, and air sacs for HPAI and spleen, cecal tonsils, and bursa of Fabricius for EDS-76 were collected and composted with poultry carcasses. At the end of the first 10 days of composting, virus-isolation efforts showed that the HPAI virus had been inactivated, and only 1 of 20 tissue samples yielded the adenovirus of EDS-76. The viruses of HPAI and EDS-76 were completely inactivated at the end of the second 10-day period of the two-stage composting process. Control tissues collected at necropsy and frozen at -70°C for virus isolation were all positive for virus.

Descriptors: chickens, avian influenza virus, aviadenovirus, survival, animal diseases, carcasses, waste disposal, composting, disease control, adenoviridae, birds, domestic animals, domesticated birds, environmental protection, Galliformes, influenza virus, livestock, orthomyxoviridae, pollution control, poultry, processing, useful animals, viruses, waste management, two stage composting, inactivation.

NAL Call Number: 41.8 Av5

Abstract: From October 1973 to September 1981, 2,882,111 birds were offered for importation into the United States. All were quarantined for 30 days, and specimens were submitted to the laboratory for virus-isolation studies. Viruses were isolated from specimens from 26.3% (598/2,274) of the quarantined lots of birds. Viscerotropic velogenic Newcastle disease virus (VVNDV) was isolated from 141 lots. Nonviscerotropic velogenic Newcastle disease virus (VNDV) was isolated from six lots. All VVNDV- and VNDV-positive lots were refused entry. The percentage of lots refused entry declined from 31.6% in 1974 to 2.9% in 1981. Mesogenic Newcastle disease virus (NDV) was isolated from three lots, and lentogenic NDV was isolated from 23 lots. Lots positive for mesogenic and lentogenic NDV were allowed to enter the United States. Hemagglutinating (HA) viruses other than NDV were isolated from 24.5% (373/1,521) of the lots imported through privately owned quarantine facilities. Of the 8,563 HA viruses isolated, 1,558 were selected for identification. Forty-six percent were identified as paramyxovirus (PMV)-2, 34% were PMV-3, and 20% were influenza A viruses possessing the hemagglutinin subtypes H3, H4, H7, and H10 and the neuraminidase subtypes N1, N6, N7, and N8. The frequency of PMV-2 and PMV-3 isolations fluctuated from year to year, whereas the frequency of isolations of influenza A viruses decreased from 64% in 1974 to 0.2% in 1981. Viruses that did not agglutinate chicken red blood cells were isolated from 52 lots. Psittacine herpesvirus (Pacheco's disease) was isolated from 25 lots of psittacines. Viruses identified by electron microscopy as reoviruses were isolated from 24 lots. (ABSTRACT TRUNCATED AT 250 WORDS)

Descriptors: birds microbiology, viruses isolation and purification, animals, domestic, hemagglutination, viral, influenza A virus avian isolation and purification, Newcastle disease virus isolation and purification, Newcastle disease virus pathogenicity, quarantine, respirovirus isolation and purification, species specificity, United States, virulence.

Surveillance for H5 and H7 subtypes of avian influenza virus (AIV) in the live-bird markets (LBMs) of the northeastern United States has been in effect since 1986 when the markets were first recognized as a potential reservoir for AIV. Long-term maintenance of AIV in the LBM system has been documented. However, little is known about the influence of successive cycles of replication in unnatural avian hosts (gallinaceous birds) on the genetics of the virus, especially in the region of the hemagglutinin (HA) gene that can influence pathogenicity. Isolation of low-pathogenicity H5 AIVs from the LBMs has been sporadic; however, in 1994 a low-pathogenicity H7N2 virus was isolated that has persisted in the LBMs for more than 7 yr. Efforts to eliminate the H7 virus from the markets have been unsuccessful. During the 7-yr period, several molecular changes have occurred at the hemagglutinin cleavage site of the H7 virus. These changes include substitutions of proline for threonine and lysine for asparagine, respectively, at the -2 and -5 positions of the HA1 protein. In addition, there has been a 24 nucleotide base-pair deletion in the receptor binding region of the HA1. The accumulation of an additional basic amino acid at the cleavage site is a cause for concern to regulatory authorities, and, therefore, efforts to eliminate the virus from the LBM system have been intensified.

Descriptors: epidemiology, infection, live bird markets, molecular epidemiology, viral characteristics, biological, molecular viral pathogenicity, viral reservoir.


Cyclical and seasonal. Influenza was found mainly in the summer and paramyxoviruses in the winter.

**Descriptors:** influenza A virus avian isolation and purification, paramyxoviridae isolation and purification, poultry microbiology, antigens, viral analysis, cloaca microbiology, Hong Kong, avian immunology, Newcastle disease virus immunology, Newcastle disease virus isolation and purification, paramyxoviridae immunology, trachea microbiology.


**Abstract:** In the last two decades, influenza A viruses have been found to occur throughout the animal kingdom, mainly in birds, notably aquatic ones, in which infection is largely intestinal, waterborne, and asymptomatic. The domestic duck of southern China, raised in countless numbers all year round mainly as an adjunct to rice farming, is the principal host of influenza A viruses. Studies based on Hong Kong H3N2 viruses from southern China suggest that pandemic strains originate from the domestic duck there and are transmitted to humans via the domestic pig, which acts as a "mixing vessel" for two-way transmission of viruses. This provides further support for the hypothesis that the region is a hypothetical influenza epicenter. Rural dwellers in the epicenter show serological evidence of contact with non-human influenza A viruses. Two hypotheses are advanced for the range of hemagglutinin (HA) subtypes of viruses that can cause pandemics (1) circle or cycle limited to H1, H2, and H3 subtypes, thereby implying that a virus of the H2 subtype will cause the next pandemic; and (2) spiral, by which any one of the 14 HA subtypes recorded to date may be involved. Consideration is given to the temporal and geographical factors and range of hosts, namely the duck, pig, and human, that need to be submitted to virus surveillance in China and beyond to attempt to anticipate a future pandemic. Evidence is presented that points strongly to pandemic influenza being a zoonosis.

**Descriptors:** ducks microbiology, influenza transmission, influenza A virus avian pathogenicity, human pathogenicity, porcine pathogenicity, swine microbiology, zoonoses transmission, China epidemiology, chronology, disease outbreaks prevention and control, feces microbiology, fresh water, influenza epidemiology, influenza microbiology, avian isolation and purification, human isolation and purification, porcine isolation and purification, reassortant viruses genetics.


**NAL Call Number:** QR189.V32

**Descriptors:** disease outbreaks, influenza epidemiology, chickens, Hong Kong epidemiology, influenza A virus avian isolation and purification.


**NAL Call Number:** SF601.V44

**Abstract:** This account takes stock of events and involvements, particularly on the avian side of the influenza H5N1 'bird flu' incident in Hong Kong SAR in 1997. It highlights the role of the chicken in the many live poultry markets as the source of the virus for humans. The slaughter of chicken and other poultry across the SAR seemingly averted an influenza pandemic. This perspective from Hong Kong SAR marks the coming-of-age of acceptance of the role of avian hosts as a source of pandemic human influenza viruses and offers the prospect of providing a good baseline for influenza pandemic preparedness in the future. Improved surveillance is the key. This is illustrated through the H9N2 virus which appears to have provided the 'replicating' genes for the H5N1 virus and which has since been isolated in the SAR from poultry, pigs and humans highlighting its propensity for interspecies transmission.

**Descriptors:** influenza transmission, influenza A virus avian pathogenicity, zoonoses transmission, chickens, disease outbreaks prevention and control, fowl plague transmission, Hong Kong epidemiology, influenza mortality, influenza virology, avian genetics.

virusom. [Isolation of the influenza virus from the tree sparrow and a study of the infectivity of this virus in wild birds of the central Dnieper River area]. Voprosy Virusologii 30(6): 657-61. ISSN: 0507-4088.

NAL Call Number: 448.8 P942

Abstract: An influenza virus belonging to the serovariant A/H3N2 and registered as A/sparrow/Ukraine/83 was isolated from a member of synanthropic birds, a tree sparrow, near Kanev. This virus showed low pathogenicity and immunologic activity in experimental infection of sparrows and other birds. Sera from a number of avian and mammal species had antibodies to this virus which indicates that synanthropic and semi-synanthropic birds may be a connecting link in spread of influenza virus.

Descriptors: birds microbiology, fowl plague microbiology, influenza A virus avian isolation and purification, antibodies, viral analysis, antigens, viral analysis, chick embryo, disease vectors, epitopes analysis, avian classification, avian ultrastructure, microscopy, electron, serotyping, Ukraine, virion classification, virion isolation and purification, virion ultrastructure.


NAL Call Number: SF602.M8

Descriptors: avian influenza virus, human, zoonoses, diagnosis, disease distribution, disease prevalence, disease transmission, epidemiology, poultry, zoonoses.


NAL Call Number: SF604.J342

Abstract: Two-day-old specific-pathogen free chicks were inoculated with type A influenza virus (A/whistling swan/Shimane/499/83 (H5N3) through the air sac. Inoculated chicks showed mild to severe diarrhea and lesions of pancreatitis and atrophy of the pancreas, thymus and bursa of Fabricius. One chick died on each of days 4, 6 and 14 postinoculation (PI). Reduced weight gain was conspicuous from day 22 PI. Positive immunoreaction to the virus antigen was detected in the pancreas, kidneys, liver, lungs and air sacs, and cecal lamina propria. Virus recovery persisted longer in the pancreas. Some of these findings conformed to those of stunting syndrome.

Descriptors: chickens, growth disorders veterinary, influenza A virus avian physiology, poultry diseases virology, air sacs immunology, air sacs virology, antigens, viral analysis, antigens, viral immunology, atrophy, bursa of fabricius pathology, growth disorders pathology, growth disorders virology, avian immunology, kidney immunology, kidney virology, liver immunology, liver virology, lung immunology, lung virology, pancreas pathology, pancreatitis etiology, pancreatitis pathology, pancreatitis veterinary, poultry diseases pathology, poultry diseases physiopathology, regression analysis, syndrome, thymus gland pathology, weight gain physiology.


NAL Call Number: 41.8 J93

Descriptors: avian influenza, virus properties, epidemiology.


NAL Call Number: 41.8 Av5

Abstract: An outbreak of highly pathogenic avian influenza caused by multiple genotypes of H5N1 virus occurred in Hong Kong, commencing in January 2002. Infection in local chicken farms was preceded by the detection of virus in multiple retail markets and the main poultry wholesale market. The first case of this disease on a local farm was detected on February 1, 2002. By February 9, 2002, 15 farms were infected, and by late March a total of 22 infected farms had been identified. Three main clusters of infected farms were seen, suggesting multiple incursions of virus, and subsequent limited lateral spread to neighboring
farms. Control of this disease has been effected through a combination of quarantine, tightening of biosecurity measures, and depopulation of infected and contact farms. About 950,000 birds have been destroyed. Vaccination using a killed H5 vaccine was introduced in April 2002 to farms in one zone where infection has persisted. None of the viruses isolated contained the internal genes found in the 1997 H5N1 virus.

Descriptors: epidemiology, infection, avian influenza, infectious disease, respiratory system disease, viral disease, genotyping genetic techniques, laboratory techniques, poultry farm, poultry wholesale markets, viral pathogenesis.


Descriptors: communicable disease control trends, disease outbreaks prevention and control, disease outbreaks veterinary, influenza epidemiology, avian influenza epidemiology, birds, communicable disease control economics, communicable disease control history, disease outbreaks history, history, 20th century, influenza history, world health.


NAL Call Number: 41.8 Am3

Descriptors: fowl plague epidemiology, influenza A virus avian pathogenicity, birds, disease outbreaks veterinary, fowl plague mortality, avian isolation and purification, Virginia epidemiology, virulence.


NAL Call Number: 41.8 Ex7

Descriptors: influenza A virus genetics, mutation, recombination, genetic, disease outbreaks, gene frequency, influenza A virus avian genetics, influenza A virus, porcine genetics, influenza A virus metabolism, neuraminidase metabolism.


NAL Call Number: 448.3 AC85

Descriptors: antibodies, viral immunology, ducks immunology, influenza A virus avian immunology, epidemiologic methods, fowl plague epidemiology.


NAL Call Number: 41.8 V6426

Descriptors: influenza veterinary, poultry diseases epidemiology, influenza epidemiology, poultry, poultry diseases microbiology, Russia.


NAL Call Number: 41.8 AV5

Abstract: This is the first report of the isolation of H13N2 avian influenza virus (AIV) subtype from domestic turkeys. This subtype was also isolated from nearby surface water. The observation of large numbers of gulls in close association with turkeys on range before the virus isolations suggests that this virus subtype was transmitted from gulls to range turkeys. Turkey flocks infected by this virus subtype did not show any clinical signs of the disease, although seroconversion did occur. The H13N2 isolates were found to be non-pathogenic in chickens.

Descriptors: fowl plague microbiology, influenza A virus avian isolation and purification, turkeys, water microbiology, birds, chickens, cloaca microbiology, fowl plague transmission, Minnesota, specific pathogen free organisms, trachea microbiology.


**Abstract:** Type-A influenza viruses were commonly recovered from cloacal swab specimens from migratory waterfowl. Experiments indicated that the virus replicated in various cells of the digestive tract.

**Descriptors:** ducks microbiology, feces microbiology, influenza A virus avian isolation and purification, cloaca microbiology, intestines microbiology, trachea microbiology.

Slemons, R.D., W.R. Hansen, K.A. Converse, and D.A. Senne (2003). **Type A influenza virus surveillance in free-flying, nonmigratory ducks residing on the eastern shore of Maryland.** *Avian Diseases* 47(Special Issue): 1107-1110. ISSN: 0005-2086.

**Abstract:** Virus surveillance in free-flying, nonmigratory ducks living on the eastern shore of Maryland indicated that influenza A viruses were introduced into the area or that the prevalence of endemic infections increased between July 15 and August 27, 1998. Cloacal swabs collected between May 28 and July 15, 1998, were negative for influenza A virus recovery (0/233), whereas 13.9% (29/209) of swabs collected between August 27 and September 2, 1998, were positive for influenza A virus recovery. Five hemagglutinin subtypes (H2, H3, H6, H9, and H12), six neuraminidase subtypes (N1, N2, N4, N5, N6, and N8), and nine HA-NA combinations were identified among 29 influenza A isolates. Interestingly, 18 of the 29 isolates initially appeared to contain two or more HA and/or NA subtypes. The free-flying, nonmigratory ducks served as excellent sentinels for the early detection of type A influenza viruses in the southern half of the Atlantic Migratory Waterfowl Flyway during the earliest phase of the yearly southern migration.

**Descriptors:** epidemiology, infection, avian influenza, infectious disease, respiratory system disease, viral disease, Atlantic migratory waterfowl flyway, southern migration, virus surveillance.


**Abstract:** Seventy-six type A influenza viruses recovered from waterfowl in Wisconsin, California, South Dakota, Florida, Texas, Alabama, and Nebraska were tested for virulence in chickens. The challenge to chickens was intravenous inoculation of first-, second-, or third-egg-passage virus. Each of the virus strains was tested separately in three or four chickens. Eighteen of the 76 viruses caused the death of one or more chickens following inoculation. Postmortem lesions were similar in all dead birds. In decreasing order of frequency, gross lesions included: swollen kidneys evident as accentuated lobular patterns, urates in the pericardial sac, and urates on the surface of the liver. Microscopic lesions present in kidneys were consistent with visceral gout. Mortality was associated with inoculations having higher concentrations of infectious virus. These results indicate that the influenza A viruses circulating in duck populations may include strains potentially pathogenic for chickens.

**Descriptors:** chickens, fowl plague pathology, influenza A virus avian pathogenicity, kidney pathology, animals, wild, antibodies, viral biosynthesis, birds, ducks, fowl plague microbiology, fowl plague mortality, geese, avian immunology, avian isolation and purification, virulence.


**Abstract:** Because ducks are considered an important reservoir for type A influenza virus, and type A influenza viruses had not been recovered from ducks in Ohio, a 3-year virus surveillance study was
conducted in Ohio waterfowl and waterfowl passing through Ohio to determine if domestic turkeys were at risk of exposure to avian influenza (AI) viruses from the waterfowl reservoir. The prevalence of AI infections in ducks during the fall migration averaged about 5.9%. The 55 waterfowl-origin type A influenza viruses recovered from ducks during fall 1986, 1987, and 1988 represented 23 different hemagglutinin-neuraminidase sub-type combinations of type A influenza viruses. Virus recovery frequencies ranged from 3.6% to 7.8% between years, from 2.0% to 8.2% between study sites, from 0.0% to 16.7% for sampling days, and from 0.0% to 14.3% among species of ducks sampled. **Descriptors:** disease reservoirs, ducks, fowl plague epidemiology, influenza A virus avian isolation and purification, turkeys, animals, domestic, animals, wild, birds, cloaca microbiology, hemagglutination inhibition tests, avian classification, neuraminidase analysis, Ohio epidemiology, prevalence, seasons, trachea microbiology.

**NAL Call Number:** 41.8 Av5  
**Abstract:** Intravenous inoculation of chickens with a waterfowl-origin type A influenza virus resulted in high titers of virus in kidney tissues and viral nucleoprotein in renal tubular epithelial cells and in intestinal mucosal epithelial cells. Virus titers in kidneys of four of eight clinically normal chickens sampled on days 3 and 5 postinoculation (PI), one dead chicken on day 3 PI, and one dead chicken on day 7 PI exceeded 10(6) mean embryo infectious dose per gram of tissue. Using immunofluorescent and immunoperoxidase staining, viral nucleoprotein was identified in the cytoplasm and nucleus of tubular epithelial cells in kidneys and in nucleus of mucosal epithelial cells lining villi in the lower small intestine. Based on the low intravenous pathogenicity index for this virus (0.3) along with the high virus titers in kidney tissues and localization of viral antigen in kidney important site for replication of avian influenza (AI) virus of low pathogenicity. Recovery of type A influenza viruses from cloacal swabs could result from viral replication in kidneys as well as in the lower intestine and/or the bursa of Fabricius.  
**Descriptors:** chickens microbiology, fowl plague microbiology, influenza A virus avian physiology, intestine, small microbiology, kidney microbiology, fluorescent antibody technique, immunoenzyme techniques, immunohistochemistry, virus replication.

**NAL Call Number:** 41.8 Av5  
**Abstract:** Waterfowl-origin influenza (WFOI) viruses were evaluated for their tissue tropism and replicative properties in chickens. The 14 WFOI isolates used in this study represented 13 different hemagglutinin-neuraminidase combinations recovered during 1987 and 1988 and included isolates possessing the H5 and H7 hemagglutinin subtypes and one isolate possessing the H5N2 combination. Following intravenous challenge, the frequencies of virus recovery within individual experiments were generally higher for the lower digestive tract and kidney samples. Virus titers ranged up to 10(8.5) mean embryo infective doses per gram of kidney tissue in clinically normal chickens. Differences in frequencies of virus recovery and virus titers in tissues indicated that some of these uniformly nonpathogenic and low-pathogenicity WFOI virus isolates replicated more extensively in chickens than did others. This enhanced ability to replicate in chickens should be further evaluated as a potential factor associated with the threat WFOI viruses present to poultry.  
**Descriptors:** ducks virology, influenza A virus avian isolation and purification, avian physiology, organ specificity, virus replication, bursa of fabricius virology, chickens, cloaca virology, fowl plague virology, avian classification, intestine, small microbiology, kidney virology.

**NAL Call Number:** QR375.V6  
**Abstract:** Avian H5N1 influenza A viruses are considered to be of high pandemic potential as they are able to cross the avian-human species barrier and cause disease in humans. In the present study we assessed the impact of amino acid substitutions in the hemagglutinin (HA) of antigenic escape mutants of influenza
A/Mallard/Pennsylvania/10218/84 (H5N2) (Mld/PA/84-MA) virus on the level of neutralizing antibodies and
the ability to protect mice against challenge with the wild type H5 influenza virus. beta-Propiolactone-
inactivated vaccines prepared from eight different H5 escape mutants could be separated into two groups
based on levels of protection. One group of escape mutants [m46(7), m46(7)-24B9, m46(7)-55, and
m46(7)-55-24B9] was characterized by providing high levels of protection (90.0-95.4% survival) to mice
against subsequent challenge with 5 LD(50) of wild type Mld/PA/84-MA virus. The other group of escape
mutants [m176/26, m55(2), m55(2)-24B9, and m24B9-176/26] provided moderate level of protection (57.1-
66.6% survival) in mice. Analysis of the amino acid substitutions in the HA revealed that two amino acid
changes in antigenic site B of the HA molecule (D(126)-->N and K(152)-->N) were associated for decreases
in the levels of antibody and the immune protection afforded by vaccination with these H5 virus escape
mutants. The phenotypic effects of mutations in HA gene of H5 virus may be of importance to appraise the
extent and direction of H5 influenza viruses antigenic evolution.

Descriptors: antibodies, viral blood, hemagglutinin glycoproteins, influenza virus genetics, hemagglutinin
glycoproteins, influenza virus immunology, influenza prevention and control, avian influenza A virus
immunology, influenza vaccines immunology, amino acid substitution, antigens, viral genetics, antigens, viral immunology, genes, viral, influenza virology, avian influenza A virus
growth and development, mice, mutation, missense, neutralization tests, vaccines, inactivated immunology,
virus inactivation.

NAL Call Number: 41.9 W64B
Abstract: Four hemagglutinating agents were isolated from 100 cloacal samples collected from migratory
waterfowl during the 1977 hunting season in Michigan. Three of the isolates are paramyxoviruses and they
show no reactivity with antisera to Newcastle disease virus. The fourth isolate is an orthomyxovirus,
A/Duck/Michigan/77 (Hsw1 Nav2). Under experimental conditions two of the paramyxoviruses were
recovered from the intestinal tract of chicks, and the third paramyxovirus was recovered from both the
respiratory and intestinal tract of chicks. One paramyxovirus was pathogenic for chicks. The type A influenza
virus was recovered from both the respiratory and intestinal tracts of chicks and caused subclinical
infections.
Descriptors: birds microbiology, influenza A virus avian isolation and purification, paramyxoviridae isolation
and purification, cloaca microbiology, ducks microbiology, geese microbiology, Michigan.

virusonositel'stva pri grippe kur. [The virus carrier state in avian influenza]. Voprosy Virusologii (4.):
411-417. ISSN: 0507-4088.
NAL Call Number: 448.8 P942
Descriptors: avian influenza virus, carrier state, clinical symptoms.

Smolenskii, V.I., N.G. Osidze, and A.I. Kalashnikov (1976). Izuchenie putei vydeleniya i sposobov peredachi
virusa grippa ptits v ekspermente. [Experimental study of routes of excretion and methods of
transmission of avian influenzavirus]. Sbornik Nauchnykh Trudov, Moskovskaya Veterinarnaya
Akademiya 87: 77-82.
Descriptors: avian influenza virus, epidemiology, excretion routes, transmission, secretions.

Sokolov, M.I. (1972). Nekotorye aktual'nye voprosy genetiki virusov pozvonochnykh. [Genetics of vertebrate
Descriptors: orthomyxoviridae radiation effects, genetics, microbial, influenza A virus avian radiation
effects, mutation, nucleic acid hybridization, RNA, viral, radiation genetics, recombination, genetic, ultraviolet
rays, virulence, virus replication.

NAL Call Number: 41.8 V6426
Descriptors: influenza veterinary, poultry diseases microbiology, antibodies, viral isolation and purification, hemagglutination inhibition tests, influenza microbiology, orthomyxoviridae immunology, poultry.


NAL Call Number: SF995.W4

Descriptors: avian influenza virus, microbiological analysis, identification, Mexico, America, biological analysis, influenza virus, Latin America, North America, orthomyxoviridae, viruses.


NAL Call Number: 448.8 V81

Descriptors: genes viral, influenza A virus avian genetics, human genetics, RNA viral genetics, variation genetics, base sequence, ducks, nucleic acid hybridization, RNA viral analysis.


NAL Call Number: SF601.V38

Abstract: Isolation of avian influenza virus (AIV) has been reported from 12 orders and 88 species of free-living birds. Most isolations are reported from species in the orders Anseriformes and Charadriiformes and it is recognized that species in Anseriformes represent important reservoirs of AIV. Morbidity and mortality among free-living birds attributable to AIV infection are rare, but differences in prevalence of AIV occur within and between avian species. Seasonal variation has been reported from free-living and sentinel ducks with peak AIV infection occurring in late summer and early fall. Prevalence of AIV is age-related, with highest isolation rates reported from juvenile birds. Differences in susceptibility to AIV infection among species have been demonstrated under experimental conditions. The dynamics and epidemiology of species-related variation in populations of free-living birds require further study.

Descriptors: fowl plague epidemiology, influenza A virus avian isolation and purification, aging, birds, fowl plague microbiology, seasons, species specificity.


NAL Call Number: 41.8 Av5

Abstract: Persistence of five avian influenza viruses (AIVs) derived from four waterfowl species in Louisiana and representing five hemagglutinin and neuraminidase subtypes was determined in distilled water at 17 C and 28 C. Infectivity was determined over 60 days by microtiter endpoint titration. One AIV was tested over 91 days at 4 C. Linear regression models for these viruses predicted that an initial concentration of 1 x 10(6) TCID50/ml water could remain infective for up to 207 days at 17 C and up to 102 days at 28 C. Significant differences in slopes for AIV persistence models were detected between treatment temperatures and among viruses. Results suggest that these viruses are adapted to transmission on waterfowl wintering habitats. Results also suggest a potential risk associated with waterfowl and domestic poultry sharing a common water source.

Descriptors: influenza A virus avian growth and development, water microbiology, chick embryo, ducks, fresh water, linear models, regression analysis, specific pathogen free organisms.


NAL Call Number: 41.8 Av5

Abstract: Cloacal and tracheal swabs were collected from 1389 hunter-killed ducks in Cameron Parish, Louisiana, during the 1986 and 1987 waterfowl seasons. Twenty-eight avian influenza viruses (AIVs) were isolated from 605 blue-winged teal (Anas discors), 75 mottled ducks (A. fulvigula), 375 gadwalls (A. stpeera) and 334 green-winged teal (A. crecca). Prevalence estimates of AIV in ducks sampled during September, November, and December through January were 3.1%, 2.0%, and 0.4%, respectively. Differences in prevalence were detected by season (P = 0.044) and age class (P = 0.036). Two isolations from resident
mottled ducks document transmission of AIV on these wintering areas. Much subtype diversity was present, with nine of 13 hemagglutinin (HA) and nine of nine neuraminidase (NA) subtypes recovered. Predominant HA and NA subtypes were typical of AIVs commonly associated with waterfowl. Results indicate that AIVs are transmitted in the wintering areas, and, although prevalence is low, these viruses continue to circulate within these duck populations during winter.

Descriptors: ducks microbiology, fowl plague epidemiology, influenza A virus avian isolation and purification, age factors, fowl plague microbiology, hemagglutination inhibition tests, avian classification, Louisiana epidemiology, prevalence, seasons.


NAL Call Number: 448.3 Ar23

Abstract: A comprehensive study using virological and serological approaches was carried out to determine the status of live healthy mallard ducks (*Anas platyrhynchos*) in New Zealand for infections with avian paramyxoviruses (APMV) and influenza viruses (AIV). Thirty-three viruses isolated from 321 tracheal and cloacal swabs were characterized as: 6 AIV (two H5N2 and four H4N6), 10 APMV-1 and 17 APMV-4. Of 335 sera samples tested for AIV antibodies, 109 (32.5%) sera were positive by nucleoprotein-blocking ELISA (NP-B-ELISA). Serum samples (315) were examined for antibody to APMV-1, -2, -3, -4, -6, -7, -8, -9 by the haemagglutination inhibition test. The largest number of reactions, with titres up to $>\text{or } =1/64$, was to APMV-1 (93.1%), followed by APMV-6 (85.1%), APMV-8 (56%), APMV-4 (51.7%), APMV-7 (47%), APMV-9 (15.9%), APMV-2 (13.3%) and APMV-3 (6.0%). All of the H5N2 isolates of AIV and the APMV-1 isolates from this and earlier New Zealand studies had low pathogenicity indices assessed by the Intravenous Pathogenicity Index (IVPI) with the result 0.00 and Intracerebral Pathogenicity Index (ICPI) with results 0.00-0.16. Partial genomic and antigenic analyses were also consistent with the isolates being non-pathogenic. Phylogenetic analysis of the 10 APMV-1 isolates showed 9 to be most similar to the reference APMV-1 strain D26/76 originally isolated in Japan and also to the Que/66 strain, which was isolated in Australia. The other isolate was very similar to a virus (MC 110/77) obtained from a shelduck in France.

Descriptors: avulavirus isolation and purification, ducks virology, influenza A virus avian isolation and purification, antibodies, viral analysis, antibodies, viral blood, avulavirus genetics, avulavirus pathogenicity, base sequence, cloaca virology, ducks blood, ducks immunology, enzyme linked immunosorbent assay, hemagglutination inhibition tests, avian pathogenicity, molecular sequence data, New Zealand, population surveillance, reverse transcriptase polymerase chain reaction, sequence alignment, trachea virology.


Abstract: Influenza remains a globally important cause of febrile respiratory illness. Influenza virus activity in the community results in significant mortality, morbidity and economic disruption, particularly in those at high risk of developing complications, such as the elderly and those with underlying chronic medical conditions, including pulmonary disease and diabetes mellitus. The occurrence in Hong Kong in 1997 of avian influenza H5N1 in man, which resulted in six deaths, served to remind us of the importance of continuing surveillance and preparation for the next pandemic.

Descriptors: influenza epidemiology, antigenic variation, influenza genetics, mutation genetics, population surveillance, prevalence, risk factors.


NAL Call Number: 470 Sci2

Abstract: The 1918 "Spanish" influenza pandemic represents the largest recorded outbreak of any infectious disease. The crystal structure of the uncleaved precursor of the major surface antigen of the extinct 1918 virus was determined at 3.0 angstrom resolution after reassembly of the hemagglutinin gene from viral RNA fragments preserved in 1918 formalin-fixed lung tissues. A narrow avian-like receptor-binding site, two previously unobserved histidine patches, and a less exposed surface loop at the cleavage site that
activates viral membrane fusion reveal structural features primarily found in avian viruses, which may have contributed to the extraordinarily high infectivity and mortality rates observed during 1918.


NAL Call Number: 470 Sci2

Descriptors: disease outbreaks, influenza epidemiology, influenza prevention and control, influenza vaccines supply and distribution, clinical trials, drug industry, influenza virology, influenza A virus, avian immunology, avian pathogenicity, human immunology, influenza vaccines administration and dosage, influenza vaccines economics, international cooperation, population surveillance, public policy, World Health Organization.


NAL Call Number: 448.3 C33(1)

Abstract: In the course of a study which was made in order to contribute to the knowledge about influenza viruses in birds, 18 strains of avian Influenza-A-subtypes were isolated from cloaca swabs. From the Central European bird species, one strain of Influenza A/England/62 was isolated from a mallard. All other species of birds obtained from three different biotopes from Austria and Hungary showed negative results. The other 17 influenza strains were isolated from imported birds from Senegal. Nine of these strains corresponded to subtype A/duck/England/62, five to subtype duck/England/56. One isolated strain showed a relation to A/duck/England/56 in terms of the hemagglutinin and to chicken/Brescia/1902 in terms of the neuraminidase. Two other strains reacted best with antisera against duck/England/62 in the hemagglutination inhibition test; the neuraminidase inhibition test showed a relation to subtype quail/Italy/65. The Newcastle disease-Virus was not isolated in any sample.

Descriptors: birds microbiology, influenza A virus avian isolation and purification, Argentina, Austria, cloaca microbiology, hemagglutination inhibition tests, Hungary, Senegal.


NAL Call Number: QR180.D4

Abstract: Avian influenza virus can cause serious disease in a wide variety of birds and mammals, but its natural host range is in wild ducks, gulls, and shorebirds. Infections in poultry can be inapparent or cause respiratory disease, decreases in production, or a rapidly fatal systemic disease known as highly pathogenic avian influenza (HPAI). For the protection of poultry, neutralizing antibody to the hemagglutinin and neuraminidase proteins provide the primary protection against disease. A variety of vaccines elicit neutralizing antibody, including killed whole virus vaccines and fowl-pox recombinant vaccines. Antigenic drift of influenza viruses appears to be less important in causing vaccine failures in poultry as compared to humans. The cytotoxic T lymphocyte response can reduce viral shedding in mildly pathogenic avian influenza viruses, but provides questionable protection against HPAI. Influenza viruses can directly affect the immune response of infected birds, and the role of the Mx gene, interferons, and other cytokines in protection from disease remains unknown.

Descriptors: immune system, infection, highly pathogenic avian influenza, viral disease, avian influenza virus vaccination immunization method, antigenic drift cellular immunity.

influenza virus infections in poultry in North America. Avian Diseases 47(Special Issue): 888-897. ISSN: 0005-2086.
NAL Call Number: 41.8 Av5

Abstract: Avian influenza is endemic in wild birds in North America, and the virus routinely has been transmitted from this reservoir to poultry. Influenza, once introduced into poultry, can become endemic within the poultry population. It may be successfully eradicated by human intervention, or the virus may fail to successfully spread on its own. In the last 5 yr, influenza virus has been isolated from poultry in the United States on numerous occasions, and, with the use of molecular epidemiology, the relationships of these different viruses can be determined. There are 15 different hemagglutinin subtypes of avian influenza viruses, but infections with virus of H5 and H7 subtypes are of the most concern because of the potential for these viruses to mutate to the highly pathogenic form of the virus. Most of the influenza isolations in the United States have been associated with the live-bird markets (LBMs) in the Northeast. This has included primarily H7N2 influenza viruses, but also H7N3, H5N2, and other subtypes. Most of the H7N2 viruses were part of a single lineage that was first observed in 1994, but new introductions of H7N2 and H7N3 were also observed. The predominant H7N2 LBM lineage of virus spread to large commercial poultry operations on at least three occasions since 1997, with the largest outbreak occurring in Virginia in 2002. The H5N2 viruses in the LBMs included viruses from domestic ducks, gamebirds, and environmental samples. Some H5N2 viruses isolated in different years and in different locations had a high degree of sequence relatedness, although the reservoir source, if it is endemic, has not been identified. Finally, an H1N2 virus, associated with a drop in egg production, was isolated from turkeys in Missouri in 1999. This virus was a complex reassortant with swine, human, and avian influenza genes that was similar to recent swine isolates from the Midwest. Additional serologic evidence suggests that flocks in other states were infected with a H1N2 virus.

Descriptors: epidemiology, immune system, infection, avian influenza, infectious disease, respiratory system disease, viral disease, serology, clinical techniques, diagnostic techniques, disease control, egg production, molecular epidemiology, poultry population, viral reservoir, viral transmission.

NAL Call Number: SF995.W4
Descriptors: avian influenza virus, Newcastle disease, poultry diseases, poultry industry, United States.

NAL Call Number: SF601.V44

Abstract: Although influenza viruses can infect a wide variety of birds and mammals, the natural host of the virus is wild waterfowl, shorebirds, and gulls. When other species of animals, including chickens, turkeys, swine, horses, and humans, are infected with influenza viruses, they are considered aberrant hosts. The distinction between the normal and aberrant host is important when describing virus evolution in the different host groups. The evolutionary rate of influenza virus in the natural host reservoirs is believed to be slow, while in mammals the rate is much higher. The higher rate of evolution in mammals is thought to be a result of selective pressure on the virus to adapt to an aberrant host species. Chickens and turkey influenza virus isolates have previously and incorrectly been lumped together with wild waterfowl, gull, and shorebird influenza viruses when determining rates of evolutionary change. To determine mutational and evolutionary rates of a virus in any host species, two primary assumptions must be met: first, all isolates included in the analysis must have descended from a single introduction of the virus, and second, the outbreak must continue long enough to determine a trend. For poultry, three recent outbreaks of avian influenza meet these criteria, and the sequences of the hemagglutinin and nonstructural genes were compared. Sequences from all three outbreaks were compared to an avian influenza virus consensus sequence, which at the amino acid level is highly conserved for all the internal viral proteins. The consensus sequence also provides a common point of origin to compare all influenza viruses. The evolutionary rates determined for all three outbreaks were similar to what is observed in mammals, providing strong evidence of adaptation of influenza to the new host species, chickens and turkeys.

Descriptors: animal husbandry, evolution and adaptation, infection, avian influenza virus infection, viral disease, adaptation evolution mutations.

**NAL Call Number:** SF602.M8

**Descriptors:** infection, veterinary medicine, avian influenza, clinical pathology, diagnosis, viral disease, swine influenza, clinical pathology, viral disease, antibody response vaccine.


**NAL Call Number:** QR360.J6

**Abstract:** The single gene reassortant virus that derives its PB2 gene from the avian influenza A/Mallard/NY/78 virus and remaining genes from the human influenza A/Los Angeles/2/87 virus exhibits a host range restriction (hr) phenotype characterized by efficient replication in avian tissue and failure to produce plaques in mammalian Madin-Darby canine kidney cells. The hr phenotype is associated with restriction of viral replication in the respiratory tract of squirrel monkeys and humans. To identify the genetic basis of the hr phenotype, we isolated four phenotypic hr mutant viruses that acquired the ability to replicate efficiently in mammalian tissue. Segregational analysis indicated that the loss of the hr phenotype was due to a mutation in the PB2 gene itself. The nucleotide sequences of the PB2 gene of each of the four hr mutants revealed that a single amino acid substitution at position 627 (Glu replaced by Lys) was responsible for the restoration of the ability of the PB2 single gene reassortant to replicate in Madin-Darby canine kidney cells. Interestingly, the amino acid at position 627 in every avian influenza A virus PB2 protein analyzed to date is glutamic acid, and in every human influenza A virus PB2 protein, it is lysine. Thus, the amino acid at residue 627 of PB2 is an important determinant of host range of influenza A viruses.

**Descriptors:** avian influenza virus, influenza virus, structural genes, viral proteins, nucleotide sequences, amino acid sequences, hybrids, host range, replication, cell lines, kidneys, chickens, dogs, mutations, mutants, molecular sequence data, GENBANK l02352, reassortants.


**Abstract:** The virulence of influenza viruses results from the interplay between the virus and host and depends upon specific virulence markers in one or more gene segment of the virus and the level of immune protection in an individual or population. The viral surface glycoproteins, the hemagglutinin (HA) and neuraminidase (NA), are the targets of the protective immune response. Drift and shift are the two major mechanisms of antigenic variation in influenza. Antigenic drift resulting from point mutations in the HA and/or NA in and around the antibody binding site is seen in influenza A and B viruses. Over time these accumulated mutations alter the viral antigens enough so that antibodies elicited by prior infections or vaccines no longer neutralize the virus. Although genetic markers of virulence in circulating human influenza viruses are not well defined, H3N2 viruses are associated with higher peaks of pneumonia and influenza mortality in the US population than H1N1 or influenza B viruses. Antigenic shift occurs when a novel influenza A HA or NA subtype is introduced from an animal influenza A virus reservoir into a human population that lacks preexisting immunity to influenza; spread of such a virus can result in a pandemic. Three pandemics in the 21st century occurred with the introduction of H1N1, H2N2 and H3N2 viruses, respectively into the human population and were associated with significant morbidity and mortality. In 1997 avian H5N1 viruses caused an outbreak of 18 cases of human disease in Hong Kong. Older age was a host factor that was associated with severe disease. Virulence determinants are present in at least 2 gene segments of these viruses. In 1999, avian H9N2 viruses were recovered from 2 children with mild illness in Hong Kong. The Hong Kong H9N2 and H5N1 viruses had identical internal protein genes suggesting that the ability of an avian influenza virus to infect humans may be determined by a specific gene constellation while the surface glycoprotein genes may confer virulence. In summary, while studies in humans and animal models and the application of reverse genetics techniques have identified virulence determinants in several influenza virus genes, the severity of disease is determined by a combination of viral and host factors.

**Descriptors:** epidemiology, immune system, infection, molecular genetics, public health, influenza, epidemiology, etiology, prevention and control, respiratory system disease, viral disease, gene function, host protective immunity, infection outbreaks, lessons, past pandemics, viral genetics, viral reservoirs, viral

**NAL Call Number:** 448.8 P942

**Descriptors:** hemolysis, influenza A virus avian pathogenicity, chick embryo, hydrogen-ion concentration, kinetics, light, scattering, radiation, time factors, virus cultivation.


**Descriptors:** chickens, influenza virology, avian influenza A virus pathogenicity, avian influenza virology, poultry diseases virology, zoonoses virology, acetamides therapeutic use, amantadine therapeutic use, antiviral agents therapeutic use, disease outbreaks, influenza epidemiology, influenza therapy, influenza transmission, influenza vaccines, avian influenza epidemiology, avian influenza transmission, neuraminidase antagonists and inhibitors, poultry diseases epidemiology, poultry diseases transmission, sialic acids therapeutic use, zoonoses epidemiology, zoonoses transmission.


**Abstract:** The gene pool of influenza A viruses in aquatic birds provides all of the genetic diversity required for human and lower animals. Host range selection of the receptor binding specificity of the influenza virus hemagglutinin occurs during maintenance of the virus in different host cells that express different receptor sialo-sugar chains. In this paper, functional roles of the hemagglutinin and neuraminidase spikes of influenza viruses are described in the relation to 1) host range of influenza viruses, 2) receptor binding specificity of human and other animal influenza viruses, 3) recognition of sialyl sugar chains by Spanish influenza virus hemagglutinin, 4) highly pathogenic and potentially pandemic H5N1, H9N2, and H7N7 avian influenza viruses and molecular mechanism of host range variation of influenza viruses, 5) role of the neuraminidase spike for the host range of influenza viruses, and 6) Development of anti-influenza drugs.

**Descriptors:** influenza, viruses, host range, molecular mechanism, sialobiology, influenza A, gene pool, drugs, aquatic birds, human.


**NAL Call Number:** SF481.M54

**Descriptors:** avian influenza virus, virulence, disease transmission, pathology, disease control, poultry.


**NAL Call Number:** 41.8 Av5

**Abstract:** Pathobiologic characteristics were determined for three mildly pathogenic (MP) ratite-origin avian influenza viruses (AIVs). Ratite-origin AIVs produced respiratory disease in rheas, and virus was reisolated from oropharyngeal and cloacal swabs on days 2-6 postinoculation. Inoculation of two ratite-origin AIVs in the upper respiratory tract of chickens resulted in viral infections, but the mean chicken infectious dose (CID50) for A/emu/Texas/39924/93 (H5N2) (Emu/Texas) virus was 500-fold lower than the CID50 for the A/rhea/North Carolina/39482/93 (H7N1) virus. In ovo and in vivo passage of the MP parent Emu/Texas isolate resulted in emergence of a highly pathogenic (HP) variant that had high plaquing efficiency in chicken embryo fibroblast cultures and was highly lethal in chicken pathotyping tests. This variant virus produced gross lesions in chickens similar to those reported for other HP AIVs. These findings demonstrated that ratite-origin AIVs can produce significant clinical disease in rheas and have a realistic potential for interspecies transmission to domestic poultry. Furthermore, HP variants can emerge from MP H5 ratite-origin AIVs if introduced and allowed to circulate in chicken populations.

**Descriptors:** rheas, chickens, avian influenza virus, pathogenicity, experimental infection, in vivo experimentation, disease transmission, biological differences, biological properties, birds, disease
transmission, domestic animals, domesticated birds, experimentation, Galliformes, infection, influenza virus, livestock, microbial properties, orthomyxoviridae, pathogenesis, poultry, Rheiformes, useful animals, viruses, interspecies transmission, infectivity, strain differences.

NAL Call Number: 41.8 Am3
Descriptors: diagnosis, disease prevalence, disease transmission, epidemiology, Newcastle disease, outbreaks, reservoir hosts, wild birds, zoonoses, avian influenza virus, ducks, human, United States.

NAL Call Number: 41.8 Av5
Abstract: Five-week-old specific-pathogen-free chickens were inoculated intravenously with one of 16 low-pathogenicity type A influenza virus isolates; 14 were of wild duck origin, and two were of turkey origin. Tubulointerstitial nephritis was the most frequent specific histopathologic change. The frequency and severity of kidney lesions were independent of the virus hemagglutinin-neuraminidase subtype or titer of the challenge virus. Influenza nucleoprotein was most frequently demonstrated in the kidney and was consistently localized to necrotic proximal and/or distal renal tubule epithelium. Common nonspecific histopathologic changes were lymphoid hyperplasia of the spleen and cecal tonsils, as well as lymphocyte depletion in the cloacal bursa. Uncommon histopathologic changes, in decreasing order of frequency, were interstitial pneumonia, lymphoid follicular hyperplasia in the myocardium, and lymphocytic tracheitis. Histopathologic changes were rare or absent in the jejunum, duodenum, pancreas, and brain. The low-pathogenicity avian-origin type A influenza virus isolates were epitheliotropic in chickens, primarily nephrotropic. Such findings were dissimilar from findings with highly pathogenic avian-origin type A influenza virus isolates both in severity and in tissue distribution of histopathologic changes and influenza viral antigen.
Descriptors: fowl plague pathology, influenza A virus avian pathogenicity, antigens, viral analysis, chickens, ducks, immunohistochemistry, avian isolation and purification, nephritis pathology, nephritis virology, organ specificity, species specificity, turkeys.

NAL Call Number: 41.8 Av5
Abstract: One-day-old chickens were inoculated intravenously with one of three low-pathogenicity avian-origin influenza isolates. On day 5 postinoculation (PI), the frequency of influenza virus isolation from cloacal swabs following challenge with each isolate ranged from 83% to 100% for clinically normal euthanatized chickens. Influenza virus was also frequently isolated from kidneys of these chickens (47%) and from chickens that died (100%). Kidneys positive for virus isolation had lesions of nephrosis and/or acute nephritis, and influenza viral nucleoprotein was demonstrated in nuclei and cytoplasm of necrotic renal tubule epithelium. On sampling days 28 and 45/60 PI, influenza virus was neither isolated from nor immunohistochemically demonstrated in kidneys (0/125); however, the kidneys (47%) did have chronic histologic lesions that suggested previous influenza virus infection of the kidneys. Influenza virus was isolated from cloacal swabs of two of 44 chickens on day 28 PI, but all cloacal swabs were negative for virus recovery on sampling day 45/60 PI (0/81). These results indicate that replication of influenza virus in renal tubule epithelial cells did not result in persistence of type A influenza virus in this immunologically privileged site.
Descriptors: chicks, avian influenza virus, kidneys, cloaca, persistence, experimental infections, replication.

NAL Call Number: SF781.R4
Abstract: Highly pathogenic (HP) avian influenza (AI) (HPAI) is an extremely contagious, multi-organ systemic disease of poultry leading to high mortality, and caused by some H5 and H7 subtypes of type A
Influenza virus, family Orthomyxoviridae. However, most AI virus strains are mildly pathogenic (MP) and produce either subclinical infections or respiratory and/or reproductive diseases in a variety of domestic and wild bird species. Highly pathogenic avian influenza is a List A disease of the Office International des Epizooties, while MPAI is neither a List A nor List B disease. Eighteen outbreaks of HPAI have been documented since the identification of AI virus as the cause of fowl plague in 1955. Mildly pathogenic avian influenza viruses are maintained in wild aquatic bird reservoirs, occasionally crossing over to domestic poultry and causing outbreaks of mild disease. Highly pathogenic avian influenza viruses do not have a recognised wild bird reservoir, but can occasionally be isolated from wild birds during outbreaks in domestic poultry. Highly pathogenic avian influenza viruses have been documented to arise from MPAI viruses through mutations in the haemagglutinin surface protein. Prevention of exposure to the virus and eradication are the accepted methods for dealing with HPAI. Control programmes, which imply allowing a low incidence of infection, are not an acceptable method for managing HPAI, but have been used during some outbreaks of MPAI. The components of a strategy to deal with MPAI or HPAI include surveillance and diagnosis, biosecurity, education, quarantine and depopulation. Vaccination has been used in some control and eradication programmes for AI.

Descriptors: veterinary medicine, highly pathogenic avian influenza, viral disease, mortality.


NAL Call Number: SF781.R4

Abstract: L'influenza aviaire hautement pathogene est une maladie extremement contagieuse de la volaille, a tropisme multiple et systemique, qui s'accompagne d'une mortalite elevee. Elle est due a certains sous-types H5 et H7 du virus influenza de type A, de la famille des Orthomyxoviridae. Toutefois, la plupart des souches virales de l'influenza aviaire sont moderement pathogenes et provoquent soit des infections infracliniques, soit des maladies respiratoires et/ou de la reproduction chez plusieurs especes d'oiseaux domestiques et sauvages. L'influenza aviaire hautement pathogene fait partie de la Liste A de l'Office international des epizooties (OIE), alors que l'influenza aviaire moderement pathogene ne figure ni sur la Liste A ni sur la Liste B de l'OIE. Dix-huit episodes d'influenza aviaire hautement pathogene ont ete decrits depuis que l'origine de la peste aviaire de 1955 a ete imputee au virus de l'influenza aviaire. Les virus de l'influenza aviaire moderement pathogene sont presents chez les oiseaux migrateurs aquatiques, qui servent de reservoir; ces virus atteignent occasionnellement des volailles domestiques, entrainant l'apparition de maladies peu severes. Les virus de l'influenza aviaire hautement pathogene n'ont pas de reservoir reconnu chez les oiseaux sauvages, mais ils peuvent parfois etre isoles chez ces derniers lors d'epidemies affectant les volailles domestiques. D'apres la documentation existante, les virus de l'influenza aviaire hautement pathogene proviendraient des virus de l'influenza aviaire moderement pathogene suite a des mutations de la proteine de surface de l'hemagglutinine. La strategie recommandee en cas d'influenza aviaire hautement pathogene consiste a eviter toute exposition au virus et a eradiquer la maladie. Les programmes de prophylaxie qui tolerent une faible incidence de l'infection ne constituent pas une methode acceptable pour faire face a des cas d'influenza aviaire hautement pathogene, mais ils ont ete utilisees lors de certaines epidemies d'influenza aviaire moderement pathogene. Les strategies de lutte contre l'influenza aviaire hautement et moderement pathogene, reposent essentiellement sur le diagnostic, l'hygiene, l'éducation, la quarantaine et la reduction de la taille des elevages. La vaccination a ete utilisee dans certains programmes de prophylaxie et d' eradication de l'influenza aviaire.

Descriptors: poultry, viroses, avian influenza virus, orthomyxoviridae, etiology, pathogenicity, microbial ecology, epidemiology, diagnosis, public health, disease control, biological properties, domestic animals, ecology, infectious diseases, influenza virus, livestock, microbial properties, orthomyxoviridae, useful animals, viruses.


**Descriptors:** Aves, virus transmission, avian influenza viruses, ecology, epidemiology, zoonotic potential implications.


**Abstract:** Comprehensive guidelines were developed and used to train poultry company personnel on in-house composting procedures. Results to date suggest in-house composting of avian influenza infected flocks is a biosecure, cost-effective, and efficient means of disposal of broiler carcasses in clear-span houses.

**Descriptors:** poultry, avian influenza, composting, in-house composting, infected flocks.

Tacken, G.M.L. (2003). **Ketenconsequenties van de uitbraak van vogelpest. [Supply chain consequences of the avian influenza outbreak].** Rapport Landbouw Economisch Instituut (LEI) 6.03.06: 53. ISSN: 9052428077.

**Descriptors:** agricultural economics, agricultural policy, avian influenza virus, fowl plague virus, poultry farming, disasters, Netherlands, economic impact.


**Descriptors:** disease outbreaks, encephalitis, viral epidemiology, fowl plague epidemiology, respirovirus infections epidemiology, zoonoses, influenza A virus avian pathogenicity, Malaysia epidemiology, population surveillance, public health, respirovirus pathogenicity, Singapore epidemiology.

Tanyi, J. (1997). **Place and role of avian influenza within the influenza entity.** *Magyar Allatorvosok Lapja* 119(12): 718-723. ISSN: 0025-004X.

**Abstract:** Starting from the principled similarity and possibilities of variation of the antigen components (Figure 1) of type A influenza viruses extremely widespread in nature, the author discusses the role and importance of avian influenza within the influenza entity. Based upon the two external antigens, at present 14 haemagglutinin and 9 neuraminidase subtypes or serotypes are known (Table 1). The influenza viruses isolated in Hungary, at the Veterinary Institute of Debrecen since 1969 are grouped by subtype and avian species in Table 2. Influenza studies conducted in South China and Northern America suggest that waterfowl act as the natural reservoirs of influenza virus, which is explained by the high incidence of symptomless infection, the intestinal form, and by the aquatic origin of life. Although influenza viruses mostly persist in the species to which they have adapted themselves, they may cross the species barrier. With regard to the animal kingdom and humans, this is most likely to occur in South China, a region considered to be an influenza epicentre, where the transmission of influenza viruses from waterfowl to men most probably takes place through pigs, after much variation (Figure 2 and Table 3). Namely, in that region the close coexistence of the three species, the high density of the human and animal population, the optimal climatic and geographic conditions and the existing high susceptibility create a possibility for a chain of infection to develop. This is why avian influenza, especially the influenza of waterfowl, has great importance both in historic perspective and at the present time.

**Descriptors:** infection, vector biology, avian influenza, respiratory system disease, epizootiology.


Taubenberger, J.K., A.H. Reid, A.E. Krafft, K.E. Bijwaard, and T.G. Fanning (1997). *Initial genetic characterization of the 1918 "Spanish" influenza virus.* Science 275(5307): 1793-6. ISSN: 0036-8075. NAL Call Number: 470 Sci2 Abstract: The "Spanish" influenza pandemic killed at least 20 million people in 1918-1919, making it the worst infectious pandemic in history. Understanding the origins of the 1918 virus and the basis for its exceptional virulence may aid in the prediction of future influenza pandemics. RNA from a victim of the 1918 pandemic was isolated from a formalin-fixed, paraffin-embedded, lung tissue sample. Nine fragments of viral RNA were sequenced from the coding regions of hemagglutinin, neuraminidase, nucleoprotein, matrix protein 1, and matrix protein 2. The sequences are consistent with a novel H1N1 influenza A virus that belongs to the subgroup of strains that infect humans and swine, not the avian subgroup. Descriptors: genes viral, influenza virology, influenza A virus human genetics, porcine genetics, RNA viral genetics, algorithms, base sequence, hemagglutinin glycoproteins, influenza virus genetics, history of medicine, 20th century, influenza history, avian genetics, human classification, human pathogenicity, porcine classification, porcine pathogenicity, lung virology, molecular sequence data, neuraminidase genetics, nucleoproteins genetics, phylogeny, polymerase chain reaction, viral core proteins genetics, viral matrix proteins genetics, virulence.


Tollis, M. and T.L. Di (2002). *Recent developments in avian influenza research: Epidemiology and immunoprophylaxis.* Veterinary Journal 164(3): 202-215. ISSN: 1090-0233. NAL Call Number: SF601.V484 Abstract: Influenza A viruses have been isolated from humans, from several other mammalian species and a wide variety of avian species, among which, wild aquatic birds represent the natural hosts of influenza viruses. The majority of the possible combinations of the 15 haemagglutinin (HA) and nine neuraminidase (NA) subtypes recognized have been identified in isolates from domestic and wild birds. Infection of birds can cause a wide range of clinical signs, which may vary according to the host, the virus strain, the host's immune status, the presence of any secondary exacerbating microorganisms and environmental factors. Most infections are inapparent, especially in waterfowl and other wild birds. In contrast, infections caused by viruses of H5 and H7 subtypes can be responsible for devastating epidemics in poultry. Despite the warnings to the poultry industry about these viruses, in 1997 an avian H5N1 influenza virus was directly transmitted from birds to humans in Hong Kong and resulted in 18 confirmed infections, thus strengthening the pandemic threat posed by avian influenza (AI). Indeed, reassortant viruses, harbouring a combination of avian and human viral genomes, have been responsible for major pandemics of human influenza. These considerations warrant the need to continue and broaden efforts in the surveillance of AI. Control programmes have varied from no intervention, as in the case of the occurrence of low pathogenic (LP) AI (LPAI) viruses, to extreme, expensive total quarantine-slaughter programmes carried out to eradicate highly pathogenic (HP) AI (HPAI) viruses. The adoption of a vaccination policy, targeted either to control or to prevent infection in poultry, is generally banned or discouraged. Nevertheless, the need to boost eradication efforts in order to limit further spread of infection and avoid heavy economic losses, and advances in modern
vaccine technologies, have prompted a re-evaluation of the potential use of vaccination in poultry as an additional tool in comprehensive disease control strategies. This review presents a synthesis of the most recent research on AI that has contributed to a better understanding of the ecology of the virus and to the development of safe and efficacious vaccines for poultry.

Descriptors: animal husbandry, epidemiology, immune system, infection, veterinary medicine, virology, avian influenza, respiratory system disease, viral disease, avian influenza research: epidemiology, immunoprophylaxis, recent developments avian influenza vaccine development immunoprophylaxis poultry vaccine development: efficacy, safety.


Descriptors: ecology, wild birds, vector biology, avian influenza, transmission, Australia.


NAL Call Number: 448.8 M45

Abstract: In December 2003, the largest outbreak of highly pathogenic avian influenza H5N1 occurred among poultry in 8 Asian countries. A limited number of human H5N1 infections have been reported from Vietnam and Thailand, with a mortality rate approaching 70%. Deaths have occurred in otherwise healthy young individuals, which is reminiscent of the 1918 Spanish influenza pandemic. The main presenting features were fever, pneumonitis, lymphopenia, and diarrhea. Notably, sore throat, conjunctivitis, and coryza were absent. The H5N1 strains are resistant to amantadine and rimantadine but are susceptible to neuraminidase inhibitors, which can be used for treatment and prophylaxis. The widespread epidemic of avian influenza in domestic birds increases the likelihood for mutational events and genetic reassortment. The threat of a future pandemic from avian influenza is real. Adequate surveillance, development of vaccines, outbreak preparedness, and pandemic influenza planning are important. This article summarizes the current knowledge on avian influenza, including the virology, epidemiology, diagnosis, and management of this emerging disease.

Descriptors: communicable diseases, emerging epidemiology, disease outbreaks statistics and numerical data, influenza A virus, avian genetics, avian influenza pathogenicity, avian influenza epidemiology, poultry diseases epidemiology, world health, amantadine therapeutic use, antiviral agents therapeutic use, Asia epidemiology, communicable diseases, emerging diagnosis, emerging prevention and control, emerging virology, disease outbreaks prevention and control, drug resistance, multiple, viral, family characteristics, forecasting, avian influenza diagnosis, avian influenza prevention and control, avian influenza virology, mutation genetics, neuraminidase antagonists and inhibitors, patient isolation, population surveillance, poultry, poultry diseases diagnosis, poultry diseases prevention and control, poultry diseases virology, recombination, genetics, rimantadine therapeutic use, vaccination, zoonoses epidemiology, zoonoses virology.


Descriptors: antibodies, avian infectious bursitis, disease surveys, seasonal variation, serological surveys, vaccination, avian influenza virus, Newcastle disease virus, Vietnam.


NAL Call Number: QH323.5.J6

Abstract: This paper is concerned with a stochastic model, describing outbreaks of infectious diseases that have potentially great animal or human health consequences, and which can result in such severe economic losses that immediate sets of measures need to be taken to curb the spread. During an outbreak of such a disease, the environment that the infectious agent experiences is therefore changing due to the subsequent control measures taken. In our model, we introduce a general branching process in a changing (but not
random) environment. With this branching process, we estimate the probability of extinction and the expected number of infected individuals for different control measures. We also use this branching process to calculate the generating function of the number of infected individuals at any given moment. The model and methods are designed using important infections of farmed animals, such as classical swine fever, foot-and-mouth disease and avian influenza as motivating examples, but have a wider application, for example to emerging human infections that lead to strict quarantine of cases and suspected cases (e.g. SARS) and contact and movement restrictions.

Descriptors: classical swine fever epidemiology, classical swine fever virus growth and development, veterinary disease outbreaks, biological models, classical swine fever prevention and control, classical swine fever transmission, epidemiologic methods, Netherlands epidemiology, stochastic processes, swine.

NAL Call Number: SF604.V463
Descriptors: avian influenza virus, consequences, birds.

NAL Call Number: 41.8 Av5
Abstract: Low-pathogenic avian influenza virus (AIV) continues to be isolated from the live bird markets (LBMs) in the Northeastern United States. Recent years have seen increasing numbers of these markets opening and an expansion of the type of animals they sell in conjunction with traditional live poultry. Specific-pathogen-free chickens were released into the livestock area of 13 New York City LBMs and then tested for evidence of AIV. We were able to recover virus or demonstrate seroconversion among the chickens introduced to four of the markets.
Descriptors: epidemiology, infection, avian influenza, infectious disease, respiratory system disease, viral disease, live bird markets livestock areas.


NAL Call Number: 448.8 J826
Descriptors: antibodies analysis, antigens analysis, orthomyxoviridae immunology, adult, age factors, aged, antigen antibody reactions, depression, chemical, ducks, hemagglutination inhibition tests, influenza A virus avian immunology, middle aged, neutralization tests, periodic acid pharmacology, potassium pharmacology, turkeys.

NAL Call Number: 41.8 Av5
Abstract: During the spring of 2002, a low pathogenic avian influenza (LPAI) A (H7N2) virus caused a major outbreak among commercial poultry in Virginia and adjacent states. The virus primarily affected turkey flocks, causing respiratory distress and decreased egg production. Experimentally, turkeys were more susceptible than chickens to H7N2 virus infection, with 50% bird infectious dose titers equal to 10(0.8) and 10(2.8-3.2), respectively. Comparison of virus shedding from the cloaca and oropharynx demonstrated that recent H7N2 virus isolates were readily isolated from the upper respiratory tract but rarely from the
gastrointestinal tract. The outbreak of H7N2 virus raised concerns regarding the availability of vaccines that could be used for the prevention and control of this virus in poultry. We sought to determine if an existing commercial avian influenza (AI) vaccine prepared from a 1997 seed stock virus could provide protection against a 2002 LPAI H7N2 virus isolated from a turkey (A/turkey/Virginia/158512/02 [TV/02]) in Virginia that was from the same lineage as the vaccine virus. The inactivated AI vaccine, prepared from A/chicken/Pennsylvania/21342/97 (CP/97) virus, significantly reduced viral shedding from vaccinated turkeys in comparison with sham controls but did not prevent infection. The protective effect of vaccination correlated with the level of virus-specific antibody because a second dose of vaccine increased antiviral serum immunoglobulin G and hemagglutination inhibition (HI) reactivity titers in two different turkey age groups. Serum from CP/97-vaccinated turkeys reacted equally well to CP/97 and TV/02 antigens by HI and enzyme-linked immunosorbent assay. These results demonstrate the potential benefit of using an antigenically related 1997 H7N2 virus as a vaccine candidate for protection in poultry against a H7N2 virus isolate from 2002.

Descriptors: chickens, influenza A virus, avian pathogenicity, avian etiology, poultry diseases etiology, turkeys, antibodies, viral blood, avian classification, avian immunology, prevention and control, poultry diseases immunology, poultry diseases prevention and control, species specificity, viral vaccines pharmacology.


NAL Call Number: 448.3 AC85

Abstract: One strain of influenza A virus (H4N6), three strains of Newcastle disease virus (NDV) and one strain of paramyxovirus (PMV) type 4 were isolated from tracheal and cloacal swabs of sentinel domestic ducks by inoculation of tested samples into the amniotic and allantoic cavities of chick embryos (CE).

Descriptors: ducks microbiology, influenza A virus avian isolation and purification, Newcastle disease virus isolation and purification, paramyxoviridae isolation and purification, cloaca microbiology, Czechoslovakia, seasons, trachea microbiology.


NAL Call Number: aSF995.6.I6I5 1981a

Descriptors: avian influenza virus, domestic fowl, economic impact.


NAL Call Number: 41.8 Au72

Descriptors: fowl plague microbiology, influenza A virus, avian isolation and purification, poultry.


NAL Call Number: 41.8 Au72

Descriptors: epidemiological surveys, mutations, outbreaks, pathogenicity, serological surveys, disease distribution, disease prevalence, disease surveys, disease transmission, disease vectors, waterfowl, wild birds, Anseriformes, avian influenza virus, Charadriiformes, ducks, fowl.


NAL Call Number: 41.8 V6426

Descriptors: fowl plague diagnosis, Newcastle disease diagnosis, chick embryo, chickens, diagnosis, differential, influenza A virus avian isolation and purification, methods, Newcastle disease virus isolation and purification.

Ungchusak, K., P. Auewarakul, S.F. Dowell, R. Kitphati, W. Auwanit, P. Puthavathana, M. Uiprasertkul, K. Boonnak,

**Descriptors:** disease transmission, vertical, influenza transmission, influenza A virus, avian genetics, adult, child, fatal outcome, influenza virology, avian influenza isolation and purification, avian influenza transmission, lung radiography, phylogeny, poultry, reverse transcriptase polymerase chain reaction, zoonoses transmission.


**NAL Call Number:** 1 Ag84Pro no. 1704

**Descriptors:** nonindigenous pests control, United States, avian influenza, threat, poultry.


**NAL Call Number:** 1 Ag84Pro

**Descriptors:** avian influenza, threat, poultry, USDA.


**NAL Call Number:** SF995.6.I6I58 1992

**Descriptors:** avian influenza virus, infectious diseases, influenza virus, viruses, international symposium, U.S. Animal Health Association.


**NAL Call Number:** 41.8 Av5

**Abstract:** High-pathogenicity avian influenza (HPAI) viruses emerged from low-pathogenicity avian influenza (LPAI) viruses in Pennsylvania (1983-84), Mexico (1994-95), and Italy (1999-2000). Here we focus on the question of why the HPAI virus supersedes the LPAI virus, once it has appeared during the epidemic. To study this, we used an experimental model in chickens that enabled us to estimate the reproduction ratio (R0). Using this model, we determined the R0 of the A/Chicken/Pennsylvania/21525/83 (LPAI) and of the A/Chicken/Pennsylvania/1370/83 (HPAI). Comparing the R0 of both viruses, we concluded that the R0 of the HPAI virus is significantly higher than the R0 of the LPAI.

**Descriptors:** epidemiology, infection, avian influenza, infectious disease, respiratory system disease, viral disease, transmission dynamics.


**NAL Call Number:** SF601.V523

**Abstract:** Recombinant technology is relatively new to veterinary medicine. It combines safety, purity, potency, and efficacy in the vaccine. Its positive features include not exposing the vaccinate to the pathogen, the lack of need for adjuvants, and stability that allows some vaccine to remain viable at ambient temperatures. These recombinants can receive multiple genetic inserts and present an opportunity to have multiple combination vaccines for use in animals. Licensed recombinant vaccines in veterinary medicine include those protecting against Lyme disease, pseudorabies, rabies, canine distemper, Newcastle disease, and a strain of avian influenza.

**Descriptors:** animal diseases prevention and control, vaccines, synthetic, veterinary medicine trends.

van Rooijen, J. (2004). Veterinair vooroordeel. [Veterinary pre-judgement]. *Tijdschrift Voor Diergeneeskunde*

**Abstract:** Only a limited number of A-subtypes of influenza virus so far caused disease in human subjects, pigs and horses; this occurred in more or less defined areas which occasionally showed epidemic aggravations, becoming apparent as rapidly spreading epidemics or otherwise in even the form of pandemics. However this number of antigenic subtypes was found to be fairly constant and host-specific. Earlier studies were done in domesticated fowl and birds, though particularly in water birds in recent years, and numerous subtypes were detected, only a small number of these subtypes also being found to occur in man, pigs and horses. It became increasingly apparent that particularly mallards, but also other water birds play an extremely important role in the maintenance as well as in the distribution and circulation of these orthomyxoviruses in nature. These infections in water birds were not merely caused by a single subtype but occasionally by two or more antigenically different subtypes. This could be conducive to the appearance of recombinants as a result of genetic rearrangement in the cells lining the alimentary tracts of birds. Occasionally, subtypes observed in man were also found to occur in birds, which gave rise to the question of the extent to which birds are the origin or sources of infections of human epidemics caused by these subtypes. This also holds good for the subtypes in pigs. In addition to a number of oecological and ornithological considerations, reference was also made to systematic facts and routes along which further investigations on the presence of influenza viruses in the world of birds could be taken up, particular attention being paid to migratory birds. As birds of passage pass over and find their way into isolated areas as well as human population centres, these birds play a role which is yet unknown both in the distribution and in the overwintering of influenza viruses. Conditions in which wild and domesticated (water) birds, pigs, horses and man form a chain of close contact, and the areas in which new influenza viruses pathogenic for man are most likely to appear. Studies on the transgression of these barriers of species by subtypes of influenza virus still are entirely separate matter. The fact that a multidisciplinary approach is essential admits of no discussion.

**Descriptors:** bird diseases microbiology, ducks microbiology, influenza veterinary, influenza A virus avian isolation and purification, birds microbiology, disease reservoirs, influenza transmission, avian classification, avian pathogenicity, porcine isolation and purification, serotyping, swine microbiology.


**Descriptors:** disease outbreaks veterinary, avian influenza, prevention and control, avian influenza transmission, public health, zoonoses, birds, disease outbreaks prevention and control, feces virology, avian imortality, risk factors, vaccination veterinary.


**Descriptors:** bird diseases transmission, bird diseases virology, orthomyxoviridae infections transmission, orthomyxoviridae infections virology, influenza A virus, avian genetics, avian immunology.


**NAL Call Number:** 47.8 Am33P

**Abstract:** Infectious bronchitis, Newcastle disease, infectious laryngotracheitis, avian influenza, and pneumovirus are the viruses that more frequently affect the respiratory tract of chickens. Because of the tendency to change its antigenic properties, infectious bronchitis is currently the viral disease present in most poultry producing areas of the world. New serotypes and variant strains are reported in several countries. Current commercially available vaccines do not always provide protection against new field isolates. Vaccination programs are constantly adjusted in an attempt to improve protection against this disease. Infectious laryngotracheitis has appeared in the broiler industry as a serious disease. Improved vaccines are needed to control the disease in broilers. In the U.S., the control of the highly pathogenic forms of avian influenza and the velogenic forms of Newcastle disease have been achieved by eradication. In other countries, effective vaccines have been used to control Newcastle and avian influenza. Avian pneumovirus infection is also an emerging disease of chickens and turkeys.

**Descriptors:** poultry diseases virology, respiratory tract infections veterinary, viral vaccines, virus diseases veterinary, chickens, poultry diseases immunology, poultry diseases prevention and control, respiratory tract infections immunology, respiratory tract infections prevention and control, vaccination veterinary, virus diseases immunology, virus diseases prevention and control.


**NAL Call Number:** 41.8 T431

**Descriptors:** avian influenza epidemiology, poultry diseases epidemiology, birds, avian influenza prevention and control, Netherlands epidemiology, poultry, poultry diseases prevention and control.


**NAL Call Number:** 41.8 T431

**Descriptors:** bird diseases epidemiology, euthanasia, animal legislation and jurisprudence, influenza, avian epidemiology, legislation, veterinary, poultry diseases epidemiology, domestic animals, bird diseases prevention and control, birds, Europe epidemiology, avian influenza prevention and control, Netherlands epidemiology, poultry, poultry diseases prevention and control.


**NAL Call Number:** 470 Sci2

**Descriptors:** hemagglutinin glycoproteins, influenza virus genetics, influenza virology, influenza A virus avian genetics, avian pathogenicity, chickens, child, preschool, disease outbreaks, fowl plague virology, genes viral, hemagglutinin glycoproteins, influenza virus chemistry, Hong Kong epidemiology, influenza epidemiology, influenza transmission, avian physiology, sequence analysis, DNA, virus replication.


**NAL Call Number:** 448.8 P942

**Abstract:** Three hemagglutinating agents were isolated from mixed pools of the viscera from black-headed gulls (*Larus ridibundus*) and robin (*Erithacus rubecula*) collected in the Byelorussian SSA and the Kaliningrad region of the RSFSR. Typing of the viruses by double immunodiffusion technique revealed antigenic relationships of the viruses with swine hemagglutinin (Hsw1) and human hemagglutinin H0. One of the strains had neuraminidase N2 the other two Nav2. An analysis of the polypeptide composition of the virus showed the molecular weights of the heavy (HA1) and light (HA2) hemagglutinin chains to be similar in both strains (about 50,000 and 25,000 daltons, respectively). The strains had a low content of the light
hemagglutinin chain (HA2) which is typical for viruses having Hsw1 hemagglutinin.

**Descriptors:** animal population groups microbiology, animals, wild microbiology, antigens, viral analysis, birds microbiology, influenza A virus avian isolation and purification, Byelarus, hemagglutination inhibition tests, immunodiffusion, avian analysis, peptides analysis, Russia, serotyping.


**NAL Call Number:** 41.8 OF2

**Descriptors:** influenza A virus avian, humidity, hydrogen-ion concentration, temperature, virus cultivation.


**NAL Call Number:** 41.8 OF2

**Descriptors:** influenza A virus avian analysis, orthomyxoviridae infections veterinary, chick embryo, chickens, feces microbiology, orthomyxoviridae infections immunology, orthomyxoviridae infections prevention and control, urine microbiology, vaccination, viral vaccines.


**Descriptors:** fowl plague epidemiology, influenza epidemiology, disease outbreaks, fowl plague virology, Hong Kong epidemiology, influenza virology.


**NAL Call Number:** SF601.J6

**Descriptors:** epidemiological surveys, avian influenza virus, adenovirus, zoo animals, aviary birds, ducks, captive waterfowl, exposure.


**NAL Call Number:** 44.8 In282

**Descriptors:** bovine spongiform encephalopathy, avian influenza virus, Coronavirus, disease control, disease distribution, disease prevalence, disease prevention, epidemiology, livestock, zoonoses, human, prions.


**Descriptors:** strains, pathogenicity, viral morphology, ducks, avian influenza virus, Galliformes.


**NAL Call Number:** 448.8 J273

**Abstract:** Analysis of the NS and M genes of the archetype H6N5 influenza virus strain A/shearwater/Australia/1/72 shows it to be a typical example of the avian host reservoir, containing Old World/Eurasian internal proteins with divergent surface proteins, which is a potential source of new pandemic strains.

**Descriptors:** genes viral, influenza A virus avian genetics, viral matrix proteins genetics, viral nonstructural proteins genetics, amino acid sequence, base sequence, DNA, complementary genetics, disease outbreaks, disease reservoirs, evolution, molecular, gene library, molecular sequence data, sequence analysis, DNA.


**Descriptors:** orthomyxoviridae classification, paramyxoviridae classification, influenza A virus avian, measles virus, Newcastle disease virus.

**Abstract:** BACKGROUND: In response to the emergence of severe infection capable of rapid global spread, WHO will issue a pandemic alert. Such alerts are rare; however, on Feb 19, 2003, a pandemic alert was issued in response to human infections caused by an avian H5N1 influenza virus, A/Hong Kong/213/03. H5N1 had been noted once before in human beings in 1997 and killed a third (6/18) of infected people. The 2003 variant seemed to have been transmitted directly from birds to human beings and caused fatal pneumonia in one of two infected individuals. Candidate vaccines were sought, but no avirulent viruses antigenically similar to the pathogen were available, and the isolate killed embryonated chicken eggs. Since traditional strategies of vaccine production were not viable, we sought to produce a candidate reference virus using reverse genetics. METHODS: We removed the polybasic aminoacids that are associated with high virulence from the haemagglutinin cleavage site of A/Hong Kong/213/03 using influenza reverse genetics techniques. A reference vaccine virus was then produced on an A/Puerto Rico/8/34 (PR8) backbone on WHO-approved Vero cells. We assessed this reference virus for pathogenicity in in-vivo and in-vitro assays. FINDINGS: A reference vaccine virus was produced in Good Manufacturing Practice (GMP)-grade facilities in less than 4 weeks from the time of virus isolation. This virus proved to be non-pathogenic in chickens and ferrets and was shown to be stable after multiple passages in embryonated chicken eggs. INTERPRETATION: The ability to produce a candidate reference virus in such a short period of time sets a new standard for rapid response to emerging infectious disease threats and clearly shows the usefulness of reverse genetics for influenza vaccine development. The same technologies and procedures are currently being used to create reference vaccine viruses against the 2004 H5N1 viruses circulating in Asia.

Descriptors: disease outbreaks prevention and control, influenza vaccines immunology, orthomyxoviridae immunology, orthomyxoviridae infections prevention and control, antibodies, viral immunology, Asia epidemiology, birds, communicable disease control methods, drug design, genetic engineering, Hong Kong epidemiology, influenza A virus, avian immunology, human immunology, avian influenza prevention and control, avian influenza virology, orthomyxoviridae chemistry, orthomyxoviridae growth and development, orthomyxoviridae infections immunology, orthomyxoviridae infections virology, plasmids immunology, poultry diseases immunology, poultry diseases prevention and control, poultry diseases virology, reassortant viruses chemistry, reassortant viruses growth and development, reassortant viruses immunology, transformation, genetic immunology, virulence factors isolation and purification.


**NAL Call Number:** 41.8 Av5

**Abstract:** From February 2000 through September 2001, a limited number of H6N2 influenza viruses were isolated from chickens in California. This report describes the genetic characterization of nine of these H6N2 viruses. All of the viruses analyzed had phylogenetically similar hemagglutinin (HA) and neuraminidase molecules that suggested the viruses shared a recent common ancestor. The analysis of the HA sequence of these viruses with all available H6 viruses from different hosts and locations showed that these genes do not separate into well-defined North American and Eurasian lineages. The neuraminidase genes of the California viruses contain an 18 amino acid deletion, a possible adaptation to growth in chickens. Analysis of the remaining gene segments of the California viruses revealed that three distinct genotypes of H6N2
viruses were present.

Descriptors: epidemiology, infection, molecular genetics, virology, genetic characterization, genetic techniques, laboratory techniques, genotyping, phylogenetic analysis, mathematical and computer techniques, viral isolation, immunologic techniques, amino acid deletion.

NAL Call Number: 470 Sci2

NAL Call Number: 470 Sci2
Descriptors: influenza epidemiology, influenza virology, influenza A virus pathogenicity, chickens virology, evolution, molecular, genes viral genetics, genetic engineering, genome, viral, hemagglutinin glycoproteins, influenza virus chemistry, hemagglutinin glycoproteins, influenza virus genetics, hemagglutinin glycoproteins, influenza virus immunology, influenza mortality, influenza transmission, influenza A virus avian genetics, avian pathogenicity, human genetics, human immunology, human pathogenicity, porcine genetics, porcine pathogenicity, influenza A virus genetics, influenza A virus immunology, influenza vaccine biosynthesis, influenza vaccine immunology, mice, multifactorial inheritance genetics, mutation genetics, phylogeny, protein structure, tertiary, RNA viral analysis, RNA viral genetics, RNA viral isolation and purification, reassortant viruses genetics, reassortant viruses immunology, reassortant viruses pathogenicity, recombination, genetic genetics, risk, species specificity, swine virology, variation genetics genetics.

NAL Call Number: 448.8 L22
Abstract: CONTEXT: Live-animal markets (wet markets) provide a source of vertebrate and invertebrate animals for customers in tropical and subtropical regions of the world. Wet markets sell live poultry, fish, reptiles, and mammals of every kind. Live-poultry markets (mostly chicken, pigeon, quail, ducks, geese, and a wide range of exotic wild-caught and farm-raised fowl) are usually separated from markets selling fish or red-meat animals, but the stalls can be near each other with no physical separation. Despite the widespread availability of affordable refrigeration, many Asian people prefer live animals for fresh produce. Wet markets are widespread in Asian countries and in countries where Asian people have migrated. Live-poultry markets were the source of the H5N1 bird-influenza virus that transmitted to and killed six of 18 people in Hong Kong. STARTING POINT: Yi Guan and colleagues (Science 2003; 302: 276-78) recently reported the isolation of severe acute respiratory syndrome (SARS) coronavirus (CoV) from Himalayan palm civets (Paguna larvata) in wet markets in Shenzen, southern China. These researchers also found serological evidence of infection in raccoon dogs (Nyctereutes procyonoides). Serological evidence for SARS CoV in human beings working in these markets, taken together with the earliest cases of SARS in restaurant workers, supports the contention of a potential zoonotic origin for SARS. WHERE NEXT? Will SARS reappear? This question confronts public-health officials worldwide, particularly infectious disease personnel in those regions of the world most affected by the disease and the economic burden of SARS, including China, Taiwan, and Canada. Will the virus re-emerge from wet markets or from laboratories working with SARS CoV, or are asymptomatic infections ongoing in human beings? Similar questions can be asked about a pandemic of influenza that is probably imminent. Knowledge of the ecology of influenza in wet markets can be used as an early-warning system to detect the reappearance of SARS or pandemic influenza.
Descriptors: food industry methods, influenza epidemiology, severe acute respiratory syndrome epidemiology, zoonoses transmission, communicable diseases, emerging epidemiology, communicable diseases, emerging transmission, communicable diseases, emerging veterinary, disease outbreaks statistics and numerical data, disease reservoirs veterinary, disease vectors, Hong Kong epidemiology, influenza transmission, influenza veterinary, influenza A virus avian isolation and purification, poultry diseases epidemiology, poultry diseases transmission, severe acute respiratory syndrome transmission, severe acute
respiratory syndrome veterinary, zoonoses epidemiology, zoonoses virology.


NAL Call Number: 448.8 V81

Descriptors: orthomyxoviridae isolation and purification, recombination, genetic, antigens, heterophile, chickens, epitopes, genetics, microbial, hemagglutination inhibition tests, hemagglutinins viral analysis, hybridization, genetic, immunization, influenza A virus avian enzymology, avian immunology, lung, neuraminidase, neutralization tests, orthomyxoviridae enzymology, orthomyxoviridae immunology, tissue extracts, turkeys, viral vaccines.


NAL Call Number: 448.8 V81

Descriptors: orthomyxoviridae enzymology, orthomyxoviridae growth and development, orthomyxoviridae immunology, orthomyxoviridae isolation and purification, orthomyxoviridae pathogenicity, recombination, genetic, antigens analysis, centrifugation, density gradient, chick embryo, fetal membranes, fibroblasts, hemagglutination inhibition tests, hemagglutination tests, hemagglutinins viral analysis, hybridization, genetic, immune sera, influenza microbiology, influenza A virus avian enzymology, avian growth and development, avian immunology, avian pathogenicity, lung microbiology, neuraminidase analysis, rabbits, sucrose, swine, tissue culture, turkeys, virulence, virus replication.


NAL Call Number: 501 L84Pb

Abstract: The only direct evidence for transmission of influenza viruses between species comes from studies on swine influenza viruses. Antigenically and genetically identical Hsw1N1 influenza viruses were isolated from pigs and man on the same farm in Wisconsin, U.S.A. The isolation of H3N2 influenza viruses from a wide range of lower animals and birds suggests that influenza viruses of man can spread to the lower orders. Under some conditions the H3N2 viruses can persist for a number of years in some species. The isolation, from aquatic birds, of a large number of influenza A viruses that possess surface proteins antigenically similar to the viruses isolated from man, pigs and horses provides indirect evidence for inter-species transmission. There is now a considerable body of evidence which suggests that influenza viruses of lower animals and birds may play a role in the origin of some of the pandemic strains of influenza A viruses. There is no direct evidence that the influenza viruses in aquatic birds are transmitted to man, but they may serve as a genetic pool from which some genes may be introduced into humans by recombination. Preliminary evidence suggests that the molecular basis of host range and virulence may be related to the RNA segments coding for one of the polymerase proteins (P3) and for the nucleoprotein (NP).

Descriptors: influenza transmission, influenza A virus genetics, orthomyxoviridae infections veterinary, birds microbiology, ducks microbiology, fowl plague transmission, genes viral, influenza A virus avian genetics, mammals microbiology, RNA viral genetics, recombination, genetic, species specificity.


NAL Call Number: QR180.3.D4

Abstract: Studies on influenza viruses from feral ducks trapped in Canada in August 1976, gave a 26% isolation rate from cloacal samples of juvenile birds. Several different influenza A viruses were isolated, some of which possessed novel hemagglutinin and/or neuraminidase antigens. Influenza A viruses isolated from the rectum of feral ducks replicate in the upper respiratory tract and also in the intestinal tract of feral and domestic ducks. Representative human influenza viruses of the H0N1, H3N2 and Hsw1 N1 subtypes replicate in the upper respiratory tract of ducks but not in the intestinal tract. The A/Hong Kong/68 [H3N2]
influenza virus that has not been isolated from man for several years was recently isolated from pigs originating from The People's Republic of China. A/Victoria/3/75-like influenza viruses that are currently circulating in man were also isolated from pigs. Both the A/Hong Kong/68 and the A/Victoria/75-like viruses transmitted readily from pig to pig in experimental studies. The susceptibility of ducks and pigs to infection with human influenza viruses suggests that these animals may play an important role in the ecology of influenza A viruses.

Descriptors: influenza etiology, influenza A virus avian immunology, avian isolation and purification, porcine immunology, porcine isolation and purification, influenza A virus isolation and purification, antibodies, viral, cloaca microbiology, disease outbreaks, ducks microbiology, hemagglutinins viral isolation and purification, swine microbiology, virus replication.

NAL Call Number: 449.9 W892B
Descriptors: influenza A virus avian classification, recombination, genetic, birds microbiology, serotyping, USSR.

NAL Call Number: 448.8 V81
Abstract: A large pool of avirulent influenza viruses are maintained in the wild ducks and shorebirds of the world, but we know little about their potential to become virulent. It is well established that the hemagglutinin (HA) is pivotal in determining virulence and that a constellation of other genes is also necessary (R. Rott, M. Orlich, and C. Scholtissek, 1976, J. Virol. 19, 54-60). The question we are asking here is the ability of avirulent influenza viruses to provide the gene constellation that will complement the HA from a highly virulent virus and for the reassortant to be virulent. Reassortant influenza viruses were prepared between ultraviolet treated A/Chicken/Pennsylvania/1370/83 (H5N2) [Ck/Penn] and influenza viruses from natural reservoirs. These viruses included examples of the predominant subtypes in wild ducks, shorebirds, and domestic poultry. Attention was given to the influenza viruses from live poultry markets, for it is possible that these establishments may be important in mixing of influenza genes from different species and the possible transmission to domestic and mammalian species. The reassortants were genotyped by partial sequencing of each gene and were tested for virulence in chickens. Each of the reassortants contained the hemagglutinin and matrix (M) genes from Ck/Penn and a majority of genes from the viruses from natural reservoirs indicating a preferential association between the HA and M genes. The reassortants containing multiple genes from wild ducks and a cleavable HA were avirulent indicating that the gene pool in ducks may not have a high potential to provide genes that are potentially virulent. In contrast, a disproportionate number of viruses from shorebirds and all avirulent H5N2 influenza viruses from city markets provided a gene constellation that in association with cleavable H5 HA were highly virulent in chickens. An evolutionary tree based on oligonucleotide mapping established that the H5N2 influenza viruses from birds in city markets are closely related.
Descriptors: hemagglutinin viral genetics, influenza A virus avian pathogenicity, poultry diseases microbiology, animals, wild microbiology, antibodies, monoclonal, birds microbiology, disease reservoirs, genes viral, hn protein, hemagglutinins viral immunology, avian genetics, oligonucleotides analysis, poultry microbiology, viral envelope proteins genetics, viral envelope proteins immunology, viral matrix proteins genetics, virus replication.

NAL Call Number: QR360.J6
Abstract: The influenza A virus [A/Chicken/Pennsylvania/1370/83 (H5N2)] that caused up to 80% mortality among chickens provided a model system for testing the efficacy of chemotherapeutic agents against highly virulent influenza virus. Amantadine and rimantadine administered in drinking water were efficacious both
prophylactically and therapeutically. However, under conditions simulating natural transmission of virus, amantadine- and rimantadine-resistant viruses arose and were transmitted to other birds in contact with the infected chickens, causing mortality. Simultaneous administration of inactivated H5N2 vaccine and amantadine provided protection. Thus, chemotherapy may be useful in the treatment of a highly pathogenic influenza virus outbreak in humans or other animals when used in combination with vaccine.

**Descriptors:** adamantan analogs and derivatives, amantadine therapeutic use, fowl plague prevention and control, influenza A virus avian immunology, rimantadine therapeutic use, chickens, drug resistance, microbial, fowl plague drug therapy, fowl plague transmission, vaccination, viral vaccines immunology.


**NAL Call Number:** QR175.P47

**Descriptors:** avian influenza virus, pests, parasites, outbreaks, Australia, New Zealand, United States.


**NAL Call Number:** 448.8 V81

**Descriptors:** influenza A virus avian growth and development, intestines microbiology, virus replication, ducks, feces microbiology, hydrogen-ion concentration, avian ultrastructure, human growth and development, porcine growth and development, lung microbiology.


**Abstract:** Fifty years ago, the age-old scourge of infectious disease was receding in the developed world in response to improved public health measures, while the advent of antibiotics, better vaccines, insecticides and improved surveillance held the promise of eradicating residual problems. By the late twentieth century, however, an increase in the emergence and re-emergence of infectious diseases was evident in many parts of the world. This upturn looms as the fourth major transition in human-microbe relationships since the advent of agriculture around 10,000 years ago. About 30 new diseases have been identified, including Legionnaires’ disease, human immunodeficiency virus (HIV)/acquired immune deficiency syndrome (AIDS), hepatitis C, bovine spongiform encephalopathy (BSE)/variant Creutzfeldt-Jakob disease (vCJD), Nipah virus, several viral hemorrhagic fevers and, most recently, severe acute respiratory syndrome (SARS) and avian influenza. The emergence of these diseases, and resurgence of old ones like tuberculosis and cholera, reflects various changes in human ecology: rural-to-urban migration resulting in high-density peri-urban slums; increasing long-distance mobility and trade; the social disruption of war and conflict; changes in personal behavior; and, increasingly, human-induced global changes, including widespread forest clearance and climate change. Political ignorance, denial and obduracy (as with HIV/AIDS) further compound the risks. The use and misuse of medical technology also pose risks, such as drug-resistant microbes and contaminated equipment or biological medicines. A better understanding of the evolving social dynamics of emerging infectious diseases ought to help us to anticipate and hopefully ameliorate current and future risks.

**Descriptors:** communicable diseases diagnosis, communicable diseases etiology, cardiovascular diseases diagnosis, cardiovascular diseases etiology, communicable disease control, communicable diseases, emerging, demography, disease outbreaks, health, international cooperation, neoplasms diagnosis, neoplasms etiology, public health, risk, risk factors, time factors, world health.


**NAL Call Number:** 41.8 Ex7

**Abstract:** Seven different hyperimmune serum samples from chickens or rabbits were conjugated with fluorescein isothiocyanate and reacted with reference influenza A strains. Conclusions are that direct immunofluorescence reliably detected avian influenza viruses and distinguished them from Newcastle disease virus. A diagnostic set of nine inactivated influenza A viruses is available, covering subtypes from
NAL Call Number: 41.8 Au72

Descriptors: disease outbreaks veterinary, fowl plague epidemiology, Australia epidemiology, birds, fowl plague diagnosis, influenza A virus avian isolation and purification, avian pathogenicity.

NAL Call Number: SF995.A1A9

Descriptors: disease transmission, differences, strains, avian influenza virus, spread, chickens.

NAL Call Number: QR360.J6

Abstract: Wild aquatic birds are the primary reservoir of influenza A viruses, but little is known about the viruses' gene pool in wild birds. Therefore, we investigated the ecology and emergence of influenza viruses by conducting phylogenetic analysis of 70 matrix (M) genes of influenza viruses isolated from shorebirds and gulls in the Delaware Bay region and from ducks in Alberta, Canada, during >18 years of surveillance. In our analysis, we included 61 published M genes of isolates from various hosts. We showed that M genes of Canadian duck viruses and those of shorebird and gull viruses in the Delaware Bay shared ancestors with the M genes of North American poultry viruses. We found that North American and Eurasian avian-like lineages are divided into sublineages, indicating that multiple branches of virus evolution may be maintained in wild aquatic birds. The presence of non-H13 gull viruses in the gull-like lineage and of H13 gull viruses in other avian lineages suggested that gulls' M genes do not preferentially associate with the H13 subtype or segregate into a distinct lineage. Some North American avian influenza viruses contained M genes closely related to those of Eurasian avian viruses. Therefore, there may be interregional mixing of the two clades. Reassortment of shorebird M and HA genes was evident, but there was no correlation among the HA or NA subtype, M gene sequence, and isolation time. Overall, these results support the hypothesis that influenza viruses in wild waterfowl contain distinguishable lineages of M genes.

Descriptors: animals, wild virology, birds virology, ecology, evolution, molecular, influenza A virus, avian genetics, viral matrix proteins genetics, ducks virology, avian classification, avian isolation and purification, molecular sequence data, phylogeny, sequence analysis, DNA.

NAL Call Number: 41.8 M463

Abstract: A dynamic development of African ostrich breeding (Struthio camelus) has been observed in the recent years all over the world and since 1993 in Poland as well. In natural conditions the birds inhabit semidesert and grassy regions of African savannah. However, they can adapt easily to different European climatic conditions. Despite the high popularity of ostrich breeding in Poland, breeders and veterinarians face various problems connected with the birds' acclimatization to new environmental and feeding conditions. The ostriches' state of health is affected not only by numerous etiologic factors such as viruses, bacteria or fungi, but also breeding and feeding conditions. The most threatening viral infections in ostrich are: Newcastle disease, Avian influenza, Avian pox and adenovirus infections. Bacterial infections are also an important issue in intensive ostrich breeding. The most alarming thing is a high level of ostriches' infection with *Salmonella*, *Escherichia coli*, *Pseudomonas* sp. instantly after hatching. In older birds the etiologic agents of diseases are often *Mycoplasma* sp., *Campylobacter* sp., *Megabacteria*, *Chlamydia psittaci* or *Clostridium*.

Descriptors: animal husbandry, infection, veterinary medicine, avian influenza, viral disease, avian pox, viral disease, *Campylobacter* infection, bacterial disease, *Chlamydia psittaci* infection, bacterial disease,
Clostridium infection, bacterial disease, Escherichia coli infection, bacterial disease, Megabacteria infection, bacterial disease, Mycoplasma infection, bacterial disease, Newcastle disease, viral disease, Pseudomonas infection, bacterial disease, Salmonella infection, bacterial disease, adenovirus infection, viral disease, environmental acclimatization, feeding conditions, ostrich breeding, savannah.


**Descriptors:** infectious bursal disease virus, fowl plague virus, Newcastle disease virus, avian influenza virus, Galliformes, avian paramyxovirus, poultry.


**Descriptors:** fowl plague history, influenza A virus avian, virology history, viruses, chick embryo, history of medicine, 19th century, history of medicine, 20th century.


**Abstract:** The Animal and Plant Health Inspection Service (APHIS) has a long history of rapid direction, control, and eradication of devastating diseases. Our immediate response mechanisms to diseases such as avian influenza, Venezuelan equine encephalomyelitis, and Newcastle disease, have long been recognized by the global emergency response community as models of control and eradication. APHIS and the U.S. livestock industries, in partnership with the Animal Agriculture Coalition, re-evaluated the Nation's animal health emergency preparedness and response systems. The group identified areas that negatively impact, biologically and/or economically, the Nation's animal and food production industries. To counter the increased risks including bioterrorism, APHIS plans to establish a world-class "Center of Excellence for Animal Health Emergency Management." APHIS, Intelligence agencies, other Federal departments, State governments, and industries are working together to provide accurate information on the foreign and domestic threats posed to the U.S. agricultural sector by biological weapons. Additionally, the same agencies and organizations are evaluating, updating, and improving the coordination and training mechanisms necessary to respond in the even of a widespread pest or disease outbreak.

**Descriptors:** animal diseases prevention and control, animal diseases transmission, animal husbandry, bioterrorism prevention and control, government agencies, United States.


**Abstract:** Influenza is an emerging and re-emerging disease. Since the late 1930s influenza viruses have been isolated yearly from different parts of the world during epidemics and pandemics. The "epidemiologic success" of influenza is due largely to rapid and unpredictable antigenic changes (antigenic drift) among human influenza viruses, and the emergence of new subtypes (antigenic shift), mostly from reassortment between human and avian influenza viruses. Antigenic shifts were attributed to the global pandemic viruses of 1957 (H2N2 Asian flu) and 1968 (H3N2 Hong Kong flu). Concern over possible new pandemics has been heightened by recent reports of human infection in Asia in 1997 with avian viruses (H5N1) and in 1999 (H9N2) and isolation of human-avian reassorted viruses from pigs and humans in Europe. Influenza has a high rate of in apparent infection, short incubation and high infectivity; epidemics usually start abruptly and spread rapidly to neighboring communities and countries. Isolation and quarantine are often unsuccessful in preventing the spread of the infection. Although not perfect, immunization and chemoprophylaxis are highly effective at minimizing the spread of influenza and reducing morbidity and mortality, social disruption and economic loss. Plans for future influenza epidemics and pandemics require national and international programs to be in place for the monitoring of influenza activity, the dissemination and exchange of information and the provision of sufficient quantities of vaccines and antiviral agents. This paper reviews and discusses the antigenic variations of the influenza virus, potential influenza pandemics,
Protective efficacy of inactivated vaccines and antiviral agents and preparation for control of future epidemics and pandemics.

Descriptors: epidemiology, infection, influenza, epidemiology, prevention and control, respiratory system disease, viral disease, chemoprophylaxis clinical techniques, therapeutic and prophylactic techniques, immunization clinical techniques, therapeutic and prophylactic techniques, antigenic drift viral infectivity.


Descriptors: animal diseases, disease control, disease transmission, decision making, economic analysis, losses, epidemiology, foot and mouth disease, Aphthovirus, avian influenza virus, swine fever virus.


Descriptors: avian influenza, epidemiology, outbreaks prevention, control, mortality, transmission, Laos, poultry, rural health, veterinarians, zoonoses, emerging infectious diseases.


NAL Call Number: SF995.A1A9

Abstract: The nucleotide sequence encoding the HA1 portion of the haemagglutinin gene of the influenza virus A/turkey/Germany/2482/90, isolated from birds kept in an area of many pig farms, was determined and compared with those of recent avian and swine influenza isolates. It was found to be closest to the 'avian-like' swine H1N1 influenza viruses that have been reported in Europe since the early 1980s and may represent good evidence for transmission of these viruses back to birds after they have become established in pigs.

Descriptors: animal husbandry, genetics, infection, methods and techniques, microbiology, veterinary medicine, avian influenza virus Ha1, nucleotide sequence, hemagglutinin gene H1 isolate, infection, molecular genetics, pathogen, swine farm proximity, viral transmission.


NAL Call Number: 41.8 Av5

Abstract: The hemagglutinin concentration of beta-propiolactone-inactivated influenza vaccine containing A/Duck/N.Y./189/82 (H5N2) virus was measured by single-radial-immunodiffusion (SRD) test. After administration of vaccine to chickens in Freund's complete adjuvant, vaccine efficacy was assessed by challenge with lethal A/Chicken/Penn./1370/83 (H5N2) virus. SRD potency values correlated with post-vaccination antibody levels and protection against infection.

Descriptors: fowl plague prevention and control, influenza A virus avian immunology, influenza vaccine standards, chickens, hemagglutinins viral immunology, influenza vaccine therapeutic use, neuraminidase immunology, poultry diseases prevention and control, vaccination.


NAL Call Number: QR189.V32

Descriptors: influenza prevention and control, influenza A virus avian immunology, influenza vaccine therapeutic use, chickens, ducks, ferrets, human immunology, human isolation and purification, mice inbred BALB c.

Preparation of vaccines against H5N1 influenza. Vaccine 20(Suppl. 2): S84-7. ISSN: 0264-410X.
NAL Call Number: QR189.V32
Abstract: In response to the pandemic warning provided by the highly pathogenic H5N1 influenza virus infections in Hong Kong, there were world-wide attempts to develop vaccines. Three strategies were followed and although each was associated with some success, there were also some problems. Pre-clinical vaccine efficacy results are presented from one such strategy, that of using an apathogenic H5N3 avian strain for vaccine production.
Descriptors: influenza A virus avian immunology, influenza vaccine immunology, baculoviridae genetics, mice, vaccines, attenuated immunology, vaccines, synthetic immunology.

NAL Call Number: 41.8 Av5
Abstract: The highly pathogenic A/Chicken/Penn./1370/83 (H5N2) avian influenza virus, which caused 80% mortality in chickens in Pennsylvania, produced only mild transient illness in experimentally infected pheasants, little or no clinical signs in ring-billed gulls and pigs, and no clinical signs in pekin ducks. Virus could be recovered from only the upper respiratory tract of gulls and pigs for 1-2 days. Infection in ducks resulted in intestinal replication of virus in only 1 out of 12 ducks. By contrast, pheasants shed virus in feces (10(4.7) EID50) for at least 15 days. These studies reinforce wildlife surveillance findings indicating that gulls and ducks are unlikely to have transmitted virus between chicken farms during the 1983 outbreak. Although experimental data suggest that wild gallinaceous birds such as pheasants are potentially capable of virus transmission, there has been no evidence of this from wildlife surveillance in Pennsylvania. Experimental infection of chickens with H5N2 virus isolated from wild ducks one year before the Pennsylvania outbreak or a gull virus (H5N1) isolated in the quarantine area in 1983 resulted in asymptomatic infections and virus replication occurring only in the upper respiratory tract. These studies suggest that if the first H5N2 virus infecting chickens in Pennsylvania originated from waterbirds, changes in host specificity and pathogenicity for chickens and other gallinaceous birds probably occurred during emergence of the Chicken/Penn./83 virus. It is recommended that attention be given in the future to the isolation of domestic poultry from contact with wild aquatic birds.
Descriptors: chickens, disease outbreaks veterinary, ducks, fowl plague transmission, influenza A virus avian pathogenicity, swine diseases transmission, antibodies, viral analysis, birds, cloaca microbiology, disease susceptibility, fowl plague microbiology, hemagglutination tests veterinary, avian growth and development, avian immunology, Pennsylvania, species specificity, swine, trachea microbiology, virulence, virus replication.

NAL Call Number: 41.8 Av5
Abstract: Avian influenza virus was isolated from the conjunctiva of a male emu chick. Clinical observations included ocular discharge, dyspnea, and mild respiratory signs. Lesions included conjunctivitis, tracheitis, bronchopneumonia, and airsacculitis. Escherichia coli was isolated from the conjunctiva and the sinus, and Staphylococcus sp. was isolated from the conjunctiva. Influenza A viral nucleoprotein was detected immunohistochemically in epithelial cells of the bronchi, lung parenchyma and tracheal mucosa, and mononuclear inflammatory cells within the exudate of the bronchial lumen; conjunctiva, air sacs, kidney, intestine, and liver were negative for the viral nucleoprotein. The isolated influenza virus was typed as H10N7 and was determined to be nonpathogenic for chickens.
Descriptors: veterinary medicine, respiratory system, sense organs, virology, airsacculitis, respiratory system disease, bronchopneumonia, respiratory system disease, conjunctivitis, eye disease, dyspnea, respiratory system disease, ocular discharge, eye disease, respiratory disease, respiratory system disease, tracheitis, respiratory system disease, case study.

During 2000, 2001, and January 2002, avian influenza virus was isolated from chickens from 12 different locations in California. All the isolates were typed as H6N2 and determined to be of low pathogenicity for chickens. Nine of the isolates came from commercial layer flocks; one from a backyard flock; one from a mixed age flock, where ducks and squabs were also present; and one from a primary broiler breeder. Although a drop in egg production and increased mortality were among the disease signs reported in the layer flocks, the pathological changes observed in the early cases were primarily associated with mild respiratory infections. It was not until August 2001 that yolk peritonitis was observed; this has been a feature of all the remaining cases through 2001 and 2002. All the isolates clustered as a unique group separate from other influenza viruses based upon sequence data of the H6, neuraminidase (N2), and matrix (MA) genes, indicating a common ancestor for these three gene segments. However, sequencing of the nonstructural (NS) gene indicates introductions from two separate origins. With the first isolate CK/CA/431/00 as the index case, the N2, MA, and NS genes are more closely related to North American isolates, as is the NP gene of CK/CA/650/00. In contrast, the H6 gene is more closely related to a Eurasian influenza isolate. Comparison of amino acid sequences of the N2 and MA genes of these isolates with available type A influenza viruses identified two unique changes in the MA gene and nine in the N2 gene, as well as four progressive changes. These results are discussed in relation to available clinical and epidemiological data.

Descriptors: epidemiology, infection, clinical data, commercial layer flock, egg production, epidemiological data, viral pathogenicity.
may not be frequent participants in interspecies genetic exchange and reassortment of influenza viruses in the United States. In contrast, 73% of the turkey influenza virus isolates contained genes of swine origin. One turkey isolate was a reassortant having three genes characteristic of avian influenza virus and three of swine origin. These findings document a high degree of genetic exchange and reassortment of influenza A viruses in domestic turkeys in the United States. The molecular biologic techniques used by the authors should aid future epidemiologic studies of influenza pandemics.

Descriptors: disease vectors, influenza transmission, influenza A virus, porcine genetics, reassortant viruses genetics, swine microbiology, turkeys microbiology, immunoblotting, influenza microbiology, human genetics, polymerase chain reaction, United States.


NAL Call Number: 470 Sci2
Descriptors: chickens virology, disease outbreaks veterinary, fowl plague epidemiology, influenza A virus avian pathogenicity, disease outbreaks prevention and control, fowl plague virology, avian genetics, avian immunology, Mexico epidemiology, mutation, viral vaccines, virulence.

Descriptors: disease control, incidence, avian influenza virus, China, Galliformes, poultry.

Descriptors: avian influenza A virus, avian influenza epidemiology, birds virology, disease transmission prevention and control, Hong Kong epidemiology, avian influenza diagnosis, avian influenza transmission.


NAL Call Number: 448.8 P942
Abstract: A total of 288 influenza A strains with different combinations of hemagglutinin and neuraminidase, including serovariants causing diseases in mammals (H3, H4, H5, H6, H9, and H13) were isolated in 1976-1999 in Northern Caspian region from birds of 37 species belonging to Laridae, Caradridae, Anatidae, Ardeidae, Phalacrocoracidae. Serovariant H13N6 predominated. Detection of different neuraminidase subtypes (N2, N3, N6, N8) suggests introduction of genes of different viruses in previous variants of seagull viruses, but this did not subside the H13 subtype. Study of antigenic structure of A/H13 strains showed their heterogeneity, uncommon for avian influenza viruses. 3-4 antigenic variants circulated during the same period. Receptor specificity of A/H13 viruses differs from that of viruses isolated from ducks. Essential differences in the primary structure of NS gene fragments were revealed in influenza viruses isolated from seagulls (H13 and H14) at the same time and in the same place.
Descriptors: infection, circulation, influenza A virus, wild birds.


NAL Call Number: 448.3 Ar23
Descriptors: antibodies, viral immunology, fowl plague immunology, hemagglutination, viral, influenza A virus avian immunology, chickens, ducks, hemagglutination inhibition tests, mice, mink, neutralization tests,
species specificity.

Descriptors: avian influenza,symposium, summary.

Descriptors: disease surveys, epidemiology, carrier state, influenza virus, USSR, Europe.

NAL Call Number: 448.8 L22
Descriptors: influenza epidemiology, influenza transmission, disease outbreaks statistics and numerical data, influenza virology, influenza A virus, avian genetics, avian growth and development, human genetics, human growth and development, population surveillance, poultry diseases epidemiology, poultry diseases transmission, poultry diseases virology, probability, virus replication, zoonoses epidemiology, zoonoses transmission.

Abstract: The recent alert over bird flu (influenza A H5N1) in Hong Kong has ruffled feathers in some countries, including the United Kingdom, as to how the virus should be handled in clinical and research laboratories.
Descriptors: disease outbreaks prevention and control, influenza prevention and control, influenza A virus avian pathogenicity, laboratory personnel, occupational exposure prevention and control, birds, Great Britain, Hong Kong.

NAL Call Number: RM260.J6
Abstract: Influenza A, B and C all have a segmented genome, although only certain influenza A subtypes and influenza B cause severe disease in humans. The two major proteins of influenza are the surface glycoproteins-haemagglutinin (HA) and neuraminidase (NA). HA is the major antigen for neutralizing antibodies and is involved in the binding of virus particles to receptors on host cells. Pandemics are a result of novel virus subtypes of influenza A, created by reassortment of the segmented genome (antigenic shift), whereas annual epidemics are a result of evolution of the surface antigens of influenza A and B virus (antigenic drift). The rapid evolution of influenza viruses highlights the importance of surveillance in identifying novel circulating strains. Infectivity of influenza depends on the cleavage of HA by specific host proteases, whereas NA is involved in the release of progeny virions from the cell surface and prevents clumping of newly formed virus. In birds, the natural hosts of influenza, the virus causes gastrointestinal infection and is transmitted via the faeco-oral route. Virulent avian influenza strains, which cause systemic disease, have an HA that is cleaved by proteases present in all cells of the body, rather than by proteases restricted to the intestinal tract. In mammals, replication of influenza subtypes appears restricted to respiratory epithelial cells. Most symptoms and complications, therefore, involve the respiratory tract. However, systemic complications are sometimes observed and other viral genes besides the HA, including the NA, may be involved in determination of virulence of influenza strains in mammals.
Descriptors: antigenic variation physiology, hemagglutinin glycoproteins, influenza virus physiology, influenza epidemiology, neuraminidase physiology, antiviral agents therapeutic use, influenza drug therapy, influenza virology, influenza A virus human pathogenicity, neuraminidase antagonists and inhibitors, sialic acids therapeutic use.

**Descriptors:** antigenic variation physiology, influenza virology, orthomyxoviridae pathogenicity, orthomyxoviridae physiology, antigenic variation genetics, birds virology, disease reservoirs, evolution, molecular, hemagglutinin glycoproteins, influenza virus chemistry, hemagglutinin glycoproteins, influenza virus genetics, hemagglutinin glycoproteins, influenza virus metabolism, influenza epidemiology, influenza transmission, neuraminidase genetics, neuraminidase metabolism, orthomyxoviridae enzymology, orthomyxoviridae genetics.


**Abstract:** AIM: To prepare monoclonal antibodies (mAb) against the hemagglutinin(HA) of H9 subtype of avian influenza virus (AIV). METHODS: 8 week-old female BALB/c mice were immunized with the inactivated vaccine of H9 subtype of AIV. Splenocytes from the immunized mice were fused with Sp2/0 myeloma cells, and positive hybridoma clones were screened by indirect ELISA and hemagglutination inhibition test (HI). The specificity of the mAb was characterized by ELISA, HI test, indirect immunofluorescence (IF) staining and Western blot. RESULTS: Three hybridoma cell lines named 2H1, 2A3 and 1C8 against HA of AIV H9 were obtained. The HI titers of 3 mAbs were 1 x 2(8)-1 x 2(13), and the ELISA titers were 1 x 10(-7), 1 x 10(-5) and 5 x 10(-6), respectively. The immunoglobulin subclass of all 3 mAbs was IgG1. Western blot analysis confirmed that mAb 2H1 could recognize HA and reacted to 31 out of 32 isolates of H9 subtype of AIV. CONCLUSION: Three mAbs recognizing HA of H9 subtype of AIV were obtained, which may provide an useful tool for the antigenic analysis, the serological diagnosis, the epidemiological survey and the evaluation of AIV vaccine.

**Descriptors:** characterization, H9, avian influenza, virus, monoclonal antibodies, mAb, HA, AIV, subtype, ELISA, titers, vaccine.


**Descriptors:** avian influenza virus, disease control, disease prevalence, disease prevention, epidemiological surveys, pathogenicity, virulence, wild birds, ducks, fowl, ostriches, peafowl, quail, Sturnidae, turkeys.


**NAL Call Number:** SF604.C485

**Descriptors:** chickens, influenza virus, epidemics, symptoms, pathology, immunology, birds, domestic animals, domesticated birds, epidemiology, Galliformes, livestock, poultry, useful animals, viruses.


**Descriptors:** influenza prevention and control, avian influenza A virus pathogenicity, avian influenza prevention and control, birds, influenza etiology, avian influenza A virus classification, avian influenza complications, avian influenza virology.


**Descriptors:** influenza prevention and control, avian influenza A virus isolation and purification, avian influenza transmission, zoonoses transmission, influenza transmission, influenza veterinary, avian influenza A virus pathogenicity, poultry.

Zhou, N.N., D.A. Senne, J.S. Landgraf, S.L. Swenson, G. Erickson, K. Rossow, L. Liu, K. Yoon, S. Krauss, and

NAL Call Number: QR360.J6

Abstract: In late summer through early winter of 1998, there were several outbreaks of respiratory disease in the swine herds of North Carolina, Texas, Minnesota, and Iowa. Four viral isolates from outbreaks in different states were analyzed genetically. Genotyping and phylogenetic analyses demonstrated that the four swine viruses had emerged through two different pathways. The North Carolina isolate is the product of genetic reassortment between H3N2 human and classic swine H1N1 influenza viruses, while the others arose from reassortment of human H3N2, classic swine H1N1, and avian viral genes. The hemagglutinin genes of the four isolates were all derived from the human H3N2 virus circulating in 1995. It remains to be determined if either of these recently emerged viruses will become established in the pigs in North America and whether they will become an economic burden.

Descriptors: genome, viral, influenza A virus avian genetics, human genetics, porcine genetics, reassortant viruses, amino acid sequence, birds virology, molecular sequence data, swine virology.


NAL Call Number: SF995.W4

Descriptors: avian influenza virus, chickens, Pennsylvania.


NAL Call Number: 47.8 R523

Descriptors: avian influenza virus, Newcastle disease virus, pathogenicity, microbial properties, epidemiology, disease control, disease transmission, vaccines, livestock, Italy.

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**NAL Call Number:** 41.8 Av5

**Abstract:** Four- and six-week-old turkeys were vaccinated subcutaneously using avian influenza virus (AIV) A/Duck/613/MN/79 (H4N2) killed oil-emulsion vaccine. Sequential serological tests using agar gel precipitin (AGP), hemagglutination inhibition (HI), and enzyme-linked immunosorbent assay (ELISA) for measuring antibodies to AIV were performed up to 4 weeks postvaccination, when birds were challenged intranasally using A/Turkey/MN/80 (H4N2) live AIV. The ELISA was 25 to 1600 times more sensitive than the HI test and was able to detect antibody production earlier than the HI test. All turkeys with an ELISA titer of greater than or equal to 800 were protected against homologous challenge, as measured by virus recovery 3 days postchallenge. Four turkeys out of 20 serologically negative by AGP and HI tests but ELISA-positive were protected.

**Descriptors:** influenza A virus avian immunology, sensitivity and specificity, turkeys immunology, viral vaccines immunology, antibodies, viral analysis, enzyme linked immunosorbent assay veterinary, fowl plague immunology, fowl plague prevention and control, hemagglutination inhibition tests veterinary, influenza A virus avian isolation and purification, precipitin tests veterinary, vaccines, inactivated immunology.


**NAL Call Number:** Z5055.U49D53

**Descriptors:** viral diseases, avian influenza., turkeys, immunization, ELISA.


**NAL Call Number:** SF605.C59

**Descriptors:** avian influenza, turkeys, vaccine, serological evaluation, abstract.


**NAL Call Number:** 41.8 J82

**Descriptors:** fowl plague epidemiology, Newcastle disease epidemiology, animal husbandry, animals, domestic, birds, disease outbreaks prevention and control, disease outbreaks veterinary, fowl plague prevention and control, fowl plague transmission, influenza A virus avian classification, Newcastle disease prevention and control, Newcastle disease transmission, Newcastle disease virus classification, poultry, vaccination veterinary.


**NAL Call Number:** SF771.M36 2000

**Descriptors:** fowl plague virus, influenza virus A, immunization, diagnosis, techniques, mortality, pathogenicity, diagnostic tests, manual of standards, vaccines, *Gallus gallus*, poultry.


**NAL Call Number:** QR360.A1J6

**Descriptors:** antigens, immunization, orthomyxoviridae immunology, antigens, viral, birds, chickens, cross reactions, erythrocytes immunology, glycoproteins, hemagglutination inhibition tests, hemagglutinins viral
analysis, immune sera, injections, intramuscular, neuraminidase analysis, orthomyxoviridae enzymology, serologic tests, species specificity, turkeys.


**Descriptors:** avian influenza virology, Asia, birds virology, influenza A virus, avian physiology, avian influenza prevention and control, avian influenza transmission.


**NAL Call Number:** 448.8 L22

**Descriptors:** influenza prevention and control, avian influenza A virus immunology, influenza epidemiology, influenza transmission, influenza virology, influenza vaccines, avian influenza prevention and control, avian influenza transmission, international cooperation, poultry.


**Descriptors:** influenza epidemiology, influenza A virus, avian isolation and purification, human isolation and purification, avian influenza epidemiology, birds, incidence, influenza prevention and control, avian influenza prevention and control, poultry, risk assessment, survival rate, World Health Organization.


**NAL Call Number:** 448.8 L22

**Descriptors:** public health practice standards, social change, China epidemiology, communicable disease control standards, communicable disease control trends, disease outbreaks prevention and control, disease outbreaks statistics and numerical data, influenza, avian epidemiology, avian influenza prevention and control, population surveillance methods, poultry, severe acute respiratory syndrome epidemiology, severe acute respiratory syndrome prevention and control, world health.


**NAL Call Number:** R11.H3

**Descriptors:** disease outbreaks prevention and control, disease outbreaks veterinary, influenza epidemiology, influenza, avian prevention and control, child, influenza, avian epidemiology, poultry.


**Descriptors:** chickens virology, influenza epidemiology, influenza virology, influenza A virus, avian immunology, influenza vaccines, influenza prevention and control, influenza, avian epidemiology, zoonoses epidemiology.


**Descriptors:** disease outbreaks prevention and control, avian influenza transmission, poultry diseases transmission, vaccination, animals, domestic animals, wild birds, disease notification, avian influenza epidemiology, avian influenza prevention and control, poultry, poultry diseases epidemiology, poultry diseases prevention and control, zoonoses.


**NAL Call Number:** 449.9 W892B

**Descriptors:** disease outbreaks prevention and control, influenza epidemiology, world health, Asia epidemiology, influenza prevention and control, influenza virology, influenza A virus, avian influenza pathogenicity, avian influenza epidemiology, avian influenza prevention and control, avian influenza virology, public health practice.


**NAL Call Number:** RC111.R4

**Abstract:** After the initial atypical presentation of a patient with avian influenza (H5N1) infection, paired acute-phase and convalescent-phase serum samples obtained from 25 health care workers (HCWs) who were exposed to the patient were compared with paired serum samples obtained from 24 HCWs who worked at different units in the same hospital and were not exposed to the patient. There was no serologic evidence of anti-H5 antibody reactivity or subclinical infection in either of the groups.

**Descriptors:** H5N1, seroprevalence, anti-H5 antibody, health care workers, avian influenza, patient, serum samples, exposure.

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**NAL Call Number:** 449.9 Un3r

**Descriptors:** fowl plague prevention and control, turkeys, fowl plague epidemiology, fowl plague transmission, Minnesota.


**NAL Call Number:** SF481.M54

**Descriptors:** avian influenza virus, vaccination, disease control, disease prevention, poultry.


**NAL Call Number:** aSF995.6.I6I5 1981a

**Descriptors:** avian influenza virus, control, prevention, immunization, vaccines, symposium.


**NAL Call Number:** 41.8 V641

**Descriptors:** fowl plague prevention and control, turkeys, vaccination veterinary, influenza A virus avian immunology, viral vaccines.


**NAL Call Number:** 41.8 Av5

**Abstract:** A recombinant fowlpox vaccine virus containing the H5 hemagglutinin gene of avian influenza virus was administered to susceptible chickens via wing-web puncture, eye drop, instillation into the nares, and drinking water. Even though there was a negligible hemagglutination-inhibition (HI) serologic response, all 10 chickens vaccinated by wing-web puncture remained without obvious signs of disease and survived challenge with a highly pathogenic strain of H5N2 avian influenza virus. All unvaccinated chickens and those vaccinated by nasal and drinking-water routes died following challenge. Eight of 10 chickens vaccinated with the recombinant by eyedrop died. All vaccinates were negative on the agar gel precipitin (AGP) test, and only one chicken had a positive HI titer before challenge. All chickens that survived challenge had high levels of HI antibody and were positive on the AGP test, indicating that they were infected by the challenge virus.

**Descriptors:** chickens immunology, fowl plague prevention and control, fowlpox virus immunology, poultry diseases prevention and control, viral vaccines administration and dosage, evaluation studies, fowl plague pathology, poultry diseases microbiology, poultry diseases pathology, vaccines, synthetic administration and dosage, vaccines, synthetic immunology, viral vaccines immunology.

Two recombinant fowlpox viruses containing the avian influenza H5 hemagglutinin (HA) gene were evaluated for their ability to protect chickens against challenge with a highly pathogenic isolate of avian influenza virus (H5N2). Susceptible chickens were vaccinated with the parent fowlpox vaccine virus or recombinant viruses either by wing-web puncture or comb scarification. Following challenge 4 weeks later with highly pathogenic avian influenza virus, all birds vaccinated by the wing-web method were protected by both recombinants, while 50% and 70% mortality occurred in the two groups of birds vaccinated by comb scarification. Birds vaccinated with the unaltered parent fowlpox vaccine virus or unvaccinated controls experienced 90% and 100% mortality, respectively, following challenge. Hemagglutination-inhibition (HI) antibody levels were low, and agar-gel precipitin results were negative before challenge. Very high HI titers and positive precipitating antibody responses were observed in all survivors following challenge.

Descriptors: fowls, avian influenza virus, recombinant vaccines, fowl pox virus, disease prevention, vaccination, mortality, wing web puncture, comb scarification.
several genes into the large genome of fowlpox may enable the development of multivalent vaccines and vaccines incorporating immune response modifiers such as lymphokines. Newcastle disease, avian influenza, infectious bursal disease and Marek’s disease antigens expressed by rFPV have been shown to be effective vaccines in poultry. None appear, however, to provide a substantial improvement in vaccine efficacy. Recombinant FPV will be a valuable adjunct to conventional vaccines currently in widespread use. Whether rFPV or other vector based vaccines can circumvent the problems of vaccination in the presence of high maternally derived antibodies is yet to be resolved. The observation that avipoxvirus recombinants may be suitable for the vaccination of non-avian species provides an added dimension to vaccines based on FPV or other avipoxviruses. Recombinant FPV will be a valuable adjunct to conventional vaccines currently in widespread use. Whether rFPV or other find a useful role in poultry disease control when used in conjunction with conventional vaccines.

Descriptors: genetics, immune system, infection, microbiology, pharmacology, veterinary medicine, avian influenza virus biotechnology genetic engineering.


NAL Call Number: 41.8 Au72

Abstract: OBJECTIVE: To evaluate the vaccine efficacy of a fowlpox virus recombinant expressing the H7 haemagglutinin of avian influenza virus in poultry. PROCEDURE: Specific-pathogen-free poultry were vaccinated with fowlpox recombinants expressing H7 or H1 haemagglutinins of influenza virus. Chickens were vaccinated at 2 or 7 days of age and challenged with virulent Australian avian influenza virus at 10 and 21 days later, respectively. Morbidity and mortality, body weight change and the development of immune responses to influenza haemagglutinin and nucleoprotein were recorded. RESULTS: Vaccination of poultry with fowlpox H7 avian influenza virus recombinants induced protective immune responses. All chickens vaccinated at 7 days of age and challenged 21 days later were protected from death. Few clinical signs of infection developed. In contrast, unvaccinated or chickens vaccinated with a non-recombinant fowlpox or a fowlpox expressing the H1 haemagglutinin of human influenza were highly susceptible to avian influenza. All those chickens died within 72 h of challenge. In younger chickens, vaccinated at 2 days of age and challenged 10 days later the protection was lower with 80% of chickens protected from death. Chickens surviving vaccination and challenge had high antibody responses to haemagglutinin and primary antibody responses to nucleoprotein suggesting that although vaccination protected substantially against disease it failed to completely prevent replication of the challenge avian influenza virus. CONCLUSION: Vaccination of chickens with fowlpox virus expressing the avian influenza H7 haemagglutinin provided good protection against experimental challenge with virulent avian influenza of H7 type. Although eradication will remain the method of first choice for control of avian influenza, in the circumstances of a continuing and widespread outbreak the availability of vaccines based upon fowlpox recombinants provides an additional method for disease control.

Descriptors: chickens, fowl plague immunology, fowl plague prevention and control, fowlpox virus immunology, influenza A virus avian immunology, vaccines, synthetic, viral vaccines, antibodies, viral blood, DNA primers, enzyme linked immunosorbent assay, fowl plague blood, fowlpox virus classification, fowlpox virus genetics, hemagglutinin glycoproteins, influenza virus genetics, hemagglutinin glycoproteins, influenza virus immunology, influenza A virus avian genetics, reverse transcriptase polymerase chain reaction, specific pathogen free organisms.


NAL Call Number: 448.8 V81

Abstract: Avian H5N1 influenza viruses isolated from humans in Hong Kong in 1997 were divided into two antigenic groups based on the presence or absence of a potential glycosylation site at amino acid residues 154-156 in the HA1 region of the viral hemagglutinin (HA) surface glycoprotein. To assess the impact of glycosylation on the immunogenicity of an HA-expressing DNA vaccine, a series of plasmid vaccine constructs that differed in the presence of potential glycosylation sites at amino acid residues 154-156, 165-167, and 286-288 were used to immunize BALB/c mice. Postvaccination serum IgG, hemagglutination
inhibition, and neutralizing antibody titers as well as the morbidity and mortality following a lethal H5N1 viral challenge did not vary significantly among any of the experimental groups. We conclude that the glycosylation pattern of the influenza virus HA1 domain has little impact on the murine antibody response raised to a DNA vaccine encoding the H5 HA, thereby minimizing the concern that the pattern of glycosylation sites encoded by the vaccine match those of closely related H5 viruses.

Descriptors: immune system, pharmacology, antibody response glycosylation.


Abstract: PURPOSE OF REVIEW: The emergence of severe acute respiratory syndrome in late 2002 and the recent outbreaks of avian influenza in Asia are timely reminders of the ever present risks from respiratory viral diseases. Apart from influenza, there are no vaccines and very few antiviral chemotherapeutic agents available for the prevention and treatment of respiratory viral infections-the most common cause of human illness. If the current H5N1 avian influenza outbreak ever assumes the role of a pandemic, formidable technical difficulties relating to the properties of the agent, itself, will ensure that vaccines will only become available after a significant lead time and then only to a relatively small percentage of the population. The use of existing antivirals could be critical in limiting the initial spread of a pandemic, although their use in the control of epidemics caused by nonpandemic viruses has not been evaluated. It is against this background that a review of recent developments in respiratory antivirals has been undertaken. RECENT FINDINGS: The late 1990s were a period of unprecedented activity in the development of new and much superior antivirals for the treatment of influenza infections. However, during the past 2 to 3 years and largely for commercial reasons, there has been a decline in interest in their further development by major drug companies. This situation may soon change with the possible advent of new pandemic viruses, and moves are afoot in several countries to consider the stockpiling of antivirals. The neuraminidase inhibitors zanamivir and oseltamivir, and the M2 inhibitors amantadine and rimantadine, remain the only options for controlling respiratory disease caused by influenza viruses, although the latter two could not be used against very recent H5N1 strains. There are several other neuraminidase inhibitors in development. Compounds with activity against other respiratory viruses, notably rhinoviruses, are also in development, many based on a newer knowledge of viral protein structure and function (rational drug design). SUMMARY: The following is an overview of recent papers on the further development of neuraminidase inhibitors against influenza viruses and on recent development of newer antivirals against RSV and rhinoviruses. Where possible, comparisons are made with existing antivirals. For considerations of space, this review has been structured around stages in the replication cycle of significant respiratory viruses that have been traditionally used as targets for inhibition.

Descriptors: antiviral agents therapeutic use, respiratory tract infections drug therapy, respiratory tract infections virology, virus diseases drug therapy, antiviral agents pharmacology, drugs investigational pharmacology, drugs investigational therapeutic use, enzyme inhibitors pharmacology, enzyme inhibitors therapeutic use, ion channels antagonists and inhibitors.


NAL Call Number: QH506.E46

Descriptors: influenza, vaccine, variability, avian influenza, epidemic, shortages.


NAL Call Number: 41.8 AV5

Abstract: Hemagglutinin-based influenza vaccines stimulate protection in chickens that is limited to the serotype of the expressed hemagglutinin. To evaluate whether a more highly conserved influenza virus protein might stimulate a broader protective response, the influenza virus nucleoprotein (NP) was introduced into a retroviral vector (mRCAS/NP). NP is an internal influenza virus protein that has been shown to stimulate cytotoxic T-cell responses in influenza-virus-infected mice. Cells infected with mRCAS/NP...
expressed approximately 10% of the level of NP observed in influenza-virus-infected chicken embryo fibroblasts. Immunocompetent chicks were vaccinated intramuscularly with approximately $1 \times 10^5$ NP-expressing units of mRCAS/NP. Four weeks later, chicks were bled and challenged with a highly pathogenic avian influenza virus (A/Chicken/Victoria/1/85). The NP-expressing vector stimulated an influenza-virus-specific response, as indicated by the presence of antibody to NP, but failed to protect against the lethal challenge.

Descriptors: chickens immunology, influenza A virus avian immunology, influenza vaccine immunology, nucleoproteins immunology, poultry diseases immunology, viral core proteins immunology, antibodies, viral blood, fowl plague immunology, genetic vectors immunology, influenza vaccine biosynthesis, leukosis virus, avian metabolism, nucleoproteins biosynthesis, poultry diseases microbiology, vaccines, synthetic biosynthesis, vaccines, synthetic immunology, viral core proteins biosynthesis.


NAL Call Number: 41.8 Am3A

Abstract: Chickens and turkeys vaccinated with inactivated virus oil-emulsion vaccines containing different concentrations of either 1 (monovalent) or 4 (polyvalent) strains of avian influenza virus (AIV) were challenged-exposed with virulent AIV A/chicken/Scotland/59 or A/turkey/Ontario/7732/66. Four of 6 vaccines protected completely against postexposure mortality. Vaccine valency did not alter the serologic and challenge-exposure responses of chickens vaccinated with AIV A/turkey/Wisconsin/68, which was the virus component common to both monovalent and polyvalent vaccines. The magnitude of the serologic responses and protection against challenge-exposure were dependent on the concentration of virus in the vaccines. These data indicate that control of virulent AIV in chickens and turkeys by vaccination with inactivated vaccines may be feasible.

Descriptors: chickens, influenza veterinary, influenza vaccine administration and dosage, poultry diseases prevention and control, turkeys, vaccination veterinary, antigens, viral immunology, emulsions, hemagglutinins viral analysis, immunity, influenza immunology, influenza prevention and control, influenza A virus immunology, oils, poultry diseases immunology.


NAL Call Number: 41.8 Am3A

Abstract: Influenza A/turkey/Oregon/71 virus has antigenic characteristics of fowl plague virus but is avirulent for chickens. The virus was inoculated intratracheally in chickens at several dosage levels and resulted in the formation of antibody and immunity against fowl plague. The avirulent virus replicated in chickens and was recoverable by tracheal swab specimens up to 4 days after inoculation. Although the virus was transmitted to contact controls at the time when their cagemates were inoculated, it was not transmitted to contact controls placed with chickens inoculated 24 hours earlier. After 10 passages in chickens, the virus remained avirulent for chickens and turkeys.

Descriptors: chickens, fowl plague prevention and control, vaccination veterinary, antibodies, viral analysis, influenza A virus avian growth and development, avian immunology, avian isolation and purification, trachea microbiology, viral vaccines, virulence.


NAL Call Number: 449.9 Un3r

Descriptors: fowl plague prevention and control, influenza A virus avian growth and development, immunology, chickens, cloaca microbiology, fowl plague immunology, vaccination.


**Abstract:** The present paper reports on the development, validation and field application of a control strategy for avian influenza infections in poultry. The "DIVA" (Differentiating Infected from Vaccinated Animals) strategy is based on the use of an inactivated oil emulsion vaccine containing the same haemagglutinin (H) subtype as the challenge virus, but a different neuraminidase (N). The possibility of using the heterologous N subtype, to differentiate between vaccinated and naturally infected birds, was investigated through the development of an "ad hoc" serological test based on the detection of specific anti-N antibodies. This test is based on an indirect fluorescent antibody assay, using as an antigen a baculovirus expressing recombinant N proteins. The vaccination strategy has been tested in the laboratory and shown to be efficacious both against challenge with highly pathogenic AI viruses and with low pathogenicity AI viruses, ensuring clinical protection, reduction of duration and titre of shedding. In addition, vaccination resulted in an increased resistance to infection. The companion diagnostic tests directed to the detection of anti-N1 and anti-N3 antibodies have been validated in the laboratory and using field samples. The serological assay showed an "almost perfect agreement" (Kappa value) with the HI test, with relative sensitivity and specificity values of 98.1 and 95.7, respectively. The results of the present investigation suggest that the "DIVA" control strategy may represent a tool to support the eradication of avian influenza infections in poultry.

**Descriptors:** animals, viral blood antibodies, viral immunology antibodies, genetic engineering, avian influenza A virus enzymology, avian influenza diagnosis, avian influenza prevention and control, neuraminidase genetics, poultry, sensitivity and specificity, veterinary serologic tests, marker vaccines, viral vaccines immunology, virus shedding.


**NAL Call Number:** SF481.M54

**Descriptors:** poultry, disease control, epidemics, immune response, immunization, avian influenza virus, DIVA, Italy.


**NAL Call Number:** SF600.Z6

**Descriptors:** avian influenza virus, disease control, inactivated vaccines, recombinant vaccines, vaccination, regulations, fowl.


**NAL Call Number:** 41.8 V641

**Descriptors:** avian influenza, control, distribution, prevalence, European Union, Italy, outbreaks, poultry, vaccination.


**NAL Call Number:** QR180.3.D4 v. 114

**Descriptors:** avian influenza virus, control programs, disease control, immunization, poultry, Italy.


**NAL Call Number:** 41.8 V641

**Descriptors:** disease outbreaks veterinary, fowl plague epidemiology, fowl plague prevention and control, influenza veterinary, influenza A virus avian immunology, vaccination veterinary, influenza epidemiology, human diseases, immunization, influenza, occupational hazards, infected poultry.

NAL Call Number: SF995.A1A9

Descriptors: avian influenza virus, disease control, disease prevention, disease resistance, experimental infection, immune response, vaccination, turkeys.


NAL Call Number: SF995.A1A9

Abstract: Recent epidemics of highly contagious animal diseases included in list A of the Office International des Epizooties, such as foot-and-mouth disease, classical swine fever and avian influenza (AI), have led to the implementation of stamping-out policies resulting in the depopulation of millions of animals. The enforcement of a control strategy based on culling animals that are infected, suspected of being infected or suspected of being contaminated, which is based only on the application of sanitary restrictions on farms, may not be sufficient to avoid the spread of infection, particularly in areas that have high animal densities, thus resulting in mass depopulation. In the European Union, the directive that imposes the enforcement of a stamping-out policy (92/40/EC) for AI was adopted in 1992 but was drafted in the 1980s. The poultry industry has undergone substantial changes in the past 20 years, mainly resulting in shorter production cycles and in higher animal densities per territorial unit. Due to these organizational changes, infectious diseases are significantly more difficult to control because of the greater number of susceptible animals reared per given unit of time and due to the difficulties in applying adequate biosecurity measures. The slaughter and destruction of great numbers of animals is also questionable from an ethical point of view. For this reason, mass depopulation has raised serious concerns for the general public and has recently led to very high costs and economic losses for national and federal governments, stakeholders and, ultimately, for consumers. In the past, the use of vaccines in such emergencies has been limited by the impossibility of differentiating vaccinated/infected from vaccinated/noninfected animals. The major concern was that through trade or movement of apparently uninfected animals or products, the disease could spread further or might be exported to other countries. For this reason, export bans have been imposed on countries enforcing a vaccination policy. This review considers the possible strategies for the control of avian influenza infections, bearing in mind the new proposed definition of AI, including the advantages and disadvantages of using conventional inactivated (homologous and heterologous) vaccines and recombinant vaccines. Reference is made to the different control strategies, including the restriction measures to be applied in case of the enforcement of a vaccination policy. In addition, the implications of a vaccination policy on trade are discussed. It is concluded that if vaccination is accepted as an option for the control of AI, vaccine banks, including companion diagnostic tests, must be established and made available for immediate use.

Descriptors: epidemiology, infection, public health, veterinary medicine, avian influenza, epidemiology, infectious disease, prevention and control, respiratory system disease, viral disease, vaccination, clinical techniques, biosecurity, disease control strategies, disease control vaccination policy, epizootics, slaughter and destruction, disease control.


NAL Call Number: QR189.V32

Descriptors: avian influenza, infection, vaccination, prevention and control, Food and Agriculture Organization, Asia.


NAL Call Number: SF995.A1A9

Abstract: The present paper reports of the development and validation of a control strategy for avian
influenza infections in poultry. The "DIVA" (Differentiating Infected from Vaccinated Animals) strategy is based on the use of an inactivated oil emulsion vaccine containing the same haemagglutinin (H) subtype as the challenge virus, but a different neuraminidase (N). The possibility of using the heterologous N subtype, to differentiate between vaccinated and naturally infected birds, was investigated through the development of an "ad hoc" serological test based on the detection of specific anti-N1 antibodies. This was achieved using a baculovirus expressing a recombinant N1 protein. The A/ck/Pakistan/H7N3 virus was used as a vaccine and birds were challenged with the HPAI A/ty/Italy/4580/V99/H7N1 strain. The homologous H group ensured a clinical protection of 93% regardless of the vaccination scheme used, and was able to prevent viraemia and muscle colonization in the clinically healthy challenged birds. However, it was not able to prevent viral shedding. The "ad hoc" serological assay was developed as an indirect immunofluorescence test, and was validated using 608 field sera, and showed an "almost perfect agreement" (Kappa value) with the HI test, with relative sensitivity and specificity values of 98.1 and 95.7, respectively. The results of the present investigation suggest that the "DIVA" control strategy may represent a tool for the control of avian influenza infections in poultry.

Descriptors: immune system, infection, pharmacology, avian influenza, infectious disease, viral disease, differentiating infected from vaccinated animals strategy (DIVA strategy) clinical techniques, laboratory techniques, poultry vaccination clinical techniques, therapeutic and prophylactic techniques, serological assay clinical techniques, diagnostic techniques, laboratory techniques, viral challenge clinical techniques.

NAL Call Number: 41.8 V641
Descriptors: fowl plague prevention and control, influenza A virus avian isolation and purification, birds, Italy.

Abstract: En virtud de la sero-conversion observada, en pollos centinelas, al virus de Influenza Aviar (IA) en ciertas zonas avícolas del pais, los productores de pollo introducen en sus granjas pollos con anticuerpos maternos como una medida de prevencion. El objeto del presente trabajo fue el de determinar si los pollos con anticuerpos maternos, como una medida de la inmunidad pasiva, tenian una respuesta diferencial con respecto a los pollos sin anticuerpos, al ser vacunados al primer dia de edad con la vacuna recombinante de Viruela-Influenza Aviar. Se realizaron 2 estudios en los que grupos de 15 y 30 pollos respectivamente para cada estudio, se siguieron serologicamente despues de vacunarlos al dia de edad. Se realizaron desafios a los 7, 21, 35 y 49 dias post-vacunacion para el primer estudio y a los 7, 21 y 49 dias para el segundo. En todos los casos, los pollos a los 49 dias post-vacunacion fueron serologicamente negativos en la prueba de inhibicion de la hemaglutinacion. comparados con pollos que fueron vacunados con vacuna emulsionada en que mostraron el 100% de sero-conversion en este periodo. En cuanto a la proteccion al desafio tanto los pollos con anticuerpos como los sin anticuerpos maternos estuvieron protegidos con la vacuna recombinante al momento de los desafios. Los resultados indican que la vacuna recombinante aqui probada induce una buena proteccion al ser aplicada en pollos comerciales de engorda tanto aquellos que tienen inmunidad pasiva como a los que no la tienen. De tal manera que este estado no limita la utilizacion de la vacuna.
Descriptors: broiler chickens, avian influenza virus, synthetic vaccines, immune response, maternal immunity, birds, chickens, domestic animals, Galliformes, immunity, influenza virus, livestock, meat animals, orthomyxoviridae, passive immunity, poultry, useful animals, vaccines, viruses.

NAL Call Number: 448.8 V81
Abstract: The influenza A/chicken/Pennsylvania/1/83 (H5N2) virus is the first known example of an influenza virus isolated from a natural infection which contained primarily defective interfering particles (T. M. Chambers and R. G. Webster, J. Virol. 61, 1517-1523, 1987). In chickens, coinoculation of this virus together with the closely related but highly virulent influenza A/chicken/Pennsylvania/1370/83 virus results in reduced mortality compared to virulent virus infection alone (Bean et al., J. Virol. 54, 151-160, 1985). The biological basis of this protective effect has not been established. Protective activity required greater than or equal to 100-fold excess input of protecting virus over virulent virus, functioned effectively during the first generations of virulent virus multiplication, and also functioned against an antigenically heterologous (H7N7) virulent influenza virus. Protection was correlated with the complete inhibition of virulent virus spread to the brain of infected chickens. Plaque-purified chicken/Pennsylvania/1/83 virus depleted of defective interfering particles, and beta-propiolactone-inactivated virus, had no protective effect. These characteristics are consistent with the hypothesis that protection was the result of defective interfering particle-mediated interference with virulent virus multiplication within the respiratory tract of the chicken.

Descriptors: influenza prevention and control, influenza A virus avian pathogenicity, viral vaccines therapeutic use, chickens, disease outbreaks, influenza epidemiology, avian growth and development, propiolactone pharmacology, United States epidemiology, virulence, virus activation.

NAL Call Number: 41.8 Av5

Abstract: H9N2 subtype avian influenza viruses have been identified in avian species worldwide, and infections in pigs were confirmed in Hong Kong in 1998. Subsequently, H9N2 viruses were isolated from two children in Hong Kong in 1999, and five human infections were reported from China, raising the possibility that H9N2 viruses pose a potential pandemic threat for humans. These events prompted us to develop a vaccine candidate to protect humans against this subtype of influenza A viruses. Reassortant H1N1 and H3N2 human influenza A viruses with the six internal gene segments of A/Ann Arbor/6/60 (H2N2)(AA) cold-adapted (ca) virus have been tested extensively in humans and have proved to be attenuated and safe as live virus vaccines. Using classical genetic reassortment, we generated a reassortant that contains the hemagglutinin and neuraminidase genes from A/chicken/Hong Kong/G9/97 (H9N2) and six internal gene segments from the AAca virus. The G9/AAca reassortant virus exhibits the ca phenotype and the temperature-sensitive phenotypes of the AAca virus and was attenuated in mice. The reassortant virus was immunogenic and protected mice from wild-type H9N2 virus challenge. The G9/AAca virus bears the in vitro and in vivo phenotypes specified by the AAca virus and will be evaluated as a potential vaccine candidate in humans.

Descriptors: infection, pharmaceuticals, avian influenza, infectious disease, respiratory system disease, viral disease, candidate vaccine strains, genetic reassortment, temperature sensitive phenotypes.

NAL Call Number: S471.C6N89
Descriptors: immune response, DNA vaccines, vaccine development, avian influenza virus, chickens.

NAL Call Number: QR189.V32
Abstract: H9N2 subtype avian influenza viruses (AIVs) are widely distributed in avian species and were isolated from humans in Hong Kong and Guangdong province, China in 1999 raising concern of their potential for pandemic spread. We generated a high-growth reassortant virus (G9/PR8) that contains the hemagglutinin (HA) and neuraminidase (NA) genes from the H9N2 avian influenza virus A/chicken/Hong Kong/G9/97 (G9) and six internal genes from A/Puerto Rico/8/34 (PR8) by genetic reassortment, for evaluation as a potential vaccine candidate in humans. Pathogenicity studies showed that the G9/PR8
reassortant was not highly pathogenic for mice or chickens. Two doses of a formalin-inactivated G9/PR8 virus vaccine induced hemagglutination inhibiting antibodies and conferred complete protection against challenge with G9 and the antigenically distinct H9N2 A/Hong Kong/1073/99 (G1-like) virus in a mouse model. These results indicate that the high growth G9/PR8 reassortant has properties that are desirable in a vaccine seed virus and is suitable for evaluation in humans for use in the event of an H9 pandemic.

Descriptors: immune system, infection, influenza A virus infection, prevention and control, viral disease.


NAL Call Number: SF604.C58

Descriptors: immune system, leokocytes, lymphocytes, avian influenza virus, experimental infection, chicken.


Descriptors: DNA vaccines, genes, human diseases, immune response, immunization, influenza A, influenza B, reviews, influenza virus B.


Descriptors: recombinant vaccines, avian influenza virus, fowl pox virus, hemagglutinins, interferon, chickens.


NAL Call Number: 448.3 Ac83

Abstract: The hemagglutinin (HA) gene from the AIV, A/Chicken/China/F/1998 (H9N2) was amplified with the RT-PCR technique and directionally inserted into transferring vector 1175, resulted in recombinant transferring vector 1175HA. In order to generate recombinant fowlpox virus expressing HA (rFPV-HA), the recombinant transferring vector 1175HA was used to transfect the chicken embryo fibroblasts (CEF) pre-infected with wide type fowlpox virus. Then, by selection of blue plaques on the CEF overlaid with agar containing X-gal, rFPV-HA was obtained and purified. The expression of HA by rFPV-HA was detected in the recombinant virus-infected CEF by indirect immunofluorescence. Experiments on chickens demonstrated that rFPV-HA could induce detectable HI antibodies 7 days post-vaccination and those HI antibodies of relatively high titers could persist 55 days. rFPV-HA also had the same protective efficacies to suppress SPF chickens or commercial broiler chickens with antibodies against FPV from shedding challenged virus from intestine as inactivated vaccine in oil emulsion.

Descriptors: immune system, infection, methods and techniques, avian influenza, viral disease, protective immunity.


NAL Call Number: 41.8 Av5

Abstract: Eukaryotic expression plasmids encoding either the avian influenza hemagglutinin or matrix genes (pCMV-HA and pCMV-M, respectively) were constructed. The viral genes were derived from a low-pathogenicity H7N1 strain, A/Chicken/Italy/1067/99, isolated during the 1999-2001 epizootic in Italy. The plasmid was administered to 4-to-5-wk-old specific-pathogen-free chickens by several different injection methods. For the initial studies comparing methods of vaccine injection, results were compared based on hemagglutination inhibition (HI) response following immunization with pCMV-HA. Additional studies with
Coadministration of both pCMV-HA and pCMV-M was evaluated based on HI response and viral isolation after homologous challenge. Preliminary results indicate that a device intended to inject insulin in humans (Medijector) and the coadministration of both plasmids improved protection against H7 infection.

Descriptors: epidemiology, infection, pharmaceuticals, public health, avian influenza, infectious disease, respiratory system disease, viral disease, immunization clinical techniques, therapeutic and prophylactic techniques, epizootic.


Descriptors: communicable disease control organization and administration, influenza A virus, avian isolation and purification, virus diseases epidemiology, birds, communicable diseases epidemiology, incidence, influenza epidemiology, influenza prevention and control, avian influenza epidemiology, avian influenza prevention and control, risk assessment, severe acute respiratory syndrome epidemiology, severe acute respiratory syndrome prevention and control, virus diseases prevention and control, world health.


Descriptors: disease control, disease surveys, geographical information systems, intensive production, monitoring, outbreaks, poultry diseases, risk factors, avian influenza virus, Delmarva Peninsula, United States.


NAL Call Number: SF995.W4

Descriptors: chickens, vaccines, avian influenza virus, birds, domestic animals, domesticated birds, Galliformes, influenza virus, livestock, orthomyxoviridae, poultry, useful animals, viruses.


NAL Call Number: QR189.V32

Abstract: Baculoviruses were engineered to express hemagglutinin (HA) genes of recent avian influenza (AI) isolates of the H5 and H7 subtypes. The proteins were expressed as either intact (H7) or slightly truncated versions (H5). In both cases purified HA proteins from insect cell cultures retained hemagglutination activity and formed rosettes in solution, indicating proper folding. Although immunogenic in this form, these proteins were more effective when administered subcutaneously in a water-in-oil emulsion. One or two-day-old specific pathogen free (SPF) White Rock chickens, free of maternal AI antibodies, responded with variable serum HI titers, but in some cases the titers were comparable to those achieved using whole virus preparations. Vaccination of three-week-old chickens with 1.0 microg of protein per bird generated a more consistent serum antibody response with an average geometric mean titer (GMT) of 121 (H5) and 293 (H7) at 21 days postvaccination. When challenged with highly pathogenic strains of the corresponding AI subtypes, the vaccinated birds were completely protected against lethal infection and in some cases exhibited reduced or no cloacal shedding at 3 days postinfection. Vaccine protocols employing these recombinant HA proteins will not elicit an immune response against internal AI proteins and thus will not interfere with epidemiological surveys of natural influenza infections in the field.

Descriptors: baculoviridae immunology, fowl plague immunology, fowl plague prevention and control, hemagglutinins viral immunology, influenza vaccine immunology, amino acid sequence, chickens, cloning, molecular, hemagglutinins viral chemistry, hemagglutinins viral genetics, influenza A virus avian immunology, molecular sequence data, recombinant proteins chemistry, recombinant proteins genetics, recombinant proteins immunology, turkeys.


**NAL Call Number:** 41.8 Av5

**Abstract:** Vaccination against highly pathogenic (HP) subtypes of avian influenza (AI) virus in poultry has been prohibited in the United States. Recently, policy has been changed to potentially allow use of inactivated vaccines in emergency programs to control HP H5 and H7 AI. Vaccination with inactivated virus against non-highly pathogenic AI viruses has been allowed in the U.S. turkey industry since 1979 (1) but requires expensive handling of individual birds for parenteral inoculation. Oral immunization would provide a less expensive method to protect commercial poultry from AI. Prime candidates for oral vaccines are waterfowl-origin (WFO) isolates, which have a tropism for the alimentary tract. One WFO isolate, A/mallard/Ohio/556/1987 (H5N9) (MOh87), was characterized by determining the complete nucleotide sequence of its hemagglutinin (HA) gene. The HA protein of this isolate possessed a deduced amino acid sequence nearly identical to the consensus amino acid sequence for all published H5 genes, indicating that it has potential as a broadly effective vaccine. Experimental results demonstrated measurable serum antibody responses to orally delivered live and inactivated preparations of MOh87. Oral vaccination also protected chickens from diverse, lethal H5 AI virus challenge strains and blocked cloacal shedding of challenge virus.

**Descriptors:** avian influenza virus, chickens, hemagglutinins, immunization, oral administration, genes, oral vaccination, virulence, live vaccines, inactivated vaccines, experimental infections, strain differences, nucleotide sequences, amino acid sequences, immune response, molecular sequence data, GENBANK u67783.


**Descriptors:** influenza virology, influenza A virus, avian pathogenicity, zoonoses virology, chickens virology, influenza epidemiology, influenza prevention and control, influenza transmission, isolation and purification, Japan epidemiology, respiratory protective devices, zoonoses epidemiology, zoonoses transmission.


**NAL Call Number:** SF600.C82

**Descriptors:** avian influenza virus, control, outbreaks, Italy.


**Descriptors:** avian influenza virus, poultry, disease control, disinfection, immunization, farm animals, pathology.


**NAL Call Number:** 41.8 Av5

**Abstract:** In the winter of 1997 and 1998, in the midst of the H7N2 avian influenza outbreak in Pennsylvania, producers added antifreeze or windshield washer fluid to disinfectant solutions in wash stations to prevent freezing. The purpose of this study was to determine if the addition of these products to the disinfectant solutions would have deleterious effects. Four disinfectants (two phenols, one quaternary ammonium, and one combination product: quaternary ammonium and formaldehyde) and one sodium hypochlorite detergent product currently used in the poultry industry were studied. Each product was diluted according to the manufacturer's recommendation in sterile distilled water and compared with dilutions of the disinfectants with the addition of antifreeze products (ethylene glycol or propylene glycol) or windshield washer fluid for their effectiveness in killing nonpathogenic H7N2 avian influenza virus. All products diluted according to the manufacturer's recommendation killed the nonpathogenic H7N2 avian influenza virus in this test system. The phenol products and the quaternary ammonium product were still efficacious with the
addition of the antifreeze containing ethylene glycol. Both the combination product and the sodium hypochlorite detergent had decreased efficacy when the ethylene glycol product was added. When the propylene glycol product was added, the efficacy of all disinfectants remained unaffected, whereas the efficacy of the sodium hypochlorite detergent decreased. With the addition of the windshield washer fluid (methyl alcohol), all products remained efficacious except for the combination product.

Descriptors: avian influenza virus, disinfectants, efficacy, propylene glycol, ethylene glycol, fluids, methanol, freezing point, windshield washer fluid.


NAL Call Number: QR189.V32

Abstract: A cloned cDNA copy of the haemagglutinin (HA) gene of A/Chicken/Scotland/59 (H5N1) influenza virus has been expressed in vaccinia virus. This pox virus is poorly infectious or non-infectious for chickens. However, immunization of chickens with lysates of cell cultures infected with the recombinant vaccinia virus, that had been emulsified with adjuvant and which contained an estimated 0.5 microgram influenza HA, elicited a substantial neutralizing antibody response to influenza virus. Challenges of immunized and non-immunized adult chickens with virulent A/Chicken/Scotland/59 influenza virus showed that the immunized animals were highly protected while the non-immunized controls died. Immunized birds were also protected against infection with the recent virulent H5 avian influenza virus, A/Chicken/Pennsylvania/83 (H5N2).

Descriptors: antigens immunology, fowl plague prevention and control, influenza A virus avian immunology, vaccines, synthetic immunology, vaccinia virus immunology, viral vaccines immunology, chickens, fluorescent antibody technique, hemagglutinins viral analysis, immunochemistry, immunoenzyme techniques, neutralization tests.


Abstract: During the recent devastating epidemics of foot-and-mouth disease (FMD), bluetongue (BT), the highly pathogenic avian influenza (HPAI) and New Castle disease, more than 115 million animals were culled. The mass slaughter of animals raised serious ethical questions. These epidemics showed that the use of emergency vaccination is an essential element in disease control. During the last decade the FMD antigen banks have proved to be effective and this module should be extended. An international vaccine stock should be considered for classical swine fever and HPAI. Agreements with vaccine producers should be made easily available, with instant access to a vaccine reserve for rinderpest, peste des petits ruminants, BT, African horse sickness and Rift valley fever. These vaccines should meet international standards and should allow distinction between vaccinated and infected animals. Information should be gathered proactively on the use of vaccines for lumpy skin disease, sheep and goat pox and contagious bovine pleuropneumonia.

Descriptors: animals, Australia, communicable disease control methods, disease outbreaks prevention and control, veterinary disease outbreaks, drug storage, emergency treatment methods, veterinary emergency treatment, animal euthanasia, foot-and-mouth disease prevention and control, international cooperation, viral vaccines immunology, viral vaccines supply and distribution.


Abstract: To prepare candidate influenza pandemic vaccines, we are developing an approach based on reassortment of antigenically appropriate nonpathogenic avian viruses of different subtypes (H5, H9, H7) with the cold-adapted master strain (MS) A/Leningrad/134/17/57 (Len/17) that is currently used in Russia for preparing licensed live attenuated vaccines for adults and children. In the present study, reassortants between A/Duck/Potsdam/1402-6/86(H5N2) (H5N2-wt) and Len/17 were obtained. One of the clones, A/17/Duck/Potsdam/86-92(H5N2) (Len17/H5), was chosen for further detailed genetic and antigenic analysis. Len17/H5 inherited the HA gene from the H5N2-wt and all other genes from Len/17 (7:1 genome composition). The HA gene sequence of Len17/H5 was identical to that of the parent H5N2-wt virus. The
antigenic profile of the reassortant virus was similar to that of the H5N2-wt parent strain in the hemagglutination-inhibition (HI) test with a panel of antisera to different avian and human H5 viruses. The reassortant demonstrated high growth ability (9.3+0.3 lg EID50/ml) in embryonated hens' eggs (CE) at optimal (34 [deg]C) temperature, comparable with that of the parent Len/17 MS. Also, Len17/H5 demonstrated cold-adapted (ca) and temperature-sensitive (ts) phenotypes similar to those of Len/17 and was attenuated for mice.

Descriptors: avian influenza, live attenuated reassortant vaccine.


NAL Call Number: 41.8 Av5

Abstract: The minimum requirements for assessing the immunogenicity of an experimental avian influenza (AI) vaccine prepared from inactivated A/Turkey/Italy/2676/99 (H7N1) low-pathogenicity (LP) AI (LPAI) virus were determined in chickens of different ages. A correlation between the amount of hemagglutinin (HA) per dose of vaccine and the protection against clinical signs of disease and infection by A/Chicken/Italy/13474/99 highly pathogenic (HP) AI (HPAI) virus was established. Depending on the vaccination schedule, one or two administrations of 0.5 mug of hemagglutinin protected chickens against clinical signs and death and completely prevented virus shedding from birds challenged at different times after vaccination.

Descriptors: epidemiology, infection, avian influenza, epidemiology, infectious disease, prevention and control, respiratory system disease, transmission, viral disease, vaccination clinical techniques, immunogenicity, viral shedding.


NAL Call Number: 448.3 AC85

Abstract: Seventeen nucleoside derivatives (derived from arabinosylcytosine, resp. cytidine, 5-fluorouracil and uracil) were tested by agar-diffusion plaque-inhibition test for their antiviral activity with herpes simplex, vaccinia, fowl plague, Newcastle disease and western equine encephalomyelitis viruses. The highest antiviral activity against DNA viruses exhibited arabinosylcytosine, N4-acylarabinosylcytosines, arabinosylthiouracil, cyclocytidine and its 5'-chloroderivative. RNA viruses were inhibited by 5-fluorouridine only, whereas other tested compounds were ineffective or showing marginal activity only. By search for relationship between chemical structure and antiviral activity a tendency was found of higher antiviral activity at lower lipophilicity. This is probably due to better transport of the studied compounds into cell. The chemical structure, however, is the main reason of antiviral activity.

Descriptors: antiviral agents chemistry, pyrimidine nucleosides pharmacology, encephalitis virus, western equine drug effects, encephalitis virus, western equine growth and development, influenza A virus avian drug effects, avian growth and development, Newcastle disease virus drug effects, Newcastle disease virus growth and development, plaque assay, pyrimidine nucleosides chemistry, simplexvirus drug effects, simplexvirus growth and development, structure activity relationship, vaccinia virus drug effects, vaccinia virus growth and development.


NAL Call Number: 41.8 Am3A

Descriptors: antibody formation, antigens, viral, bird diseases immunology, influenza veterinary, orthomyxoviridae immunology, birds microbiology, chickens microbiology, cross reactions, ducks microbiology, hemagglutinins viral, immunization, influenza immunology, influenza A virus avian immunology, influenza vaccine, neuraminidase metabolism, orthomyxoviridae enzymology, orthomyxoviridae isolation and purification, poultry diseases immunology, turkeys microbiology.


**Descriptors:** Newcastle disease, avian influenza virus, immunity, immunization, reviews, poultry.


**Descriptors:** fowls, avian influenza virus, vaccines, vaccination, USDA, disease control, Pennsylvania.


**Descriptors:** disease outbreaks veterinary, influenza A virus, avian, influenza, avian epidemiology, poultry diseases prevention and control, vaccination, agriculture methods, chickens, disease outbreaks prevention and control, Hong Kong epidemiology, prevention and control, transmission, poultry diseases epidemiology, poultry diseases virology.


**Descriptors:** avian influenza virus, chemotherapy, antiviral agents.


**Abstract:** La vacuna recombinante de Viruela-Influenza Aviar ha sido evaluada en el laboratorio y en el campo, en pollos comerciales de engorda con anticuerpos maternos para el virus de Influenza Aviar (IA). En este estudio se pretendio evaluar los parametros productivos incluyendo la mortalidad observada durante las 4 primeras semanas despues de la vacunacion en pollos sin y con anticuerpos maternos para el virus de IA. Se vacunaron 36,000 pollos en la incubadora, al dia de edad, los cuales fueron divididos en 2 casetas en una granja localizada en el estado de Queretaro. Estudios serologicos semanales fueron conducidos en 50 pollos vacunados y elegidos arbitrariamente en cada muestreo. Asi como en 25 pollos sin vacunar de cada caseta. Se realizo un desafio a las 3 semanas post-vacunacion Los resultados indicaron al igual que en un estudio anterior, que la vacunacion no tuvo ningun efecto adverso en los indices de produccion de la parvada ni tampoco se observaron lesiones en la mortalidad atribuibles al producto. Los indices de produccion asi como los datos de necropsias de los pollos vacunados con el producto recombinante, fueron comparados con los datos obtenidos del resto de las casetas de la seccion y de la granja. La reciproca de las medias geometricas de anticuerpos para IA, detectados en los muestreos, fueron despresiables al compararse con los titulos observados en pollos vacunados con vacuna inactivada, aplicada a los 10 dias de edad en los pollos de otras casetas. La mortalidad al desafio, realizado a las 3 semanas de edad,
indicaron un 100% de protección obtenido en los pollos originalmente libres de anticuerpos, con un 80% de protección en los pollos que provenían de reproductoras vacunadas para IA. Los resultados de este estudio señalan que la vacuna recombinante de Viruela-IA es confiable, no afecta los índices productivos y es eficaz para evitar la mortalidad causada por virus de IA de alta patogenicidad y que puede ser usada como un producto adicional en la campaña de erradicación, ya que esta no contiene el genoma completo de virus de IA, por lo que es incapaz de causar la enfermedad en aves vacunadas.

Descripciones: pollo broiler, virus de la influenza aviar, vacunas sintéticas, respuesta inmune, aves, pollos, animales domésticos, Galliformes, inmunidad, influenza del virus, ganado, animales de carne, Orthomyxoviridae, pollo, animales útiles, vacunas, virus.


NAL Call Number: SF995.W4
Descripciones: virus de la influenza aviar inactivado, vacunación, control, brotes.


NAL Call Number: 41.8 Av5
Descripciones: turcos, virus de la influenza aviar, antígenos, vacunas, congelamiento, almacenamiento, temperatura, tiempo, álcoholes, polietileno, vacunación, aves, control de enfermedad, Galliformes, inmunización, factores inmunológicos, inmunología, inmunestimulación, inmunoterapia, influenza del virus, polímeros, procesamiento, terapia, virus, antígenos virales, potencia, polietileno de glicol.


NAL Call Number: QR189.V32
Descripciones: aves de corral, virus de la influenza aviar, antígenos, vacunas, congelamiento, almacenamiento, temperatura, tiempo, alcoholes, polietileno, vacunación, aves, control de enfermedad, Galliformes, inmunización, factores inmunológicos, inmunología, inmunestimulación, inmunoterapia, influenza del virus, polímeros, procesamiento, terapia, virus, antígenos virales, potencia, polietileno de glicol.


**Abstract:** The fermentation and isolation procedures of the antibiotic granatominic produced by *Streptomyces lateritius* are described. Furthermore, the producing strain ZIMET 43 627 and the main constituents of granatominic will be characterized. Granatominic is a red-violet pigment antibiotic of the naphthoquinone type. The physicochemical properties of granatominic resemble those of granaticin. The antibiotic can be isolated from culture filtrates and from the mycelium by extraction with lower aliphatic alcohols. It can be purified by gel filtration methods. Granatominic displays antimicrobial activity, particularly against grampositive and gramnegative bacteria, and antiviral activity against fowl-plaque-virus in mammalian cells. Granatominic is useful in selection of resistant mutants of bacteria and viruses with decreased virulence but high immunogenity suitable for use as life vaccines against infection diseases. The physicochemical properties of the main constituents of granatominic studied confirm the identity of granatominic C with granaticin and the identity of granatominic D with dihydrogranaticin Granatominic A is identical with the well-known semisynthetic methylester of dihydrogranaticin. Therefore, the production of granatominic A is the first possibility to produce this derivative of granaticin biosynthetically.

**Descriptors:** anti bacterial agents isolation and purification, naphthoquinones isolation and purification, *Streptomyces* metabolism, anti bacterial agents analysis, anti bacterial agents pharmacology, bacteria drug effects, chemistry, influenza A virus avian drug effects.


**NAL Call Number:** SF481.M54

**Descriptors:** avian influenza virus, outbreaks, vaccines, disease control, poultry.


**NAL Call Number:** SF995.W4

**Descriptors:** avian influenza, vaccination program, turkeys, results.


**NAL Call Number:** QH443.D5

**Abstract:** Recently, we demonstrated that direct inoculation of a hemagglutinin 7 (H7)-expressing DNA could vaccinate chickens against a lethal H7 influenza virus challenge. These experiments used a defective-retroviral-based vector to express H7 (p188) (Robinson et al., 1993). Here, we report protective immunizations using a non-retroviral-based vector for H7 expression (pCMV/H7). Unlike the previously used retroviral-based vector, this vector cannot be transmitted as an infectious agent (as a consequence of phenotypic mixing with exogenous or endogenous virus proteins). Vaccination was accomplished by inoculating young, immunocompetent chickens by each of three routes (intravenous, intraperitoneal, and intramuscular) with 100 micrograms of cesium chloride-purified pCMV/H7 DNA in saline. After two immunizations, birds were challenged via the nares with a lethal dose of a highly virulent chicken influenza virus of the H7 subtype. The results of five independent vaccine trials demonstrated protective immunizations in approximately 60% of the pCMV/H7 DNA-inoculated chickens. By contrast, only 3% of the chickens inoculated with control DNA survived the lethal challenge.

**Descriptors:** hemagglutinins viral immunology, influenza A virus avian immunology, influenza vaccine genetics, poultry diseases prevention and control, vaccines, synthetic immunology, antibodies, viral biosynthesis, chickens, DNA, viral genetics, gene expression, genes, structural, viral, genetic vectors,
hemagglutinins viral genetics, neutralization tests.


**NAL Call Number:** 500 N21P

**Abstract:** Plasmid DNAs expressing influenza virus hemagglutinin glycoproteins have been tested for their ability to raise protective immunity against lethal influenza challenges of the same subtype. In trials using two inoculations of from 50 to 300 micrograms of purified DNA in saline, 67-95% of test mice and 25-63% of test chickens have been protected against a lethal influenza challenge. Parenteral routes of inoculation that achieved good protection included intramuscular and intravenous injections. Successful mucosal routes of vaccination included DNA drops administered to the nares or trachea. By far the most efficient DNA immunizations were achieved by using a gene gun to deliver DNA-coated gold beads to the epidermis. In mice, 95% protection was achieved by two immunizations with beads loaded with as little as 0.4 micrograms of DNA. The breadth of routes supporting successful DNA immunizations, coupled with the very small amounts of DNA required for gene-gun immunizations, highlight the potential of this remarkably simple technique for the development of subunit vaccines.

**Descriptors:** DNA, viral administration and dosage, fowl plague prevention and control, hemagglutinins viral genetics, influenza prevention and control, influenza A virus avian immunology, human immunology, cell line, chickens, DNA, viral immunology, fowl plague immunology, genes viral, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral biosynthesis, influenza immunology, avian genetics, human genetics, injections, injections, intramuscular, injections, intravenous, mice, mice inbred BALB c, mucous membrane, restriction mapping, transfection, viral envelope proteins biosynthesis, viral envelope proteins genetics.


**NAL Call Number:** 41.8 Av5

**Abstract:** The control and eventual eradication of H5N2 influenza virus from domestic poultry in Mexico is dependent on the use of avian influenza (AI) vaccine strategies. This study was performed to determine the amount of hemagglutinin (HA) antigen required to control the signs of disease from a highly pathogenic H5N2 influenza virus (A/Chicken/Queretaro/19/95) and the amount of antigen required to prevent shedding of virus from vaccinated birds. Six commercial inactivated water in oil H5N2 vaccines available in Mexico were compared with standardized vaccines to assess their efficacy. The amount of HA required to prevent the signs of disease from A/Chicken/Queretaro/19/95 influenza virus was approximately 0.4 microgram per dose. Each of the six commercially available vaccines prevented disease signs, and half of the vaccines significantly reduced viral shedding from vaccinated birds. There is a need for standardization of AI virus vaccine, and the antigen content should be increased in some of the commercially available AI vaccines in Mexico.

**Descriptors:** Mexico, chickens, avian influenza virus, vaccines, vaccination, disease control, symptoms, pathogenicity, agglutinins, antigens, disease transmission, dosage, mortality, America, biological properties, birds, domestic animals, Galliformes, immunization, immunological factors, immunostimulation, immunotherapy, influenza virus, livestock, microbial properties, North America, orthomyxoviridae, pathogenesis, poultry, proteins, therapy, useful animals, viruses, inactivated vaccines, virulence, hemagglutinins, shedding.


**Abstract:** El virus de viruela aviar es miembro de la familia Poxviridae, y afecta solo a ciertas especies de aves. El objeto del presente estudio fue determinar que el virus de viruela aviar utilizado, en la vacuna recombinante, como vector para acarrear el DNA complementario del gene de la hemoaglutinina 5 del virus...
de Influenza Aviar (I.A) no causara reacciones adversas al aplicarse una dosis mayor que la recomendada en pollos y que este virus no se trasmite en forma horizontal de pollos vacunados a pollos susceptibles. Para lo cual grupos de 20 pollos fueron vacunados mediante punción en el ala y por vía subcutanea con 10 dosis de la vacuna recombinante. 2 días después de la vacunación se introdujeron a la jaula 20 pollos de la misma edad, sin vacunar. Ambos grupos fueron observados diariamente durante 21 días. Se realizaron estudios serológicos y al final del periodo de observación se desafiaron tanto a los pollos vacunados como a los contactos, con una cepa de virus de I.A. de alta patogenicidad. Ninguno de los pollos vacunados con 10 dosis del producto, por cualquiera de las vías utilizadas, mostraron signos de enfermedad o lesiones patológicas durante el periodo de observación. Serológicamente los pollos en contacto fueron negativos a la prueba de inhibición de la hemoaglutinación (IH) para IA y ambos grupos negativos en las pruebas de inmunodifusión. La seropositividad por IH fue de 1 a 3 pollos con títulos de 1:10 a 1:40 en los grupos de pollos vacunados con la recombinante. Posterior al desafío todos los pollos vacunados mostraron títulos serológicos con medias geometricas mayores a 1:40. Los pollos en contacto fueron susceptibles al desafío y en todos los casos no se demostró la presencia de anticuerpos para el virus de I.A. Se concluye que la vacuna es segura, ya que no causo reacciones adversas inclusive al aplicar 10 veces la dosis recomendada, que la inserción no modifica el tropismo del virus de viruela a otros órganos y que no se transmite en forma horizontal por contacto directo.

Descriptors: broiler chickens, avian influenza virus, synthetic vaccines, immune response, birds, chickens, domestic animals, Galliformes, immunity, influenza virus, livestock, meat animals, orthomyxoviridae, poultry, useful animals, vaccines, viruses.


NAL Call Number: 396.8 An84
Abstract: The effect of 9 analogues of distamycin A was studied in a tissue culture with respect to the virus of a smallpox vaccine and classical avian plague. Three analogues of distamycin A (I, VI, VII) were studied in chick embryos with respect to the smallpox and influenza viruses. The analogues were characterized by a loss or decrease of the activity against the smallpox vaccine virus as compared to distamycin A. In contrast to distamycin A analogue VII had an inhibitory effect on influenza infection in chick embryos.
Descriptors: antiviral agents, distamycins pharmacology, influenza A virus avian drug effects, orthomyxoviridae drug effects, pyrroles pharmacology, variola virus drug effects.

Descriptors: communicable disease control organization and administration, influenza epidemiology, influenza A virus, avian isolation and purification, avian influenza epidemiology, birds, influenza prevention and control, avian influenza prevention and control, primary prevention organization and administration, risk assessment, vaccination methods, world health.


NAL Call Number: 41.8 R312
Abstract: Vaccination of fowls with inactivated Newcastle disease (ND) virus and avian influenza (AI) virus oil emulsion vaccines containing an interferon inducer (BRL 5907) produced an enhanced immunological response. The Newcastle disease vaccine containing BRL 5907 induced earlier protection to challenge than Newcastle disease vaccine by itself and also produced an increase immune response when administered to day-old maternally immune and susceptible chicks.
Descriptors: adjuvants, immunologic, chickens immunology, influenza vaccine, interferon inducers, Newcastle disease virus immunology, RNA viral pharmacology, viral vaccines, antibody formation, influenza immunology, influenza veterinary, Newcastle disease immunology, orthomyxoviridae immunology, poultry diseases immunology.

Descriptors: infection, pharmacology, respiratory system, influenza, respiratory system disease, treatment, viral disease, ELISA analytical method, detection, labeling techniques, viral disease transmission, viral replication, inhibition, meeting abstract, meeting slide.


NAL Call Number: RM265.A5132

Abstract: The orally administered neuraminidase (NA) inhibitor RWJ-270201 was tested in parallel with zanamivir and oseltamivir against a panel of avian influenza viruses for inhibition of NA activity and replication in tissue culture. The agents were then tested for protection of mice against lethal H5N1 and H9N2 virus infection. In vitro, RWJ-270201 was highly effective against all nine NA subtypes. NA inhibition by RWJ-270201 (50% inhibitory concentration, 0.9 to 4.3 nM) was superior to that by zanamivir and oseltamivir carboxylate. RWJ-270201 inhibited the replication of avian influenza viruses of both Eurasian and American lineages in MDCK cells (50% effective concentration, 0.5 to 11.8 microM). Mice given 10 mg of RWJ-270201 per kg of body weight per day were completely protected against lethal challenge with influenza A/Hong Kong/156/97 (H5N1) and A/quail/Hong Kong/G1/97 (H9N2) viruses. Both RWJ-270201 and oseltamivir significantly reduced virus titers in mouse lungs at daily dosages of 1.0 and 10 mg/kg and prevented the spread of virus to the brain. When treatment began 48 h after exposure to H5N1 virus, 10 mg of RWJ-270201/kg/day protected 50% of mice from death. These results suggest that RWJ-270201 is at least as effective as either zanamivir or oseltamivir against avian influenza viruses and may be of potential clinical use for treatment of emerging influenza viruses that may be transmitted from birds to humans.

Descriptors: antiviral agents pharmacology, influenza prevention and control, influenza A virus avian drug effects, virus replication drug effects, acetamides pharmacology, acetamides therapeutic use, antiviral agents therapeutic use, body weight drug effects, brain drug effects, brain virology, cyclopentanes pharmacology, cyclopentanes therapeutic use, disease models, animal, dogs, influenza A virus avian enzymology, influenza A virus avian physiology, lung drug effects, lung virology, mice, mice inbred BALB c, neuraminidase antagonists and inhibitors, sialic acids pharmacology, sialic acids therapeutic use, treatment outcome.


NAL Call Number: 448.3 AC85

Abstract: Cross-protection of mice immunized with inactivated preparations of human and avian influenza A (H2) viruses was determined after lethal infection with mouse-adapted (MA) variants of human A/Jap x Bell/57 (H2N1) and avian A/NJers/78 (H2N3) viruses. The MA variants differed from the original strains by acquired virulence for mice and changes in the HA antigenicity. These studies indicated that mice vaccinated with human influenza A (H2) viruses were satisfactorily protected against challenge with A/Jap x Bell/57-MA variant; the survival rate was in the range of 61%-88.9%. Immunization of mice with the same viral preparations provided lower levels of protection against challenge with A/NJers/78-MA variant. Vaccination of mice with the avian influenza A (H2) viruses induced better protection than with human strains against challenge with both MA variants. Challenge with A/NJers/78-MA variant revealed that 76.2%-95.2% of animals were protected when vaccinated with avian influenza virus strains isolated before 1980, and that the protection reached only 52.4%-60.0% in animals vaccinated with strains isolated in 1980-1985. The present study revealed that cross-protection experiments in a mouse model could provide necessary information for the development of appropriate influenza A (H2) virus vaccines with a potential for these viruses to reappear in a human population.

Descriptors: influenza prevention and control, influenza A virus avian immunology, influenza A virus human immunology, influenza vaccine immunology, cross reactions, disease models, animal, influenza mortality, influenza A virus avian classification, influenza A virus avian pathogenicity, influenza A virus human
classification, influenza A virus human pathogenicity, mice, vaccination, vaccines, attenuated immunology.

Descriptors: avian influenza virus, Newcastle disease, Salmonellosis, antibiotics, disease control, drug resistance, EU regulations, poultry, public health, reviews.

NAL Call Number: 41.8 T445
Descriptors: avian influenza virus, fowl plague virus, disease control, European Union, poultry, zoonoses.

NAL Call Number: S451.M6M582
Descriptors: poultry, Minnesota, avian influenza virus, disease transmission, hosts, disease control, monitoring, vaccination, America, disease control, domestic animals, domesticated birds, immunization, immunostimulation, immunotherapy, influenza virus, lake states United States, livestock, North America, north central states United States, orthomyxoviridae, pathogenesis, therapy, United States, useful animals, viruses, reservoir hosts, disease prevention.

NAL Call Number: SF995.W4
Descriptors: avian influenza virus, turkeys, chickens, disease control.

NAL Call Number: 47.8 N219
Descriptors: avian influenza virus, immunization, disease control, prevention, turkeys, United States, Minnesota.

NAL Call Number: SF995.A1A9
Abstract: Biosecurity is the first line of defence in the prevention and control of mildly pathogenic avian influenza (MPAI). Its use has been highly successful in keeping avian influenza (AI) out of commercial poultry worldwide. However, sometimes AI becomes introduced into poultry populations and, when that occurs, biosecurity again is the primary means of controlling the disease. There is agreement that routine serological monitoring, disease reporting, isolation or quarantine of affected flocks, application of strict measures to prevent the contamination of and movement of people and equipment, and changing flock schedules are necessities for controlling AI. There is disagreement as to the disposition of MPAI-infected flocks: some advocate their destruction and others advocate controlled marketing. Sometimes biosecurity is not enough to stop the spread of MPAI. In general, influenza virus requires a dense population of susceptible hosts to maintain itself. When there is a large population of susceptible poultry in an area, use of an inactivated AI vaccine can contribute to AI control by reducing the susceptibility of the population.Does use of inactivated vaccine assist, complicate or interfere with AI control and eradication? Yes, it assists MPAI control (which may reduce the risk of highly pathogenic AI (HPAI)) but, unless steps are taken to prevent it, vaccination may interfere with sero-epidemiology in the case of an HPAI outbreak.Does lack of vaccine assist, complicate or interfere with AI control and eradication? Yes, it assists in identification of sero-positive (convalescent) flocks in a HPAI eradication program, but it interferes with MPAI control (which in turn may increase the risk of emergence of HPAI).A number of hypothetical concerns have been raised about the use of inactivated AI vaccines. Infection of vaccinated flocks, serology complications and spreading of virus by vaccine crews are some of the hypothetical concerns. The discussion of these concerns should take
place in a scientific framework and should recognize that control of MPAI reduces the risk of HPAI. That
inactivated vaccines have reduced a flock's susceptibility to AI infection, have reduced the quantity of virus
shed post-challenge, have reduced transmission and have markedly reduced disease losses, are scientific
facts. The current regulations preventing vaccination against H5 or H7 MPAI have had the effect of
promoting circulation of MPAI virus in commercial poultry and live poultry markets. In the absence of highly
pathogenic avian influenza, there is no justification for forbidding the use of inactivated vaccine.

Descriptors: influenza prevention and control, influenza veterinary, influenza A virus avian immunology,
poultry virology, poultry diseases immunology, poultry diseases virology, vaccines, inactivated immunology,
influenza immunology, influenza transmission, poultry immunology, poultry diseases epidemiology, poultry
diseases transmission.

Poultry Diseases Conference 44: 15-19.
NAL Call Number: SF995.W4
Descriptors: avian influenza virus, Minnesota, America, influenza virus, lake states United States, North
America, north central states United States, orthomyxoviridae, United States, viruses.

NAL Call Number: SF481.M54
Descriptors: avian influenza virus, disease control, prevention, transmission, biosecurity.

expression and sequence of an avian influenza nucleoprotein gene: potential use in diagnosis.
Archives of Virology 113(1-2): 133-41. ISSN: 0304-8608.
NAL Call Number: 448.3 Ar23
Abstract: The nucleoprotein (NP) gene from avian influenza strain A/Shearwater/Aust/1/72 (H6N5) was
cloned, sequenced, and expressed in vaccinia virus for the production of potent sera in immunised rabbits.
The NP gene is 1565 bp and shares greater than 95% amino acid sequence identity with other NPs of the
avian subtype. The recombinant NP expressed by vaccinia virus comigrated with endogenous
A/Shearwater/Aust/1/72 NP by Western blot analysis. Polyclonal rabbit sera raised against recombinant NP
was evaluated in an antigen capture ELISA system as a potential diagnostic tool for the detection of avian
influenza. All type A strains, comprising several HA and NA subtypes, but not type B nor other avian viruses,
were detected.
Descriptors: fowl plague diagnosis, genes viral, influenza A virus avian genetics, nucleoproteins genetics,
vaccinia virus genetics, viral core proteins, viral proteins genetics, amino acid sequence, antibodies, viral
immunology, base sequence, blotting, southern, cloning, molecular, DNA, viral, enzyme linked
immunosorbent assay, avian immunology, molecular sequence data, nucleoproteins immunology, predictive
value of tests, thymidine kinase genetics, vaccinia virus immunology, viral proteins immunology.

hydrogen peroxide against exotic animal viruses. Applied and Environmental Microbiology 63(10): 3916-
3918. ISSN: 0099-2240.
NAL Call Number: 448.3 Ap5
Abstract: The efficacy of vapor-phase hydrogen peroxide in a pass-through box for the decontamination of
equipment and inanimate materials potentially contaminated with exotic animal viruses was evaluated. Tests
were conducted with a variety of viral agents, which included representatives of several virus families
(Orthomyxoviridae, Reoviridae, Flaviviridae, Paramyxoviridae, Herpesviridae, Picornaviridae, Caliciviridae,
and Rhabdoviridae) from both avian and mammalian species, with particular emphasis on animal viruses
exotic to Canada. The effects of the gas on a variety of laboratory equipment were also studied. Virus
suspensions in cell culture media, egg fluid, or blood were dried onto glass and stainless steel. Virus viability
was assessed after exposure to vaporphase hydrogen peroxide for 30 min. For all viruses tested and under
all conditions (except one), the decontamination process reduced the virus titer to 0 embryo-lethal doses for
the avian viruses (avian influenza and Newcastle disease viruses) or less than 10 tissue culture infective
doses for the mammalian viruses (African swine fever, bluetongue, hog cholera, pseudorabies, swine
vesicular disease, vesicular exanthema, and vesicular stomatitis viruses). The laboratory equipment exposed to the gas appeared to suffer no adverse effects. Vaporphase hydrogen peroxide decontamination can be recommended as a safe and efficacious way of removing potentially virus-contaminated objects from biocontainment level III laboratories in which exotic animal disease virus agents are handled.

**Descriptors:** biochemistry and molecular biophysics, methods and techniques, microbiology, pharmacology, veterinary medicine, biocontainment level III laboratories, disinfectant, disinfection efficacy, equipment decontamination, hydrogen peroxide, methodology, microbiology, pass through box, vaporized virus, titer reduction, virus viability.


**NAL Call Number:** 41.8 Av5

**Abstract:** An outbreak of H7N2 low-pathogenicity (LP) avian influenza (AI) occurred in a two-county area in Pennsylvania from December of 1996 through April of 1998. The outbreak resulted in infection of 2,623,116 commercial birds on 25 premises encompassing 47 flocks. Twenty-one (one premise with infection twice) of the twenty-five infected premises housed egg-laying chickens and one premise each had turkeys, layer pullets, quail, and a mixed backyard dealer flock. Despite close proximity of infected flocks to commercial broiler flocks, no infected broilers were identified. Experimentally, when market age broilers were placed on an influenza-infected premise they seroconverted and developed oviduct lesions. The outbreak was believed to have originated from two separate introductions into commercial layer flocks from premises and by individuals dealing in sales of live fowl in the metropolitan New York and New Jersey live-bird markets. Source flocks for these markets are primarily in the northeast and mid-Atlantic areas, including Pennsylvania. Mixed fowl sold include ducks, geese, guinea hens, quail, chukar partridges, and a variety of chickens grown on perhaps hundreds of small farms. Infections with the H7N2 AI virus were associated with variable morbidity and temporary decreases in egg production ranging from 1.6% to 29.1% in commercial egg-laying chickens. Egg production losses averaged 4.0 weeks duration. Mortality ranged from 1.5 to 18.3 times normal (mean of 4.3 times normal). Duration of mortality ranged from 2 to 13 weeks (average of 3.9 weeks) in flocks not depopulated. Lesions observed were primarily oviducts filled with a mucous and white gelatinous exudates and atypical egg yolk peritonitis. Quarantine of premises and complete depopulation were the early measures employed in control of this outbreak. Epidemiological studies suggested that depopulation furthered the spread of influenza to nearby flocks. Thereafter, later control measures included quarantine, strict biosecurity, and controlled marketing of products.

**Descriptors:** animal husbandry, epidemiology, infection, biosecurity, disease control measures, disease outbreak, live fowl markets, production losses, quarantine.

Hernandez Magdaleno, A., H.M. Ceron, V.H. Rodriguez, and G.J. Garcia (1996). **Proteccion por cuatro vacunas de influenza aviar (H5N2) en codornices (Coturnix coturnix japonica).** [*Protection of quail (Coturnix coturnix japonica) with 4 avian influenza (H5N2) vaccines*]. *Proceedings of the Western Poultry Diseases Conference* 45: 296-298.

**NAL Call Number:** SF995.W4

**Descriptors:** quails, vaccines, birds, Galliformes.


**Abstract:** El objetivo de la presente investigacion fue estudiar la patogenia del virus de influenza aviar (H5N2) altamente patogeno (AP) en aves susceptibles (Av-Susc) y en aves inmunizadas (Av-Inm), durante las primeras 72 horas post-inoculacion (hpi). Se formaron dos grupos de 100 aves libres de patogenos especificos. A los 8 dias de edad, uno de los grupos fue inmunizado con una vacuna emulsionada contra influenza aviar (IA) y el otro grupo permanecio sin inmunizar. A las cuatro semanas de edad, ambos grupos
fueron inoculados por vía intranasal con 1 x 103 DLEP50 del virus A/Chicken/Queretaro/14588-19/95 (H5N2) altamente patogeno. Se tomaron aleatoriamente 3 aves de cada grupo a las 2, 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68 y 72 hpi. De cada ave se tomo una muestra de sangre para el aislamiento y titulación viral; posteriormente, fueron sacrificadas humanitariamente y se tomaron muestras para histopatología e inmunohistoquímica de los siguientes órganos: cresta, timo, cometas nasales, laringe, traquea, pulmón, proventriculo, duodeno, pancreas, tonsilas ceceales, ileón y bolsa de Fabricio. Se realizaron seis diferentes procedimientos de la técnica de inmunohistoquímica. Al examen microscópico, las lesiones fueron calificadas con un método numérico para calcular la media histológica de lesiones (MHL). Las Av-Susc mostraron signos clínicos, mortalidad y fue detectado virus circulante en la sangre, a partir de las 28 hpi. En las Av-Inm, a pesar de que hubo lesiones a nivel microscópico, estas fueron generalmente menos severas e incluso en la cresta no se observaron lesiones, a diferencia de las Av-Susc, en que la cresta fue el tejido más afectado tal como se reflejo en la MHL. Las diferencias en la manifestación de la enfermedad entre ambos grupos fueron marcadas y a pesar de que no se pudo demostrar mediante inmunohistoquímica la presencia del virus en los tejidos, en las Av-Susc hubo viremia, situación que no sucedió en las Av-Inm. En las Av-Sus el dano al endotelio capilar producido por el virus pudo ser uno de los mecanismos responsables de la muerte de los animales, al desencadenar un colapso vascular generalizado. Así mismo, el virus AP produjo apoptosis linfoides severa. La inmunidad conferida por la vacuna emulsionada contra la IA, protegió a las aves de la presentación de signos clínicos y mortalidad, debido a que evitó la viremia, con lo que el virus no pudo causar dano en los centros vitales de las aves.

**Descriptors:** broiler chickens, avian influenza virus, pathogenicity, immunity, biological properties, birds, chickens, domestic animals, Galliformes, influenza virus, livestock, meat animals, microbial properties, orthomyxoviridae, poultry, useful animals, viruses.


**NAL Call Number:** 41.8 Av5

**Abstract:** To examine the specificity of the antibody response to the influenza hemagglutinin and the generation of antigenic variants, chickens were immunized against the highly virulent H5 virus A/Ty/Ont/7732/66 (H5N9) and then challenged with a lethal dose of the virus. The antibody responses of these chickens to the hemagglutinin (HA) were examined with an enzyme-linked immunosorbent assay (ELISA) in which their sera were titrated for the ability to block the binding of monoclonal antibodies (MAbs) to five distinct neutralizing epitopes on the viral HA. Based on the ELISA results, a majority (5/6) of the chickens produced antibodies to three of the five neutralizing epitopes on the viral HA. After challenge, two of six immunized chickens shed virus and died; antigenic comparisons of isolates from these two chickens indicated the presence of an antigenic variant; i.e., there was a change in one neutralizing epitope on the HA of virus shed by one chicken. None of the chickens had produced antibodies to this particular epitope on the viral HA. Inoculation of chickens with this variant resulted in 100% mortality, demonstrating that a change in this particular epitope did not alter the virulence of the virus. These studies indicate that chickens immunized against highly virulent influenza viruses may excrete virulent variants following challenge with live virus.

**Descriptors:** antibodies, viral biosynthesis, antigens, viral immunology, chickens, fowl plague immunology, influenza A virus avian immunology, antibodies, monoclonal immunology, antigenic variation, enzyme linked immunosorbent assay, epitopes immunology, fowl plague prevention and control, hemagglutination inhibition tests, hemagglutinins viral immunology, avian pathogenicity, nucleoproteins immunology, virulence.


**NAL Call Number:** QR189.V32

**Descriptors:** genetic vectors genetics, influenza A virus avian genetics, human genetics, influenza vaccine biosynthesis, reassortant viruses genetics, antigenic variation genetics, birds virology, cell line, chick embryo, China, Czechoslovakia, DNA, recombinant genetics, dogs, genes viral, avian immunology, avian isolation and purification, human immunology, human isolation and purification, influenza vaccine genetics, influenza vaccine immunology, influenza vaccine isolation and purification, New Caledonia, Panama, phenotype, reassortant viruses immunology, reassortant viruses isolation and purification, reproducibility of
results, reverse transcriptase polymerase chain reaction, transfection, virus cultivation.


NAL Call Number: 47.8 Ar2

Descriptors: disease control, consequences, outbreaks, poultry, vaccination, avian influenza virus, Netherlands, Germany, Belgium.


NAL Call Number: QH301.F3

Descriptors: biochemistry and molecular biophysics, immune system, infection, pharmacology, influenza, respiratory system disease, viral disease, functional hemagglutination assay characterization method, immunoprecipitation technique characterization method, radiolabeling technique characterization method, agrobacterium mediated technique transformation method, western blot characterization method, immune responses, microsomal retention signal, plant expressing, cassettes, vaccine delivery, vaccine development, viral challenge, viral envelope, meeting, abstract.


Descriptors: disease control, diagnosis, avian influenza virus, China.


Descriptors: communicable disease control organization and administration, communicable diseases, emerging prevention and control, disease outbreaks prevention and control, influenza epidemiology, influenza A virus, avian, avian influenza prevention and control, antiviral agents therapeutic use, Australia epidemiology, birds, emerging epidemiology, immunization programs organization and administration, influenza diagnosis, influenza drug therapy.


Abstract: Emergence of highly virulent influenza A/H5N1 viruses in Hong Kong in 1997 posed a threat of pandemic and brought an urgent need to develop a suitable seed virus for vaccine production. The virulence of the H5N1 viruses to chicken embryos should hamper the efficient production of the vaccine. In addition, potential virulence to humans raised safety issue in manufacturing vaccine. Toward vaccine development, one approach is to use an avirulent avian influenza virus antigenically similar to the virulent ones as a surrogate vaccine strain. The other approach is based on the attenuation of pathogenicity of virulent H5N1 virus by genetic engineering of the hemagglutinin gene and selection of a gene constellation. The reverse genetics technique can make the latter approach possible. Candidate strains suitable for vaccine production could be prepared by using either approach.

Descriptors: influenza transmission, influenza A virus human genetics, human immunology, influenza vaccine, chick embryo, genes viral, genetic engineering, hemagglutinins chemistry, hemagglutinins genetics, vaccines, attenuated, virulence.


NAL Call Number: 41.9 R24

Descriptors: influenza A virus avian, orthomyxoviridae infections veterinary, poultry diseases prevention.
and control, viral vaccines, chickens, orthomyxoviridae infections prevention and control, vaccines.


**NAL Call Number:** S19.Y36

**Descriptors:** antibodies, immune response, immunization, avian influenza virus, fowl pox virus, chickens.


**NAL Call Number:** SF604.C58

**Descriptors:** antibodies, genetic stability, hemagglutinins, immunity, avian influenza virus, fowl pox virus, chickens.


**NAL Call Number:** S19.Y36

**Descriptors:** immunization, potency, recombinant vaccines, hemagglutinins, avian influenza virus, fowl pox virus, chickens.


**NAL Call Number:** SF604.C58

**Descriptors:** chicks, immune response, immunization, dosage, maternal antibodies, mortality, recombinant vaccines, avian influenza, fowl pox virus.


**Descriptors:** birds virology, disease outbreaks prevention and control, influenza A virus, avian genetics, avian influenza transmission, India, avian influenza pathogenicity, avian influenza diagnosis.


**NAL Call Number:** SF995.W4

**Descriptors:** vaccines, avian influenza virus, influenza virus, orthomyxoviridae, viruses.


**NAL Call Number:** SF995.W4

**Descriptors:** avian influenza virus, vaccines, Mexico, America, influenza virus, Latin America, North America, orthomyxoviridae, viruses.

Kalidari, G.A., N. Harzandi, and S.A.D. Moghadam (2002). **Evaluation of the half life of maternal antibodies against Avian Influenza (AI) in broiler and layer chicks in Mashhad.** *Journal of the Faculty of Veterinary Medicine, University of Tehran* 57(1): 47-50. ISSN: 1022-646X.

Abstract: The potency and efficacy of an inactivated oil-emulsion influenza vaccine against infection, illness, and virus shed was studied in market turkeys. No undesirable local or systemic reactions occurred following vaccination. The vaccine induced measurable antibody to nucleocapsid and hemagglutinin antigens of the virus. Challenged unvaccinated controls experienced airsacculitis, but none of the vaccinates were affected. The percent of the birds shedding virus following intranasal challenge was lower in the vaccinated groups than in the controls, and the quantity of virus shed was also smaller in vaccinated groups than in the controls.

Descriptors: antibodies, viral biosynthesis, fowl plague immunology, influenza A virus avian immunology, turkeys, viral vaccines immunology, antigens, viral immunology, capsid immunology, fowl plague prevention and control, hemagglutination inhibition tests veterinary, hemagglutinins viral immunology, immunodiffusion veterinary, vaccination veterinary, viral core proteins immunology.


Abstract: Influenza viruses cause annual epidemics and occasional pandemics of acute respiratory disease. Improved vaccines that can overcome the decline in immune function with aging and/or can induce broader immunity to novel pandemic strains are a high priority. To design improved vaccines for the elderly, we need to better understand the effects of age on both innate and adaptive immunity. In a murine model, we have determined that defects in antigen-presenting cell (APC) expression of pattern-recognition molecules, co-stimulatory molecules, and cytokine production may play an important role in the reduced clonal expansion of T cells in aging. The use of immunomodulators such as adjuvants may overcome some of the defects of aging immunity and may also be useful in the development of improved vaccines for avian influenza A subtypes that pose a pandemic threat. Several novel strategies including the use of ISCOM-formulated vaccines, mucosal delivery, or DNA vaccination provided cross-subtype protection that could provide an important component of immunity in the event of a pandemic.

Descriptors: aging immunology, disease outbreaks prevention and control, influenza prevention and control, influenza vaccines immunology, adjuvants, immunologic pharmacology, aged, immunity, active immunology, immunity, natural, influenza epidemiology, influenza immunology, influenza A virus, avian immunology, avian pathogenicity, membrane glycoproteins genetics, membrane glycoproteins metabolism, mice, orthomyxoviridae immunology, orthomyxoviridae pathogenicity, receptors, cell surface genetics, receptors, cell surface metabolism.

**NAL Call Number:** 41.8 Av5

**Abstract:** Viruses conveyed in shipments of eggs, viral diagnostic reagents, or avian serum samples are a potential hazard for susceptible poultry. Different methods of treatment of those materials to eliminate the hazard of virulent and avirulent strains of Newcastle disease virus (NDV) or avian influenza virus (AIV) were evaluated. The NDV strains tested were more thermostable than the AIV strains. The results suggest that standard pasteurization methods would not reliably inactivate the concentrations of NDV used. Beta-propiolactone (BPL) (greater than or equal to 0.025%) inactivated NDV or AIV in allantoic fluid, but higher concentrations were needed to inactivate virus diluted in serum. Hemagglutination (HA) of NDV and AIV and hemolysis (HL) activity of NDV were reduced or eliminated by 0.4% BPL. Formalin (greater than or equal to 0.04%) inactivated either virus but adversely affected HA and HL activity. NDV or AIV was inactivated by binary ethylenimine (BEI) (0.01 M) with no adverse effect on HA or HL. Heat (56 C) or BEI (0.01 M) had no apparent effect on hemagglutination-inhibition (HI) titers of NDV and AIV antisera, the effect of formalin (0.1%) was variable, and BPL (greater than or equal to 0.25%) depressed the HI titers of both antisera. The optimum method should achieve virus inactivation without harming the treated material.

**Descriptors:** egg yolk, egg albumen, allantoic fluid, blood serum, Newcastle disease virus, inactivation, avian influenza virus, virulence.


**NAL Call Number:** SF602.M8

**Descriptors:** Newcastle disease, avian influenza, classical swine fever, foot and mouth disease, vaccination, clinical techniques, slaughtered, transmission, outbreaks.


**NAL Call Number:** QR360.J6

**Abstract:** In Hong Kong in 1997, a highly lethal H5N1 avian influenza virus was apparently transmitted directly from chickens to humans with no intermediate mammalian host and caused 18 confirmed infections and six deaths. Strategies must be developed to deal with this virus if it should reappear, and prospective vaccines must be developed to anticipate a future pandemic. We have determined that unadapted H5N1 viruses are pathogenic in mice, which provides a well-defined mammalian system for immunological studies of lethal avian influenza virus infection. We report that a DNA vaccine encoding hemagglutinin from the index human influenza isolate A/HK/156/97 provides immunity against H5N1 infection of mice. This immunity was induced against both the homologous A/HK/156/97 (H5N1) virus, which has no glycosylation site at residue 154, and chicken isolate A/Ck/HK/258/97 (H5N1), which does have a glycosylation site at residue 154. The mouse model system should allow rapid evaluation of the vaccine's protective efficacy in a mammalian host. In our previous study using an avian model, DNA encoding hemagglutinin conferred protection against challenge with antigenic variants that differed from the primary antigen by 11 to 13% in the HA1 region. However, in our current study we found that a DNA vaccine encoding the hemagglutinin from A/Ty/Ir/1/83 (H5N8), which differs from A/HK/156/97 (H5N1) by 12% in HA1, prevented death but not H5N1 infection in mice. Therefore, a DNA vaccine made with a heterologous H5 strain did not prevent infection by H5N1 avian influenza viruses in mice but was useful in preventing death.

**Descriptors:** hemagglutinin glycoproteins, influenza virus immunology, influenza prevention and control, influenza A virus avian immunology, influenza vaccine immunology, vaccines, DNA immunology, antibodies, viral blood, hemagglutinin glycoproteins, influenza virus genetics, immunization, mice, mice inbred BALB c.


**NAL Call Number:** QR189.V32

**Abstract:** The cross-species transfer of a H5N1 influenza virus from birds to humans, and the systemic spread of this virus in mice, has accelerated the efforts to devise protective strategies against lethal...
influenza viruses. DNA vaccination with the highly conserved nucleoprotein gene appears to provide cross protection against influenza A viruses in murine models. Whether such vaccines would protect human hosts against different influenza A viruses, including strains with pandemic potential, is unclear. Our aim in this study is to evaluate the ability of a combination DNA vaccine consisting of two plasmids encoding the HA genes from two different subtypes and a DNA vaccine encoding the viral nucleoprotein gene from a H5 virus to induce protection against highly lethal infection caused by H5 and H7 influenza viruses in chickens. Chickens given a single dose of plasmids expressing H5 and H7 hemagglutinins protected the birds from infection by either subtype. However, birds immunized with nucleoprotein DNA and challenged with either A/Ck/Vic/1/85(H7N7) or A/Ty/Ir/1/83 (H5N8) showed definite signs of infection, suggesting inadequate immunity against viral infection. Fifty percent of the nucleoprotein DNA immunized birds survived infection by influenza A/Ty/Ir/1/83 (H5N8) virus (virus of same subtype) while 42% survived infection by influenza A/Ck/Vic/1/85/(H7N7) virus (virus of a different subtype). These studies demonstrate that immunization with DNA encoding a type-specific gene may not be effective against either homologous or heterologous strains of virus, particularly if the challenge virus causes a highly lethal infection. However, the combination of HA subtype vaccines are effective against lethal infection caused by viruses expressing any of the HA subtypes used in the combination preparation.

Descriptors: chickens immunology, hemagglutinin glycoproteins, influenza virus immunology, influenza veterinary, influenza A virus avian immunology, influenza vaccine immunology, nucleoproteins, poultry diseases prevention and control, vaccination veterinary, vaccines, DNA immunology, viral core proteins immunology, cos cells, Cercopithecus aethiops, evaluation studies, hemagglutinin glycoproteins, influenza virus genetics, influenza immunology, influenza prevention and control, influenza transmission, avian genetics, mice, plasmids immunology, poultry diseases immunology, recombinant fusion proteins immunology, species specificity, transfection, viral core proteins genetics, zoonoses.


NAL Call Number: QR189.V32

Abstract: The fraction NP/HA (nucleoprotein/haemagglutinin) obtained from n-octyl-beta-D-glucopyranoside-treated influenza A H5N2 virus was highly enriched for NP with residual haemagglutinin. This preparation was incorporated in ISCOMs. This potent 'immunostimulating complex' induced the production of high antibody titres in turkeys. The NP/HA ISCOMs preparation was found to protect turkeys from both homologous and heterologous challenge infection as shown by reduced viral titres in the lung and trachea of vaccinated turkeys. Clearance of the virus from trachea and lungs was seen at late stages of infection. The vaccine also induced a cellular immune response as measured by T-cell proliferation and a delayed-type hypersensitivity response. The results reported in this study demonstrate that the NP/HA ISCOM vaccine is capable of inducing type-specific immunity and that it has potential utility as a vaccine in turkeys.

Descriptors: fowl plague prevention and control, influenza A virus avian immunology, influenza vaccine immunology, antibodies, viral biosynthesis, cell division drug effects, cell division immunology, fowl plague immunology, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral immunology, hypersensitivity, delayed, immunity, cellular, avian isolation and purification, lung virology, lymphocytes cytology, lymphocytes drug effects, lymphocytes immunology, mitogens pharmacology, nucleoproteins isolation and purification, trachea virology, turkeys.


Descriptors: avian influenza, diagnosis, control, turkeys.


NAL Call Number: SF600.C82

Descriptors: inactivated vaccines, immune response, avian influenza virus, chickens, experimental infection.
NAL Call Number: SF995.W4
Descriptors: disease control, egg production, safety, animal production, production, disease prevention.

NAL Call Number: RS160.J6
Abstract: Propolis samples from different geographic origins were investigated for their antibacterial (against Staphylococcus aureus and Escherichia coli), antifungal (against Candida albicans) and antiviral (against Avian influenza virus) activities. All samples were active against the fungal and Gram-positive bacterial test strains, and most showed antiviral activity. The activities of all samples were similar in spite of the differences in their chemical composition. In samples from the temperate zone, flavonoids and esters of phenolic acids are known to be responsible for the above mentioned activities of bee glue; tropical samples did not contain such substances but showed similar activities. Obviously, in different samples, different substance combinations are essential for the biological activity of the bee glue. It seems that propolis has general pharmacological value as a natural mixture and not as a source of new powerful antimicrobial, antifungal and antiviral compounds.
Descriptors: Candida albicans drug effects, Escherichia coli drug effects, influenza A virus avian drug effects, propolis pharmacology, Staphylococcus aureus drug effects, anti bacterial agents, anti infective agents pharmacology, antifungal agents pharmacology, antiviral agents pharmacology, antiviral agents toxicity, cell culture, chick embryo, fibroblasts virology, flavonoids analysis, phenols analysis.

NAL Call Number: 41.8 Av5
Abstract: Retail live poultry markets (LPMs) may act as a reservoir of avian influenza viruses (AlV). In this study we test the hypothesis that a rest day in the LPMs where the stalls are completely emptied of poultry, cleansed, and restocked will reduce the isolation rates of avian influenza viruses. The isolation rate of H9N2 subtype viruses from chicken was significantly lower after the rest day than prior to it, indicating its impact in reducing transmission. In contrast, Newcastle disease virus (NDV) isolation rates appear unaffected by this intervention, possibly reflecting differences in herd immunity or virus transmission dynamics.
Descriptors: epidemiology, infection, herd immunity, monthly rest day, retail live poultry markets, viral isolation rates, virus transmission dynamics.

Descriptors: vaccines, immunity, avian influenza virus, chicks.

Descriptors: avian influenza, classical swine fever, foot and mouth disease, diagnostic techniques, vaccination, European Union, O.I.E. List A diseases, disease control, disease eradication, ethics, legislation.


NAL Call Number: 41.8 V6426

Descriptors: chemotherapy, antiviral agents, avian influenza virus, chickens.


NAL Call Number: 41.8 R3224

Descriptors: disease outbreaks veterinary, fowl plague epidemiology, poultry diseases epidemiology, animals, wild microbiology, Canada, fowl plague prevention and control, influenza A virus classification, poultry diseases microbiology, poultry diseases prevention and control, turkeys microbiology.


NAL Call Number: 448.3 Ar23

Descriptors: amantadine administration and dosage, influenza veterinary, poultry diseases prevention and control, administration, oral, animal feed, antibodies analysis, body fluids, chick embryo, chlorides, hemagglutination inhibition tests, hemagglutination, viral, influenza blood, influenza immunology, influenza mortality, influenza prevention and control, orthomyxoviridae isolation and purification, time factors, turkeys.

Laver, G. (2004). **From the great barrier reef to a "cure" for the flu - tall tales, but true.** *Perspectives in Biology and Medicine* 47(4): 590-596. ISSN: 0031-5982.

NAL Call Number: 442.8 P43

Descriptors: infection, prevention and control, sea birds, drug development.


NAL Call Number: SF995.W4

Descriptors: immune response, vaccination, broiler chickens, avian influenza virus, birds, chickens, disease control, domestic animals, domesticated birds, Galliformes, immunity, immunization, immunostimulation, immunotherapy, influenza virus, livestock, meat animals, orthomyxoviridae, poultry, therapy, useful animals, viruses.


NAL Call Number: 41.8 Av5

Abstract: Previously, we have shown that intramuscular vaccination of chickens with the eukaryotic expression vector (EEV), expressing the influenza H5 hemagglutinin (H) protein, can stimulate a measurable and protective antibody response. Based on these results, we cloned other H genes from Eurasian H5, North American and Eurasian H7, and H15 influenza viruses into the EEV for use in vaccination of chickens to produce reference antibodies for diagnostic purposes, such as the hemagglutination inhibition (HI) test. Three-week-old specific pathogen free (SPF) chickens were vaccinated with 100 µg of EEV mixed with a cationic lipid by intramuscular injection. Then the birds were boostered twice at monthly intervals after the original vaccination. Measurable antibody titers were present for most birds after 1 month and generally increased after each boost. To examine the cross reactivity of the sera with other subtypes, HI test was conducted with antigens prepared from 15 subtypes of influenza virus. Subtype specificity of the antisera prepared by DNA vaccination were comparable or better than the antisera prepared by traditional method using whole virus vaccination. Preparation of reference antisera by DNA vaccination holds good promise because it is safe and allows for the production of H specific antibodies without producing antibodies specific
to other influenza viral proteins.

Descriptors: epidemiology, immune system, infection, DNA vaccination genetic techniques, laboratory techniques, intramuscular vaccination, clinical techniques, therapeutic and prophylactic techniques, antibody titers, protective antibody response.

NAL Call Number: QR360.J6

Abstract: An outbreak of avian influenza (AI) caused by a low-pathogenic H5N2 type A influenza virus began in Mexico in 1993 and several highly pathogenic strains of the virus emerged in 1994-1995. The highly pathogenic virus has not been reported since 1996, but the low-pathogenic virus remains endemic in Mexico and has spread to two adjacent countries, Guatemala and El Salvador. Measures implemented to control the outbreak and eradicate the virus in Mexico have included a widespread vaccination program in effect since 1995. Because this is the first case of long-term use of AI vaccines in poultry, the Mexican lineage virus presented us with a unique opportunity to examine the evolution of type A influenza virus circulating in poultry populations where there was elevated herd immunity due to maternal and active immunity. We analyzed the coding sequence of the HA1 subunit and the NS gene of 52 Mexican lineage viruses that were isolated between 1993 and 2002. Phylogenetic analysis indicated the presence of multiple sublineages of Mexican lineage isolates at the time vaccine was introduced. Further, most of the viruses isolated after the introduction of vaccine belonged to sublineages separate from the vaccine's sublineage. Serologic analysis using hemagglutination inhibition and virus neutralization tests showed major antigenic differences among isolates belonging to the different sublineages. Vaccine protection studies further confirmed the in vitro serologic results indicating that commercial vaccine was not able to prevent virus shedding when chickens were challenged with antigenically different isolates. These findings indicate that multilinear antigenic drift, which has not been observed in AI virus, is occurring in the Mexican lineage AI viruses and the persistence of the virus in the field is likely aided by its large antigenic difference from the vaccine strain.

Descriptors: influenza A virus, avian genetics, avian pathogenicity, avian immunology, influenza vaccines immunology, amino acid sequence, chickens, evolution, hemagglutination inhibition tests, hemagglutinin glycoproteins, influenza virus genetics, immune sera immunology, molecular sequence data, phylogeny.

NAL Call Number: QR189.V32

Abstract: Vaccination of poultry with inactivated influenza vaccine can be an effective tool in the control of avian influenza (AI). One major concern of using inactivated vaccine is vaccine-induced antibody interference with serologic surveillance and epidemiology. In the United States, low pathogenicity H5 and H7 subtype AI viruses have caused serious economic losses in the poultry industry. Most of these viruses also have the accompanying N2 subtype and no H5N1 or H7N8 subtype AI viruses have been identified in poultry in the US. In order to allow the Differentiation of Infected from Vaccinated Animals (DIVA) while maintaining maximum efficacy of the vaccine, we generated reassortant viruses by reverse genetics that contained the same H5 and H7 hemagglutinin (HA) gene as the challenge virus, but a heterologous N1 or N8 neuraminidase (NA) gene. In vaccination-challenge experiments in 2-week-old specific pathogen free chickens, reassortant influenza vaccines (rH5N1 and rH7N8) demonstrated similar antibody profiles and comparable protection rates as vaccines prepared with parent H5N2 and H7N2 viruses. Further, we were able to differentiate the sera from infected and vaccinated birds by neuraminidase inhibition test and indirect immunofluorescent antibody assay on the basis of different antibodies elicited by their NA proteins. These results demonstrate the usefulness of a reverse genetics system for the rapid generation of reassortant AI virus that allows utilization of the DIVA strategy for the control of AI infections in poultry.

Descriptors: influenza A virus, avian immunology, influenza vaccines therapeutic use, avian influenza immunology, avian influenza prevention and control, poultry diseases immunology, poultry diseases prevention and control, antibodies, viral analysis, viral biosynthesis, chickens, fluorescent antibody technique, indirect, avian influenza A virus genetics, influenza vaccines genetics, plasmids genetics, reverse
Efficacy of zanamivir against avian influenza A viruses that possess genes encoding H5N1 internal proteins and are pathogenic in mammals. Antimicrobial Agents and Chemotherapy 45(4): 1216-24. ISSN: 0066-4804.

Abstract: In 1997, an avian H5N1 influenza virus, A/Hong Kong/156/97 (A/HK/156/97), caused six deaths in Hong Kong, and in 1999, an avian H9N2 influenza virus infected two children in Hong Kong. These viruses and a third avian virus [A/Teal/HK/W312/97 (H6N1)] have six highly related genes encoding internal proteins. Additionally, A/Chicken/HK/G9/97 (H9N2) virus has PB1 and PB2 genes that are highly related to those of A/HK/156/97 (H5N1), A/Teal/HK/W312/97 (H6N1), and A/Quail/HK/G1/97 (H9N2) viruses. Because of their similarities with the H5N1 virus, these H6N1 and H9N2 viruses may have the potential for interspecies transmission. We demonstrate that these H6N1 and H9N2 viruses are pathogenic in mice but that their pathogenicities are less than that of A/HK/156/97 (H5N1). Unadapted virus replicated in lungs, but only A/HK/156/97 (H5N1) was found in the brain. After three passages (P3) in mouse lungs, the pathogenicity of the viruses increased, with both A/Teal/HK/W312/97 (H6N1) (P3) and A/Quail/HK/G1/97 (H9N2) (P3) viruses being found in the brain. The neuraminidase inhibitor Zanamivir inhibited viral replication in Madin-Darby canine kidney cells in virus yield assays (50% effective concentration, 8.5 to 14.0 microM) and inhibited viral neuraminidase activity (50% inhibitory concentration, 5 to 10 nM). Twice daily intranasal administration of Zanamivir (50 and 100 mg/kg of body weight) completely protected infected mice from death. At a dose of 10 mg/kg, Zanamivir completely protected mice from infection with H9N2 viruses and increased the mean survival day and the number of survivors infected with H6N1 and H5N1 viruses. Zanamivir, at all doses tested, significantly reduced the virus titers in the lungs and completely blocked the spread of virus to the brain. Thus, Zanamivir is efficacious in treating avian influenza viruses that can be transmitted to mammals.

Descriptors: antiviral agents therapeutic use, enzyme inhibitors therapeutic use, influenza A virus avian drug effects, neuraminidase antagonists and inhibitors, sialic acids therapeutic use, administration, intranasal, antiviral agents administration and dosage, antiviral agents pharmacology, brain virology, cell line, dogs, enzyme inhibitors administration and dosage, enzyme inhibitors pharmacology, genes viral, influenza virology, avian genetics, avian pathogenicity, kinetics, lung virology, mice, mice inbred BALB c, microbial sensitivity tests, sialic acids administration and dosage, sialic acids pharmacology, species specificity, virus replication drug effects.

The neuraminidase inhibitor GS4104 (oseltamivir phosphate) is efficacious against A/Hong Kong/156/97 (H5N1) and A/Hong Kong/1074/99 (H9N2) influenza viruses. Antiviral Research 48(2): 101-15. ISSN: 0166-3542.

Abstract: In 1997, an H5N1 avian influenza A/Hong Kong/156/97 virus transmitted directly to humans and killed six of the 18 people infected. In 1999, another avian A/Hong Kong/1074/99 (H9N2) virus caused influenza in two children. In such cases in which vaccines are unavailable, antiviral drugs are crucial for prophylaxis and therapy. Here we demonstrate the efficacy of the neuraminidase inhibitor GS4104 (oseltamivir phosphate) against these H5N1 and H9N2 viruses. GS4071 (the active metabolite of oseltamivir) inhibited viral replication in MDCK cells (EC(50) values, 7.5-12 microM) and neuraminidase activity (IC(50) values, 7.0-15 nM). When orally administered at doses of 1 and 10 mg/kg per day, GS4104 prevented death of mice infected with A/Hong Kong/156/97 (H5N1), mouse-adapted A/Quail/Hong Kong/G1/97 (H9N2), or human A/Hong Kong/1074/99 (H9N2) viruses and reduced virus titers in the lungs and prevented the spread of virus to the brain of mice infected with A/Hong Kong/156/97 (H5N1) and mouse-adapted A/Quail/Hong Kong/G1/97 (H9N2) viruses. When therapy was delayed until 36 h after exposure to the H5N1 virus, GS4104 was still effective and significantly increased the number of survivors as compared with control. Oral administration of GS4104 (0.1 mg/kg per day) in combination with rimantadine (1 mg/kg per day) reduced the number of deaths of mice infected with 100 MLD(50) of H9N2 virus and prevented the deaths of mice infected with 5 MLD(50) of virus. Thus, GS4104 is efficacious in treating infections caused by H5N1 and H9N2 influenza viruses in mice.

Descriptors: acetamides pharmacology, antiviral agents pharmacology, influenza drug therapy, influenza A

**NAL Call Number:** QR180.3.D4

**Abstract:** An influenza pandemic could arise unexpectedly with rapid spread across the world. The efficiency of production of a vaccine and the ability to administer it widely will be among the most important factors in the ability to protect public health. The current process for producing inactivated or live attenuated influenza vaccines requires six to nine months. That reduces considerably the likelihood that the vaccine will be available during the first wave of the pandemic. Therefore, a key element of preparedness is to optimize the production process and to reduce the vaccine development time. During the 1997 H5N1 outbreak in Hong Kong, seed viruses were prepared for production of inactivated and live-attenuated vaccines. We used the cold-adapted A/Ann Arbor/6/60 as the donor virus to generate live attenuated vaccines containing genetically modified HA and NA genes from H5N1 influenza viruses. These reassortants were shown to be safe and protective in animal models. This study indicates that production of live attenuated avian influenza vaccines is feasible and that development of a library of reassortants containing different subtype HA and NA genes may reduce the vaccine preparation time for future influenza pandemics.

**Descriptors:** antigens, viral immunology, influenza prevention and control, influenza A virus avian immunology, influenza epidemiology, influenza vaccine administration and dosage.


**NAL Call Number:** 448.3 AC85

**Abstract:** The protective properties of monoclonal antibody (MoAb) C179 directed to the stem region of haemagglutinin (HA) H2 that possessed fusion-inhibition and unique broad cross-neutralizing activities were examined in a mouse model. The MoAb efficiently protected mice against a lethal challenge with pneumovirulent human (H1) and avian (H2) strains of influenza A virus. Survival rates in mice that received intraperitonealy (i.p.) 1000 micrograms of the MoAb per mouse a day before the virus challenge were 90% for H1 and 100% for H2 strain. The dose of the MoAb of 100 micrograms per mouse significantly decreased mortality in mice. Moreover, the MoAb was also efficient in treatment of lethal bronchopneumonia caused by H2 influenza virus. The survival rate in mice that received 1000 micrograms of the MoAb per mouse 2 days after the virus challenge was 90%, while that in the control group was 30% only. These results indicate that the MoAb was effective in protection of animals against lethal influenza A infection without significant difference between H1 and H2 subtypes. The MoAb exerted significant effect in treatment of mice infected with H2 influenza virus. Thus, these data allow to suggest that the stem region of HA might be a potential target for prevention of influenza virus infection and antiviral therapy.

**Descriptors:** antibodies, monoclonal therapeutic use, bronchopneumonia therapy, hemagglutinins viral immunology, influenza therapy, influenza A virus avian immunology, human immunology, pneumonia, viral therapy, antibodies, monoclonal immunology, bronchopneumonia prevention and control, dose response relationship, immunologic, influenza prevention and control, mice, pneumonia, viral prevention and control, random allocation, time factors.


**Descriptors:** vaccination, avian influenza virus, genetic mutations, poultry.

Lopez, H.C., E.R. Cruz, and M.I. Enrich (1996). *Situacion y perspectivas del programa de erradicacion de la*

Abstract: El estudio se concreto en evaluar la respuesta serologica y la resistencia al desafio de una vacuna sola y una vacuna combinada de I.A-ENC. que contenia 9.2 DIEP50 por ml del virus de IA. Grupos de 20 pollos fueron vacunados al dia de edad con la dosis completa de las vacunas y con 0.25 ml del producto, y fueron estudiados serologicamente a los 0, 3, 7, 10 y 14 dias post-vacunacion (PV), para despus hacerlo cada 8 dias hasta el dia 96. Se realizaron 4 desafios para IA a los 14, 28, 63 y 96 dias PV. Se colocaron pollos en contacto, 3 dias despues del desafio, para evaluar si el virus de IA replicaba en las aves vacunadas, en cantidad suficiente para causar morbidad y/o mortalidad en pollos susceptibles. Los resultados indican que a los 14 dias PV, un bajo porcentaje de las aves mostraron anticuerpos para la vacuna de I.A. sola o combinada aplicada a dosis completa. Las aves vacunadas con media dosis de I.A. permanecieron sero-negativas en este muestreo. A partir de los 21 dias PV se detectaron anticuerpos para I.A. En todos los grupos con porcentajes de 83 a 100% de sero-conversion, el ultimo unicamente fue alcanzado en el grupo de pollos que recibieron la dosis completa de vacuna de I.A. sola. Porcentajes de proteccion al desafio del 100%, con una cepa de alta patogenicidad, fueron alcanzados en pollos vacunados con I.A. o combinada con ENC aplicada en dosis completa. La vacuna bivalente de I.A.- ENC aplicada a media dosis, gradualmente incremento la proteccion hasta alcanzar el 100% a los 63 dias PV. Sin embargo, es importante senalar de que a pesar de haberse observado una buena proteccion cuando se aplica la vacuna sola de I.A. a media dosis, esta en ningun caso alcanzo el 100% de proteccion. En este estudio se confirma que no hay una relacion que permita asociar la proteccion con la excrecion viral, de tal manera que las aves vacunadas con dosis completa de vacuna tanto sola o combinada eliminaron virus en cantidad suficiente para causar la muerte de las aves en contacto.

Descriptors: broiler chickens, avian influenza virus, vaccines, application rates, Newcastle disease, birds, chickens, domestic animals, Galliformes, infectious diseases, influenza virus, livestock, meat animals, orthomyxoviridae, poultry, useful animals, viroses, viruses.
antibody. Mice injected intramuscularly with inactivated G1 whole virus vaccine were completely protected from challenge with either H9N2 virus. In contrast, mice administered inactivated G9 vaccine were only partially protected against heterologous challenge with the G1 virus. These results have implications for the development of human vaccines against H9N2 viruses, a priority for pandemic preparedness.

Descriptors: influenza A virus avian immunology, influenza vaccine immunology, cross reactions, disease models, animal, influenza immunology, influenza prevention and control, avian physiology, mice, inbred BALB c, vaccination, vaccines, inactivated, virus replication.

Descriptors: immune system, infection, pharmacognosy, HIV infection, human immunodeficiency virus infection, blood and lymphatic disease, drug therapy, immune system disease, viral disease, avian influenza, viral disease, viral diseases, drug therapy, viral disease, HAART (highly active antiretroviral therapy) clinical techniques, therapeutic and prophylactic techniques, drug resistance, drug sources, phagocytic activity synergism, viral replication cycle.

Descriptors: avian influenza virus, histopathology, immunization, inactivated vaccines, fowl.

Descriptors: disease control, avian influenza virus, emulsion preparation, China.

NAL Call Number: SF604.C58
Descriptors: avian influenza virus, infectious bronchitis virus, Newcastle disease virus, immune response, polyvalent vaccines.

NAL Call Number: QR189.V32
Abstract: The H5 hemagglutinin (HA) gene of a highly pathogenic avian influenza virus (AIV) isolate (A/chicken/Italy/8/98) was cloned and sequenced, and inserted at the non-essential UL50 (dUTPase) gene locus of a virulent strain of infectious laryngotracheitis virus (ILTV). Northern and Western blot analyses of the obtained ILTV recombinants demonstrated stable expression of the HA gene under control of the human cytomegalovirus immediate-early gene promoter. In vitro replication of the HA-expressing ILTV mutants was not affected, and infection of chickens revealed a reduced but still considerable virulence, similar to that of a UL50 gene deletion mutant without foreign gene insertion. The immunized animals produced specific antibodies against ILTV and AIV HA, and were protected against challenge infections with either virulent ILTV, or two different highly pathogenic AIV strains (A/chicken/Italy/8/98, A/chicken/Scotland/59). After challenge, no ILTV could be reisolated from protected animals, and shedding of AIV was considerably reduced. Thus, although attenuation remains to be improved, genetically engineered ILTV live-virus vaccines might be used as vectors to protect chickens also against other pathogens.
Descriptors: hemagglutinin glycoproteins, influenza virus immunology, herpesvirus 1, gallid genetics, influenza A virus avian immunology, influenza vaccine immunology, vaccines, synthetic immunology, chickens, hemagglutinin glycoproteins, influenza virus genetics, vaccination.

NAL Call Number: 41.8 V6426
Descriptors: fowl plague immunology, avian influenza virus, viral vaccines, aerosols, chickens.

Abstract: An efficiency of various ways of immunization applied when obtaining hybridomas releasing monoclonal antibodies (mABs) against avian influenza virus has been estimated. It is shown that the intraspleen immunization can be successfully used together with routine methods without decrease of virus specific clones outcome.
Descriptors: laboratory animals, avian influenza virus, monoclonal antibodies, hybridomas, immunization, mice, animal biotechnology, veterinary medicine, antibodies, biotechnology, cells, disease control, immunological factors, immunostimulation, immunotherapy, influenza virus, mammals, orthomyxoviridae, Rodentia, therapy, useful animals, viruses.

NAL Call Number: 41.8 Av5
Abstract: In 1999-2000, Italy was affected by the most severe avian influenza (AI) epidemic that has ever occurred in Europe. The epidemic was caused by a type A influenza virus of the H7N1 subtype, which originated from the mutation of a low-pathogenicity (LP) AI virus of the same subtype. From August to November 2000, 4 months after the eradication of the highly pathogenic (HP) AI virus, the LPAI strain re-emerged and infected 55 poultry farms mainly located in the southern area of Verona province (Veneto region). To supplement disease control measures already in force, an emergency vaccination program against the disease was implemented in the area. Vaccination was carried out using an inactivated heterologous vaccine (A/chicken/Pakistan/1995-H7N3). In order to establish whether LPAI infection was circulating in the area, regular serological testing of sentinel birds in vaccinated flocks and a discriminatory test able to distinguish the different types of antineuraminidase antibodies (anti-N1 and anti-N3) were performed. Shortly after the beginning of the vaccination campaign (December 2000 to March 2001), the H7N1 LPAI virus emerged again, infecting 23 farms. Among these, only one vaccinated flock was affected, and infection did not spread further to other vaccinated farms. The data reported in the present paper indicate that the combination of biosecurity measures, official control, and vaccination can be considered successful for the control of LPAI infections in densely populated poultry areas.
Descriptors: epidemiology, infection, public health, avian influenza, epidemiology, infectious disease, prevention and control, respiratory system disease, transmission, viral disease, serology, clinical techniques, diagnostic techniques, vaccination, disease control, emergency vaccination program.

Abstract: From 1997 to 2003, Italy has been affected by two epidemics of highly pathogenic avian influenza (HPAI) and by several outbreaks of low pathogenic avian influenza (LPAI). In 1999-2000 a severe HPAI epidemic affected the country, causing 413 outbreaks: a total of about 16 million birds died or were stamped out. From August 2000 to March 2001, a H7N1 LPAI strain infected 78 poultry farms. The last affected flock was stamped out on the 26th of March 2001. In October 2002, another LPAI virus of the H7N3 subtype emerged and infected a total of 388 poultry holdings. Eradication measures were based on stamping out or controlled marketing of slaughtered birds on infected farms and on the prohibition of restocking. Restriction measures on the movement of live poultry, vehicles and staff were also imposed. To supplement these disease control measures, two emergency vaccination programmes, based on the "DIVA" (Differentiating Infected from Vaccinated Animals) strategy were implemented. The two vaccination campaigns (2000-2002 and 2002-2003) both resulted in the eradication of infection. However, the first campaign appeared to be
more successful that the second and possible explanations are discussed.

Descriptors: animals, disease outbreaks prevention and control, veterinary disease outbreaks, avian influenza A virus immunology, avian influenza epidemiology, avian influenza prevention and control, Italy epidemiology, population density, poultry, veterinary vaccination, viral vaccines.


NAL Call Number: QR355.A5

Abstract: The effectiveness of the novel sialidase inhibitor 4-guanidino-Neu5Ac2en, which is highly effective in mouse and ferret models of influenza virus infection (von Itzstein et al. (1993) Nature 363, 418-423), has been assessed as a prophylactic agent in the prevention of infection of chickens with highly pathogenic avian influenza viruses. At best a small delay in the onset of pyrexia and death was observed with one strain of fowl plague virus, but not with two other strains. These results demonstrate that a locally acting drug may be ineffective if virus can escape from the site of inoculation and replicate elsewhere.

Descriptors: antiviral agents pharmacology, chickens, fowl plague prevention and control, sialic acids pharmacology, body temperature, cell line, fowl plague mortality, influenza A virus avian drug effects, avian pathogenicity.


NAL Call Number: 41.8 Au72

Descriptors: chickens, disease outbreaks veterinary, avian influenza, prevention and control, southeastern Asia, epidemiology, disease outbreaks prevention and control, influenza A virus.


NAL Call Number: SF995.A1A9

Descriptors: avian influenza virus, immunization, vaccines, neuramidase, hemagglutination, poultry.


NAL Call Number: SF600.C82

Descriptors: avian influenza virus, diagnosis, vaccination.


Abstract: The effect of the neuraminidase inhibitors zanamivir and oseltamivir on the transmission of highly pathogenic avian influenza (HPAI) in chickens was studied. Per group, five chickens inoculated with HPAI A/Chicken/Pennsylvania/1370/83 H5N2 virus were placed 1 day post-inoculation (p.i.) in one cage with five contact chickens. Inoculated and contact chickens were treated twice daily from 1 day before inoculation up to day 7 p.i. All untreated inoculated and contact chickens became infected and four inoculated and two contact chickens died. Similarly, all of the zanamivir-treated inoculated and contact chickens became infected and all inoculated and four contact chickens died. Obviously, locally active zanamivir has no effect. In contrast, although oseltamivir could not prevent tracheal infection of the inoculated chickens, none had an infected cloaca and only one died. More important, only after stopping treatment three contact chickens became positive, suggesting limited transmission within or after the treatment period. In conclusion, treatment with systemically active oseltamivir limits to a large extent a severe outcome and chicken-to-chicken transmission of HPAI virus.

Descriptors: highly pathogenic avian influenza virus, chicken, transmission, antiviral treatment, antiviral prophylaxis, neuraminidase inhibitors, zanamivir, oseltamivir.

**NAL Call Number:** 449.9 Un3r  
**Descriptors:** recombinant vaccines, recombinant fowl pox virus gene, immunization, Cox regression model, avian influenza virus, turkeys, poultry.


**NAL Call Number:** SF995.W4  
**Descriptors:** avian influenza virus, vaccines, avipoxvirus, influenza virus, orthomyxoviridae, poxviridae, viruses.


**NAL Call Number:** 448.9 Am37  
**Descriptors:** influenza prevention and control, influenza vaccines supply and distribution, influenza epidemiology, influenza A virus, avian, influenza vaccines administration and dosage, seasons, United States epidemiology.


**NAL Call Number:** 41.9 T23  
**Descriptors:** antibodies, disease control, disease prevention, immunization, inactivated vaccines, hemagglutination inhibition test, immune response, avian influenza A virus, Iran, poultry, chickens, broilers.


**NAL Call Number:** 41.8 Am3  
**Descriptors:** influenza prevention and control, influenza A virus avian physiology, influenza vaccine, avian immunology, poultry, swine.


**NAL Call Number:** SF481.A9  
**Descriptors:** reviews, avian influenza virus, epidemiology, diagnosis, control.


**NAL Call Number:** QR180.I52  
**Abstract:** The immunomodulatory activity of Isoprinosine treatments have been experimentally verified on chicken infected by three different viruses: Newcastle disease, fowl plague and avian infectious bronchitis. In protection tests, positive variations in the mean day of death rather than in the mortality rate were found depending on the modality of treatment. A stimulatory influence on primary anti-Newcastle disease virus antibody response was observed. In the avian model the Isoprinosine antiviral effect appears as due mainly to the enhancement of interferon production and to a synergistic interferon-isoprinosine interaction.  
**Descriptors:** adjuvants, immunologic pharmacology, inosine analogs and derivatives, inosine pranobex pharmacology, virus diseases immunology, antibodies, viral biosynthesis, chickens, hemagglutination inhibition tests, infectious bronchitis virus immunology, influenza A virus avian immunology, interferons
therapeutic use, kinetics, Newcastle disease virus immunology, vesicular stomatitis Indiana virus immunology, virus diseases drug therapy.


**Descriptors:** disease control, disinfectants, formaldehyde, pH, phenol, evaluation, chemical treatment, ultraviolet radiation, efficacy, avian influenza virus, poultry.


**NAL Call Number:** 475 P172

**Descriptors:** avian influenza virus, passive immunity, immunization, disease control, immunostimulation, immunotherapy, chickens, broilers, poultry.


**NAL Call Number:** 41.8 Av5

**Abstract:** Zanamivir has been shown to inhibit both human and avian influenza viral neuraminidases (NAs) and has been approved in several countries for the treatment and prophylaxis of influenza infection. Reliable monitoring of drug resistance is important for assessment of the impact of drug therapy on circulating virus populations. This study compares the current fluorometric (FL) method for evaluating zanamivir susceptibility with a recently developed chemiluminescent (CL) NA activity assay using viruses representative of all nine NA subtypes. The CL assay displayed signal/noise ratios that are 50-100 times greater than those associated with the FL assay. Human H3N2 strains appeared to exhibit greater NA activity relative to avian subtypes with the FL substrate but not with the CL substrate. Additionally, the CL assay remained linear over three orders of magnitude compared to only one order of magnitude for the FL assay. Four of the nine NA subtypes tested in this study displayed slightly higher inhibitor concentration that inhibits 50% of neuraminidase activity values by CL than by FL, while four displayed the opposite effect. Implications for the routine determination of resistance to NA inhibitors are discussed.

**Descriptors:** infection, avian influenza, infectious disease, respiratory system disease, viral disease, chemiluminescent neuraminidase assay bioassay techniques, clinical techniques, diagnostic techniques, laboratory techniques, antiviral susceptibility, drug resistance.


**NAL Call Number:** 475 P173

**Abstract:** An epidemic of avian influenza was recorded in broiler flocks in Karachi area in 1999. Samples were collected for serosurveillance, isolation, stereotyping, development of inactivated (alum precipitated and oil based vaccines, to study immune response of broilers to these vaccines. Results of the project indicated that H9N2-AIV was associated with the epidemic occurred in the area of Karachi and inactivated alum precipitated and oil based vaccines developed from local isolate when inoculated to broilers (primed on day-5 with alum precipitated and boosted with oil based on day-21) provoked a GM-titer (range) 64-256 in the vaccinates.

**Descriptors:** broiler chickens, avian influenza virus, vaccines, immune response, Pakistan, Asia, birds, chickens, domestic animals, Galliformes, immunity, livestock, meat animals, poultry, South Asia, useful animals.


**NAL Call Number:** 448.8 J821


**NAL Call Number:** 41.8 Av5

**Abstract:** During the past decade, several examples of the ability of H5 and H7 low-pathogenicity avian influenza (LPAI) viruses to mutate to high-pathogenicity (HP) viruses have been documented worldwide. During this time, the introduction and persistence of an H7N2 LPAI virus in the northeast live-bird marketing system in the United States has raised concern on how to prevent the possibility of such a mutation occurring in this country. The United States has periodically experienced trade restrictions based on the occasional introduction of H5 and H7 LPAI viruses into commercial poultry and based on AI-related changes in the import requirements for poultry and poultry products of several of our trading partners. Consequently, the U.S. Department of Agriculture (USDA) is exploring options for how our regulatory response to H5 and H7 LPAI viruses might be revised to better protect our domestic poultry flocks from HPAI and to ensure that any interruptions in trade are scientifically supportable. The options under consideration include mandatory and voluntary measures to improve the surveillance for and control of H5 and H7 LPAI virus infections.

Descriptors: epidemiology, infection, avian influenza, epidemiology, infectious disease, prevention and control, respiratory system disease, viral disease, influenza control, regulation, live bird markets, trade restrictions.


**NAL Call Number:** 47.8 Am33P

**Abstract:** The effect of microaerosolized H2O2 on bacterial and viral poultry pathogens was investigated. Bacterial cultures and viruses were dried on sterile glass Petri dishes and subjected to direct and indirect 5% (H2O2) microaerosol mist. In the trials using *Escherichia coli* and *Staphylococcus aureus*, there was complete inactivation following exposure to H2O2. Using *Salmonella typhimurium*, indirect exposure resulted in only partial inactivation whereas direct exposure to H2O2 gave complete inactivation. For the viruses studied, 5% H2O2 microaerosol mist completely inactivated infectious laryngotracheitis virus. Newcastle disease virus, infectious bronchitis virus, and avian influenza virus showed reduced infectivity but were not completely inactivated. Avian reovirus susceptibility varied with the method of exposure and infectious bursal disease virus was highly resistant. The use of 10% H2O2 mist, however, resulted in total inactivation of infectious bursal disease virus. The effect of 10% H2O2 on equipment and selected materials representative of a hatcher or poultry house was investigated. A solar cell calculator, a thermostat containing a microswitch, and samples of uncoated steel, galvanized steel, and uncoated aluminum were subjected to 10 fumigation cycles. No damage was detected in the calculator and the thermostat. Both the uncoated steel and the galvanized steel showed signs of oxidation. The aluminum did not show signs of oxidation.


**NAL Call Number:** 41.8 Av5

**Abstract:** Avian influenza viruses are major contributors to viral disease in poultry as well as humans. Outbreaks of high-pathogenicity avian influenza viruses cause high mortality in poultry, resulting in...
significant economic losses. The potential of avian influenza viruses to reassort with human strains resulted in global pandemics in 1957 and 1968, while the introduction of an entirely avian virus into humans claimed several lives in Hong Kong in 1997. Despite considerable research, the mechanisms that determine the pathogenic potential of a virus or its ability to cross the species barrier are poorly understood. Reverse genetics methods, i.e., methods that allow the generation of an influenza virus entirely from cloned cDNAs, have provided us with one means to address these issues. In addition, reverse genetics is an excellent tool for vaccine production and development. This technology should increase our preparedness for future influenza virus outbreaks.

Descriptors: epidemiology, infection, molecular genetics, avian influenza, genetics, infectious disease, prevention and control, respiratory system disease, viral disease, disease control, economic losses, global pandemics, reverse genetics, viral outbreaks, viral pathogenicity.


NAL Call Number: RS1.A7

Abstract: benzoxazolone-5-(2'-nitro)-sulphonanilides were synthesized by acylation of o-nitroanilines with benzoxazolone-5-sulphochloride or 3-methylbenzoxazolone-5-sulphochloride. The nitro group in these compounds was subjected to reduction and the resulting amino derivatives were cyclised to yield the corresponding 1-(benzoazolone-5'-sulphonyl)-benzotriazoles. Decyclization of the oxazolone cycle of benzoxazolone-5-(2'-amino)-sulphonanilides resulted in 4-hydroxy-3,2'-diaminobenzenesulphonanilides. In vitro testing of the antiviral activity of the compounds obtained during successive synthetic steps revealed that some of them exhibited marked antiviral effect against toga, orthomixo, oncorna and herpes viruses.

Descriptors: antiviral agents chemical synthesis, benzoxazoles chemical synthesis, sulfanilamides chemical synthesis, antiviral agents pharmacology, benzoxazoles pharmacology, chemistry, cytopathogenic effect, viral drug effects, herpesvirus 1, suid drug effects, influenza A virus avian drug effects, mice, mice inbred BALB c, moloney murine leukemia virus drug effects, Semliki Forest virus drug effects, sulfanilamides pharmacology, triazoles chemical synthesis, triazoles pharmacology.


NAL Call Number: 448.8 L22

Abstract: Background: In 1997, pathogenic avian influenza A/Hong Kong/97 (H5N1) viruses emerged as a pandemic threat to human beings. A non-pathogenic variant, influenza A/Duck/Singapore/97 (H5N3), was identified as a leading vaccine candidate. We did an observer-blind, phase I, randomised trial in healthy volunteers to assess safety, tolerability, and antigenicity of MF59-adjuvanted and non-adjuvanted vaccines. Methods: 32 participants were randomly assigned MF59, and 33 non-adjuvanted vaccine. Two doses were given 3 weeks apart, of 7.5, 15, or 30 mug haemagglutinin surface-antigen influenza A H5N3 vaccine. Antibody responses were measured by haemagglutination inhibition, microneutralisation, and single radial haemolysis (SRH). The primary outcome was geometric mean antibody titre 21 days after vaccination. Findings: The A/Duck/Singapore vaccines were safe and well tolerated. Antibody response to non-adjuvanted vaccine was poor, the best response occurring after two 30 mug doses: one, four, four, and one person of eleven seroconverted by haemagglutination inhibition, microneutralisation, H5N3 SRH, and H5N1 SRH, respectively. The geometric mean titres of antibody, and seroconversion rates, were significantly higher after MF59 adjuvanted vaccine. Two 7.5 mug doses of MF59 adjuvanted vaccine gave the highest seroconversion rates: haemagglutination inhibition, six of ten; microneutralisation, eight of ten; H5N3 SRH, ten of ten; H5N1 SRH, nine of ten. Geometric mean titre of antibody to the pathogenic virus, A/Hong Kong/489/97 (H5N1), was about half that to A/Duck/Singapore virus. Interpretation: Non-adjuvanted A/Duck/Singapore/97 (H5N3) vaccines are poorly immunogenic and doses of 7.5-30 mug haemagglutinin alone are unlikely to give protection from A/Hong Kong/97 (H5N1) virus. Addition of MF59 to A/Duck/Singapore/97 vaccines boost the antibody response to protection levels. Our findings have
implications for development and assessment of vaccines for future pandemics.

**Descriptors:** infection, pharmacology, influenza, respiratory system disease, viral disease, antigenicity safety.


**NAL Call Number:** 470 Sci2

**Descriptors:** agricultural workers' diseases virology, antibodies, viral blood, influenza virology, influenza A virus, avian immunology, acetamides therapeutic use, agricultural workers' diseases immunology, agricultural workers' diseases prevention and control, antiviral agents therapeutic use, disease outbreaks, influenza epidemiology, influenza immunology, influenza prevention and control, Japan epidemiology, protective clothing.


**NAL Call Number:** 470 Sci2

**Descriptors:** influenza prevention and control, influenza A virus, avian immunology, influenza vaccines, World Health Organization, cloning, molecular, hemagglutinins, viral genetics, viral immunology, influenza transmission, influenza virology, avian genetics, neuraminidase genetics, neuraminidase immunology, patents, vaccines, synthetic.


**NAL Call Number:** 470 Sci2

**Descriptors:** disease outbreaks veterinary, influenza A virus, avian immunology, influenza vaccines immunology, avian influenza prevention and control, poultry, vaccination veterinary, Asia epidemiology, chickens, disease outbreaks prevention and control, immunization programs, influenza prevention and control, influenza transmission, influenza virology, avian influenza, epidemiology, avian influenza, transmission, risk assessment.


**NAL Call Number:** 41.8 V6426

**Descriptors:** chemoprophylaxis, antiviral agents, amantadine, avian influenza, mortality rate, drinking water, chicks, poultry.


**Descriptors:** influenza prevention and control, influenza vaccines therapeutic use, vaccines, inactivated therapeutic use, adolescent, adult, advisory committees, child, preschool child, enzyme inhibitors therapeutic use, immunization programs, infant, influenza epidemiology, influenza veterinary, influenza virology, influenza A virus, avian pathogenicity, influenza vaccines administration and dosage, influenza vaccines adverse effects, influenza vaccines immunology, middle aged, neuraminidase antagonists and inhibitors, Ontario epidemiology, population surveillance, United States epidemiology, vaccines, inactivated administration and dosage, vaccines, inactivated adverse effects, vaccines, inactivated immunology.


**Descriptors:** avian influenza virus, maternal immunity, immune response, inactivated vaccines, results, acquired antibody, chicks.

Osidze, N.G., V.I. Smolenskii, A.I. Kalashnikov, and V.N. Syrin (1977). *Safety, antigenicity and immunogenicity*

Descriptors: avian influenza virus, experimental inactivated vaccine, safety, antigenicity, immunogenicity.


NAL Call Number: 41.8 AC84

Descriptors: fowl plague prevention and control, viral vaccines, influenza A virus avian, vaccination.


NAL Call Number: SF995.W4

Descriptors: avian influenza virus, vaccines, influenza virus, orthomyxoviridae, viruses.


Abstract: En el laboratorio y bajo condiciones de confinamiento, los ensayos con la vacuna recombinante de Viruela-Influenza Aviar, demostraron que el producto no representa riesgos relativos para los pollos ni para otras especies animales. El presente estudio tuvo como objetivo determinar si la vacuna tendría un efecto sobre los parámetros productivos del pollo y la mortalidad asociada a la aplicación del producto, en pollos comerciales de engorda. Para tal fin se utilizó un granja comercial localizada en el estado de Guanajuato, donde fueron instalados pollos machos, con anticuerpos maternos, vacunadas en la incubadora, al día de edad, en 2 cassetas, teniendo un total de 48,000 pollos en el tratamiento. Al resto de las cassetas de la granja se les aplico vacuna inactivada, emulsionada, bivalente de Newcastle (eNC)-Influenza Aviar.(IA) a los 10 días de edad. Los pollos recibieron el resto de las vacunas, de acuerdo al calendario de vacunacion establecido por la empresa de pollos. Los pollos vacunados fueron observados diariamente por espacio de siete semanas, Se realizo la necropsia a la mortalidad diaria, Los pollos de la prueba fueron seguidos serologicamente de tal manera que 50 pollos vacunados y 25 centinelas de las 2 cassetas de pollos vacunados con el producto recombinante, fueron sangrados semanalmente. Se hicieron 2 desafíos, a las 3 y 6 semanas de edad, con el virus de alta patogenicidad de IA. Los resultados indican que la vacunacion no tuvo efectos negativos en los indices de produccion de los pollos utilizados, ni tampoco causo alguna mortalidad asociada a la vacunacion. Los pollos vacunados con el producto recombinante fueron serologicamente negativos a partir de las 4 semanas de edad hasta el momento de salir al mercado. Se obtuvo el 95% de proteccion en los pollos vacunados, cuando estos fueron desafiados experimentalmente en unidades de aislamiento, y que la mortalidad observada post-desafio estuvo asociada a la presencia de otros microorganismos involucrados así como a la incidencia de ascitis en la parvada. El estudio senala que la vacuna no tuvo ningun efecto adverso en el campo, que induce una adecuada proteccion al desafio con cepas de alta patogenicidad del virus de IA a pesar de que, las aves vacunadas mostraron serologias negativas al final del ciclo de produccion.

Descriptors: broiler chickens, avian influenza virus, synthetic vaccines, immune response, birds, chickens, domestic animals, Galliformes, immunity, influenza virus, livestock, meat animals, orthomyxoviridae, poultry, useful animals, vaccines, viruses.


Abstract: En enero de 1995, la DGSA autorizo la elaboracion de vacunas inactivadas, emulsionadas en
aceite para controlar la Influenza Aviar (I.A) de alta patogenicidad. Los estudios iniciales demostraron la eficiencia de la vacuna para prevenir los signos y lesiones, así como la mortalidad ante el desafío con las cepas de alta patogenicidad, aisladas en Puebla y Queretaro. Meses después de haber sido autorizados 6 laboratorios a elaborar las vacunas, se realizó el siguiente trabajo de evaluación. Se seleccionaron en forma aleatoria 3 vacunas inactivadas con formol, 2 vacunas inactivadas con beta-propriolactona y 2 vacunas bivalentes para prevenir además, la enfermedad de Newcastle, inactivadas con formol. Se vacunaron grupos de 20 pollos SPF con cada uno de los productos, se determinó la presencia de anticuerpos inhibidores de la hemoaglutinación a los 0, 7, 10, 14 y 21 días pos-vacunación (PV). A los 21 días PV grupos de 18 pollos vacunados con cada producto fueron desafiados con un virus de alta patogenicidad, aislado en Queretaro. Los resultados serológicos indicaron que cuando menos una vacuna de cada grupo indujo el 100% de sero conversion al día 21 PV con medias geométricas (MG) que variaron de 28 a 264 (reciproca de la MG). No se detectó ninguna asociación entre el inactivante utilizado o en la combinación con otro antígeno, con la capacidad del producto para inducir la formación de anticuerpos. Independientemente de la presencia y del nivel de anticuerpos detectados en el suero, el 100% de los pollos vacunados estuvieron protegidos cuando de desafiaron con el virus de alta patogenicidad, lo cual demuestra que los laboratorios productores de vacuna elaboraron un producto de buena calidad que permite ayudar en el control de la enfermedad, que a los 21 días PV encontramos del 84 al 100% de sero-conversion y el 100% de protección al desafío; por lo que la inmunidad humoral parece no ser la más importante en la protección. La utilización de pollos en contacto con las aves vacunadas y desafiadas permitió identificar que las aves vacunadas después del desafío replican y eliminan virus de progenie, en cantidad suficiente para causar la enfermedad y muerte de pollos susceptibles.

Descriptors: broiler chickens, avian influenza virus, vaccines, immune response, birds, chickens, domestic animals, Galliformes, immunity, influenza virus, livestock, meat animals, orthomyxoviridae, poultry, useful animals, viruses.


Descriptors: recombinant veterinary vaccines, fowl pox virus, influenza virus, rabies virus, risk assessment, agricultural biotechnology, poultry.


NAL Call Number: 41.8 Av5

Abstract: The Office International des Epizooties (OIE) has developed international standards to reduce the risk of the spread of high-pathogenicity avian influenza though international trade. These standards include providing a definition of high-pathogenicity avian influenza (HPAI), procedures for prompt reporting of HPAI outbreaks, requirements that must be met for a country or zone to be defined as free of HPAI, requirements that should be met to import live birds and avian products into a HPAI-free country or zone, and the general provisions that countries should meet to reduce the risk of spread of HPAI through trade. The goal of these standards is to facilitate trade while minimizing the risk of the introduction of HPAI.

Descriptors: epidemiology, infection, avian influenza, epidemiology, infectious disease, prevention and control, respiratory system disease, viral disease, disease spread international, influenza control standards.


NAL Call Number: SF605.C59

Descriptors: avian influenza virus, vaccine, turkeys, immune response.


Descriptors: antibodies, immune response, immunization, avian influenza virus, fowl, poultry.
NAL Call Number: aSF995.6.I6I5 1981a
Descriptors: avian influenza virus, control, prevention, commercial vaccines, poultry, symposium.

NAL Call Number: SF995.W4
Descriptors: avian influenza virus, vaccines, evaluation, influenza virus, orthomyxoviridae, viruses.

NAL Call Number: SF995.A1A9
Abstract: Inactivated whole avian influenza virus (AIV) vaccine provides protection against homologous haemagglutinin (HA) subtype virus, but poor protection against a heterologous HA virus. Moreover, it induces chickens to produce antibodies to cross-reactive antigens, especially nucleoprotein, which is limits AIV serological surveillance. In this study, a recombinant fowlpox virus co-expressing HA (H5 subtype) and NA (N1 subtype) genes of AIV was evaluated for its ability to protect chickens against intramuscular challenge with a lethal dose of highly pathogenic (HP) AIV. Susceptible chickens were also vaccinated by wing-web puncture with the parent fowlpox vaccine virus. Following challenge 4 weeks later with HPAIV, all chickens vaccinated with recombinant virus were protected, while the chickens vaccinated with either the unaltered parent fowlpox vaccine virus or unvaccinated controls experienced 100% mortality following challenge. This protection was accompanied by the high levels of specific antibody to the respective components of the recombinant vaccine. The above results showed that rFPV-HA-NA could be a potential vaccine to replace current inactivated vaccines for preventing AI.
Descriptors: animal husbandry, infection, pharmacology, intramuscular immune challenge clinical techniques, wing web puncture vaccination clinical techniques.

NAL Call Number: S417.C6Z462
Descriptors: antibodies, experimental infections, gene expression, immunity, potency, recombinant vaccines, vaccine development, viral hemagglutinins, avian influenza virus, fowl pox virus, chickens, poultry, fowl, mortality.

NAL Call Number: S471.C6N89
Descriptors: antibodies, nucleoproteins, avian influenza virus, fowl pox virus, poultry.

Descriptors: influenza prevention and control, influenza A virus, avian immunology, influenza vaccines supply and distribution, drug industry, United States, vaccination.

Descriptors: disease outbreaks prevention and control, influenza A virus, avian influenza, avian influenza prevention and control, avian influenza transmission, international cooperation, zoonoses transmission.


Abstract: Studies of the pathogenesis of influenza infection have involved the extensive use of animal models. The development of the current concepts of immunity to influenza and of the contribution the secretory immune system makes toward the protection of mucosal surfaces against influenza infection would have been impossible without this use of animals. The pathology and clinical signs of influenza infection in both natural and experimental hosts, the advantages and disadvantages of the most common experimental influenza infection models, and the contribution of animal models to the understanding of local and systemic immunity to influenza infection are discussed.
Descriptors: influenza immunology, influenza veterinary, antibody formation, disease models, animal, ferrets, fowl plague immunology, hamsters, haplorhini, horse diseases immunology, horses, influenza A virus avian, influenza A virus human, influenza A virus, porcine, influenza A virus, influenza vaccine administration and dosage, mice.

Abstract: The question of how best to protect the human population against a potential influenza pandemic has been raised by the recent outbreak caused by an avian H5N1 virus in Hong Kong. The likely strategy would be to vaccinate with a less virulent, laboratory-adapted H5N1 strain isolated previously from birds. Little attention has been given, however, to dissecting the consequences of sequential exposure to serologically related influenza A viruses using contemporary immunology techniques. Such experiments with the H5N1 viruses are limited by the potential risk to humans. An extremely virulent H3N8 avian influenza A virus has been used to infect both immunoglobulin-expressing (Ig+/+) and Ig-/ mice primed previously with a laboratory-adapted H3N2 virus. The cross-reactive antibody response was very protective, while the recall of CD8(+) T-cell memory in the Ig-/ mice provided some small measure of resistance to a low-dose H3N8 challenge. The H3N8 virus also replicated in the respiratory tracts of the H3N2-primed Ig+/+ mice, generating secondary CD8(+) and CD4(+) T-cell responses that may contribute to recovery. The results indicate that the various components of immune memory operate together to provide optimal protection, and they support the idea that related viruses of nonhuman origin can be used as vaccines.
Descriptors: influenza prevention and control, influenza A virus avian immunology, influenza vaccine immunology, base sequence, birds, CD4 positive T lymphocytes immunology, CD8 positive T lymphocytes immunology, DNA, viral, disease models, animal, immunoglobulins immunology, influenza immunology, mice, mice inbred BALB c, mice, inbred c57bl, molecular sequence data.

Abstract: La produccion de pollo en areas en donde se ha observado la sero-conversion de aves centinelas para Influenza Aviar (I:A:) ha propiciado que los productores introduzcan pollos con anticuerpos maternos para esta enfermedad. La practica de vacunacion en el campo es comun hacerla al dia de edad en la incubadora, o bien entre los 8 y 12 dias en la granja. La existencia de otras enfermedades como la enfermedad de Newcastle (eNC) y la hepatitis con cuerpos de inclusion (HCI) que se previenen con vacunas oleosas inactivadas, causan que estas se incluyan en el mismo producto. El presente estudio tuvo como objetivo el evaluar en terminos de sero-conversion y proteccion al desafio de I.A. pollos sin anticuerpos y con anticuerpos para IA, vacunados al dia y a los 10 dias de edad, con productos que contienen el virus solo o combinados con eNC y eNC HCI. Los resultados indican que en aves sin anticuerpos, vacunadas al dia de edad, se logran porcentajes de proteccion al desafio de I.A. del 67 al 100% a los 14 dias post-vacunacion (PV). Que concentrar el virus de I.A. En un producto no reditua en una mejor proteccion. La aplicacion de vacunas a los 10 dias de edad en aves con anticuerpos maternos brindaron una mejor proteccion al desafio 7 dias PV que en pollos libres de anticuerpos. En todos los casos las aves sin anticuerpos vacunadas con cualquier producto, al dia de edad, mostraron una importante baja proteccion al desafio realizado 7 dias PV; lo anterior contrasta con la proteccion observada en pollos con anticuerpos maternos vacunados a los 10 dias de edad, los cuales mostraron el 73% de proteccion con vacuna sola y el 100% de proteccion con vacuna combinada con eNC. En este estudio, al igual que otros realizados, es importante senalar que los resultados serologicos no estuvieron relacionados con el indice de proteccion observado, ni tampoco con la eliminacion del virus de desafio, el cual en todos los casos causo morbibilidad y mortalidad en pollos susceptibles introducidos a la jaula 3 dias despues del desafio.

Descriptors: broiler chickens, avian influenza virus, vaccination, maternal immunity, birds, chickens, domestic animals, Galliformes, immunity, immunization, immunostimulation, immunotherapy, influenza virus, livestock, meat animals, orthomyxoviridae, passive immunity, poultry, therapy, useful animals, viruses.


NAL Call Number: QR189.V32

Abstract: Recently avian influenza A viruses of the H5N1 subtype were shown to infect humans in the Hong Kong area, resulting in the death of six people. Although these viruses did not efficiently spread amongst humans, these events illustrated that influenza viruses of subtypes not previously detected in humans could be at the basis of a new pandemic. In the light of this pandemic threat we evaluated and compared the efficacy of a classical non-adjuvanted subunit vaccine and a vaccine based on immune stimulating complexes (ISCOM) prepared with the membrane glycoproteins of the human influenza virus A/Hong Kong/156/97 (H5N1) to protect roosters against a lethal challenge with this virus. The ISCOM vaccine induced protective immunity against the challenge infection whereas the non-adjuvanted subunit vaccine proved to be poorly immunogenic and failed to induce protection in this model.

Descriptors: immune system, infection, pharmacology, lethal viral challenge pandemic protective immunity, induction.


NAL Call Number: QR189.V32

Abstract: Direct DNA inoculations have been used to demonstrate that in vivo transfections can be used to elicit protective immune responses. The direct inoculation of an H7 haemagglutinin-expressing DNA protected chickens against lethal challenge with an H7N7 influenza virus. Three-week-old chickens were
vaccinated by inoculating 100 micrograms of plasma DNA by each of three routes (intravenous, intraperitoneal and subcutaneous). One month later, chickens were boosted with 100 micrograms of DNA by each of the three routes. At 1-2 weeks postboost, chickens were challenged via the nares with 100 lethal doses of an H7N7 virus. Low to undetectable levels of H7-specific antibodies were present postvaccination and boost. High titres of H7-specific antibodies appeared within 1 week of challenge. In a series of four experiments, 50% (28/56) of the DNA-vaccinated and < 2% (1/67) of the control chickens survived the challenge. This exceptionally simple method of immunization holds high promise for the development of subunit vaccines.

Descriptors: DNA, viral genetics, defective viruses immunology, genetic vectors, hemagglutinin viral immunology, influenza prevention and control, influenza A virus avian immunology, influenza vaccine immunology, leukosis virus, avian genetics, plasmids, recombinant fusion proteins immunology, amantadine pharmacology, chickens immunology, defective viruses drug effects, defective viruses genetics, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral biosynthesis, hemagglutinins viral genetics, immunity, active, immunization, influenza A virus avian drug effects, influenza A virus avian genetics, recombinant fusion proteins biosynthesis, recombinant fusion proteins genetics, specific pathogen free organisms, transfection.

NAL Call Number: SF995.W4
Descriptors: avian influenza virus, vaccination, disease control, immunization, immunostimulation, immunotherapy, influenza virus, orthomyxoviridae, therapy, viruses.

NAL Call Number: SF995.W4
Descriptors: broiler chickens, avian influenza virus, birds, chickens, domestic animals, domesticated birds, Galliformes, influenza virus, livestock, meat animals, orthomyxoviridae, poultry, useful animals, viruses.

Abstract: Los laboratorios farmaceuticos, que han desarrollado productos derivados de la biotecnologia moderna, en la que se han manipulado genes de microorganismos, han empezado a solicitar el uso de esos productos tanto a nivel internacional como nacional. En Mexico una vez que se presentaron los brotes de Influenza Aviar (I.A.) de alta patogenicidad, se considero conveniente evaluar una vacuna recombinante, que fue construida mediante la insercion del DNA complementario, al gene que codifica para la hemoaglutinina 5 del virus de I.A., en el genoma del virus de viruela de las aves. Las ventajas que ofrece este producto es el que no utiliza el virus completo de I.A., y que por la serologia podrian diferenciarse pollos vacunados de infectados en el campo. El presente estudio se realizo en confinamiento, en unidades de aislamiento, teniendo como objetivo, evaluar la respuesta serologica y la proteccion al desafio de pollos vacunados al dia de edad con este producto, por 2 vias de administracion, subcutanea y en el pliegue del ala. La proteccion observada fue del 40-45% a los 7 dias post-vacunacion (PV) alcanzando el 95% a los 14 dias PV y llegando al 100% a los 21 dias PV por ambas rutas de administracion. Los resultados serologicos indican que mediante la prueba de inhibicion de la hemoaglutinacion, un limitado numero de pollos dieron una reaccion positiva, dando como resultado una inapreciable media geometrica. En todos los casos las aves vacunadas dieron una reaccion negativa en la prueba de precipitacion en agar. Los pollos vacunados
y desafiados mostraron una sero-conversion en el 100% de ellos, 7 días después del desafío. Las conclusiones de este trabajo indican que la vacuna recombinante administrada por cualquiera de estas vías en el pollo de un día de edad induce una adecuada protección al desafío, y que se pueden diferenciar pollos vacunados de pollos infectados experimentalmente.

**Descriptors:** broiler chickens, avian influenza virus, synthetic vaccines, immune response, birds, chickens, domestic animals, Galliformes, immunity, influenza virus, livestock, meat animals, orthomyxoviridae, poultry, useful animals, vaccines, viruses.


**Abstract:** Las vacunas inactivadas, oleosas de Influenza Aviar (IA), elaboradas por seis laboratorios, demostraron que previnieron la morbilidad y mortalidad, de aves vacunadas, causadas por el desafío, con una cepa de alta patogenicidad del virus de IA. Con el fin de complementar estos estudios se decidió realizar 2 experimentos adicionales, para determinar la adecuada inactivación del virus en el producto elaborado, demostrar que fueran seguras a la sobre-dosificación y que si al aplicar dosis menores a la recomendada protegieran a los pollos ante el desafío con cepas de alta patogenicidad del virus de IA. A siete grupos, de 5 pollos cada uno, de 2 semanas de edad, se les aplicaron 4 dosis de vacuna, por vía subcutanea, administrándola en 2 sitios diferentes. Las aves vacunadas de esta manera se observaron diariamente por un período de 21 días. El día de la vacunación se introdujeron en cada grupo 5 pollos susceptibles. Tanto a los pollos vacunados como a los pollos en contacto fueron sangrados para determinar los niveles de anticuerpos en el suero por pruebas de inhibiciónde la hemoaglutinacion y se desafiaron a los 21 días post-vacunacion. Por otro lado a grupos de 9 pollos por vacuna, se les aplico a 3 de ellos la dosis normal, a 3 pollos 0.05 ml de la vacuna y 0.005 del producto a los 3 pollos restantes. Al igual que en el otro estudio se determinaron los títulos de anticuerpos y la protección al desafio. Los resultados indicaron que los pollos puestos en contacto con las aves que fueron vacunadas con 4 dosis de cada producto no sero-convirtieron al virus de I:A, y fueron susceptibles al desafío con la cepa de alta patogenicidad. Variaciones en cuanto a la sero-conversion, fueron observadas dependiendo de la dosis utilizada para cada producto, así como una morbilidad y mortalidad variable a dosis de una decima o una centesima de la vacuna aplicada. Las vacunas probadas demostraron estar adecuadamente inactivadas y que no son capaces de causar trastornos en los pollos vacunados, inclusive hasta con 4 dosis. En este estudio se confirma que estas vacunas, utilizadas a la dosis indicada, confieren el 100% de protección al desafío; pero que dosis menores a la recomendada causaron morbilidad e inclusive mortalidad cuando a los pollos se les expuso a un virus altamente patogeno.

**Descriptors:** broiler chickens, avian influenza virus, vaccines, application rates, immune response, birds, chickens, domestic animals, Galliformes, immunity, influenza virus, livestock, meat animals, orthomyxoviridae, poultry, useful animals, viruses.


**Descriptors:** pharmacology, pathology, prevention, control, African horse sickness, Newcastle disease, bluetongue, contagious bovine pleuropneumonia, foot and mouth disease, goat pox, highly pathogenic avian influenza, lumpy skin disease, peste des petits ruminants, Rift Valley fever, rinderpest, sheep pox, swine fever, vesicular stomatitis, Office International des Epizooties, OIE, List A diseases, member countries, symposium.


**NAL Call Number:** QR360.A1J6

**Descriptors:** antibody formation, antigens, viral, fowl plague immunology, influenza A virus avian immunology, neuraminidase analysis, orthomyxoviridae immunology, chickens immunology, hemagglutination inhibition tests, hemagglutinins viral analysis, immune sera, immunization, influenza
NAL Call Number: 47.8 B77
Descriptors: avian influenza virus, low pathogenic H7N1, experimental challenge, model, protection.

NAL Call Number: 448.3 Ar23
Abstract: In order to develop a surrogate virus strain for production of an inactivated influenza vaccine against a human H9N2 virus, A/Hong Kong/1073/99 (HK1073: H9N2) was co-infected in embryonated chicken eggs with an apathogenic avian influenza virus, A/Duck/Czechoslovakia/56 (Dk/Cz: H4N6), for gene segment reassortment. Multiple-gene reassortants obtained were examined for replication in mammalian hosts in vitro and in vivo by infecting MDCK cells and by intranasal administration to hamsters, respectively. A 2-6 gene reassortant with both surface glycoproteins of HK1073 origin and the rest of Dk/Cz origin, HK/CZ-13, was shown to replicate poorly in the mammalian hosts both in vivo and in vitro comparing with HK1073, although this reassortant replicated as efficiently as each parental strain in embryonated eggs. No sequence difference was observed in the HA1 region between HK1073 and HK/CZ-13, indicating that the reassortant would be equivalent in its immunogenicity to the parental HK1073 strain when it is used as an inactivated vaccine. A virus strain with attenuation in mammalian hosts is preferable for production of an H9 vaccine, since it should reduce the risk of manufacturing-related infections of employees during the vaccine production. HK/CZ-13 can therefore be a surrogate strain for production of an inactivated vaccine as well as diagnostic antigens in case of a possible future pandemic caused by an HK1073-like H9 influenza virus.
Descriptors: influenza A virus, avian genetics, human genetics, influenza vaccines, reassortant viruses genetics, reassortant viruses physiology, administration, intranasal, cell line, chick embryo, DNA complementary chemistry, DNA complementary isolation and purification, hamsters, hemagglutinin glycoproteins, influenza virus immunology, avian pathogenicity, avian physiology, human pathogenicity, human physiology, mesocricetus, neuraminidase immunology, RNA, viral isolation and purification, viral metabolism, reassortant viruses immunology, reassortant viruses pathogenicity, reverse transcriptase polymerase chain reaction, sequence analysis, specific pathogen free organisms, vaccines, attenuated, virus replication.

Abstract: For the prediction of future influenza pandemics, global surveillance of avian influenza has been continuing since 1991 and carried out in Russia, Mongolia, China and Japan from 2000 to 2003. Influenza virus isolates of 50 combinations of HA and NA subtypes have been identified and 3 strains selected from each of those are stocked. In addition, 47 other combinations have been generated by standard genetic reassortment procedure in the laboratory. Since we have already shown that influenza viruses have been fully adapted to ducks and cause no disease signs and are in evolutionary stasis in their natural reservoirs, virus isolates from ducks are ideal as vaccine strains. Thus, influenza viruses of 97 combinations of HA and NA subtypes are now available as vaccine strain candidates against emerging pandemic influenza in humans, domestic animals and poultry.
Descriptors: global surveillance, vaccine, avian influenza virus, pandemic, prediction.

Descriptors: avian influenza virus, immunity, inactivated vaccines, turkeys.

**NAL Call Number:** 41.8 T445

**Descriptors:** avian influenza, strains, vaccines, immunology, ducks.


**Descriptors:** pharmacology, prevention, control, foot and mouth disease, Newcastle disease, avian influenza, Office International des Epizooties, OIE, World Trade Organization, WTO, international standards, international animal health code, List A diseases.


**NAL Call Number:** QR355.A5

**Descriptors:** antiviral agents, biperiden pharmacology, influenza A virus avian drug effects, human drug effects, piperidines pharmacology, amantadine pharmacology, cell line, chick embryo, drug interactions, drug resistance, microbial, genes viral drug effects, hemagglutination, viral drug effects, hemolysis drug effects, avian physiology, human growth and development, human physiology, interferon type I biosynthesis, interferons pharmacology, measles virus drug effects, mutation, virus replication drug effects.


**NAL Call Number:** 448.8 J821

**Abstract:** The infectivity, immunogenicity, and efficacy of live, attenuated influenza A/Texas/1/85 (H1N1) and A/Bethesda/1/85 (H3N2) avian-human (ah) and cold-adapted (ca) reassortant vaccines were compared in 252 seronegative adult volunteers. The immunogenicity and efficacy of the H1N1 reassortant vaccine were also compared with those of the trivalent inactivated virus vaccine. Each reassortant vaccine was satisfactorily attenuated. The 50% human infectious dose was 10(4.9) for ca H1N1, 10(5.4) for ah H1N1, 10(6.4) for ca H3N2, and 10(6.5) TCID50 for ah H3N2 reassortant virus. Within a subtype, the immunogenicities of ah and ca vaccines were comparable. Five to seven weeks after vaccination, volunteers were challenged with homologous wild-type influenza A virus. The magnitude of shedding of virus after challenge was greater than 100-fold less in H1N1 vaccinees and greater than 10-fold less in H3N2 vaccinees compared with unimmunized controls. The vaccines were equally efficacious, as indicated by an 86%-100% reduction in illness. Thus, the ah A/Mallard/New York/6750/78 and the ca A/Ann Arbor/6/60 reassortant viruses are comparable.

**Descriptors:** influenza prevention and control, influenza A virus avian immunology, human immunology, influenza vaccine, adult, antibodies, viral biosynthesis, cold, double blind method, enzyme linked immunosorbent assay, hemagglutination inhibition tests, avian pathogenicity, avian physiology, human pathogenicity, human physiology, random allocation, vaccines, attenuated, vaccines, synthetic, virus replication.


**NAL Call Number:** 41.8 Av5

**Abstract:** Eight-week-old chickens were inoculated with one of two exotic viruses to determine the effect of composting on virus survival. Group 1 chickens were inoculated with highly pathogenic avian influenza (HPAI) virus via the caudal thoracic air sac. Group 2 chickens were inoculated with the adenovirus that causes egg drop syndrome-76 (EDS-76) by the oral route. Five days after inoculation, lung, trachea, and air sacs for HPAI and spleen, cecal tonsils, and bursa of Fabricius for EDS-76 were collected and composted.
with poultry carcasses. At the end of the first 10 days of composting, virus-isolation efforts showed that the HPAI virus had been inactivated, and only 1 of 20 tissue samples yielded the adenovirus of EDS-76. The viruses of HPAI and EDS-76 were completely inactivated at the end of the second 10-day period of the two-stage composting process. Control tissues collected at necropsy and frozen at -70°C for virus isolation were all positive for virus.

Descriptors: chickens, avian influenza virus, aviadenovirus, survival, animal diseases, carcasses, waste disposal, composting, disease control, adenoviridae, birds, domestic animals, domesticated birds, environmental protection, Galliformes, influenza virus, livestock, orthomyxoviridae, pollution control, poultry, processing, useful animals, viruses, waste management, two stage composting, inactivation.


NAL Call Number: QR360.J6

Abstract: In 1997, avian H5N1 influenza virus transmitted from chickens to humans resulted in 18 confirmed infections. Despite harboring lethal H5N1 influenza viruses, most chickens in the Hong Kong poultry markets showed no disease signs. At this time, H9N2 influenza viruses were co-circulating in the markets. We investigated the role of H9N2 influenza viruses in protecting chickens from lethal H5N1 influenza virus infections. Sera from chickens infected with an H9N2 influenza virus did not cross-react with an H5N1 influenza virus in neutralization or hemagglutination inhibition assays. Most chickens primed with an H9N2 influenza virus 3 to 70 days earlier survived the lethal challenge of an H5N1 influenza virus, but infected birds shed H5N1 influenza virus in their feces. Adoptive transfer of T lymphocytes or CD8+ T cells from inbred chickens (B(2)/B(2)) infected with an H9N2 influenza virus to naive inbred chickens (B(2)/B(2)) protected them from lethal H5N1 influenza virus. In vitro cytotoxicity assays showed that T lymphocytes or CD8+ T cells from chickens infected with an H9N2 influenza virus recognized target cells infected with either an H5N1 or H9N2 influenza virus in a dose-dependent manner. Our findings indicate that cross-reactive cellular immunity induced by H9N2 influenza viruses protected chickens from lethal infection with H5N1 influenza viruses in the Hong Kong markets in 1997 but permitted virus shedding in the feces. Our findings are the first to suggest that cross-reactive cellular immunity can change the outcome of avian influenza virus infection in birds in live markets and create a situation for the perpetuation of H5N1 influenza viruses.

Descriptors: chickens, fowl plague immunology, fowl plague virology, influenza A virus avian immunology, T lymphocytes, cytotoxic immunology, adoptive transfer, cross reactions, fowl plague prevention and control, hemagglutination inhibition tests, Hong Kong, immunity, cellular, immunization, avian classification, avian pathogenicity.


NAL Call Number: QH301.Z4

Abstract: Sixty products, derived from marine organisms, typical of the Bulgarian Black Sea coast, were examined for inhibitory activity on the reproduction of influenza viruses in tissue cultures. The antiviral effect was investigated by the reduction of virus infectivity. Using representative strains of influenza virus it was shown that apparently the inhibitory effect was strain-specific. The most effective products were further studied in fertile hen’s eggs and in experimental influenza infection in white mice.

Descriptors: algae chemistry, antiviral agents pharmacology, influenza drug therapy, influenza A virus avian drug effects, human drug effects, plant extracts pharmacology, tissue extracts pharmacology, antiviral agents isolation and purification, chick embryo, hemagglutination inhibition tests, invertebrates, mice, seawater, species specificity.


NAL Call Number: 49 J822
NAL Call Number: 41.8 V641
Descriptors: avulavirus isolation and purification, bird diseases prevention and control, fowl plague prevention and control, influenza A virus avian isolation and purification, rubulavirus infections veterinary, avulavirus pathogenicity, birds, feces microbiology, avian pathogenicity, quarantine, rubulavirus infections prevention and control.

NAL Call Number: 448.3 AC85
Descriptors: antibodies, viral immunology, ducks immunology, influenza A virus avian immunology, epidemiologic methods, fowl plague epidemiology.

NAL Call Number: SF995.W4
Descriptors: avian influenza virus, vaccines.

Descriptors: avian influenza virus, epidemiology, excretion routes, transmission, secretions.

NAL Call Number: QR46.J6
Abstract: An avian-human reassortant influenza A virus deriving its genes coding for the hemagglutinin and neuraminidase from the human influenza A/Washington/897/80 (H3N2) virus and its six "internal" genes from the avian influenza A/Mallard/NY/6750/78 (H2N2) virus (i.e., a six-gene reassortant) was previously shown to be safe, infectious, nontransmissible, and immunogenic as a live virus vaccine in adult humans. Two additional six-gene avian-human reassortant influenza viruses derived from the mating of wild-type human influenza A/California/10/78 (H1N1) and A/Korea/1/82 (H3N2) viruses with the avian influenza A/Mallard/NY/78 virus were evaluated in seronegative (hemagglutination inhibition titer, less than or equal to 1:8) adult volunteers for safety, infectivity, and immunogenicity to determine whether human influenza A viruses can be reproducibly attenuated by the transfer of the six internal genes of the avian influenza A/Mallard/NY/78 virus. The 50% human infectious dose was 10(4.9) 50% tissue culture infectious doses for the H1N1 reassortant virus and 10(5.4) 50% tissue culture infectious doses for the H3N2 reassortant virus. Both reassortants were satisfactorily attenuated with only 5% (H1N1) and 2% (H3N2) of infected vaccines receiving less than 400 50% human infectious doses developing illness. Consistent with this level of attenuation, the magnitude of viral shedding after inoculation was reduced 100-fold (H1N1) to 10,000-fold
(H3N2) compared with that produced by wild-type virus. The duration of virus shedding by vaccines was one-third that of controls receiving wild-type virus. At 40 to 100 50% human infectious doses, virus-specific immune responses were seen in 77 to 93% of volunteers. When vaccinees who has received 10(7.5) 50% tissue culture infectious doses of the H3N2 vaccine were experimentally challenged with a homologous wild-type human virus only 2 of 19 (11%) vaccinees became ill compared with 7 of 14 (50%) unvaccinated seronegative controls ( \( P < 0.025 \); protective efficacy, 79%). Thus, three different virulent human influenza A viruses have been satisfactorily attenuated by the acquisition of the six internal genes of the avian influenza A/Mallard/NY/78 virus. The observation that this donor virus can reproducibly attenuate human influenza A viruses indicates that avian-human influenza A reassortants should be further studied as potential live influenza A virus vaccines.

Descriptors: hemagglutinins viral immunology, influenza A virus avian immunology, human immunology, neuraminidase immunology, viral vaccines immunology, adult, antibodies, viral biosynthesis, avian growth and development, human growth and development, virus replication.


Abstract: A reverse genetics approach provides a new mutant strain where a modified cleavage site within its hemagglutinin depends on proteolytic activation strictly by elastase. The new strain grows well in cell culture and is entirely attenuated to mice. It induced complete protection against a lethal challenge at a dose of \( 10^5 \) plaque-forming units. This provides an approach that allows conversion of any epidemic strain into a genetically homologous attenuated virus.

Descriptors: mutant strain A, WSN, 33, elastase, cell culture, attenuated virus, strain conversion


NAL Call Number: 448.8 J821

Abstract: Characteristics of avian-human (ah) and cold-adapted (ca) influenza A/Kawasaki/9/86 (H1N1) reassortant vaccine viruses were compared in 37 seronegative adults and 122 seronegative infants and children. The 50% human infectious dose (HID50) in infants and children was 10(2.9) and 10(2.6) TCID50 for the ah and ca vaccine, respectively. The ah influenza A/Kawasaki/9/86 reassortant was reactogenic: 24% of infants and children infected with greater than or equal to 100 HID50 had fever greater than or equal to 39.4 degrees C. Since H3N2 ah vaccines were previously shown to be adequately attenuated, it is reasonable to suggest that the genes that code for hemagglutinin and neuraminidase of the H1N1 virus apparently influence the reactogenicity of reassortant viruses derived from the avian influenza A/Mallard/New York/6750/78 donor virus. Because this avian virus does not reproducibly confer a satisfactory level of attenuation to each subtype of influenza A virus, it is not a suitable donor virus for attenuation of wild-type influenza viruses. In contrast, the ca A/Ann Arbor/6/60 donor virus reliably confers attenuation characteristics to a variety of H1N1 and H3N2 influenza A viruses.

Descriptors: influenza prevention and control, influenza A virus avian immunology, human immunology, influenza vaccine adverse effects, adult, child, preschool, infant, influenza etiology, avian pathogenicity, human pathogenicity, vaccines, attenuated adverse effects, vaccines, synthetic adverse effects, virulence.


NAL Call Number: 448.8 J821

Abstract: Antigenically well-matched vaccines against highly pathogenic avian influenza H5N1 viruses are urgently required. Human serum samples after immunization with MF59 or nonadjuvanted A/duck/Singapore/97 (H5N3) vaccine were tested for antibody to 1997-2004 human H5N1 viruses. Antibody responses to 3 doses of nonadjuvanted vaccine were poor and were higher after MF59-adjuvanted vaccine,
with seroconversion rates to A/HongKong/156/97, A/HongKong/213/03, A/Thailand/16/04, and A/Vietnam/1203/04 of 100% (P<.0001), 100% (P<.0001), 71% (P=.0004), and 43% (P=.0128) in 14 subjects, respectively, compared with 27%, 27%, 0%, and 0% in 11 who received nonadjuvanted vaccine. These findings have implications for the rational design of pandemic vaccines against influenza H5.

Descriptors: adjuvants immunologic, cross-reactions immunology, influenza vaccines immunology, avian influenza immunology, avian influenza virology, orthomyxoviridae classification, orthomyxoviridae immunology, immunosorbsorbent assay, Hong Kong epidemiology, influenza vaccines administration and dosage, influenza vaccines supply and and distribution, avian influenza epidemiology, avian influenza prevention and control, middle-aged, neutralization tests, orthomyxoviridae genetics, orthomyxoviridae pathogenicity, Singapore epidemiology, Thailand epidemiology, vaccination, Vietnam epidemiology.


Abstract: Sporadic human infection with avian influenza viruses has raised concern that reassortment between human and avian subtypes could generate viruses of pandemic potential. Vaccination is the principal means to combat the impact of influenza. During an influenza pandemic the immune status of the population would differ from that which exists during interpandemic periods. An emerging pandemic virus will create a surge in worldwide vaccine demand and new approaches in immunisation strategies may be needed to ensure optimum protection of unprimed individuals when vaccine antigen may be limited. The manufacture of vaccines from pathogenic avian influenza viruses by traditional methods is not feasible for safety reasons as well as technical issues. Strategies adopted to overcome these issues include the use of reverse genetic systems to generate reassortant strains, the use of baculovirus-expressed haemagglutinin or related non-pathogenic avian influenza strains, and the use of adjuvants to enhance immunogenicity. In clinical trials, conventional surface-antigen influenza virus vaccines produced from avian viruses have proved poorly immunogenic in immunologically naive populations. Adjuvanted or whole-virus preparations may improve immunogenicity and allow sparing of antigen.


NAL Call Number: QR375.V6

Abstract: Haemagglutination-inhibition (HI) tests are a simple method used to assess immune responses to influenza haemagglutinin. However, HI tests are insensitive at detection of antibody responses to avian haemagglutinin after vaccination or natural infection, even in the presence of high titres of neutralising antibody or virus isolation. Avian influenza viruses preferentially bind to sialic acid receptors that contain N-acetylneuraminic acid alpha2,3-galactose (alpha2,3Gal) linkages while human viruses preferentially bind to those containing N-acetylneuraminic acid alpha2,6-galactose (alpha2,6Gal) linkages. By using horse erythrocytes in the HI test and thereby increasing the proportion of alpha2,3Gal linkages available for binding, we are able to demonstrate improved detection of antibody to avian H5 in human sera following vaccination with MF59-adjuvanted A/Duck/Singapore/97 surface antigen vaccine. This modified HI test was more sensitive in detection of anti-H5 antibody evoked by revaccination of primed subjects and may be useful in assessing potential avian HA vaccine candidates.

Descriptors: antibodies, viral blood, erythrocytes, hemagglutinin glycoproteins, influenza virus immunology, horses, influenza A virus, avian immunology, influenza vaccines immunology, squalene immunology, adjuvants, immunologic, hemagglutination inhibition tests methods, influenza vaccines administration and dosage, polysorbates administration and dosage, receptors, virus metabolism, squalene administration and dosage, turkeys.
NAL Call Number: 448.8 L22
Descriptors: clinical immunology, humans, infection, vaccination, clinical techniques, immune response.

NAL Call Number: 470 Sci2
Descriptors: disease outbreaks, influenza epidemiology, influenza prevention and control, influenza vaccines supply and distribution, clinical trials, drug industry, influenza virology, influenza A virus, avian immunology, avian pathogenicity, human immunology, influenza vaccines administration and dosage, influenza vaccines economics, international cooperation, population surveillance, public policy, World Health Organization.

NAL Call Number: 41.8 Av5
Abstract: Inactivated oil-emulsion (OE) Newcastle disease (ND) and avian influenza (AI) vaccines were injected into 18-day-old white rock (WR) and white leghorn (WL) chicken embryos to evaluate their immunologic efficacy and their effects on hatchability. Embryonating eggs were inoculated at 1.5 inches depth with various vaccine volumes and antigen concentrations. Serum hemagglutination-inhibition (HI) titers were first detected in chickens at 2 wk posthatch. Protection against morbidity and mortality was demonstrated in all of 10 chickens vaccinated as embryos and challenged with viscerotropic velogenic ND virus at 53 days of age and also in all of eight in ovo- vaccinated chickens challenged with highly pathogenic AI virus at 34 days of age. All of five unvaccinated control chickens for each respective ND- and AI- vaccinated group died. In pooled groups from successive hatches, the hatchability of WR or WL embryos injected with 100 microliters of vaccine was not significantly different (P > 0.05) from unvaccinated hatchmate controls when needle gauges of 22, 20, and 18 were used. Seroconversion rates of chickens vaccinated as embryos ranged from 27% to 100% with ND vaccination and 85% to 100% for AI vaccination. For ND, geometric mean HI titers of chickens per vaccine group ranged from 11 to 733, and in pooled groups, the range was 49 to 531. Titers for AI vaccine groups ranged from 156 to 1178. This study demonstrated that acceptable hatchability, seroconversion rates, and protective immunity can be attained with in ovo inoculation of ND or AI OE vaccines if the vaccines are prepared with sufficient antigen and administered properly.
Descriptors: chicks, vaccination, Newcastle disease virus, avian influenza virus, viroses, vaccines, evaluation, egg hatchability, dosage, antigens, morbidity, mortality, pathogenicity, application methods, equipment, immune response, immunity, formulations, needle gauges, efficacy, seroconversion.

NAL Call Number: 41.8 Av5
Abstract: An experimental avian influenza (AI) oil-emulsion vaccine was formulated with 1 part inactivated A/turkey/Wisconsin/68 (H5N9) AI virus emulsified in 4 parts oil. Broilers were vaccinated subcutaneously (SC) either at 1 or 3 days old or at 4 or 5 wks old. Commercial white leghorn (WL) layers were vaccinated SC at 12 and 20 wks old or at only 20 wks old. Maximum geometric mean hemagglutination-inhibition titers postvaccination (PV) were 1:86-1:320 for broilers, 1:597 for twice-vaccinated layers, and 1:422 for once-vaccinated layers. Ninety to 100% of vaccinated broilers were protected against death and morbidity when challenged with highly pathogenic A/chicken/Penn/83 (H5N2) AI virus 4 weeks PV, and all were protected when challenged 8 wks PV. All controls and most vaccinates were infected by challenge virus, and 90-100% of controls died or exhibited clinical signs. Vaccinated commercial pullets were protected against morbidity, death, and egg-production decline at either peak of lay (25 wks old) or at 55 wks old. All unvaccinated
controls became morbid or died, and egg production ceased 72 hours after challenge. The 0.5-ml vaccine dose was determined to contain 251 and 528 mean protective doses (PD50s) in 4-wk-old and 1-year-old SPF WL chickens, respectively, challenged 4 wks PV.

Descriptors: chickens, fowl plague prevention and control, influenza A virus avian immunology, vaccination veterinary, viral vaccines, specific pathogen free organisms.

NAL Call Number: 41.8 Av5
Abstract: Acceptable oil-emulsion vaccines were sought to replace mineral oil-emulsion vaccines that, by regulations, require a 42-day minimum holding period for poultry between injection and slaughter for consumption. Water-in-oil emulsions were prepared using animal or vegetable oils in a ratio of 4 parts oil to 1 part Newcastle disease or avian influenza aqueous antigen. Beeswax particles suspended in the oil at the 5% or 10% level (wt:vol) served as the oil-phase surfactant. Hemagglutination-inhibition titers induced by mineral-oil vaccines were not significantly different from those induced by the most efficacious formulations prepared from animal and vegetable oils. Tissue reaction from injection of animal- and vegetable-oil vaccines was less than that induced by mineral-oil vaccines. An inactivated avian influenza vaccine formulated from peanut oil induced protection against morbidity and death when vaccinated chickens were challenged with a virulent isolate of avian influenza virus.
Descriptors: chickens, vaccines, plant oils, animal oils, emulsions, vaccination, Newcastle disease, avian influenza virus, animal tissues, side effects, animal morphology, birds, disease control, domestic animals, domesticated birds, Galliformes, immunization, immunostimulation, immunotherapy, infectious diseases, influenza virus, livestock, oils, physical states, poultry, processed plant products, processed products, therapy, toxicity, useful animals, viroses, viruses, adverse effects.

NAL Call Number: 41.8 Av5
Abstract: Preparations of inactivated Newcastle disease (ND) and avian influenza (AI) oil-emulsion vaccines with surfactant hydrophile-lipophile-balance (HLB) values between 4.3 and 9.5 were evaluated for their efficacy in broiler-type white rock chickens. Chickens were vaccinated at 3-4 weeks of age and bled at 2-week intervals over 8 weeks. Post-vaccinal hemagglutination-inhibition (HI) geometric mean titers (reciprocals) ranged from 197 to 485 for ND vaccines and from 184 to 1040 for AI vaccines. Based on the HI response, an HLB value of 7.0 induced the greatest stimulation of antibody titers. Ten percent surfactant in the oil phase of the vaccines induced maximum titers at this HLB. The oil:aqueous ratios of the vaccines did not greatly influence the overall serologic response when the vaccines had an HLB of 7.0. These results indicate that manipulating surfactant HLB values of OE vaccine may maximize the HI response in broilers.
Descriptors: chickens immunology, fowl plague prevention and control, Newcastle disease prevention and control, surface active agents, viral vaccines therapeutic use, hemagglutination inhibition tests veterinary, poultry.

NAL Call Number: 41.8 Av5
Abstract: The influence of the composition of water-in-oil emulsions on their physical characteristics was determined by preparing experimental emulsions with various water-to-oil ratios and various emulsifiers. Emulsions containing Tween 80 in the aqueous phase and Arlacel A or Arlacel 80 in the oil phase were lower in viscosity than emulsions containing only an oil-phase emulsifier. Viscosity decreased as the concentration of oil increased. Oil-emulsion vaccines prepared with aqueous- and oil-phase emulsifiers had low viscosity, were stable for more than 12 weeks at 37 C, and induced a marked primary antibody response in chickens.
Descriptors: bacterial vaccines administration and dosage, Mycoplasma immunology, RNA viruses immunology, viral vaccines administration and dosage, antibody formation, chickens immunology,
emulsions, infectious bronchitis virus immunology, influenza A virus avian immunology, methods, mineral oil, Newcastle disease virus immunology, viscosity.

NAL Call Number: SF481.M54
Descriptors: immunization, vaccines, avian influenza virus, disease control, poultry, disease prevention.

NAL Call Number: QR180.D4
Abstract: Avian influenza virus can cause serious disease in a wide variety of birds and mammals, but its natural host range is in wild ducks, gulls, and shorebirds. Infections in poultry can be inapparent or cause respiratory disease, decreases in production, or a rapidly fatal systemic disease known as highly pathogenic avian influenza (HPAI). For the protection of poultry, neutralizing antibody to the hemagglutinin and neuraminidase proteins provide the primary protection against disease. A variety of vaccines elicit neutralizing antibody, including killed whole virus vaccines and fowl-pox recombinant vaccines. Antigenic drift of influenza viruses appears to be less important in causing vaccine failures in poultry as compared to humans. The cytotoxic T lymphocyte response can reduce viral shedding in mildly pathogenic avian influenza viruses, but provides questionable protection against HPAI. Influenza viruses can directly affect the immune response of infected birds, and the role of the Mx gene, interferons, and other cytokines in protection from disease remains unknown.
Descriptors: immune system, infection, highly pathogenic avian influenza, viral disease, avian influenza virus vaccination immunization method, antigenic drift cellular immunity.

NAL Call Number: 41.8 Av5
Abstract: Vaccination of poultry with naked plasmid DNA has been successfully demonstrated with several different poultry pathogens, but the technology needs to be further developed before it can be practically implemented. Many different methods can conceivably enhance the efficacy of DNA vaccines, and this report examines the use of different eukaryotic expression vectors with different promoters and different adjuvants to express the influenza hemagglutinin protein. Four different promoters in five different plasmids were used to express the hemagglutinin protein of an H5 avian influenza virus, including two different immediate early cytomegaloviruses (CMVs), Rous sarcoma virus, chicken actin, and simian virus 40 promoters. All five constructs expressed detectable hemagglutinin protein in cell culture, but the pCI-neo HA plasmid with the CMV promoter provided the best response in chickens when vaccinated intramuscularly at 1 day of age on the basis of antibody titer and survivability after challenge with a highly pathogenic avian influenza virus at 6 wk postinoculation. A beneficial response was observed in birds boostered at 3 wk of age, in birds given larger amounts of DNA, and with the use of multiple injection sites to administer the vaccine. With the use of the pCI-neo construct, the effects of different adjuvants designed to increase the uptake of plasmid DNA, including 25% sucrose, diethylaminoethyl dextran, calcium phosphate, polybrene, and two different cationic liposomes, were examined. Both liposomes tested enhanced antibody titers as compared with the positive controls, but the other chemical adjuvants decreased the antibody response as compared with the control chickens that received just the plasmid alone. The results observed are promising for continued studies, but continued improvements in vaccine response and reduced costs are necessary before the technology can be commercially developed.
Descriptors: molecular genetics, immune system, influenza, respiratory system disease, viral disease, avian influenza model physical model, vaccination preventative method, antibody response, eukaryotic expression, vectors.

Abstract: Avian influenza A H5N1 viruses similar to those that infected humans in Hong Kong in 1997 continue to circulate in waterfowl and have reemerged in poultry in the region, raising concerns that these viruses could reappear in humans. The currently licensed trivalent inactivated influenza vaccines contain hemagglutinin (HA) and neuraminidase genes from epidemic strains in a background of internal genes derived from the vaccine donor strain, A/Puerto Rico/8/34 (PR8). Such reassortant candidate vaccine viruses are currently not licensed for the prevention of human infections by H5N1 influenza viruses. A transfectant H5N1/PR8 virus was generated by plasmid-based reverse genetics. The removal of the multibasic amino acid motif in the HA gene associated with high pathogenicity in chickens, and the new genotype of the H5N1/PR8 transfectant virus, attenuated the virus for chickens and mice without altering the antigenicity of the HA. A Formalin-inactivated vaccine prepared from this virus was immunogenic and protected mice from subsequent wild-type H5N1 virus challenge. This is the first successful attempt to develop an H5N1 vaccine seed virus resembling those used in currently licensed influenza A vaccines with properties that make it a promising candidate for further evaluation in humans.

Descriptors: infection, molecular genetics, pharmacology, influenza A virus infection, viral disease, plasmid based reverse genetics genetic techniques, laboratory techniques.


Abstract: Vaccines have played an important role in the control of diseases of livestock and poultry, including Transboundary Diseases. In the future, vaccines will play a greater role in controlling these diseases. Historically, inactivated whole viruses in various adjuvant systems have been used and will continue to be used in the near future. For the future, emerging technologies will allow targeted use of only the protective antigens of the pathogen and will provide the opportunity for differentiating between vaccinated and field-exposed animals. Furthermore, the expression of cytokines by vaccines will afford earlier or greater enhancement of protection than can be achieved by the protective response elicited by the antigenic epitopes of the pathogen alone. Avian influenza (AI) is a good case for studying future trends in vaccine design and use. Inactivated AI virus (AIV) vaccines will continue as the primary vaccines used over the next 10 years. These vaccines will use homologous haemagglutinin sub-types, either from the use of field strains or the generation of new strains through the use of infectious clones produced in the laboratory. The latter will allow creation of high growth reassortants, which will provide consistent high yields of antigen and result in potent vaccines. New viral and bacterial vectors with inserts of AIV haemagglutinin gene will be developed and potentially used in the field. Such new vectors will include herpesvirus-turkey, infectious laryngotraechitis virus, adenoviruses, various types of paramyxoviruses and Salmonella sp. In addition, there is a theoretical possibility of gene-deleted mutants that would allow the use of live AIV vaccines, but the application of such vaccines has inherent dangers for gene reassortment with field viruses in the generation of disease-causing strains. Subunit haemagglutinin protein and DNA haemagglutinin gene vaccines are possible, but with current technologies, the cost is prohibitive. In the future, effective AI vaccines must prevent clinical signs and death, increase resistance of the host to infection, decrease the rate of replication and shedding of a challenge or field virus and provide uniform protection following single immunization. Mass application technologies of new virus or bacterial vector systems will provide economic incentives for adoption over current labour-intensive manual individual bird injection methods used with today's AI vaccines.

Descriptors: animals, biotechnology, communicable disease control methods, avian influenza A virus genetics, avian influenza A virus immunology, avian influenza A virus pathogenicity, influenza vaccines genetics, influenza vaccines immunology, avian influenza immunology, avian influenza prevention and control, poultry, vaccination methods, vaccination standards, veterinary vaccination, inactivated vaccines genetics, inactivated vaccines immunology, viral vaccines.


NAL Call Number: 449.9 Un3r

Descriptors: poultry, recombinant vaccines, avian influenza virus, chickens, highly pathogenic, Mexican

**NAL Call Number:** QR180.3.D4 v. 114

**Descriptors:** disease prevention, disease resistance, DNA vaccines, hemagglutinins, immune response, immunization, Newcastle disease, poultry, recombinant vaccines, avian influenza virus, turkeys.


**NAL Call Number:** SF995.A1A9

**Abstract:** The influence of vaccine strain and antigen mass on the ability of inactivated avian influenza (AI) viruses to protect chicks from a lethal, highly pathogenic (HP) AI virus challenge was studied. Groups of 4-week-old chickens were immunized with inactivated vaccines containing one of 10 haemagglutinin subtype H5 AI viruses, one heterologous H7 AI virus or normal allantoic fluid (sham), and challenged 3 weeks later by intra-nasal inoculation with a HP H5 chicken-origin AI virus. All 10 H5 vaccines provided good protection from clinical signs and death, and produced positive serological reactions on agar gel immunodiffusion and haemagglutination inhibition tests. In experiment 1, challenge virus was recovered from the oropharynx of 80% of chickens in the H5 vaccine group. In five H5 vaccine groups, challenge virus was not recovered from the cloaca of chickens. In the other five H5 vaccine groups, the number of chickens with detection of challenge virus from the cloaca was lower than in the sham group (P < 0.05). Reductions in the quantity of challenge virus shed from the cloaca and oropharynx were also evident in some H5 vaccinate groups when compared to the sham group. However, there was no positive correlation between the sequence identity of the haemagglutinin gene from the vaccine strain and challenge virus, and the ability to reduce the quantity of challenge virus shed from the cloaca or oropharynx. As the quantity of AI antigen in the vaccines increased, all parameters of protection improved and were virus strain dependent. A/turkey/Wisconsin/68 (H5N9) was the best vaccine candidate of the H5 strains tested (PD50 = 0.006 mug AI antigen). These data demonstrate that chickens vaccinated with inactivated H5 whole virus AI vaccines were protected from clinical signs and death, but usage of vaccine generally did not prevent infection by the challenge virus, as indicated by recovery of virus from the oropharynx. Vaccine use reduced cloacal detection rates, and quantity of virus shed from the cloaca and oropharynx in some vaccine groups, which would potentially reduce environmental contamination and disease transmission in the field.

**Descriptors:** immune system, infection, veterinary medicine, avian influenza, prevention, viral disease, H5 avian influenza inactivated vaccine, antigen mass influence, efficacy, virus strain influence.


**NAL Call Number:** 41.8 Av5

**Abstract:** Vaccines against mildly pathogenic avian influenza (AI) have been used in turkeys within the United States as part of a comprehensive control strategy. Recently, AI vaccines have been used in control programs against highly pathogenic (HP) AI of chickens in Pakistan and Mexico. A recombinant fowl pox-AI hemagglutinin subtype (H) 5 gene insert vaccine has been shown to protect specific-pathogen-free chickens from HP H5 AI virus (AIV) challenge and has been licensed by the USDA for emergency use. The ability of the recombinant fowl pox vaccine to protect chickens preimmunized against fowl pox is unknown. In the current study, broiler breeders (BB) and white leghorn (WL) pullets vaccinated with a control fowl poxvirus vaccine (FP-C) and/or a recombinant fowl poxvirus vaccine containing an H5 hemagglutinin gene insert (FP-HA) were challenged with a HP H5N2 AIV isolated from chickens in Mexico. When used alone, the FP-HA vaccine protected BB and WL chickens from lethal challenge, but when given as a secondary vaccine after a primary FP-C immunization, protection against a HP AIV challenge was inconsistent. Both vaccines protected against virulent fowl pox challenge. This lack of consistent protection against HPAl may limit use to chickens without previous fowl pox vaccinations. In addition, prior exposure to field fowl poxvirus could be expected to limit protection induced by this vaccine.

**Descriptors:** chickens, fowl pox virus, recombinant vaccines, genes, vaccination, efficacy, pathogenicity,

**NAL Call Number:** 41.8 Av5

**Abstract:** Internationally and nationally, governments and the poultry industries have used various strategies to control avian influenza (AI), ranging from a minimum of living with mildly pathogenic AI virus (AIV) infections to the other extreme of implementing a total quarantine-slaughter approach for eradication of highly pathogenic (HP) forms of the disease. However, recent economic considerations in various countries have prompted a broader reevaluation of vaccination as one of several tools to be used in AI control programs, including H5 and H7 HP AI. In the current study, 1-day-old chickens were immunized with a recombinant fowl poxvirus vaccine containing a hemagglutinin gene insert (Vector-HA) from an H5 AIV. Vertor-HA- and negative control (vector-control)-vaccinated chicks were challenged with a HP H5N2 AIV isolated from chickens in Mexico. All immunized chickens were antibody negative on the agar gel precipitin test, indicating that vaccination would not interfere with routine AI serologic surveillance programs in the United States. However, in the hemagglutinin-inhibition test, a few immunized chickens (8%) had low serologic titers. Protection against illness (90-100%) and death (90-100%) was provided by the vector-HA vaccine from 3 wk of age to the end of the 20-wk study. The number of chickens shedding the challenge AIV from their enteric tracts was significantly reduced (50-75%) and the quantity of challenge AIV shed from respiratory and enteric tracts was significantly reduced (10(1)-10(2.1) mean embryo lethal dose/ml) in most vector-HA vaccine groups when compared with vector-control groups. Furthermore, vector-HA vaccination reduced in contact transmission of HP AI challenge virus to both vector-HA- and vector-control-vaccinated chickens. These findings indicate the recombinant fowl poxvirus vaccine can be a useful tool in an AI control program by preventing illness and death in chickens and reducing intestinal and respiratory shedding of H5 AIV.

**Descriptors:** chickens, avipoxvirus, avian influenza virus, pathogenicity, biological differences, synthetic vaccines, disease control, antibodies, experimental infection, in vivo experimentation, morbidity, mortality, digestive system, vaccination, dosage, injection, wings, application methods, biological properties, birds, body parts, body regions, disease transmission, domestic animals, epidemiology, experimentation, Galliformes, immunization, immunological factors, immunostimulation, immunotherapy, infection, influenza virus, limbs, livestock, microbial properties, orthomyxoviridae, pathogenesis, poultry, poxviridae, therapy, useful animals, vaccines, viruses, fowl pox virus, strain differences, recombinant vaccines, subcutaneous injection.

Protection against diverse highly pathogenic H5 avian influenza viruses in chickens immunized with a recombinant fowlpox vaccine containing an H5 avian influenza hemagglutinin gene insert. *Vaccine* 18(11-12): 1088-95. ISSN: 0264-410X.

**NAL Call Number:** QR189.V32

**Abstract:** A recombinant fowlpox vaccine with an H5 hemagglutinin gene insert protected chickens against clinical signs and death following challenge by nine different highly pathogenic H5 avian influenza viruses. The challenge viruses had 87.3 to 100% deduced hemagglutinin amino acid sequence similarity with the recombinant vaccine, and represented diversely geographic and spatial backgrounds; i.e. isolated from four different continents over a 38 year period. The recombinant vaccine reduced detectable infection rates and shedding titers by some challenge viruses. There was a significant positive correlation in hemagglutinin sequence similarity between challenge viruses and vaccine, and the ability to reduce titers of challenge virus isolated from the oropharynx (r(s)=0.783, P=0.009), but there was no similar correlation for reducing cloacal virus titers (r(s)=-0.100, P=0.78). This recombinant fowlpox-H5 avian influenza hemagglutinin vaccine can provide protection against a variety of different highly pathogenic H5 avian influenza viruses and frequent optimizing of the hemagglutinin insert to overcome genetic drift in the vaccine may not be necessary to provide adequate field protection.

**Descriptors:** fowlpox virus genetics, hemagglutinin glycoproteins, influenza virus immunology, influenza A virus avian immunology, vaccines, synthetic immunology, viral vaccines immunology, chickens, cloaca

NAL Call Number: SF601.V44

**Abstract:** Inactivated whole avian influenza (AI) virus vaccines, baculovirus-derived AI haemagglutinin vaccine and recombinant fowlpoxvirus-AI haemagglutinin vaccine were tested for the ability to protect chickens against multiple highly pathogenic (HP) H5 AI viruses. The vaccine and challenge viruses, or their haemagglutinin protein components, were obtained from field AI viruses of diverse backgrounds and included strains obtained from four continents, six host species, and isolated over a 38-year-period. The vaccines protected against clinical signs and death, and reduced the number of chickens shedding virus and the titre of the virus shed following a HP H5 AI virus challenge. Immunization with these vaccines should decrease AI virus shedding from the respiratory and digestive tracts of AI virus exposed chickens and reduce bird-to-bird transmission. Although most consistent reduction in respiratory shedding was afforded when vaccine was more similar to the challenge virus, the genetic drift of avian influenza virus did not interfere with general protection as has been reported for human influenza viruses.

**Descriptors:** antigenic variation, fowl plague prevention and control, influenza A virus avian genetics, influenza vaccine immunology, baculoviridae, chickens, gene frequency, hemagglutinin glycoproteins, influenza virus immunology, avian immunology, vaccination veterinary.


NAL Call Number: SF995.W4

**Descriptors:** avian influenza virus, vaccines, influenza virus, orthomyxoviridae, viruses.


NAL Call Number: 41.8 Av5

**Abstract:** Current vaccines to prevent avian influenza rely upon labor-intensive parenteral injection. A more advantageous vaccine would be capable of administration by mass immunization methods such as spray or water vaccination. A recombinant vaccine (rNDV-AIV-H7) was constructed by using a lentogenic paramyxovirus type 1 vector (Newcastle disease virus (NDV) B1 strain) with insertion of the hemagglutinin (HA) gene from avian influenza virus (AIV) A/chicken/NY/13142-5/94 (H7N2). The recombinant virus had stable insertion and expression of the H7 AIV HA gene as evident by detection of HA expression via immunofluorescence in infected Vero cells. The rNDV-AIV-H7 replicated in 9-10 day embryonating chicken eggs and exhibited hemagglutinating activity from both NDV and AI proteins that was inhibited by antisera against both NDV and AI proteins that was inhibited by antisera against both NDV and AIV H7. Groups of 2-week-old white Leghorn chickens were vaccinated with transfected NDV vector (tNDV), rNDV-AIV-H7, or sterile allantoic fluid and were challenged 2 weeks later with viscerotrophic velogenic NDV (vvNDV) or highly pathogenic (HP) AIV. The sham-vaccinated birds were not protected from vvNDV or HP AIV challenge. The transfected NDV vaccine provided 70% protection for NDV challenge but did not protect against AIV challenge. The rNDV-AIV-H7 vaccine provided partial protection (40%) from vvNDV and HP AIV challenge. The serologic response was examined in chickens that received one or two immunizations of the rNDV-AIV-H7 vaccine. Based on hemagglutination inhibition and enzyme-linked immunosorbent assay (ELISA) tests, chickens that received a vaccine boost seroconverted to AIV H7, but the serologic response was weak in birds that received only one vaccination. This demonstrates the potential for NDV for use as a vaccine vector in expressing AIV proteins.

**Descriptors:** animal husbandry, immune system, infection, veterinary medicine, Newcastle disease, infectious disease, viral disease, influenza, respiratory system disease, ELISA, immunologic techniques, laboratory techniques, hemagglutination test, mass immunization, clinical techniques, therapeutic and prophylactic techniques, seroconversion.

**NAL Call Number:** 41.8 Av5

**Abstract:** In 1997, highly pathogenic (HP) H5N1 avian influenza virus (AIV) caused infections in poultry in Hong Kong and crossed into humans, resulting in a limited number of infections including 18 hospitalized cases and six associated deaths. The unique ability of this, AIV to infect both poultry and people raised a concern for the potential of humans to be biological as well as mechanical vectors of this AIV to poultry. The current study was undertaken to determine if existing vaccines and their technologies could be used during an outbreak to protect poultry. Commercial and experimental inactivated whole H5 AIV and baculovirus-expressed AIV H5 hemagglutinin protein vaccines provided protection from clinical signs and death in chickens after lethal challenge by human-origin HP H5N1 Hong Kong strains 156/97 and 483/97. The commercial and experimental inactivated vaccines had mean protective doses ranging from 0.25 to 0.89, which represents the milligrams of viral protein in the vaccines that provided protection from death in half of the birds. Furthermore, the vaccines reduced the ability of the challenge AIV to replicate in chickens and decreased the recovery of challenge AIV from the enteric and respiratory tracts, but the use of a vaccine will not totally prevent AI virus replication and shedding. Existing vaccines will protect poultry from mortality and reduce virus replication from the new HP AIV strain that can infect both poultry and humans.

**Descriptors:** immune system, infection, pharmacology, vector biology, avian influenza virus infection, viral disease, vaccination immunologic method, mortality.

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**NAL Call Number:** 448.39 B87

**Descriptors:** ammonium chloride pharmacology, influenza A virus avian drug effects, orthomyxoviridae drug effects, virus replication drug effects, ammonium sulfate pharmacology, cattle immunology, kidney, tissue culture, virus cultivation.

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**NAL Call Number:** SF604.P32

**Descriptors:** immunization, chickens, antibodies, vaccines, immune response, avian influenza virus.

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**NAL Call Number:** QR360.J6

**Abstract:** In the influenza H5N1 virus incident in Hong Kong in 1997, viruses that are closely related to H5N1 viruses initially isolated in a severe outbreak of avian influenza in chickens were isolated from humans, signaling the possibility of an incipient pandemic. However, it was not possible to prepare a vaccine against the virus in the conventional embryonated egg system because of the lethality of the virus for chicken embryos and the high level of biosafety therefore required for vaccine production. Alternative approaches, including an avirulent H5N4 virus isolated from a migratory duck as a surrogate virus, H5N1 virus as a reassortant with avian virus H3N1 and an avirulent recombinant H5N1 virus generated by reverse genetics, have been explored. All vaccines were formalin inactivated. Intraperitoneal immunization of mice with each of vaccines elicited the production of hemagglutination-inhibiting and virus-neutralizing antibodies, while intranasal vaccination without adjuvant induced both mucosal and systemic antibody responses that protected the mice from lethal H5N1 virus challenge. Surveillance of birds and animals, particularly aquatic birds, for viruses to provide vaccine strains, especially surrogate viruses, for a future pandemic is stressed.

**Descriptors:** influenza immunology, influenza A virus avian immunology, influenza vaccine immunology, communicable disease control, disease outbreaks, influenza prevention and control, influenza vaccine administration and dosage, mice, vaccination.

**NAL Call Number:** QR189.V32

**Abstract:** Fowlpox virus, the prototypic virus of the genus *Avipoxvirus* has a natural host range limited to avian species. As such, fowlpox virus provides a suitable candidate for the development of a species-specific recombinant viral vector. This paper reports the development of a fowlpox virus recombinant expressing the haemagglutinin molecule from a highly virulent avian influenza virus. On immunization of chickens and turkeys with the recombinant, protection is afforded against a lethal challenge with either the homologous or a heterologous influenza virus strain.

**Descriptors:** fowlpox virus genetics, hemagglutinins genetics, influenza immunology, poxviridae genetics, viral vaccines therapeutic use, chickens, fluorescent antibody technique, influenza prevention and control, orthomyxoviridae, poultry diseases prevention and control, recombinant proteins pharmacology, species specificity, turkeys, vaccination.


**NAL Call Number:** QR360.A1J6

**Descriptors:** vian influenza virus, avian laryngotracheitis virus, avian herpesvirus, herpesviridae, disease prevention, disease resistance, genes, hemagglutinins, immunodiagnosis, laryngotracheitis, vaccination, vaccines, achickens.


**NAL Call Number:** QR355.A5

**Abstract:** The sialidase inhibitor 4-guanidino-2,4-dideoxy-2,3-dehydro-N-acetylneuraminic acid was tested for growth inhibitory effects against a panel of avian influenza A viruses encompassing all nine neuraminidase subtypes. Growth in tissue culture of viruses from each subtype was inhibited by this compound at concentrations within a range previously found effective against human N1 and N2 viruses. This compound may prove a selective agent for the treatment (and prevention) of influenza virus infections.

**Descriptors:** enzymology, microbiology, pharmacology, antiviral drug avian influenza viruses human influenza viruses neuraminidase inhibition pharmacodynamics 4-guanidino-2,4-dideoxy-N-acetylneuraminic acid.


**NAL Call Number:** 396.8 J824

**Abstract:** A new antibiotic complex has been isolated from cultures of *Streptomyces* strain No. JA 10124. On the basis of taxonomic studies, the producing microorganism is described as *Streptomyces griseoflavus* (Krainsky, 1914) Waksman et Henrici, 1948, subsp. thuringiensis subsp. nov., type strain JA 10124. The antibiotic complex, designated as streptovirudin, was isolated from extracts of both mycelium and culture filtrate. It is a white amorphous material which consists of ten closely related components including streptovirudins A, B, C, D and E. The streptovirudin complex exhibits antibiotic activity against Gram-positive bacteria, *Mycobacteria*, and various DNA- and RNA-viruses.

**Descriptors:** anti bacterial agents isolation and purification, antiviral agents isolation and purification, administration, oral, anti bacterial agents administration and dosage, anti bacterial agents pharmacology, antiviral agents pharmacology, *Chlamydia* drug effects, fermentation, herpesvirus 1, suid drug effects, influenza A virus avian drug effects, injections, intraperitoneal, injections, intravenous, injections, subcutaneous, mice, *Mycobacterium* drug effects, Newcastle disease virus drug effects, sheep, sindbis virus drug effects, *Streptomyces* analysis, *Streptomyces* classification, vaccinia virus drug effects.

NAL Call Number: 500 N21P

Abstract: Influenza virus infection is responsible for hundreds of thousands of deaths annually. Current vaccination strategies and antiviral drugs provide limited protection; therefore, new strategies are needed. RNA interference is an effective means of suppressing virus replication in vitro. Here we demonstrate that treatment with small interfering RNAs (siRNAs) specific for highly conserved regions of the nucleoprotein or acidic polymerase inhibits influenza A virus replication in vivo. Delivery of these siRNAs significantly reduced lung virus titers in infected mice and protected animals from lethal challenge. This protection was specific and not mediated by an antiviral IFN response. Moreover, influenza-specific siRNA treatment was broadly effective and protected animals against lethal challenge with highly pathogenic avian influenza A viruses of the H5 and H7 subtypes. These results indicate that RNA interference is promising for control of influenza virus infection, as well as other viral infections.

Descriptors: influenza prevention and control, RNA interference, base sequence, influenza A virus, avian genetics, avian physiology, mice, inbred balb c, RNA, small interfering administration and dosage, small interfering genetics, viral genetics, virus replication.


NAL Call Number: 448.3 AC85

Abstract: Dipyridamole proved to be active against influenza viruses A/England 42/72, A/Bangkok 1/79 and A/fowl plague (FPV). The antiviral activities assayed by various methods varied from 90-99 per cent. No inhibition was found against influenza virus B/Leningrad 235/74 in vitro. Three dipyridamole derivatives were significantly active in tissue cultures against influenza virus A/England 42/72 and A/FPV. In white mice infected with influenza virus A/England 42/72 dipyridamole administered orally showed a protection rate of 62.5 per cent.

Descriptors: antiviral agents pharmacology, dipyridamole pharmacology, influenza A virus drug effects, dipyridamole analogs and derivatives, dipyridamole therapeutic use, influenza drug therapy, influenza A virus avian drug effects, mice, rimantadine therapeutic use.


NAL Call Number: 41.8 Av5

Descriptors: immunization, lymphocytes, avian influenza virus, turkeys, vaccines, immune response.


NAL Call Number: QR189.V32

Abstract: Recent outbreaks of avian influenza in humans have demonstrated the need for vaccines for influenza viruses with pandemic potential. Recombinant hemagglutinins are an attractive option for such vaccines because they do not require handling potentially highly pathogenic influenza viruses for vaccine production. In order to evaluate the immunogenicity, optimum dosing and timing of administration of a recombinant baculovirus-expressed H5 HA (rH5) in humans, 147 healthy adults were assigned randomly to receive intramuscular rH5 as two doses of 25, 45 or 90 microg each, one dose of 90 microg followed by a dose of 10 microg, or two doses of placebo, at intervals between doses of 21, 28 or 42 days. All doses of rH5 were well tolerated. The rH5 vaccine was modestly immunogenic at high dose. Neutralizing antibody responses to a titer of 1:80 or greater were seen in 23% (14/60) of individuals after a single dose of 90 microg, and in 52% (15/29) after two doses of 90 microg. Varying intervals between doses from 21 to 42 days had no significant effect on antibody responses to vaccination. These results suggest that baculovirus-expressed H5 HA can induce functional antibody in individuals who have not had prior exposure to H5 viruses, but that further studies to improve the immunogenicity of the vaccine are needed.
Descriptive terms:
- hemagglutinin glycoproteins
- influenza virus immunology
- influenza A virus human immunology
- influenza vaccine adverse effects
- influenza vaccine immunology
- vaccines, synthetic adverse effects
- vaccines, synthetic immunology
- adult, antibodies
- viral immunology
- dose response relationship
- immunologic
- enzyme linked immunosorbent assay
- hemagglutinin glycoproteins
- influenza virus genetics
- immunization schedule
- kinetics
- neutralization tests
- vaccination


**NAL Call Number:** QR189.2.R425 1994

Descriptive terms:
- recombinant vaccines
- synthetic vaccines
- avipoxvirus
- Galliformes
- avian influenza
- hemagglutinin gene


**NAL Call Number:** 41.8 Av5

**Abstract:**
A vaccine strain of fowlpox virus (FPV) was genetically engineered to produce avian influenza virus hemagglutinin (HA). This was accomplished by inserting a cDNA copy of the avian influenza virus HA gene, which was regulated by a vaccinia virus promoter, into the FPV thymidine kinase (TK) gene. Two types of recombinant viruses, differing only in the orientation of the HA gene relative to an adjacent foreign gene (lacZ), were created. Following preliminary identification of FPV recombinants based on the generation of beta-galactosidase (lacZ gene product), correct insertion of the HA gene into the genomes of these viruses was verified by hybridization studies. Susceptible chickens vaccinated with these FPV recombinants produced specific hemagglutination-inhibiting antibodies against the HA antigen. In view of this immune response, these viruses may serve as vaccines against avian influenza virus. In this regard, they appeared to be less virulent than the parental virus.

Descriptive terms:
- fowls
- recombinant vaccines
- avian influenza virus
- genes
- hemagglutinins
- fowl pox virus
- immune response
- virulence
- genetic engineering
- chickens


**NAL Call Number:** 41.8 Av5

**Abstract:**
During the spring of 2002, a low pathogenic avian influenza (LPAI) A (H7N2) virus caused a major outbreak among commercial poultry in Virginia and adjacent states. The virus primarily affected turkey flocks, causing respiratory distress and decreased egg production. Experimentally, turkeys were more susceptible than chickens to H7N2 virus infection, with 50% bird infectious dose titers equal to 10(0.8) and 10(2.8-3.2), respectively. Comparison of virus shedding from the cloaca and oropharynx demonstrated that recent H7N2 virus isolates were readily isolated from the upper respiratory tract but rarely from the gastrointestinal tract. The outbreak of H7N2 virus raised concerns regarding the availability of vaccines that could be used for the prevention and control of this virus in poultry. We sought to determine if an existing commercial avian influenza (AI) vaccine prepared from a 1997 seed stock virus could provide protection against a 2002 LPAI H7N2 virus isolated from a turkey (A/turkey/Virginia/158512/02 [TV/02]) in Virginia that was from the same lineage as the vaccine virus. The inactivated AI vaccine, prepared from A/chicken/Pennsylvania/21342/97 (CP/97) virus, significantly reduced viral shedding from vaccinated turkeys in comparison with sham controls but did not prevent infection. The protective effect of vaccination correlated with the level of virus-specific antibody because a second dose of vaccine increased antiviral serum immunoglobulin G and hemagglutination inhibition (HI) reactivity titers in two different turkey age groups. Serum from CP/97-vaccinated turkeys reacted equally well to CP/97 and TV/02 antigens by HI and enzyme-linked immunosorbent assay. These results demonstrate the potential benefit of using an antigenically related 1997 H7N2 virus as a vaccine candidate for protection in poultry against a H7N2 virus isolate from 2002.

Descriptive terms:
- chickens
- influenza A virus
- avian pathogenicity
- avian etiology
- poultry diseases etiology
- turkeys
- antibodies
- viral blood
- avian classification
- avian immunology
- prevention and control
- poultry

**NAL Call Number:** QR360.J6

**Abstract:** Influenza vaccines that induce greater cross-reactive or heterosubtypic immunity (Het-I) may overcome limitations in vaccine efficacy imposed by the antigenic variability of influenza A viruses. We have compared mucosal versus traditional parenteral administration of inactivated influenza vaccine for the ability to induce Het-I in BALB/c mice and evaluated a modified *Escherichia coli* heat-labile enterotoxin adjuvant, LT(R192G), for augmentation of Het-I. Mice that received three intranasal (i.n.) immunizations of H3N2 vaccine in the presence of LT(R192G) were completely protected against lethal challenge with a highly pathogenic human H5N1 virus and had nasal and lung viral titers that were at least 2,500-fold lower than those of control mice receiving LT(R192G) alone. In contrast, mice that received three vaccinations of H3N2 vaccine subcutaneously in the presence or absence of LT(R192G) or incomplete Freund's adjuvant were not protected against lethal challenge and had no significant reductions in tissue virus titers observed on day 5 post-H5N1 virus challenge. Mice that were i.n. administered H3N2 vaccine alone, without LT(R192G), displayed partial protection against heterosubtypic challenge. The immune mediators of Het-I were investigated. The functional role of B and CD8+ T cells in Het-I were evaluated by using gene-targeted B-cell (IgH-6(-/-))- or beta2-microglobulin (beta2m(-/-))-deficient mice, respectively. beta2m(-/-) but not IgH-6(-/-) vaccinated mice were protected by Het-I and survived a lethal infection with H5N1, suggesting that B cells, but not CD8+ T cells, were vital for protection of mice against heterosubtypic challenge. Nevertheless, CD8+ T cells contributed to viral clearance in the lungs and brain tissues of heterotypically immune mice. Mucosal but not parenteral vaccination induced subtype cross-reactive lung immunoglobulin G (IgG), IgA, and serum IgG anti-hemagglutinin antibodies, suggesting the presence of a common cross-reactive epitope in the hemagglutinins of H3 and H5. These results suggest a strategy of mucosal vaccination that stimulates cross-protection against multiple influenza virus subtypes, including viruses with pandemic potential.

**Descriptors:** B lymphocytes immunology, fowl plague prevention and control, influenza A virus avian immunology, influenza vaccine immunology, adjuvants, immunologic administration and dosage, administration, cutaneous, administration, intranasal, antibodies, viral analysis, antibodies, viral blood, bacterial toxins administration and dosage, CD8 positive T lymphocytes immunology, cross reactions, enterotoxins administration and dosage, *Escherichia coli* immunology, fowl plague immunology, fowl plague virology, Freund's adjuvant administration and dosage, hemagglutinins viral immunology, immunoglobulin A analysis, immunoglobulin A blood, immunoglobulin G analysis, immunoglobulin G blood, influenza A virus avian isolation and purification, lung immunology, lung virology, mice inbred BALB c, mice, inbred c57bl, mice, knockout, species specificity, vaccines, inactivated immunology.


**NAL Call Number:** 41.8 V6426

**Descriptors:** fowl plague diagnosis, Newcastle disease diagnosis, chick embryo, chickens, diagnosis, differential, influenza A virus avian isolation and purification, methods, Newcastle disease virus isolation and purification.


**NAL Call Number:** SF601.V523

**Abstract:** Recombinant technology is relatively new to veterinary medicine. It combines safety, purity, potency, and efficacy in the vaccine. Its positive features include not exposing the vaccinate to the pathogen, the lack of need for adjuvants, and stability that allows some vaccine to remain viable at ambient temperatures. These recombinants can receive multiple genetic inserts and present an opportunity to have multiple combination vaccines for use in animals. Licensed recombinant vaccines in veterinary medicine...
include those protecting against Lyme disease, pseudorabies, rabies, canine distemper, Newcastle disease, and a strain of avian influenza.

Descriptors: animal diseases prevention and control, vaccines, synthetic, veterinary medicine trends.

NAL Call Number: QR189.A73
Descriptors: avian influenza virus, efficacy, antibodies, hemagglutination inhibition test, immune response, inactivated vaccines, pullets, broilers, hens, vaccination, Galliformes.

NAL Call Number: 448.9 Am37
Descriptors: disease outbreaks prevention and control, influenza epidemiology, influenza prevention and control, influenza A virus avian immunology, influenza vaccine, world health, centers for disease control and prevention United States, influenza veterinary, poultry virology, poultry diseases epidemiology, poultry diseases virology, United States.

NAL Call Number: QR360.A1J6
Descriptors: infection, fowl plague, infectious laryngotracheitis virus infection, immunofluorescence, immunologic techniques, western blot, genetic techniques.

NAL Call Number: 41.8 T431
Descriptors: avian influenza epidemiology, poultry diseases epidemiology, birds, avian influenza prevention and control, Netherlands epidemiology, poultry, poultry diseases prevention and control.

NAL Call Number: 41.8 OF2
Descriptors: influenza A virus avian, humidity, hydrogen-ion concentration, temperature, virus cultivation.

NAL Call Number: 41.8 Av5
Abstract: Several avian influenza virus strains of hemagglutinin subtype 5 were assayed for sensitivity to the antiviral drug amantadine. Most strains exhibited little sensitivity to the drug as measured by plaque reduction. The A/Chicken/Scotland/59 (CS59), however, was highly sensitive, making it easily distinguishable from the other H5 strains. Drug sensitivity of the viruses was also assayed in chicken embryos. The in ovo patterns of amantadine sensitivity differed from those detected in cell culture. The CS59 isolate could not be distinguished from all the other strains on the basis of its response to amantadine in ovo. Although amantadine protected chickens inoculated with CS59 from morbidity and mortality, drug-resistant viruses were readily isolated from the infected birds. As found with other amantadine-resistant variants, the structure of the matrix gene was altered in the resistant isolates. These results demonstrate that amantadine resistance is widespread among avian influenza viruses of the H5 subtype, that drug sensitivity in cell culture does not necessarily reflect responses to amantadine in ovo and in vivo, and, as previously found, amantadine-resistant derivatives of H5 strains may be isolated from birds protected by the drug.
Descriptors: fowls, avian influenza virus, amantadine, susceptibility, drug resistance, strain differences, cell culture, ova, chickens.

NAL Call Number: 44.8 In282
Descriptors: bovine spongiform encephalopathy, avian influenza virus, Coronavirus, disease control, disease distribution, disease prevalence, disease prevention, epidemiology, livestock, zoonoses, human, prions.

NAL Call Number: S19.C58
Descriptors: antibodies, antigens, disease control, disease prevention, dosage, immune response, inactivated vaccines, vaccination, vaccine development, avian influenza virus, fowl, embryos.

Descriptors: disease prevention, disease control, disease transmission, diagnosis, quarantine, outbreaks, antibiotics, vaccination, avian influenza virus, China, Galliformes, reviews.

NAL Call Number: 448.8 L22
Abstract: BACKGROUND: In response to the emergence of severe infection capable of rapid global spread, WHO will issue a pandemic alert. Such alerts are rare; however, on Feb 19, 2003, a pandemic alert was issued in response to human infections caused by an avian H5N1 influenza virus, A/Hong Kong/213/03. H5N1 had been noted once before in human beings in 1997 and killed a third (6/18) of infected people. The 2003 variant seemed to have been transmitted directly from birds to human beings and caused fatal pneumonia in one of two infected individuals. Candidate vaccines were sought, but no avirulent viruses antigenically similar to the pathogen were available, and the isolate killed embryonated chicken eggs. Since traditional strategies of vaccine production were not viable, we sought to produce a candidate reference virus using reverse genetics. METHODS: We removed the polybasic aminoacids that are associated with high virulence from the haemagglutinin cleavage site of A/Hong Kong/213/03 using influenza reverse genetics techniques. A reference vaccine virus was then produced on an A/Puerto Rico/8/34 (PR8) backbone on WHO-approved Vero cells. We assessed this reference virus for pathogenicity in in-vivo and in-vitro assays. FINDINGS: A reference vaccine virus was produced in Good Manufacturing Practice (GMP)-grade facilities in less than 4 weeks from the time of virus isolation. This virus proved to be non-pathogenic in chickens and ferrets and was shown to be stable after multiple passages in embryonated chicken eggs. INTERPRETATION: The ability to produce a candidate reference virus in such a short period of time sets a new standard for rapid response to emerging infectious disease threats and clearly shows the usefulness of reverse genetics for influenza vaccine development. The same technologies and procedures are currently being used to create reference vaccine viruses against the 2004 H5N1 viruses circulating in Asia.
Descriptors: disease outbreaks prevention and control, influenza vaccines immunology, orthomyxoviridae immunology, orthomyxoviridae infections prevention and control, antibodies, viral immunology, Asia epidemiology, birds, communicable disease control methods, drug design, genetic engineering, Hong Kong epidemiology, influenza A virus, avian immunology, human immunology, avian influenza prevention and control, avian influenza virology, orthomyxoviridae chemistry, orthomyxoviridae growth and development, orthomyxoviridae infections immunology, orthomyxoviridae infections virology, plasmids immunology, poultry diseases immunology, poultry diseases prevention and control, poultry diseases virology, reassortant viruses chemistry, reassortant viruses growth and development, reassortant viruses immunology, transformation, genetic immunology, virulence factors isolation and purification.

**NAL Call Number:** QR360.J6

**Abstract:** The influenza A virus [A/Chicken/Pennsylvania/1370/83 (H5N2)] that caused up to 80% mortality among chickens provided a model system for testing the efficacy of chemotherapeutic agents against highly virulent influenza virus. Amantadine and rimantadine administered in drinking water were efficacious both prophylactically and therapeutically. However, under conditions simulating natural transmission of virus, amantadine- and rimantadine-resistant viruses arose and were transmitted to other birds in contact with the infected chickens, causing mortality. Simultaneous administration of inactivated H5N2 vaccine and amantadine provided protection. Thus, chemotherapy may be useful in the treatment of a highly pathogenic influenza virus outbreak in humans or other animals when used in combination with vaccine.

**Descriptors:** adamantane analogs and derivatives, amantadine therapeutic use, fowl plague prevention and control, influenza A virus avian immunology, rimantadine therapeutic use, chickens, drug resistance, microbial, fowl plague drug therapy, fowl plague transmission, vaccination, viral vaccines immunology.


**NAL Call Number:** 41.8 Av5

**Abstract:** The presence of highly pathogenic H5N2 avian influenza in domestic poultry in Mexico that is not being eradicated by conventional depopulation methods constitutes an imminent problem for poultry producers and agricultural authorities in the United States. The present report considers the candidate vaccines available to H5N2 influenza virus and establishes that a fowl pox-H5 recombinant can provide protection from lethal Mexican H5N2, and prevent shedding in the feces and transmission to contact birds. Inactivated and recombinant vaccines may be useful adjuncts to eradication if the H5N2 influenza virus spreads to the United States or the countries in Central America.

**Descriptors:** Mexico, chickens, avian influenza virus, synthetic vaccines, avipoxvirus, disease control, immunity, agglutinins, genes, America, birds, cell structure, chromosomes, domestic animals, domesticated birds, Galliformes, influenza virus, Latin America, livestock, North America, nucleus, orthomyxoviridae, poultry, poxviridae, proteins, useful animals, vaccines, viruses, recombinant vaccines, fowl pox virus, disease prevention, hemagglutinins.


**NAL Call Number:** T223.A21

**Descriptors:** methods and techniques, pharmacology, veterinary medicine, avian vaccination method protective method.


**Abstract:** Influenza is an emerging and re-emerging disease. Since the late 1930s influenza viruses have been isolated yearly from different parts of the world during epidemics and pandemics. The "epidemiologic success" of influenza is due largely to rapid and unpredictable antigenic changes (antigenic drift) among human influenza viruses, and the emergence of new subtypes (antigenic shift), mostly from reassortment between human and avian influenza viruses. Antigenic shifts were attributed to the global pandemic viruses of 1957 (H2N2 Asian flu) and 1968 (H3N2 Hong Kong flu). Concern over possible new pandemics has been heightened by recent reports of human infection in Asia in 1997 with avian viruses (H5N1) and in 1999 (H9N2) and isolation of human-avian reassorted viruses from pigs and humans in Europe. Influenza has a high rate of in apparent infection, short incubation and high infectivity; epidemics usually start abruptly and spread rapidly to neighboring communities and countries. Isolation and quarantine are often unsuccessful in preventing the spread of the infection. Although not perfect, immunization and chemoprophylaxis are highly effective at minimizing the spread of influenza and reducing morbidity and mortality, social disruption and
economic loss. Plans for future influenza epidemics and pandemics require national and international programs to be in place for the monitoring of influenza activity, the dissemination and exchange of information and the provision and delivery of sufficient quantities of vaccines and antiviral agents. This paper reviews and discusses the antigenic variations of the influenza virus, potential influenza pandemics, protective efficacy of inactivated vaccines and antiviral agents and preparation for control of future epidemics and pandemics.

Descriptors: epidemiology, infection, influenza, epidemiology, prevention and control, respiratory system disease, viral disease, chemoprophylaxis clinical techniques, therapeutic and prophylactic techniques, immunization clinical techniques, therapeutic and prophylactic techniques, antigenic drift viral infectivity.


Descriptors: animal diseases, disease control, disease transmission, decision making, economic analysis, losses, epidemiology, foot and mouth disease, Aphthovirus, avian influenza virus, swine fever virus.


NAL Call Number: 41.8 Av5
Abstract: The hemagglutinin concentration of beta-propiolactone-inactivated influenza vaccine containing A/Duck/N.Y./189/82 (H5N2) virus was measured by single-radial-immunodiffusion (SRD) test. After administration of vaccine to chickens in Freund's complete adjuvant, vaccine efficacy was assessed by challenge with lethal A/Chicken/Penn./1370/83 (H5N2) virus. SRD potency values correlated with post-vaccination antibody levels and protection against infection.

Descriptors: fowl plague prevention and control, influenza A virus avian immunology, influenza vaccine standards, chickens, hemagglutinins viral immunology, influenza vaccine therapeutic use, neuraminidase immunology, poultry diseases prevention and control, vaccination.


NAL Call Number: QR189.V32
Descriptors: influenza prevention and control, influenza A virus avian immunology, influenza vaccine therapeutic use, chickens, ducks, ferrets, human immunology, human isolation and purification, mice inbred BALB c.


NAL Call Number: QR189.V32
Abstract: In response to the pandemic warning provided by the highly pathogenic H5N1 influenza virus infections in Hong Kong, there were world-wide attempts to develop vaccines. Three strategies were followed and although each was associated with some success, there were also some problems. Pre-clinical vaccine efficacy results are presented from one such strategy, that of using an apathogenic H5N3 avian strain for vaccine production.

Descriptors: influenza A virus avian immunology, influenza vaccine immunology, baculoviridae genetics, mice, vaccines, attenuated immunology, vaccines, synthetic immunology.


NAL Call Number: QR180.3.D4
Abstract: Single-radial-immunodiffusion (SRD) provides a sensitive and reproducible in vitro assay for haemagglutinin (HA) concentration in inactivated influenza vaccines. The use of SRD for human influenza
vaccine standardization and application for equine and avian influenza vaccines is discussed. In clinical trials, vaccine HA concentration measured by SRD has been shown to be directly related to antibody responses and to protection against challenge. The use of SRD may considerably reduce the usage of animals for potency testing of veterinary influenza vaccines.

Descriptors: influenza vaccine standards, vaccines, attenuated standards, antibodies, viral biosynthesis, chickens, horses, immunodiffusion standards, influenza prevention and control, influenza veterinary.


Abstract: During normal interpandemic influenza seasons, immune responses to vaccines are quite predictable and meet the licensing criteria of the European Union (EU) Committee for Proprietary Medicinal Products (CPMP). In a pandemic situation, large sections, if not all of the community will be immunologically naive and therefore new immunisation strategies will be needed. In 1976 and 1977 H1N1 vaccines were prepared and tested clinically. To stimulate 'protective' antibody responses, two doses of vaccine were needed in people below the age of 24 years (no previous experience of H1N1 virus), whereas one conventional dose was adequate in older people. In 1997, the highly pathogenic avian influenza H5N1 virus caused widespread concern when it infected man, with lethal effects. Due to safety concerns it was necessary to adopt new strategies for vaccine development and one such strategy was to produce vaccine from an avirulent H5N3 virus, A/Duck/Singapore-Q/F119-2/97. Clinical trials of a subunit vaccine prepared from A/Duck/Sing/97 virus revealed that even two doses of twice the normal vaccine concentration (i.e. 30 mug haemagglutinin) were poorly immunogenic, whereas an H5N3 vaccine adjuvanted with microfluidised emulsion (MF) 59 stimulated antibody levels that complied with CPMP criteria after two half strength doses (i.e. 7.5 mug haemagglutinin).

Descriptors: clinical immunology, epidemiology, infection, pharmacology, public health, pulmonary medicine, influenza, immunology, prevention and control, respiratory system disease, viral disease, pandemic prevention, vaccine development.


Abstract: Over the past eight years, cases of human infection with highly pathogenic avian influenza viruses have raised international concern that we could be on the brink of a global influenza pandemic. Many of these human infections have proved fatal and if the viruses had been able to transmit efficiently from person to person, the effects would have been devastating. How can we arm ourselves against this pandemic threat when these viruses are too dangerous to use in conventional vaccine production? Recent technological developments (reverse genetics) have allowed us to manipulate the influenza virus genome so that we can construct safe, high-yielding vaccine strains. However, the transition of reverse-genetic technologies from the research laboratory to the manufacturing environment has presented new challenges for vaccine manufacturers as well as veterinary and public health authorities.

Descriptors: influenza vaccines isolation and purification, disease outbreaks prevention and control, genetic engineering, influenza prevention and control, influenza A virus, avian genetics, avian pathogenicity, avian ultrastructure, influenza vaccines genetics, safety, vaccines, inactivated genetics, vaccines, inactivated isolation and purification.


NAL Call Number: 501 L84Pb

Abstract: Pandemic influenza presents special problems for vaccine development. There must be a balance between rapid availability of vaccine and the safeguards to ensure safety, quality and efficacy of vaccine. Vaccine was developed for the pandemics of 1957, 1968, 1977 and for the pandemic alert of 1976. This experience is compared with that gained in developing vaccines for a possible H5N1 pandemic in 1997-1998. Our ability to mass produce influenza vaccines against a pandemic threat was well illustrated by the production of over 150 million doses of 'swine flu' vaccine in the USA within a 3 month period in 1976. However, there is cause for concern that the lead time to begin vaccine production is likely to be about 7-8
months. Attempts to reduce this time should receive urgent attention. Immunogenicity of vaccines in pandemic situations is compared over the period 1968-1998. A consistent feature of the vaccine trials is the demonstration that one conventional 15 µg haemagglutinin dose of vaccine is not sufficiently immunogenic in naive individuals. Much larger doses or two lower doses are needed to induce satisfactory immunity. There is some evidence that whole-virus vaccines are more immunogenic than split or subunit vaccines, but this needs substantiating by further studies. H5 vaccines appeared to be particularly poor immunogens and there is evidence that an adjuvant may be needed. Prospects for improving the development of pandemic vaccines are discussed.


Descriptors: influenza prevention and control, influenza A virus avian immunology, influenza vaccine, birds virology, influenza epidemiology, avian genetics, sentinel surveillance, vaccination, Vietnam.


NAL Call Number: 41.8 Av5

Abstract: Inactivated Newcastle disease virus (NDV), avian influenza virus (AIV), and infectious bronchitis virus (IBV) antigens were evaluated for immunological efficacy in monovalent and polyvalent vaccines. Vaccinated broilers were bled for hemagglutination-inhibition (HI) tests at 1- or 2-week intervals. Half of the chickens were challenged with the Largo isolate of velogenic viscerotropic (VV) NDV at 8 weeks post-vaccination, and the remainder were challenged with the Massachusetts 41 strain IBV at 9 weeks post-vaccination. Newcastle disease HI titers were reduced significantly (P less than 0.05) from those of monovalent control vaccine groups when IBV antigen was emulsified in mixtures with low (1-3x) concentrated NDV or NDV and AIV antigens. Avian influenza HI titers were significantly (P less than 0.05) lower than those of the control monovalent groups when highly concentrated NDV was part of the polyvalent vaccine. Infectious bronchitis HI titers were higher than those of control monovalent groups in 13 of 15 vaccine groups when IBV antigen was in polyvalent formulations. VV NDV challenge killed all non-NDV vaccinates and induced increased HI titers in NDV vaccinates but no morbidity or mortality. Sixty of 80 IBV vaccinates experienced a fourfold or greater HI titer increase following challenge. All non-IBV vaccinates seroconverted at 1 week post-challenge.

Descriptors: chickens immunology, coronaviridae immunology, infectious bronchitis virus immunology, influenza A virus avian immunology, Newcastle disease virus immunology, viral vaccines immunology, antibodies, viral biosynthesis, antigens, viral immunology, hemagglutination inhibition tests, specific pathogen free organisms, vaccines, inactivated immunology.


Descriptors: diagnosis, prevention, treatment, avian influenza virus, fowl, Galliformes.

Xue JingShan, Xu HaiNie, Pan WenBo, Liao XiuYun, Yang Su, Bo QingRu, and Feng JiaWang (2001). The interference of inoculating chicks with avian influenza virus (AIV) type H9 vaccine on measuring the antibody to AIV type H5 in them. Chinese Journal of Veterinary Science and Technology 31(6): 5-8. ISSN: 1000-6419.

Descriptors: antibodies, chicks, poultry, birds, vaccines, immunization, measurement, avian influenza virus, orthomyxoviridae.

NAL Call Number: 47.8 Ar2
Descriptors: avian influenza virus, disinfectants, formaldehyde, formic acid, potency, temperature, poultry.

NAL Call Number: SF604.C58
Descriptors: avian influenza virus, disease control, disease prevention, poultry, China.

Abstract: The recent alert over bird flu (influenza A H5N1) in Hong Kong has ruffled feathers in some countries, including the United Kingdom, as to how the virus should be handled in clinical and research laboratories.
Descriptors: disease outbreaks prevention and control, influenza prevention and control, influenza A virus avian pathogenicity, laboratory personnel, occupational exposure prevention and control, birds, Great Britain, Hong Kong.

NAL Call Number: aSF995.6.I6I5 1981a
Descriptors: avian influenza virus, control, inactivated vaccines, oil emulsion.

Descriptors: antigens, attenuation, DNA vaccines, immune response, polymerase chain reaction, reverse transcription, strains, vaccination, vaccine development, pathogenicity, avian influenza virus, poultry, fowl, mice, Salmonella typhimurium, genetic vectors.

Descriptors: avian influenza virus, disease control, disease prevalence, disease prevention, epidemiological surveys, pathogenicity, virulence, wild birds, ducks, fowl, ostriches, peafowl, quail, Stumidae, turkeys.

Descriptors: hygiene, disinfectants, avian influenza virus, disease control, China, Galliformes.

NAL Call Number: 41.8 Av5
Abstract: Emu antibody responses to avian influenza virus (AM infection were evaluated by the competitive enzyme-linked immunosorbent assay (C-ELISA), agar gel immunodiffusion (AGID) and hemaggulitation inhibition (HI) tests. AU birds infected with AIV H5N1, H5N3, or H7N7 developed antinucleoprotein (NP) antibodies as early as 7 days postinfection as detected by the C-ELISA. The responses lasted 49 days for
the emus receiving H5N3 and at least 56 days for emus receiving the other two viruses. By evaluating 50 emu field serum samples, the C-ELISA was found more sensitive than the AGID test for the detection of anti-NP antibodies. This study indicates that emus experimentally infected with AIV developed antibody responses that can be detected by C-ELISA, AGID, and HI tests. The results from this and our previous studies demonstrate the use of the C-ELISA as a substitute for the AGID test in a routine serodiagnostic screening for detection of antibodies to AIV infection in multiple avian species.

**Descriptors:** immune system, infection, veterinary medicine, avian influenza virus infection, serodiagnosis, viral disease, agar gel immunodiffusion analytical method, competitive ELISA analytical method, hemagglutination inhibition test analytical method, antibody response: evaluation.


**NAL Call Number:** SF604.C485

**Descriptors:** immunoprecipitation tests, serological surveys, avian influenza virus, diagnosis, management, outbreaks, pheasants, China.


**Abstract:** Influenza disease continues to cause thousands of deaths in the United States. Due to the burden of influenza hospitalizations among children, inactivated influenza vaccine is now routinely recommended for children age 6-23 months. A live, attenuated influenza vaccine was licensed in 2003 for healthy persons age 5-49 years.

**Descriptors:** influenza epidemiology, influenza vaccines administration and dosage, vaccination standards, age factors, influenza prevention and control, influenza virology, influenza vaccines adverse effects, avian influenza epidemiology, avian influenza prevention and control, avian influenza virology, attenuated vaccines administration and dosage, attenuated vaccines adverse effects, inactivated vaccines administration and dosage, inactivated vaccines adverse effects.

**Return to:** Contents

**NAL Call Number:** 41.8 Av5

**Abstract:** An outbreak of low-pathogenicity H7N2 avian influenza virus (AIV) in the Shenandoah Valley of Virginia during the spring and summer of 2002 affected 197 farms and resulted in the destruction of over 4.7 million birds. The outbreak affected primarily turkey farms (28 breeders, 125 grow out) with some spillover into chicken farms (29 breeders, 13 grow out, 2 table-egg layers). Although no direct link was established, the strain of H7N2 AIV in this outbreak had a molecular fingerprint that was essentially identical to the H7N2 AIV strain that has circulated in the live bird markets of the northeastern United States for the last 8 yr. After an initial delay caused by lack of viable disposal options, depopulation and disposal, primarily in sanitary landfills, was carried out within 24 hr of detection of a positive flock. Increased surveillance efforts included once-a-week testing of the daily mortality of all poultry farms in the region, testing of all breeder farms every 2 wk, and testing of all flocks prior to movement for any reason. A statistical sampling of backyard flocks and wild birds found no evidence of the virus. The successful eradication of this outbreak was the result of the efforts of a highly effective task force of industry, state, and federal personnel.

**Descriptors:** epidemiology, infection, avian influenza, infectious disease, respiratory system disease, viral disease, disease control measures, disease outbreak, poultry farms.


**NAL Call Number:** SF600.Z6

**Descriptors:** avian influenza virus, *Gallus gallus*, Pakistan.


**NAL Call Number:** 41.8 Av5

**Abstract:** Since the Fourth International Symposium on Avian Influenza (AI) there has been considerable AI activity in the Eastern Hemisphere. The higher profile of AI resulting from the human infections with H5N1 and H9N2 viruses in Hong Kong, in 1997 and 1999, respectively, resulted in increased reporting and active surveillance. There have been three reported incidents of high-pathogenicity (HP) AI: H5N2 in northeastern Italy in 1997 (eight outbreaks); H5N1 in Hong Kong in 1997 recurring in 2001 and 2002; H7N1 in northeastern Italy resulting in 413 outbreaks in 1999-00. The Italian HPAI outbreaks were preceded by 199 H7N1 low-pathogenicity (LP) AI outbreaks in 1999, and this virus continued to cause some problems after the eradication of HPAI. During the second half of the 1990s outbreaks of LPAI due to H9N2 subtype have been reported in Germany, Italy, Ireland, South Africa, Hungary, Korea, China, Hong Kong, countries of the Middle East, Iran, and Pakistan. The continued presence of virus of this subtype in the Middle and Far East may mean it is becoming an established endemic disease in those regions. Other more restricted outbreaks in poultry have resulted in the isolation of LPAI viruses of H5, H6, H7, and H10 subtypes.

**Descriptors:** epidemiology, infection, veterinary medicine, avian influenza, infectious disease, respiratory system disease, viral disease, Fourth International Symposium on Avian Influenza, disease outbreaks.


**NAL Call Number:** 41.8 V641

**Descriptors:** disease outbreaks veterinary, fowl plague epidemiology, influenza A virus avian, poultry diseases epidemiology, turkeys, Great Britain epidemiology, incidence, poultry diseases microbiology.


**Descriptors:** influenza epidemiology, adult, Canada, chickens virology, child, influenza A virus, human, influenza B virus, influenza, avian epidemiology.


**NAL Call Number:** 41.8 In2

**Descriptors:** avian influenza virus infection, quarantine, clinical techniques, Food and Agriculture Organization, United Nations, World Health Organization, Office International des Epizooties, Asia.


**NAL Call Number:** 41.8 Au72

**Descriptors:** birds virology, disease reservoirs veterinary, influenza, avian epidemiology, avian influenza, transmission, wild animals, Australia epidemiology, etiology.


**NAL Call Number:** HD9000.9.A8A84

**Descriptors:** avian influenza virus, disease control, broilers, ducks, Australia.


**NAL Call Number:** aSF995.6.I6I5 1981a

**Descriptors:** poultry, avian influenza virus, symposium.


**NAL Call Number:** aSF995.6.I6I5 1981a

**Descriptors:** avian influenza virus, surveys, wild birds, France.


**Descriptors:** avian influenza A, human diseases, animal diseases, clinical aspects, disease transmission, reviews, Hong Kong.


**Abstract:** The European Scientific Working group on Influenza (ESWI) was established in 1992. Its main task is to reduce impact of influenza in Europe by increase of awareness about influenza, dangers, methods of its prevention among physicians and in the society, stimulation of scientific studies, organizing of conferences, including those on the preparedness plans for the next pandemic. Infections, and in some cases also deaths, caused in humans by avian influenza viruses A(H5N1) in 1997 and 2003, A(H9N2) in 1999 and A(H7N7) in 2003 show that the outbreak of the next pandemic is a matter of time. Considering the above facts ESWI prepared a pilot study to introduce in Poland, Germany and Sweden. The main aim of this project is to achieve a better and more effective control of influenza by an increase of knowledge about influenza, promoting of vaccinations and new antinfluenza drugs--neuraminidase inhibitors. In Poland project is coordinated by the National Influenza Center located at the National Institute of Hygiene, Warsaw. This is only one center in Poland and one of 112 similar centers in 83 countries of the world participating in the international program of influenza surveillance in cooperation with WHO, ESWI and European Influenza Surveillance Scheme.

**Descriptors:** health planning, influenza epidemiology, influenza prevention and control, respiratory tract
infections prevention and control, world health, Europe epidemiology, Poland, practice guidelines, respiratory tract infections epidemiology, World Health Organization.


**NAL Call Number:** 449.9 Un3r

**Descriptors:** avian influenza virus, outbreak, Maryland, Pennsylvania.


**NAL Call Number:** 41.8 Av5

**Abstract:** Low pathogenicity avian influenza virus (AIV) H7N2 has been isolated since 1994 from retail live-bird markets (LBMs) in the northeastern United States. This study examines the suppliers to the LBMs in New York and New Jersey. In 2001, 185 supplier premises in nine states were surveyed for the presence of AIV by virus isolation (VI) in embryonating chicken eggs. No H7 or H5 virus was isolated. In addition, 104 producer premises in two states were serologically negative for H7 and H5 AIV. Information on management practices was obtained via questionnaire for 191 premises in 12 states. The survey results suggest that current biosecurity practices at supplier premises could be improved, especially regarding movement of birds. The study supports the hypothesis that H7N2 AIV is primarily maintained within the LBMs and, if reintroduction from suppliers is occurring, it is likely reintroduced at a very low level or from suppliers not included in this study.

**Descriptors:** epidemiology, infection, public health, avian influenza, infectious disease, respiratory system disease, viral disease, viral isolation, clinical techniques, diagnostic techniques, immunologic techniques, laboratory techniques, biosecurity, disease surveillance, food safety, retail, live bird markets.


**NAL Call Number:** 41.8 Av5

**Abstract:** In 2001, all 109 retail live-bird markets (LBMs) in New York and New Jersey were surveyed for the presence of avian influenza virus (AIV) by a real time reverse transcriptase/polymer chain reaction assay (RRT/PCR) and results compared to virus isolation (VI) in embryonating chicken eggs. The RRT/PCR had a 91.9% sensitivity and 97.9% specificity in detecting presence of AIV at the market level. However, the sensitivity at the sample level is 65.87%. The RRT/PCR is a reliable method to identify AIV at the market level. In addition, a cross-sectional epidemiologic study of the LBMs showed that, during the past 12 months, markets that were open 7 days per week and those that also sold rabbits had the highest risk for being positive for AIV. Markets that were closed one or more days per week and those that performed daily cleaning and disinfecting had the lowest risk for being AIV positive.

**Descriptors:** epidemiology, infection, avian influenza, infectious disease, respiratory system disease, viral disease, reverse transcriptase polymerase chain reaction, RT PCR, genetic techniques, laboratory techniques, viral isolation, immunologic techniques, disease surveillance data, epidemiological data, live bird markets, viral detection, efficacy.


**NAL Call Number:** 41.8 Au72

**Descriptors:** wild aquatic birds, avian influenza virus, disease distribution, disease prevalence, disease transmission, disease vectors, outbreaks, reservoir hosts.


**NAL Call Number:** 449.9 Un3r

NAL Call Number: 448.8 V81

Abstract: Since the "bird flu" incident in Hong Kong SAR in 1997, several studies have highlighted the substantial role of domestic birds, such as turkeys and chickens, in the ecology of influenza A viruses. Even if recent evidence suggests that chickens can maintain several influenza serotypes, avian influenza viruses (AIVs) circulating in domestic species are believed to be introduced each time from the wild bird reservoir. However, so far the direct precursor of influenza viruses from domestic birds has never been identified. In this report, we describe the antigenic and genetic characterization of the surface proteins of H7N3 viruses isolated from wild ducks in Italy in 2001 in comparison to H7N3 strains that circulated in Italian turkeys in 2002-2003. The wild and domestic avian strains appeared strictly related at both phenotypic and genetic level: homology percentages in seven of their genes were comprised between 99.8% (for PB2) and 99.1% (for M), and their NA genes differed mainly because of a 23-aminoacid deletion in the NA stalk. Outside this region of the molecule, the NAs of the two virus groups showed 99% similarity. These findings indicate that turkey H7N3 viruses were derived "in toto" from avian influenza strains circulating in wild waterfowl 1 year earlier, and represent an important step towards the comprehension of the mechanisms leading to interspecies transmission and emergence of potentially pandemic influenza viruses.

Descriptors: bird diseases transmission, ducks virology, influenza A virus, avian isolation and purification, avian influenza transmission, poultry diseases transmission, turkeys virology, amino acid sequence, animals, wild virology, bird diseases virology, evolution, molecular, hemagglutinin glycoproteins, influenza virus, avian influenza A virus genetics, avian influenza, virology, Italy, molecular sequence data, neuraminidase, phylogeny, poultry diseases virology, viral proteins.


NAL Call Number: 41.8 OF2

Descriptors: avian influenza, status in Mexico, poultry, control, immunization.


NAL Call Number: SF995.A1A9

Abstract: This paper reviews the worldwide situation regarding avian influenza infections in poultry from 1997 to March 2004. The increase in the number of primary introductions and the scientific data available on the molecular basis of pathogenicity have generated concerns particularly for legislative purposes and for international trade. This has led to a new proposed definition of ‘avian influenza’ to extend all infections caused by H5 and H7 viruses regardless of their virulence as notifiable diseases, although this has encountered some difficulties in being approved. The paper also reviews the major outbreaks caused by viruses of the H5 or H7 subtype and the control measures applied. The zoonotic aspects of avian influenza, which until 1997 were considered to be of limited relevance in human medicine, are also discussed. The human health implications have now gained importance, both for illness and fatalities that have occurred following natural infection with avian viruses, and for the potential of generating a reassortant virus that could give rise to the next human influenza pandemic. Copyright 2004 Houghton Trust Ltd


NAL Call Number: 241.71 B75

**NAL Call Number:** 41.8 V641

**Abstract:** Among the consequences of the epidemic of highly pathogenic avian influenza which affected Italy between 1999 and 2000 was an epidemic of Newcastle disease in northern and central Italy. It affected industrially reared poultry, dealer flocks and backyard flocks, with a total of 254 outbreaks notified up to December 31, 2000. Virological investigations yielded virulent isolates of Newcastle disease virus, which produced intracerebral pathogenicity indices ranging from 1.6 to 2.0 and which, on the basis of their monoclonal antibody binding patterns, could be classified as belonging to group C1. The clinical, gross and microscopical findings were typical of Newcastle disease, and different avian species were susceptible to different degrees. Chickens and guinea fowl appeared to be the most susceptible, followed by pheasants, turkeys and ostriches. The epidemiological inquiry highlighted the crucial role of a broiler hatchery in initiating the epidemic, and of dealers in perpetuating it. The control measures imposed by Directive 92/66/EEC are discussed with reference to the outbreaks in backyard flocks.

**Descriptors:** disease outbreaks, Newcastle disease epidemiology, animal husbandry, Italy epidemiology, Newcastle disease virus classification, Newcastle disease virus isolation and purification, Newcastle disease virus pathogenicity, poultry, serotyping.


**NAL Call Number:** 41.8 V641

**Descriptors:** disease outbreaks veterinary, influenza A virus, avian immunology, influenza vaccines, avian influenza prevention and control, turkeys, disease notification, disease outbreaks prevention and control, avian pathogenicity, avian influenza epidemiology, avian influenza virology, Italy epidemiology, poultry diseases epidemiology, poultry diseases prevention and control, vaccination veterinary.


**NAL Call Number:** SF601.V38

**Descriptors:** avian influenza A virus, disease control, disease distribution, outbreaks, mortality, vaccination, ducks, guineafowl, ostriches, pheasants, quails, turkeys, Italy.


**NAL Call Number:** 41.8 V641

**Descriptors:** fowl plague virology, influenza A virus avian classification, turkeys, disease outbreaks veterinary, fowl plague epidemiology, fowl plague prevention and control, hemagglutination inhibition tests veterinary, avian pathogenicity, Italy epidemiology, phylogeny.


**NAL Call Number:** 41.8 Av5

**Abstract:** From 1997 to 2001, Italy has been affected by two epidemics of high-pathogenicity avian influenza. The first epidemic was caused by a virus of the H5N2 subtype and was limited to eight premises in backyard and semi-intensive flocks. The prompt identification of the disease was followed by the implementation of European Union (EU) directive 92/40/EEC and resulted in the eradication of infection without serious consequences to the poultry industry. The 1999-00 epidemic was caused by a virus of the H7N1 subtype that originated from the mutation of a low pathogenic virus and resulted instead in a devastating epidemic that affected industrially reared poultry, culminating in the infection of 413 flocks. The description of the epidemics and the result of the control policies are reported.

**Descriptors:** epidemiology, infection, avian influenza, infectious disease, respiratory system disease, viral disease, European Union Directive 92, 40, EEC, disease eradication, poultry flocks.
NAL Call Number: SF995.A1A9

Abstract: Between the month of October 1997 and January 1998, eight outbreaks of highly pathogenic avian influenza were diagnosed in the Veneto and Friuli-Venezia Giulia regions in north-eastern Italy. For each of the eight outbreaks, influenza A virus of subtype H5N2 was isolated and the inoculation of susceptible chickens confirmed these viruses to be extremely virulent with intravenous pathogenicity indices in 6-week-old chickens of 2.98 to 3.00. Although it was not possible to trace the origin of infection, the epidemiological investigation revealed connections between several outbreaks and emphasized the well-known risk factors for avian influenza such as bird movement, rearing of mixed populations and contact with migratory waterfowl. Control measures listed in European Union directive 92/40/EEC were implemented promptly and spread of the infection to intensively-reared domestic poultry was avoided.

Descriptors: avian influenza virus, outbreaks, chickens, virulence, epidemiology, risk factors, disease control, diagnosis, viral antigens, antigen testing.


NAL Call Number: SF995.W4

Descriptors: avian influenza virus, Newcastle disease, epidemics, pathogenicity, Italy.


NAL Call Number: SF995.W4

Descriptors: avian influenza virus, epidemics, pathogenicity, poultry, Italy.


NAL Call Number: SF481.I58

Descriptors: avian influenza virus, epidemics, pathogenicity, Italy.


NAL Call Number: 41.8 V641

Descriptors: avian paramyxovirus, disease prevalence, disease surveys, migratory waterfowl, Anas crecca, Anas platyrhynchos.


Abstract: The present paper reviews the worldwide situation regarding avian influenza (AI) infections caused by viruses of the H5 and H7 subtype in poultry from 1999 to date. The increase in the number of primary introductions and the scientific data available on the molecular basis of pathogenicity have generated concerns particularly for legislative purposes, for international trade and on novel control strategies, including vaccination. This has led to a new proposed definition of "avian influenza" to extend to all infections caused by H5 and H7 viruses regardless of their virulence as notifiable diseases, although this has encountered some difficulties in being approved. Reference is also made to the zoonotic aspects of avian influenza which until 1997 were considered to be of limited relevance in human medicine, and have now gained importance, both for illness and fatalities which have occurred following natural infection with avian viruses, and for the potential of generating a reassortant virus which could give rise to the next human influenza pandemic.

Descriptors: avian influenza, outbreaks, control, zoonosis, poultry, avian influenza A virus, definition.

NAL Call Number: SF995.A1A9

Abstract: During 1999, northern Italy has been affected by an epidemic of low pathogenicity avian influenza (LPAI) caused by a virus of the H7N1 subtype. Due to the characteristics of the poultry industry in the area and to the absence of specific legislative tools to eradicate infection, the virus continued to circulate for several months until a highly pathogenic virus of the same subtype emerged. The highly pathogenic virus had caused death, at the time of writing, of over 13 million birds in 3 months. The consequences of the highly pathogenic avian influenza (HPAI) epidemic appear to be devastating for the poultry industry and the social community. Several conditions generated the current situation, including the high density of susceptible animals and the structure of the poultry industry in the infected area. In addition, the circulation of LPAI virus for a number of months inevitably delayed the prompt identification of HPAI and complicated the interpretation of diagnostic results. A reconsideration of current European legislation and a reorganization of the poultry industry are suggested to prevent the occurrence of similar situations in countries of the European Union.

Descriptors: animal husbandry, infection, epidemiology, enrichment broth, highly pathogenic avian influenza (HPAI), viral disease, low pathogenicity avian influenza (LPAI), H7N1 subtype, viral disease, epidemic.


NAL Call Number: RA407.3.M56

Abstract: Since mid-December 2003, eight Asian countries (Cambodia, China, Indonesia, Japan, Laos, South Korea, Thailand, and Vietnam) have reported an epizootic of highly pathogenic avian influenza in poultry and various other birds caused by influenza A (H5N1). As of February 9, 2004, a total of 23 laboratory-confirmed human cases of influenza A (H5N1) had been reported in Thailand and Vietnam. In 18 (78%) of these cases, the patients died. Clinical experience with avian H5N1 disease in humans is limited. The human H5N1 viruses identified in Asia in 2004 are antigenically and genetically distinguishable from the 1997 and February 2003 viruses. To aid surveillance and clinical activities, this report provides a preliminary clinical description of the initial five confirmed cases in Thailand.

Descriptors: influenza virology, influenza A virus, avian, child, fatal outcome, influenza diagnosis, influenza epidemiology, middle aged, Thailand epidemiology.


NAL Call Number: RA407.3.M56

Abstract: During December 2003-February 2004, outbreaks of highly pathogenic avian influenza A (H5N1) among poultry were reported in Cambodia, China, Indonesia, Japan, Laos, South Korea, Thailand, and Vietnam. As of February 9, 2004, a total of 23 cases of laboratory-confirmed influenza A (H5N1) virus infections in humans, resulting in 18 deaths, had been reported in Thailand and Vietnam. In addition, approximately 100 suspected cases in humans are under investigation by national health authorities in Thailand and Vietnam. CDC, the World Health Organization (WHO), and national health authorities in Asian countries are working to assess and monitor the situation, provide epidemiologic and laboratory support, and assist with control efforts. This report summarizes information about the human infections and avian outbreaks in Asia and provides recommendations to guide influenza A (H5N1) surveillance, diagnosis, and testing in the United States.

Descriptors: disease outbreaks prevention and control, influenza virology, influenza A virus, avian influenza isolation and purification, avian influenza epidemiology, Asia epidemiology, influenza epidemiology, influenza prevention and control, avian influenza virology, poultry, poultry diseases epidemiology, poultry diseases virology, public health practice, United States epidemiology.

This report summarizes influenza activity in the United States during September 29, 2003-March 27, 2004, and updates the previous summary. This report also summarizes human infections with avian influenza viruses related to poultry outbreaks in North America. Preliminary data collected through CDC influenza surveillance indicate that national influenza activity peaked during late November-December. The most frequently isolated viruses were influenza A (H3N2), and approximately 87% of these were similar to the drift variant A/Fujian/411/2002.

Descriptors: influenza epidemiology, influenza A virus isolation and purification, adult, child, influenza mortality, influenza virology, influenza B virus isolation and purification, avian influenza epidemiology, poultry, seasons, United States epidemiology.


Abstract: In 1998, a novel H3N2 reassortant virus emerged in the United States swine population. We report the interspecies transmission of this virus to turkeys in two geographically distant farms in the United States in 2003. This event is of concern, considering the reassortment capacity of this virus and the susceptibility of turkey to infection by avian influenza viruses. Two H3N2 isolates, A/turkey/NC/16108/03 and A/turkey/MN/764/03, had 98.0% to 99.9% nucleotide sequence identity to each other in all eight gene segments. All protein components of the turkey isolates had 97% to 98% sequence identity to swine H3N2 viruses, thus demonstrating interspecies transmission from pigs to turkeys. The turkey isolates were better adapted to avian hosts than were their closest swine counterparts, which suggests that the viruses had already begun to evolve in the new host. The isolation of swine-like H3N2 influenza viruses from turkeys raises new concerns for the generation of novel viruses that could affect humans.

Descriptors: influenza veterinary, influenza A virus, porcine pathogenicity, poultry diseases transmission, swine diseases transmission, turkeys virology, antigenic variation, influenza transmission, porcine genetics, phylogeny, poultry diseases virology, swine, swine diseases virology, United States epidemiology.


Abstract: H9N2 influenza viruses are panzootic in domestic poultry in Eurasia and since 1999 have caused transient infections in humans and pigs. To investigate the zoonotic potential of H9N2 viruses, we studied the evolution of the viruses in live-poultry markets in Hong Kong in 2003. H9N2 was the most prevalent influenza virus subtype in the live-poultry markets between 2001 and 2003. Antigenic and phylogenetic analysis of hemagglutinin (HA) showed that all of the 19 isolates found except one belonged to the lineage represented by A/Duck/Hong Kong/Y280/97 (H9N2). The exception was A/Guinea fowl/NT184/03 (H9N2), whose HA is most closely related to that of the human isolate A/Guangzhou/333/99 (H9N2), a virus belonging to the A/Chicken/Beijing/1/94-like (H9N2) lineage. At least six different genotypes were recognized. The majority of the viruses had nonstructural (and HA) genes derived from the A/Duck/Hong Kong/Y280/97-like virus lineage but had other genes of mixed avian virus origin, including genes similar to those of H5N1 viruses isolated in 2001. Viruses of all six genotypes of H9N2 found were able to replicate in chickens and mice without adaptation. The infected chickens showed no signs of disease, but representatives of two viral genotypes were lethal to mice. Three genotypes of virus replicated in the respiratory tracts of swine, which shed virus for at least 5 days. These results show an increasing genetic and biologic diversity of H9N2 viruses in Hong Kong and support their potential role as pandemic influenza agents.

Descriptors: evolution, molecular, influenza A virus, avian classification, avian genetics, poultry virology, chickens virology, China, hemagglutination inhibition tests, avian growth and development, avian isolation and purification, lung virology, mice, mice, inbred balb c, phylogeny, swine virology, virus replication.


Abstract: We surveyed live-poultry markets in Korea in 2003 and isolated 9 H9N2, 6 H3N2, and 1 H6N1 influenza viruses. Antigenic and phylogenetic analyses showed that all 9 H9N2 isolates were of A/Chicken/Korea/25232-96006/96-like lineage (which caused disease in chickens in Korea in 1996) but were different from H9N2 viruses of southeastern China. They had at least 4 genotypes and replicated in chickens but not in mice. The H3N2 and H6N1 viruses were new to Korea and were probably reassortants of avian influenza viruses from southeastern China and recent Korean H9N2 viruses. All 8 segments of the H3N2 viruses formed a single phylogenetic cluster with 99.1 to 100% homology. The H3N2 viruses replicated in chickens and mice without preadaptation, but the H6N1 virus did not. Our results show an increasingly diverse pool of avian influenza viruses in Korea that are potential pandemic influenza agents.

Descriptors: avian influenza A virus pathogenicity, poultry virology, amino acid sequence, chickens virology, conserved sequence, avian influenza A virus classification, avian influenza A virus isolation and purification, Korea, mice, molecular sequence data, phylogeny, poultry diseases virology, rodent diseases.
Cornell University - Department of Population Medicine & Diagnostic Sciences - Animal Health Diagnostic Center - College of Veterinary Medicine (2005). **Canine Influenza Virus - Detection and Sampling.**

Online: http://www.diaglab.vet.cornell.edu/issues/civ-dect.asp

Abstract: Canine influenza virus is a relatively new pathogen of dogs. It was first identified in racing greyhounds in 2004 and this virus appears to have been involved with significant respiratory problems on the dog tracks throughout the US for the last 2-3 years. The Virology Lab at Cornell isolated the first influenza virus from an animal that died during one of these clinical episodes. Evidence of infection of non-greyhounds by influenza virus has been found in Florida within the past year as part of the ongoing research efforts by Dr Cynda Crawford at the University of Florida on respiratory disease in dogs.


**NAL Call Number:** 472 N21

**Descriptors:** influenza diagnosis, influenza veterinary, influenza A virus, avian isolation and purification, adult, Cambodia epidemiology, chickens virology, child, developing countries economics, influenza epidemiology, influenza prevention and control, Laos epidemiology, public health economics, Thailand, Vietnam, zoonoses epidemiology, zoonoses transmission, zoonoses virology.


**NAL Call Number:** 472 N21

**Descriptors:** biomedical research, birds virology, influenza veterinary, influenza A virus, avian isolation and purification, language, periodicals, swine virology, southeastern Asia epidemiology, China epidemiology, communicable disease control, communication barriers, influenza epidemiology, influenza transmission, influenza virology, avian classification, publishing, time factors, zoonoses transmission, zoonoses virology.


**Descriptors:** chickens, disease outbreaks veterinary, influenza A virus, avian growth and development, avian influenza epidemiology, poultry diseases epidemiology, West Nile fever epidemiology, West Nile virus growth and development, Arizona epidemiology, California epidemiology, China epidemiology, influenza, avian virology, middle aged, poultry diseases virology, Vietnam epidemiology, West Nile fever virology.


**NAL Call Number:** 41.8 Av5

**Abstract:** The nonpathogenic avian influenza (AI) outbreak in Pennsylvania began in December 1996 when there was a trace back from a New York live bird market to a dealer's flock. A total of 18 commercial layer flocks, two commercial layer pullet flocks, and a commercial meat turkey flock were diagnosed with nonpathogenic AI (H7N2) viral infection with an economic loss estimated at between dollar sign3 and dollar sign4 million. Clinical histories of flocks infected with the disease included respiratory disease, elevated morbidity and mortality throughout the house, egg production drops, depression, and lethargy. A unique gross lesion in the commercial layers was a severe, transmural oviduct edema with white to gray flocculent purulent material in the lumen. Layer flocks on two separate premises were quarantined but permitted to remain in the facilities until cessation of virus shed was determined through virus isolation. Several months later, clinical AI appeared again in these flocks. It is not known whether the recurrence of disease in these cases is due to persistence of the organism in the birds or the environment. In addition to serologic testing and virologic testing by chicken embryo inoculation, an antigen capture enzyme immunoassay was
evaluated as a diagnostic tool for AI. Research projects related to disinfection, burial pits, and geographical system technology were developed because of questions raised concerning transmission, diagnosis, and control of nonpathogenic AI (H7N2).

Descriptors: epidemiology, infection, avian influenza, infectious disease, respiratory system disease, viral disease, serology, clinical techniques, diagnostic techniques, commercial layer flocks, disease outbreak, disease transmission, economic losses, live bird market.


NAL Call Number: 41.8 Am3

Descriptors: economic losses, economic analysis, outbreaks, disease control, avian influenza virus, turkeys, United States, Pennsylvania.


NAL Call Number: SF601.V44

Abstract: We report the results of a 6-year serological and virological monitoring performed in ducks and coots in Italy, in order to assess the degree of influenza A virus circulation in these birds during wintering. A total of 1039 sera collected from 1992 to 1998 was screened by a double antibody sandwich blocking ELISA (NP-ELISA): seroprevalence of antibodies to influenza A viruses was significantly higher in ducks compared to coots (52.2% vs. 7.1%, respectively). The hemagglutination-inhibition (HI) assay, performed on NP-ELISA positive sera, showed that 16.9% of these duck sera and 33.3% of these coot sera had antibodies to at least one influenza virus HA subtype: ducks showed HI antibodies against most of the HA subtypes, except for the H3, H4, H7, and H12; coots were seropositive to the H3 and H10 subtypes, only. From 1993 to 1998, 22 virus strains were obtained from 802 cloacal swabs, with an overall virus isolation frequency of 2.7%. Viruses belonging to the H1N1 subtype were by far the most commonly circulating strains (18/22) and were isolated mainly from ducks (17/18). The remaining viruses were representative of the H10N8, H5N2 and H3N8 subtypes. Our data indicate some differences between influenza A virus circulation in sympatic ducks and coots and a significant antigenic diversity between some reference strains and viruses recently isolated in Italy.

Descriptors: bird diseases virology, disease reservoirs veterinary, ducks, influenza veterinary, influenza A virus, avian isolation and purification, antibodies, viral blood, cloaca virology, ecosystem, enzyme linked immunosorbent assay veterinary, hemagglutination inhibition tests veterinary, influenza blood, influenza epidemiology, influenza virology, Italy epidemiology, seroepidemiologic studies.


NAL Call Number: SF601.V38

Descriptors: avian influenza virus, disease distribution, disease prevalence, predatory birds, waterfowl, wild birds, Italy.


NAL Call Number: 41.8 T431

Abstract: To get an impression of the presence of pathogens in multi-aged flocks of old fancy chicken breeds in the Netherlands, plasma samples originating from 24 flocks were examined for antibodies against 17 chicken pathogens. These flocks were housed mainly in the centre and east of the Netherlands, regions with a high poultry density. The owners of the tested flocks showed their chicken at national and international poultry exhibitions. Antibodies against Avian Influenza, Egg Drop Syndrome '76 virus, Pox...
virus, Salmonella pullorum/gallinarum, Salmonella Enteritidis or Salmonella Typhimurium were not detected. However, antibodies against other Salmonella species, Mycoplasma gallisepticum, infectious bursal disease virus, infectious bronchitis virus, avian encephalomyelitis virus, chicken anaemia virus, infectious laryngotracheitis virus, and avian leukosis virus, subgroups A and B, and subgroup J were detected in a varying proportion of the flocks. This study shows that antibodies against many chicken pathogens are present among the flocks of old fancy chicken breeds that are exhibited at international poultry exhibitions. **Descriptors:** bacterial infections veterinary, chickens, poultry diseases epidemiology, virus diseases veterinary, antibodies, bacterial blood, viral blood, bacterial infections epidemiology, Netherlands epidemiology, poultry diseases microbiology, prevalence, risk factors, seroepidemiologic studies, virus diseases epidemiology.
positive flocks were euthanatized in-house within 11 days of the original case submission date. Increased surveillance of poultry flocks within 10-mile radius zones centered at the foci of the positive farms continued until March 1, 2002. No additional cases were detected.

Descriptors: epidemiology, infection, avian influenza, infectious disease, respiratory system disease, viral disease, broiler breeder flocks, disease outbreak, seroconversion.


NAL Call Number: RJ1.J6


NAL Call Number: SF995.W4


NAL Call Number: 41.8 Av5
Abstract: A Geographic Information System (GIS) is a very powerful and flexible software tool for effective management of spatially referenced data (e.g., geodata). Coupling database and GIS technology provides the tools for a detailed analysis of spatial patterns and distributions in veterinary applications. A specific veterinary GIS (VetGIS) toolbox was developed to perform the calculation of indices such as Lorenz curve, GINI index, and a kernel-based animal density estimation. This software was employed for the analysis and management of avian influenza in Italy during the 1999-2000 epidemic.
Descriptors: epidemiology, infection, avian influenza, epidemiology, infectious disease, respiratory system disease, viral disease, geographic information system (GIS) applied and field techniques, epidemic contingency plan, epidemiological data.


NAL Call Number: 41.8 Av5
Abstract: Clinical signs and gross lesions observed in poultry submitted for postmortem examination (PME) from the first five infected poultry flocks preceding the detection of the primary outbreak of highly pathogenic avian influenza (HPAI) of subtype H7N7 during the 2003 epidemic in the Netherlands are described. The absence of HPAI from the Netherlands for more than 75 yr created a situation in which poultry farmers and veterinary practitioners did not think of AI in the differential diagnosis as a possible cause of the clinical problems seen. Increased and progressive mortality was not reported to the governmental authorities by farmers or veterinary practitioners. It took 4 days from the first entry of postmortem material to notify the governmental authorities of a strong suspicion of an AI outbreak on the basis of a positive immunofluorescence test result. The gross lesions observed at PME did not comply with the descriptions in literature, especially the lack of hemorrhagic changes in tissues, and the lack of edema and cyanosis in comb and wattles is noted. The following lessons are learned from this epidemic: a) in the future, increased and progressive mortality should be a signal to exclude AI as cause of disease problems on poultry farms; b) intensive contact between the veterinary practitioner in the field and the veterinarian executing PME is necessary to have all relevant data and developments at one's disposal to come to a conclusive diagnosis; c) in an anamnesis, reporting of high or increased mortality should be quantified in the future (number of dead birds in relation to the number of birds brought to the farm to start production, together with the timing within the production cycle), or else this mortality cannot be interpreted properly; d) if clinical findings such as high mortality indicate the possibility of HPAI, the pathologist should submit clinical samples to the
reference laboratory, even if PME gives no specific indications for HPAI; e) the best way to facilitate early
detection of an HPAI outbreak is to have the poultry farmer and/or veterinary practitioner immediately report
to the syndrome-reporting system currently in operation the occurrence of high mortality, a large decrease in
feed or water intake, or a considerable drop in egg production; f) in order to detect low pathogenic avian
influences infections that could possibly change to HPAI, a continuous serologic monitoring system has been
set up, in which commercial poultry flocks are screened for antibodies against AI virus of subtypes H5 and
H7.

**Descriptors:** disease outbreaks veterinary, influenza A virus, avian influenza, avian epidemiology, poultry
diseases epidemiology, disease outbreaks history, epidemiologic methods veterinary, fluorescent antibody
technique, veterinary history, 21st century, avian mortality, avian pathology, Netherlands epidemiology,
poultry, poultry diseases pathology, poultry diseases virology.


**Abstract:** Outbreaks of highly pathogenic H5N1 avian influenza have occurred in Hong Kong in chickens
and other gallinaceous poultry in 1997, 2001, twice in 2002 and 2003. High mortality rates were seen in
gallinaceous birds but not in domestic or wild waterfowl or other wild birds until late 2002 when highly
pathogenic H5N1 avian influenza occurred in waterfowl (geese, ducks and swans), captive Greater
Flamingo (Phoenicopterus ruber) and other wild birds (Little Egret Egretta garzetta) at two waterfowl parks
and from two dead wild Grey Heron (Ardea cinerea) and a Black-headed Gull (Larus ridibundus) in Hong
Kong. H5N1 avian influenza virus was also isolated from a dead feral pigeon (Columba livia) and a dead tree
sparrow (Passer montanus) during the second outbreak. The first waterfowl outbreak was controlled by
immediate strict quarantine and depopulation 1 week before the second outbreak commenced. Control
measures implemented for the second outbreak included strict isolation, culling, increased sanitation and
vaccination. Outbreaks in gallinaceous birds occurred in some live poultry markets concurrently with the
second waterfowl outbreak, and infection on a chicken farm was detected 1 week after the second waterfowl
park outbreak was detected, on the same day the second grey heron case was detected. Subsequent virus
surveillance showed the outbreaks had been contained.

**Descriptors:** bird diseases epidemiology, bird diseases virology, communicable disease control, disease
outbreaks veterinary, influenza A virus, avian pathogenicity, influenza, avian epidemiology, bird diseases
transmission, birds, Hong Kong, immunoassay veterinary, immunoenzyme techniques veterinary, avian
transmission, reverse transcriptase polymerase chain reaction veterinary.

590. ISSN: 1095-9203.

**NAL Call Number:** 470 Sci2

**Descriptors:** antibodies, viral blood, conjunctivitis, viral virology, influenza A virus, avian immunology,
occupational diseases epidemiology, orthomyxoviridae infections epidemiology, agricultural workers'
diseases epidemiology, agricultural workers' diseases virology, viral epidemiology, disease outbreaks
veterinary, hemagglutination inhibition tests, influenza, avian epidemiology, Netherlands epidemiology,
occupational diseases virology, orthomyxoviridae infections transmission, orthomyxoviridae infections
virology, poultry, zoonoses.

1095-9203.

**NAL Call Number:** 470 Sci2

**Descriptors:** Carnivora virology, cat diseases virology, influenza veterinary, influenza A virus, avian
pathogenic, avian genetics, avian influenza transmission, avian influenza virology, poultry, swine, swine
diseases virology.

NAL Call Number: 47.8 So89
Descriptors: avian influenza virus, genomes, pathogenicity, hosts, disease control, monitoring, immunization, immunostimulation, immunotherapy, South Africa, poultry.

NAL Call Number: 470 Sci2

NAL Call Number: 449.9 Un3r
Descriptors: avian influenza virus, disease control, eradication, problems.

NAL Call Number: 41.8 C61
Descriptors: wild birds, avian influenza virus, monitoring.

Descriptors: disease outbreaks prevention and control, influenza epidemiology, influenza A virus classification, influenza A virus genetics, influenza A virus pathogenicity, zoonoses virology, birds, communicable disease control, influenza prevention and control, influenza transmission, avian influenza transmission, poultry, world health, zoonoses transmission.

NAL Call Number: 47.8 R523
Descriptors: avian influenza virus, disease control, epidemic, poultry, zoonoses, South East Asia.

NAL Call Number: SF995.W4
Descriptors: turkeys, avian influenza virus, diagnosis, disease transmission, disease distribution, economic impact, California.

NAL Call Number: QR360.J6
Abstract: The 2004 outbreaks of H5N1 influenza viruses in Vietnam and Thailand were highly lethal to humans and to poultry; therefore, newly emerging avian influenza A viruses pose a continued threat, not only to avian species but also to humans. We studied the pathogenicity of four human and nine avian

Abstract: The 2004 outbreaks of H5N1 influenza viruses in Vietnam and Thailand were highly lethal to humans and to poultry; therefore, newly emerging avian influenza A viruses pose a continued threat, not only to avian species but also to humans. We studied the pathogenicity of four human and nine avian...
H5N1/04 influenza viruses in ferrets (an excellent model for influenza studies). All four human isolates were fatal to intranasally inoculated ferrets. The human isolate A/Vietnam/1203/04 (H5N1) was the most pathogenic isolate; the severity of disease was associated with a broad tissue tropism and high virus titers in multiple organs, including the brain. High fever, weight loss, anorexia, extreme lethargy, and diarrhea were observed. Two avian H5N1/04 isolates were as pathogenic as the human viruses, causing lethal systemic infections in ferrets. Seven of nine H5N1/04 viruses isolated from avian species caused mild infections, with virus replication restricted to the upper respiratory tract. All chicken isolates were nonlethal to ferrets. A sequence analysis revealed polybasic amino acids in the hemagglutinin connecting peptides of all H5N1/04 viruses, indicating that multiple molecular differences in other genes are important for a high level of virulence. Interestingly, the human A/Vietnam/1203/04 isolate had a lysine substitution at position 627 of PB2 and had one to eight amino acid changes in all gene products except that of the M1 gene, unlike the A/chicken/Vietnam/C58/04 and A/quail/Vietnam/36/04 viruses. Our results indicate that viruses that are lethal to mammals are circulating among birds in Asia and suggest that pathogenicity in ferrets, and perhaps humans, reflects a complex combination of different residues rather than a single amino acid difference.

Descriptors: influenza virus infection, respiratory system disease, viral disease complications, etiology, mortality, pathology, transmission, Vietnam, Thailand, ferrets, chickens, humans.


Abstract: Influenza viruses from chickens (H5N1) have caused outbreaks in children from both Vietnam and Thailand in 2004. All infected patients presented with fever and cough. Striking laboratory findings included leukopenia and thrombocytopenia. All children who developed progressive pneumonia with acute respiratory distress syndrome died. However, very few children received antiviral therapy.


Descriptors: disease outbreaks prevention and control, influenza epidemiology, world health, antiviral agents therapeutic use, influenza drug therapy, influenza prevention and control, influenza virology, influenza vaccine administration and dosage, orthomyxoviridae genetics, orthomyxoviridae immunology, practice guidelines, vaccination, World Health Organization.


NAL Call Number: 500 N484

Abstract: Avian influenza (AI) viruses are Type A influenza viruses of the Orthomyxoviridae family. There are 15 subtypes of the virus widespread in migratory waterfowl throughout the world. It has become increasingly evident that some low pathogenic avian influenza (LPAI) H5 or H7 viruses have the capacity to mutate into the more virulent strains that cause extensive economic losses and high mortality. Recent AI disease outbreaks in several countries have increased attention and concern over low pathogenic H5 and H7 AI viruses. This heightened international concern increases the risk of unnecessary trade bans. For the US poultry industry, avian influenza continues to be a challenge to the flow of trade. On one hand, there is the increased focus of world attention on the H5 and H7 low pathogenic AI virus and the possibility of mutation. On the other hand, there are the factors contributing to our finding of infected flocks. Among these, perhaps the most important is the ever-present reservoir of virus in the migratory waterfowl population. With the discovery of exposed flocks comes the threat of trade bans.

Descriptors: commerce, disease outbreaks, influenza A virus, pathogenicity, prevention and control, transmission, poultry, wild animals, ducks, avian genetics, epidemiology, public policy, United States.

occurring in Italy. *Tijdschrift Voor Diergeneeskunde* 125(6): 188-189. ISSN: 0040-7453.
NAL Call Number: 41.8 T431
Descriptors: outbreaks, pathogenesis, avian influenza virus, Italy, Netherlands.

NAL Call Number: RA648.5.E46
Abstract: Genome sequences of chicken (low pathogenic avian influenza [LPAI] and highly pathogenic avian influenza [HPAI]) and human isolates from a 2004 outbreak of H7N3 avian influenza in Canada showed a novel insertion in the HA0 cleavage site of the human and HPAI isolate. This insertion likely occurred by recombination between the hemagglutination and matrix genes in the LPAI virus.
Descriptors: disease outbreaks veterinary, influenza A virus, avian genetics, avian influenza epidemiology, amino acid sequence, British Columbia epidemiology, chickens, avian influenza pathogenicity, avian influenza virology, models, molecular, molecular sequence data, mutagenesis, insertion, protein conformation, sequence alignment, viral proteins chemistry.

NAL Call Number: 47.8 Ar2
Descriptors: disease control, consequences, outbreaks, poultry, vaccination, avian influenza virus, Netherlands, Germany, Belgium.

NAL Call Number: RC960.S6
Abstract: Influenza surveillance networks in Guangdong were established to investigate the epidemiological characteristics of influenza and influenza epidemics. Influenza activity peaked annually from March to July in Guangdong in 1991-2000; influenza H3N2 predominated in the epidemic (7 years of 10); the outbreak of influenza in 1996 was the remarkable result of antigenic drift of H3N2 strain. Ten isolates of H9N2 strains were discovered from human subjects in 1998 and 1999: chicken strains isolated after the Hong Kong fowl influenza outbreak. It was found that there was just one influenza activity season per annum in Guangdong and that the influenza H3N2 subtype still predominates in Guangdong. Further research into the pathogenicity of influenza H9N2 in humans warranted.
Descriptors: disease outbreaks, influenza epidemiology, animals, domestic virology, chickens virology, China epidemiology, disease notification, influenza A virus avian isolation and purification, avian pathogenicity, population surveillance.

Descriptors: monitoring, disease surveys, control programs, disease transmission, prevalence, disinfection, hygiene, avian influenza virus, northeast, United States.

NAL Call Number: aSF601.U5

**NAL Call Number:** RA648.5.E46

**Descriptors:** avian influenza virus, outbreaks, disease control, risk assessment, Pennsylvania.


**NAL Call Number:** QD431.T3

**Descriptors:** influenza A virus, avian pathogenicity, SARS virus pathogenicity, severe acute respiratory syndrome virology, Asia epidemiology, disease outbreaks, avian influenza epidemiology, avian influenza transmission, avian influenza virology, poultry diseases epidemiology, poultry diseases transmission, virulence, zoonoses epidemiology, zoonoses transmission.


**NAL Call Number:** R99.N4

**Descriptors:** influenza, avian epidemiology, public health, communicable disease control methods, disease outbreaks statistics and numerical data, influenza A virus isolation and purification, avian influenza transmission, avian influenza virology, New Zealand epidemiology, poultry, risk factors, world health, zoonoses epidemiology, zoonoses transmission, zoonoses virology.


**Abstract:** The paper explores the social representation of the 2001 Hong Kong avian bird flu epidemic from the perspective of local women. Fifty women were asked to describe their first thoughts about the flu, and these were subsequently explored. Thematic analysis of the semi-structured interviews revealed that the first thoughts were characterized by: (a) the origin of the epidemic, (b) anchors for it, (c) emotions about it, and (d) images of it. Aspersion concerning the lack of hygiene of Mainland Chinese chicken rearers and chicken sellers in Hong Kong dominated the interviews. Other environmental factors were also stressed, as was regulation leniency and a drive to profit. Comparisons between old traditions and newer practices formed a central feature. The findings are discussed in terms of their continuity with western risk findings as well as their specific cultural nuances.

**Descriptors:** bird diseases epidemiology, food, social behavior, adult, bird diseases virology, culture, disease outbreaks, health behavior, Hong Kong epidemiology, hygiene, influenza A virus, avian isolation and purification, middle aged, questionnaires.


**NAL Call Number:** 41.8 Av5

**Abstract:** The epidemiology of the first reported non-fowl-plague avian influenza (AI) virus, A/Chicken/Alabama/75 (Hav4Neq2), isolated from chickens in the United States is discussed. The signs and pathologic changes have been described. The environment, nutrition, and stress factors are discussed as possible contributors to the disease syndrome observed in 3 commercial egg-laying flocks. Avian influenza antibody was demonstrated by agargel precipitation in convalescent chickens through 83 days postinfection. A serological survey of 321 additional poultry flocks was negative for antibodies against avian influenza. A survey was made by serology and virus isolation techniques on 387 wild free-flying birds that fed and roosted in the area. Wild waterfowl are discussed as a possible source of the AI virus.

**Descriptors:** chickens, disease outbreaks veterinary, influenza veterinary, poultry diseases epidemiology, Alabama, bird diseases immunology, birds, influenza epidemiology, influenza immunology, poultry diseases.
immunology.


**Descriptors**: disease outbreaks prevention and control, influenza epidemiology, influenza A virus, avian pathogenicity, avian influenza epidemiology, southeastern Asia epidemiology, birds, influenza prevention and control, influenza transmission, avian influenza prevention and control, avian influenza transmission.


**NAL Call Number**: 41.8 AC83

**Abstract**: A large number of diseases occur in domestic, farm-raised poultry. Only two of the many different diseases are notifiable and subject to governmental control: highly pathogenic avian influenza and Newcastle disease. Diagnosis and treatment or prevention of all other conditions are left to the skills of farmers and their veterinarians. Poultry production is aimed at providing more and tastier food for the ever growing human community. Infectious diseases and technical errors during production and processing need to be minimised. The concept of hazard analysis critical control point (HACCP) has already been introduced into food processing and quality assessment. The regulations laid down in ISO 9000 will soon become a powerful and practical tool for monitoring and improving the productivity of live poultry. Approved epidemiological concepts and tools will enable the poultry industry to achieve constant and safe production. Certification on the basis of ISO 9000 of all areas of poultry production is a new approach for maintaining the health of poultry, for tracing and subsequently eliminating breaks in productivity, and securing production without health hazards for the consumer.

**Descriptors**: chickens, communicable diseases veterinary, poultry diseases epidemiology, turkeys, communicable diseases epidemiology, consumer product safety standards, disease outbreaks, food handling standards, guidelines, incidence, meat standards, poultry diseases diagnosis, poultry diseases etiology, poultry products standards, proportional hazards models.


**NAL Call Number**: 41.8 D482

**Abstract**: The scientific literature of the past century is reviewed on fowl plague (presently termed highly pathogenic avian influenza, HPAI) in pigeons. HPAI viruses cause epidemic disease outbreaks with high rates of losses in many avian species, particularly in chickens and turkeys. Also susceptible to disease are quails, guinea fowl, ducks, geese, ostriches, passerine birds, and birds of prey whereas conflicting reports on the susceptibility of the domestic pigeon exist. Based on literature reports and on own experiments, and applying as criteria for judgements clinically overt forms of disease, virus multiplication plus shedding and seroconversion, it is concluded that domestic pigeons are only partially susceptible to influenza A viruses of the haemagglutinin subtype H7. Infection of pigeons with H7 viruses results only in some of them in signs, virus shedding and seroconversion. Using the same criteria, pigeons appear to be even less susceptible to infection with influenza A viruses of the H5 subtype. Only one of five publications describe in 1/19 pigeons exposed to H5 influenza A virus depression one day before death, and only 2/19 multiplied and excreted virus, and 1/19 developed circulating antibodies. Consequently, pigeons play only a minor role in the epidemiology of H5 influenza viruses. In contrast, following infection with influenza A virus of the subtype H7 clinical signs in pigeons consist of conjunctivitis, tremor, paresis of wings and legs, and wet droppings. H7-infected pigeons multiply and excrete H7 viruses and develop circulating antibodies. Albeit of the status of infection, free-flying domestic pigeons can act as mechanical vectors and vehicles for long-distance transmission of any influenza A virus if plumage or feet were contaminated.

**Descriptors**: Columbidae virology, influenza A virus, avian pathogenicity, avian influenza virology, chick embryo, chickens, disease susceptibility veterinary, ducks, avian classification, avian influenza pathology, avian influenza transmission, species specificity, virus shedding.

NAL Call Number: aSF601.U5
Descriptors: poultry, north eastern states United States, avian influenza virus, epidemiology, America, domestic animals, domesticated birds, influenza virus, livestock, North America, United States, useful animals, viruses.


NAL Call Number: 100 M66 1
Descriptors: turkeys, avian influenza virus, viral diseases, epidemiology, disease transmission, diagnosis, vaccination, Minnesota.


Abstract: In February 2003, the highly pathogenic avian influenza-A virus, subtype H7N7, was the causative agent of a large outbreak of fowl plague in the Netherlands. Two days after visiting a poultry farm that was infected by fowl plague, a 57-year-old male veterinarian developed malaise, headache and fever. After 8 days he was admitted to hospital with signs of pneumonia. Five days later, his condition deteriorated alarmingly. Despite extensive pharmacotherapy he died 4 days later of acute pneumonia. Influenza-A virus, subtype H7N7, was identified by means of reverse transcriptase/PCR in broncho-alveolar washings that had been obtained earlier; routine virus culture yielded the isolate A/Nederland/219/03, which differs by 14 amino-acid substitutions from the first isolate in a chicken (A/kip/Nederland/1/03). Partly as a result of this case, the preventive measures were then adjusted; people who came into contact with infected poultry were given increased possibilities for vaccination and the administration of oseltamivir.


Descriptors: influenza, avian epidemiology, Canada epidemiology, poultry.


Abstract: Recent outbreaks of highly pathogenic avian influenza in chickens and ducks that occurred in 9 Asian countries including Japan alarmed to realize that there is no border for infections and gave a rise to great concern for human health as well as for agriculture. This H5N1 virus jumped the species barrier and caused severe disease with high mortality in humans in Viet Nam and Thailand; 15 deaths of 22 cases and 8 of 12, respectively. A second concern was the possibility that the situation could give rise to another influenza pandemic in humans since genetic reassortment may occur between avian and human influenza viruses when a person is concurrently infected with viruses from both species. This process of gene swapping inside the human body can give rise to a new subtype of the influenza virus to which humans would not have immunity. The outbreaks also emphasized the need to continue active surveillance on avian influenza throughout the year to undertake aggressive emergency control measures as soon as an infection is detected.

Descriptors: influenza A virus, avian genetics, avian pathogenicity, Asia epidemiology, disease outbreaks, Europe epidemiology, influenza epidemiology, influenza virology, avian influenza epidemiology, avian influenza virology, poultry, zoonoses epidemiology, zoonoses transmission, zoonoses virology.

**Abstract:** Between February 2000 and February 2002, the California Animal Health and Food Safety Laboratory System diagnosed 26 cases of low-pathogenic H6N2 avian influenza from 12 commercial egg-laying farms. The most common gross and histologic lesions observed in infected chickens were fibrinous yolk peritonitis, salpingitis, oophoritis, and nephritis. Edema of the mesentery of the oviduct and pale, swollen kidneys were also observed. Mortality in infected flocks ranged from 0.25% to 3%, and egg production dropped 7% to 40%.

**Descriptors:** infection, veterinary medicine, avian influenza, infectious disease, respiratory system disease, viral disease, fibrinous yolk peritonitis, digestive system disease, reproductive system disease, female, nephritis, urologic disease, oophoritis, endocrine disease, gonads, reproductive system disease, female, salpingitis, reproductive system disease, female, clinicopathology commercial egg laying farms commercial layer flocks.


**Descriptors:** disease outbreaks history, disease outbreaks veterinary, fowl plague history, influenza A virus avian isolation and purification, Austria epidemiology, filtration instrumentation, fowl plague diagnosis, fowl plague epidemiology, fowl plague etiology, Germany epidemiology, history of medicine, 19th century, history of medicine, 20th century, Italy epidemiology, poultry.


**Abstract:** PURPOSE OF REVIEW: New emerging infections over the last few years demonstrate the potential for the introduction of epidemic illness through global migration. The increasing number of children adopted internationally (>20,000 in 2003, from the United States State Department) provides a unique situation for the spread of emerging infections through the combination of international travel by parents through areas where such infections may be contracted and the nature of the living conditions for many of the orphans being placed by this process. RECENT FINDINGS: The recent literature on three emerging infections—avian influenza, severe acute respiratory syndrome (SARS) and measles—describes clinical aspects of the illnesses and their epidemiology. For avian influenza aspects of the agrarian economy in southeast Asia enabled the virus to reach the human population. The potential for further adaptation to people could set the stage for a new pandemic. SARS evolved in rural China and spread worldwide in one season with an approximate 10% mortality. Attention to public-health measures led to control of this new illness. Most recently, outbreaks of measles in Chinese orphanages have been documented. These findings demonstrate the potential of such infections to be transmitted during the process of international adoption, and in the case of measles the realization of this potential in recent reported cases from Chinese orphanages brought to the United States on commercial airlines. SUMMARY: Clinicians involved in international adoption and public-health officials assessing emerging infections need to work together in monitoring these issues.

**Descriptors:** adoption, communicable diseases, emerging epidemiology, emigration and immigration, severe acute respiratory syndrome epidemiology, adolescent, adult, child, preschool child, communicable disease control, communicable diseases, emerging transmission, infant, influenza epidemiology, influenza transmission, influenza A virus, avian, SARS virus, severe acute respiratory syndrome transmission.


**NAL Call Number:** aSF995.6.i6l5 1981a

**Descriptors:** avian influenza virus, ducks, turkeys, pheasants, wild birds, Canada, outbreaks.


**NAL Call Number:** 448.8 J821

**Abstract:** Influenza type A virus periodically undergoes major antigenic shifts in which the hemagglutinin (HAG) and sometimes the neuraminidase (NA) antigens are replaced by HAG and NA antigens of another subtype. Three such shifts have taken place since the virus was first isolated, and all appear to have occurred in China. The way in which these "new" influenza type A viruses suddenly appear (or reappear) in the human population is not known. At a meeting held in Beijing, China, on November 10-12, 1982, participants discussed the latest findings on the molecular biology of influenza viruses and on aspects of their ecology that may offer insight into the factors responsible for the origin of pandemic influenza viruses. Information obtained in earlier studies has provided some clues about how the antigenic shifts may occur. For example, the H3N2 virus has been found to be a recombinant deriving seven of its eight genes from an H2N2 strain and gene 4 (which encodes for the HAG) from some other virus, possibly an avian influenza virus of the H3 subtype [1-3]. In addition, studies of the genome of the H1N1 virus that appeared in Anshan, China, in 1977 have shown that this virus almost certainly underwent no replication for 27 years. This finding suggests that the virus existed in an animal reservoir during this period [4, 5].

**Descriptors:** influenza microbiology, influenza A virus human physiology, orthomyxoviridae physiology, antigens, viral immunology, China, disease reservoirs, ecology, epitopes immunology, genes viral, hemagglutinis viral immunology, influenza therapy, human genetics, influenza A virus physiology, influenza vaccine immunology, macromolecular systems, neuraminidase genetics, neuraminidase immunology, orthomyxoviridae genetics, orthomyxoviridae immunology, recombination, genetic, T lymphocytes, cytotoxic immunology, virus replication.

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**NAL Call Number:** SF995.A1A9

**Abstract:** In the US, the isolation of H5 subtype avian influenza (AI) viruses has been uncommon in commercial chickens and turkeys, although sporadic isolations have been made from the live bird markets or its supply chain since 1986. In 2002, two different outbreaks of H5 AI occurred in commercial chicken or turkey operations. The first occurred in Texas and was identified as a H5N3 subtype AI virus. The second outbreak was caused by a H5N2 virus isolated from a turkey farm in California. In this study we analyzed recent H5 subtype AI viruses from different avian species and different sources in the US. Most recent H5 subtype isolates shared a high sequence identity and phylogenetically assorted into a separate clade from the Pennsylvania/83 lineage isolates. However, no established lineage was found within this clade and the recent H5 subtype isolates seemed to be the result of separate introductions from the wild bird reservoir. The Texas H5N3 isolate shared the lowest homology with the other recent isolates in the haemagglutinin gene and had a unique haemagglutinin cleavage site sequence of REKR/G (other recent isolates have the typical avirulent motif, RETR/G). Furthermore, this isolate had a 28 amino acid deletion in the stalk region of the neuraminidase protein, a common characteristic of chicken adapted influenza viruses, and may indicate that this virus had actually been circulating in poultry for an extended period of time before it was isolated. In agreement with genetic evidence, the Texas H5N3 isolate replicated better than other H5 isolates in experimentally infected chickens. The outbreak in Texas with a more chicken-adapted H5N3 virus underscores the importance of ongoing surveillance and control efforts regarding the H5 subtype AI virus in the US.

**Descriptors:** chickens virology, disease outbreaks veterinary, influenza A virus, avian genetics, avian epidemiology, poultry diseases epidemiology, turkeys virology, amino acid sequence, base sequence, geography, hemagglutinis genetics, avian pathogenicity, avian virology, molecular sequence data, phylogeny, poultry diseases virology, reverse transcriptase polymerase chain reaction, sequence alignment, sequence analysis, DNA, sequence homology, species specificity, United States epidemiology.

Abstract: OBJECTIVE: To understand the epidemic status of avian influenza A virus in chickens and men in Guangzhou area and to prevent men suffering from avian influenza A (H5N1) virus. METHODS: Etiologic and serological surveys were conducted in chickens and men who were working in the poultry farms and slaughter house. Viruses were isolated with both MDCK cells and embryonated chicken eggs. Hemagglutination inhibition tests were performed by routine method. RESULTS: Anti-H9N2 antibody was found in 12.8% of the chickens and 5.1% of the workers. CONCLUSIONS: Avian influenza virus H9N2 subtype existed in chickens and this subtype of influenza A virus might infect men.

Descriptors: antibodies, influenza A virus, blood serum, epidemics, fowl diseases, human diseases, poultry, serological surveys, viral diseases, zoonoses, Asia, Gallus gallus, avian influenza virus, developing countries, China, birds.


NAL Call Number: 472 N21

Abstract: A highly pathogenic avian influenza virus, H5N1, caused disease outbreaks in poultry in China and seven other east Asian countries between late 2003 and early 2004; the same virus was fatal to humans in Thailand and Vietnam. Here we demonstrate a series of genetic reassortment events traceable to the precursor of the H5N1 viruses that caused the initial human outbreak in Hong Kong in 1997 (refs 2-4) and subsequent avian outbreaks in 2001 and 2002 (refs 5, 6). These events gave rise to a dominant H5N1 genotype (Z) in chickens and ducks that was responsible for the regional outbreak in 2003-04. Our findings indicate that domestic ducks in southern China had a central role in the generation and maintenance of this virus, and that wild birds may have contributed to the increasingly wide spread of the virus in Asia. Our results suggest that H5N1 viruses with pandemic potential have become endemic in the region and are not easily eradicable. These developments pose a threat to public and veterinary health in the region and potentially the world, and suggest that long-term control measures are required.

Descriptors: evolution, molecular, influenza epidemiology, influenza virology, orthomyxoviridae genetics, orthomyxoviridae pathogenicity, birds virology, far east epidemiology, genes, viral genetics, genotype, influenza transmission, molecular sequence data, mutation genetics, orthomyxoviridae isolation and purification, phylogeny, reassortant viruses genetics, reassortant viruses isolation and purification, reassortant viruses pathogenicity, time factors.

NAL Call Number: aSF995.6.1615 1981a
Descriptors: avian influenza virus, cloacal swabs, poultry, wild birds, Israel, ecological studies.

NAL Call Number: SF995.W4
Descriptors: avian influenza virus, Mexico, America, influenza virus, Latin America, North America, orthomyxoviridae, viruses.

NAL Call Number: 41.8 Av5
Abstract: An avian influenza (AI) outbreak occurred in meat-type chickens in central Pennsylvania from December 2001 to January 2002. Two broiler breeder flocks were initially infected almost simultaneously in early December. Avian influenza virus (AIV), H7N2 subtype, was isolated from the two premises in our
The H7N2 isolates were characterized as a low pathogenic strain at the National Veterinary Services Laboratories based on molecular sequencing of the virus hemagglutinin cleavage site and virus challenge studies in specific-pathogen-free leghorn chickens. However, clinical observations and pathologic findings indicated that this H7N2 virus appeared to be significantly pathogenic in meat-type chickens under field conditions. Follow-up investigation indicated that this H7N2 virus spread rapidly within each flock. Within 7 days of the recognized start of the outbreak, over 90% seroconversion was observed in the birds by the hemagglutination inhibition test. A diagnosis of AI was made within 24 hr of bird submission during this outbreak using a combination of virus detection by a same-day dot-enzyme-linked immunosorbent assay and virus isolation in embryonating chicken eggs. Follow-up investigation revealed that heavy virus shedding (90%-100% of birds shedding AIV) occurred between 4 and 7 days after disease onset, and a few birds (15%) continued to shed virus at 13 days post-disease onset, as detected by virus isolation on tracheal and cloacal swabs. AIV was not detected in or on eggs laid by the breeders during the testing phase of the outbreak. The two flocks were depopulated at 14 days after disease onset, and AIV was not detected on the two premises 23 days after depopulation.


NAL Call Number: SF780.9.S63
Descriptors: disease distribution, disease surveys, disease transmission, epidemiological surveys, epidemics, outbreaks, logistic regression analysis, risk factors, survival analysis, susceptibility, temporal variation, avian influenza virus, turkeys, poultry, fowl, Italy.


NAL Call Number: SF481.M54
Descriptors: poultry, vaccines, immunization, disease prevention, disease control, avian influenza virus, Mexico, developing countries.


NAL Call Number: SF781.D57
Descriptors: avian influenza virus, pathogenicity, poultry, turkeys, quails, guineafowls, Italy.


NAL Call Number: 241.71 B75
Descriptors: outbreaks, poultry, avian influenza virus, turkeys, guineafowl, Italy.


NAL Call Number: SF481.R485
Descriptors: diagnosis, disease control, prevention, disease surveys, poultry, reviews, avian influenza virus, Newcastle disease virus, Brazil, South America.


NAL Call Number: 448.9 Am37
Descriptors: influenza virology, influenza A virus avian genetics, disease outbreaks, Hong Kong epidemiology, influenza epidemiology, poultry virology.
NAL Call Number: SF995.W4
Descriptors: avian influenza virus, Mexico, America, influenza virus, Latin America, North America, orthomyxoviridae, viruses.

Abstract: During the outbreak of highly pathogenic avian influenza (HPAI) A(H7N7) in the Netherlands in 2003, human infection occurred in unexpectedly high numbers. Initially, all those involved in the culling of poultry were advised to wear protective clothing, goggles, and nose-mouth masks, and to wash their hands after work. In a later stage, vaccination and antiviral prophylaxis of all poultry workers and antiviral treatment of all cases was initiated. Case finding was implemented immediately. Conjunctival and nose/throat swabs were collected from 453 persons. Eighty-nine persons were A(H7) positive, 78 with conjunctivitis only, 5 with conjunctivitis and influenza-like illness (ILI), 2 with ILI only and 4 did not fit the case definitions. Nine A(H7) cases had both positive conjunctival and nose/throat swabs. One A(H7) case had an A(H7) positive nose/throat swab only. Of the two A(H7) cases presenting with ILI only, a veterinarian who developed a respiratory distress syndrome died. Three contacts of two A(H7) positive poultry workers developed A(H7) conjunctivitis. One of these, the 12-year-old daughter of a poultry worker, additionally developed ILI. Since they had no direct exposure to infected poultry, these observations strongly suggest human-to-human transmission. No simultaneous infection with A(H7) and human influenza virus in one patient was detected.
Descriptors: highly pathogenic avian influenza A, H7N7, poultry, epizootic, poultry to human transmission, conjunctivitis, Netherlands, human to human transmission.

NAL Call Number: aSF995.6.l6l5 1981a
Descriptors: avian influenza virus, ducks, laying hens, poultry, Belgium.

NAL Call Number: SF995.W4
Descriptors: broilers, avian influenza virus, outbreaks, Virginia.

NAL Call Number: aSF601.U5
Descriptors: avian influenza virus, Newcastle disease virus, disease surveys, poultry, turkey, duck, guineafowl, New York, New Jersey.

NAL Call Number: aSF601.U5
Descriptors: antibodies, avian influenza virus, poultry, Virginia, Florida.

Abstract: (1) Seroepidemiological analysis of influenza pandemics (1986-2003) in Shizuoka Prefecture and all Japan revealed differences in geographical, annual, seasonal, and age distributions. (2) For 17 years, the pandemics generally began at the 50th week every year showing over 1.0 patient/clinic, reached the peak at 5th week the following year, and ended over 10-15th week. Two big A/H3N2 pandemics were seen in
1989/1990 and 1997/1998 seasons, claiming over 1 million patients in Japan. (3) As herald strains, A/H3N2 strains (A/Sydney-like) were found in October 1999, and B strains (B/Victoria- and B/Yamagata-like) were detected in July and November 1998 and, in August and December 2000 in Shizuoka. B/Shizuoka/1/98 strain was registered internationally as a vaccine-recommended strain. (4) A/H3N2 and B viruses were detected in 55-78% of flu patients (almost under 10 years) with encephalopathy in 1999/2000 and 78-91% in 2000/2001 by MDCK and reverse transcription polymerase chain reaction (RT-PCR) methods. (5) High hemagglutination inhibition (HI) titers over 40 in 250 persons were shown against A/Sydney/5/97 (H3N2), A/Yokohama/8/98 (H3N2), A/Panama/2007/99 (H3N2) and A/Moscow/10/99 (H1N1) strains, while low titers showed against A/Beijing/262/95 (H1N1) and A/New Caledonia/20/99 (H1N1), and B/Beijing/243/97, B/Shandong/7/97 and B/Yamanashi/106/98 strains in 1998-2000. (6) In anti-HA titers against A/H3N2, A/H1N1 and B subtypes, clear generation gaps were observed between children (0-19 years), adults (20-59 years) and old men (over 60 years). (7) The pandemics are dependent on host immunity (acquired and vaccinated) and climatic conditions (low temperature, low humidity and limited rainfall), considering highly pathogenic avian influenza (HPAI) viruses (A/H5N1, A/H7N7) like severe acute respiratory syndrome (SARS) corona virus in 2002-2003.

Descriptors: active dynamic surveillance, Herald strain, vaccine recommended strain, influenza associated encephalopathy, highly pathogenic avian influenza, reverse transcription polymerase chain reaction, hemagglutination inhibition, SARS, severe acute respiratory syndrome, coronavirus, Japan.

NAL Call Number: 41.8 Au72
Abstract: In May 1985 an outbreak of avian influenza, a disease exotic to the Australian poultry industry, occurred on a farm in central Victoria. The outbreak was contained on that farm by immediate depopulation and disinfection measures. Although the origin of the infection was not established, it is considered most likely that wild birds introduced the virus. The infection status of wild bird populations in the area has not been ascertained but sampling surveys of the poultry industry indicated that there were no other infected flocks in the state. The infection may have entered the affected flock as long as 2 weeks prior to the clinical outbreak although the exact timing could not be ascertained. The spread of disease on the farm appeared to be largely due to humans acting as mechanical vectors.
Descriptors: poultry, broiler chickens, viroses, avian influenza virus, epidemiology, Victoria, Australia, birds, chickens, domestic animals, domesticated birds, Galliformes, infectious diseases, influenza virus, livestock, meat animals, Oceania, poultry, useful animals, viruses.

NAL Call Number: QR180.C62
Descriptors: disease outbreaks veterinary, fowl plague epidemiology, fowl plague economics, fowl plague prevention and control, influenza A virus avian isolation and purification, Minnesota, turkeys microbiology.

NAL Call Number: SF481.M54
Descriptors: avian influenza virus, Hong Kong, birds, primates, mammals, humans, poultry, contributing factors, outbreaks, zoonoses, disease control.

NAL Call Number: 41.8 D482
Abstract: This brief review summarises some structural and biological properties of the highly pathogenic avian influenza virus and its biological significance for animal and man. Sources of actual information in case of an acute disease outbreak are also given.
Descriptors: infection, veterinary medicine, avian influenza virus infection, viral disease.

**Descriptors:** clinical aspects, disease distribution, disease prevalence, epidemiology, avian influenza virus, outbreaks, poultry, hens, fowl, Pakistan.


**NAL Call Number:** 41.8 Av5  
**Abstract:** Over the last 10 years, low-pathogenicity avian influenza (LPAI) viruses have been isolated from the live-bird markets (LBMs) of the Northeast. Despite educational efforts, surveillance, and increased state regulatory efforts, the number of positive markets has persisted and increased. In an effort to address the continued levels of LPAI in the retail LBM and address the question of persistence and circulation of the virus within the LBM system itself, these markets were closed for a continuous 3-day period. This effort was a cooperative effort between the State Departments of Agriculture and coordinated by the U.S. Department of Agriculture and led to the first successful system-wide closure of the retail LBMs in the Northeast.

**Descriptors:** epidemiology, infection, public health, avian influenza, infectious disease, respiratory system disease, viral disease, disease surveillance live bird markets market closure.


**Descriptors:** fowl diseases, avian influenza, outbreaks, symptoms, mortality, egg production, Tadzhikstan.


**NAL Call Number:** 41.8 Av5  
**Descriptors:** chicken, turkey, guinea fowl, quail, ostrich, water fowl, pheasant, poultry, avian influenza epidemic, clinical aspects, diagnostic techniques, epidemiology, histopathology, immunohistochemistry, pathogenicity, postmortem examinations, Italy.


**NAL Call Number:** SF604.R48  
**Descriptors:** epidemiology, avian influenza virus, disease transmission, reviews, zoonoses, poultry, fowl.


**NAL Call Number:** 41.8 V641  
**Descriptors:** disease outbreaks veterinary, fowl plague epidemiology, influenza A virus avian classification, fowl plague complications, fowl plague prevention and control, fowl plague virology, avian isolation and purification, Pakistan epidemiology, poultry.


**NAL Call Number:** 41.8 Av5  
**Abstract:** An epidemic of avian influenza (AI) (H9N2) occurred in broiler chicken farms in Iran during 1998-2001. Mortality between 20% and 60% was commonly observed on the affected farms. Mixed infections of the influenza virus with other respiratory pathogens, particularly infectious bronchitis virus and *Mycoplasma gallisepticum*, were thought to be responsible for such high mortality, which resulted in great economic losses. Clinical signs included swelling of the periorbital tissues and sinuses, typical respiratory discharge, and severe respiratory distress. Gross lesions included extensive hyperemia of the respiratory system followed by exudation and cast formation in the tracheal bifurcation extending into the secondary bronchi. Light microscopy lesions were characterized by severe necrotizing tracheatis. Serological examination using...
H9N2 AI viral antigen produced inconsistent results. Ultrastructural findings showed typical viral replication through budding processes on cell membranes of the tracheal epithelium.

Descriptors: epidemiology, infection, respiratory system, avian influenza, infectious disease, mortality, respiratory system disease, viral disease, mixed respiratory infection, light microscopy imaging and microscopy techniques, laboratory techniques, serology, clinical techniques, diagnostic techniques, broiler chicken farm, disease mortality, economic losses, viral replication.


NAL Call Number: SF995.A1A9

Abstract: Since 1998, an epidemic of avian influenza has occurred in the Iranian poultry industry. The agent was pathotyped as non-highly pathogenic and subtyped as an H9N2 avian influenza virus. Therefore it did not require eradication. However, frequent incidences of high mortality were observed commonly on broiler farms. No other species of bird were affected. The circulation of the virus and mixed infection with other respiratory pathogens, particularly infectious bronchitis virus and Mycoplasma gallisepticum, were incriminated in the high mortality on poultry farms and resulting great economic losses. Clinical signs in both field and experimental studies included swelling of the periorbital tissues and sinuses, nasal and ocular discharge, and severe respiratory distress. However, in the experimental study, the mortality rate was much lower than in the natural outbreak. Gross lesions identified included extensive congestion of the respiratory tissues, and exudation with cast formation in the tracheal bifurcation, which extended to the secondary bronchi. Severe necrotizing tracheitis was the predominate histological lesion. Ultrastructurally, orthomyxovirus-like particles were identified in the inoculum used for the experimental study. An inactivated H9N2 avian influenza vaccine prevented mortality in experimentally challenged chickens.

Descriptors: epidemiology, infection, respiratory system, veterinary medicine, Mycoplasma gallisepticum infection, bacterial disease, avian influenza virus infection, prevention and control, viral disease, infectious bronchitis virus infection, respiratory system disease, viral disease, mortality ultrastructure.


NAL Call Number: 470 Sci2

Descriptors: influenza epidemiology, influenza virology, influenza A virus, avian, influenza, avian epidemiology, population surveillance, adult, southeastern Asia epidemiology, Cambodia epidemiology, disease outbreaks veterinary, influenza transmission, poultry.


NAL Call Number: 470 Sci2

Descriptors: ducks, influenza transmission, influenza A virus, avian pathogenicity, avian physiology, influenza, avian virology, Asia, chickens, influenza prevention and control, influenza virology, avian influenza prevention and control, poultry diseases prevention and control, poultry diseases virology, virus replication, virus shedding, World Health Organization.


Abstract: This report contains two parts: part one provides reports on the animal health status and disease control methods and tables on incidence of list "A" diseases and part two contains tables on animal health status and diseases control methods and number of veterinarians and animal health auxiliary personnel. The reports on animal health and disease control methods covers disease status worldwide in the year 2000, wildlife diseases, and country reports. The list "A" diseases are foot and mouth disease, vesicular stomatitis, swine vesicular disease, rinderpest, peste des petits ruminants, contagious bovine pleuropneumonia, lumpy skin disease, Rift Valley fever, bluetongue, sheep pox and goat pox, African horse sickness, African swine fever, classical swine fever, highly pathogenic avian influenza, and Newcastle disease. The country reports includes reports from most of the countries in the world and they contain sections on new activities of the veterinary services, list "A" diseases, comments on selected list "B" diseases, and other diseases. The reports are presented in English, French, Spanish, or Russian.
NAL Call Number: SF781.D57
Descriptors: case reports, diagnostic techniques, disease control, epidemiology, avian influenza, Honduras, swine fever, Spain, foot and mouth disease, Argentina, Uruguay, Newcastle disease, Turkey, rabies, France, outbreaks, seroprevalence, surveys, immunity, mortality, vaccination, livestock, poultry.

NAL Call Number: SF604.A76
Abstract: The presence of antibodies to the avian influenza virus subtypes H1N1 and H3N2, was studied through the technique of hemagglutination inhibition in the plasma of 225 birds of RIO-ZOO Foundation, Bwana Park and of small flocks of the Rio de Janeiro State. Among the studied birds, 60 (26.6%) were seropositives, being 22 (9.8%) for the subtype H1N1, 28 (12.4%) for the subtype H3N2 and 10 (4.4%) for both subtypes. These results indicate the occurrence of these avian influenza virus subtypes in Rio de Janeiro and point out the potential risk of their transmission for the industrial poultry and humans.
Descriptors: epidemiology, infection, veterinary medicine, hemagglutination inhibition technique detection method, serological survey survey method.

NAL Call Number: SF995.W4
Descriptors: avian influenza virus, Mexico, America, influenza virus, Latin America, North America, orthomyxoviridae, viruses.

NAL Call Number: SF995.W4
Descriptors: avian influenza virus, influenza virus, orthomyxoviridae, viruses.

Descriptors: avian influenza, study, diagnosis, economics, USSR, congress, exposition.

Descriptors: disease outbreaks, influenza epidemiology, influenza history, Alaska epidemiology, France epidemiology, Great Britain epidemiology, history of medicine, 20th century, Hong Kong epidemiology, influenza pathology, influenza virology, Norway epidemiology, United States epidemiology.

ISSN: 0005-2086.
NAL Call Number: 41.8 Av5
Abstract: Between 1993 and 2000, gallinaceous birds, waterfowl, and environmental specimens from the
live bird markets (LBMs) of the northeastern United States and non-LBM premises were tested for the presence of avian influenza virus (AIV), pathogenic properties of AIV subtypes, especially of hemagglutinin (H) subtypes H5 and H7, and a possible association between LBM and non-LBM infections. Ten H subtypes of AIV were isolated from the LBM specimens: H1, H2, H3, H4, H5, H6, H7, H9, H10, and H11. During this period, the 10 subtypes also were isolated from birds in non-LBM premises. In the LBMs, subtypes H2, H3, H4, H6, H7, and H11 were present for 5-8 yr despite efforts to clean and disinfect the premises. The H5 or H7 subtypes present during the same year in both LBMs and non-LBMs within a state or in contiguous states were (subtype/year): H5N2/1993, 1999, and H7N2/1994-99. The AIV subtypes including the H5 and H7 that were evaluated for pathogenicity in chickens were low pathogenic. The deduced amino acid sequence at the H cleavage site of H5 and H7 subtypes was consistent with those of low pathogenic AIV. Although the H5N2 and H7N2 subtypes remained low pathogenic, they did undergo mutations and acquired an additional basic amino acid at the H cleavage site; however, the minimum number of basic amino acids in correct sequence (B-X-B-R, where B = basic amino acid, X = need not be basic amino acid, and R = arginine) required for high pathogenicity was lacking. A low pathogenic H5 or H7 subtype may become highly pathogenic by acquiring additional basic amino acids at the H cleavage site. The LBMs have been and will likely continue to be a source of AIV for commercial poultry.

Descriptors: chickens, fowl plague virology, hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian classification, amino acid sequence, birds, cloaca pathology, cloaca virology, fowl plague epidemiology, hemagglutinin glycoproteins, influenza virus chemistry, influenza A virus avian genetics, influenza A virus avian pathogenicity, New England epidemiology, polymerase chain reaction methods, polymerase chain reaction veterinary, specific pathogen free organisms, trachea pathology, trachea virology, virulence.

Descriptors: epidemiology, avian influenza virus, disease prevalence, chickens, turkeys, Greece, wild birds.

Descriptors: avian influenza virus, Netherlands, mortality, poultry, outbreak, highly pathogenic.

Descriptors: disease outbreaks, influenza epidemiology, influenza A virus, avian, Cambodia epidemiology, influenza virology.


Descriptors: avian influenza virus, disease prevalence, disease control, vaccination, epidemiology, poultry, turkeys, guinea fowl, Italy.

Abstract: Human disease associated with influenza A subtype H5N1 re-emerged in January, 2003, for the first time since an outbreak in Hong Kong in 1997. Patients with H5N1 disease had unusually high serum concentrations of chemokines (e.g., interferon induced protein-10 [IP-10] and monokine induced by interferon gamma [MIG]). Taken together with a previous report that H5N1 influenza viruses induce large amounts of proinflammatory cytokines from macrophage cultures in vitro, our findings suggest that cytokine dysfunction contributes to the pathogenesis of H5N1 disease. Development of vaccines against influenza A (H5N1) virus should be made a priority.

Descriptors: influenza epidemiology, influenza transmission, influenza, avian epidemiology, zoonoses epidemiology, China epidemiology, disease outbreaks statistics and numerical data, Hong Kong epidemiology, influenza virology, influenza A virus, avian isolation and purification, human isolation and purification, influenza, avian influenza transmission, avian influenza virology, poultry, poultry diseases epidemiology, poultry diseases transmission.


Abstract: Avian influenza (AI) viruses comprise the vast majority of the type A Orthomyxoviridae. Evolution has produced an enormous array of viral antigenic subtypes and variants based upon the structure of the two surface glycoproteins, the hemagglutinin (HA) and the neuraminidase (NA). These viruses appear to be perpetuated in nature in a select few wild avian species, but some strains are capable of sporadic and unpredictable entry into other animal populations, including humans. The fate of these occasional entries is likewise unpredictable, and investigators are left only with retrospective analysis. It is clear, however, that AI viruses (or some of their genes) have fixed themselves into circulating lineages in some mammalian hosts. In birds, particularly commercial poultry, AI can undergo a dramatic shift and take the unique form of a highly lethal and systemic disease. This has happened at least eight times in this decade on four different continents. In this review we explore these outbreaks and what we have learned from them regarding virulence acquisition and interspecies transmission. We further attempt to explore the implications of these outbreaks for the future of both avian and non-avian species and discuss current methods of diagnosis and control of AI.

Descriptors: infection, veterinary medicine, avian influenza, clinical pathology, control, diagnosis, epidemiology, interspecies transmission, outbreak, viral disease, epizootiology phylogenetic tahara vaccination.

Perez Brena, P. and I. Casas (2004). Infecciones producidas por los virus de la gripe aviar A (H5N1) en las poblaciones de aves del sudeste asiatico y en la especie humana. [Avian influenza A (H5N1) infectious in both birds and humans in South-Eastern Asian countries]. Enfermedades Infecciosas y Microbiologia Clinica 22(7): 412-8. ISSN: 0213-005X.

Abstract: Avian influenza affects most types of birds and occurs in epidemics on poultry farms. The fatal disease is named "highly pathogenic avian influenza" and is caused by influenza A virus subtypes H5 and H7. The natural reservoir is the migratory waterfowl that occasionally infects domestic poultry. In 1997 in Hong Kong, 18 persons were infected and 6 of them died. At the end of 2003 and the beginning of 2004, avian influenza H5N1 infected numerous farms in several South-Eastern Asian countries. The virus was transmitted to humans in close contact with infected birds. A total of 34 persons were infected and 23 of them died. There is currently a considerable concern about the H5N1 avian influenza that has infected humans: the high virulence, evolution rate, the possibility of recombination with other influenza viruses, how H5N1 variants that infect humans or different approaches to the development of influenza vaccines.

Descriptors: influenza epidemiology, influenza A virus, avian isolation and purification, avian influenza pathogenicity, avian influenza epidemiology, southeastern Asia epidemiology, birds, influenza prevention and control, influenza virology, virulence, world health.

NAL Call Number: aSF995.6.I6I5 1981a
Descriptors: avian influenza virus, turkeys, outbreaks, control measures, hygiene, Italy, symposium.

Descriptors: epidemiology, infection, infectious disease, emerging, infectious disease, influenza, complications, respiratory system disease, viral disease, neutralization assay detection method.

NAL Call Number: aSF995.6.I6I5 1981a
Descriptors: avian influenza virus, poultry, turkeys, history, United States, symposium.

NAL Call Number: 449.9 Un3r
Descriptors: avian influenza virus, poultry, turkeys, United States.

NAL Call Number: SF481.M54
Descriptors: control methods, culling, disease control, disease prevention, disease surveys, economic impact, influenza, losses, outbreaks, zoonoses, avian influenza virus, poultry, fowl, Thailand.

Abstract: Annual outbreaks of influenza A infection are an ongoing public health threat and novel influenza strains can periodically emerge to which humans have little immunity, resulting in devastating pandemics. The 1918 pandemic killed at least 40 million people worldwide and pandemics in 1957 and 1968 caused hundreds of thousands of deaths. The influenza A virus is capable of enormous genetic variation, both by continuous, gradual mutation and by reassortment of genome segments between viruses. Both the 1957 and 1968 pandemic strains are thought to have originated as reassortants in which one or both human-adapted viral surface proteins were replaced by proteins from avian influenza strains. Analyses of the genes of the 1918 pandemic virus, however, indicate that this strain might have had a different origin. The haemagglutinin and nucleoprotein genome segments in particular are unlikely to have come directly from an avian source that is similar to those that are currently being sequenced. Determining whether a pandemic influenza virus can emerge by different mechanisms will affect the scope and focus of surveillance and prevention efforts.
Descriptors: influenza history, influenza virology, influenza A virus, human genetics, variation genetics, viral proteins genetics, disease outbreaks, hemagglutinin glycoproteins, influenza virus genetics, history, 20th century, influenza epidemiology, mutation, neuraminidase genetics, nucleoproteins genetics, reassortant viruses genetics, viral matrix proteins genetics, viral nonstructural proteins genetics.

NAL Call Number: QR360.A1J6
Abstract: Influenza A virus is a major public health threat, killing more than 30 000 per year in the USA alone, sickening millions and inflicting substantial economic costs. Novel influenza virus strains emerge
periodically to which humans have little immunity, resulting in devastating pandemics. The 1918 pandemic killed nearly 700,000 Americans and 40 million people worldwide. Pandemics in 1957 and 1968, while much less devastating than 1918, also caused tens of thousands of deaths in the USA. The influenza A virus is capable of enormous genetic variability, both by continuous, gradual mutation and by reassortment of gene segments between viruses. Both the 1957 and 1968 pandemic strains are thought to have originated as reassortants, in which one or both human-adapted viral surface proteins were replaced by proteins from avian influenza virus strains. Analyses of the surface proteins of the 1918 pandemic strain, however, suggest that this strain may have had a different origin. The haemagglutinin gene segment of the virus may have come directly from an avian source different from those currently circulating. Alternatively, the virus, or some of its gene segments, may have evolved in an intermediate host before emerging as a human pathogen. Determining whether pandemic influenza virus strains can emerge via different pathways will affect the scope and focus of surveillance and prevention efforts.

Descriptors: epidemiology, infection, molecular genetics, influenza, respiratory system disease, viral disease.

Descriptors: clinical aspects, diagnosis, incidence, disease prevention, treatment, avian influenza virus, poultry.


NAL Call Number: 449.9 Un3r
Descriptors: avian influenza virus, quarantine, outbreaks, poultry, carcass disposal, disease control.

NAL Call Number: RA648.5.E46
Abstract: We describe the enhanced rumor surveillance during the avian influenza H5N1 outbreak in 2004. The World Health Organization’s Western Pacific Regional Office identified 40 rumors; 9 were verified to be true. Rumor surveillance informed immediate public health action and prevented unnecessary and costly responses.
Descriptors: influenza prevention and control, avian influenza A virus, population surveillance methods, communication, disease outbreaks, influenza epidemiology, avian influenza epidemiology, World Health Organization.

NAL Call Number: 41.8 R25
Descriptors: epidemiology, avian influenza virus, outbreaks, egg production, turkeys, Israel.

NAL Call Number: 448.8 V81
Abstract: H2N2 influenza A viruses caused the Asian pandemic of 1957 and then disappeared from the human population 10 years later. To assess the potential for similar outbreaks in the future, we determined the antigenicity of H2 hemagglutinins (HAs) from representative human and avian H2 viruses and then
analyzed the nucleotide and amino acid sequences to determine their evolutionary characteristics in different hosts. The results of longitudinal virus surveillance studies were also examined to estimate the prevalence of avian H2 isolates among samples collected from wild ducks and domestic poultry. Reactivity patterns obtained with a large panel of monoclonal antibodies indicated antigenic drift in the HA of human H2 influenza viruses, beginning in 1962. Amino acid changes were clustered in two regions of HA1 that correspond to antigenic sites A and D of the H3 HA. By contrast, the antigenic profiles of the majority of avian H2 HAs were remarkably conserved through 1991, resembling the prototype Japan 57 (H2N2) strain. Amino acid changes were distributed throughout HA1, indicating that antibodies do not play a major role in the selection of avian H2 viruses. Phylogenetic analysis revealed two geographic site-specific lineages of avian H2 HAs: North American and Eurasian. Evidence is presented to support interregion transmission of gull H2 viruses. The human H2 HAs that circulated in 1957-1968 form a separate phylogenetic lineage, most closely related to the Eurasian avian H2 HAs. There was an increased prevalence of H2 influenza viruses among wild ducks in 1988 in North America, preceding the appearance of H2N2 viruses in domestic fowl. As the prevalence of avian H2N2 influenza viruses increased on turkey farms and in live bird markets in New York City and elsewhere, greater numbers of these viruses have come into direct contact with susceptible humans. We conclude that antigenically conserved counterparts of the human Asian pandemic strain of 1957 continue to circulate in the avian reservoir and are coming into closer proximity to susceptible human populations.

Descriptors: disease outbreaks, disease reservoirs, hemagglutinins viral genetics, influenza epidemiology, influenza A virus genetics, orthomyxoviridae infections epidemiology, Americas epidemiology, antibodies, monoclonal, antibodies, viral immunology, Asia epidemiology, birds microbiology, Europe epidemiology, evolution, fowl plague epidemiology, fowl plague genetics, genes viral genetics, hemagglutinin glycoproteins, influenza virus, influenza genetics, influenza A virus avian genetics, avian immunology, human genetics, human immunology, influenza A virus immunology, molecular sequence data, orthomyxoviridae infections genetics, phylogeny, population surveillance, time factors.


NAL Call Number: 41.8 Av5

Abstract: Between 1997 and 2001, there was one report of highly pathogenic avian influenza (HPAI) in the Western Hemisphere and Pacific Basin. In 1997, in New South Wales, Australia, an outbreak caused by avian influenza (AI) virus subtype H7N4 involved both chickens and emus. All other reports of infections in poultry and isolations from wild bird species in the region pertained to low pathogenicity (LP) AI virus. Animal Health Officials in Canada reported isolations of subtypes HI, H6, H7, and H10 from domestic poultry and subtypes H3 and H13 from imported and wild bird species. In Mexico, the H5N2 LPAI virus, the precursor of the HPAI outbreak in 1994-95, was isolated from poultry in each year from 1997 to 2001. Since 1997, Mexico has used approximately 708 million doses of a killed H5N2 vaccine and an additional 459 million doses of a recombinant fowlpox-H5 vaccine in their H5N2 control program. In Central America, avian influenza was diagnosed for the first time when H5N2 LPAI virus was isolated from chickens in Guatemala and El Salvador in 2000 and 2001, respectively. The H5N2 virus was genetically similar to the H5N2 virus found in Mexico. Surveillance activities in the United States resulted in the detection of AI virus or specific antibodies in domestic poultry from 24 states. Eleven of the fifteen hemagglutinin (H1, H2, H3, H4, H5, H6, H7, H9, H10, H11, and H13) and eight of the nine neuraminidase (N1, N2, N3, N4, N6, N7, N8, and N9) subtypes were identified. Two outbreaks of LPAI virus were reported in commercial table-egg producing chickens; one caused by H7N2 virus in Pennsylvania in 1996-98 and the other caused by H6N2 virus in California in 2000-01. In addition, isolations of H5 and H7 LPAI virus were recovered from the live-bird markets (LBMs) in the northeast United States.

Descriptors: epidemiology, infection, avian influenza, infectious disease, respiratory system disease, viral disease, animal health, live bird markets.


Abstract: Epidemiological information on currently circulating influenza viruses in poultry in Korea has not been available. We performed the surveillance of avian influenza viruses in the live poultry markets where
chickens, ducks, geese, and doves are sold. H9N2, H3N2, and H6N1 influenza viruses were isolated from poultry in the Korean live bird markets. H9N2 influenza viruses were mainly isolated from chickens; H3N2 influenza viruses were isolated from ducks and a dove, and an H6N1 influenza virus was isolated from a duck. Serological surveillance in chickens showed that chickens were infected over 50% with H9N2 viruses. **Descriptors:** poultry market, surveillance, H9N2, epidemiology, avian influenza virus, poultry, Korea, chickens, ducks, geese, doves, live bird markets.

**NAL Call Number:** RA648.5.E46
**Descriptors:** epidemiology, infection, pharmacology, infectious diseases, global strategy, response, infectious disease, surveillance, influenza, avian, pandemic, respiratory system disease, viral disease, antibiotic resistance, behavioral problem, medical problem, bioterrorism, pandemic, 1918 influenza pandemic.

**NAL Call Number:** SF600.Z6
**Descriptors:** avian influenza virus, epidemiology, pathology, diagnosis, control, prevention, poultry.

**NAL Call Number:** SF600.Z6
**Descriptors:** avian influenza virus, outbreaks, diagnosis, poultry, epidemiology, control, Mexico.

**NAL Call Number:** SF600.Z6
**Descriptors:** avian influenza virus, poultry, epidemiology, control, United States.

**NAL Call Number:** SF481.2.W6 1992
**Descriptors:** avian influenza virus, surveillance, chickens, Taiwan.

**NAL Call Number:** 49 J822
**Descriptors:** serotypes, disease surveys, avian influenza virus, pathogenicity, identification, chickens, Taiwan.

**NAL Call Number:** SF781.D57
**Descriptors:** avian influenza virus, disease prevalence, poultry, turkeys, Israel.

**NAL Call Number:** SF781.D57
**Descriptors:** avian influenza virus, Israel.

**NAL Call Number:** aSF995.6.I6I5 1981a
Descriptors: avian influenza virus, poultry, ducks, geese, chickens, Hong Kong, market surveillance, symposium.


NAL Call Number: QR189.V32
Abstract: Recent studies in Hong Kong and Singapore suggest that the annual impact of influenza in these wealthy tropical cities may be substantial, but little is known about the burden in middle-income tropical countries. We reviewed the status of influenza surveillance, vaccination, research, and policy in Thailand as of January 2004. From 1993 to 2002, 64-91 cases of clinically diagnosed influenza were reported per 100,000 persons per year. Influenza viruses were isolated in 34% of 4305 specimens submitted to the national influenza laboratory. Vaccine distribution figures suggest that less than 1% of the population is immunized against influenza each year. In January 2004, Thailand reported its first documented outbreak of influenza A H5N1 infection in poultry and the country's first human cases of avian influenza. Thailand's growing economy, well-developed public health infrastructure, and effective national immunization program could enable the country to take more active steps towards influenza control.
Descriptors: disease prevalence, epidemiology, human diseases, immunization, influenza, middle classes, outbreaks, poultry, surveillance, vaccination, viral diseases, avian influenza A virus, Thailand.


Abstract: In 1997, a high-pathogenicity H5N1 avian influenza virus caused serious disease in both man and poultry in Hong Kong, China. Eighteen human cases of disease were recorded, six of which were fatal. This unique virus was eliminated through total depopulation of all poultry markets and chicken farms in December 1997. Other outbreaks of high-pathogenicity avian influenza (HPAI) caused by H5N1 viruses occurred in poultry in 2001 and 2002. These H5N1 viruses isolated had different internal gene constellations to those isolated in 1997. No new cases of infection or disease in man due to these or other H5N1 viruses have been reported. This paper provides an overview and chronology of the events in Hong Kong relating to avian influenza, covering the period from March 1997 to March 2002.
Descriptors: epidemiology, infection, avian influenza, infectious disease, respiratory system disease, viral disease, chicken farms, epidemic chronology, inteRNAI gene constellations, poultry markets.


**Abstract:** A reverse genetics approach provides a new mutant strain where a modified cleavage site within its hemagglutinin depends on proteolytic activation strictly by elastase. The new strain grows well in cell culture and is entirely attenuated to mice. It induced complete protection against a lethal challenge at a dose of $10^5$ plaque-forming units. This provides an approach that allows conversion of any epidemic strain into a genetically homologous attenuated virus.

Descriptors: human diseases, influenza, poultry, avian influenza virus.


**Abstract:** An epidemic of high-pathogenicity avian influenza (HPAI) A virus subtype H7N7 occurred in The Netherlands in 2003 that affected 255 flocks and led to the culling of 30 million birds. To evaluate the effectiveness of the control measures, we quantified between-flock transmission characteristics of the virus in 2 affected areas, using the reproduction ratio $R_h$. The control measures markedly reduced the transmission of HPAI virus: $R_h$ before detection of the outbreak in the first infected flock was 6.5 (95% confidence interval [CI], 3.1-9.9) in one area and 3.1 in another area, and it decreased to 1.2 (95% CI, 0.6-1.9) after detection of the first outbreak in both areas. The observation that $R_h$ remained >1 suggests that the containment of the epidemic was probably due to the reduction in the number of susceptible flocks by complete depopulation of the infected areas rather than to the reduction of the transmission by the other control measures.

Descriptors: disease outbreaks veterinary, influenza A virus, avian influenza isolation and purification, avian influenza epidemiology, disease outbreaks prevention and control, avian influenza prevention and control, avian influenza transmission, models, statistical, Netherlands epidemiology, poultry.


**Abstract:** Waterfowl are the natural reservoir of all influenza A viruses, which are usually nonpathogenic in wild aquatic birds. However, in late 2002, outbreaks of highly pathogenic H5N1 influenza virus caused deaths among wild migratory birds and resident waterfowl, including ducks, in two Hong Kong parks. In February 2003, an avian H5N1 virus closely related to one of these viruses was isolated from two humans with acute respiratory distress, one of whom died. Antigenic analysis of the new avian isolates showed a reactivity pattern different from that of H5N1 viruses isolated in 1997 and 2001. This finding suggests that significant antigenic variation has recently occurred among H5N1 viruses. We inoculated mallards with antigenically different H5N1 influenza viruses isolated between 1997 and 2003. The new 2002 avian isolates caused systemic infection in the ducks, with high virus titers and pathology in multiple organs, particularly the brain. Ducks developed acute disease, including severe neurological dysfunction and death. Virus was also isolated at high titers from the birds’ drinking water and from contact birds, demonstrating efficient
transmission. In contrast, H5N1 isolates from 1997 and 2001 were not consistently transmitted efficiently
among ducks and did not cause significant disease. Despite a high level of genomic homology, the human
isolate showed striking biological differences from its avian homologue in a duck model. This is the first
reported case of lethal influenza virus infection in wild aquatic birds since 1961.

Descriptors: bird diseases virology, communicable diseases, emerging virology, ducks virology, influenza A
virus, avian pathogenicity, avian classification, avian isolation and purification, avian physiopathology, avian
transmission, virus replication, influenza, avian virology, bird diseases physiopathology, bird diseases
transmission, communicable diseases, emerging mortality, emerging transmission, hemagglutination
inhibition tests, Hong Kong.

influenza viruses isolated from the live bird markets of the Northeast United States.** *Journal of
Virology* 73(5): 3567-73. ISSN: 0022-538X.

**NAL Call Number:** QR360.J6

**Abstract:** The presence of low-pathogenic H7 avian influenza virus (AIV), which is associated with live-bird
markets (LBM) in the Northeast United States, was first detected in 1994 and, despite efforts to eradicate the
virus, surveillance of these markets has resulted in numerous isolations of H7 AIVs from several states from
1994 through 1998. The hemagglutinin, nonstructural, and matrix genes from representative H7 isolates
from the LBM and elsewhere were sequenced, and the sequences were compared phylogenetically. The
hemagglutinin gene of most LBM isolates examined appeared to have been the result of a single
introduction of the hemagglutinin gene. Evidence for evolutionary changes were observed with three
definable steps. The first isolate from 1994 had the amino acid threonine at the -2 position of the
hemagglutinin cleavage site, which is the most commonly observed amino acid at this site for North
American H7 AIVs. In January 1995 a new genotype with a proline at the -2 position was detected, and this
genotype eventually became the predominant virus isolate. A third viral genotype, detected in November
1996, had an eight-amino-acid deletion within the putative receptor binding site. This viral genotype
appeared to be the predominant isolate, although isolates with proline at the -2 position without the deletion
were still observed in viruses from the last sampling date. Evidence for reassortment of multiple viral genes
was evident. The combination of possible adaptive evolution of the virus and reassortment with different
influenza virus genes makes it difficult to determine the risk of pathogenesis of this group of H7 AIVs.

Descriptors: fowl plague virology, hemagglutinin glycoproteins, influenza virus genetics, influenza A virus
avian genetics, viral matrix proteins genetics, viral nonstructural proteins genetics, amino acid sequence,
base sequence, birds virology, DNA, viral, fowl plague epidemiology, avian classification, avian isolation and
purification, molecular sequence data, New England epidemiology, phylogeny, sequence homology, amino
acid.

Suarez, D.L. and D.A. Senne (2000). **Sequence analysis of related low-pathogenic and highly pathogenic
H5N2 avian influenza isolates from United States live bird markets and poultry farms from 1983-1989.**
*Avian Diseases* 44(2): 356-364. ISSN: 0005-2086.

**NAL Call Number:** 41.8 Av5

**Abstract:** The last highly pathogenic outbreak of avian influenza in the United States was caused by an
H5N2 influenza virus in Pennsylvania and New Jersey in 1983-84. Through a combined federal and state
eradication effort, the outbreak was controlled. However, in 1986-89, multiple H5N2 viruses were isolated
from poultry farms and the live bird markets (LBMs) in the United States. To determine the epidemiologic
relationships of these viruses, the complete coding sequence of the nonstructural gene and the
hemagglutinin protein subunit I of the hemagglutinin gene was determined for 11 H5N2 viruses and
compared with previously available influenza sequences. The H5N2 isolates from 1986-89 were all closely
related to the isolates from the 1983-84 Pennsylvania outbreak by nucleotide and amino acid sequence
analysis for both genes, providing additional evidence that the Pennsylvania/83 (PA/83) virus lineage was
not completely eradicated. The PA/83 lineage also had a large number of unique amino acid changes not
found in other avian influenza viruses, which was suggestive that this lineage of virus had been circulating in
poultry for an extended period of time before the first isolation of virus in 1983. High substitution and
evolutionary rates were measured by examining the number of nucleotide or amino acid substitutions over
time as compared with the index case, CK/PA/21525/83. These rates, however, were similar to other
outbreaks of avian influenza in poultry. This study provides another example of the long-term maintenance and evolution of influenza viruses in the U.S. LBMs and provides further evidence of the connection of the LBMs and the Pennsylvania 1983 H5N2 outbreak.

**Descriptors:** avian influenza virus, poultry, outbreaks, phylogenetics, DNA sequencing, nucleotide sequences, amino acid sequences, pathogenicity, evolution, hemagglutinins, genes, United States, nonstructural genes.


**NAL Call Number:** RA648.5.E46

**Abstract:** Influenza A viruses occur worldwide in wild birds and are occasionally associated with outbreaks in commercial chickens and turkeys. However, avian influenza viruses have not been isolated from wild birds or poultry in South America. A recent outbreak in chickens of H7N3 low pathogenic avian influenza (LPAI) occurred in Chile. One month later, after a sudden increase in deaths, H7N3 highly pathogenic avian influenza (HPAI) virus was isolated. Sequence analysis of all eight genes of the LPAI virus and the HPAI viruses showed minor differences between the viruses except at the hemagglutinin (HA) cleavage site. The LPAI virus had a cleavage site similar to other low pathogenic H7 viruses, but the HPAI isolates had a 30-nucleotide insert. The insertion likely occurred by recombination between the HA and nucleoprotein genes of the LPAI virus, resulting in a virulence shift. Sequence comparison of all eight gene segments showed the Chilean viruses were also distinct from all other avian influenza viruses and represent a distinct South American clade.

**Descriptors:** disease outbreaks, influenza A virus, avian influenza genetics, avian influenza epidemiology, recombination, genetic, amino acid sequence, Chile epidemiology, avian influenza classification, avian influenza pathogenicity, avian influenza virology, molecular sequence data, phylogeny, virulence.


**NAL Call Number:** 448.3 Ar23

**Abstract:** We report the findings of a 12-year surveillance study (1977-89) of avian influenza A viruses in eastern Germany. Viruses were isolated directly from feral ducks (n = 236) and other wild birds (n = 89); from domestic ducks (n = 735) living on a single farm; and from white Pekin ducks (n = 193) used as sentinels for populations of wild aquatic birds; mainly sea birds. The efficiency of virus isolation was 9.9% overall, with considerable variability noted among species: 8.7% in wild ducks, 0.9% in other feral birds and 38% in Pekin ducks. Use of sentinel ducks in wild pelagic bird colonies improved virus detection rates fivefold, suggesting that this approach is advantageous in ecological studies. Among the 40 different combinations of hemagglutinin (HA) and neuraminidase (NA) subtypes we identified, H6N1 predominated (23.6% for all avian species), followed by H4N6 (11%). Among individual species, the frequency profiles favored H2N3 (20.8%) and H4N6 (20.3%) in feral ducks; H7N7 (22.3%), H4N6 (24.4%) and H2N3 (10.4%) in Pekin ducks used as sentinels; and H6N1 (34.8%) and H6N6 (15.1%) in domestic ducks maintained on a single farm. By relying on sentinel birds for serological assays, it was possible to trace an "influenza season" in feral swan populations, beginning in August and continuing through the winter months. Comparison of subtype distribution of influenza viruses for Europe and North America showed significant differences. This supports the fact of two geographically distinct gene pools of influenza viruses in birds connected with their distinct flyways of each hemisphere. The high frequency of isolation of H2 influenza viruses is of considerable interest to those interested in the recycling of this subtype in humans. Similarly the frequent isolation of H7N7 influenza viruses raises concern about reservoirs of potentially pathogenic influenza virus for domestic poultry. Out results confirm the existence of a vast reservoir of influenza A viruses in European aquatic birds, which possesses sufficient diversity to account for strains that infect lower animals and humans.

**Descriptors:** ducks, avian influenza virus, *Anas platyrhynchos*, sentinel animals, waterfowl, disease prevalence, geographical distribution, species differences, epizootiology, reservoir hosts, seasonal variation, Germany, North America, virus subtypes.
Descriptors: virus strains, strain differences, zoonoses, outbreaks, avian influenza virus, poultry, pigs, human, horses, United States, Italy, Australia, Hong Kong.

NAL Call Number: 41.8 Av5
Descriptors: diagnosis, disease control, disease distribution, disease prevalence, disinfection, drug therapy, epidemiology, outbreaks, pathogenesis, pathogenicity, public health, quarantine, regulations, risk assessment, strains, trade, vaccination, vaccines, avian influenza virus, ducks, fowl, quails, turkeys, China, Hong Kong, Italy, symposium.

NAL Call Number: 41.8 Av5
Descriptors: disease surveys, disease transmission, viral proteins, wild birds, avian influenza virus A.

NAL Call Number: SF995.6.I6I58 1997
Descriptors: avian influenza congresses, proceedings, symposium, avian influenza.

NAL Call Number: 280.9 L23
Descriptors: broilers, hens, outbreaks, poultry farming, avian influenza virus, fowl plague virus, Netherlands.

Descriptors: public health, emerging infections, Centers for Disease Control and Prevention, avian influenza virus, Asia, United States, reporting.

NAL Call Number: QR189.V32
Abstract: Worldwide pandemics of human influenza virus caused extensive morbidity and mortality around the world had been documented in the 20th century. However, the mechanisms involved in the emergence of novel influenza virus and the epidemiological factors leading to pandemics are unpredictable. Southern China is postulated as the epicentre of influenza epidemics due to its agricultural-based communities and high population density. Pandemic influenza viruses are through to arise from avian viruses through genetic reassortment among influenza viruses. An influenza virus (H5N1) known to infect only birds previously was found to infect human causing disease and death in Hong Kong in 1997 and the outbreak involved 18 patients with six deaths. Prior to the human outbreak, the H5N1 virus was found to cause extensive death in chickens in three farms in Hong Kong. The significance of this outbreak raised worldwide concern on the possibilities that such an influenza virus may become the next influenza pandemic strain. Investigations were initiated to find the source of the virus. In addition the extend of spread in individuals in contact with the
index case and infected poultry was studied by H5-specific serology. Results demonstrated that individuals in close contact with the index case or with exposure to poultry were at risk of being infected. Out of the 18 cases of human infection, eleven had severe infection with symptoms of pneumonia and multi-organ failure. All severe cases presented with lower respiratory infection and lymphopenia and six eventually died. Case-fatality ratio was high among patients over 12 years of age (five out of nine). Control measures aimed at reducing exposure of human to potential H5-positive poultry were instituted which included culling of all poultry in Hong Kong, the segregation of water fowls and chicken, and the introduction of import control measures for chickens. Such measures had successfully controlled the outbreak and continuous surveillance of the poultry in Hong Kong of H5N1 infection is maintained to minimize future human exposure.

Descriptors: chickens virology, disease outbreaks, fowl plague transmission, influenza epidemiology, influenza A virus avian isolation and purification, zoonoses epidemiology, adult, child, preschool, Hong Kong epidemiology, influenza diagnosis, influenza etiology.


NAL Call Number: 241.71 B75

Abstract: From January to May 2000 a serological survey on AI virus subtype H7N1 was carried out in the flocks of Emilia-Romagna region of Italy. 153 out of the 51,997 samples examined by HI resulted positive. One LPAI outbreak in turkeys was detected. Most of the positive sera samples was collected from ducks and geese, pheasants and partridges. A flock of one day-old chickens showing transitory seropositivity was recorded. Survey results seem to indicate a limited spread of AI in Emilia-Romagna region during the HPAI epidemics involving the other regions of Northern Italy.

Descriptors: broiler chickens, layer chickens, turkeys, pigeons, guinea fowl, game birds, geese, ducks, ostriches, pathogenicity, identification, serotypes, disease surveys, epidemiology, avian influenza virus, monitoring, Emilia Romagna, Anseriformes, biological differences, biological properties, birds, chickens, Columbiformes, domestic animals, Europe, Galliformes, game, influenza virus, Italy, livestock, meat animals, microbial properties, orthomyxoviridae, poultry, Struthioniformes, surveys, useful animals, viruses, western Europe, wild animals, wildlife.


NAL Call Number: 41.8 V644

Descriptors: avian influenza virus, turkeys, eggs, hatchability, outbreak.s, Hungary.


NAL Call Number: SF995.W4

Descriptors: turkeys, avian influenza virus, disease distribution, disease transmission, epidemics, egg production, economic impact, California.


NAL Call Number: 501 L84Pb

Abstract: The Spanish influenza pandemic of 1918-1919 caused acute illness in 25-30% of the world's population and resulted in the death of 40 million people. The complete genomic sequence of the 1918 influenza virus will be deduced using fixed and frozen tissues of 1918 influenza victims. Sequence and phylogenetic analyses of the complete 1918 haemagglutinin (HA) and neuraminidase (NA) genes show them to be the most avian-like of mammalian sequences and support the hypothesis that the pandemic virus contained surface protein-encoding genes derived from an avian influenza strain and that the 1918 virus is
very similar to the common ancestor of human and classical swine H1N1 influenza strains. Neither the 1918 HA genes nor the NA genes possessed mutations that are known to increase tissue tropicity, which accounts for the virulence of other influenza strains such as A/WSN/33 or fowl plague viruses. The complete sequence of the non-structural (NS) gene segment of the 1918 virus was deduced and tested for the hypothesis that the enhanced virulence in 1918 could have been due to type I interferon inhibition by the NS1 protein. The results from these experiments were inconclusive. Sequence analysis of the 1918 pandemic influenza virus is allowing us to test hypotheses as to the origin and virulence of this strain. This information should help to elucidate how pandemic influenza strains emerge and what genetic features contribute to their virulence.

Descriptors: epidemiology, history, infection, molecular genetics, pandemic influenza, epidemiology, respiratory system disease, viral disease, 1918 Spanish influenza pandemic, tissue tropicity, virulence.


NAL Call Number: RA407.3.M56


NAL Call Number: aSF995.6.16I5 1981a

Descriptors: chickens, avian influenza virus, virus isolation, Australia.


NAL Call Number: 286.81 F322

Descriptors: avian influenza virus, domestic fowl, economic impact, Australia.


NAL Call Number: aSF601.U5

Descriptors: poultry, avian influenza virus, outbreaks, economic impact, United States.


NAL Call Number: RA648.5.E46

Abstract: Avian influenza that infects poultry in close proximity to humans is a concern because of its pandemic potential. In 2004, an outbreak of highly pathogenic avian influenza H7N3 occurred in poultry in British Columbia, Canada. Surveillance identified two persons with confirmed avian influenza infection. Symptoms included conjunctivitis and mild influenzalike illness.

Descriptors: disease outbreaks veterinary, influenza transmission, influenza A virus, avian pathogenicity, adolescent, adult, aged, British Columbia epidemiology, chickens, child, preschool child, infant, influenza virology, avian influenza epidemiology, avian influenza transmission, middle aged, mutagenesis, insertional, population surveillance.


NAL Call Number: 280.8 N47

Descriptors: influenza, avian epidemiology, disease outbreaks, Hong Kong epidemiology, influenza, avian virology.

United States. Animal and Plant Health Inspection Service. Veterinary Services. Centers for Epidemiology and
Descriptors: avian influenza United States, poultry virus diseases United States, avian influenza Mexico, poultry virus diseases Mexico, food safety.

NAL Call Number: SF481.M54
Descriptors: avian influenza virus, outbreaks, economics, public health, Hong Kong.

NAL Call Number: SF995.W4
Descriptors: avian influenza virus, slaughter, losses, disinfection, turkeys, guineafowls, Pennsylvania, Virginia, United States.

NAL Call Number: SF481.M54
Descriptors: avian influenza virus, outbreaks, disease control, disease prevention, _vaccination, Asia, Pakistan.

NAL Call Number: 41.8 T431
Abstract: Only a limited number of A-subtypes of influenza virus so far caused disease in human subjects, pigs and horses; this occurred in more or less defined areas which occasionally showed epidemic aggravations, becoming apparent as rapidly spreading epidemics or otherwise in even the form of pandemics. However this number of antigenic subtypes was found to be fairly constant and host-specific. Earlier studies were done in domesticated fowl and birds, though particularly in water birds in recent years, and numerous subtypes were detected, only a small number of these subtypes also being found to occur in man, pigs and horses. It became increasingly apparent that particularly mallards, but also other water birds play an extremely important role in the maintenance as well as in the distribution and circulation of these orthomyxoviruses in nature. These infections in water birds were not merely caused by a single subtype but occasionally by two or more antigenically different subtypes. This could be conducive to the appearance of recombinants as a result of genetic rearrangement in the cells lining the alimentary tracts of birds. Occasionally, subtypes observed in man were also found to occur in birds, which gave rise to the question of the extent to which birds are the origin or sources of infections of human epidemics caused by these subtypes. This also holds good for the subtypes in pigs. In addition to a number of oecological and ornithological considerations, reference was also made to systematic facts and routes along which further investigations on the presence of influenza viruses in the world of birds could be taken up, particular attention being paid to migratory birds. As birds of passage pass over and find their way into isolated areas as well as human population centres, these birds play a role which is yet unknown both in the distribution and in the overwintering of influenza viruses. Conditions in which wild and domesticated (water) birds, pigs, horses and man form a chain of close contact, and the areas in which new influenza viruses pathogenic for man are most likely to appear. Studies on the transgression of these barriers of species by subtypes of influenza virus still are entirely separate matter. The fact that a multidisciplinary approach is essential admits of no discussion.
Descriptors: bird diseases microbiology, ducks microbiology, influenza veterinary, influenza A virus avian isolation and purification, birds microbiology, disease reservoirs, influenza transmission, avian classification, avian pathogenicity, porcine isolation and purification, serotyping, swine microbiology.

**NAL Call Number:** 47.8 So89

**Descriptors:** poultry, avian influenza virus, diagnosis, disease control, vaccination, case studies, Europe, Middle East, domestic animals, immunization, immunostimulation, immunotherapy, livestock, therapy, useful animals.


**NAL Call Number:** 41.8 Av5

**Abstract:** The avian influenza high-pathogenicity virus was eradicated in poultry of Mexico in a relatively short period by the use of inactivated emulsified vaccine, enforcing biosecurity, and controlling movement of poultry and poultry products. Mexico maintains a permanent and reliable monitoring program for AI. H5N2 is the only avian influenza subtype identified. It is possible to control and eradicate the avian influenza low-pathogenicity virus mainly by controlled depopulation of positive poultry, reinforcing biosecurity, and the use of vaccines.

**Descriptors:** epidemiology, infection, avian influenza, epidemiology, infectious disease, prevention and control, respiratory system disease, transmission, viral disease.


**NAL Call Number:** 448.8 V81

**Abstract:** In this report, the genome of the Thai avian influenza virus A (H5N1); A/Chicken/Nakorn-Pathom/Thailand/CU-K2/04, isolated from the Thai avian influenza A (AI) epidemic during the early of 2004 was sequenced. Phylogenetic analyses were performed in comparison to AI viruses from Hong Kong 1997 outbreaks and other AI (H5N1) isolates reported during 2001-2004. Molecular characterization of the Thai AI (H5N1) HA gene revealed a common characteristic of a highly pathogenic AI (HPAI), a 20-codon deletion in the neuraminidase gene, a 5-codon deletion in the NS gene and polymorphisms of the M2 and PB2 genes. Moreover, the HA and NA genes of the Thai AI displayed high similarity to those of the AI viruses isolated from human cases during the same epidemic. Finally, our results demonstrated that the Thai AI emerged as a member of 2000’s AI lineage with most of the genetic sequences closely related to the Influenza A/Duck/China/E319.2/03 (H5N1).

**Descriptors:** disease outbreaks veterinary, genome, viral, influenza A virus, avian genetics, avian influenza virology, amino acid sequence, codon, gene deletion, avian influenza A virus isolation and purification, avian influenza A virus pathogenicity, avian influenza epidemiology, molecular sequence data, phylogeny, polymorphism, genetic, poultry, sequence alignment, Thailand epidemiology, viral proteins genetics.


**NAL Call Number:** 41.8 T431

**Descriptors:** risk assessment, avian influenza virus, Netherlands, western Europe, European Union countries, hobby chicken, poultry farming.


**Descriptors:** fowl plague epidemiology, influenza epidemiology, disease outbreaks, fowl plague virology, Hong Kong epidemiology, influenza virology.


**Abstract:** In order to investigate the prevalence and ecology of the Avian Influenza A virus (AIV) in western Palearctic wild birds, migrating ducks, mainly Mallards (*Anas platyrhynchos*), have been caught in a funnel.
trap at the Ottenby Bird Observatory on the Swedish Island Oland. After banding and collection of biometrical data, every individual was sampled for AIV. Since the fall of 2002, more than 3200 samples from 1900 birds have been collected showing a prevalence of AIV of 12%. Several subtypes have been found, including the low pathogenic H5N2. Some ducks are re-caught both during fall and spring migration, and the recruiting and wintering areas of the birds are known enabling us to draw conclusions about the geographical and reservoir distribution of AIV.


NAL Call Number: QR175.P47

Descriptors: avian influenza virus, pests, parasites, outbreaks, Australia, New Zealand, United States.


NAL Call Number: R11.C3

Descriptors: avian influenza, outbreak, update.


NAL Call Number: aSF601.U5

Descriptors: poultry, avian influenza virus, viroses, monitoring, United States, America, domestic animals, domesticated birds, infectious diseases, influenza virus, livestock, North America, useful animals, viruses.


NAL Call Number: 41.8 Au72

Descriptors: poultry, avian influenza virus, diagnosis, epidemiology, Australia, domestic animals, domesticated birds, influenza virus, livestock, Oceania, useful animals, viruses.


NAL Call Number: SF604.P65

Abstract: The health status of ring-necked pheasants in view of the prevalence of infectious diseases was estimated in Polish pheasantries in the years 1997-2000. Anatomicopathological, microbiological and serological examinations were carried out on birds derived from 26 pheasantries, including birds randomly selected from 18 flocks and sick or dead birds sent from 8 pheasantries. Antibodies specific to the following viruses were detected in serum blood samples: HE, AE, AP, REO, AI, Adeno group 1, MD, ND, as well as *Mycoplasma gallisepticum* specific antibodies. However, in none of the examined flocks was the presence of antibodies against reticuloendoteliosis virus found. Marble spleen disease and salmonellosis proved to be the most frequent cause of death during the growing period.

Descriptors: epidemiology, infection, veterinary medicine, avian influenza virus infection, viral disease, avian pox virus infection, viral disease, hemorrhagic enteritis virus infection, viral disease, Marek's disease, blood and lymphatic disease, immune system disease, neoplastic disease, viral disease, *Mycoplasma gallisepticum* infection, bacterial disease, reticuloendotheliosis virus infection, viral disease, adenovirus group I infection, viral disease, avian encephalomyelitis virus infection, viral disease, marble spleen disease, blood and lymphatic disease, immune system disease, viral disease, reovirus infection, viral disease, salmonellosis, bacterial disease, serology clinical techniques, diagnostic techniques, health status mortality pheasantry.


Descriptors: animal husbandry, government and law, infection, Newcastle disease, viral disease, avian influenza, viral disease, classic swine fever, hog cholera, viral disease, foot and mouth disease, viral disease, infectious animal diseases, infectious disease, agroterrorism, biological crimes, biological terrorism, biowarfare, clinical features, clinical signs, differential diagnosis, disease control, disease definition, disease eradication, epidemiology, etiology, geographic distribution, host range, incubation period, intentional outbreak, morbidity, mortality, natural outbreak, pathology, public health, transmission, zoonotic potential.


Abstract: After the discovery of poultry infected with highly pathogenic avian influenza (HPAI) virus of subtype H7N7 in the central area of the Netherlands on 28 February 2003, the hypothesis was put forward that an outbreak of the low pathogenic (LP) variant of H7N7 had preceded, unnoticed, the occurrence of the HPAI virus. Consequently, a cross-sectional serological survey of the Dutch poultry population was executed in the second week of March 2003. The basic requirements set were detection of a 5% prevalence of flocks exposed to LPAI virus with 95% confidence within the production type stratification level within each province in the Netherlands. Because of supposed higher risk of avian influenza infections in ducks, turkeys and free-range poultry, all the commercial flocks of these production types present in the Netherlands were sampled. The serological screening of 28018 sera from 1193 randomly selected poultry farms, located outside surveillance zones showed that LPAI H7 virus infections had occurred on three neighbouring farms all located in the southwest of the Netherlands. No antibodies against the neuraminidase N7 subtype were detected in the sera of these farms, indicating that the subtype was different from the HPAI H7N7 subtype that caused the avian influenza epidemic in 2003. In addition, evidence of infections with non-H5 or non-H7 subtypes of influenza A virus were obtained in two other farms located in the northeast and the southeast of the Netherlands. It was concluded that the HPAI subtype H7N7 outbreak was most likely not preceded by a significant circulation of a LPAI subtype H7N7 virus. Based on the Dutch experience, recommendations are made to detect avian influenza infections faster in the future.

Descriptors: antibodies, disease prevalence, egg production, ELISA, poultry, serology, avian influenza virus, ducks, turkeys, Netherlands epidemiology, avian influenza A virus pathogenicity, avian influenza epidemiology, viral antibodies, cross-sectional studies, disease outbreaks, chickens virology, ducks virology, oviposition, seroepidemiologic studies, time factors, virulence, turkeys virology, virulence.


Descriptors: disease outbreaks, avian influenza A virus pathogenicity, avian influenza epidemiology, poultry diseases epidemiology, zoonoses epidemiology, southeastern Asia epidemiology, China epidemiology, avian influenza transmission, Japan epidemiology, poultry diseases transmission, risk assessment.


Descriptors: avian influenza, WHO, weekly record.

World Health Organization (2004). Avian influenza A(H5N1)--situation (poultry) in Asia as at 2 March 2004:
need for a long-term response, comparison with previous outbreaks. Weekly Epidemiological Record; Releve Epidemiolelique Hebdomadaire 79(10): 96-9. ISSN: 0049-8114.


Descriptors: birds, disease outbreaks, avian influenza epidemiology, Vietnam epidemiology.


Descriptors: disease outbreaks, influenza, avian epidemiology, adult, middle aged, Vietnam epidemiology.


Descriptors: human disease outbreaks, viral diseases, epidemiology, transmission, influenza virus, Hong Kong, avian influenza, primates, mammals, case control study, China, Asia.


Descriptors: disease outbreaks, health priorities, influenza epidemiology, avian influenza A virus pathogenicity, public health, World Health Organization, Asia epidemiology avian influenza epidemiology.


Descriptors: disease outbreaks prevention and control, influenza epidemiology, avian influenza epidemiology, avian influenza prevention and control, birds, Hong Kong epidemiology, poultry, public health, public health administration.


NAL Call Number: QR189.V32

Abstract: During 1989-1999, influenza A H3N2 and H1N1 subtypes and B type viruses were still co-circulating in human population in China, while influenza A (H3N2) virus was predominant strain. The two antigenically and genetically distinguishable strains of influenza B virus were also still co-circulating in men in southern China. The antigenic analysis indicated that most of the H3N2 viruses were A/Panama/2007/99 (H3N2)-like strain, the most of the H1N1 viruses were antigenically similar to A/Beijing/262/95 (H1N1) virus. However, most of the influenza B viruses were B/Beijing/184/93-like strain, but few of them were antigenically similar to B/Shandong/7/97 virus. In the summer of 1998, the influenza outbreaks caused by H3N2 subtype of influenza A virus occurred widely in southern China. Afterwards, during 1998-1999 influenza season, a severe influenza epidemic caused by H3N2 virus emerged in northern China. The morbidity was reached as high as 10% in Beijing area. It was interesting that during influenza, surveillance from 1998 to 1999, five strains of avian influenza A (H9N2) virus were isolated from outpatients with
influenza-like illness in July-August of 1998, and another one was repeatedly isolated from a child suffering from influenza-like disease in November of 1999 in Guangdong province. The genetic analysis revealed that the five strains isolated in 1998 were genetically closely related to H9N2 viruses being isolated from chickens (G9 lineage virus), whereas, A/Guangzhou/333/99 (H9N2) virus was a reassortant derived from reassortment between G9 and G1 lineage of avian influenza A (H9N2) viruses due to its genes encoding the HA, NA, NP and NS proteins, closely related to G9 lineage virus, the rest of the genes encoding the M and three polymerase (PB2, PB1 and PA) were closely related to G1 lineage strain of H9N2 virus. However, no avian influenza A (H5N1) virus has so far been isolated neither from in or outpatients with influenza-like disease in mainland China. Unfortunately, where did the reassortment occur and how did the reassortant transmit to men? These questions are still unknown.

Descriptors: epidemiology, infection, influenza, respiratory system disease, viral disease.

NAL Call Number: 41.8 Av5
Abstract: In March 1999 a syndrome characterized by depression, anorexia, fever, and respiratory and enteric signs appeared in many flocks of turkeys and, to a lesser extent, chickens in the densely populated poultry-rearing regions of Northeastern Italy. Initially the disease was characterized by sinusitis, tracheitis, peritonitis, and pancreatitis. The responsible agent was identified as low-pathogenicity (LP) avian influenza (AI) of H7N1 subtype. Concerning the light layers, the mortality was variable, from 1.7% to 9.5%, whereas egg production decreased by 10% to 40%. According to the epidemiologic data, chickens seemed to be less sensitive to the virus than were turkeys. Nine months later, the AI virus changed to a highly pathogenic (HP) AI virus and affected, besides turkeys, a great number of pullet and layer flocks, with high mortality (80%-100%) in a few days. However, the course of disease was more prolonged in pullets. Within 3 1/2 mo, over 100 outbreaks were reported. Following the HPAI outbreaks, in late 2000 and early 2001, LPAI reemerged, but only one flock of layers was affected.
Descriptors: epidemiology, infection, veterinary medicine, avian influenza, infectious disease, respiratory system disease, viral disease, epidemiological data, poultry flocks.

NAL Call Number: SF481.M54
Descriptors: avian influenza virus, disease control, outbreaks, pathogenicity, poultry housing, vaccination, turkeys, Italy, biosecurity.

NAL Call Number: 41.8 Av5
Abstract: Beginning at the end of March 1999, a syndrome characterized by severe depression, anorexia, fever, and respiratory and enteric symptoms appeared in flocks of turkeys and, to a lesser extent, of chickens in the densely populated poultry-rearing regions of northeast Italy. The disease was characterized by sinusitis, tracheitis, peritonitis, and pancreatitis. The mortality varied between 5% and 90%. The disease was diagnosed as low pathogenic avian influenza, H7N1 serotype. After a summer period of declining cases, the disease reappeared in autumn exclusively in turkeys. Since the middle of December 1999, many farms of chickens, turkeys, and guinea fowl were abruptly affected by a highly pathogenic H7N1 virus, with very severe depression and mortality up to 100% in a few days. By the end of March 2000, nearly 500 farms, representing over 15 million birds, were affected or depopulated. To date, control measures have focused on improved biosecurity measures. Vaccine was not allowed, but its use was debated.
Descriptors: fowl plague epidemiology, poultry diseases epidemiology, chickens, influenza A virus avian, Italy epidemiology, pancreatitis complications, peritonitis veterinary, peritonitis complications, peritonitis veterinary, serotyping, sinusitis complications, sinusitis veterinary, tracheitis complications, tracheitis veterinary, turkeys.

International 23(11): 54-60. ISSN: 0392-0593.

NAL Call Number:  SF600.Z6

Descriptors: avian influenza virus, serovars, Galliformes, epidemic, Italy.


NAL Call Number:  SF995.W4

Descriptors: Italy, chickens, turkeys, avian influenza virus.


NAL Call Number:  241.71 B75

Abstract: Some outbreaks of avian influenza due to H7N1 serotype in light egg layers are reported. The mortality resulted variable from 1.7 to 9.5%, whereas the laying decrease resulted variable from 10 to 40% in the different farms. According to epidemiological data, the light layers appeared less sensitive to avian influenza virus than turkeys and broiler breeders.


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Pathology and Pathogenesis

NAL Call Number: SF769.A54

NAL Call Number: 41.8 P27
Abstract: Fifteen chickens, five broilers and ten layers, from the Pennsylvania 1983 outbreak of highly pathogenic avian influenza virus infection, were examined. Gross lesions in the broilers were limited to serosal petechiae and dehydration. In the layers there was comb edema, vesiculation, and necrosis. Microscopic lesions were mild to severe diffuse nonsuppurative encephalitis, very mild to severe diffuse necrotizing pancreatitis, and very mild to severe subacute necrotizing myositis involving numerous skeletal muscles and most severe in the external ocular muscles and limbs. While many of these lesions have been seen in experimental infections of chickens with influenza viruses, the pattern of organs involved in this group of chickens is distinctive.
Descriptors: chickens, disease outbreaks veterinary, fowl plague pathology, brain pathology, fowl plague epidemiology, inclusion bodies, viral ultrastructure, muscles pathology, myocardium pathology, pancreas pathology, pancreas ultrastructure, Pennsylvania, proventriculus pathology.

NAL Call Number: SF604.P32
Descriptors: experimental infection, histopathology, clinical signs, lesions, mortality, avian influenza virus, Gallus gallus, Phasianidae, Galliformes, Pakistan.

NAL Call Number: 41.8 R312
Abstract: Groups of 10 two-week-old chicks, turkey poultis and ducklings were each infected by the intranasal route with one of four avian influenza viruses: a/fowl/Germany/34 (Hav 1N))--Rostock, A/FPV/Dutch/27 (Hav 1 Neq 1)--Dutch, A/fowl/Victoria/75 (Hav 1 Neq 1)--Australian, and A/parrot/Ulster/73 (Hav 1 N1)--Ulster. Eight hours after infection 10 birds of the same age and species were placed in contact with each group and allowed to mix. The clinical signs of disease and onset of sickness and death were recorded. Ulster virus was completely avirulent for all birds. Rostock, Dutch and Australian viruses were virulent for fowls and turkeys causing death in all birds with the exception of 3/10 in contact fowls from the Rostock virus group and 2/10 in contact fowls from the Australian virus group. Only Rostock virus caused sicked sickness or death in ducks, 9/10 intranasally infected and 6/7 in contact birds showed clinical signs and 2/10 intranasally infected and 3/7 in contact ducks died. Intranasal and in contact pathogenicity indices were calculated for each virus in each bird species and indicated quantitatively the differences in virulence of the four virus strains. Virus isolation and immune response studies indicated that surviving in contact fowls in the Rostock virus group had never been infected but that surviving Australian virus in contact fowls had recovered from infection. Infection was not established in Ulster virus in contact fowls and Australian virus intranasally infected and in contact ducks. The birds in all other groups showed positive virus isolations and a high incidence of positive immune response. The last virus isolation was made at 22 days after intranasal infection of ducks with Ulster virus.
Descriptors: chickens, ducks, fowl plague etiology, influenza A virus avian pathogenicity, turkeys, antibodies, viral analysis, fowl plague immunology, fowl plague microbiology, avian immunology, virulence.

**NAL Call Number:** 448.9 R814

**Descriptors:** orthomyxoviridae pathogenicity, poultry diseases etiology, chickens, eggs, *Mycoplasma* infections complications, poultry diseases diagnosis, serologic tests.


**NAL Call Number:** 41.8 J82

**Abstract:** Eighteen specific pathogen-free chickens (nine hens older than 1 year and nine 15-week-old males) were inoculated with highly pathogenic avian influenza virus A/Chicken/Pennsylvania/1370/1983 (H5N2). Birds were serially killed and tissues collected for histological and immunohistochemical evaluation. In the group of older hens, disease was acute or peracute. By immunohistochemistry, antigen was abundant in capillary endothelium in multiple organs, and staining for antigen in parenchymal cells was marked in brain and heart. In the group of younger male birds, disease was subacute. Immunohistochemical staining of capillary endothelium was less pronounced and viral antigen staining was evident in the parenchymal cells of the heart, brain and kidney.

**Descriptors:** antigens, viral analysis, brain immunology, endothelium, vascular immunology, fowl plague pathology, influenza A virus avian pathogenicity, myocardium immunology, chickens, fowl plague immunology, immunohistochemistry, avian classification.


**NAL Call Number:** 41.8 Av5

**Abstract:** A combination of in vitro and in vivo selection procedures was used to examine the possibility that certain mildly pathogenic field isolates of avian influenza (AI) virus may contain minority subpopulations of highly pathogenic virus. Two mildly pathogenic H5N2 isolates, A/chicken/New Jersey/12508/86 (NJ12508) and A/chicken/Florida/27716/86 (FL27716), recovered from chickens epidemiologically associated with urban live-bird markets, were cloned in trypsin-free chicken embryo fibroblast cultures. Selected clones were inoculated intranasally and intratracheally (IN/IT) into specific-pathogen-free laying hens, and virus reisolated from the hens that died was serially passed in hens by IN/IT inoculation. Several highly pathogenic reisolates were recovered from hens infected with the cloned NJ12508 or FL27716 virus. A highly pathogenic NJ12508 reisolate killed 19 of 24 IN/IT-inoculated hens, and a FL27716 reisolate killed all 24 inoculated hens; signs and lesions were typical of fowl plague. In contrast, uncloned NJ12508 stock virus killed 1 of 24 hens and FL27716 stock virus killed 4 of 24 hens, and neither produced the complete spectrum of lesions associated with fowl plague. Recovery of highly pathogenic viruses from these isolates demonstrates the coexistence of pathogenically distinct subpopulations of virus. Competition for dominance among such subpopulations could explain the variable pathogenicity of some AI viruses.

**Descriptors:** chickens microbiology, influenza A virus avian pathogenicity, cultured cells, cytopathogenic effect, viral, fowl plague microbiology, fowl plague mortality, avian isolation and purification, serial passage, species specificity, trypsin diagnostic use.


**NAL Call Number:** 41.8 Av5

**Abstract:** Pronounced host effects on clinical responses to influenza virus infection were not observed in any of seven trials in which young (26-43 weeks) and old (65-94 weeks) leghorn hens were inoculated with low pathogenic subtype H5N2, H4N8, or H3N2 virus. In two of seven trials, where hens were infected with H4N8 or H3N2 virus, morbidity rates were slightly higher for old hens than for young hens. These observations indicate that host age effects on the severity of uncomplicated influenza virus infections are likely to be minimal in sexually mature chickens.

**Descriptors:** chickens, females, avian influenza virus, pathogenicity, age, morbidity, mortality, symptoms,
maturity, biological properties, birds, developmental stages, domestic animals, domesticated birds, epidemiology, Galliformes, influenza virus, livestock, microbial properties, orthomyxoviridae, poultry, sex, useful animals, viruses, age differences, maturity stage.


**Abstract:** Avian influenza (AI) virus A/chicken/Alabama/7395/75 (H4N8), a putatively non-pathogenic virus associated with a self-limiting outbreak of severe disease in commercial layers, was selectively passed in chickens or in cell cultures and then in chickens to determine whether virus with increased pathogenicity would emerge. When 20 derivatives of the parental virus were each inoculated intranasally and intratracheally in leghorn hens, mortality rates ranged from zero (0/24) to 25% (6/24); mortality was 4% (1/24) for hens inoculated with the parental virus. Many virus reisolates (51/144) from hens that died exhibited high pathogenicity, killing at least six of eight intravenously inoculated 4-week-old chickens. Most derivatives examined produced plaques in trypsin-free cell cultures more efficiently than the parental virus, but the highest plaquing efficiencies observed (10%) were lower than would be expected (100%) for highly pathogenic subtype H5 or H7 AI viruses. These results confirm that the Alabama H4N8 virus can acquire increased pathogenicity upon passage in chickens and suggest that it may have acted alone in producing the severe disease observed in laying chickens in Alabama.

**Descriptors:** chickens, avian influenza virus, pathogenicity, cell culture, mortality, biological properties, birds, culture techniques, domestic animals, domesticated birds, Galliformes, in vitro culture, influenza virus, livestock, microbial properties, poultry, useful animals, viruses.


**Abstract:** An investigation was carried out on 700 sera obtained from imported ostriches between 1994 and 1997 for the detection of antibodies against selected viral and bacterial avian pathogens. Sera were tested for antibodies against Newcastle disease, avian influenza and Crimean-Congo haemorrhagic fever (CCHF), according to OM 6/6/1992 and 24/10/1992. Sera were also processed for the detection of antibodies against PMV3, PMV6, IBV, EDS’76, TRT, HEV, IBD and S. enteritidis. All samples were negative for NDV, influenza and CCHF. Low positivities were detected for other viral antigens, while a high prevalence was recorded for S. enteritidis.

**Descriptors:** ostriches, antibodies, *Salmonella enteritidis*, animal health, legislation, Italy, disease surveillance, introduced breeds, disease surveys, immunological techniques, blood serum, Newcastle disease, avian influenza virus, paramyxovirus aviare, avian infectious bronchitis virus, enteritis, rhinotracheitis, animal viruses, bacteria, birds, blood, breeds animals, coronaviridae, digestive system diseases, enterobacteriaceae, epidemiology, Europe, immunological factors, infectious diseases, influenza virus, intestinal diseases, organic diseases, orthomyxoviridae, respiratory diseases, *Salmonella*, Struthioniformes, surveys, taxa, viroses, viruses, Western Europe.


**Abstract:** The clinical, virological and pathological findings observed in a natural outbreak of highly pathogenic avian influenza in intensively farmed ostriches (*Struthio camelus*) are reported. Clinical signs characterized by anorexia, depression, nervous and enteric signs were observed in young birds, which resulted in death of 30% of the affected birds. Virus isolation performed in accordance with the guidelines listed in European Union Directive 92/40/EEC yielded an influenza A virus of the H7N1 subtype with a deduced cleavage site motif containing multiple basic amino acids, typical of highly pathogenic viruses. Gross lesions, mainly haemorrhagic enteritis and liver degeneration and necrosis, were confirmed by
histopathology and immunohistochemistry, resulting in the detection of necrotic lesions and influenza A nucleoprotein in selected organs. The findings reported indicate that ostriches are susceptible to highly pathogenic avian influenza.

Descriptors: animal husbandry, infection, respiratory system, anorexia nervosa, behavioral and mental disorders, avian influenza A, natural outbreak, respiratory system disease, viral disease, depression, behavioral and mental disorders, hemorrhagic enteritis, vascular disease, histopathological analysis, analytical method, immunohistochemistry, immunohistochemical, immunocytochemical techniques, analytical method, European Union Directive 92 40 EEC, guidelines, death, necrosis, ostrich farming, case study.


Abstract: Se plantearon 2 hipotesis referentes a la posible patogenia de dichas lesiones, y se llevo a cabo un estudio morfologico preliminar, al respecto. En el CENID Microbiologia, se inocularon 16 aves, 8 Indian River de 7 semanas de edad y 8 Leghorn de 4 semanas de edad, instilando 0.2ml de liquido alantoideo por via intravenosa y 1ml traqueal, con virus de la cepa A/Ck/Queretaro/14588-619/95 (H5 N2) Alta patogenicidad (106 DLP 50% 3 semanas/ml de liquido alantoideo). La toma de muestras para histopatologia y microscopia electronica de llevaron a cabo a los 8 dias postinoculacion en los pollos de engorda y a los 5 dias los Leghorn. La morfopatologia macroscopica y microscopica de las lesiones cutaneas resultaron ser mas severas en los pollos de engorda que en las aves Leghorn, encontrandose en los primeros: blefaritis serohemorragica severa con focos de necrosis. El epitelio de las barbillas, cresta, region esternal, metatarsos, dedos y cojinete plantar se encontro muy tumefacto debido a acumulo de abundante exudado serohemorragico en tejido subcutaneo, cianotico y con varias areas de necrosis de la epidermis que sufria descamacion mientras que, en las aves Leghorn no se apreciaron areas de necrosis en epidermis y la tumefaccion fue moderada. En el estudio microscopico de los cortes de epitelio fue sorprendente la gran cantidad de pigmento de origen hematico disperso en todo el corte y la hiperemia severa en los numerosos capilares subepidermicos asociados especialmente a areas de necrosis de la epidermis, que se encontraban ocluidos por globulos rojos lisados (nucleos desnudos) a pesar de que el resto de la muestra estaba bien preservada. El tejido conjuntivo de la dermis se aprecio severamente infiltrado por exudado serohemorragico pero con moderada cantidad de heterofilos y leucocitos mononucleares. Los resultados no son totalmente concluyentes respecto a que estas lesiones cutaneas pudieran ser originadas por hemaglutinacion in vivo pero si se logro constatar que el virus de IA altamente patogeno se replica en gran variedad de celulas incluyendo las endoteliales, lo que pudiera explicar el dano vascular, el incremento de permeabilidad vascular, la extravasacion de gran cantidad de exudado serohemorragico con escasa cantidad de leucocitos, la irrigacion tisular deficiente y por ende, la necrosis de epidermis.

Descriptors: chickens, avian influenza virus, lesions, Veracruz, America, birds, domestic animals, Galliformes, influenza virus, livestock, Mexico, North America, orthomyxoviridae, poultry, useful animals, viruses.


NAL Call Number: SF995.W4

Descriptors: skin, lesions, avian influenza virus, Mexico, America, body parts, influenza virus, integument, Latin America, North America, orthomyxoviridae, viruses.


NAL Call Number: 500 N21P
Abstract: The pathogenicity of avian H5N1 influenza viruses to mammals has been evolving since the mid-1980s. Here, we demonstrate that H5N1 influenza viruses, isolated from apparently healthy domestic ducks in mainland China from 1999 through 2002, were becoming progressively more pathogenic for mammals, and we present a hypothesis explaining the mechanism of this evolutionary direction. Twenty-one viruses isolated from apparently healthy ducks in southern China from 1999 through 2002 were confirmed to be H5N1 subtype influenza A viruses. These isolates are antigenically similar to A/Goose/Guangdong/1/96 (H5N1) virus, which was the source of the 1997 Hong Kong "bird flu" hemagglutinin gene, and all are highly pathogenic in chickens. The viruses form four pathotypes on the basis of their replication and lethality in mice. There is a clear temporal pattern in the progressively increasing pathogenicity of these isolates in the mammalian model. Five of six H5N1 isolates tested replicated in inoculated ducks and were shed from trachea or cloaca, but none caused disease signs or death. Phylogenetic analysis of the full genome indicated that most of the viruses are reassortants containing the A/Goose/Guangdong/1/96-like hemagglutinin gene and the other genes from unknown Eurasian avian influenza viruses. This study is a characterization of the H5N1 avian influenza viruses recently circulating in ducks in mainland China. Our findings suggest that immediate action is needed to prevent the transmission of highly pathogenic avian influenza viruses from the apparently healthy ducks into chickens or mammalian hosts.

Descriptors: ducks virology, evolution, molecular, influenza A virus, avian genetics, avian pathogenicity, influenza, avian virology, chickens, China, genes, viral genetics, genotype, avian transmission, mice, molecular sequence data, phylogeny, virulence.

NAL Call Number: SF995.A1A9

Abstract: Ostriches were inoculated with a laboratory-derived highly pathogenic avian influenza (HPAI) virus of emu origin, A/emu/TX/39924/93 (H5N2) clone c1B. The aim of this study was to evaluate the pathogenicity of this isolate for ostriches and assess the ability of routine virological and serological tests to detect infection. Avian influenza virus (AIV) was isolated from cloacal and tracheal swabs from 2 to 12 days post-infection. AIV was also isolated from brain, thymus, eyelid, spleen, ovary/testis, liver, air sac, proventriculurum, duodenum, caecal tonsil, heart, pancreas, kidney, nasal gland and lung. Virus isolation was also possible from swabs of the luminal surfaces of the cloaca, jejunum, lower ileum, bursa of Fabricius, trachea and bone marrow. Birds seroconverted as early as 7 days post-infection. This study suggests that HPAI virus of emu origin replicates extensively in infected ostriches without causing significant clinical disease or mortality.

Descriptors: ostriches, influenza virus A, pathogenicity, viral replication, trachea, cloaca, animal tissues, isolation, seroconversion, clinical aspects.

NAL Call Number: 41.8 Av5

Abstract: Ostriches were inoculated with a highly pathogenic avian influenza (HPAI) virus of ratite origin, A/emu/Texas/39924/93 (H5N2) clone c1B. The aim of this study was to evaluate the pathogenicity of this isolate for ostriches and to assess the ability of routine virologic and serologic tests to detect infection. Avian influenza virus (AIV) was isolated from tracheal swabs from 2 to 12 days post-infection and from cloacal swabs from 3 to 10 days postinfection. AIV was also isolated from a wide range of tissues. Birds seroconverted as early as 7 days postinfection. This study indicates that HPAI virus of ratite origin replicates extensively in infected ostriches without causing significant clinical disease or mortality.

Descriptors: infection, virology, influenza, respiratory system disease, viral disease, serology clinical techniques, diagnostic techniques, viral pathogenicity.

NAL Call Number: Z5055.U49D53

NAL Call Number: 41.8 P27

NAL Call Number: 41.8 P27

Abstract: To determine histopathological damage in the respiratory tract, ducks were inoculated with five different influenza A viruses, including viruses virulent for other avian hosts. Lungs were collected for detection of virus and histopathological examination. Small amounts of infectious virus were recovered from lungs, and viral antigens were demonstrated by immunoperoxidase staining with monoclonal antibodies to the viral nucleoprotein. Although clinical signs were not detected, lungs of ducks infected with both virulent and avirulent viruses had mild pneumonia characterized by infiltrates of lymphocytes and macrophages. These findings show that although clinical signs are not evident, ducks may have damage to the respiratory tract during influenza.
Descriptors: ducks, fowl plague pathology, lung pathology, immunoenzyme techniques, influenza A virus avian pathogenicity, virulence.

NAL Call Number: 442.8 R326

Abstract: In the present paper the pathogenicity of equine subtype A/equi 1 (H7N7) and A/equi 2 (H3N8) for chicks was studied. Strains previously isolated in Brazil, representatives of both subtypes, were used. Eight experiments were performed for A/equi 2, using 89 chicks (4 to 18-day old). Six hundred thirty three samples of cloacal material were collected from 01 to 15 days post-infection (p.i.) and inoculated in 11-day old chick embryos for recuperation of virus. Twelve samples showed positive results. The recuperated viruses were identified with specific antiserum in hemagglutination inhibition test (HI). Blood samples of all chicks collected prior to infection showed no antibodies to both subtypes. Chicks inoculated with A/equi 2 virus were bled 18 to 21 days p.i. Out of 89, seventy one (79.8%) serums showed different levels of antibodies at HI tests. Seventy chicks were inoculated with A/equi 1 subtype. Five hundred forty three samples of cloacal material were harvested and inoculated in embryonated chick eggs. No recuperation of virus occurred. However, all the inoculated chickens showed seroconversion. Chicks infected with A/equi 2 may shed virus in feces. No signs of disease were noted in the inoculated chicks.
Descriptors: chickens microbiology, influenza A virus avian pathogenicity, pathogenicity, chick embryo, cloaca microbiology, hemagglutinins viral immunology, avian immunology, immunology, time factors.

NAL Call Number: QR360.J6

Abstract: In 1997, an outbreak of virulent H5N1 avian influenza virus occurred in poultry in Hong Kong (HK) and was linked to a direct transmission to humans. The factors associated with transmission of avian influenza virus to mammals are not fully understood, and the potential risk of other highly virulent avian influenza A viruses infecting and causing disease in mammals is not known. In this study, two avian and one human HK-origin H5N1 virus along with four additional highly pathogenic H5 avian influenza viruses were analyzed for their pathogenicity in 6- to 8-week-old BALB/c mice. Both the avian and human HK H5 influenza virus isolates caused severe disease in mice, characterized by induced hypothermia, clinical signs, rapid weight loss, and 75 to 100% mortality by 6 to 8 days postinfection. Three of the non-HK-origin isolates caused no detectable clinical signs. One isolate, A/tk/England/91 (H5N1), induced measurable disease, and all but one of the animals recovered. Infections resulted in mild to severe lesions in both the upper and lower
Most consistently, the viruses caused necrosis in respiratory epithelium of the nasal cavity, trachea, bronchi, and bronchioles with accompanying inflammation. The most severe and widespread lesions were observed in the lungs of HK avian influenza virus-infected mice, while no lesions or only mild lesions were evident with A/ck/Scotland/59 (H5N1) and A/ck/Queretaro/95 (H5N2). The A/ck/Italy/97 (H5N2) and the A/tk/England/91 (H5N1) viruses exhibited intermediate pathogenicity, producing mild to moderate respiratory tract lesions. In addition, infection by the different isolates could be further distinguished by the mouse immune response. The non-HK-origin isolates all induced production of increased levels of active transforming growth factor beta following infection, while the HK-origin isolates did not.

Descriptors: influenza virology, influenza A virus avian pathogenicity, human pathogenicity, hn protein, Hong Kong, immunohistochemistry, influenza pathology, avian isolation and purification, avian physiology, human isolation and purification, human physiology, mice, mice inbred BALB c, respiratory system pathology, respiratory system virology, transforming growth factor beta blood, virulence, virus replication.


Descriptors: ducks, avian influenza virus, hemagglutination tests, antibodies, isolation techniques, identification, pathogenicity, Egypt, agglutination tests, Anseriformes, biological properties, birds, domestic animals, immunological factors, immunological techniques, influenza virus, livestock, microbial properties, North Africa, orthomyxoviridae, poultry, useful animals, viruses.


DAL Call Number: 41.8 Au72

Abstract: An influenza virus (H7N7) isolated from an outbreak of disease in chickens in Victoria, was examined for its ability to cause disease in inoculated chickens, turkeys and ducks. The virus was highly pathogenic in chickens and turkeys but produced no clinical disease in ducks. Transmission of infection occurred from inoculated chickens to those in direct contact but other chickens separated by a distance of 3m directly downwind developed neither clinical disease nor antibody to the virus.

Descriptors: chickens microbiology, fowl plague microbiology, influenza A virus avian isolation and purification, poultry diseases microbiology, Australia, avian pathogenicity.


NAL Call Number: 41.8 Au72

Descriptors: disease outbreaks veterinary, fowl plague epidemiology, influenza A virus avian immunology, antibodies, viral analysis, chickens, Victoria epidemiology.


NAL Call Number: 448.3 Ar23

Descriptors: influenza A virus avian pathogenicity, mutation, polioviruses pathogenicity, brain microbiology, chick embryo, chickens, cytopathogenic effect, viral, genetic complementation test, haplorhini, HeLa cells, influenza A virus avian growth and development, influenza A virus avian isolation and purification, Macaca, mutagens, phenotype, polioviruses growth and development, polioviruses isolation and purification, spinal cord microbiology, temperature, tissue culture, virus cultivation, virus replication.


Descriptors: avian influenza virus, H9N2 subtype, pathogenicity, biological properties, microbial properties.

NAL Call Number: 448.8 V81

Abstract: The reported transmission of avian H9N2 influenza viruses to humans and the isolation of these viruses from Hong Kong poultry markets lend urgency to studies of their ecology and pathogenicity. We found that H9N2 viruses from North America differ from those of Asia. The North American viruses, which infect primarily domestic turkeys, replicated poorly in inoculated chickens. Phylogenetic analysis of the hemagglutinin and nucleoprotein genes indicated that the Asian H9N2 influenza viruses could be divided into three sublineages. Initial biological characterization of at least one virus from each lineage was done in animals. Early isolates of one lineage (A/Chicken/Beijing/1/94, H9N2) caused as high as 80% mortality rates in inoculated chickens, whereas all other strains were nonpathogenic. Sequence analysis showed that some isolates, including the pathogenic isolate, had one additional basic amino acid (A-R/K-S-S-R-) at the hemagglutinin cleavage site. Later isolates of the same lineage (A/Chicken/Hong Kong/G9/97, H9N2) that contains the PB1 and PB2 genes similar to Hong Kong/97 H5N1 viruses replicated in chickens, ducks, mice, and pigs but were pathogenic only in mice. A/Quail/Hong Kong/G1/97 (H9N2), from a second lineage that possesses the replicative complex similar to Hong Kong/97 H5N1 virus, replicated in chickens and ducks without producing disease signs, was pathogenic in mice, and spread to the brain without adaptation. Examples of the third Asian H9N2 sublineage (A/Chicken/Korea/323/96, Duck/Hong Kong/Y439/97) replicated in chickens, ducks, and mice without producing disease signs. The available evidence supports the notion of differences in pathogenicity of H9N2 viruses in the different lineages and suggests that viruses possessing genome segments similar to 1997 H5N1-like viruses are potentially pathogenic in mammals.

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Descriptors: influenza A virus avian genetics, influenza A virus avian pathogenicity, binding sites genetics, chickens virology, DNA complementary chemistry, DNA complementary genetics, glycosylation, hemagglutinins viral genetics, hemagglutinins viral metabolism, Hong Kong epidemiology, mice, mice inbred BALB c virology, molecular sequence data, phylogeny, poultry diseases epidemiology, RNA viral genetics, reverse transcriptase polymerase chain reaction, sequence analysis, DNA, virulence genetics, virus replication.


NAL Call Number: 41.8 T445

Abstract: "Highly pathogenic" avian influenza viruses cause fowl plague. The disease is a notifiable disease. In 2003 infections with highly pathogenic avian influenza were reported in the Netherlands, Belgium and Germany. Influenza viruses seem to be host specific. The risk of infection of humans with avian influenza A viruses is very low, however, in some cases people can attract infections. This observation should be seriously evaluated. The measures adopted to control and eradicate avian influenza are based on the strategy of stamping-out infected flocks and controlling the movement of poultry, poultry products and other contaminated materials. In general vaccinations against HPAI are only allowed as a supplement to the control measures. The decision to introduce the vaccine is accompanied with several restrictions. This paper explores the characteristics of avian influenza viruses, epidemiology, the disease and public health aspects. Finally, the current control strategy in the European communities is discussed.

Descriptors: epidemiology, infection, veterinary medicine, avian influenza, diagnosis, epidemiology, etiology, pathology, respiratory system disease, symptom, therapy, transmission, viral disease, vaccination clinical techniques, differential diagnosis, public health, zoonosis.


NAL Call Number: 41.8 Au72

Abstract: In groups receiving intranasal inoculations, 22 of 24 birds became affected. Illnesses were usually less than 2 d with clinical signs generally depression and dullness. Examination of lesions showed that this strain of virus produced in the laboratory a consistent, characteristic disease pattern, affecting predominantly the bursa of Fabricius, the pancreas and the brain.
Descriptors: chickens, avian influenza virus, wounds, pathology, birds, domestic animals, domesticated birds, Galliformes, influenza virus, lesions, livestock, poultry, useful animals, viruses.

NAL Call Number: 41.8 P27

Abstract: Avian pneumovirus (APV) is the cause of a respiratory disease of turkeys characterized by coughing, ocular and nasal discharge, and swelling of the infraorbital sinuses. Sixty turkey poults were reared in isolation conditions. At 3 weeks of age, serum samples were collected and determined to be free of antibodies against APV, avian influenza, hemorrhagic enteritis, Newcastle disease, *Mycoplasma gallisepticum*, *Mycoplasma synoviae*, *Mycoplasma meleagridis*, *Ornithobacterium rhinotracheale*, and *Bordetella avium*. When the poults were 4 weeks old, they were inoculated with cell culture-propagated APV (APV/Minnesota/turkey/2a/97) via the conjunctival spaces and nostrils. After inoculation, four poults were euthanatized every 2 days for 14 days, and blood, swabs, and tissues were collected. Clinical signs consisting of nasal discharge, swelling of the infraorbital sinuses, and frothy ocular discharge were evident by 2 days postinoculation (PI) and persisted until day 12 PI. Mild inflammation of the mucosa of the nasal turbinates and infraorbital sinuses was present between days 2 and 10 PI. Mild inflammatory changes were seen in tracheas of poults euthanatized between days 4 and 10 PI. Antibody to APV was detected by day 7 PI. The virus was detected in tissue preparations and swabs of nasal turbinates and infraorbital sinuses by reverse transcription polymerase chain reaction, virus isolation, and immunohistochemical staining methods between days 2 and 10 PI. Virus was detected in tracheal tissue and swabs between days 2 and 6 PI using the same methods. In this experiment, turkey poults inoculated with tissue culture-propagated APV developed clinical signs similar to those seen in field cases associated with infection with this virus.

Descriptors: metapneumovirus growth and development, paramyxoviridae infections veterinary, poultry diseases pathology, turkeys, antibodies, viral blood, *Cercopithecus aethiops*, cytopathogenic effect, viral, DNA, viral chemistry, DNA, viral genetics, enzyme linked immunosorbent assay veterinary, fluorescent antibody technique veterinary, histocytochemistry veterinary, metapneumovirus genetics, Minnesota, nasal mucosa pathology, nasal mucosa virology, paramyxoviridae infections blood, paramyxoviridae infections pathology, paramyxoviridae infections virology, poultry diseases virology, reverse transcriptase polymerase chain reaction veterinary, vero cells.

NAL Call Number: 41.8 Av5

Abstract: Chickens were intranasally inoculated with Chilean H7N3 avian influenza (AI) viruses of low pathogenicity (LP) (H7N3/LP), high pathogenicity (HP) (H7N3/HP), and a laboratory derivative (02-AI-15-#9) (H7N3/14D) from the LPAI virus to determine pathobiologic effects. All chickens inoculated with H7N3/HP AI virus became infected and abruptly died 2 or 3 days postinoculation, but a few showed moderate depression before death. The H7N3/HP AI virus produced focal hemorrhages of the comb, petechial hemorrhage at the esophageal-proventricular junction and proventricular mucosa, edema and congestion of the lung, petechiation of the spleen, and generalized decrease in body fat. Histologically, severe necrosis, hemorrhage, and inflammation were primarily identified in lungs and the lymphoid tissues. All tissues sampled from the H7N3/HP AI group were positive for the AI viral antigen, predominantly in endothelium of blood vessels throughout most tissues and less frequently in histiocytes and cellular debris of lymphoid tissues. Even less consistently, cardiac myocytes, hepatocytes, Kupffer cells, glandular epithelial cells, microglial cells, and neurons became infected. These studies suggest the Chilean H7N3/LP AI virus was poorly infectious for chickens and may have been recently introduced from a nongalliform host. By contrast, the H7N3/HP AI virus became infected and abruptly died 2 or 3 days postinoculation, but a few showed moderate depression before death. The H7N3/HP AI virus produced focal hemorrhages of the comb, petechial hemorrhage at the esophageal-proventricular junction and proventricular mucosa, edema and congestion of the lung, petechiation of the spleen, and generalized decrease in body fat. Histologically, severe necrosis, hemorrhage, and inflammation were primarily identified in lungs and the lymphoid tissues. All tissues sampled from the H7N3/HP AI group were positive for the AI viral antigen, predominantly in endothelium of blood vessels throughout most tissues and less frequently in histiocytes and cellular debris of lymphoid tissues. Even less consistently, cardiac myocytes, hepatocytes, Kupffer cells, glandular epithelial cells, microglial cells, and neurons became infected. These studies suggest the Chilean H7N3/LP AI virus was poorly infectious for chickens and may have been recently introduced from a nongalliform host. By contrast, the H7N3/HP AI virus was highly infectious and lethal for chickens. The H7N3/HP AI virus had a strong tropism for the cardiovascular system, principally vascular endothelium, which is similar to the viral tropism demonstrated previously with other H5 and H7 HPAI viruses. Interestingly, the H7N3/LP AI virus on intravenous inoculation replicated in cardiac myocytes, a feature of HPAI and not LPAI viruses, which further supports the theory that the H7N3/LP AI virus was in transition from LP to HP.

Descriptors: chickens, influenza A virus, avian pathogenicity, avian virology, chick embryo, Chile, avian classification, avian isolation and purification, avian pathology, virulence.

**NAL Call Number:** 41.8 Av5

**Abstract:** Groups of turkeys were exposed to different isolates of avian influenza virus from wild mallard ducks and domestic turkeys by the intracerebral, intravenous, intratracheal, and intra-airsac routes, and pathogenicity indices were calculated. For the intracerebral pathogenicity study, body weight was also measured. For intravenous, intratracheal, and intra-airsac pathogenicity studies, necropsy lesions were scored and serological responses were recorded. Only the intracerebral pathogenicity index and body weight gain post intracerebral infection demonstrated any differences between isolates. The other procedures failed to demonstrate any pathogenicity whatsoever. There was a correlation (R = 0.73) between intracerebral pathogenicity index and reduced weight gain postinfection. These studies suggest that growth suppression may be an objective measure of pathogenic potential of influenza viruses found to be nonpathogenic by other methods.

**Descriptors:** ducks microbiology, influenza A virus avian pathogenicity, turkeys microbiology, body weight veterinary, ducks growth and development, ducks immunology, fowl plague immunology, fowl plague physiopathology, hemagglutination inhibition tests veterinary, avian immunology, turkeys growth and development, turkeys immunology.


**NAL Call Number:** R41.B52

**Abstract:** In 1997 in Hong Kong, 18 human cases of respiratory illness were caused by an avian influenza A H5N1 virus. Although avian influenza viruses had not previously been known to cause respiratory illness in humans, the H5N1 viruses caused severe illness and death, primarily in individuals aged > 12 years. The introduction of H5N1 viruses into humans raised concerns about the potential of these viruses to cause a pandemic. We have used the BALB/c mouse to better understand the pathogenesis of and immunity to the H5N1 viruses in a mammalian model. Previously, we demonstrated that H5N1 viruses isolated from humans replicated efficiently in the lungs of mice without prior adaptation to this host. Two general phenotypes of pathogenicity of H5N1 viruses, based on high and low lethality for mice, were observed. We now demonstrate that in addition to a lethal outcome, H5N1 viruses with a high pathogenicity phenotype exhibit additional features that include rapid and uncontrolled replication in the lungs of infected mice, dissemination and replication of the virus in other organs, and depletion of peripheral blood leukocytes. The BALB/c mouse model was also used to better understand the parameters of protective immunity to the H5N1 viruses. Prior infection with H5N1 viruses of low pathogenicity or an antigenically related non-pathogenic H5N3 virus protected mice from death by infection with a highly pathogenic HK/483 virus. Serum hemagglutination-inhibition antibody titers of 40 or greater were associated with protection of mice from death. Immunization of mice with baculovirus-expressed recombinant H5 hemagglutinin protein or a previously defined HS-specific synthetic peptide induced MHC class II restricted CTL activity. Mice that had CTL activity but no serum hemagglutination-inhibition antibody were not protected from a lethal challenge with H5N1 virus. These results suggest that antibody is required for protection of mice against lethal challenge with H5N1 viruses of the high pathogenicity phenotype.

**Descriptors:** influenza A virus avian immunology, avian pathogenicity, antibodies, viral blood, antigens, viral analysis, immunization, influenza virology, influenza vaccine immunology, mice, mice inbred BALB c, T lymphocytes, cytotoxic immunology, virus replication.


**NAL Call Number:** SF604.J342

**Descriptors:** chickens microbiology, influenza A virus avian physiology, porcine physiology, influenza A virus physiology, mice microbiology, cloaca microbiology, avian pathogenicity, porcine pathogenicity,

**NAL Call Number:** SF995.A1A9

**Abstract:** Lesions of chickens inoculated with two highly pathogenic avian influenza virus strains, A/turkey/England/50-92/91 (H5N1) and A/chicken/Victoria/1/85 (H7N7) were examined histologically and immunohistochemically. Birds of both treatment groups died within 5 days post-inoculation. The most significant lesions induced by these two viruses consisted of swelling of the microvascular endothelium, systemic congestion, multifocal haemorrhages, perivascular mononuclear cell infiltration, and thrombosis associated with viral antigen in the vascular endothelium and/or perivascular parenchymatous cells. Viral antigen in the cardiac myocytes was consistently detected in all birds. In addition, severe pulmonary congestion and oedema was found in A/turkey/England/50-92/91 virus-inoculated birds that died within 1 day post-inoculation. The other chickens of both groups showed necrotic and inflammatory changes associated with viral antigen in various organs and tissues. These findings suggested that cardiovascular system involvement played an important role in the pathogenesis of these virus infections.

**Descriptors:** animal husbandry, immune system, infection, methods and techniques, morphology, pathology, veterinary medicine, avian influenza virus, avian pathology, experimental infections, histological, immunohistochemical examination, infection lesions, necrotic, inflammatory changes, pathological studies, pathology, viral antigen, viral infection pathogenesis.


**NAL Call Number:** 41.8 J82

**Abstract:** Central nervous system lesions of chickens inoculated with three highly pathogenic avian influenza virus strains, A/chicken/Victoria/1/85 (H7N7), A/turkey/England/50-92/91 (H5N1), and A/tern/South Africa/61 (H5N3), were examined histologically and immunohistochemically. The chickens either died within 7 days of inoculation or were killed 2 weeks after inoculation. No significant differences were observed in the lesions induced by these three viruses. The lesions were divided into two types, disseminated foci of microgliosis and necrosis, and ventriculitis. The former lesions were associated with infection of the vascular endothelium and dissemination of the virus to the peripheral parenchymal cells of the chickens that died within 3 days of inoculation. The ventriculitis lesions, however, were observed mainly in the chickens that died between 4 and 7 days after inoculation. These findings suggest that viral infection of the vascular endothelium and subsequent involvement of ependymal cells play important roles in the pathogenesis of the central nervous system lesions.

**Descriptors:** animal husbandry, cell biology, infection, morphology, nervous system, pathology, veterinary medicine, central nervous system, lesion, comparative pathology, ependymal cell microgliosis, necrosis, pathogenesis, photomicrograph, vascular endothelium, ventriculitis.


**NAL Call Number:** SF604.K42

**Abstract:** The sequential pathologic changes in the chick embryo infected with influenza virus were described. Degenerative and necrotic changes were seen in most of the organs. Oedema was very prominent. Heterophilic involvement was not a characteristic feature of the embryo response to Avian influenza virus.

**Descriptors:** animal husbandry, development, infection, veterinary medicine.


**Descriptors:** avian influenza, mallard ducks, pathogenesis, infection.

**Descriptors:** antibody formation, diagnostic techniques, experimental infection, hemagglutination inhibition test, immune response, pathogenicity, strain differences, virulence, avian influenza virus, chickens, mice.


**NAL Call Number:** 41.8 V644

**Descriptors:** disease prevalence, epidemiology, evolution, pathogenicity, Newcastle disease, avian influenza virus.


**Descriptors:** avian influenza virus, histopathology, immunization, inactivated vaccines, fowl.


**NAL Call Number:** 41.8 Av5

**Abstract:** Infections of ostriches with avian influenza A viruses are generally associated with clinical disease, but the occasional high mortality in young birds does not appear to be related directly to virus pathotype. In this study we investigated the pathogenesis of two H7 viruses for 11-wk-old ostriches inoculated intranasally, and clinical symptoms, virus excretion, and immune response were studied. One of the viruses (A/Ostrich/Italy/1038/00) was highly pathogenic for chickens, whereas the other (A/Ostrich/South Africa/1609/91) was of low pathogenicity for chickens. Clinical signs in ostriches receiving virulent virus were slight depression and hemorrhagic diarrhea, while the group receiving avirulent virus was clinically normal except for green diarrhea. Both viruses were transmitted to in-contact sentinel birds housed with the infected groups 3 days postinfection. Postmortem examination of the birds infected (including the sentinel bird) with virus highly pathogenic for chickens were grossly normal except for localized pneumonic lesions. The results of the study are presented and discussed.

**Descriptors:** infection, veterinary medicine, avian influenza, infectious disease, respiratory system disease, viral disease, disease pathogenesis, immune response, virus excretion, ostrich.


**NAL Call Number:** 41.8 Av5

**Abstract:** Pathologic changes and distribution of viral antigen as determined by immunohistochemistry were compared among 4-wk-old specific-pathogen-free chickens inoculated intratracheally with avian influenza virus (AIV) isolates of either low or high pathogenicity. Viruses of low pathogenicity previously characterized as mildly pathogenic (MP), included A/chicken/Pennsylvania/21525/83 (H5N2) (MP-Penn) and A/chicken/Alabama/7395/75 (H4N8) (MP-Alab). Viruses of high pathogenicity included A/chicken/Pennsylvania/1370/83 (H5N2), A/chicken/Victoria/A185/85 (H7N7), and A/turkey/Ontario/7732/66 (H5N9). Extremely variable clinical signs ranging from mild respiratory distress to high mortality were present among chickens inoculated with these viruses. Chickens inoculated with highly pathogenic (HP) virus had histologic lesions of necrosis and inflammation in cloacal bursa, thymus, spleen, heart, pancreas, kidney, brain, trachea, lung, and skeletal muscle, whereas chickens inoculated with HP virus had histologic lesions most frequently in lung and trachea or lacked histologic lesions. Immunospecific staining for avian influenza viral proteins was most common in cells within heart, lung, kidney, brain, and pancreas of chickens.
inoculated with HP viruses, but immunospecific staining was present only and infrequently in trachea and lung of chickens inoculated with MP-Penn AIV. MP-Alab did not produce lesions nor have vital antigen in inoculated chickens but did produce serologic evidence of infection. The pattern of organ involvement and viral antigen distribution in chickens intratracheally inoculated with HP MV isolates indicates a common capability to spread beyond the respiratory tract and confirms the pantrophic replicative, pathobiologic, and lethal nature of the viruses. However, variability in severity and lesion distribution exists between different HP AIVs.

Descriptors: chickens, avian influenza virus, pathogenicity, experimental infection, in vivo experimentation, histopathology, lesions, antigens, animal tissues, biological properties, birds, body parts, disease transmission, domestic animals, domesticated birds, experimentation, Galliformes, immunological factors, infection, influenza virus, livestock, microbial properties, orthomyxoviridae, pathogenesis, pathology, poultry, useful animals, viruses, viral antigens.

NAL Call Number: SF995.W4
Descriptors: avian influenza virus, pathogenicity, pathotypes, birds.

NAL Call Number: 41.8 Av5
Abstract: An immunohistochemical investigation was performed to assess tissue tropism and viral replication of Italian H7N1 isolates belonging to different lineages in developing chicken, turkey, Muscovy duck, and mallard duck embryos. Low-pathogenic avian influenza (LPAI) isolates were selected on the basis of the location in the phylogenetic tree; a progenitor strain, A/turkey/Italy/977/V99 (exhibiting no additional glycosylation sites, nAGS), strain A/turkey/Italy/2379/V99 (AGS in position 123), and strain A/turkey/Italy/3675/V99 (AGS in position 149) were selected. The latter two strains belonged to distinct lineages originating from the pool of progenitor strains. The highly pathogenic avian influenza (HPAI) isolate A/turkey/Italy/4580/V99 was also included in the test. All the embryos tested supported the growth of HPAI. The LPAI isolates replicated readily in the allantoic layer of the chorioallantoic membrane of all the species tested and did not replicate to detectable levels in the developing chicken, turkey, and Muscovy duck embryos. In contrast, they replicated to different extents in the respiratory tract of the developing mallard embryo. The findings indicate that the pathogenesis of LPAI infections in mallard embryos is different to that observed in other species and should be investigated further.
Descriptors: development, infection, avian influenza, infectious disease, respiratory system disease, viral disease, immunohistochemistry immunologic techniques, laboratory techniques, avian embryo infection susceptibility pathogenesis viral replication.

NAL Call Number: 448.3 Ar23
Abstract: The virulence of influenza A viruses was determined using the intracerebral pathogenicity index test for chickens. The viruses were divided into high virulent, low virulent and avirulent strains. A low virulent strain was recovered from the jejunum and faeces of infected chickens.
Descriptors: brain microbiology, chickens microbiology, influenza A virus pathogenicity, feces microbiology, influenza A virus avian pathogenicity, influenza A virus human pathogenicity, influenza A virus, porcine pathogenicity, influenza A virus growth and development, jejunum microbiology.

NAL Call Number: 41.8 Av5
Abstract: We isolated 24 Hav1 Neq1 and 18 Hav6 Nav3 influenza viruses from such free-living wild

**Abstract:** The pathogenicity for chickens of 91 strains of avian influenza A virus isolated from such free-living waterfowl as whistling swan, pintail, tufted duck, mallard and black-tailed gull in Japan was tested. The majority of the virus strains infected and were pathogenic for the chickens. The virulence of these viruses seemed not to be as high as that of fowl plague virus. There were no significant differences in the intracerebral index score among the viruses belonging to the same subtype, irrespective of year of isolation or host.

**Descriptors:** birds microbiology, brain diseases veterinary, chickens microbiology, fowl plague microbiology, influenza A virus avian pathogenicity, brain diseases microbiology, fowl plague transmission, influenza A virus avian isolation and purification, seasons, virulence.


**NAL Call Number:** SF604.V485

**Descriptors:** infection, acute renal tubular necrosis, avian influenza, non suppurative encephalitis, vasculitis, reverse transcription polymerase chain reaction, clinical techniques, diagnostic techniques, viral replication, chickens.


**NAL Call Number:** SF481.M54

**Descriptors:** avian influenza virus, highly pathogenic, mutations, poultry.


**NAL Call Number:** 41.8 P27

**Abstract:** Direct bird-to-human transmission, with the production of severe respiratory disease and human mortality, is unique to the Hong Kong-origin H5N1 highly pathogenic avian influenza (HPAI) virus, which was originally isolated from a disease outbreak in chickens. The pathobiology of the A/chicken/Hong Kong/220/97 (H5N1) (HK/220) HPAI virus was investigated in chickens, turkeys, Japanese and Bobwhite quail, guinea fowl, pheasants, and partridges, where it produced 75-100% mortality within 10 days. Depression, mucoid diarrhea, and neurologic dysfunction were common clinical manifestations of disease. Grossly, the most severe and consistent lesions included splenomegaly, pulmonary edema and congestion, and hemorrhages in enteric lymphoid areas, on serosal surfaces, and in skeletal muscle. Histologic lesions were observed in multiple organs and were characterized by exudation, hemorrhage, necrosis, inflammation, or a combination of these features. The lung, heart, brain, spleen, and adrenal glands were the most consistently affected, and viral antigen was most often detected by immunohistochemistry in the parenchyma of these organs. The pathogenesis of infection with the HK/220 HPAI virus in these species...
was twofold. Early mortality occurring at 1-2 days postinoculation (DPI) corresponded to severe pulmonary edema and congestion and virus localization within the vascular endothelium. Mortality occurring after 2 DPI was related to systemic biochemical imbalance, multiorgan failure, or a combination of these factors. The pathobiologic features were analogous to those experimentally induced with other HPAI viruses in domestic poultry.

Descriptors: birds virology, fowl plague pathology, influenza A virus avian pathogenicity, poultry diseases virology, adrenal glands pathology, antigens, viral blood, brain pathology, chick embryo, fowl plague virology, hemorrhage veterinary, immunohistochemistry veterinary, lung pathology, poultry diseases pathology, pulmonary edema veterinary, specific pathogen free organisms, splenomegaly veterinary.


Descriptors: avian influenza virus, experimental infections, lesions, pathogenicity, species differences, wild birds, budgerigars, Passer domesticus, Carpodacus mexicanus, Sternum vulgaris, Taeniopygia guttata.


Abstract: The H5N1 type A influenza viruses that emerged in Hong Kong in 1997 are a unique lineage of type A influenza viruses with the capacity to transmit directly from chickens to humans and produce significant disease and mortality in both of these hosts. The objective of this study was to ascertain the susceptibility of emus (Dromaius novaehollandiae), domestic geese (Anser anser domesticus), domestic ducks (Anas platyrhynchos), and pigeons (Columbia livia) to intranasal (i.n.) inoculation with the A/chicken/Hong Kong/220/97 (H5N1) highly pathogenic avian influenza virus. No mortality occurred within 10 days postinoculation (DPI) in the four species investigated, and clinical disease, evident as neurologic dysfunction, was observed exclusively in emus and geese. Grossly, pancreatic mottling and splenomegaly were identified in these two species. In addition, the geese had cerebral malacia and thymic and bursal atrophy. Histologically, both the emus and geese developed pancreatitis, meningoencephalitis, and mild myocarditis. Influenza viral antigen was demonstrated in areas with histologic lesions up to 10 DPI in the geese. Virus was reisolated from oropharyngeal and cloacal swabs and from the lung, brain, and kidney of the emus and geese. Moderate splenomegaly was observed grossly in the ducks. Viral infection of the ducks was pneumotropic, as evidenced by mild inflammatory lesions in the respiratory tract and virus reisolation from oropharyngeal swabs and from a lung. Pigeons were resistant to HK/220 infection, lacking gross and histologic lesions, viral antigen, and reisolation of virus. These results imply that emus and geese are susceptible to i.n. inoculation with the HK/220 virus, whereas ducks and pigeons are more resistant. These latter two species probably played a minimal epidemiologic role in the perpetuation of the H5N1 Hong Kong-origin influenza viruses.

Descriptors: infection, veterinary medicine, H5N1 avian influenza virus infection, etiology, mortality, viral disease, bursal atrophy, joint disease, cerebral malacia, nervous system disease, meningoencephalitis, nervous system disease, myocarditis, heart disease, neurologic dysfunction, nervous system disease, pancreatic mottling, digestive system disease, endocrine disease, pancreas, pancreatitis, digestive system disease, respiratory tract inflammation, respiratory system disease, splenomegaly, blood and lymphatic disease, thymic atrophy, endocrine disease, thymus.


**NAL Call Number**: 41.8 Av5

**Descriptors**: Mycoplasma infections pathology, orthomyxoviridae infections pathology, poultry diseases, antibody formation, hemagglutination inhibition tests, immune sera analysis, lung diseases pathology, lung diseases veterinary, mycoplasma pathogenicity, *Mycoplasma* infections immunology, orthomyxoviridae pathogenicity, orthomyxoviridae infections immunology, pulmonary alveoli immunology, pulmonary alveoli microbiology, pulmonary alveoli pathology, turkeys.


**NAL Call Number**: 448.8 L11

**Abstract**: Coinfection of a cell culture with a human and avian influenza A virus had yielded a recombinant virus with high neurovirulence for mice. This study reports on the comparative pathogenesis of central nervous system infection in mice between the parental human and the recombinant virus using the immunohistologic peroxidase-antiperoxidase method and virus assay of tissue suspensions. The human virus replicated poorly in mice and did not replicate in the brain even after intracerebral inoculation. In contrast, the recombinant virus replicated to high titer in the lung and brain with resulting viremia after inoculation of young mice by the intracerebral, intraperitoneal, or intranasal routes. Different populations of cells in the brain became infected after inoculation by each of the three routes: choroid plexus, and ependymal and subependymal cells after intracerebral inoculation; cells in perivenous areas, neurons in the olfactory bulbs and trigeminal ganglia and nuclear groups in the brainstem and midbrain after intranasal inoculation. Intraperitoneal inoculation resulted almost exclusively in the perivenous spread of the virus. The intranasal inoculation suggested that virus entry into the brain both by spread along nerve cell processes from the nasal mucosa to the brain and trigeminal ganglia and subsequent perivenous spread after viremia developed following virus replication in the lung. To dissect these two mechanisms we inoculated neonatal mice that had acquired high levels of serum antibody by nursing from actively immunized mothers. Intraperitoneal inoculation of these mice failed to cause infection, whereas intranasal inoculation resulted in the same pattern of cellular spread through the olfactory and trigeminal pathways as noted previously. This proved that this recombinant influenza virus could invade the central nervous system after infection via a natural route of infection. This highly neuroinvasive agent provides one example of the extent of virulence which can be acquired by recombination of apathogenic influenza viruses and raises a note of caution for adequate control of those agents generated in the laboratory.


**NAL Call Number**: Z5055.U49D53

**Descriptors**: avian influenza virus, turkeys, pathogenesis.


**NAL Call Number**: 41.8 Av5

**Abstract**: Cynomolgus macaques (*Macaca fascicularis*) infected with influenza virus A/HongKong/156/97 (H5N1) developed acute respiratory distress syndrome (ARDS) with fever. Reverse
transcriptase/polymerase chain reaction (RT/PCR) and virus isolation showed that the respiratory tract is the major target of the virus. The main lesion observed upon necropsy, performed 4 or 7 days postinfection, was a necrotizing bronchointerstitial pneumonia, similar to that found in primary influenza pneumonia in human beings. By immunohistochemistry, influenza virus antigen proved to be limited to pulmonary tissue and tonsils. The data indicate that ARDS and multiple organ dysfunction syndrome (MODS), observed in both humans and monkeys infected with this virus, are caused by diffuse alveolar damage from virus replication in the lungs alone.

Descriptors: 
infection, acute respiratory distress syndrome (ARDS), respiratory system disease, avian influenza, infectious disease, respiratory system disease, viral disease, bronchointerstitial pneumonia, respiratory system disease, multiple organ dysfunction syndrome (MODS), disease miscellaneous, immunohistochemistry immunologic techniques, laboratory techniques, necropsy clinical techniques, reverse transcriptase polymerase chain reaction (RT PCR) genetic techniques, laboratory techniques, viral isolation laboratory techniques, influenza pathogenesis viral replication.


NAL Call Number: 384 Z38

Descriptors: orthomyxoviridae pathogenicity, amino acid sequence, cell transformation, viral, hemagglutins, influenza A virus avian genetics, avian pathogenicity, orthomyxoviridae genetics, plaque assay, RNA viral genetics, species specificity, viral proteins genetics.


NAL Call Number: 41.8 B45

Descriptors: influenza A virus avian classification, microbiological techniques veterinary, chick embryo, fibroblasts, hemagglutination tests, avian pathogenicity, plaque assay veterinary, tissue culture, virulence, virus cultivation.


NAL Call Number: aSF995.6.I6I5 1981a

Descriptors: avian influenza viruses, pathogenicity, infectivity, hemagglutinins, symposium.


Abstract: Proteolytic cleavage of the influenza virus hemagglutinin glycoprotein (HA) by cellular proteases is a prerequisite for virus infectivity, spread of the virus in the infected organism, tissue tropism, and viral pathogenicity. Production of infectious virus depends upon the structure at the HA cleavage site as well as the substrate specificity and the distribution of appropriate enzymes. Differences exist in the specificities of the endoproteases that recognize the different sequence motifs at the cleavage site. With avian influenza viruses that cause lethal systemic infections, the cleavage site consists of multibasic amino acids. Furin, which activates this type of HA, is a member of the subtilisin family and represents the prototype of ubiquitously occurring membrane-bound proteases. On the other hand, serine proteases secreted from a restricted number of cell types and some bacterial enzymes recognize a monobasic cleavage signal at HA of the mammalian and the apathogenic avian influenza viruses. The limited occurrence of these proteases results in only localized infection. Implementation of these defined conditions for virus activation may represent a novel type of disease control.

Descriptors: hemagglutinins viral physiology, orthomyxoviridae enzymology, orthomyxoviridae pathogenicity, serine endopeptidases physiology, subtilisins physiology, furin, hemagglutinins viral chemistry, substrate specificity.

Influenzaviren. [Significance of hemagglutinins for the pathogenicity of avian influenza viruses].
Zentralblatt Fur Bakteriologie, Mikrobiologie, Und Hygiene. Series A, Medical Microbiology, Infectious Diseases, Virology, Parasitology 258(2-3): 337-49. ISSN: 0176-6724.
NAL Call Number: 448.3 C33 (1)

Abstract: In addition to acute viral diseases, persistent infections have attained considerable interest in recent years. Such persistent infections are characterized by extended time periods in which the infecting virus remains within the organism before the eventual appearance of manifest symptoms. These infections may be evoked by a variety of virus species resulting in a diversity of pathogenic reactions and clinical manifestations. The mechanisms of viral persistence, where known, also appear to be quite diverse. As far as space permits, some examples of persistent infections will be presented and the mechanisms of the pathogenesis of the resulting diseases will be discussed.

Descriptors: hemagglutinins viral analysis, hemagglutinins viral genetics, hemagglutinins viral immunology, influenza A virus avian pathogenicity, amino acid sequence, cell membrane microbiology, chick embryo, fetal membranes microbiology, genes viral, avian genetics, avian growth and development, avian ultrastructure, models, molecular, mutation, virulence.

NAL Call Number: QP356.3.O4 1983

Descriptors: avian influenza viruses, pathogenicity.

NAL Call Number: QR360.A1J6

Abstract: We have demonstrated by recombination of two highly pathogenic avian influenza viruses [A/FPV/Rostock (Hav1N1) x A/turkey/England/63 (Hav1Nav3)] that recombinants can be isolated which are pathogenic as well as non-pathogenic for chickens. They carried the glycoproteins of either parent strains, and all are produced in infectious form in chick embryo cells. Genetic analysis revealed that the non-pathogenic recombinants possess a mixed RNA polymerase complex, consisting of pol 1, pol 2, ptra and NP gene products, while, with one exception, the pathogenic recombinants have the genes coding for the polymerase activity from one or other parent virus. The biological properties of the recombinant viruses did not correlate with their pathogenicity for chickens.

Descriptors: genes viral, influenza A virus avian genetics, recombination, genetic, chickens, DNA directed RNA polymerases genetics, fowl plague microbiology, avian pathogenicity, neuraminidase genetics, turkeys.


Descriptors: avian influenza A viruses, cytopathogenicity, cell lines.

NAL Call Number: QR375.V6

Abstract: The reversion of temperature-sensitive (ts) mutants of fowl plague virus to the ts+ phenotype was correlated with pathogenicity for chicken. Two types of ts mutants were investigated: those obtained by mutagenesis with 5-fluorouracil and those obtained by undiluted passages at 33 degrees C. The reversion frequency of the former mutants depended on the RNA segment in which the ts defect was located, mutations in RNA segments 1 and 2 having the highest reversion frequency, those in the RNA segments coding for the glycoproteins the lowest. ts mutants obtained by undiluted passages behaved differently in this respect. There was an approximate correlation between frequency of reversion and pathogenicity for chicken. Double mutants induced by 5-fluorouracil, having one tight and one leaky mutation, reverted easily without loss of the leaky mutation. These double mutants were still to a limited extent pathogenic for the
chicken. Only one double mutant with two tight mutations (ts 293) was completely nonpathogenic after intramuscular inoculation. Two ts mutants with multiple tight defects (ts 1/1 and ts 3/18) obtained by undiluted passage did not revert to wild-type after injection into embryonated eggs and incubation at 33 degrees C, but they were still slightly pathogenic for the chicken. There was no obvious correlation between the shut-off temperature and pathogenicity of mutants carrying a single ts defect. However, for mutants with multiple tight mutations a high shut-off temperature seemed to be essential for reversion during serial passages as well as for pathogenicity in the chicken, when different routes of inoculation were examined. ts mutants seem to be safe as live vaccines only, (1) if they carry at least two tight ts defects, (2) if they have a relatively low shut-off temperature, and (3) if they could be administered other than via the respiratory tract. Descriptors: influenza A virus, avian genetics, mutation, temperature, chickens, microbiology, fluorouracil, pharmacology, avian pathogenicity.


NAL Call Number: SF995.A1A9

Abstract: Specific-pathogen-free (SPF), 2-day-old chicks were inoculated with type A influenza virus (A/whistling swan/Shimane/499/83/(H5N3)) into their caudal thoracic air sac. The original isolate of the virus was of low virulence (ICPI 0.20 to 0.40), and was passaged 10 times through the respiratory organs of SPF chicks. Most of the chicks inoculated with the passaged virus (strain 499) showed respiratory and alimentary signs. Three of 30 chicks died on days 2, 6 and 7 post-inoculation (p.i.). Almost half of the infected chicks showed poor growth, and the variation of body size in the flock became prominent from day 10 p.i. Infected chicks consistently had pathological changes in the pancreas, liver, kidneys and respiratory tracts, and occasionally in the brain, duodenum and bone marrow. Positive immunoreaction to avian influenza virus (AIV) antigen and recovery of the virus persisted for longer period in the pancreas than in other organs. The pancreatic lesions were caused by a direct, lytic virus infection of the acinar cells and contributed to poor growth of the chicks.

Descriptors: chicks, avian influenza virus, pancreas, atrophy, pathogenesis, virulence, symptoms, histopathology, growth retardation, acinar cells.


NAL Call Number: SF604.J342

Abstract: Three-day-old, specific-pathogen-free (SPF) chicks were inoculated with the strains of influenza A/whistling swan/Shimane/499/83 (H5N3) via the air sac route. The strains had been passaged through air sacs or air sacs and brains of SPF chicks. Two experiments were undertaken to examine the pathogenicity of these strains and the development of brain lesions based on time-interval changes. In experiment 1, original strain (4e) showed low pathogenicity with mild respiratory signs and zero mortality. Air sac passaged strains (18a and 24a) of 4e demonstrated mortalities of 50% and 67%, respectively, and inoculated chicks showed hemorrhages and necrotic lesions in major organs. Air sac-brain passaged strain (24a5b) of 4e produced 100% mortality and severe nervous signs. Severe circulatory disturbance with multiple foci of necrosis in major organs including the brain was found in chicks inoculated with 24a5b. The 24a5b was analogous to highly pathogenic avian influenza virus in regard to its pathogenicity to chicks. Hence, low pathogenic influenza virus (4e) gradually aggravated its pathogenicity to highly pathogenic virus (24a5b) by air sac and brain passages. In experiment 2, chicks were inoculated with 24a5b, and the earliest histological lesion was the enlargement of the vascular endothelial cells at 18 hr post-inoculation (PI) followed by necrotizing encephalitis at 24 to 48 hr PI. Immunohistological staining revealed avian influenza virus antigen initially in the vascular endothelial cells and then in the astrocytes, neurons and ependyma.

Descriptors: air sacs virology, brain virology, chickens, fowl plague pathology, influenza A virus pathogenicity, air sacs pathology, antigens, viral analysis, brain immunology, brain pathology, endothelium, vascular pathology, influenza A virus immunology, microscopy, electron methods, microscopy, electron veterinary, necrosis, neurons ultrastructure, serial passage, specific pathogen free organisms, time factors.


NAL Call Number: 41.8 Av5

Abstract: Intravenous pathogenicity index (IVPI) tests on 29 wild duck-origin type A influenza viruses, two turkey-origin type A influenza viruses, and one chicken-origin type A influenza virus resulted in indices ranging from 0.0 to 0.49. Most of the wild duck-origin viruses and the two turkey-origin viruses had indices of 0.0, indicating they are not pathogenic. Six of the duck-origin viruses had indices ranging from 0.25 to 0.49, and the IVPI for A/chicken/Alabama/75 (H4N8) was 0.49, indicating they had low pathogenic potential. An IVPI of 1.25 up to the maximum score of 3.0 is necessary for a type A influenza virus to be classified as highly pathogenic. Gross lesions observed in chickens dying following intravenous viral challenge included kidney swelling with more prominent lobular patterns, but visceral urate deposits were not present. The usefulness of the IVPI test in evaluating the pathogenicity potential of nonpathogenic and low-pathogenic strains of avian influenza virus may be limited.

Descriptors: fowls, avian influenza virus, waterfowl, ducks, pathogenicity, kidneys, lesions, mortality, Ohio.

NAL Call Number: 41.8 Av5

Abstract: Seventy-six type A influenza viruses recovered from waterfowl in Wisconsin, California, South Dakota, Florida, Texas, Alabama, and Nebraska were tested for virulence in chickens. The challenge to chickens was intravenous inoculation of first-, second-, or third-egg-passage virus. Each of the virus strains tested separately in three or four chickens. Eighteen of the 76 viruses caused the death of one or more chickens following inoculation. Postmortem lesions were similar in all dead birds. In decreasing order of frequency, gross lesions included: swollen kidneys evident as accentuated lobular patterns, urates in the pericardial sac, and urates on the surface of the liver. Microscopic lesions present in kidneys were consistent with visceral gout. Mortality was associated with inoculations having higher concentrations of infectious virus. These results indicate that the influenza A viruses circulating in duck populations may include strains potentially pathogenic for chickens.

Descriptors: chickens, fowl plague pathology, influenza A virus avian pathogenicity, kidney pathology, animals, wild, antibodies, viral biosynthesis, birds, ducks, fowl plague microbiology, fowl plague mortality, geese, avian immunology, avian isolation and purification, virulence.


Descriptors: avian influenza virus, immunofluorescence technique, pathogenesis.


NAL Call Number: 41.8 P27

Abstract: To determine the association between specific structural changes in the hemagglutinin gene and pathogenicity of avian influenza viruses (AIVs), groups of 4-week-old White Plymouth Rock chickens were inoculated intravenously or intranasally with AIVs of varying pathogenicities isolated from chickens in central Mexico during 1994-1995. Mildly pathogenic (MP) viruses had a common hemagglutinin-connecting peptide sequence of Pro-Gln-Arg-Glu-Thr-Arg decreases Gly and had restricted capability for replication and production of lesions in tissues. The principle targets for virus replication or lesion production were the lungs, lymphoid organs, and visceral organs containing epithelial cells, such as kidney and pancreas. Death was associated with respiratory and/or renal failure. By contrast, highly pathogenic (HP) AIVs had one substitution and the addition of two basic amino acids in the hemagglutinin connecting peptide, for a sequence of Pro-Gln-Arg-Lys-Arg-Lys-Thr-Arg decreases Gly. The HP AIVs were pantropic in virus replication and lesion production ability. However, the most severe histologic lesions were produced in the brain, heart, adrenal glands, and pancreas, and failure of multiple critical organs was responsible for disease pathogenesis and death. No differences in lesion distribution patterns or in sites of AIV replication were evident to explain the variation in mortality rates for different HP AIVs, but HP AIVs that produced the highest mortality rates had more severe necrosis in heart and pancreas. The ability of individual HP AIVs to produce low or high mortality rates could not be explained by changes in sequence of the hemagglutinin-connecting peptide alone, but probably required the addition of other undetermined genomic changes.

Descriptors: chickens, fowl plague pathology, influenza A virus avian genetics, avian pathogenicity, avian physiology, adrenal glands chemistry, adrenal glands pathology, adrenal glands virology, brain pathology, brain virology, brain chemistry, fowl plague epidemiology, fowl plaque mortality, hemagglutinins viral chemistry, hemagglutinins viral genetics, immunohistochemistry, kidney chemistry, kidney pathology, kidney virology, Mexico epidemiology, myocardium chemistry, myocardium pathology, pancreas chemistry, pancreas pathology, pancreas virology, specific pathogen free organisms, spleen chemistry, spleen pathology, spleen virology, viral proteins analysis, viral proteins metabolism, virus replication.


NAL Call Number: 41.8 Av5

Abstract: Chickens were inoculated with one of five H5N2 Mexican-origin avian influenza virus (AIV)
isolates to determine their pathogenicity for chickens and to determine the ability of routine virologic and serologic tests to detect infections. In laboratory infections, three AIVs, H5/94, M5/94, and J12/94, produced sporadic illness and death and were categorized as mildly pathogenic. Q1/95 produced illness and death in all inoculated chickens and was categorized as highly lethal and highly pathogenic (HP). P11/94B commonly produced clinical illness, but deaths were infrequent. During the presence of clinical signs, oropharyngeal swabs were superior for isolation of AIV; but cloacal swabs were more successful after disappearance of clinical signs. Agar gel precipitin (AGP) serologic test was superior for detecting AIV infection during the clinical phase, but AGP and hemagglutinin inhibition tests were equally effective in detecting infections after recovery from clinical illness. Passage of P11/94B parent stock and selected 14-day-embryo-passed AIVs in adult hens resulted in emergence of some HP AIV derivatives. The hemagglutinin of Q1/95 and P11/94B parent stock and derivative AIVs had an identical proteolytic cleavage site of: Pro- Gln-Arg-Lys-Arg-Lys-Thr-Arg decreased Gly, consistent with AIVs of high pathogenicity. However, no consistent differences were identified in the sequence of the hemagglutinin gene to explain the discrepancy in lethality patterns of the P11/94B AIVs. This suggests that genes other than the hemagglutinin impact the full expression of high lethality of Mexican-origin AIV infections in chickens.

Descriptors: Mexico, chickens, avian influenza virus, pathogenicity, diagnosis, immunodiffusion tests, hemagglutination tests, chemical composition, agglutination tests, America, biological properties, birds, domestic animals, domesticated birds, Galliformes, immunological techniques, immunoprecipitation tests, influenza virus, Latin America, livestock, microbial properties, North America, orthomyxoviridae, poultry, useful animals, viruses, oropharyngeal swabs, cloacal swabs, molecular sequence data, hemagglutination inhibition test, amino acid sequences.

NAL Call Number: 41.8 P27
Abstract: Forty-nine 5-week-old chickens were inoculated by the intravenous (i.v.), intratracheal (IT), or intranasal (IN) routes with either a chicken-origin or one of two duck-origin type A influenza virus isolates. Twelve control chickens were inoculated with sterile chorioallantoic fluid. For all viruses, i.v. inoculation produced predominate lesions of renal tubule necrosis (nephrosis) and nephritis, and influenza virus nucleoprotein was localized in nuclei and cytoplasm of necrotic renal tubule epithelium. Chickens inoculated by the IT route, and to a lesser extent the IN route, had mild to severe tracheitis, bronchitis, and ventromedial pneumonia associated with secondary bronchi but lacked renal tubule necrosis and nephritis. These data indicate low-virulence avian-origin influenza viruses were nephrotropic during simulated systemic infection (i.v. inoculation) and pneumotropic during simulated local infection (IT and IN inoculation). Gross and histologic kidney lesions produced by i.v. inoculation of the chicken-origin influenza virus were similar to changes reported in outbreaks of low-virulence influenza virus in laying chickens.
Descriptors: chickens microbiology, ducks microbiology, fowl plague pathology, influenza A virus avian pathogenicity, poultry diseases pathology, acute disease, administration, intranasal, immunohistochemistry, injections, intravenous, intubation, intratracheal, virulence.

NAL Call Number: 41.8 Av5
Abstract: Five-week-old specific-pathogen-free chickens were inoculated intravenously with one of 16 low-pathogenicity type A influenza virus isolates; 14 were of wild duck origin, and two were of turkey origin. Tubulointerstitial nephritis was the most frequent specific histopathologic change. The frequency and severity of kidney lesions were independent of the virus hemagglutinin-neuraminidase subtype or titer of the challenge virus. Influenza nucleoprotein was most frequently demonstrated in the kidney and was consistently localized to necrotic proximal and/or distal renal tubule epithelium. Common nonspecific histopathologic changes were lymphoid hyperplasia of the spleen and cecal tonsils, as well as lymphocyte depletion in the cloacal bursa. Uncommon histopathologic changes, in decreasing order of frequency, were interstitial pneumonia, lymphoid follicular hyperplasia in the myocardium, and lymphocytic tracheitis. Histopathologic changes were rare or absent in the jejunum, duodenum, pancreas, and brain. The low-
pathogenicity avian-origin type A influenza virus isolates were epitheliotropist in chickens, primarily nephrotropic. Such findings were dissimilar from findings with highly pathogenic avian-origin type A influenza virus isolates both in severity and in tissue distribution of histopathologic changes and influenza viral antigen.

Descriptors: fowl plague pathology, influenza A virus avian pathogenicity, antigens, viral analysis, chickens, ducks, immunohistochemistry, avian isolation and purification, nephritis pathology, nephritis virology, organ specificity, species specificity, turkeys.


NAL Call Number: 448.3 Ar23

Abstract: Influenza virus A/turkey/Ontario/7732/66 (H 5 N 9), which is highly pathogenic to chickens, is nonpathogenic to quails. After intratracheal or intramuscular inoculation of quails, virus replication was limited to the respiratory tract, genital organs, and pancreas. However, aggravation of the pathogenicity was achieved through adaptation only by several passages of lung homogenates in quails. The adapted virus caused a fatal generalized infection in quails as well as in chickens. The pathogenic change of the virus could not be explained by a change in the proteolytic cleavability of the hemagglutinin, because no difference was found in the cleavability between the original and the adapted viruses. The adapted virus formed larger plaques and grew a little faster than the original one in both chicken embryo and quail embryo cells. The faster multiplication of the adapted virus at the site of infection might be the reason for its change in pathogenicity. The original virus could circulate among quails by a direct contact transmission without causing disease. The shed virus, however, caused a fatal infection in chickens when they were kept in contact with the infected quails. The epidemiological significance of this observation is discussed.

Descriptors: Coturnix microbiology, fowl plague microbiology, influenza A virus avian pathogenicity, quail microbiology, adaptation, physiological, antibodies, viral analysis, antigens, viral analysis, central nervous system microbiology, chickens microbiology, hemagglutinins viral analysis, avian immunology, ribonucleoproteins analysis, turkeys microbiology, virus replication.


Abstract: Eighteen cases of human influenza A H5N1 infection were identified in Hong Kong from May to December 1997. Two of the six fatal cases had undergone a full post-mortem which showed reactive hemophagocytic syndrome as the most prominent feature. Other findings included organizing diffuse alveolar damage with interstitial fibrosis, extensive hepatic central lobular necrosis, acute renal tubular necrosis and lymphoid depletion. Elevation of soluble interleukin-2 receptor, interleukin-6 and interferon-gamma was demonstrated in both patients, whereas secondary bacterial pneumonia was not observed. Virus detection using isolation, reverse transcription-polymerase chain reaction and immunostaining were all negative. It is postulated that in fatal human infections with this avian subtype, initial virus replication in the respiratory tract triggers hypercytokinemia complicated by the reactive hemophagocytic syndrome. These findings suggest that the pathogenesis of influenza A H51N1 infection might be different from that of the usual human subtypes H1-H3.

Descriptors: influenza pathology, influenza virology, influenza A virus avian isolation and purification, adolescent, adult, bone marrow pathology, cytokines blood, disease outbreaks, fatal outcome, Hong Kong epidemiology, influenza epidemiology, lung pathology, lymphoid tissue pathology, postmortem changes.


NAL Call Number: 41.8 Av5

Abstract: The introduction of an influenza A virus possessing a novel hemagglutinin (HA) into an immunologically naive human population has the potential to cause severe disease and death. Such was the case in 1997 in Hong Kong, where H51N1 influenza was transmitted to humans from infected poultry. Because H5N1 viruses are still isolated from domestic poultry in southern China, there needs to be
continued surveillance of poultry and characterization of virus subtypes and variants. This study provides molecular characterization and evaluation of pathogenesis of a recent H5N1 virus isolated from duck meat that had been imported to South Korea from China. The HA gene of A/Duck/Anyang/AVL-1/01 (H5N1) isolate was found to be closely related to the Hong Kong/97 H5N1 viruses. This virus also contained multiple basic amino acids adjacent to the cleavage site between HA1 and HA2, characteristic of high-pathogenicity avian influenza viruses (HPAI). The pathogenesis of this virus was characterized in chickens, ducks, and mice. The DK/Anyang/AVL-1/01 isolate replicated well in all species and resulted in 100% and 22% lethality for chickens and mice, respectively. No clinical signs of disease were observed in DK/Anyang/AVL-1/01-inoculated ducks, but high titers of infectious virus could be detected in multiple tissues and oropharyngeal swabs. The presence of an H5N1 influenza virus in ducks bearing a HA gene that is highly similar to those of the pathogenic 1997 human/poultry H5N1 viruses raises the possibility of reintroduction of HPAI to chickens and humans.

Descriptors: epidemiology, infection, duck meat, contamination, poultry product, immunologically naive populations, pathogenesis, viral introduction, viral transmission.


NAL Call Number: 1 Ag84Pro no. 1704

Descriptors: nonindigenous pests control, United States, avian influenza, threat, poultry.


NAL Call Number: 41.8 Av5

Abstract: High-pathogenicity avian influenza (HPAI) viruses emerged from low-pathogenicity avian influenza (LPAI) viruses in Pennsylvania (1983-84), Mexico (1994-95), and Italy (1999-2000). Here we focus on the question of why the HPAI virus supersedes the LPAI virus, once it has appeared during the epidemic. To study this, we used an experimental model in chickens that enabled us to estimate the reproduction ratio (R0). Using this model, we determined the R0 of the A/Chicken/Pennsylvania/21525/83 (LPAI) and of the A/Chicken/Pennsylvania/1370/83 (HPAI). Comparing the R0 of both viruses, we concluded that the R0 of the HPAI virus is significantly higher than the R0 of the LPAI.

Descriptors: epidemiology, infection, avian influenza, infectious disease, respiratory system disease, viral disease, transmission dynamics.


Descriptors: pathology, fowl, lesions, symptoms, Moscow region, avian influenza.


NAL Call Number: 41.8 J27

Descriptors: central nervous system pathology, fowl plague pathology, chickens, China, influenza A virus avian, virus cultivation.


NAL Call Number: RM260.J6

Abstract: Influenza A, B and C all have a segmented genome, although only certain influenza A subtypes and influenza B cause severe disease in humans. The two major proteins of influenza are the surface glycoproteins-haemagglutinin (HA) and neuraminidase (NA). HA is the major antigen for neutralizing antibodies and is involved in the binding of virus particles to receptors on host cells. Pandemics are a result of novel virus subtypes of influenza A, created by reassortment of the segmented genome (antigenic shift),
whereas annual epidemics are a result of evolution of the surface antigens of influenza A and B virus (antigenic drift). The rapid evolution of influenza viruses highlights the importance of surveillance in identifying novel circulating strains. Infectivity of influenza depends on the cleavage of HA by specific host proteases, whereas NA is involved in the release of progeny virions from the cell surface and prevents clumping of newly formed virus. In birds, the natural hosts of influenza, the virus causes gastrointestinal infection and is transmitted via the faeco-oral route. Virulent avian influenza strains, which cause systemic disease, have an HA that is cleaved by proteases present in all cells of the body, rather than by proteases restricted to the intestinal tract. In mammals, replication of influenza subtypes appears restricted to respiratory epithelial cells. Most symptoms and complications, therefore, involve the respiratory tract. However, systemic complications are sometimes observed and other viral genes besides the HA, including the NA, may be involved in determination of virulence of influenza strains in mammals.

Descriptors: antigenic variation physiology, hemagglutinin glycoproteins, influenza virus physiology, influenza epidemiology, neuraminidase physiology, antiviral agents therapeutic use, influenza drug therapy, influenza virology, influenza A virus human pathogenicity, neuraminidase antagonists and inhibitors, sialic acids therapeutic use.


Descriptors: antigenic variation physiology, influenza virology, orthomyxoviridae pathogenicity, orthomyxoviridae physiology, antigenic variation genetics, birds virology, disease reservoirs, evolution, molecular, hemagglutinin glycoproteins, influenza virus chemistry, hemagglutinin glycoproteins, influenza virus genetics, hemagglutinin glycoproteins, influenza virus metabolism, influenza epidemiology, influenza transmission, neuraminidase genetics, neuraminidase metabolism, orthomyxoviridae enzymology, orthomyxoviridae genetics.


NAL Call Number: QR360.J6

Abstract: Highly pathogenic avian influenza A H5N1 viruses caused outbreaks of disease in domestic poultry and humans in Hong Kong in 1997. Direct transmission of the H5N1 viruses from birds to humans resulted in 18 documented cases of respiratory illness, including six deaths. Here we evaluated two of the avian H5N1 viruses isolated from humans for their ability to replicate and cause disease in outbred ferrets. A/Hong Kong/483/97 virus was isolated from a fatal case and was highly pathogenic in the BALB/c mouse model, whereas A/Hong Kong/486/97 virus was isolated from a case with mild illness and exhibited a low-pathogenicity phenotype in mice. Ferrets infected intranasally with 10(7) 50% egg infectious doses (EID(50)) of either H5N1 virus exhibited severe lethargy, fever, weight loss, transient lymphopenia, and replication in the upper and lower respiratory tract, as well as multiple systemic organs, including the brain. Gastrointestinal symptoms were seen in some animals. In contrast, weight loss and severe lethargy were not noted in ferrets infected with 10(7) EID(50) of two recent human H3N2 viruses, although these viruses were also isolated from the brains, but not other extrapulmonary organs, of infected animals. The results demonstrate that both H5N1 viruses were highly virulent in the outbred ferret model, unlike the differential pathogenicity documented in inbred BALB/c mice. We propose the ferret as an alternative model system for the study of these highly pathogenic avian viruses.

Descriptors: disease models, animal, ferrets, influenza physiopathology, influenza A virus avian pathogenicity, adolescent, child, preschool, influenza pathology, influenza virology, lung pathology, lung virology, virulence, virus replication.

**Abstract:** El estudio fue disenado para desarrollar un nuevo sistema de deteccion de la expresion in vitro de la molecula de HA, utilizando como marcador citoquimico una fetoproteina y un sistema de deteccion mediante microscopia confocal. El gene de la HA del virus de la influenza aviar A/DW/WI/1938/80 (H1N1), fue insertado en el vector pREP10 y clonado en E. coli DH5 alfa. Monoestratos de celulas MDBK y MDCK con indices de confluencia de entre 30 y 50% fueron transformados mediante la tecnica de transfeccion con liposomas. La seleccion de celulas transformadas se llevo a cabo con el tratamiento de los cultivos con higromicina como marcador de seleccion (600 micro l/ml en medio DME completocon 10% v/v suero bovino fetal) por un periodo de 3 a 4 semanas. Los cultivos celulares transformados en forma estable fueron crecidos en cubreobjetos y fijados en paraformaldehido (3.7% en PBS pH 7.2). La expresion temporal o constitutiva del gene de la HA en celulas mamiferas transformadas fue monitoreada con las tecnicas estandarizadas de IFI (con anticuerpos mono y policlonales), hemoadsorcion y hemoaglutinacion. La nueva tecnica alternativa desarrollada se baso en la reaccion de acoplamiento mediada por la alta afinidad entre el sitio de reconocimiento del recptor, situado en los polipeptidos de la molecula de HA y el acido sialico de la fetoproteina bovina (0.2% acido acetilneuroamidico) conjugada con oro coloidal (10nm). Los ensayos incluyeron los analisis de la reaccion a nivel de citoplasma y de superficie. Para este efecto se utilizaron monoestratos permeabilizados con el detergente Tween 20 (0.05%) y monoestratos no permeabilizadas. Los controles incluyeron celulas infectadas con virus homologos y heterologos (WSN). Se concluye que la nueva tecnica descrita, ofrece una alta especificidad y sensibilidad analitica en la deteccion de HA expresada in vitro a la vez que es rapida y sencilla. Ademas, el potencial de esta tecnica puede ser extrapolado en ensayos utilizando microscopia optica.

**Descriptors:** avian influenza virus, cytochemistry, cell structure, confocal microscopy, influenza virus, viruses.


**NAL Call Number:** 448.8 V81

**Abstract:** An influenza virus neuraminidase (NA) of the N9 subtype also has hemagglutinin (HA) activity (W. G. Laver, P. M. Colman, R. G. Webster, V. S. Hinshaw, and G. M. Air (1984), Virology 137, 314-323). To determine sequence relationships between this NA and other known NA and HA subtype sequences, and as a necessary step toward a complete structure determination, we have cloned a full-length copy of the coding sequence of the N9 NA of influenza virus A/tern/Australia/G70C/75 into the plasmid pUC9 using SalI linkers. The gene was sequenced by directed subcloning into the single-stranded phage vectors M13mp19 and M13mp18 and use of the dideoxy procedure. Most of the NA sequence was also obtained by direct protein sequencing of tryptic peptides. The N9 NA has 43 and 44% homology when compared to N1 or N2 sequences, respectively. There is no significant homology to any known HA sequence, or to the HN protein of the paramyxovirus SV5. Like the other NA molecules, the N9 NA is anchored in the membrane by an N-terminal hydrophobic region, from which biologically active heads can be released by pronase.

**Descriptors:** genes viral, hemagglutinins viral, influenza A virus avian enzymology, influenza A virus enzymology, neuraminidase genetics, amino acid sequence, base sequence, cloning, molecular, influenza A virus avian genetics, avian immunology, influenza A virus genetics, influenza A virus immunology.


**NAL Call Number:** 448.8 P942
Abstract: The results of studies of physico-chemical and biological properties of virus-specific ribonucleoproteins (RNP) in influenza infection are presented. Particular attention is given to the infectious properties of RNP. The earliest infectivity was found to be associated with RNP structures sedimenting from nuclear extract in a zone of 30-40S.

Descriptors: nucleoproteins pharmacology, ribonucleoproteins pharmacology, cell nucleus microbiology, chemistry, physical, chick embryo, cytoplasm microbiology, influenza A virus avian pathogenicity, ribonucleoproteins isolation and purification, species specificity, time factors, virus cultivation.


NAL Call Number: 448.3 Ar23

Abstract: Antigenic reactivity of the three polymerase proteins PB1, PB2, and PA of type A influenza viruses of animal and human origin were analysed by radioimmunoprecipitation using monospecific antisera. Each of the polymerase monospecific antisera made against the polymerase proteins of the human A/WSN/33 (H1N1) influenza virus reacted efficiently with the homologous proteins of all the known thirteen HA subtype viruses of avian influenza virus, three subtypes of human influenza virus, swine and equine influenza viruses. This broad reactivity of each of the antisera indicated that the polymerase proteins are antigenically related among the type A influenza viruses and therefore can be considered as type specific antigens similar to the other viral internal proteins nucleoprotein (NP) and matrix protein (M). No electrophoretic migrational heterogeneity was found among the PB2 proteins of different subtype viruses, whereas PB1 protein exhibited minor variation. However, PA protein from among various viral subtypes showed considerable heterogeneity. Each of the polymerase antisera also immunoprecipitated additional antigenically related polypeptides with distinct electrophoretic mobilities from cells infected with each of the influenza viral subtypes.

Descriptors: DNA directed RNA polymerases immunology, influenza A virus human enzymology, influenza A virus enzymology, viral proteins immunology, antigens, viral immunology, human immunology, influenza A virus immunology, precipitin tests.


NAL Call Number: aSF995.6.I6I5 1981a

Descriptors: avian influenza A virus, virulence, hemagglutinin, cells, chickens.


NAL Call Number: SF995.A1A9

Descriptors: avian influenza virus, chickens, turkeys, ducks, quails, chickens, immune response, disease transmission, clinical signs, mortality.


NAL Call Number: SF995.W4

Descriptors: Newcastle disease virus, avian influenza virus, influenza virus, orthomyxoviridae, paramyxoviridae, viruses.


NAL Call Number: QR360.A1J6

Abstract: Rapid treatment of influenza virus directly on the microscope grid with non-ionic detergent had allowed better visualization of the internal component. Many micrographs show that this ribonucleoprotein
(RNP) is present as a continuous stand of 6 nm diam. arranged in the form of a double coil or helix. In spite of the minimal treatment to which the virus was subjected most helices still showed signs of degradation. The findings that we have obtained lead us to suggest that the RNP component of influenza virus must be very sensitive to both chemical and physical manipulations, any of which could cause it to fracture from one continuous strand into several pieces, although such breakages could possibly occur at specific points along its length.

Descriptors: orthomyxoviridae ultrastructure, RNA, viral, viral proteins, chick embryo, cyprinidae, influenza A virus avian ultrastructure, microscopy, electron, phostotungstic acid, recombination, genetic, surface active agents, tissue culture.

NAL Call Number: 448.3 J823
Descriptors: influenza A virus avian, lipoproteins analysis, microscopy, electron, viral proteins analysis.

NAL Call Number: 472 N21
Descriptors: genes viral, influenza A virus avian genetics, virus replication, cell line, DNA directed RNA polymerases genetics, DNA directed RNA polymerases metabolism, avian physiology, RNA viral genetics, viral proteins genetics, viral proteins physiology.

NAL Call Number: 448.8 V81
Descriptors: genes viral, influenza A virus avian genetics, RNA viral genetics, electrophoresis, polyacrylamide gel, avian analysis, viral analysis, recombination, genetic, viral proteins analysis, viral proteins biosynthesis.

NAL Call Number: QR360.A1J6
Abstract: High resolution polyacrylamide gel electrophoresis (PAGE) of chick embryo fibroblast cells infected with the avian influenza virus FPV-Rostock revealed two distinct polypeptides migrating in the region of the nucleoprotein (NP). One-dimensional fingerprinting of these polypeptides showed that they were both nucleoprotein, and [32P]orthophosphate labelling revealed that they differed with respect to their state of phosphorylation. Pulse-chase studies using [35S]methionine indicated that phosphorylation of a certain proportion of NP occurs rapidly after synthesis and is associated with transport to the nucleus. Nucleoprotein which remained in the cytoplasm was predominantly non-phosphorylated. Both the phosphorylated and the non-phosphorylated types of NP were found in ribonucleoprotein complexes (RNP)s of different densities isolated on renografin gradients, but RNP isolated from the nucleus contained much more phosphorylated NP than those from the cytoplasm. The kinase responsible for nucleoprotein phosphorylation appears to be influenced by temperature of incubation of the infected cells.
Descriptors: influenza A virus avian metabolism, nucleoproteins metabolism, viral proteins metabolism, cell line, cell nucleus analysis, cell nucleus metabolism, chick embryo, cytoplasm analysis, fibroblasts, phosphorylation, protein kinases metabolism, ribonucleoproteins analysis, temperature.

NAL Call Number: 448.8 V81
Descriptors: genes, influenza A virus avian growth and development, mutation, chick embryo, avian analysis, avian radiation effects, peptides analysis, RNA viral analysis, recombination, genetic, temperature, tissue culture, ultraviolet rays, viral proteins analysis, virus replication.
NAL Call Number: 448.8 V81
Descriptors: genes viral, influenza A virus avian genetics, recombination, genetic, avian analysis, mutation, temperature, viral proteins analysis, viral proteins biosynthesis.

NAL Call Number: QR360.A1J6
Abstract: There is a significant difference in the ability of human influenza A virus H1N1 strains isolated up to 1977 and those isolated later to rescue temperature-sensitive mutants of fowl plague virus with a defect in the nucleoprotein (NP) gene. Therefore the NP genes of five human H1N1 and H3N2 influenza A virus strains, isolated between 1950 and 1978, have been sequenced. By comparison with previous and more recent isolates, an evolutionary pathway has been established. Three amino acid replacements were found which might be responsible for the functional difference between the USSR (1977) and the Brazil (1978) strains. The California (H1N1) strain isolated in 1978 had acquired by reassortment the NP gene of a human H3N2 virus circulating at about 1977 as had been previously suggested by investigations involving RNase fingerprint or hybridization techniques.
Descriptors: evolution, genes viral, influenza A virus human genetics, nucleoproteins genetics, viral core proteins, viral proteins genetics, amino acid sequence, base sequence, chick embryo, chickens, influenza A virus avian genetics, molecular sequence data, mutation, sequence homology, nucleic acid.

NAL Call Number: QR375.V6
Abstract: The sequences of nucleoprotein (NP) genes of recent human and turkey isolates of influenza A viruses, which serologically could be correlated to contemporary swine viruses, were determined. These sequences were closely related to the NPs of these swine viruses and they formed a separate branch on the phylogenetic tree. While the early swine virus from 1931 resembled the avian strains in consensus amino acids of the NP and in its ability to rescue NP ts mutants of fowl plague virus in chicken embryo cells, the later strains on that branch were different: at 15 positions they have their own amino acids and they rescued the NP ts mutants only poorly. Of the NPs of the human New Jersey/76 isolates analysed, one clustered with the recent H1N1 swine viruses of the U.S.A., the other one with contemporary human strains. Since the NP is one of the main determinants of species specificity it is concluded that, although the H1N1 swine isolates from the U.S.A. form their own branch in the phylogenetic tree, they can be transmitted to humans and turkeys, but they do not spread further in these populations and so far have not contributed to human pandemics. It is not very likely that they will do so in future, since its branch in the phylogenetic tree develops further away from the human and avian branch.
Descriptors: influenza A virus avian genetics, human genetics, porcine genetics, nucleoproteins genetics, fowl plague microbiology, influenza microbiology, phylogeny, sequence homology, nucleic acid, turkeys.

NAL Call Number: QR360.A1J6
Abstract: Ultrastructural changes developing in chick embryo fibroblast cultures infected with a wild-type strain of fowl plague virus (FPV) or one of six FPV temperature-sensitive (ts) mutants belonging to different complementation groups were studied. Cells infected with wild-type FPV and incubated at optimal (36 degrees C) or nonpermissive temperature (42 degrees C) displayed changes similar to those described for orthomyxoviruses. The same patterns of changes were observed at 36 degrees C in cells infected with ts mutants belonging to five of the complementation groups. Mutant ts 303, possessing mutation-altered haemagglutinin, induced at 36 degrees C the formation of virions carrying a considerably reduced number of spikes on their surfaces. At 42 degrees C, cells infected with ts mutant 131, with a defective primary
transcription stage, showed no morphological changes and no formation of electron-dense inclusions. Cells infected with ts mutants with defective secondary transcription or replication displayed nuclear inclusions but no formation of filamentous cytoplasmic structures or virions. Mutant ts 5 with defective late morphogenesis induced formation of considerably enhanced numbers of nuclear inclusions.

**Descriptors:** cell transformation, viral, influenza A virus avian, cell nucleus ultrastructure, cultured cells, chick embryo, fibroblasts ultrastructure, inclusion bodies, viral ultrastructure, microscopy, electron, mutation, temperature, virion ultrastructure.


**NAL Call Number:** 448.9 Am37

**Descriptors:** influenza epidemiology, influenza A virus avian isolation and purification, adolescent, adult, child, child, preschool, Hong Kong epidemiology, influenza virology, middle aged.


**NAL Call Number:** 448.9 Am37

**Descriptors:** influenza epidemiology, influenza virology, influenza A virus avian isolation and purification, Hong Kong epidemiology, seroepidemiologic studies.


**Descriptors:** influenza strains, influenza A virus, genetic relationships, Hong Kong.


**NAL Call Number:** QR360.A1J6

**Descriptors:** influenza A virus avian metabolism, RNA viral biosynthesis, autoradiography, cell nucleus enzymology, cell nucleus metabolism, cultured cells, chick embryo, cytoplasm enzymology, DNA directed RNA polymerases metabolism, deoxyadenosines pharmacology, fibroblasts, avian enzymology, avian growth and development, mycotoxins pharmacology, Newcastle disease virus growth and development, Newcastle disease virus metabolism, time factors, tritium, uracil nucleotides metabolism, uridine metabolism, virus replication.


**NAL Call Number:** QR360.A1J6

**Abstract:** Quantitative relationships between neutralization, aggregation and attachment to monolayers of chick embryo fibroblast (CEF) cells have been studied using a constant amount of influenza A/fowl plague virus/Rostock/34 (H7N1) and varying amounts of purified mouse polyclonal IgM directed against the haemagglutinin, the major viral neutralization antigen. There are two major types of interaction. (i) At low concentrations of IgM there is aggregation of virus, but no neutralization provided that the aggregates are dispersed by vortexing and dilution. Maximum aggregation occurs at less than seven molecules of IgM per virion and the IgM is probably bound in the 'staple' or 'crab' conformation at these concentrations. (ii) At higher concentrations there is neutralization and this coincides with inhibition of attachment of virus to CEF cells. Neutralization of 50% infectivity requires about 35 molecules of IgM per virion. The maximum neutralization observed was only 87%. Quantitative data and electron microscopy observations suggest that molecules of IgM at the higher concentrations adopt a planar stance approximately perpendicular to the viral surface. It appears that IgM neutralizes fowl plague virus in vitro primarily by interfering with its attachment to cells; the fraction of neutralized virus that does attach is known not to be internalized.

**Descriptors:** antibodies, viral immunology, immunoglobulin M immunology, influenza A virus avian immunology, antigen antibody complex, immunohistochemistry, avian ultrastructure, microscopy, electron,
neutralization tests.

NAL Call Number: 448.8 P942
Abstract: When Ehrlich ascitic carcinoma cells infected with classical fowl plague virus and treated with actinomycin D were pulse labeled for 10 min with 3H-uridine, it was mainly incorporated into nucleoplasm structures sedimenting in sucrose gradients at 120S. At 2-hr exposure of the infected cells to 3H-uridine radioactivity was found in nucleoplasm in the area of 65S and in the cytoplasm in 30-40S zone. The analysis of RNA isolated from these structures gave the following results. The RNA isolated from 120S structures sedimented in two zones of sucrose gradient: 11S and 16-23S. The 11S RNA was resistant to RNA-ase, while 16-23S RNA was sensitive to RNA-ase. A similar (16-23S) RNA was isolated from virus-specific structures 65S and 30-40S.
Descriptors: influenza A virus avian, RNA viral biosynthesis, viral isolation and purification, virus replication, carcinoma, Ehrlich tumor analysis, carcinoma, Ehrlich tumor microbiology, catalysis, cell nucleus metabolism, centrifugation, density gradient, ribonucleases, transcription, genetic, uridine metabolism.

NAL Call Number: 448.8 P942
Abstract: In the course of classical fowl plague virus reproduction in Ehrlich ascites carcinoma cells both hemagglutinins and S-antigen accumulate and titers of the infectious activity increase. However virus reproduction does not terminate in formation of virus, and subviral structures are found in the liquid fraction of the infected cells. Analysis of these structures has shown them to have a sedimentation coefficient of 350-370S and buoyant density 1.29 g/ml. The rapidly sedimenting structure has complement-fixing hemagglutinating activity but bow infectivity.
Descriptors: carcinoma, Ehrlich tumor microbiology, influenza A virus avian growth and development, virus replication, amino acids, antigens, viral analysis, carcinoma, Ehrlich tumor analysis, centrifugation, density gradient, complement fixation tests, hemagglutinins viral analysis, methionine, sulfur radioisotopes, tritium.

NAL Call Number: QR360.A1J6
Abstract: An RNA-synthesizing complex was found in the nucleoplasm of fowl plague virus-infected chicken fibroblast and Ehrlich tumour cells. The complex sedimented at 120 S and banded in caesium chloride at 1-39 to 1-41 g/ml. It contained an influenza nucleocapsid protein as a major protein constituent. The complex functioned late in infection, and RNA synthesis in it was resistant to actinomycin D, the properties expected of influenza virus replicative complex.
Descriptors: cell nucleus metabolism, influenza A virus avian metabolism, RNA viral biosynthesis, carcinoma, Ehrlich tumor, chick embryo, dactinomycin pharmacology, fibroblasts, avian growth and development, mice, tissue culture, viral proteins biosynthesis, virus replication.

NAL Call Number: 41.8 V6426
Descriptors: influenza A virus avian cytology, chick embryo, microscopy, electron.


Abstract: This study presents the first nucleotide sequence and deduced primary amino acid sequence of a subtype H1 haemagglutinin from the avian influenza virus A/duck/Alberta/35/76 (H1N1). The molecule is structurally, antigenically and molecularly similar to H1 haemagglutinins of human viruses but sequence homology differences indicate that there has not been a recent transfer of haemagglutinin genetic information between them.

Descriptors: hemagglutinins viral genetics, influenza A virus avian genetics, amino acid sequence, base sequence, genes, structural, viral, avian immunology, molecular sequence data.


Abstract: Monoclonal antibodies to the haemagglutinin (HA) of the avian H1 influenza virus A/duck/Alberta/35/76 were used to construct an operational antigenic map of the HA molecule and to study the interrelationships of H1 viruses from different hosts. Haemagglutination inhibition tests between the monoclonal antibodies and variants selected by them provided evidence of four antigenic regions which overlap to varying degrees. Avian H1 influenza viruses displayed a spectrum of reactivities to the monoclonal antibody panel. Representatives of the epidemic strains of human H1 influenza viruses and early swine influenza viruses showed little or no reactivity with the monoclonal antibodies but swine influenza-like viruses isolated from pigs and humans in the last decade reacted with 11 of 17 antibodies. The antigenic similarity of these viruses to many avian isolates suggests that there has been a transfer of HA genetic information between mammalian and avian H1 influenza viruses.

Descriptors: hemagglutinins viral immunology, influenza A virus avian immunology, antibodies, monoclonal diagnostic use, epitopes, human immunology, porcine immunology, species specificity.


Abstract: Influenza virus multiplies productively in chick cells and abortively in L cells. The infecting influenza virus RNA genomes are less stable in infected L cells than in infected chick cells. However, transcription of the virus genome in L cells, while reduced in rate, is not decreased in extent. There is no detectable synthesis of virion RNA in L cells, and this is the most likely cause of the abortive infection.

Descriptors: influenza A virus avian metabolism, L cells cell line, RNA viral biosynthesis, chick embryo, fibroblasts, avian growth and development, mice, nucleic acid hybridization, phosphorus radioisotopes, tissue culture, transcription, genetic, virus replication.


Descriptors: influenza A virus avian growth and development, RNA viral analysis, virus replication, base sequence, cell nucleus analysis, chick embryo, cytoplasm analysis, nucleic acid hybridization, RNA, ribosomal analysis, ribonucleases, time factors, tritium, uridine.


**Abstract:** The nucleotide sequence of the NS gene of the human influenza virus A/PR/8/34 was determined and found to be the same length (890 nucleotides) as the NS gene of another human influenza virus A/Udorn/72 and of the avian isolate A/FPV/Rostock/34. Comparison of the sequences of the NS genes of the two human influenza viruses shows an 8.9% difference whereas the NS gene of the avian isolate differs by only 8% from that of the human strain A/PR/8/34. The extensive sequence similarity among these three genes does not support the notion of species specific homology groups among NS genes of avian and human influenza virus strains. The primary sequence of the A/PR/8/34 NS gene is consistent with the findings that the influenza virus NS gene may code for two overlapping polypeptides. In addition, an open reading frame potentially coding for a polypeptide 167 amino acids in length was found in the negative strand RNA of the A/PR/8/34 virus NS gene.

**Descriptors:** genes viral, influenza A virus avian genetics, human genetics, RNA viral genetics, amino acid sequence, base sequence, cloning, molecular, peptides genetics, species specificity.


**Abstract:** The influence on virus replication in culture of the presence and location of glycosylation sites on the haemagglutinin (HA) glycoprotein of avian influenza viruses and differences in length of the stalk region of their neuraminidase (NA) glycoprotein was examined using reassortant viruses. Plaque size was measured in the presence or absence of bacterial neuraminidase (CPNA) and/or an influenza virus NA inhibitor, zanamivir, to assess the relative contribution of the NA to replication efficiency in tissue culture. The following conclusions were drawn, (1) HA lacking glycosylation at 158 gives inefficient growth when combined with short-stalked NAs, and efficient growth when combined with long-stalked NAs. (2) Glycosylation at 158 of HA makes the virus less dependent on NA for release from its receptors. (3) HA with glycosylation at 158 gives efficient growth when combined with short-stalked NAs but, when combined with long-stalked NAs, growth is very efficient and excess NA activity is disadvantageous. (4) HA having glycosylation at 158 combined with short-stalked NAs, or HA lacking glycosylation at 158 combined with long-stalked NAs may represent optimal combinations. The results reinforce the importance of a balance of HA and NA activity for efficient virus exit from, and entry into cells.

**Descriptors:** hemagglutinin glycoproteins, influenza virus metabolism, influenza A virus avian growth and metabolism, sialic acids, avian influenza virus replication.
development, neuraminidase metabolism, antiviral agents pharmacology, chick embryo, *Clostridium perfringens* enzymology, enzyme inhibitors pharmacology, glycosylation, hemagglutinin glycoproteins, influenza virus chemistry, hemagglutinin glycoproteins, influenza virus genetics, avian drug effects, avian genetics, avian physiology, neuraminidase antagonists and inhibitors, plaque assay, protein structure, tertiary, sialic acids pharmacology.


**Abstract:** Neuraminidases from different subtypes of influenza virus are characterized by the absence of serological cross-reactivity and an amino acid sequence homology of approximately 50%. The three-dimensional structure of the neuraminidase antigen of subtype N9 from an avian influenza virus (A/tern/Australia/G70c/75) has been determined by X-ray crystallography and shown to be folded similarly to neuraminidase of subtype N2 isolated from a human influenza virus. This result demonstrates that absence of immunological cross-reactivity is no measure of dissimilarity of polypeptide chain folding. Small differences in the way in which the subunits are organized around the molecular fourfold axis are observed. Insertions and deletions with respect to subtype N2 neuraminidase occur in four regions, only one of which is located within the major antigenic determinants around the enzyme active site.

Descriptors: influenza A virus avian enzymology, neuraminidase immunology, neuraminidase metabolism, amino acid sequence, antigens, viral, binding sites, avian classification, models, molecular, molecular sequence data, N acetylneuraminic acid, protein conformation, sialic acids metabolism.


**Abstract:** Reassortants possessing the hemagglutinin (HA) gene from A/Equine/London/1416/73 (H7N7) [Eq/Lond] and five or more genes from A/Chicken/Pennsylvania/1370/83 (H5N2) [Ck/Penn] were lethal in chickens. This result demonstrates that horses can maintain influenza viruses whose HAs are capable of promoting virulence. Thus, reassortment of equine and avian influenza virus genes could generate viruses that might be lethal in domestic poultry.

Descriptors: fowls, horses, avian influenza virus, equine influenza virus, hemagglutinins, genes, amino acids, virulence, pathogenicity, mortality, molecular sequence data, EMBL m58657, GENBANK m58657.


Descriptors: interferon, viral diseases, poultry.


**Abstract:** A 945 nucleotide region (bases 76-1020) of the HA1 part of the HA gene was obtained for 31 influenza viruses of H7 subtype isolated primarily from Europe, Asia and Australia over the last 20 years. These were analysed phylogenetically and compared with sequences of the same region from 23 H7 subtype viruses available in Genbank. The overall results showed two geographically distinct lineages of North American and Eurasian viruses with major sublineages of Australian, historical European and equine viruses. Genetically related sublineages and clades within these major groups appeared to reflect geographical and temporal parameters rather than being defined by host avian species. Viruses of high and low virulence shared the same phylogenetic branches, supporting the theory that virulent viruses are not maintained as a separate entity in waterfowl.

Descriptors: hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian classification, avian genetics, amino acid sequence, fowl plague virology, genes viral, avian isolation and purification, phylogeny, poultry, sequence homology, amino acid.
Changes in the haemagglutinin and the neuraminidase genes prior to the emergence of highly pathogenic H7N1 avian influenza viruses in Italy. Archives of Virology 146(5): 963-73. ISSN: 0304-8608.

Abstract: Outbreaks of avian influenza due to an H7N1 virus of low pathogenicity occurred in domestic poultry in northern Italy from March 1999 until December 1999 when a highly pathogenic avian influenza (HPAI) virus emerged. Nucleotide sequences were determined for the HA1 and the stalk region of the neuraminidase (NA) for viruses from the outbreaks. The HPAI viruses have an unusual multibasic haemagglutinin (HA) cleavage site motif, PEIPKGSRRGLF. Phylogenetic analysis showed that the HPAI viruses arose from low pathogenicity viruses and that they are most closely related to a wild bird isolate, A/teal/Taiwan/98. Additional glycosylation sites were present at amino acid position 149 of the HA for two separate lineages, and at position 123 for all HPAI and some low pathogenicity viruses. Other viruses had no additional glycosylation sites. All viruses examined from the Italian outbreaks had a 22 amino acid deletion in the NA stalk that is not present in the N1 genes of the wild bird viruses examined. We conclude that the Italian HPAI viruses arose from low pathogenicity strains, and that a deletion in the NA stalk followed by the acquisition of additional glycosylation near the receptor binding site of HA1 may be an adaptation of H7 viruses to a new host species i.e. domestic poultry.

Descriptors: fowl plague virology, hemagglutinins viral genetics, influenza A virus avian genetics, neuraminidase genetics, poultry diseases virology, amino acid motifs, amino acid sequence, birds virology, chickens virology, disease outbreaks, evolution, molecular, fowl plague epidemiology, genes, structural, viral, glycosylation, influenza A virus avian isolation and purification, influenza A virus avian pathogenicity, Italy epidemiology, molecular sequence data, phylogeny, poultry diseases epidemiology, protein processing, post translational, sequence deletion, sequence homology, turkeys virology, virulence genetics.

Evaluation of pathogenic potential of avian influenza virus serotype H9N2 in chickens. Avian Diseases 47(Special Issue): 817-822. ISSN: 0005-2086.

Abstract: Recently seven isolates of avian influenza virus (AIV) serotype H9N2 recovered from an outbreak of AI were analyzed on the basis of their biological and molecular characteristics. All the isolates belonged to the low-pathogenicity group of AIV. To further evaluate their pathogenic potential in association with other organisms, an isolate was inoculated experimentally in chickens using different routes and subsequently challenged with infectious bronchitis virus, Ornithobacterium rhinotracheale or Escherichia coli. The virus isolation and seromonitoring data revealed a significant role of Escherichia coli in aggravating the clinical condition of the birds earlier infected with AIV (H9N2). The AIV-antigen was detected in lung, trachea, kidney, and cloacal bursa among the infected birds, using immunofluorescent antibody technique. In another experiment, chickens that were immunosuppressed chemically showed high mortality when challenged with AIV H9N2. The results indicated that this low pathogenicity AIV (H9N2) isolate could produce severe infection depending on the type of secondary opportunistic pathogens present under field conditions. This may explain the severity of infection with the present H9N2 outbreak in the field. A prolonged antibacterial therapy in flocks infected with AIV H9N2 and use of oil-based vaccine at an early age in new flocks has helped to control this infection and the disease.

Descriptors: epidemiology, infection, avian influenza, infectious disease, respiratory system disease, viral disease, immunofluorescence, immunologic techniques, laboratory techniques, viral isolation, disease outbreak, secondary opportunistic pathogens, seromonitoring data.
against the three epitopes of NP protein failed to reveal any antigenic difference between the negative strand or positive strand-containing nucleocapsids. On the other hand, the sensitivity of virus-specific RNA in the nucleocapsids to digestion by the pancreatic ribonuclease proved to be lower for the positive strand-containing nucleocapsids.

Descriptors: influenza A virus avian genetics, RNA viral chemistry, ribonucleoproteins analysis, chick embryo, epitopes immunology, ribonucleoproteins immunology.


NAL Call Number: 449.8 J82
Descriptors: isoquinolines pharmacology, orthomyxoviridae drug effects, chick embryo, fetal membranes, hemagglutination tests, immune sera, influenza A virus avian drug effects, orthomyxoviridae growth and development, virus inhibitors pharmacology.


NAL Call Number: 448.8 V81
Abstract: The biological and antigenic roles of glycosylation were investigated in the influenza hemagglutinin (HA) glycoprotein using the glycosylation inhibitor tunicamycin (TM). Under conditions where only the nonglycosylated form of HA was detected by immunoprecipitation and gel electrophoresis, the migration of glycoproteins to the cell surface was observed by immunofluorescence using either monospecific or monoclonal antibody to the HA polypeptide. Analysis of the surface fluorescence in TM-treated infected cells by a fluorescence-activated cell sorter (FACS) showed that all cells exhibited fluorescence in the complete absence of glycosylation. The relative amount of HA antigen on cell surfaces was found to be reduced by only 30-40% in TM-treated cells, and this reflected a similar reduction in intracellular synthesis. Electron microscopic studies using ferritin labeling also demonstrated that the nonglycosylated HA glycoprotein was present in significant amounts on surfaces of infected cells. Virions with nonglycosylated glycoproteins were purified, and were found to have an approximate 30-fold decrease in both hemagglutinin and neuraminidase specific activities. The possible role of oligosaccharides in antigenic variation among various H1N1 strains was investigated. Immunoprecipitation reactions involving five different monoclonal antibodies and five antigenic variants of A/USSR/90/77 revealed no major antigenic differences between the glycosylated and nonglycosylated forms of HA.

Descriptors: cell membrane analysis, hemagglutinins viral analysis, influenza A virus avian analysis, human analysis, antibodies, monoclonal immunology, antibodies, viral immunology, epitopes immunology, hemagglutination, viral, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral immunology, neuraminidase metabolism, tunicamycin pharmacology.


NAL Call Number: 41.8 Au72
Descriptors: chickens, disease outbreaks veterinary, fowl plague microbiology, influenza A virus avian classification, RNA viral analysis, amino acid sequence, base sequence, DNA, viral chemistry, fowl plague epidemiology, hemagglutinins viral chemistry, hemagglutinins viral genetics, influenza A virus avian genetics, molecular sequence data, polymerase chain reaction, viral chemistry, Victoria epidemiology.


NAL Call Number: 384 AC8
Abstract: Human H3 strains of influenza A virus preferentially bind cell-surface oligosaccharides containing the sequence NeuAc alpha 2,6Gal, while avian influenza strains preferentially recognize the sequence NeuAc alpha 2,3Gal. The distribution of these two types of sialic acid linkages on host respiratory epithelium, the target of influenza infection, may be a factor in the selection of the different receptor specificities observed in human and avian influenza strains. To examine the distribution of these two structures on
human tracheal epithelial cells, two sialic acid specific lectins were used. The Sambucus nigra lectin (SNA), which recognizes the sequence NeuAc alpha 2,6Gal/GalNac, primarily binds to the surface of the ciliated tracheal epithelial cells, and only weakly binds to mucsins in the surface goblet cells. In contrast, the Maackia amurensis lectin (MAL), which is specific for the NeuAc alpha 2,3Gal sequence, binds strongly to mucus droplets in goblet cells, but not to the surface of ciliated cells. Thus, human ciliated tracheal cells appear to contain sialylligosaccharides preferentially recognized by human influenza strains. These findings suggest that human H3 influenza strains may have evolved a receptor specificity which favors binding to ciliated cells, and minimizes binding inhibition by respiratory mucus.

Descriptor: influenza A virus human metabolism, oligosaccharides metabolism, receptors, virus metabolism, trachea ultrastructure, epithelial cells, epithelium metabolism, epithelium ultrastructure, fluorescent antibody technique, fluorescent dyes diagnostic use, histocytochemistry, protein binding, receptors, virus ultrastructure, trachea cytology, trachea metabolism.


NAL Call Number: 448.8 V81

Abstract: The RNAs coding for the nucleoproteins of a panel of influenza isolates from human and nonhuman hosts were compared by RNA-RNA hybridization to determine the extent of genetic diversity of this protein and to determine if related nucleoproteins (NP) are consistently found in viruses from certain hosts. Five nucleoprotein groups were defined. Group 1 contains nearly all of the avian influenza viruses, group 2 includes only certain viruses isolated from gulls, group 3 includes all recent equine influenza strains, group 4 contains only equine/Prague/1/56, and group 5 contains all human and swine influenza isolates. The maintenance of specific nucleoproteins in viruses from certain species suggests that these proteins have evolved functionally significant differences that favor their replication in a specific host.

Descriptor: cell transformation, viral, genes, structural, genes viral, influenza A virus genetics, nucleoproteins genetics, human genetics, porcine genetics, nucleic acid hybridization, RNA viral genetics, species specificity.


NAL Call Number: QR360.J6

Abstract: In April 1983, an influenza virus of low virulence appeared in chickens in Pennsylvania. Subsequently, in October 1983, the virus became virulent and caused high mortality in poultry. The causative agent has been identified as an influenza virus of the H5N2 serotype. The hemagglutinin is antigenically closely related to tern/South Africa/61 (H5N3) and the neuraminidase is similar to that from human H2N2 strains (e.g., A/Japan/305/57) and from some avian influenza virus strains (e.g., A/turkey/Mass/66 [H6N2]). Comparison of the genome RNAs of chicken/Penn with other influenza virus isolates by RNA-RNA hybridization indicated that all of the genes of this virus were closely related to those of various other influenza virus isolates from wild birds. Chickens infected with the virulent strain shed high concentrations of virus in their feces (10(7) 50% egg infective dose per g), and the virus was isolated from the albumin and yolk of eggs layed just before death. Virus was also isolated from house flies in chicken houses. Serological and virological studies showed that humans are not susceptible to infection with the virus, but can serve as short-term mechanical carriers. Analysis of the RNA of the viruses isolated in April and October by gel migration and RNA-RNA hybridization suggested that these strains were very closely related. Oligonucleotide mapping of the individual genes of virulent and avirulent strains showed a limited number of changes in the genome RNAs, but no consistent differences between the virulent and avirulent strains that could be correlated with pathogenicity were found. Polyacrylamide gel analysis of the early (avirulent) isolates demonstrated the presence of low-molecular-weight RNA bands which is indicative of defective-interfering particles. These RNAs were not present in the virulent isolates. Experimental infection of chickens with mixtures of the avirulent and virulent strains demonstrated that the avirulent virus interferes with the pathogenicity of the virulent virus. The results suggest that the original avirulent virus was probably derived from influenza viruses from wild birds and that the virulent strain was derived from the avirulent strain by selective adaptation rather than by recombination or the introduction of a new virus into the
population. This adaptation may have involved the loss of defective RNAs, as well as mutations, and thus provides a possible model for a role of defective-interfering particles in nature.

Descriptors: chickens microbiology, influenza A virus avian pathogenicity, RNA viral analysis, antigens, viral analysis, defective viruses genetics, Diptera microbiology, ducks microbiology, avian genetics, avian immunology, swine microbiology, viral interference, virus replication.

NAL Call Number: 448.8 J821
Abstract: Amantadine has been accepted for both the treatment and prophylaxis of influenza A virus infections. Although amantadine-resistant mutants have been shown to be readily generated both in the laboratory and in children treated with rimantadine, little is known about their biologic properties, such as genetic stability, transmissibility, or pathogenicity, compared with the parental virus. This study examined these properties using an avian influenza virus, A/chicken/Pennsylvania/1370/83 (H5N2). Variants that were amantadine-resistant, virulent, and capable of competing with wild-type virus for transmission to susceptible hosts in the absence of the drug were selected. These amantadine-resistant variants were also genetically stable, showing no reversion to wild-type after six passages in birds over a period of greater than 20 d. Thus, these virus variants had no detectable biologic impairment. The mutations conferring drug resistance were in the M2 polypeptide and were identical to mutations previously described in human amantadine-resistant virus. These results suggest that resistant mutants may have the potential to threaten the effective use of amantadine and rimantadine for the control of epidemic influenza.

Descriptors: amantadine pharmacology, fowl plague microbiology, influenza A virus avian drug effects, amantadine therapeutic use, chickens, drug resistance, microbial, fowl plague drug therapy, fowl plague transmission, avian genetics, avian pathogenicity, mutation, RNA viral genetics, virulence.

NAL Call Number: 41.8 Av5
Abstract: An experiment was designed to simulate field conditions in which preventive treatment is not initiated until after some chickens in a flock are infected with avian influenza (AI). Twelve hens began to receive amantadine hydrochloride on the day they were inoculated (day 0) with highly pathogenic AI virus, A/chicken/Pa/1370/83. These hens remained clinically normal through 8 days postinoculation (PI), but five died after day 9; mean death time (MDT) was 18 days. Three of 12 hens given amantadine beginning 1 day PI died (MDT 5.4 days), seven of 12 hens given amantadine beginning 3 days PI died (MDT 3.7 days), and all 12 inoculated hens not given amantadine died (MDT 4.9 days). The delayed mortality in the day 0 treatment group was likely due not to the original inoculum but to the emergence of a drug-resistant virus population. Virus isolated from a dead hen from that group was resistant to the actions of amantadine in both in ovo and in vivo tests. The lack of late mortality due to the drug-resistant virus in the day 1 and day 3 treatment groups, which were in close contact with the day 0 treatment group, was attributed to their becoming infected before treatment with the drug and to the development of protective immunity.

Descriptors: amantadine pharmacology, chickens, fowl plague prevention and control, influenza A virus avian drug effects, amantadine therapeutic use, chick embryo, drug resistance, microbial, fowl plague drug therapy.

NAL Call Number: QR360.J6
Descriptors: arginine metabolism, cultured cells metabolism, cytoplasm metabolism, influenza A virus avian pathogenicity, proteins biosynthesis, autoradiography, cell line, cell nucleus metabolism, chick embryo, ethanol, fibroblasts, hamsters, hydrochloric acid, kidney, precipitation, solvents, trichloroacetic acid, tritium.

NAL Call Number: QR360.A1J6

**NAL Call Number:** 448.8 J8232

**Descriptors:** antigens, erythrocytes, hemagglutination tests, indicators and reagents, orthomyxoviridae, salicylic acids, sulfonic acids, complement fixation tests, immune sera, influenza A virus avian, nucleoproteins, sheep.


**NAL Call Number:** 449.8 Z3

**Descriptors:** antigens biosynthesis, influenza A virus avian immunology, antigens, viral biosynthesis, arginine, autoradiography, AZO compounds pharmacology, cell nucleus metabolism, chick embryo, fibroblasts, hemagglutinins viral biosynthesis, membranes, nucleoproteins biosynthesis, ribose, serotyping, viral proteins biosynthesis.


**NAL Call Number:** QR360.A1J6

**Descriptors:** azo compounds pharmacology, influenza A virus avian drug effects, neuraminidase antagonists and inhibitors, Newcastle disease virus drug effects, arboviruses drug effects, arboviruses growth and development, chick embryo, complement fixation tests, Congo red pharmacology, hemagglutination tests, avian growth and development, neuraminidase metabolism, Newcastle disease virus growth and development.


**Abstract:** Influenza A virus M protein was prepared by electrophoresis in SDS polyacrylamide gel from virus particles which had been pretreated with octylglucoside to remove the surface glycoproteins; M antigens from the influenza virus strains A/Victoria/3/75 (H3N2), A/FPV/Rostock (Hav1N1) and A/chick/Germany/49 (Hav2Neq1) did not protect mice against a lethal challenge infection with the virulent Victoria strain.

**Descriptors:** antigens, viral immunology, influenza A virus avian immunology, human immunology, viral proteins immunology, antibodies, viral biosynthesis, hemagglutination inhibition tests, immunization, influenza immunology, influenza prevention and control, mice.


**Abstract:** The indirect hemagglutination technique has been improved by fixing the carrier erythrocytes successively with glutaraldehyde and sulfosalicylic acid. Sensitization by covalent conjugation of influenza virus antigens to the erythrocytes with various coupling reagents, which resulted in stable and highly sensitive test cells, has been defined. An economical affinity chromatography procedure using antibody-coated agarose has been developed to prepare sufficiently pure antigens from fowl plague virus-infected choriollantoic membranes.

**Descriptors:** antibodies, viral analysis, erythrocytes immunology, hemagglutination tests methods, antibody specificity, blood preservation, chromatography, affinity, cytological techniques, glutaral, hemagglutinins viral
isolation and purification, influenza A virus avian immunology, salicylic acids.


**NAL Call Number:** QR360.A1J6

**Descriptors:** agglutination drug effects, lectins pharmacology, RNA viruses, agglutination tests, arboviruses, cattle, cell line, cell membrane drug effects, cultured cells microbiology, chick embryo, concanavalin A pharmacology, fibroblasts, hamsters, HeLa cells microbiology, influenza A virus avian, kidney, cell line microbiology, Newcastle disease virus, orthomyxoviridae, polioviruses, Semliki Forest virus, simian virus 40, sindbis virus, vesicular stomatitis Indiana virus, virus diseases.


**NAL Call Number:** 448.8 P942

**Descriptors:** defective viruses pathogenicity, orthomyxoviridae pathogenicity, influenza A virus avian, interferons biosynthesis, mice, viral interference, virus replication.


**Descriptors:** genetic engineering methods, influenza A virus human genetics, influenza B virus genetics, influenza vaccine genetics, adult, infant, avian immunology, human immunology, human pathogenicity, influenza B virus immunology, influenza B virus pathogenicity, influenza vaccine immunology, vaccines, attenuated genetics, vaccines, attenuated immunology, vaccines, combined genetics, vaccines, combined immunology.


**NAL Call Number:** QP501.E8

**Abstract:** The ganglioside composition of Ehrlich ascites carcinoma (EAC) cells and the role of the individual gangliosides in binding and penetration into the cell of influenza virus were determined. EAC gangliosides identical with or close to GM3, GM2, GM1, GT1a and GT1b were characterized by thin-layer chromatography, compositional analyses, methylation analysis and mass-spectrometry. The ganglioside uptake capacity of native and neuraminidase-treated EAC cells was studied with tritium-labeled gangliosides of definite structure and the binding of influenza virus to cells was determined by using [3H]uridine-labeled virus and by hemagglutination studies. Treatment of the cells with Vibrio cholerae neuraminidase largely decreased binding of the virus. Exogenous gangliosides with a terminal galactose unit or a penultimate galactose masked by neuraminic acid were able to restore the virus-binding capacity of neuraminidase-treated cells, however, the main ganglioside of EAC cells, GM2, which carbohydrate chain is terminated by N-acetylgalactosamine, was completely ineffective. The common carbohydrate sequence of the gangliosides showing binding activity (formula; see text) is proposed to be the main recognition structure of the influenza virus receptor on the surface of EAC cells. Penetration of labeled influenza virus into the nuclei of EAC cells was evaluated by measuring the radioactivity of the nuclei of neuraminidase-treated ganglioside-loaded cells after exposition to the labeled virus. Of all gangliosides tested only trisialogangliosides of the GT1b type were able to induce increased entry of the virus into the cells and accumulation of its radioactive component into the nuclei. It is suggested that GT1b gangliosides react specifically with the virus protein responsible for membrane fusion (apparently the hemagglutinin HA2 subunit) and thus are involved in virus penetration and delivery of the virus genome to the nuclei.

**Descriptors:** carcinoma, ehrlich tumor microbiology, gangliosides metabolism, influenza A virus avian physiology, receptors, virus metabolism, carbohydrate sequence, hemagglutination tests, kinetics, mice, neuraminidase pharmacology, receptors, virus drug effects, structure activity relationship, vibrio cholerae enzymology.

**NAL Call Number:** QR375.V6

**Abstract:** Entry of enveloped viruses is often mediated by an aminoterminal hydrophobic fusion peptide of a viral surface protein. The S domain of the hepatitis B virus surface protein contains a putative fusion peptide at position 7-18, but no systems are available to study its function directly. We tested the functionality of this peptide and a related peptide from another hepadnavirus in the context of the well-characterized influenza virus hemagglutinin H7 using gene mutation. The chimeric hemagglutinins could be expressed stably in CV 1 cells and were transported to the cell surface. The chimeras were incompletely cleaved by cellular proteases but cleavage could be completed by trypsin treatment of the cells. The chimeras did not differ in receptor binding, i.e. erythrocyte binding. Hemifusion and fusion pore formation were detected with membrane or cytosolic fluorescent dye-labeled erythrocytes as target structures of the hemagglutinin. Five of six different chimeras mediated hemifusion in 20-54% of the hemagglutinin-expressing cells, complete fusion and syncytium formation was not observed. The data suggest that the sequence 7-18 of the hepatitis B S domain may indeed initiate the first step of viral entry, i.e. hemifusion.

**Descriptors:** hemagglutinin glycoproteins, influenza virus metabolism, hepatitis B virus metabolism, membrane fusion, viral fusion proteins metabolism, amino acid sequence, cell line, chimeric proteins genetics, chimeric proteins metabolism, hemagglutinin glycoproteins, influenza virus genetics, hepatitis B virus genetics, molecular sequence data, peptides chemistry, peptides genetics, receptors, virus metabolism, viral fusion proteins chemistry, viral fusion proteins genetics.


**NAL Call Number:** QR360.A1J6

**Abstract:** The influenza A virus M2 proton channel plays a role in two stages of virus replication. The proteins of two closely related strains of the avian H7 subtype of influenza A virus, Rostock and Weybridge, were found to differ in their pH-modulating activities and activation characteristics. Of three amino acid differences at residues 27, 38 and 44 within the membrane-spanning domain, substitution at residue 44 was necessary and sufficient to account for differences in trans-Golgi pH-modulating activity, whereas changes in all three were required to switch the activation characteristics of the Weybridge M2 to those of the Rostock M2. These results not only separate the two phenomena genetically, but also indicate that the 'unique' activation characteristics of the Rostock M2 channel were selected specifically. In addition, they point to the importance of functional complementarity between the activation characteristics of the M2 channel and the pH of membrane fusion by haemagglutinin during virus entry.

**Descriptors:** influenza A virus, avian metabolism, ion channels metabolism, viral matrix proteins metabolism, amino acid sequence, cell line, Golgi apparatus chemistry, Golgi apparatus metabolism, hemagglutinins, viral metabolism, hydroein-ion concentration, ion channels chemistry, molecular sequence data, protein structure, tertiary, protons, sequence alignment, viral matrix proteins chemistry, virus replication.


**NAL Call Number:** 448.3 AC85

**Abstract:** The activities, the temperature and pH optima of in vitro functioning and stability upon heating of virion transcriptase of 10 human influenza virus A strains differing in reactogenicity and isolated in different epidemiological situations, and of fowl plague virus (FVP) were compared. As compared with virion transcriptase of human influenza virus strains studied, that of FPV had a higher pH optimum, was capable of functioning in vitro at a higher temperature and was more stable on heating. Freshly isolated and vaccine influenza virus strains on the one hand and strains isolated at the peak and in the end of an epidemic did not differ in the virion transcriptase properties. The virion transcriptase of a strain isolated from a local influenza outbreak was much less active than transcriptase of a highly epidemicle strain.

**Descriptors:** influenza A virus avian enzymology, human enzymology, RNA nucleotidytransferases metabolism, RNA replicase metabolism, heat, hydrogen-ion concentration, influenza vaccine, species.
specificity, temperature, virion enzymology.

NAL Call Number: 448.8 P942
Abstract: The authors tried to decode the mechanism of influenza viruses species adaptation in the process of host changing. The functionally important replacement in the surface pocket domains were revealed, particularly in the conservative region 221-241, involving fibronectin-like part. Close replacements were revealed in the region 141-161. The method of construction of heteroduplexes between hemagglutinin RNA of duck, pig, and human viruses was used. The method showed that all heteroduplexes formed recombinogene structures. An unexpected effect of directional recombination was elicited for hemagglutinin RNA heteroduplexes in cases of duck-pig and human-pig viruses. During the directional recombination the following processes took place: the receptor-binding site of animal type was transmitted to the duck virus, while the human receptor-binding site was transmitted to the pig virus. According to the experimental data, a new hypothesis is formulated: the cascade mechanism of directional recombination for duck, animal and human viruses makes it possible for the recombinant viruses to overcome interspecies barriers.
Descriptors: adaptation, physiological genetics, genes viral genetics, hemagglutinins viral genetics, influenza A virus avian genetics, porcine genetics, recombination, genetic genetics, amino acid sequence, ducks microbiology, human genetics, molecular sequence data, nucleic acid heteroduplexes genetics, RNA viral genetics, swine microbiology, variation genetics genetics.

Descriptors: influenza viruses, wild birds, terns, humans, virus recombination.

Descriptors: avian influenza virus, DEAE cellulose, neuraminidase, chromatography.

NAL Call Number: S1.S68
Descriptors: avian influenza virus, neuraminidase, immunoenzymology, antibodies.

Descriptors: avian influenza viruses, neuraminidase, antigens, physio-chemical properties, techniques.

NAL Call Number: 448.3 Ar23
Abstract: Recombinants with known gene constellations between fowl plague virus (FPV) and various prototype influenza virus strains have been examined for neurovirulence in suckling mice. Strongly neurotropic recombinants were obtained from crosses between FPV and the strains virus N, Hong Kong, and PR8, but not between FPV and equi 2 or swine viruses. All highly neurotropic recombinants had RNA segment 4 (HA) derived from FPV and RNA segment 2 (Ptra gene) from the other prototype strain. The derivation of two other RNA segments of the polymerase complex, namely RNA segments 3 (Pol 2) and 5
(NP) and also segment 8 (NS) can modulate these properties. For example, if in recombinants between FPV and virus N in addition to RNA segment 2 also RNA segments 3 and/or 8 are derived from virus N, neurovirulence is further enhanced, while replacement of RNA segment 5 of FPV by the corresponding segment of virus N decreases or abolishes neurovirulence. The derivation of the other genes does not seem to be relevant for neurovirulence in the crosses mentioned above. Of the prototype strains tested, the turkey England (t. Engl.) strain is the only one which was highly neurotropic for suckling mice. Recombinants between FPV and t. Engl. which have kept the HA gene of t. Engl. were still neurotropic, while those with the HA gene of FPV were completely avirulent. The results obtained demonstrated that 1. the creation of influenza virus recombinants neurotropic for mice is not a rare event; 2. one of the parents should multiply well in mouse lungs; 3. the presence of a cleavable hemagglutinin is necessary, but not sufficient. In the pair FPV/turkey England the hemagglutinin of turkey England seems to determine neurovirulence.

Descriptors: influenza A virus, genetics, recombination, genetic, brain microbiology, cultured cells, embryo microbiology, fibroblasts, genes viral, avian genetics, pathogenicity, kidney, lung microbiology, mice, virulence.

NAL Call Number: 448.8 Sch9
Abstract: An avian influenza A virus which grows well in human leukemic myeloblasts was unable to replicate in normal human leukocytes. The virus adhered during the first hours of incubation to plastic surfaces and to leukocytes and was then released into the supernatant; care should be taken not to confuse this with viral growth.
Descriptors: influenza A virus, avian growth and development, leukocytes microbiology, adaptation, physiological, adsorption, adult, cell adhesion, granulocytes microbiology, leukemia, myelocytic, acute, lymphocytes microbiology, monocytes microbiology, plastics, tissue culture, virus replication.

NAL Call Number: QR360.J6
Descriptors: DNA, viral metabolism, fibroblasts enzymology, influenza A virus avian metabolism, RNA biosynthesis, RNA nucleotidyltransferases biosynthesis, chick embryo, dactinomycin pharmacology, hemagglutination, viral, RNA viral biosynthesis, tissue culture, virus replication.

NAL Call Number: 448.3 Ar23
Descriptors: cytopathogenic effect, viral, lung metabolism, orthomyxoviridae pathogenicity, proteins biosynthesis, RNA biosynthesis, tissue culture, carbon isotopes, centrifugation, density gradient, chick embryo, dactinomycin pharmacology, hemadsorption, hemagglutination, influenza A virus avian growth and development, avian pathogenicity, lung pathology, orthomyxoviridae growth and development, species specificity, sucrose, tritium, uridine metabolism, valine metabolism, virus replication.

NAL Call Number: 448.3 Ar23
Abstract: The heterogeneity in charge of the influenza virus glycoproteins, hemagglutinin (HA) and neuraminidase (NA) is retained, when glycosylation is inhibited by tunicamycin (TM) or 2-deoxyglucose (2-dg). This is in contrast to the charge heterogeneity of the G protein of vesicular stomatitis virus (VSV), which is mainly due to heterogeneous sulfation of the carbohydrate side chains and therefore is abolished by the above mentioned inhibitors of glycosylation. Thus, the charge heterogeneity of influenza virus glycoproteins might be attributable to some as yet unidentified modifications of the polypeptide backbone.
Descriptors: hemagglutinins viral, influenza A virus avian analysis, membrane glycoproteins, neuraminidase, viral envelope proteins, viral proteins, cultured cells, chick embryo, deoxyglucose pharmacology, electrophoresis, polyacrylamide gel, hemagglutinin glycoproteins, influenza virus, avian
enzymology, avian metabolism, human analysis, isoelectric focusing, isoelectric point, translation, genetic, tunicamycin pharmacology, vesicular stomatitis Indiana virus analysis.

Descriptors: hemagglutinins viral analysis, influenza A virus avian immunology, peptide hydrolases metabolism, amino acid sequence, human immunology, human pathogenicity, isoelectric point.

Abstract: The hemagglutinin (HA) and neuraminidase (NA) of influenza viruses, as well as the fusion protein (F) and hemagglutinin-neuraminidase (HN) of paramyxoviruses, have been separated in native form using a two-step procedure. The glycoproteins are efficiently extracted from virions using the on-ionic detergent octyl-beta-D-glucoside and are then applied to a column of agarose beads coupled with tyrosine-sulfanilic acid. Pure HA and F are obtained in good yield in the flow-through from this column. NA and HN bind strongly and can be eluted, albeit somewhat contaminated with HA or F, by raising the pH of the column buffer. The separated non-denatured fractions can be used for structural, functional, and antigenic studies.
Descriptors: glycoproteins isolation and purification, influenza A virus avian analysis, human analysis, Newcastle disease virus analysis, viral proteins isolation and purification, chromatography, affinity, detergents, hemagglutinins viral analysis and purification, neuraminidase isolation and purification.

Abstract: The glycosylation inhibitors tunicamycin (TM), 2-deoxyglucose (2-dg), bromoconduritol (BC; 3,5/4,6-bromo 3,4,5-trihydroxycyclohex-1-ene), and N-methyl-deoxynojirimycin (MdN) have been used to study the role of glycosylation in the two proteolytic reactions involved in the biological activation of H7 influenza virus hemagglutinins (HAs): trypsinlike cleavage and subsequent elimination of the connecting peptide. The results obtained revealed that trypsin-like cleavage of the HAs of pathogenic strains does not require glycosylation, since these HAs were efficiently cleaved in the presence of TM and 2-dg. The elimination of the connecting peptide between HA1 and HA2, however, appears to require the transfer of oligosaccharides onto the HA polypeptide, since this activity was blocked by TM and by 2-dg. Elimination was not blocked by BC or MdN, which inhibit glucose trimming and subsequent conversion of the high-mannose type to the complex type of carbohydrate.
Descriptors: 1 deoxynojirimycin analogs and derivatives, carbohydrates metabolism, hemagglutinin viral metabolism, influenza A virus avian analysis, trypsin metabolism, deoxyglucose pharmacology, glucosamine analogs and derivatives, glucosamine pharmacology, inositol analogs and derivatives, inositol pharmacology, tunicamycin pharmacology, virion analysis.

Abstract: It has been shown previously that the pathogenicity of avian influenza A viruses depends strictly on the proteolytic cleavability of their haemagglutinin (HAs) in infected cells. In this communication, pathogenic and non-pathogenic strains of the H7 subtype have been studied by comparing the genetic relatedness of their HA genes. Some of the cleavable HAs of pathogenic strains were genetically more closely related to the uncleaved HAs than to other cleavable HAs. These data clearly demonstrate that the overall evolution of the H7 haemagglutinin is different from the evolution of the specific cleavage site.
Descriptors: genes viral, hemagglutinin viral genetics, influenza A virus avian immunology, evolution,
hemagglutinins viral analysis, avian genetics, avian pathogenicity, nucleic acid hybridization.

NAL Call Number: 442.8 J8224
Abstract: We present here the three-dimensional structure of neuraminidase (E.C. 3.2.1.18) from influenza virus A/Tern/Australia/G70c/75 (N9), determined by the method of multiple isomorphous replacement, and the structure of the neuraminidase complexed with an inhibitor, 2-deoxy-2,3-dehydro-N-acetyl neuraminic acid (DANA). Native and inhibitor complex crystals are isomorphous and belong to space group I432 with unit cell dimensions of 183.78 Å. The native enzyme structure and the inhibitor complex structure have been refined at 2.5 Å and 2.8 Å resolution, respectively, with crystallographic R-factor values of 0.193 for the native enzyme, and 0.179 for the inhibitor complex. The current enzyme model includes 387 amino acid residues which comprise the asymmetric unit. The root-mean-square deviation from ideal values is 0.013 Å for bond lengths and 1.6 degree for bond angles. The neuraminidase (NA), as proteolytically cleaved from the virus, retains full enzymatic and antigenic activity, and is a box-shaped tetramer with edge lengths of 90 Å and a maximal depth of 60 Å. The NA tetramers are composed of crystallographically equivalent monomers related by circular 4-fold symmetry. Each monomer folds into six antiparallel beta-sheets of four strands. The secondary structure composition is 50% beta-sheet. The remaining 50% of the residues form 24 strand-connecting loops or turns. One of the loops contains a small alpha-helix. The structure of the complex of NA with DANA, a transition state analog, has enabled us to identify and characterize the site of enzyme catalysis. The center of mass of bound inhibitor is 32 Å from the 4-fold axis of the tetramer, lodged at the end of a shallow crater of diameter 16 Å with a depth of 8 to 10 Å. There are 12 amino acid residues that directly bind DANA, with a further six conserved amino acids lining the active site pocket. The neuraminidase inhibitor complex provides a three-dimensional model which will be used to further the understanding of enzymatic hydrolysis and aid the design of specific, antineuraminidase antiviral compounds.
Descriptors: influenza A virus avian enzymology, neuraminidase antagonists and inhibitors, neuraminidase chemistry, sialic acids chemistry, binding sites, influenza B virus enzymology, mercury chemistry, models, molecular, molecular conformation, N-acetylneuraminic acid, platinum chemistry, protein conformation, sialic acids metabolism, x-ray diffraction.

NAL Call Number: 448.8 V81
Descriptors: antibodies, influenza A virus avian growth and development, neuraminidase isolation and purification, neuraminidase metabolism, orthomyxoviridae growth and development, centrifugation, density gradient, chick embryo, chromatography, DEAE-cellulose, fibroblasts, hemagglutination tests, immune sera, immunoglobulin g, immunoglobulins, avian enzymology, avian immunology, avian pathogenicity, neuraminic acids biosynthesis, orthomyxoviridae enzymology, orthomyxoviridae immunology, orthomyxoviridae pathogenicity, rabbits, sucrose, tissue culture, virus replication.

NAL Call Number: 41.8 Av5
Abstract: The nucleocapsid (N) gene of turkey coronavirus (TCV) was amplified by reverse transcriptase-polymerase chain reaction, cloned, and expressed in the baculovirus expression system. A recombinant baculovirus containing the TCV N gene (rBTCV/N) was identified by polymerase chain reaction and expression of TCV N protein as determined by western immunoblot analysis. Two TCV-specific proteins, 52 and 43 kDa, were expressed by rBTCV/N; one of these proteins, p52, was comparable in size to native TCV N protein. Baculovirus-expressed N proteins were used as antigen in an indirect enzyme-linked immunosorbent assay (ELISA) for detection of TCV-specific antibodies. The ELISA detected antibodies specific for TCV and infectious bronchitis virus, a closely related avian coronavirus, but did not detect antibodies specific for other avian viruses (avian influenza, avian reovirus, avian paramyxovirus 3, avian
adenovirus 1, or Newcastle disease virus). These findings indicate that baculovirus-expressed TCV N protein is a suitable source of antigen for ELISA-based detection of TCV-specific antibodies in turkeys.

Descriptors: baculoviridae metabolism, nucleocapsid biosynthesis, nucleocapsid proteins, turkeys virology, enteritis veterinary, enteritis virology, enzyme linked immunosorbent assay veterinary, North Carolina, nucleocapsid genetics, poultry diseases virology, reverse transcriptase polymerase chain reaction veterinary.


**Abstract:** Cells infected with a reassortant (113/Ho, H7N2) between A/fowl plague/Rostock/34 (FPV, H7N1) and A/Hong Kong/1/68 (H3N2) carrying RNA segments 1 and 6 of the Hong Kong virus and the residual genes of FPV, synthesized at 40 degrees a neuraminidase (NA) which is enzymatically not active and which is not incorporated into infectious particles. At 40 degrees NA accumulates in the rough endoplasmic reticulum. It contains mainly carbohydrate side chains of the mannose type, and fucose is only scarcely incorporated. At 33 degrees NA of the reassortant is overproduced, and at least some of it is active and is incorporated into viral particles. Under nonreducing conditions during PAGE its NA migrates to the same position as after heating with mercaptoethanol, in contrast to the Hong Kong parent virus. It is speculated that at 40 degrees the tetramerization of the NA in the rough endoplasmic reticulum does not function, and in this way its migration to the cytoplasmic membrane and its incorporation into infectious particles does not occur. Since 113/Ho is as pathogenic for the chicken (body temperature of 41 degrees) as is FPV, the question arises which role the NA plays in virus replication and spread in the infected organism.

Descriptors: influenza A virus avian genetics, human genetics, neuraminidase genetics, carbohydrate sequence, cell compartmentation, chick embryo, glycopeptides analysis, glycoproteins genetics, glycoproteins metabolism, hemagglutinins viral genetics, avian enzymology, influenza A virus human enzymology, mutation, neuraminidase metabolism, recombination, genetic, temperature, viral proteins metabolism, virus replication.


**Descriptors:** cell nucleus metabolism, cytoplasm metabolism, influenza A virus avian metabolism, viral proteins metabolism, capsid metabolism, cell fractionation, cell line, dogs, avian growth and development, kinetics.


**Descriptors:** influenza A virus avian analysis, RNA viral analysis, autoradiography, base sequence, centrifugation, density gradient, chick embryo, chromatography, DEAE-cellulose, chromatography, gel, densitometry, electrophoresis, polyacrylamide gel, influenza A virus avian isolation and purification, nucleic acid denaturation, phosphorus isotopes, RNA viral isolation and purification, ribonucleases, tissue culture, virus cultivation.


**Descriptors:** influenza A virus avian analysis, RNA viral analysis, base sequence, guanine analysis.


**Descriptors:** influenza A virus avian analysis, RNA viral analysis, base sequence, guanine analysis.
Abstract: We have investigated the effects of the anti-influenza drug amantadine (AMT) and the proton-ionophore monensin on the membrane fusion activity of influenza virus in a liposomal model system, using a kinetic fluorescence lipid mixing assay. Fusion of influenza virus A/turkey/Oregon/71 (H7N3) with liposomes was slowed down in the presence of 2 microM AMT. The effect of AMT was not observed with an AMT-resistant mutant virus. Fusion inhibition by AMT was reversed by the proton-ionophore monensin. In fact, 1 microM monensin stimulated fusion of AMT-sensitive or -resistant virus, irrespective of the presence of AMT. The effects of AMT and monensin increased with increasing temperature. They were not observed at 25 degrees, but were very prominent at 45 degrees. Monensin did not influence the fusion rates of reconstituted viral envelopes (virosomes), which lack the nucleocapsid and the M1 protein. These results suggest that intraviral low pH facilitates influenza virus fusion, possibly by weakening interactions of the C-terminus of the viral hemagglutinin with the M1 protein and/or the viral nucleocapsid. The effect of AMT on the fusion capacity of influenza virus may contribute to the anti-influenza action of the drug in the early stages of cellular infection. However, the limited extent of the fusion inhibition suggests that the fusion step is unlikely to be the primary target of AMT.

Descriptors: amantadine pharmacology, influenza A virus avian metabolism, monensin pharmacology, viral matrix proteins metabolism, electrophoresis, polyacrylamide gel, immunoblotting, avian drug effects, kinetics, membrane fusion drug effects.


Abstract: PURPOSE OF REVIEW: The emergence of severe acute respiratory syndrome in late 2002 and the recent outbreaks of avian influenza in Asia are timely reminders of the ever present risks from respiratory viral diseases. Apart from influenza, there are no vaccines and very few antiviral chemotherapeutic agents available for the prevention and treatment of respiratory viral infections-the most common cause of human illness. If the current H5N1 avian influenza outbreak ever assumes the role of a pandemic, formidable technical difficulties relating to the properties of the agent, itself, will ensure that vaccines will only become available after a significant lead time and then only to a relatively small percentage of the population. The use of existing antivirals could be critical in limiting the initial spread of a pandemic, although their use in the control of epidemics caused by nonpandemic viruses has not been evaluated. It is against this background that a review of recent developments in respiratory antivirals has been undertaken. RECENT FINDINGS: The late 1990s were a period of unprecedented activity in the development of new and much superior antivirals for the treatment of influenza infections. However, during the past 2 to 3 years and largely for commercial reasons, there has been a decline in interest in their further development by major drug companies. This situation may soon change with the possible advent of new pandemic viruses, and moves are afoot in several countries to consider the stockpiling of antivirals. The neuraminidase inhibitors zanamivir and oseltamivir, and the M2 inhibitors amantadine and rimantadine, remain the only options for controlling respiratory disease caused by influenza viruses, although the latter two could not be used against very recent H5N1 strains. There are several other neuraminidase inhibitors in development. Compounds with activity against other respiratory viruses, notably rhinoviruses, are also in development, many based on a newer knowledge of viral protein structure and function (rational drug design). SUMMARY: The following is an overview of recent papers on the further development of neuraminidase inhibitors against influenza viruses and on recent development of newer antivirals against RSV and rhinoviruses. Where possible, comparisons are made with existing antivirals. For considerations of space, this review has been structured around stages in the replication cycle of significant respiratory viruses that have been traditionally used as targets for inhibition.

Descriptors: antiviral agents therapeutic use, respiratory tract infections drug therapy, respiratory tract infections virology, virus diseases drug therapy, antiviral agents pharmacology, drugs investigational pharmacology, drugs investigational therapeutic use, enzyme inhibitors pharmacology, enzyme inhibitors therapeutic use, ion channels antagonists and inhibitors.

Abstract: We recently reported the first benzoic acid, 1-(4-carboxy-2-(3-pentylamino)phenyl)-5,5-bis(hydroxymethyl)pyrrolidin-2-one (8), that is a potent inhibitor of avian influenza A neuraminidase (N9) and, unlike other recently reported potent neuraminidase inhibitors, does not contain a basic aliphatic amine or guanidine nor a simple N-acetyl grouping. However, 8 was a poor inhibitor of influenza B neuraminidase. In the present study we further evaluated 8 as an inhibitor of human influenza A NA isolates, and it was effective against N2 NA but found to be 160-fold less active against N1 NA. We also synthesized analogues of 8 involving moderate modifications of essential substituents on the pyrrolidinone ring. Specifically, the aminomethyl (9), hydroxyethyl (10), and aminooethyl (11) analogues were prepared. Only the most conservative change (compound 9) resulted in continued effective inhibition of influenza A, in addition to a noteworthy increase in the activity of 9 for N1 NA. The effectiveness of 9 against influenza B neuraminidase was furthermore improved 10-fold relative to 8, but this activity remained 50-fold poorer than for type A NA.

Descriptors: methods and techniques, pharmacology, influenza, drug therapy, respiratory system disease, viral disease, chemical synthesis laboratory techniques.


Abstract: Eighteen specific pathogen-free chickens (nine hens older than 1 year and nine 15-week-old males) were inoculated with highly pathogenic avian influenza virus A/Chicken/Pennsylvania/1370/1983 (H5N2). Birds were serially killed and tissues collected for histological and immunohistochemical evaluation. In the group of older hens, disease was acute or peracute. By immunohistochemistry, antigen was abundant in capillary endothelium in multiple organs, and staining for antigen in parenchymal cells was marked in brain and heart. In the group of younger male birds, disease was subacute. Immunohistochemical staining of capillary endothelium was less pronounced and viral antigen staining was evident in the parenchymal cells of the heart, brain and kidney.

Descriptors: antigens, viral analysis, brain immunology, endothelium, vascular immunology, fowl plague pathology, influenza A virus avian pathogenicity, myocardium immunology, chickens, fowl plague immunology, immunohistochemistry, avian classification.


Abstract: Novel H1N2 influenza A viruses which were first detected in pigs in Great Britain in 1994 were examined antigenically and genetically to determine their origins and establish the potential mechanisms for genetic reassortment. The haemagglutinin (HA) of all swine H 1 N2 viruses examined was most closely related to, but clearly distinguishable both antigenically and genetically from, the HA of human H1N1 viruses which circulated in the human population during the early 1 980s. Phylogenetic analysis of the HA gene revealed that the swine H 1 N2 viruses formed a distinct branch on the human lineage and were probably introduced to pigs shortly after 1980. Following apparent transfer to pigs the HA gene underwent genetic variation resulting in the establishment and cocirculation of genetically and antigenically heterogeneous virus populations. Genetic analyses of the other RNA segments of all swine H1N2 viruses indicated that the neuraminidase gene was most closely related to those of early 'human-like' swine H3N2 viruses, whilst the RNA segments encoding PB2, PB1, PA, NP, M and NS were related most closely to those of avian viruses, which have been circulating recently in pigs in Northern Europe. The potential mechanisms and probable progenitor strains for genetic reassortment are discussed, but we propose that the swine H1N2 viruses examined originated following multiple genetic reassortment, initially involving human H1N1 and 'human-like' swine H3N2 viruses, followed by reassortment with 'avian-like' swine H1N1 virus. These findings suggest multiple reassortment and replication of influenza viruses may occur in pigs many years before their detection as clinical entities.

Descriptors: influenza A virus avian genetics, human genetics, recombination, genetic, antigens, viral

**NAL Call Number:** QR360.A1J6

**Abstract:** The effects of cell metabolic activity on the outcome of influenza virus infection were studied in partially synchronized chick embryo fibroblast cultures. There was no evidence to show that the time in the cell cycle at which cells were infected had any significant effect on the final virus yield. However, some differences were detected in the length of the latent period between infections established in synchronized or in stationary cells. Influenza virus could replicate in synchronized or normal cell cultures in which DNA synthesis was inhibited with 9-beta-D-arabinofuranosyladenine (ara-A).

**Descriptors:** influenza A virus avian growth and development, virus replication drug effects, cell cycle, cell division, chick embryo, DNA biosynthesis, fibroblasts, avian drug effects, tissue culture, vidarabine pharmacology.


**NAL Call Number:** 41.8 Av5

**Abstract:** The prototype mildly pathogenic A/chicken/Pennsylvania/21525/83 (H5N2) avian influenza virus, which was isolated more than 5 months before the emergence of highly pathogenic virus in the major 1983 Pennsylvania outbreak, was examined for the presence of minority subpopulations of highly pathogenic virus. Selective serial passage of the parental mildly pathogenic virus in leghorn hens did not lead to recovery of highly pathogenic virus. However, several highly pathogenic reisolates were recovered from hens inoculated with either of two mildly pathogenic virus clones selected for their ability to efficiently produce plaques in trypsin-free chicken embryo fibroblasts. Unlike the parental virus, these reisolates caused high mortality in chickens and produced postmortem lesions typical of highly pathogenic avian influenza. Electrophoretic mobilities of the hemagglutinin glycoproteins of the highly pathogenic derivatives resembled those of the prototype highly pathogenic A/chicken/Pennsylvania/1370/83 (H5N2) virus isolated in October 1983. These results suggest that unrecognized subpopulations of highly pathogenic virus may have infected Pennsylvania chickens for several months before emerging as the clinically manifest component of the virus population.

**Descriptors:** chickens, fibroblasts microbiology, fowl plague microbiology, influenza A virus avian pathogenicity, cultured cells, chick embryo, electrophoresis, polyacrylamide gel, glycoproteins analysis, hemagglutination inhibition tests, avian chemistry, avian genetics, avian growth and development, plaque assay, RNA viral analysis, serial passage, specific pathogen free organisms, viral proteins analysis.


**NAL Call Number:** 448.8 Sch9

**Abstract:** Using M-TUR, a macrophage-adapted avian influenza A virus (Hav1, Nav3), antiviral resistance of peritoneal macrophages obtained from specifically or nonspecifically immunized mice towards in vitro infection was assessed. M-TUR grew to high titers in macrophages from nonimmune mice thereby causing a marked cytopathic effect. In contrast, peritoneal macrophages from mice specifically immunized with TUR virus were not affected by infection with M-TUR in vitro. This antiviral immunity was specific: mice immunized with antigenetically unrelated influenza strains such as influenza A/Hong Kong/1/68 (H3, N2) or influenza B/Lee yielded susceptible macrophages. Specific macrophage immunity could be abrogated by trypsin treatment in vitro. Susceptible macrophages from nonimmune hosts became resistant following in vitro exposure to homologous anti-TUR sera. Peritoneal exudate cells from BCG-infected animals were less susceptible to in vitro challenge with M-TUR than control macrophages. In vivo treatment of mice with the unspecific immunostimulants BCG or Corynebacterium parvum did not protect the animals against lethal infection with a hepatotropic variant of TUR.

**NAL Call Number:** QR355.I5

**Abstract:** The hemagglutinin of an influenza virus isolated from a wild duck (Pintail, *Anas acuta*) in the USSR in 1976 had been found to be antigenically indistinguishable from the hemagglutinin of H2N2 viruses of human origin isolated in 1957. The hemagglutinins from viral preparations of the A/*Anas acuta*/Primorie/695/76 (H2Nav2) and A/Singapore/1/57 (H2N2) strains were purified by SDS gel chromatography as the subunits HA1 and HA2. Comparison of amino acid compositions and peptide maps of tryptic peptides containing [14C]-carboxymethylcysteine showed a striking degree of similarity between the H2 hemagglutinins.

**Descriptors:** hemagglutinins viral analysis, influenza A virus avian immunology, human immunology, amino acids analysis, ducks microbiology, peptides analysis.


**NAL Call Number:** 448.8 V81

**Abstract:** The nucleotide sequences of RNA segment 5 of an avian influenza A virus, A/Mallard/NY/6750/78 (H2N2), and a human influenza A virus, A/Udorn/307/72 (H3N2), were determined and the deduced amino acid sequences of the nucleoprotein (NP) of these viruses were compared to two other avian and two other human influenza A NP sequences. The results indicated that there are separate classes of avian and human influenza A NP genes that can be distinguished on the basis of sites containing amino acids specific for avian and human influenza viruses and also by amino acid composition. The human influenza A virus NP genes appear to follow a linear pathway of evolution with the greatest homology (96.9%) between A/NT/60/68 (H3N2) and A/Udorn/72, isolated only 4 years apart, and the least homology (91.1%) between A/PR/8/34 (H1N1) and A/Udorn/72, isolated 38 years apart. Furthermore, 84% of the nucleotide substitutions between A/PR/8/34 and A/NT/60/68 are preserved in the NP gene of the A/Udorn/72 strain. In contrast, a distinct linear pathway is not present in the avian influenza NP genes since the homology (90.3%) between the two avian influenza viruses A/Parrot/Ulster/73 (H7N1) and A/Mallard/78 isolated only 5 years apart is not significantly greater than the homology (90.1%) between strains A/FPV/Rostock/34 and A/Mallard/78 isolated 44 years apart and only 49% of the nucleotide substitutions between A/FPV/34 and A/Parrot/73 are found in A/Mallard/78. A determination of the rate of evolution of the human influenza A virus NP genes suggested that there were a greater number of nucleotide substitutions per year during the first several years immediately following the emergence of a new subtype in 1968.

**Descriptors:** influenza A virus genetics, nucleoproteins genetics, viral proteins genetics, amino acid sequence, base sequence, evolution, genes viral, nucleoproteins classification, RNA viral genetics, sequence homology, nucleic acid, viral proteins classification.


**NAL Call Number:** QR360.J6

**Abstract:** The nucleotide sequence of the region of RNA segment 7 coding for the M1 and M2 proteins of avian influenza A/Mallard/New York/6750/78 was determined, and the deduced amino acid sequences were compared to other avian and human M protein sequences. The M2 proteins of the avian and human viruses have diverged much more than the M1 proteins, although amino acids specific for avian and human viruses were found in both M1 and M2 proteins.

**Descriptors:** genes viral, influenza A virus avian genetics, RNA viral genetics, viral proteins genetics, amino acid sequence, haplorhini microbiology, avian growth and development, messenger genetics.
NAL Call Number: 448.8 P942
Descriptors: histones pharmacology, orthomyxoviridae drug effects, triazines pharmacology, virus replication drug effects, influenza A virus avian drug effects, Newcastle disease virus drug effects, RNA viral antagonists and inhibitors.

NAL Call Number: 448.8 P942
Abstract: The capacity of two gangliosides, GD1a and GT1b isolated from bovine brain to function as specific receptors of influenza virus was determined. A primary chick fibroblast culture was treated with neuraminidase to destroy natural receptors, the cells were loaded with gangliosides GD1a and GT1b, inoculated with 3H-uridine-labeled virus, and virus adsorption and penetration into the cell nucleus were determined. Both gangliosides were shown to restore virus adsorption to the cell surface and penetration of viral structures into the cell, GT1b facilitating more effective transportation of viral structures into the nuclei than GD1a and inducing penetration into the nuclei nearly 1.5-fold as much amount of viral structures as in native cells. The same ganglioside partially restored virus-induced hemolysis upon loading it on erythrocytes pre-treated with neuraminidase. It is concluded that ganglioside GT1b is a specific receptor for influenza virus. 3.9% of this ganglioside was found in chick fibroblast lipids.
Descriptors: gangliosides metabolism, orthomyxoviridae metabolism, receptors, virus metabolism, adsorption, cell nucleus metabolism, chick embryo, erythrocytes metabolism, fibroblasts metabolism, hemolysis, influenza A virus avian metabolism.

NAL Call Number: 511 P444A
Descriptors: cell transformation, viral drug effects, gangliosides pharmacology, influenza A virus avian pathogenicity, receptors, virus drug effects, adsorption, carcinoma, Ehrlich tumor microbiology, avian drug effects, neuraminidase pharmacology.

NAL Call Number: 448.3 Ar23
Abstract: Noninfectious virus particles were produced in Ehrlich ascites tumor cells infected intraperitoneally with fowl plague virus. The PFU yield of virus per cell was less than 0.1 and the ratio PFU/HA units in the progeny virus was less than 10(3). The virus particles had the same morphology and size as egg-grown virus but were more fragile. They were disrupted by centrifugation through sucrose and caesium chloride gradients, but this disruption was avoided by fixing the particles with formaldehyde before centrifugation. Analysis of polypeptides by SDS-PAGE showed that ascites-grown virus particles contained reduced amounts of matrix protein compared with egg-grown virus.
Descriptors: carcinoma, Ehrlich tumor microbiology, influenza A virus avian growth and development, centrifugation, density gradient, avian enzymology, avian ultrastructure, mice, neoplasm transplantation, neuraminidase metabolism, peptides analysis, viral proteins analysis, virus replication.

NAL Call Number: 448.3 AC85
Abstract: The properties of fowl plague virus (influenza virus A) nucleocapsids isolated from the cytoplasm...
of infected Ehrlich ascites carcinoma cells and chick embryo cells were compared. Nucleocapsids isolated from both systems possessed similar polypeptides (P and NP) but differed in their biophysical characteristics. Nucleocapsids from ascites cells sedimented in velocity sucrose gradients slower (from 25 to 50 S) and the majority of them banded at higher density in CsCl gradients (rho 1.38 as compared to 1.34 g/ml) than nucleocapsids from chick embryo cells. In the electron microscope they appeared as thin threads 3–4 nm in diameter.

Descriptors: capsid analysis, influenza A virus avian analysis, viral proteins analysis, capsid biosynthesis, carcinoma, Ehrlich tumor, cultured cells, centrifugation, density gradient, chick embryo, cytoplasm analysis, avian growth and development, avian metabolism, mice, microscopy, electron.


**NAL Call Number:** QH201.U4

**Abstract:** Electron micrographs of two-dimensional microcrystals of a complex of an avian influenza virus neuraminidase and an antibody Fab fragment, termed 32/3, have been recorded using the spot-scan method of imaging. The crystals have a large unit cell (159.5 Å x 159.5 Å x 130.5 Å) and a high solvent content (approximately 71% by volume) and are a challenging specimen for testing the spot-scan methodology. Crystalline order was preserved to beyond 4 Å resolution as demonstrated by electron diffraction, using an embedding medium of a mixture of glucose and neutral potassium phosphotungstate. Using a Philips C400 computer control system interfaced to an EM420 electron microscope, and with the inclusion of additional software in the system, we have been able to record micrographs at low temperature with a relatively narrow (1500 Å diameter) moving beam. There is evidence that the use of such a spot-scan beam reduces the effects of beam-induced specimen motion on the quality of micrographs. Conventional low-dose "flood-beam" images showed good isotropic optical diffraction in only 15% of cases whereas 30% of spot-scan images showed good diffraction. The best flood-beam images gave phases to only 15 Å resolution after computer processing, whereas the best spot-scan images gave phases to 7 Å resolution. Electron diffraction patterns were also recorded at low temperature, and the resulting diffraction amplitudes combined with phases from spot-scan images to yield a projection map of the structure. A 7 Å resolution projection map of the complex is presented, and is compared with the projection map of the same avian influenza neuraminidase complexed with a different monoclonal Fab fragment, NC41, which has been solved to high resolution by X-ray diffraction.

Descriptors: antibodies, viral chemistry, image processing, computer assisted, immunoglobulins, Fab ultrastructure, influenza A virus avian ultrastructure, neuraminidase ultrastructure, binding sites, crystallization, crystallography, immunoglobulins, Fab chemistry, avian enzymology, avian immunology, microscopy, electron, neuraminidase chemistry, x-ray diffraction.


**NAL Call Number:** QR360.A1J6

**Abstract:** A temperature-sensitive mutant (ts 1/9) obtained by undiluted passage of fowl plague virus (FPV) at 33 degrees C carried a strong ts defect in RNA segment 6 [neuraminidase (NA) gene] and a weak ts defect in RNA segment 8 [non-structural (NS) protein] Although the viral proteins have normal migration rates, the NS gene migrated during polyacrylamide gel electrophoresis (PAGE) significantly faster than the NS gene of wild-type FPV, even after denaturation by glyoxal. Despite this observation, the NS gene of ts 1/9 did not carry a deletion as shown by sequence determination. There were only five base replacements which resulted in three changes in amino acids. Three of the base replacements led to a more compact secondary structure of RNA segment 8, which seems to be responsible for the faster migration rate during PAGE and which seems to resist, at least partially, the treatment with glyoxal.

Descriptors: influenza A virus avian genetics, mutation, RNA viral isolation and purification, amino acid sequence, base sequence, cultured cells, chick embryo, cloning, molecular, genes, structural, genes viral, hemagglutinins genetics, neuraminidase genetics, plasmids, viral genetics, RNA directed DNA polymerase metabolism.

**NAL Call Number:** 501 L84Pb

**Abstract:** Severe acute respiratory syndrome coronavirus (SARS-CoV) moved into humans from a reservoir species and subsequently caused an epidemic in its new host. We know little about the processes that allowed the cross-species transfer of this previously unknown virus. I discuss what we have learned about the movement of viruses into humans from studies of influenza A, both how it crossed from birds to humans and how it subsequently evolved within the human population. Starting with a brief review of severe acute respiratory syndrome to highlight the kinds of problems we face in learning about this viral disease, I then turn to influenza A, focusing on three topics. First, I present a reanalysis of data used to test the hypothesis that swine served as a "mixing vessel" or intermediate host in the transmission of avian influenza to humans during the 1918 "Spanish flu" pandemic. Second, I review studies of archived viruses from the three recent influenza pandemics. Third, I discuss current limitations in using molecular data to study the evolution of infectious disease. Although influenza A and SARS-CoV differ in many ways, our knowledge of influenza A may provide important clues about what limits or favours cross-species transfers and subsequent epidemics of newly emerging pathogens.

**Descriptors:** evolution, molecular, influenza transmission, influenza A virus physiology, models, biological, phylogeny, SARS virus physiology, zoonoses virology, influenza genetics, influenza A virus genetics, swine virology.


**NAL Call Number:** 396.8 AN7

**Abstract:** The main contributions of the author and collaborators about sialidase (EC 3.2.1.18) of influenza virus types A and B and O-acetylesterase (EC 3.1.1.53) of type C are summarized. After a short introduction on the topic, the negative results obtained by the author on inhibitors are commented. Then, the peculiarities of the three procedures assayed, based on the NADH determination as a measurement for the sialidase activity, are discussed. The spectrofluorimetric measurement of NADH concentration is a more sensitive and convenient procedure than that by spectrophotometry, although it is less sensitive than that based on bioluminescence. Sialidase activity is generally higher in influenza virus type A than in type B; however, some differences have been found between the three sub-types A analysed. Furthermore, thermal stability and stability against changes in the pH values are higher for influenza virus from ducks, followed by those from humans and, finally, by those from pigs. O-acetylesterase of influenza virus type C shows a broad specificity; it acts on O-acetyl-containing compounds which may not be sialic acids. It seems that this enzyme might contribute to facilitate the action of sialidase of influenza virus types A and B. The peculiarities of influenza virus type C suggest to include this type as a new genus in the future classification of viruses.

**Descriptors:** carboxylic ester hydrolases analysis, neuraminidase analysis, orthomyxoviridae enzymology, ducks, fowl plague enzymology, influenza enzymology, influenza A virus avian enzymology, human enzymology, porcine enzymology, influenza B virus enzymology, influenza virus C enzymology, orthomyxoviridae infections enzymology, swine.


**NAL Call Number:** 448.8 V81

**Descriptors:** disease outbreaks veterinary, influenza veterinary, influenza A virus avian classification, human classification, poultry diseases virology, antigens, viral genetics, antigens, viral immunology, cloning, molecular, genome, viral, hemagglutination inhibition tests, hemagglutinins viral genetics, Hong Kong epidemiology, influenza epidemiology, avian genetics, avian immunology, human genetics, human immunology, molecular sequence data, Pakistan epidemiology, phylogeny, poultry diseases epidemiology, sequence analysis, protein, viral proteins genetics, viral proteins immunology.

Capua, I., F. Mutinelli, and M.H. Hablovarid (2002). *Avian embryo susceptibility to Italian H7N1 avian influenza*

**NAL Call Number:** 448.3 Ar23

**Abstract:** In the present paper we report of the results of an immunohistochemical investigation to assess tissue tropism and viral replication in developing chicken, turkey, Muscovy duck and mallard duck embryos, of Italian H7N1 isolates belonging to different genetic lineages. LPAI isolates were chosen on the basis of the location in the phylogenetic tree: a progenitor strain, A/ty/Italy/977/V99, (exhibiting no additional glycosylation site, nAGS), strain A/ty/Italy/2379/V99 (AGS in position 123) and strain A/ty/Italy/3675/V99 (AGS in position 149) were selected. The latter two strains belonged to distinct lineages originating from the pool of progenitor strains. HPAI isolate A/ty/Italy/4580/V99 was also included in the study. All the embryos tested supported the growth of HPAI. The LPAI isolates replicated readily in the allantoic layer of the CAM of all the species tested, and did not grow in the developing chicken, turkey and Muscovy duck embryos. In contrast, they replicated to different extents in the respiratory tract of the developing mallard embryo, which also presented lower mortality rates than the other species. We conclude from these findings that the pathogenesis of LPAI infections in mallard embryos is different to that observed in other species, and should be investigated further.

**Descriptors:** allantois virology, chick embryo virology, chorion virology, influenza A virus avian pathogenicity, disease susceptibility, ducks, embryo loss etiology, glycosylation, immunohistochemistry, avian genetics, turkeys.


**NAL Call Number:** SF995.A1A9

**Descriptors:** avian influenza virus, disease control, disease prevention, disease resistance, experimental infection, immune response, vaccination, turkeys.


**NAL Call Number:** 448.3 Ar23

**Abstract:** Disulfiram at concentrations between 0.1 and 0.3 mM inhibits the multiplication of Semliki Forest virus (SFV), fowl plague virus (FPV), Newcastle disease virus (NDV), vesicular stomatitis virus (VSV), and pseudorabies virus (PRV), when administered 1 hour before and during adsorption. There is, however, no inhibition of virus multiplication, when the drug is added after adsorption onto chick embryo cells. Disulfiram interferes neither with the receptors of the virus nor of erythrocytes, and it does not prevent virus adsorption. Possibly an early step in virus multiplication is affected by disulfiram. Infected cells once treated with the drug recover after some time of incubation in an inhibitor-free medium. The inhibitory state can be maintained, however, if relatively low doses of disulfiram are present in the culture medium also after adsorption. Disulfiram has no effect on macromolecular synthesis of the host cells. It has, however, a marked affect on membrane function. While virus multiplication is readily inhibited by disulfiram when chick embryo or BHK cells were investigated, virus multiplication in HeLa cells is almost resistant against the action of disulfiram.

**Descriptors:** disulfiram pharmacology, herpesviridae growth and development, herpesvirus 1, suid growth and development, influenza A virus avian growth and development, Newcastle disease virus growth and development, Semliki Forest virus growth and development, vesicular stomatitis Indiana virus growth and development, virus replication drug effects, adsorption, ditiocarb pharmacology, erythrocytes drug effects, ethanol pharmacology, influenza A virus avian drug effects, Newcastle disease virus drug effects, pseudorabies drug therapy, Semliki Forest virus drug effects, tissue culture, vesicular stomatitis Indiana virus drug effects.


**NAL Call Number:** QR375.V6

**Abstract:** Influenza viruses of contrasting receptor specificity have been examined for their ability to infect receptor-modified MDCK cells containing sialyloligosaccharide receptor determinants of defined sequence.
Cells were treated with sialidase to remove sialic acid and render them resistant to infection and were then incubated with sialyltransferase and CMP-sialic acid to restore sialic acid in the SA alpha 2,6Gal or SA alpha 2,3Gal linkages. The viruses A/RI/5 + /57 and A/duck/Ukraine/1/63, previously shown to exhibit preferential binding of SA alpha 2,6Gal and SA alpha 2,3Gal linkages, respectively, were found to exhibit differential infection of the receptor-modified cells in accord with their receptor specificity. Coinfection of SA alpha 2,3Gal derivatized cells with a mixture of the two viruses resulted in selective propagation of the SA alpha 2,3Gal-specific A/duck/Ukraine/1/63 virus. The results demonstrate the potential for cell surface receptors to mediate selection of receptor-specific variants of influenza virus.

Descriptors: influenza A virus avian metabolism, human metabolism, oligosaccharides metabolism, receptors, virus metabolism, adsorption, antibodies, viral analysis, binding sites, cell line, dogs, erythrocytes microbiology, hemagglutinins viral, avian immunology, human immunology, kidney, neuraminidase metabolism, receptors, virus genetics, receptors, virus immunology, sialic acids metabolism, sialyltransferases metabolism, species specificity, viral proteins analysis.


Abstract: Incomplete influenza A virus (fowl plague Dobson strain) was prepared by undiluted passage in primary chick embryo fibroblast cells. Analysis of released virus RNA revealed a deficiency in RNA segments 1-3, characteristic of incomplete virus formation. The virus yield from a high multiplicity infection with standard virus always showed this deficiency, even when analysed as early as 6 hours post-infection, whereas infection at low multiplicity gave rise to virus indistinguishable in RNA composition from the parent virus. The relative amounts of intracellular, non-polyadenylated, complementary RNA (template RNA) were found to reflect accurately the eventual RNA composition of released virus, and were altered in phase with PFU:HAU ratio, throughout a von Magnus cycle.

Descriptors: defective viruses growth and development, influenza A virus avian growth and development, RNA viral biosynthesis, cultured cells, chick embryo, defective viruses physiology, fibroblasts, kinetics, probability.


Abstract: Nucleotide sequence analysis of the terminal virus-coded regions of a clone of the matrix gene of influenza virus indicated that the region corresponding to the 5' end of the mRNA contains an additional 13 non-virus coded nucleotides. Using the dideoxy-chain termination sequencing method with a restriction fragment derived from this clone, we have determined that the 5' ends of matrix gene mRNAs contain a heterogenous sequence of 9-15 nucleotides. In addition, the data indicate that the 3' terminal nucleotide of matrix gene virion RNA is not transcribed into mRNA, transcription of influenza virus-specific sequences commencing with the penultimate nucleotide at the 3' end of viron RNA.

Descriptors: influenza A virus avian analysis, RNA, messenger, viral, base sequence, cloning, molecular, DNA restriction enzymes, DNA, recombinant.


Abstract: The morphology of plaques induced by Italian, H7N1, low-pathogenic avian influenza (LPAI) viruses belonging to different lineages was investigated in primary chicken, turkey, Muscovy duck, and
mallard duck kidney cells and in MDCK cells in the absence of trypsin. LPAI isolates were selected on the basis of the location in the phylogenetic tree: 977/V99 (located at the root, no additional glycosylation site (nAGS)), 2379/V99 (AGS in position 123), and 3675/V99 (AGS in position 149). Different isolates did not induce plaques with a statistically significant different size in MDCK cells. However, in primary cells of different avian origin, the presence or absence of AGS significantly influenced plaque size. Generally speaking, 977/V99 was the least efficient at plaquing in all cells, while 2379/V99 (AGS in position 123) plaqued more efficiently in turkey cells and 3675/V99 (AGS in position 149) in chicken cells. The presence of either AGS induced statistically significant larger plaques in cells of waterfowl origin.

Descriptors: cell biology, infection, avian influenza, infectious disease, respiratory system disease, viral disease, cell culture culturing techniques, laboratory techniques, glycosylation sites plaque morphology.


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**Descriptors:** poultry, avian influenza virus, DNA, nucleotide sequence, molecular cloning, acids, domestic animals, genetic engineering, genomes, influenza virus, livestock, nucleic acids, nucleic compounds, organic acids, orthomyxoviridae, useful animals, viruses.


**NAL Call Number:** 448.8 P942

**Descriptors:** influenza A virus avian isolation and purification, cellulose, chromatography, ion exchange.


**NAL Call Number:** 475 Ex7

**Descriptors:** abo blood group system analysis, antigens analysis, erythrocytes immunology, fetal membranes immunology, haptens analysis, immunodiffusion, immunoelectrophoresis, influenza A virus avian immunology, kidney immunology, Newcastle disease virus immunology, parainfluenza virus 1, human immunology, guinea pigs, immunity, cellular, methods, rabbits, rats.


**NAL Call Number:** 448.8 P942

**Descriptors:** influenza A virus avian analysis, Newcastle disease virus analysis, viral proteins analysis, antigens, viral analysis, centrifugation, density gradient, electrophoresis, disc, immunodiffusion.


**NAL Call Number:** 448.8 P942

**Descriptors:** antigens analysis, influenza A virus avian immunology, Newcastle disease virus immunology, orthomyxoviridae immunology, parainfluenza virus 1, human immunology, antigens, viral analysis, guinea pigs, immunodiffusion, immunoelectrophoresis, rabbits, rats, species specificity.


**NAL Call Number:** QH431.A1G4

**Abstract:** Mutagenic potential of the influenza virus was evaluated. Based on its capacity of inducing recessive lethal mutations in the X chromosome of *Drosophila melanogaster*, the influenza virus can be classified as a moderate-activity mutagen. Its mutagenicity does not depend on ability to reproduce in the cell system. This virus was shown to disrupt formation of the wing, particularly wing vein M1 + 2. Cytogenetic examination of polytene X chromosomes bearing recessive lethal mutations in *Drosophila* salivary glands did not reveal chromosome rearrangements. These lethals are assumed to be small deletions or point mutations. The determination of the lethal activity stage of these mutations showed that they disrupt the expression of genes functioning at various developmental stage of *Drosophila*. Two of them were conditionally lethal (temperature-sensitive). Two of 15 mutations analyzed were mapped to region 2B9-10-3C10-11.

**Descriptors:** *Drosophila melanogaster* genetics, *Drosophila melanogaster* virology, influenza A virus avian genetics, mutagenesis, X chromosome genetics, genes, lethal, genes, recessive, point mutation.


**NAL Call Number**: SF604.C54

**Abstract**: The spleen of BALB/c mice, which had been immunized five times with purified avian influenza virus, H5N9 strain, and had good antibody response, was harvested; the spleen cells were fused with NS-1 myeloma cells. After a screening for specific antibody production with the ELISA test, 18 of 460 wells showed strong positive reactions. Three further subclonings established nine strains of hybridoma with stable activities of secreting monoclonal antibodies. The isotypes of the nine monoclonal antibodies were all IgG1, and all their light chains also belong to the kappa chain. The antibodies were applied on CEF cultures infected with AIV H5N9 by means of indirect fluorescent antibody staining. Fluorescence was observed among the cell cytoplasm only. All monoclonal antibodies had HI and neutralization abilities, but formed no precipitation line in an immunodiffusion test. One antibody reacted with viral polypeptide, which was HA2 antigen with molar mass 28 kD, according to the western blotting test. In order to detect the specificity, we reacted the monoclonal antibody with AIV subtypes H1 through H12, respectively, according to the HI test. Besides H5N9, the antibody reacted with strain H8N4, but not H8N6. Viral protein analysis by means of SDS-PAGE revealed that both H5N9 and H8N4 had common peptide bands 69, 57, 48, 37 and 28 kD, especially the peptide of HA2, 28 kD.

**Descriptors**: immune system, infection, microbiology, pathology, pharmacology, veterinary medicine, vaccination viral protein analysis.


**NAL Call Number**: 448.8 P942

**Descriptors**: antiviral agents pharmacology, deoxyribonucleases pharmacology, histones pharmacology, ribonucleases pharmacology, adenoviridae drug effects, adenoviridae infections drug therapy, antiviral agents therapeutic use, aphthovirus drug effects, conjunctivitis drug therapy, DNA, viral biosynthesis, deoxyribonucleases therapeutic use, encephalitis virus, Venezuelan equine drug effects, encephalitis viruses, tick borne drug effects, herpesviridae infections drug therapy, histones therapeutic use, influenza A virus avian drug effects, keratitis, dendritic drug therapy, meningitis, viral drug therapy, Newcastle disease virus drug effects, orthomyxoviridae drug effects, polioviruses drug effects, RNA viral biosynthesis, ribonucleases therapeutic use, simplexvirus drug effects, vaccinia virus drug effects, vesicular stomatitis Indiana virus drug effects, virus replication drug effects.


**NAL Call Number**: QR375.V6

**Abstract**: Twenty-four H1N2 influenza A viruses were newly isolated from pigs in the United States. These isolates originated from 19 farms in 9 different swine producing states between 1999 and 2001. All farms had clinical histories of respiratory problem and/or abortion. The viral isolates were characterized genetically to determine the origin of all eight gene segments. The results showed that all H1N2 isolates were reassortants of classical swine H1N1 and triple reassortant H3N2 viruses. The neuraminidase (NA) and PB1 genes of the H1N2 isolates were of human origin, while the hemagglutinin (HA), nucleoprotein (NP), matrix (M), non-structural (NS), PA and PB2 polymerase genes were of avian or swine origin. Fifteen of the 24 H1N2 isolates were shown to have a close phylogenetic relationship and high amino acid homology with the first US isolate of H1N2 (A/SW/IN/9K035/99). The remaining nine isolates had a close phylogenetic relationship with classical swine influenza H1N1 in the HA gene. All other genes including NA, M, NP, NS, PA, PB1 and PB2 showed a close phylogenetic relationship with the H1N2 (A/SW/IN/9K035/99) strain and triple reassortant H3N2 viruses. However, PB1 genes of two isolates (A/SW/KS/13481-S/00, A/SW/KS/13481-T/00) were originated from avian influenza A virus lineage. These results suggest that although there are some variations in the HA genes, the H1N2 viruses prevalent in the US swine population are of a similar genetic lineage.

**Descriptors**: influenza A virus, porcine genetics, antigens, viral, hemagglutinin glycoproteins, influenza virus genetics, porcine classification, porcine enzymology, porcine isolation and purification, molecular sequence data, neuraminidase genetics, phylogeny, swine, United States, variation genetics.
NAL Call Number: 442.9 So1
Descriptors: orthomyxoviridae isolation and purification, centrifugation, density gradient, centrifugation, zonal, influenza A virus avian isolation and purification, methods, Newcastle disease virus isolation and purification, sucrose.

NAL Call Number: 448.8 V81
Abstract: Amantadine treatment of cells infected with H7 strains of influenza A viruses causes an M2 protein-mediated conversion of hemagglutinin (HA) from its native to its low pH conformation. Immunofluorescence and electron microscopic observations showed that the structural alteration and hence drug action occur shortly after HA exits from the Golgi complex during its passage through the trans Golgi region. Using the DAMP/anti-DNP pH probe it is evident that virus infection causes increased acidity of the trans Golgi region and that vesicles containing low pH HA in amantadine-treated virus-infected cells are particularly acidic. These results indicate therefore that the alteration in HA is the direct consequence of exposure to an adverse low pH and provide further support for the conclusion that the M2 protein, the target of amantadine action, is involved in regulating vesicular pH, a function important for the correct maturation of the HA glycoprotein.
Descriptors: amantadine pharmacology, Golgi apparatus metabolism, hemagglutinins viral chemistry, influenza A virus avian drug effects, cell compartmentation, cultured cells, fluorescent antibody technique, hemagglutinin glycoproteins, influenza virus, hemagglutinin viral drug effects, hemagglutinins viral metabolism, hydrogen-ion concentration, avian ultrastructure, microscopy, immunoelectron, monensin pharmacology, protein conformation drug effects, temperature.

NAL Call Number: QR375.V6
Abstract: Inhibition of the function of the M2 protein by amantadine can cause a conformational change in the haemagglutinin (HA) of H7 influenza A viruses and the consequent expression of the low pH form of the glycoprotein on the surface of virus-infected cells. Immunofluorescence studies showed that this conversion occurs shortly after HA exits from the Golgi complex apparently during its transport through the trans Golgi network and using the pH probe, DAMP/anti-DNP, that it is the direct result of reduced vesicular pH. The lowest pHs encountered were estimated using mutant HAs differing in pH stability to be approximately 5.2 and 5.6 in virus-infected CEF or MDCK cells, respectively, in the absence of functional M2. Depending on the particular M2, this protein was responsible for increases in vesicular pH of up to 0.8 units. The influence of mutations in both HA and M2 on the maturation of native HA illustrates the important relationship between the structural and functional properties of these two proteins. Using the fluorescent probe SNARF-1 the M2 protein was also shown to be largely responsible for the 0.3-0.4 unit reduction in intracellular pH of virus-infected cells. The data thus provide further evidence for the pH regulatory function of M2 and its importance for the maturation of the HA glycoprotein.
Descriptors: influenza A virus avian physiology, viral matrix proteins physiology, amantadine pharmacology, cell line, fluorescent antibody technique, hemagglutination, viral, hydrogen-ion concentration.

NAL Call Number: 448.3 AC85
Descriptors: cell nucleus microbiology, cultured cells microbiology, cytoplasm microbiology, influenza A virus avian growth and development, orthomyxoviridae growth and development, cell membrane

**NAL Call Number:** QR46.J6

**Abstract:** We compared the abilities of the six internal RNA segments of two avian influenza viruses, A/Mallard/Alberta/88/76 (H3N8) and A/Mallard/NY/6750/78 (H2N2), to confer attenuation on wild-type human influenza A/Bethesda/1/85 (H3N2) virus in seronegative adult volunteers. Live avian-human influenza A reassortant virus vaccines derived from either avian virus parent were comparable in the following properties: safety, infectivity, immunogenicity, and genetic stability. Since the avian influenza A/Mallard/Alberta/76 virus offered no clear advantage as a donor virus, we will conduct our future evaluations on live influenza A virus reassortants derived from the more extensively characterized avian influenza A/Mallard/NY/78 virus.

**Descriptors:** antibodies, viral biosynthesis, influenza prevention and control, influenza A virus avian immunology, human immunology, influenza vaccine immunology, dose response relationship, immunologic, electrophoresis, polyacrylamide gel, enzyme linked immunosorbent assay, genes viral, hemagglutination inhibition tests, avian genetics, avian physiology, human genetics, human physiology, influenza vaccine adverse effects, vaccines, attenuated adverse effects, vaccines, attenuated immunology, vaccines, synthetic adverse effects, vaccines, synthetic immunology, virus replication.


**NAL Call Number:** QR46.J6

**Abstract:** A reassortant influenza A virus was produced by mating an avian influenza A/Pintail/Alberta/119/79 (H4N6) virus with wild-type human influenza A/Washington/897/80 (H3N2) virus. The avian-human influenza A reassortant virus contained the genes coding for the hemagglutinin and neuraminidase surface antigens of the human influenza wild-type virus and the six other RNA segments (internal genes) of the avian influenza A virus donor. In the lower respiratory tract of squirrel monkeys, this avian-human influenza reassortant virus, like its avian influenza A parent virus, was restricted approximately 100-fold in replication compared with the wild-type human influenza A virus. Despite this restriction of replication, infection of monkeys with the avian-human influenza A reassortant virus induced resistance to wild-type human influenza A virus challenge. In comparison with the wild-type human influenza A virus, the avian-human influenza A reassortant was also fully attenuated when 10(5.5) to 10(7.5) 50% tissue culture infective doses were administered to susceptible adult volunteers. Attenuation was indicated by a more than 300-fold reduction in virus shedding and lack of reactogenicity. The reassortant virus did not spread to susceptible contacts and could not be isolated from the blood or stools of infected adults. The 50% human infectious dose was 10(6.2) 50% tissue culture infective dose, indicating that this reassortant virus is only slightly less infectious for adults than a similarly derived avian-human influenza A/Washington/80 X A/Mallard/78 reassortant virus. These findings suggest that the avian influenza A/Pintail/79 virus may be a satisfactory donor of attenuating genes for production of live, attenuated avian-human influenza A reassortant virus vaccines.

**Descriptors:** influenza A virus human immunology, immunology, influenza vaccine immunology, adolescent, adult, genes viral, influenza immunology, influenza prevention and control, human genetics, genetics, influenza vaccine adverse effects, saimiri, vaccines, attenuated adverse effects, vaccines, attenuated immunology, virus replication.

Abstract: The transfer of six internal RNA segments from the avian influenza A/Mallard/New York/6750/78 (H2N2) virus reproducibly attenuates human influenza A viruses for squirrel monkeys and adult humans. To identify the avian influenza A virus genes that specify the attenuation and host range restriction of avian-human (ah) influenza A reassortant viruses (referred to as ah reassortants), we isolated six single-gene reassortant viruses (SGRs), each having a single internal RNA segment of the influenza A/Mallard/New York/6750/78 virus and seven RNA segments from the human influenza A/Los Angeles/2/87 (H3N2) wild-type virus. To assess the level of attenuation, we compared each SGR with the A/Los Angeles/2/87 wild-type virus and a 6-2 gene ah reassortant (having six internal RNA segments from the avian influenza A virus parent and two genes encoding the hemagglutinin and neuraminidase glycoproteins from the wild-type human influenza A virus) for the ability to replicate in seronegative squirrel monkeys and adult human volunteers. In monkeys and humans, replication of the 6-2 gene ah reassortant was highly restricted. In humans, the NS, M, PB2, and PB1 SGRs each replicated significantly less efficiently (P less than 0.05) than the wild-type human influenza A virus parent, suggesting that each of these genes contributes to the attenuation phenotype. In monkeys, only the NP, PB2, and possibly the M genes contributed to the attenuation phenotype. These discordant observations, particularly with regard to the NP SGR, indicate that not all genetic determinants of attenuation of influenza A viruses for humans can be identified during studies of SGRs conducted with monkeys. The PB2 and M SGRs that were attenuated in humans each exhibited a new phenotype that was not observed for either parental virus. Thus, it was not possible to determine whether avian influenza virus PB2 or M gene itself or a specific constellation of avian and human influenza A virus specified restriction of virus replication in humans.

Descriptors: influenza A virus avian genetics, human genetics, adult, base sequence, genes viral, human pathogenicity, human physiology, influenza vaccine isolation and purification, molecular sequence data, RNA viral genetics, saimiri, transfection, vaccines, attenuated isolation and purification, virulence genetics, virus replication genetics.


Abstract: Using horseradish peroxidase (HRP)-conjugated lectins for pre-embedding labelling we have shown differences in ultrastructural localization of saccharides in cell compartments of fowl plague (FP) virus-infected and uninfected MDCK cells. Lectinochemical staining of the cell compartments in the case of FP virus-infected MDCK cells was less intensive as compared with uninfected cells. Also certain differences in the staining of subcompartments of cell organelles were seen. Staining of uninfected cells with Pisum sativum agglutinin (PSA)-HRP revealed an extensive visualization of Golgi complex, mainly its cis-part, TGN vesicles and lysosomes. Staining of FP virus-infected cells with the same lectin marked very lightly rough endoplasmic reticulum and not at all the Golgi complex. Staining with Erythrina cristagalli agglutinin (ECA)-HRP revealed a picture very similar to PSA-HRP staining of uninfected and FP virus-infected cells. The differences in the lectinochemical staining of cell organelles of FP virus-infected and uninfected cells may be connected with the inhibition of cell protein synthesis during FP virus morphogenesis.

Descriptors: influenza A virus avian chemistry, plant lectins, antibodies, monoclonal immunology, cell line, dogs, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral metabolism, hemagglutinins viral ultrastructure, immunoenzyme techniques, avian ultrastructure, lectins metabolism.


Abstract: The replicative abilities and tissue tropism properties of 13 non-pathogenic or low-pathogenic waterfowl-origin type A influenza isolates recovered in 1986 were examined in chickens. Following intravenous challenge, reisolation of challenge virus was attempted from swabs of the luminal surfaces of the cloaca, jejunum, ileum, bursa, trachea, and air sacs and from swabs of bone marrow and liver tissues. Virus-isolation attempts were also accomplished on brain, thymus, spleen, pancreas, gonad, kidney, blood, and lung tissues. The overall frequency of influenza virus recovery for each experiment ranged from 3.1% to
For all experiments combined, 58.3% of the kidney tissues and 62.9% of the cloacal swab samples collected on days 1 to 10 postinoculation were positive for challenge virus recovery. Virus titers up to 10(8.7) mean embryo infective dose per gram of kidney tissue were demonstrated in clinically normal chickens. Distinct biological variations and nephrotropism appear to exist among the corporate properties of virus populations making up each of the 13 waterfowl-origin type A influenza isolates.

Descriptors: chickens, fowl plague microbiology, influenza A virus avian physiology, virus replication, antibodies, viral blood, chick embryo, cloaca microbiology, avian immunology, avian isolation and purification, kidney microbiology, serial passage, specific pathogen free organisms.


NAL Call Number: 448.8 V81

Abstract: The receptor specificity of 56 H2 and H3 influenza virus isolates from various animal species has been determined to test the relevance of receptor specificity to the ecology of influenza virus. The results show that the receptor specificity of both H2 and H3 isolates evaluated for sialic acid linkage specificity and inhibition of hemagglutination by horse serum correlates with the species of origin, as postulated earlier for H3 strains based on a limited survey of five human, three avian, and one equine strain. Elucidation of the amino acid sequence of several human H2 receptor variants and analysis of known sequences of H2 and H3 isolates revealed that receptor specificity varies in association with an amino acid change at residues 228 in addition to the change at residue 226 previously documented to affect receptor specificity of H3 but not H1 isolates. Residues 226 and 228 are leucine and serine in human isolates, which preferentially bind sialic acid alpha 2,6-galactose beta 1,4-N-acetyl glucosamine (SA alpha 2,6Gal), and glutamine and glycine in avian and equine isolates, which exhibit specificity for sialic acid alpha-2,3-galactose beta-1,3-N-acetyl galactosamine (SA alpha 2,3Gal). The results demonstrate that the correlation of receptor specificity and species of origin is maintained across both H2 and H3 influenza virus serotypes and provide compelling evidence that influenza virus hosts exert selective pressure to maintain the receptor specificity characteristics of strains isolated from that species.

Descriptors: influenza A virus avian metabolism, human metabolism, metabolism, receptors, virus metabolism, amino acid sequence, amino acids genetics, carbohydrate sequence, chick embryo, hemagglutinin glycoproteins, influenza virus, hemagglutiniins viral genetics, molecular sequence data, species specificity, viral envelope proteins genetics.


NAL Call Number: QR360.J6

Abstract: Cytoplasmic poly (A)-rich RNA extracted from fowl plague virus-infected cells was found to program efficiently the translation of two major peptides in the wheat germ cell-free system. These peptides have the same electrophoretic mobility, on polyacrylamide gels, as the two major virion proteins M and NP. [35S] methionine tryptic peptide analysis by one-dimensional thin-layer ionophoresis and finger printing by two-dimensional thin-layer ionophoresis and chromatography show a high degree of similarity between the two in vitro products and the authentic viral proteins M and NP. Although virion RNA is devoid of any poly (A) sequence, it is confirmed here that the viral complementary cytoplasmic RNA contains poly (A) stretches of varying lengths. Intact purified virion was found to promote the synthesis of very low amounts of the same NP and M proteins in this cell-free system. Quantitative aspects of data would indicate that this is due to minute amounts of complementary viral RNA associated with the virion or with the virion RNA itself. In conclusion, it is shown directly by cell-free translation of authentic viral products that the influenza virion is "negative stranded" (Baltimore, 1971), at least for its two major structural proteins.

Descriptors: influenza A virus avian metabolism, RNA, messenger metabolism, RNA viral metabolism, translation, genetic, cell free system, glycoproteins biosynthesis, avian analysis, peptide synthesis, plant extracts, poly A analysis, RNA, messenger analysis, viral analysis, tissue culture, triticum, viral proteins biosynthesis.


**Abstract:** A cell-free coupled system for the transcription and translation of fowl plague virus RNA is described. The system utilizes a new nuclease-preincubated rabbit reticulocyte lysate that has a high sensitivity to exogenous mRNA and a very low level of nuclease activity. Translation of the viral proteins in the coupled system is strictly dependent upon the viral transcriptase activity. In the coupled system the optimal concentration of magnesium is intermediate between the optimum for transcription and that for translation. Translation of the viral proteins seems faithful. The products represent the major viral peptides M and NP and two peptides with the same electrophoretic mobility as HA and P2. Viron NA is not resolved in the kind of polyacrylamide gels described. Proteins M and NP were immunoprecipitable with monospecific antisera. It is concluded that the virion-associated RNA polymerase transcribes the negative-stranded segments of the viral genome coding for these major structural proteins into fully functional mRNA's.

**Descriptors:** influenza A virus avian metabolism, RNA viral metabolism, transcription, genetic, translation, genetic, cell free system, avian enzymology, magnesium metabolism, oligonucleotides pharmacology, peptide synthesis, RNA replicase metabolism, messenger metabolism, viral biosynthesis, rabbits, reticulocytes, viral proteins biosynthesis.


**Abstract:** The multiplication of Ulster 73 virus, an avian strain of type A influenza virus, was blocked in chick embryo fibroblast cells, CEF, by treatment with 0.5 microg/ml of chromomycin A3 whereas in LLC-MK2 cells no inhibition of replication was observed. Virus-induced polypeptide synthesis in chick embryo fibroblast cells was confined to the synthesis of PB2, PB1 and PA subunits of the RNA dependent-RNA polymerase, the nucleoprotein NP, the non-structural protein NS1, the haemagglutinin HA, the non-structural protein NS2; only the membrane M1 polypeptide synthesis was greatly inhibited. Viral unpolyadenylated cRNAs synthesis was studied at a late time of the infection, 8 hours p.i.: chromomycin A3 was able to inhibit the "novo" synthesis of complementary RNA poly(A)- and segment 7 of virion RNA. The mode of action of the drug in chick embryo fibroblast cells is discussed.

**Descriptors:** chromomycin A3 pharmacology, fibroblasts drug effects, influenza A virus avian drug effects, nucleic acid synthesis inhibitors pharmacology, virus replication drug effects, cell line, chick embryo, electrophoresis, polyacrylamide gel, fibroblasts virology, avian physiology, RNA viral biosynthesis, RNA viral genetics, virus cultivation.


**Abstract:** We investigated acylation of haemagglutinin (HA) of type A influenza viruses during infection of permissive chick embryo fibroblasts (CEF) treated with cerulenin. Fatty acid binding was monitored using a maintenance medium containing 3H-palmitic acid. Our results suggest that fatty acid acylation of viral haemagglutinin may be essential for production of mature viral particles. Indeed, palmitoylation was found in infected CEF cells, but was lacking during the infectious cycle when cells were treated with a dose of 30 micrograms/ml of cerulenin. We discuss the possibility that acylation of virus-induced HA is a posttranslational modification regulating correct insertion of virus haemagglutinin into the cellular membrane.
and, as a consequence, controlling the maturation of budding influenza virus.

Descriptors: antiviral agents pharmacology, cerulenin pharmacology, influenza A virus avian drug effects, virion drug effects, acylation, cells, cultured, chick embryo, dose response relationship, drug, fatty acids metabolism, fibroblasts cytology, hemagglutinin glycoproteins influenza virus, hemagglutinins viral metabolism, avian metabolism, avian physiology, virus replication drug effects.


Abstract: The growth cycle of influenza virus strain FPV, Ulster 73, was altered by treatment of LLC-MK2 cells with diamidinophenylindole. Viral protein synthesis was restricted to the early pattern of virus multiplication, and post-treatment experiments showed the ability of the drug to block virus replication until the 4th hour p.i. Drug addition (followed by removal) revealed the inhibition of synthesis of late viral products, and especially of membrane protein. Kinetic studies on the production of viral RNA indicated a decrease in the synthesis of late virus-induced RNA species, suggesting that the target of DAPI is probably the late transcription of the virus genome. The nonpermissive condition mediated by the drug could represent a suitable model to study cellular intervention during viral growth.

Descriptors: indoles pharmacology, influenza A virus avian growth and development, virus replication drug effects, capsid genetics, gene expression regulation drug effects, avian genetics, RNA viral biosynthesis, RNA viral genetics, time factors, viral core proteins genetics, viral nonstructural proteins.


Abstract: When KB cells were infected either with the fowl plague (FPV) Rostock strain (Hav1N1) or the WSN (H0N1) strain of influenza A virus the yield of cell-associated haemagglutinin and neuraminidase polypeptides was essentially comparable, but virus particles were not produced in the FPV-KB system. WSN virus-infected KB cells synthesized normal amounts of mature virus particles and had all the characteristics of a permissive replication cycle. Biosynthesis and transport of RNP antigen from nucleus to cytoplasm of infected cells were traced by immunofluorescent staining at 4 and 8 hours after the beginning of infection. While the fluorescent-stained material was totally confined to the nuclei in FPV-infected KB cells, RNP antigen migrated out of the nucleus during the replicative cycle of WSN virus in the same host cell. Patterns of virus-specific protein synthesis were studied by pulse-labelling with 35S-methionine. The most significant feature concerned the amplification of synthesis of virus-induced matrix (M) protein which did not occur in FPV-infected cells but occurred normally during WSN infection. The different patterns of replication in the same host cell when infected by different influenza A viruses is discussed.
Descriptors: influenza A virus avian growth and development, human growth and development, cell line, cytopathogenic effect, viral, hemagglutinins viral analysis, avian metabolism, human metabolism, neuraminidase metabolism, ribonucleoproteins metabolism, viral proteins biosynthesis, virus replication.

NAL Call Number: 448.3 Ar23
Abstract: The M protein of avian, but not human, strains of influenza A viruses is synthesized in infected chicken erythrocytes. In dual infections an avian strain complemented the human virus and both the human and avian M proteins were expressed.
Descriptors: erythrocytes microbiology, influenza A virus avian metabolism, human metabolism, viral proteins biosynthesis, chick embryo, dactinomycin pharmacology, avian growth and development, human growth and development.

NAL Call Number: QR1.I57
Abstract: Chicken erythrocytes can be infected by the fowl plague (Rostock) strain (FP/R) of influenza type A, Newcastle disease virus (NDV), and Semliki Forest virus (SFV). Only NDV and SFV produced infectious progeny, albeit at low levels. Infection by FP/R was monitored by de novo synthesis of viral proteins, and the proteins synthesized could be identified by comparison with infected chicken fibroblast cells. FP/R synthesized far greater amounts of viral protein than did NDV or SFV.
Descriptors: erythrocytes microbiology, chick embryo, hemagglutinins viral analysis, influenza A virus avian growth and development, avian metabolism, leukocytes microbiology, neuraminidase metabolism, Newcastle disease virus growth and development, Newcastle disease virus metabolism, Semliki Forest virus growth and development, Semliki Forest virus metabolism, viral proteins biosynthesis.

NAL Call Number: QR46.J6
Abstract: A simple molecular technique for rapid genotyping was developed to monitor the internal gene composition of currently circulating influenza A viruses. Sequence information from recent H1N1, H3N2, and H5N1 human virus isolates was used to identify conserved regions within each internal gene, and gene-specific PCR primers capable of amplifying all three virus subtypes were designed. Subtyping was based on subtype-specific restriction fragment length polymorphism (RFLP) patterns within the amplified regions. The strategy was tested in a blinded fashion using 10 control viruses of each subtype (total, 30) and was found to be very effective. Once standardized, the genotyping method was used to identify the origin of the internal genes of 51 influenza A viruses isolated from humans in Hong Kong during and immediately following the 1997-1998 H5N1 outbreak. No avian-human or H1-H3 reassortants were detected. Less than 2% (6 of 486) of the RFLP analyses were inconclusive; all were due to point mutations within a restriction site. The technique was also used to characterize the internal genes of two avian H9N2 viruses isolated from children in Hong Kong during 1999.
Descriptors: genes viral, influenza virology, influenza A virus human classification, human genetics, polymorphism, restriction fragment length, disease outbreaks, Hong Kong, avian classification, avian genetics, avian isolation and purification, human isolation and purification, reverse transcriptase polymerase chain reaction.

NAL Call Number: 381 B522
Abstract: The anomeric specificity of six sialidases (Vibrio cholerae, Arthrobacter ureafaciens, Clostridium
perfringens, Newcastle disease virus, fowl plague virus and influenza A2 virus sialidases) was assessed with sialylated antifreeze glycoprotein, ovine submandibular gland glycoprotein and alpha 1-acid glycoprotein, resialylated specifically in alpha(2-3) or alpha(2-6) linkage with N-acetylneuraminic acid or N-glycolylineuraminic acid using highly purified sialytransferases. The rate of release of sialic acid from these substrates was found to correlate well with the specificity observed earlier with the same sialidases using small oligosaccharide substrates, i.e., alpha(2-3) glycosidic linkages are hydrolyzed faster than alpha(2-6) linkages, with the exception of the enzyme from A. ureafaciens. Sialidase activity was higher with N-acetylneuraminic acid when compared with N-glycolylineuraminic acid. The studies also showed that the core oligosaccharide and protein structure in glycoproteins may influence the rate of release for different glycosidic linkages.

Descriptors: glycoproteins metabolism, neuraminidase metabolism, sialic acids metabolism, arthrobacter enzymology, Clostridium perfringens enzymology, influenza A virus avian enzymology, enzymology, Newcastle disease virus enzymology, structure activity relationship, substrate specificity, vibrio cholerae enzymology.


Abstract: 1. The action of sialidases from Newcastle disease virus (NDV), influenza A2 virus (IA2V) and fowl plague virus (FPV) on sialyloligosaccharide substrates containing alpha 2-3, alpha 2-6 or alpha 2-8 linkages was studied. 2. In all cases 2-3-linked sialic acids were preferentially released. Compared with II6Neu5AcLac, all 2-6-linked substrates, including sialyl-N-acetyllactosamine and its asparaginyl derivative, a urinary hexasaccharide and Neu5Ac(2-6)GalNAc were cleaved at improved rates by NDV and less by FPV sialidases. In the case of IA2V sialidase the asparaginyl oligosaccharide was very poorly cleaved, illustrating a variation in viral strain specificity. 3. A decrease in relative rates was observed in the order NDV greater than IA2V greater than FPV for substrates with 2-3 linkages relative to II6Neu5AcLac. The greatest relative rate was 470-fold higher. The 2-3-linked sialyl-N-acetyllactosaminylasparagine and IV3Neu5AcLcOse4 were poor substrates for the IA2V sialidase, but the rates were greater than with the 2-6 linked substrates. 4. The ganglioside substrate II3Neu5AcLacCer showed lower activity than its oligosaccharide analogue, but neither II3Neu5AcGgOse4Cer nor its oligosaccharide were substrates. 5. The Km values for 2-6-linked substrates were generally of the order 10 mM while those for the 2-3-linked substrates were approximately 1 mM. The V values were consistently higher for the 2-3-linked substrates. IV3Neu5AcLcOse4 showed high Km and very high V values, while the 2-8-linked disialyllactose showed this trend only with NDV enzyme, the IA2V and FPV sialidases exhibiting high Km and low V values. 6. The results are discussed in the light of the current knowledge of viral sialidase specificity and relative to the binding of virus particles to cell surfaces.

Descriptors: neuraminidase metabolism, oligosaccharides metabolism, viruses enzymology, colorimetry, glycoproteins metabolism, influenza A virus avian enzymology, enzymology, kinetics, Newcastle disease virus enzymology, species specificity, substrate specificity.


NAL Call Number: 448.8 V81

Descriptors: DNA analysis, influenza A virus avian analysis, nucleic acid hybridization, RNA, ribosomal analysis, viral analysis, bromelains pharmacology, genes, avian drug effects, avian isolation and purification, kinetics, temperature, transcription, genetic.


NAL Call Number: 41.8 Av5

Abstract: Vaccination against highly pathogenic (HP) subtypes of avian influenza (AI) virus in poultry has been prohibited in the United States. Recently, policy has been changed to potentially allow use of inactivated vaccines in emergency programs to control HP H5 and H7 AI. Vaccination with inactivated virus
against non-highly pathogenic AI viruses has been allowed in the U.S. turkey industry since 1979 (1) but requires expensive handling of individual birds for parenteral inoculation. Oral immunization would provide a less expensive method to protect commercial poultry from AI. Prime candidates for oral vaccines are waterfowl-origin (WFO) isolates, which have a tropism for the alimentary tract. One WFO isolate, A/mallard/Ohio/556/1987 (H5N9) (MOh87), was characterized by determining the complete nucleotide sequence of its hemagglutinin (HA) gene. The HA protein of this isolate possessed a deduced amino acid sequence nearly identical to the consensus amino acid sequence for all published H5 genes, indicating that it has potential as a broadly effective vaccine. Experimental results demonstrated measurable serum antibody responses to orally delivered live and inactivated preparations of MOh87. Oral vaccination also protected chickens from diverse, lethal H5 AI virus challenge strains and blocked cloacal shedding of challenge virus.

Descriptors: avian influenza virus, chickens, hemagglutinins, immunization, oral administration, genes, oral vaccination, virulence, live vaccines, inactivated vaccines, experimental infections, strain differences, nucleotide sequences, amino acid sequences, immune response, molecular sequence data, GENBANK u67783.


NAL Call Number: 448.8 V81

Abstract: Using a genetic system that allows the in vivo reconstitution of active ribonucleoproteins, the ability to ensure transcription/replication of a viral-like reporter RNA harboring the G(3) -> A(3), U(5) -> C(5), and C(8) -> U(8) mutations (triple 3-5-8 mutations) in the 3' arm of the promoter was examined with core proteins from human or avian strains of influenza A viruses. The efficiency of transcription/replication of the viral-like RNA with the triple 3-5-8 mutations in COS-1 cells was found to be slightly decreased as compared to the wild-type RNA when the polymerase was derived from a human virus. In contrast, it was found to be considerably increased when the polymerase was derived from an avian virus, in agreement with published observations using the avian A/FPV/Bratislava virus (G. Neumann and G. Hobom, 1995, J. Gen. Virol. 76, 1709-1717). This increase could be attributed to the compensation of the defect in transcription/replication activity in the COS-1 mammalian cell line due to the presence of a glutamic acid at PB2 residue 627, characteristic of avian strains of influenza viruses. Our results thus suggest that PB2 and/or cellular proteins interacting with PB2 could be involved in RNA conformational changes during the process of transcription/replication.

Descriptors: DNA directed RNA polymerases physiology, influenza A virus avian enzymology, human enzymology, promoter regions genetics, viral chemistry, transcription, genetic, viral proteins chemistry, virus replication, amino acid sequence, base sequence, cos cells, molecular sequence data, mutation, nucleic acid conformation, viral biosynthesis.


NAL Call Number: 448.8 V81

Descriptors: defective viruses analysis, influenza A virus avian, RNA viral analysis, defective viruses growth and development, defective viruses metabolism, viral proteins biosynthesis.


NAL Call Number: QP501.E8

Abstract: Chick embryo cells infected with an influenza A (fowl plague) virus have been labelled with (3H)-uridine for different lengths of time. Virion RNA and cellular RNA have been separated by specific hybridization with a surplus of unlabelled viral complementary RNA and RNase digestion. The ratio of the specific radioactivity in the UMP and CMP moieties of both types of RNA has been determined. Since the rate of approach to equilibrium of CMP to UMP labelling of both types of RNA is completely different it is
concluded that cellular and virion RNA are synthesized using different pyrimidine nucleoside triphosphate pools.

Descriptors: influenza A virus avian metabolism, pyrimidine nucleotides metabolism, RNA biosynthesis, RNA viral biosynthesis, cells cultured, chick embryo, nucleic acid hybridization, transcription, genetic, uridine metabolism.


NAL Call Number: QR360.A1J6

Abstract: The amino acid sequence of the haemagglutinin of A/equine/Miami/63 (H3N8), the prototype influenza virus of the H3 subtype from horses, is deduced from the nucleotide sequence of virus RNA and compared with the sequences of haemagglutinins of viruses of this subtype isolated from humans [X-31 (H3N2)] and from birds [A/duck/Ukraine/63 (H3N8)] and with the sequence of the haemagglutinin of A/equine/Fontainebleau/79 (H3N8) a virus isolated from a recent outbreak of equine influenza. The amino acid sequence differences detected are discussed with reference to the structure of the molecules, their antigenicity and antigenic drift in influenza viruses viruses isolated from horses.

Descriptors: hemagglutinin viral, influenza A virus genetics, amino acid sequence, avian genetics, immunology, RNA viral genetics, species specificity, horses.


NAL Call Number: QR355.J6

Abstract: The resolution potential of reverse-phase high-performance liquid chromatography (HPLC) for peptide analysis of hydrophobic viral membranes has been investigated, using as model the membrane (M) protein of influenza virus. Proteolytic digests of 125I-labelled M protein and CNBr fragments, extracted from radioiodinated whole virus, have been separated on a uBondapak C18 column with an isopropanol or acetonitrile solvent system. Peptide mapping of trypsin digests of M protein from A/PR/8/34 (H1N1) and A/chicken/Germany/N/49 (H10N7) viruses was identical, whereas *Staphylococcus aureus* V8 protease digests showed minor differences in at least two peptides. The results also show that HPLC is a powerful tool for the separation of proteolytic digests of viral proteins, since the peptide maps are highly reproducible and recovery was greater than 85%.

Descriptors: chromatography, high pressure liquid methods, influenza A virus avian analysis, membrane proteins analysis, peptides analysis, viral proteins analysis, electrophoresis, polyacrylamide gel, iodine radioisotopes.


NAL Call Number: 448.3 Ar23

Abstract: The alpha-glucosidase inhibitor bromoconduritol inhibits the formation of the N-linked, complex-type oligosaccharides of the glycoproteins from influenza viruses (fowl plague virus, influenza virus PR-8) and from sindbis virus. Viral glycoproteins produced in bromoconduritol-treated chicken-embryo and baby-hamster kidney cells are fully glycosylated, but accumulate N-linked, high-mannose oligosaccharides of the composition Glc1Manx (GlcNAc)2 (x = 7, 8, and 9). Other alpha-glucosidase inhibitors (nojirimycin, deoxynojirimycin, acarbose) were not specific inhibitors of oligosaccharide processing under the conditions used in the present investigation. In bromoconduritol-treated, sindbis virus-infected chicken-embryo and baby-hamster kidney cells, the sindbis glycoproteins are metabolically stable. Specific proteolytic cleavage of the polyprotein precursors to form E2 and E1 occurs in bromoconduritol-treated chicken-embryo cells, but cleavage of PE2 to E2 is prevented in the infected baby-hamster kidney cells. Yet, release of infectious sindbis virus particles is inhibited in both cell types indicating that the formation of complex oligosaccharides is required for a late step in virus formation. The release of virus particles from influenza virus PR-8-infected bromoconduritol-treated chicken-embryo cells is not inhibited, and virus with only high-mannose oligosaccharides is formed. In contrast, when chicken-embryo cells were infected with the influenza virus
fowl plague virus, release of infectious particles was inhibited. The fowl plague virus hemagglutinin is cleaved in chicken-embryo cells, in contrast to the hemagglutinin of the PR-8 virus. However, the cleavage products HA1 and HA2 do not reach the cell surface. In addition, or as a consequence, HA1 and HA2 are proteolytically broken down, whereas uncleaved hemagglutinin of PR-8 appeared metabolically stable. These results may explain the decrease in formation of fowl plague virus particles and the lack of effect on PR-8 virus in bromoconduritol-treated cells. This work thus shows different biological roles for oligosaccharide processing.

Descriptors: glycoproteins biosynthesis, influenza A virus avian growth and development, oligosaccharides metabolism, sindbis virus growth and development, viral proteins biosynthesis, cell line, chick embryo, glycoproteins isolation and purification, glycoside hydrolases antagonists and inhibitors, hamsters, avian drug effects, inositol analogs and derivatives, inositol pharmacology, kidney, oligosaccharides isolation and purification, sindbis virus drug effects, viral proteins isolation and purification.

NAL Call Number: 448.8 J8232
Descriptors: antibodies analysis, influenza immunology, influenza A virus avian immunology, adolescent, adult, aged, aging, child, child preschool, hemagglutination inhibition tests, infant, middle aged, statistics.

NAL Call Number: QH573.C42
Abstract: Using a cell-free system we have obtained fusion of vesicles from the endocytic pathway. The fusion is rapid, efficient, and requires ATP. Only vesicles derived from certain positions along the endocytic pathway are capable of fusing. Lysosomes and vesicles derived from the plasma membrane do not fuse. Descriptors: endocytosis, membrane fusion, adenosine triphosphate physiology, cell line, cell membrane physiology, cell free system, hamsters, influenza A virus avian, kidney, lysosomes physiology, mesocricetus, Semliki Forest virus, sialic acids analysis.

NAL Call Number: 472 N21
Descriptors: orthomyxoviridae analysis, RNA viral analysis, aphthovirus analysis, centrifugation, density gradient, encephalitis viruses analysis, influenza A virus avian analysis, molecular weight, Newcastle disease virus analysis, phosphorus isotopes, rauscher virus analysis, sarcoma viruses, avian analysis, spectrum analysis.

NAL Call Number: 41.8 Av5
Abstract: From 1977 to 1983, waterfowl migrating along the Atlantic flyway were annually monitored for orthomyxoviruses and paramyxoviruses in an area in central New York State. A total of 168 influenza isolates were obtained from 1,430 waterfowl. Twenty-four combinations of hemagglutinin and neuraminidase subtypes were detected, with as many as 12 found in a single year. One combination, an H5N2 isolate in 1982, was closely related to the virulent chicken virus that appeared in Pennsylvania in 1983. The prevalence of influenza varied greatly among the common waterfowl species: mallards 42%, black ducks 30%, blue-winged teal 11%, wood ducks 2%, and Canada geese 0%. A total of 89 paramyxoviruses were also from these waterfowl. In contrast to findings with influenza virus, the prevalence of paramyxoviruses did not differ significantly among the duck species. Serotype 1 (Newcastle disease virus) was predominant; three other serotypes were also identified. These findings indicated that ducks in the Atlantic flyway continually harbor influenza viruses and paramyxoviruses. The viruses may be a source of infection for other species.
Descriptors: ducks microbiology, influenza A virus avian isolation and purification, orthomyxoviridae
isolation and purification, paramyxoviridae isolation and purification, antigens, viral analysis, demography, New York, species specificity.


**NAL Call Number:** 448.8 P942

**Abstract:** The method of specific adsorption followed by the use of antisera in HI test and competitive enzyme immunoassay was used to study the antigenic composition of hemagglutinins (HA) Hsw1 in influenza viruses isolated in 1982 from humans in Bulgaria and in 1976 in Canada from ducks as well as their antigenic relationships with HA of Hsw1 variant isolated from swine and man. Hemagglutinins of Hsw1 strains isolated from man in Bulgaria and Alma-Ata were found to be similar to HA of A/New Jersey/8/76 virus in two determinants and with hemagglutinin of the classic virus of swine in three determinants. The HA of A/duck/Alberta/35/76 virus was similar in three determinants to HA of A/New Jersey/8/76 virus and in two determinants with other Hsw1 variants. The similarities and differences in antigenic determinants of HA in Hsw1 viruses isolated from man and animals attest to their common origin and different modes of variability.

**Descriptors:** epitopes analysis, hemagglutinins viral immunology, influenza A virus avian immunology, human immunology, ducks, enzyme linked immunosorbent assay, immunosorbent techniques.


**NAL Call Number:** 448.8 P942

**Abstract:** Competitive radioimmunoassay was used to study the antigenic composition of hemagglutinin of Hsw1N1 viruses isolated from man in comparison with hemagglutinin Hsw1 of influenza virus of swine and ducks. The data of oligonucleotide analysis of the 4th RNA segment coding for hemagglutinin in these viruses are presented. It has been shown that in Alma-Ata, 1984-1985, influenza viruses Hsw1N1 were isolated with the antigenic structure of hemagglutinin and with the hemagglutinin gene identical with those of the classical influenza virus of swine A/Swine/Iowa/15/30 but differing from virus A/New Jersey/8/76.

**Descriptors:** antigens, viral analysis, hemagglutinins viral analysis, influenza A virus avian immunology, human immunology, influenza A virus porcine immunology, immunology, adsorption, antigens, viral genetics, binding, competitive, ducks, genes viral, hemagglutinins viral genetics, avian genetics, avian isolation and purification, human genetics, human isolation and purification, porcine genetics, porcine isolation and purification, Kazakhstan, oligonucleotides analysis, oligonucleotides genetics, RNA viral analysis, viral genetics, radioimmunoassay methods, swine.


**Abstract:** To prepare candidate influenza pandemic vaccines, we are developing an approach based on reassortment of antigenically appropriate nonpathogenic avian viruses of different subtypes (H5, H9, H7) with the cold-adapted master strain (MS) A/Leningrad/134/17/57 (Len/17) that is currently used in Russia for preparing licensed live attenuated vaccines for adults and children. In the present study, reassortants between A/Duck/Potsdam/1402-6/86(H5N2) (H5N2-wt) and Len/17 were obtained. One of the clones, A/17/Duck/Potsdam/86-92(H5N2) (Len17/H5), was chosen for further detailed genetic and antigenic analysis. Len17/H5 inherited the HA gene from the H5N2-wt and all other genes from Len/17 (7:1 genome composition). The HA gene sequence of Len17/H5 was identical to that of the parent H5N2-wt virus. The antigenic profile of the reassortant virus was similar to that of the H5N2-wt parent strain in the hemagglutination-inhibition (HI) test with a panel of antisera to different avian and human H5 viruses. The reassortant demonstrated high growth ability (9.3+0.3 lg EID50/ml) in embryonated hens' eggs (CE) at optimal (34 [deg]C) temperature, comparable with that of the parent Len/17 MS. Also, Len17/H5
demonstrated cold-adapted (ca) and temperature-sensitive (ts) phenotypes similar to those of Len/17 and was attenuated for mice.

Descriptors: avian influenza, live attenuated reassortant vaccine.


NAL Call Number: 500 N21P

Abstract: Based on nucleotide sequence analysis of the hemagglutinin (HA) gene from the virulent and avirulent A/chicken/Pennsylvania/83 influenza viruses, it was previously postulated that acquisition of virulence was associated with a point mutation that resulted in loss of a glycosylation site. Since there are two potential glycosylation sites in this region of the HA molecule and since all Asn-Xaa-Thr/Ser sequences in the HAs of different strains are not necessarily glycosylated, the question remained open as to whether either one of these sites was glycosylated. We now provide direct evidence that a site-specific glycosylation affects cleavage of the influenza virus HA and thus virulence. We have identified the glycosylation sites on the HA1 subunit from the virulent and avirulent strains by direct structural analysis of the isolated proteins. Our results show that the only difference in glycosylation between the HA1s of the virulent and avirulent strains is the lack of an asparagine-linked carbohydrate on the virulent HA1 polypeptide at residue 11. Further, we show that the HA1s of both the avirulent and virulent viruses are not glycosylated at one potential site, while all other sites contain carbohydrate. Amino acid sequence analysis of the HA1 of an avirulent revertant of the virulent strain confirmed these findings.

Descriptors: genes, structural, genes viral, glycoproteins genetics, hemagglutinins viral genetics, influenza A virus avian pathogenicity, amino acid sequence, chick embryo, chromatography, high pressure liquid, glycopeptides analysis, hemagglutinins viral isolation and purification, avian genetics, oligosaccharides analysis, peptide fragments analysis, trypsin, virulence.


NAL Call Number: 448.8 V81

Abstract: To define the sequence changes that occurred in an avian influenza virus neuraminidase (NA) during the evolution of virulence, we have studied the NA of the virulent and avirulent A/Chick/Penn/83 (H5N2) influenza viruses. A comparison of the deduced amino acid sequence from these viruses shows that the virulent strain, which evolved from the avirulent by the accumulation of point mutations (Bean et al., 1985), acquired four amino acid changes in the NA: one in the transmembrane segment, one in the stalk, and two in the head. A comparison of the deduced amino acid sequences with those of the human N2 NAs indicates a 20-amino acid deletion in the stalk of the Chick/Penn/83 NA. Antigenic analysis of the NAs from the avirulent and virulent Chick/Penn/83 virus shows they are antigenically very closely related, but can be distinguished with two monoclonal antibodies at a site which probably involves at least one of the amino acid changes in the NA head. Antigenic analysis also shows the Chick/Penn/83 NAs are closely related to the NAs of other N2 avian influenza viruses isolated between 1965 and 1984, supporting previous studies which indicate a relative antigenic stability of the NA among avian N2 influenza viruses. The Chick/Penn/83 NAs are the first N2 NA genes of an avian virus to be sequenced. These NAs are antigenically closely related to the 1957 human N2 NAs, and show a high degree of amino acid sequence homology with the prototype 1957 human N2 NA. These data give further support to the view that the 1957 human H2N2 viruses were at least partially derived from an avian source.

Descriptors: influenza A virus avian enzymology, neuraminidase isolation and purification, amino acid sequence, antibodies monoclonal diagnostic use, base sequence, chick embryo, chickens, epitopes analysis, genes structural, genes viral, avian genetics, avian pathogenicity, models molecular, neuraminidase immunology, protein conformation, species specificity, virulence.

Oligonucleotide analysis of two avian influenza A viruses (Hav6N2 and Hav6Nav4) isolated in nature showed identical or almost identical patterns for the corresponding M and HA genes; 24 of 25 and 13 of 13 large oligonucleotides were indistinguishable by two-dimensional gel analysis. On the other hand, remarkable differences in the oligonucleotide patterns of the remaining genes were observed. Only 2 of 11 oligonucleotide spots of the NS gene, 10 of 27 spots of the NA/NP genes, and 22 of 49 spots of the P genes were indistinguishable between the two strains. On the basis of this observation that at least two genes of these viruses are virtually identical whereas others show easily detectable differences, we conclude that the two avian strains are related to each other by a recombinational event. In addition, it was found that animals in nature can be doubly infected with influenza viruses. Both lines of evidence strongly suggest that recombination is at least one mechanism by which "new" influenza virus strains emerge in nature.

Descriptors: genes viral, influenza A virus avian genetics, recombination, genetic, hemagglutinins viral analysis, avian immunology, oligoribonucleotides analysis, RNA viral analysis.
hemagglutinin genes in different regions of the world. Virology 169(2): 408-17. ISSN: 0042-6822.

NAL Call Number: 448.8 V81

Abstract: To understand the determinants of influenza virus evolution, phylogenetic relationships were determined for nine hemagglutinin (HA) genes of the H4 subtype. These genes belong to a set of viruses isolated from several avian and mammalian species from various geographic locations around the world between 1956 and 1985. We found that the HA gene of the H4 subtype is 1738 nucleotides in length and is predicted to encode a polypeptide of 564 amino acids. The connecting peptide, which is removed from the precursor polypeptide by peptidases to yield the mature HA1 and HA2 polypeptides, contains only one basic amino acid. This type of connecting peptide is a feature of all avian avirulent HAs. On the basis of pairwise nucleotide sequence homology comparisons the genes can be segregated into two groups: influenza virus genes isolated in North America and those isolated from other parts of the world. A high degree of homology exists between pairs of genes from viruses of similar geographic origin. The nucleotide sequences within a group differ by 1.5 to 10.6%; in contrast, between groups the differences range from 15.8 to 19.4%. An evolutionary tree for the nine sequences suggests that North American isolates have diverged extensively from those circulating in other parts of the world. Geographic barriers which determine flyway outlay may prevent the gene pools from extensive mixing. The lack of correlation between date of isolation and evolutionary distance suggests that different H4 HA genes cocirculate in a fashion similar to avian H3 HA genes (H. Kida et al., 1987, Virology 159, 109-119) and influenza C genes (D. Buonagurio et al., 1985, Virology 146, 221-232) implying the absence of selective pressure by antibody that would give a significant advantage to antigenic variants. In contrast to avian influenza virus genes, human influenza virus genes evolve rapidly under the selective pressure of antibody.

Descriptors: hemagglutinins viral genetics, influenza A virus genetics, amino acid sequence, base sequence, cloning, molecular, geography, molecular sequence data, sequence homology, nucleic acid.


Abstract: We have shown previously using immunofluorescence microscopy that upon infection of polarized hippocampal cells in culture with vesicular stomatitis virus (VSV) and fowl plague virus (FPV) the VSV glycoprotein is delivered to the plasma membrane of the dendrites and of the cell body whereas the FPV hemagglutinin is transported to the axonal surface (Cell, 62 (1990) 63-72). In this work electron microscopy of infected rat hippocampal neurons showed that VSV progeny budded from the plasma membrane of the dendrites and the cell body. The location of the budding virions corresponded to the distribution of the VSV glycoprotein which was detected over the somatodendritic plasma membrane by immunoelectron microscopy. In contrast, no FPV formation was seen in the infected neurons although the FPV hemagglutinin was localized to the axonal surface by immunoelectron microscopy. In Semliki Forest virus (SFV) infected hippocampal cells we observed that the viral glycoproteins were exclusively present in the dendrites and cell body but not in axons.

Descriptors: cell polarity physiology, hippocampus microbiology, membrane glycoproteins analysis, neurons microbiology, viral envelope proteins analysis, cultured cells, hippocampus cytology, influenza A virus avian isolation and purification, microscopy, microscopy, electron, microscopy, immunoelectron, rats, rats, Sprague Dawley, Semliki Forest virus isolation and purification, vesicular stomatitis Indiana virus isolation and purification.


NAL Call Number: QH573.C42

Abstract: Cultured hippocampal neurons were infected with a temperature-sensitive mutant of vesicular stomatitis virus (VSV) and a wild-type strain of the avian influenza fowl plague virus (FPV). The intracellular distribution of viral glycoproteins was monitored by immunofluorescence microscopy. In mature, fully polarized neurons the VSV glycoprotein (a basolateral protein in epithelial MDCK cells) moved from the Golgi complex to the dendritic domain, whereas the hemagglutinin protein of FPV (an apically sorted protein in MDCK cells) was targeted preferentially, but not exclusively, to the axon. The VSV glycoprotein appeared in clusters on the dendritic surface, while the hemagglutinin was distributed uniformly along the axonal
membrane. Based on the finding that the same viral glycoproteins are sorted in a polarized fashion in both neuronal and epithelial cells, we propose that the molecular mechanisms of surface protein sorting share common features in the two cell types.

Descriptors: axons microbiology, dendrites microbiology, glycoproteins analysis, hippocampus microbiology, influenza A virus avian genetics, neurons microbiology, vesicular stomatitis Indiana virus genetics, viral proteins analysis, cultured cells, embryo, fluorescent antibody technique, glycoproteins genetics, rats, viral proteins genetics.


Abstract: Seventeen nucleoside derivatives (derived from arabinosylcytosine, resp. cytidine, 5-fluorouracil and uracil) were tested by agar-diffusion plaque-inhibition test for their antiviral activity with herpes simplex, vaccinia, fowl plague, Newcastle disease and western equine encephalomyelitis viruses. The highest antiviral activity against DNA viruses exhibited arabinosylcytosine, N4-acylarabinosylcytosines, arabinosylthiouracil, cyclocytidine and its 5'-chloroderivative. RNA viruses were inhibited by 5-fluorouridine only, whereas other tested compounds were ineffective or showing marginal activity only. By search for relationship between chemical structure and antiviral activity a tendency was found of higher antiviral activity at lower lipophilicity. This is probably due to better transport of the studied compounds into cell. The chemical structure, however, is the main reason of antiviral activity.

Descriptors: antiviral agents chemistry, pyrimidine nucleosides pharmacology, encephalitis virus, western equine drug effects, encephalitis virus, western equine growth and development, influenza A virus avian drug effects, avian growth and development, Newcastle disease virus drug effects, Newcastle disease virus growth and development, plaque assay, pyrimidine nucleosides chemistry, simplexvirus drug effects, simplexvirus growth and development, structure activity relationship, vaccinia virus drug effects, vaccinia virus growth and development.


Abstract: In human lymphoblastoid cells, infected with an influenza virus, Fowl Plague Virus (FPV), glycoproteins (such as secreted IgM) are hyposialylated, through the action of viral neuraminidase. In this study, the modulation of the cellular ectosialyltransferase activity during viral infection was investigated. This activity was detectable in FPV-infected cells, was shown to be 2.5-fold higher than that of uninfected cells, and to be able to restore, at least partially, the level of sialylation of the cell surface acceptors.

Descriptors: cell transformation, viral, influenza A virus avian enzymology, neuraminidase metabolism, sialyltransferases metabolism, transferases metabolism, cell line, cell membrane metabolism, clostridium enzymology, glycoproteins metabolism, kinetics, lymphocytes, membrane proteins metabolism.


Abstract: The biosynthesis of IgM by the Epstein-Barr virus-negative RAMOS lymphoblastoid cell line infected with an influenza A virus, fowl plague virus Dobson strain (FPV-B), was investigated. The results show that FPV infection of RAMOS cells slightly inhibited overall cellular protein synthesis only at 24 h after infection.
infection, despite the synthesis of FPV-specific proteins. However, even at this time, the synthesis and secretion of IgM were not affected by virus infection. Secreted IgM contained a reduced amount of sialic acid. The quantity of the asialylated IgM increased proportionally to the amount of enzymically active neuraminidase, suggesting that the asialylation of IgM is due to the action of virus neuraminidase. No such asialylated IgM was observed in RAMOS cells infected with measles virus, which does not possess neuraminidase. These results, together with a previous observation of ours that asialylated immunoglobulins acquire an altered antigenicity, suggest that the modulation of enzyme activities in B lymphocytes in response to an exogenous aggression may lead to disturbances in the structure and in the antigenic properties of immunoglobulins.

Descriptors: immunoglobulin m metabolism, influenza A virus avian physiology, lymphocytes microbiology, cell line, immunoglobulin m analysis, lymphocytes immunology, lymphoma, neuraminidase metabolism, proteins analysis, sialic acids analysis, virus replication.


NAL Call Number: 448.8 V81

Abstract: Four avian influenza viruses have been generated, each containing a single extra defective RNA segment in addition to the eight standard segments. Three of the extra RNAs were derived from segment 1 and the fourth from segment 2. Chick embryo fibroblast cells were infected with each virus, and a wild-type virus. Virus RNA was quantified in extracts of virus-infected cells and in virus released by 10 hr postinfection using reverse transcription and by Northern blot analysis. In the case of two of the viruses the presence of the defective RNA did not markedly affect the accumulation of virus RNA within the infected cell, but significantly and selectively reduced the amount of the "parent" segment in released virus. This effect was reduced in a third virus. In a fourth virus, defective RNA was found to be present at a low-input multiplicity and results were varied. Mixed infections of one of the viruses with a closely related wild-type virus resulted in reduction of the corresponding vRNA segment of the nondefective virus. We conclude that assembly of influenza virus segments is not a purely random process.

Descriptors: chicks, avian influenza virus, RNA, infection, pathogenesis, quantitative analysis, fibroblasts, acids, analytical methods, birds, cells, chickens, disease transmission, domestic animals, domesticated birds, Galliformes, influenza virus, livestock, nucleic acids, nucleic compounds, organic acids, orthomyxoviridae, pathogenesis, poultry, useful animals, viruses, young animals, reverse transcription, virus assembly, transcription, mixed infections.


NAL Call Number: 442.9 So1

Descriptors: orthomyxoviridae pathogenicity, serologic tests, hemadsorption inhibition tests, immune sera pharmacology, influenza A virus avian pathogenicity, methods, Newcastle disease virus pathogenicity, tissue culture.


NAL Call Number: QR360.A1J6

Descriptors: antigens analysis, neuraminidase analysis, orthomyxoviridae analysis, orthomyxoviridae immunology, recombination, genetic, electrophoresis, hemagglutination inhibition tests, hemagglutinins viral analysis, hybridization, genetic, immunodiffusion, influenza A virus avian.

The influenza virus A/duck/Alberta/48/76 with the antigen formula H7N3 (16) and Hav1 Nav2 (WHO nomenclature from 1971) (15), respectively, as well as a nonpathogenic virus of the subtype Hav1 were purified to a high degree by ultracentrifugation in continuous sucrose gradients (15-40% w/w and 20-60% w/w, respectively). The activity of the RNA polymerase of this virus preparation was determined by incorporating 3H-UMP in acid insoluble material following preincubation of the virus with the nonionic detergents Nonolid P-40 for 15 min at 32 degrees C. The influence of different concentrations was investigated of dinucleotid, NaCl, MgCl2, Nonidet P-40 and different incubation temperatures. Optimal incorporation rates were found at following conditions: 0.2 mM dinucleotid ApG, 150 mM sodium chloride and 8 mM magnesium chloride by concentration of ions, 0.25-0.5% detergents Nonidet P-40 as well as a temperature of incubation of 32 degrees C. The data for optimal polymerase activity for the avian influenza virus A/duck/Alberta/48/76 are generally not different from the conditions described for the Fowl-Plague-Virus and for human strains.

Descriptors: DNA directed RNA polymerases metabolism, influenza A virus avian enzymology, bacteriological techniques, chick embryo, enzyme activation, temperature.

Rac1 and PAK1 are upstream of IKK-epsilon and TBK-1 in the viral activation of interferon regulatory factor-3. FEBS Letters 567(2-3): 230-8. ISSN: 0014-5793.

DNA binding proteins metabolism, protein serine threonine kinases metabolism, transcription factors metabolism, RACL GTP binding protein metabolism, cell line, DNA binding proteins chemistry, DNA binding proteins genetics, dimerization, dogs, enzyme activation, influenza A virus, avian pathogenicity, human pathogenicity, interferon beta genetics, nuclear proteins metabolism, phosphorylation, promoter regions genetics, protein serine threonine kinases antagonists and inhibitors, protein serine threonine kinases genetics, RNA, double stranded immunology, double stranded metabolism, signal transduction, trans activators metabolism, transcription factors chemistry, transcription factors genetics, transcription, genetic, virus replication.


Four strains of avian reovirus were ineffective inducers of interferon (IFN) in chicken kidney (CK) cell cultures. All strains were similar in single-cycle replication curves. At multiplicities of infection between 0.20 and 10 plaque-forming units per cell, IFN was not induced in CK cells. Reovirus did not produce an IFN blocker in CK cells. Attenuated reovirus did induce IFN in aged chicken embryo fibroblast (CEF) cell cultures. By priming cells with a low dose of IFN before infection with reovirus, IFN formation by CEF could be enhanced. Ultraviolet-inactivated avian reovirus was an effective inducer of IFN in both CK and CEF cell cultures. The sensitivity of avian reoviruses (Fahey-Crawley, Reo-25, S-1133, Reo-V) to chicken interferon (Ch-IFN) was studied by the plaque-reduction method. Avian reoviruses were less sensitive to Ch-IFN than was vesicular stomatitis virus or Semliki Forest virus and appeared to be as resistant to IFN as was Newcastle disease virus.

Descriptors: interferons biosynthesis, reoviridae growth and development, virus replication, cultured cells, chickens, cytopathogenic effect, viral, drug resistance, microbial, influenza A virus avian growth and development, interferons pharmacology, kidney, Newcastle disease virus growth and development, Semliki Forest virus growth and development, ultraviolet rays, vesicular stomatitis Indiana virus growth and

**NAL Call Number:** QD341.A2N8

**Abstract:** The polyadenylation of Fowl Plague Viral RNA and of Influenza A/Victoria Viral RNA using E. coli poly (A) polymerase and the subsequent reverse transcription of the polyadenylated species is reported. We have shown that all 8 genome fragments are adenylated and that an average of 25--30 adenylic acid residues per molecule is sufficient for maximal transcription with reverse transcriptase. The cDNA product is 95% sensitive to SI-nuclease and hybridisation analysis against viral RNA reveals it to be a faithful copy of the RNA. Amongst the transcription products are long, discrete copies of genes 1--8, the lengths of which are comparable with those of the vRNA determined by electrophoresis on formamide acrylamide gels. These single-stranded cDNAs have been further transcribed to form double-stranded products with hair-pin structures at one end. Analysis of this material on native acrylamide gels revealed some DNA bands corresponding to the predicted sizes for genes 4--8.

**Descriptors:** *Escherichia coli* enzymology, nucleotidyltransferases metabolism, poly A biosynthesis, polynucleotide adenylyltransferase metabolism, RNA viral metabolism, RNA directed DNA polymerase metabolism, DNA, viral biosynthesis, influenza A virus avian, kinetics, molecular weight, nucleic acid hybridization, orthomyxoviridae.


**NAL Call Number:** 472 N21

**Abstract:** A gene sequence for the fowl plague virus (FPV) haemagglutinin molecule has been inserted into a bacterial plasmid such that its transcription is under the control of a promoter derived from the tryptophan operon. Such plasmids direct the synthesis of a protein that reacts specifically with antisera to FPV haemagglutinin. Evidence is also presented that in some cases DNA inserted at the HindIII site of pBR322 is expressed.

**Descriptors:** antigens, viral genetics, DNA, recombinant, *Escherichia coli* genetics, hemagglutinins viral genetics, influenza A virus avian genetics, epitopes, genes, structural, influenza A virus avian immunology, operon, plasmids, transcription, genetic, tryptophan genetics.


**NAL Call Number:** QD320.B56

**Descriptors:** antigens, viral biosynthesis, hemagglutinins viral biosynthesis, influenza A virus avian genetics, amino acid sequence, antigens, viral genetics, antigens, viral immunology, base sequence, *Escherichia coli* genetics, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral genetics, hemagglutinins viral immunology, history of medicine, 20th century, influenza A virus avian immunology, molecular sequence data, recombinant proteins biosynthesis, recombinant proteins genetics, recombinant proteins immunology.


**NAL Call Number:** SF769.P36

**Descriptors:** avian influenza virus, chemotherapy, antiviral agents.


**NAL Call Number:** 448.8 J824

**Abstract:** Trypanosoma vivax stock V953 lysates were observed to produce neuraminidase (sialidase EC 3.2.1.18) in vitro, which cleaved neuraminic (sialic) acid from the substrate fetuin. The neuraminidase activity was proportional to the number of trypanosomes in the lysates, with 0.44, 0.88, and 1.75 X 10(6) trypanosomes producing 1.4 +/- 0.06, 3.1 +/- 0.1, and 6.7 +/- 0.1 micrograms of sialic acid liberated, respectively. Equal numbers of unlysed and lysed trypanosomes produced approximately the same amount of the enzyme. Trypanosome eluates stored at room temperature appeared to have lost neuraminidase activities within 4 days. An inhibition test for identifying the neuraminidase antigen on influenza viruses was performed in vitro on the T. vivax lysates. The inhibition test, using Type A influenza virus anti-HAV8 serum, showed a highly significant (P less than 0.0001) reduction in neuraminidase activities. The effect of equal amounts of influenza antiserum on serially diluted trypanosome lysates showed that 1 ml of influenza anti-HAV8 serum would inhibit a mean of 6.74 +/- 0.18 micrograms of T. vivax stock V953 neuraminidase activity.

**Descriptors:** antibodies, viral immunology, influenza A virus avian immunology, neuraminidase antagonists and inhibitors, Trypanosoma enzymology, immune sera, neuraminidase immunology, temperature.


**NAL Call Number:** 448.3 AC85

**Abstract:** The levels of neutral protease activity associated with allantoic and amniotic fluids of embryonated eggs during the replication of influenza strains A/PR/8/34 (H1N1) and A/turkey/Ontario/7732/66 (H5N9) were investigated. A sensitive fluorometric technique proved useful for characterization and monitoring changes of protease activities in egg fluids. The predominant type of protease in allantoic and amniotic fluids had trypsin-like specificities. Variation in protease levels of both fluids occurred throughout the course of virus replication irrespective of the virus strain or the route of inoculation used. Concomitant with the production of high levels of infectious virus there was a marked decrease in neutral protease activity in the fluid from the cavity initially infected. Translocation of virus also occurred especially with amniotically infected eggs, as evidenced by high infectious virus titers and decreased protease activities in allantoic fluids.

**Descriptors:** allantois enzymology, amniotic fluid enzymology, fetal membranes enzymology, influenza A virus physiology, peptide hydrolases metabolism, virus replication, allantois microbiology, amniotic fluid microbiology, chick embryo, influenza A virus avian physiology, protease inhibitors pharmacology, turkeys.


**NAL Call Number:** QH573.C42

**Descriptors:** genes viral, hemagglutinins viral genetics, influenza A virus avian genetics, influenza A virus human genetics, amino acid sequence, base sequence, cloning, molecular, ducks microbiology, epitopes, hemagglutinins viral immunology, influenza A virus avian immunology, influenza A virus human immunology, mutation.


**NAL Call Number:** 41.8 Av5

**Abstract:** The combined effect of time and temperature on the stability of two avian influenza virus (AlV)
isolates concentrated with polyethylene glycol (PEG), stored at different temperatures, and used in the preparation of avian influenza vaccine was evaluated in turkeys at 24 hr and at 12, 24, 30, 36, and 42 months of storage. The differences detected between antibodies raised in turkeys by vaccines made from isolates under different storage conditions, times, and temperatures were not significant (P > 0.05), especially with vaccines prepared from one isolate. Virus recovery rates following challenge studies of vaccinated birds were similar. However, birds that were vaccinated twice had lower rates of virus recovery from the trachea, lungs, pancreas, and fecal samples following challenge infection. The results suggest that if stable isolates of AIV can be identified, such isolates can be rapidly concentrated with PEG and stored at -20 C or -196 C for at least 42 months without any loss of potency in the vaccine prepared from these isolates. This would reduce the costs associated with vaccine storage and subsequent expiration dates.

Descriptors: turkeys, avian influenza virus, antigens, vaccines, freezing, storage, temperature, time, alcohols, polyethylene, vaccination, birds, disease control, Galliformes, immunization, immunological factors, immunology, immunostimulation, immunotherapy, influenza virus, polymers, processing, therapy, viruses, viral antigens, potency, polyethylene glycol.


NAL Call Number: QH573.T75

Abstract: When the Drosophila cells were infected with the mixo- and arboviruses, in case of influenza A/WSN virus a rise in the titre and slight cytopathogenic effect with the subsequent decrease in the titre was observed. Since the decrease in the virus titer was not observed when actinomycin D was added, it was supposed that interferonlike inhibitor may be produced by the infected cells. Vacuolization and increase in the size of the infected cells were caused by all the nuclear polyhedrosis viruses tested. The number of the infected cells depended on the virus type and multiplicity of the infection.

Descriptors: insect viruses, viruses, arboviruses, cultured cells, cytopathogenic effect, viral, encephalitis virus, western equine, influenza A virus avian, Newcastle disease virus, orthomyxoviridae.


NAL Call Number: QR360.J6

Abstract: The tissue tropism and spread of infection of the highly pathogenic avian influenza virus A/FPV/Rostock/34 (H7N1) (FPV) were analyzed in 11-day-old chicken embryos. As shown by in situ hybridization, the virus caused generalized infection that was strictly confined to endothelial cells in all organs. Studies with reassortants of FPV and the apathogenic avian strain A/chick/Germany/N/49 (H10N7) revealed that endotheliotropism was linked to FPV hemagglutinin (HA). To further analyze the factors determining endotheliotropism, the HA-activating protease furin was cloned from chicken tissue. Ubiquitous expression of furin and other proprotein convertases in the chick embryo indicated that proteolytic activation of HA was not responsible for restriction of infection to the endothelium. To determine the expression of virus receptors in embryonic tissues, histochemical analysis of alpha2,3- and alpha2,6-linked neuraminic acid was carried out by lectin-binding assays. These receptors were found on endothelial cells and on several epithelial cells, but not on tissues surrounding endothelia. Finally, we analyzed the polarity of virus maturation in endothelial cells. Studies on cultured human endothelial cells employing confocal laser scanning microscopy revealed that HA is specifically targeted to the apical surface of these cells, and electron microscopy of embryonic tissues showed that virus maturation occurs also at the luminal side. Taken together, these observations indicate that endotheliotropism of FPV in the chicken embryo is determined, on one hand, by the high cleavability of HA, which mediates virus entry into the vascular system, and, on the other hand, by restricted receptor expression and polar budding, which prevent spread of infection into tissues surrounding endothelia.

Descriptors: endothelium virology, influenza A virus avian pathogenicity, chick embryo, endothelium metabolism, endothelium pathology, Furin, hemagglutinin glycoproteins, influenza virus metabolism, in situ
hybridization, influenza A virus avian ultrastructure, microscopy, confocal, neuraminidase metabolism, organ specificity, proprotein convertase 5, receptors, virus analysis, serine endopeptidases metabolism, subtilisins metabolism.


Abstract: The primary structure of the hemagglutinin of the apathogenic avian influenza virus A/chick/Germany/N/49 (H10N7) and of the serologically related strain A/mink/Sweden/84 (H10N4) pathogenic for mink has been elucidated by nucleotide sequence analysis, and the carbohydrates attached to the polypeptide have been determined. The H10 hemagglutinin has 65, 52, 46, 45, and 44% amino acid sequence homology with serotypes H7, H3, H1, H2, and H5, respectively. H10 and H7 hemagglutinins are also most closely related in their glycosylation patterns. There is a high sequence homology between both H10 strains supporting the concept that the mink virus has obtained its hemagglutinin from an avian strain. The sequence homology includes the cleavage site which consists of a single arginine as is the case with most other hemagglutinins exhibiting low susceptibility to proteolytic activation. The similarity in hemagglutinin structure between both H10 strains is discussed in light of the distinct differences in the pathogenicity of both viruses.

Descriptors: hemagglutinins viral genetics, influenza A virus genetics, amino acid sequence, base sequence, carbohydrates analysis, chickens microbiology, glycosylation, hemagglutinins viral analysis, influenza A virus immunology, mink microbiology, molecular sequence data, sequence homology, nucleic acid.


Abstract: A series of reassortants has been constructed by crossing of UV-inactivated avian influenza virus of H3N8 subtype and live human influenza virus of H1N1 subtype, adapted to growth in continuous canine kidney cell line (MDCK). The analysis of RNA duplexes has shown that the reassortants contain HA gene of avian influenza virus whereas the other genes belong to human parent virus. The reassortants were efficiently reproduced in MDCK cells at low temperature (limiting for the avian parent virus). The data suggest that the avian virus HA gene does not hamper the reproduction of reassortant viruses in mammalian cells under the conditions unfavorable for the multiplication of avian influenza subtype H3N8 viruses.

Descriptors: genes viral, influenza A virus avian genetics, human genetics, virus replication, cultured cells, dogs, hemagglutinins viral genetics, hemagglutinins viral immunology, avian immunology, avian physiology, human immunology, human physiology, kidney, nucleic acid hybridization, phenotype, RNA viral genetics, temperature.


Abstract: 3-Deazaaristeromycin and 3-deazaadenosine (3DA-Ado) both interfere with the methylation of RNA, but only 3DA-Ado is metabolized to the corresponding homocysteine derivative. In contrast to 3-deazaaristeromycin, 3DA-Ado inhibits the synthesis of late influenza A virus proteins in chicken embryo cells (CEC), while it causes an overproduction of early proteins and of the nonstructural proteins NS2 and M2. Only the former effect of 3DA-Ado can be reversed by concomitant addition of adenosine, but not by guanosine. 3DA-Ado acts only early in the infectious cycle and, after removal of the drug, its effect on the yield of infectious virus is reversible. It can be significantly enhanced by homocysteine thiolactone. Except for the M gene, synthesis of viral mRNA is not significantly affected by 3DA-Ado. We conclude that 3DA-Ado acts via its homocysteine derivative by interfering with a specific post-transcriptional modification of viral
mRNA and on splicing of specifically the M mRNA. In L-cells influenza viral protein synthesis is comparable to that in CEC in the presence of 3DA-Ado in that there is only little HA and M1 synthesized, and a severe overproduction of NS2 is observed. Under the experimental conditions 3DA-Ado has no inhibiting effect on the replication of other RNA viruses like Newcastle disease virus, Semliki Forest virus, or West Nile virus whose RNA is not methylated, since they do not have a nuclear phase during replication.

Descriptors: anti bacterial agents pharmacology, influenza A virus genetics, tubercidin pharmacology, viral proteins biosynthesis, adenosine analogs and derivatives, adenosine pharmacology, aminoglycosides, capsid biosynthesis, cell line, cultured cells, chick embryo, enzyme inhibitors pharmacology, influenza A virus avian drug effects, avian physiology, influenza A virus drug effects, influenza A virus metabolism, isomerism, kinetics, mice, RNA, messenger biosynthesis, RNA viral biosynthesis, viral core proteins biosynthesis, viral nonstructural proteins, viral proteins isolation and purification, virus replication.


NAL Call Number: QR355.J6

Abstract: Neuraminidase is one of the two surface glycoproteins of influenza virions. In order to compare neuraminidases of the same subtype but isolated from different species (man, birds, pig), a new and simple method was adapted and optimized using peanut hemagglutinin. Results were very similar to those obtained with the classical method recommended by the WHO, using fetuin as a substrate. The technique was used to examine the relationship between animal and human neuraminidases belonging to serotypes N1 and N2. The results confirm the possible role of ducks as a reservoir for influenza viruses and the eventuality of interspecific exchanges.


NAL Call Number: QR355.A44

Abstract: The study of biological properties of influenza virus strains belonging to the same subtype A(H1N1) and closely antigenically related, but isolated from different animal species (man, pig and duck), demonstrated that avian strains were more resistant than those isolated from mammals to high temperature and low pH, as shown by titration of residual infectivity in cell cultures (MDCK) and by sialidase assay. The difference in behaviour could be correlated to biological adaptation of the virus to its host. Avian body temperature is 40 degrees C and influenza virus, in ducks, is enterotropic and therefore capable of passing through the low pH values in the upper digestive tract of the animal. These results do not contradict the hypothesis of a possible filiation between avian and mammalian orthomyxoviruses.

Descriptors: influenza A virus physiology, body temperature, cell line, ducks, hemagglutination tests, hydrogen-ion concentration, influenza A virus avian enzymology, avian growth and development, avian physiology, human enzymology, human growth and development, human physiology, porcine enzymology, porcine growth and development, porcine physiology, influenza A virus enzymology, influenza A virus growth and development, neuraminidase analysis, plaque assay, swine, temperature, virus replication.


NAL Call Number: QR355.I5

Abstract: In genetic recombination experiments with the mouse-lung-adapted human influenza A/Engl/1/61 (H2N2) and an avian influenza strain A/Rostock/34 (FPV) (Hav1N1) which is avirulent for the mouse lung, recombinants in which hemagglutinin and neuraminidase were either segregated (Hav1N2; H2N1) or not segregated (Hav1N1) were selected. The recombinants were studied for mouse-lung virulence and their ability to propagate in mouse kidney cells, mouse embryo fibroblasts, chick embryo kidney cells and chick embryo fibroblasts. An association between plaque formation in mouse kidney cells and mouse-lung...
virulence was found. 

Descriptors: influenza A virus human pathogenicity, antigens, viral analysis, hemagglutinins viral analysis, human growth and development, human immunology, lung microbiology, mice, neuraminidase immunology, plaque assay, recombination, genetic, tissue culture, virulence, virus replication.


NAL Call Number: QR360.J6

Descriptors: cultured cells microbiology, orthomyxoviridae growth and development, vesicular stomatitis Indiana virus growth and development, virus replication, autoradiography, carbon radioisotopes, cell line, cell nucleus microbiology, cytochalasin B pharmacology, electrophoresis, polyacrylamide gel, haplorhini, influenza A virus avian growth and development, avian metabolism, kidney, orthomyxoviridae metabolism, peptide synthesis, plaque assay, RNA viral biosynthesis, sulfur radioisotopes, tritium, vesicular stomatitis Indiana virus metabolism, viral proteins biosynthesis.


NAL Call Number: SF602.A5

Abstract: From the Revised Nomenclature of WHO, the fowl influenza virus A/Duck/Ukraine/63 (Hav7 Neq2) has the same neuraminidase as the equine virus A/equi 2/Miami/63 (Heq2 Neq2); the A/Chicken Germany "N"/49 virus has the same neuraminidase as the equine virus A/equi 1/Prague/56. A comparative study of the antigenic specificities confirms that the Neq2 neuraminidases are closely connected, whatever their animal origin, and that the fowl strain Hav7 Neq2 can be used for the titration of anti Neq2 antibodies in the sera of animals immunized with the equine virus Heq2 Neq2. The Neqi neuraminidases of various animal origins are connected, but the neuraminidase of the fowl strain Hav2 Neqi is slightly inhibited by the anti Neq1 antibodies of animals immunized with the Heq1 Neq1 virus: to titrate the anti Neq1 antibodies of equine origin, the H72 Neq1 recombinant should therefore be used. The antigenic characterization of the different equine influenza strains isolated since 1967 by the study of their neuraminidase has been completed: The various neuraminidases, like the hemagglutinins of the various strains belonging to the subtype A equi2 are closely connected; a minor antigenic variation, concerning the two surface antigens, seems to exist between the strain A equi 1/Prague/56 and the strain of the same subtype isolated in 1973. 

Descriptors: antigens, viral, neuraminidase immunology, orthomyxoviridae immunology, cross reactions, epitopes, hemagglutination inhibition tests, horse diseases immunology, horses, influenza immunology, influenza veterinary, influenza A virus avian immunology.


NAL Call Number: 41.8 Av5

Abstract: Avian influenza and hemorrhagic enteritis viral preparations were immunelectrophoresed in a phosphate-buffered system. Excellent separation and resolution of viral proteins were achieved. Reasons are given why this method might be preferred over the conventional method employing a veronal (barbital)-buffered system.

Descriptors: antigens, viral analysis, coronaviridae analysis, coronavirus, turkey analysis, influenza A virus avian analysis, viral proteins analysis, coronavirus, turkey immunology, immuneelectrophoresis methods, viral proteins immunology.


NAL Call Number: 384 Z38

Abstract: We describe here the application of 1H-NMR spectroscopy to determine the substrate specificity
of sialidases using a 1:1 mixture of NeuAc alpha 2-3Gal beta 1-4Glc and NeuAc alpha 2-6Gal beta 1-4Glc, one viral and five bacterial sialidases. This method utilizes the separate signals in NMR spectra, characteristic for the different alpha ketosidically linked NeuAc residues and also for bound and free NeuAc. The signals generally most suitable for these purposes are those of H3a, H3e and NOCH3. By observation and integration of these signals we can follow--qualitatively and quantitatively--which and how many NeuAc residues of the substrates are hydrolyzed. In contrast to the generally used colorimetric tests it is now possible to investigate with this method substrates containing two or more NeuAc residues and to determine the corresponding rate constants for hydrolysis of the differently bound NeuAc molecules. The six sialidases used show large differences in their specificities as compared with our "model substrate": The sialidase from fowl plague virus hydrolyzes NeuAc alpha 2-3Gal beta 1-4Glc nearly 18 times and the enzyme from *Clostridium perfringens* four times, from *Vibrio cholerae* two times faster than NeuAc alpha 2-6Gal beta 1-4Glc. On the contrary, the sialidase from *Arthrobacter ureafaciens* hydrolizes the alpha 2-6 linkage six times faster than the alpha 2-3 linkage. The sialidases from *Bifidobacterium* show no obvious differences in their specificities relative to the linkage.


NAL Call Number: 448.3 Ar23

Abstract: After infection of primary chick embryo cells with an influenza A virus (FPV) the synthesis of polar lipids was specifically inhibited, while mono-, di- and triacylglycerols and fatty acids accumulated. Influx of Ca++ accelerated and Ca++ accumulated in the infected cells. Since enzymes like choline phosphotransferase are sensitive to high concentrations of Ca++, specific inhibition of the synthesis of polar lipids is presumably due to an increased influx of Ca++ by the infection.

Descriptors: calcium metabolism, fowl plague metabolism, lipids metabolism, biological transport, cultured cells, chick embryo, influenza A virus avian.


NAL Call Number: 448.3 Ar23

Descriptors: hemagglutinins viral immunology, influenza A virus avian immunology, antibodies, monoclonal immunology, antibodies, viral immunology, birds microbiology, cross reactions, ducks microbiology, epitopes, hemagglutination inhibition tests, hemagglutininins viral classification, influenza A virus avian classification.


NAL Call Number: QH506.E46

Abstract: We have used filter-grown Madin-Darby canine kidney (MDCK) cells to explore the mechanism by which influenza virus facilitates secondary virus infection. Vesicular stomatitis virus (VSV) and Semliki Forest virus (SFV) infect only through the basolateral surface of these polarized epithelial cells and not through the apical surface. Prior infection with influenza virus rendered the cell susceptible to infection by VSV or SFV through either surface. The presence of both a permissive and a restrictive surface for virus entry in the same cell allowed us to determine how the influenza infection enhanced the subsequent infection of a second virus. Biochemical and morphological evidence showed that influenza haemagglutinin on the apical surface serves as a receptor for the superinfecting virus by binding to its sialic acid-bearing envelope proteins. Influenza virus also facilitates secondary virus infection in non-epithelial cells; baby hamster kidney cells (BHK-21), which are normally resistant to infection by the coronavirus (mouse hepatitis virus MHV-A59), could be infected via the haemagglutinin-sialic acid interaction. Facilitation of secondary virus infection requires only the sialic acid-binding properties of the haemagglutinin since the uncleaved haemagglutinin
could also mediate virus entry.

Descriptors: hemagglutinins viral metabolism, influenza A virus avian metabolism, receptors, virus metabolism, vesicular stomatitis Indiana virus metabolism, cell compartmentation, cultured cells, dogs, endocytosis, hamsters, kidney microbiology, murine hepatitis virus metabolism, Semliki Forest virus metabolism, sialic acids physiology, viral proteins biosynthesis, virus replication.


NAL Call Number: 500 N21P

Abstract: Plasmid DNAs expressing influenza virus hemagglutinin glycoproteins have been tested for their ability to raise protective immunity against lethal influenza challenges of the same subtype. In trials using two inoculations of from 50 to 300 micrograms of purified DNA in saline, 67-95% of test mice and 25-63% of test chickens have been protected against a lethal influenza challenge. Parenteral routes of inoculation that achieved good protection included intramuscular and intravenous injections. Successful mucosal routes of vaccination included DNA drops administered to the nares or trachea. By far the most efficient DNA immunizations were achieved by using a gene gun to deliver DNA-coated gold beads to the epidermis. In mice, 95% protection was achieved by two immunizations with beads loaded with as little as 0.4 micrograms of DNA. The breadth of routes supporting successful DNA immunizations, coupled with the very small amounts of DNA required for gene-gun immunizations, highlight the potential of this remarkably simple technique for the development of subunit vaccines.

Descriptors: DNA, viral administration and dosage, fowl plague prevention and control, hemagglutinins viral genetics, influenza prevention and control, influenza A virus avian immunology, human immunology, cell line, chickens, DNA, viral immunology, fowl plague immunology, genes viral, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral biosynthesis, influenza immunology, avian genetics, human genetics, injections, injections, intramuscular, injections, intravenous, mice, mice inbred BALB c, mucous membrane, restriction mapping, transfection, viral envelope proteins biosynthesis, viral envelope proteins genetics.


NAL Call Number: 511 P444A

Descriptors: adamantane analogs and derivatives, influenza A virus avian drug effects, rimantadine pharmacology, viral proteins biosynthesis, chick embryo, fibroblasts microbiology, avian metabolism, RNA, messenger metabolism.


NAL Call Number: 385 B523

Abstract: An anti-influenza preparation, rimantadine (alpha-methyl-1-adamantane methylamine hydrochloride) at concentrations of 10-25 mkg/ml depresses the RNA-dependent RNA polymerase induction in a culture of cells infected with influenza virus (fowl plague virus). The inhibitory effect is also observed 2 hours following cell infection. In vitro studies have demonstrated that rimantadine has no effect on the activity of virus-induced RNA-dependent RNA polymerase, as well as on that of RNA-dependent RNA polymerase associated with virus particles.

Descriptors: adamantane analogs and derivatives, antiviral agents pharmacology, bridged compounds analogs and derivatives, influenza A virus avian, RNA nucleotidyltransferases biosynthesis, RNA replicate biosynthesis, adamantane pharmacology, cultured cells, enzyme induction drug effects, virus cultivation.

NAL Call Number: 448.8 P942

Descriptors: antiviral agents pharmacology, cyclohexanes pharmacology, influenza microbiology, influenza A virus avian drug effects, virus replication drug effects, antiviral agents adverse effects, cell line, chick embryo, fibroblasts enzymology, hemagglutinins viral biosynthesis, avian isolation and purification, neuraminidase metabolism, tissue culture.


NAL Call Number: 448.3 Ar23

Abstract: H5, H7, and H9 subtype influenza viruses in land-based poultry often differ from viruses of wild aquatic birds by deletions in the stalk of the neuraminidase, by the presence of additional carbohydrates on the hemagglutinin, and by occasional changes in the receptor specificity. To test whether these differences could reflect distinctions between the virus receptors in different avian species, we compared the binding of duck, chicken and human influenza viruses to cell membranes and gangliosides from epithelial tissues of duck, chicken and African green monkey. Human viruses bound to cell membranes of monkey and chicken but not to those of duck, suggesting that chicken cells unlike duck cells contain Sia(alpha2-6)Gal-terminated receptors recognized by human viruses. Duck virus bound to gangliosides with short sugar chains that were abundant in duck intestine. Human and chicken viruses did not bind to these gangliosides and bound more strongly than duck virus to gangliosides with long sugar chains that were found in chicken intestinal and monkey lung tissues. Our data suggest that the spectrum of sialylglycoconjugates which can serve as influenza virus receptors in chicken is more similar to the spectrum of receptors in the respiratory epithelia of monkey than to that in the epithelial tissues of duck. This notion could explain the recent emergence of avian H9N2 virus lineage with human virus-like receptor specificity and emphasizes the role of the chicken as a potential intermediate host for the transmission of viruses from aquatic birds to humans.

Descriptors: chickens, ducks, influenza A virus avian metabolism, influenza A virus human metabolism, receptors, virus chemistry, receptors, virus metabolism, binding sites, cell membrane metabolism, cercopithecus aethiops, epithelial cells metabolism, gangliosides chemistry, gangliosides metabolism, oligosaccharides chemistry, oligosaccharides metabolism, receptors, cell surface chemistry, receptors, cell surface metabolism.


NAL Call Number: 41.8 Av5

Abstract: To study whether influenza virus receptors in chickens differ from those in other species, we compared the binding of lectins and influenza viruses with known receptor specificity to cell membranes and gangliosides from epithelial tissues of ducks, chickens, and African green monkeys. We found that chicken cells contained Neu5Acalpha(2-6)Gal-terminated receptors recognized by Sambucus nigra lectin and by human viruses. This finding explains how some recent H9N2 viruses replicate in chickens despite their human virus-like receptor specificity. Duck virus bound to gangliosides with short sugar chains that were abundant in duck intestine. Human and chicken viruses did not bind to these gangliosides and bound more strongly than duck virus to gangliosides with long sugar chains that were found in chicken intestinal and monkey lung tissues. Chick and duck viruses also differed by their ability to recognize the structure of the third sugar moiety in Sia2-3Gal-terminated receptors. Chicken viruses preferentially bound to Neu5Acalpha(2-3)Galbeta(1-4)GlcNAc-containing synthetic sialylglycopolymer, whereas duck viruses displayed a higher affinity for Neu5Acalpha(2-3)Galbeta(1-3)GalNAc-containing polymer. Our data indicate that sialyloligosaccharide receptors in different avian species are not identical and provide a potential explanation for the differences between the hemagglutinin and neuraminidase proteins of duck and chicken viruses.

**NAL Call Number:** 448.8 V81

**Abstract:** Synthetic sialylglycoconjugates bearing 3'-sialyllactose, 6'-sialyllactose, or 6'-sialyl(N-acetyllactosamine) moieties attached to the polyacrylic acid carrier (P-3-SL, P-6-SL, and P-6-SLN, respectively) were prepared and tested for their ability to bind to influenza virus isolates from different hosts in a competitive solid phase assay. The virus panel included egg-grown avian and porcine strains, as well as human viruses isolated and propagated solely in mammalian (MDCK) cells and their egg-adapted variants. A clear correlation was observed between the pattern of virus binding of two glycopolymers, P-3-SL and P-6-SLN, and the host species from which the virus was derived. Avian isolates displayed a high binding affinity for P-3-SL and a two to three orders of magnitude lower affinity for P-6-SLN. By contrast, all non-egg-adapted human A and B viruses bound P-6-SLN strongly but did not bind P-3-SL. Unlike the "authentic" human strains, their egg-adapted counterparts acquired an ability to bind P-3-SL, indicative of a shift in the receptor-binding phenotype toward the recognition of Neu5Ac2-3Gal-terminated sugar sequences. Among the porcine viruses and human isolates with porcine hemagglutinin, few displayed an avian-like binding phenotype, while others differed from both avian and human strains by a reduced ability to discriminate between P-3-SL and P-6-SLN. Our data show that sialylglycopolymers may become a useful tool in studies on molecular mechanisms of interspecies transfer, tissue specificity, and other structure-function relationships of the influenza virus hemagglutinin.

**Descriptors:** amino sugars metabolism, influenza A virus avian metabolism, human metabolism, porcine metabolism, influenza B virus metabolism, lactose analogs and derivatives, receptors, virus metabolism, sialic acids metabolism, amino sugars chemistry, cell line, chick embryo, dogs, glycoconjugates metabolism, human isolation and purification, influenza B virus isolation and purification, lactose chemistry, lactose metabolism, phenotype, receptors, virus chemistry, sialic acids chemistry.


**NAL Call Number:** 448.8 V81

**Abstract:** We studied receptor-binding properties of influenza virus isolates from birds and mammals using polymeric conjugates of sialooligosaccharides terminated with common Neu5Ac[alpha]2-3Gal[beta] fragment but differing by the structure of the inner part of carbohydrate chain. Viruses isolated from distinct avian species differed by their recognition of the inner part of oligosaccharide receptor. Duck viruses displayed high affinity for receptors having [beta]1-3 rather than [beta]1-4 linkage between Neu5Ac[alpha]2-3Gal-disaccharide and penultimate N-acetylhexosamine residue. Fucose and sulfate substituents at this residue had negative and low effect, respectively, on saccharide binding to duck viruses. By contrast, gull viruses preferentially bound to receptors bearing fucose at N-acetylgalcosamine residue, whereas chicken and mammalian viruses displayed increased affinity for oligosaccharides that harbored sulfo group at position 6 of ([beta]1-4)-linked GlcNAc. These data suggest that although all avian influenza viruses preferentially bind to Neu5Ac[alpha]2-3Gal-terminated receptors, the fine receptor specificity of the viruses varies depending on the avian species. Further studies are required to determine whether observed host-dependent differences in the receptor specificity of avian viruses can affect their ability to infect humans.

**Descriptors:** animals, birds, carbohydrate sequence, chickens, ducks, humans, avian influenza A virus metabolism, avian influenza A virus pathogenicity, human influenza A virus metabolism, human influenza A virus pathogenicity, porcine influenza A virus metabolism, porcine influenza A virus pathogenicity, molecular models, molecular sequence data, oligosaccharides chemistry, oligosaccharides metabolism, virus receptors chemistry, virus receptors metabolism, species specificity, swine, U.S. Government P.H.S. research support, N.I.H. extramural research support, non-U.S. Government research support.

NAL Call Number: 470 Sci2

Abstract: The 1918 influenza pandemic resulted in about 20 million deaths. This enormous impact, coupled with renewed interest in emerging infections, makes characterization of the virus involved a priority. Receptor binding, the initial event in virus infection, is a major determinant of virus transmissibility that, for influenza viruses, is mediated by the hemagglutinin (HA) membrane glycoprotein. We have determined the crystal structures of the HA from the 1918 virus and two closely related HAs in complex with receptor analogs. They explain how the 1918 HA, while retaining receptor binding site amino acids characteristic of an avian precursor HA, is able to bind human receptors and how, as a consequence, the virus was able to spread in the human population.


NAL Call Number: QR360.A1J6

Descriptors: cultured cells metabolism, influenza A virus avian pathogenicity, L cells cell line, proteins biosynthesis, RNA biosynthesis, antigens, viral metabolism, carbon isotopes, cell fractionation, cell nucleus metabolism, chick embryo, complement fixation tests, cytopathogenic effect, viral, cytoplasm metabolism, dactinomycin pharmacology, electrophoresis, disc, hemagglutinins viral metabolism, avian enzymology, avian growth and development, avian immunology avian metabolism, neuraminidase metabolism, RNA viral biosynthesis, time factors, tritium, uridine metabolism, valine metabolism, viral proteins biosynthesis, virus replication.


NAL Call Number: 448.8 V81

Abstract: The cDNA encoding the murine Mx1 protein, a mediator of resistance to influenza virus, was inserted into a replication-competent avian retroviral vector in either the sense (referred to as Mx+) or the antisense (referred to as Mx-) orientation relative to the viral structural genes. Both vectors produced virus retaining the Mx insert (Mx recombinant viruses referred to as Mx+ and Mx-) following transfection into chicken embryo fibroblasts (CEF). Mx protein of the appropriate size and nuclear localization was expressed only in CEF cells infected with the Mx+ virus. Mx expression was observed in all Mx(+)-infected cells and was stable during long-term culture. Cells infected with the Mx+ virus were resistant to infection by human influenza A/WSN/33 (H1N1) and avian influenza viruses A/Turkey/Wisconsin/68 (H5N9) and A/Turkey/Massachusetts/65 (H6N2), but were susceptible to infection by the enveloped RNA viruses Sindbis and vesicular stomatitis virus (VSV). Normal CEF and cells infected with the Mx virus were susceptible to influenza A, Sindbis, and VSV. The synthesis of influenza proteins, especially the larger polymerase and hemagglutinin proteins, was reduced in Mx+ retrovirus-infected cells superinfected by influenza A.

Descriptors: GTP binding proteins, influenza A virus avian growth and development, growth and development, proteins physiology, transfection, virus inhibitors physiology, cell line, cultured cells, chick embryo, fibroblasts cytology, fluorescent antibody technique, genetic predisposition to disease, immunoblotting, mice, mice, inbred strains, plaque assay, proteins genetics.
NAL Call Number: 448.3 M583
Descriptors: HeLa cells immunology, hemagglutination inhibition tests, influenza A virus avian immunology, methods.

NAL Call Number: QR360.A1J6
Abstract: Molecular changes in the haemagglutinin (HA)-coding regions and proteolytic cleavage sites from multiple H5N2 subtype viruses isolated during a recent outbreak of avian influenza (Al) in central Mexico have been characterized. Eighteen isolates, collected during a 15 month period (October 1993 to January 1995) from six central states, were sequenced. None of the 18 predicted HA1 amino acid sequences were identical and changes were not restricted to a specific region of the sequence. Phylogenetic analyses of the HA1 sequences demonstrated two virus lineages, designated Puebla and Jalisco, with sequence variation as high as 10.5% for amino acid and 6.2% for nucleotide sequences. During the latter months of the surveillance period, highly pathogenic (HP) strains of Al emerged causing lethal disease in commercial poultry flocks. In each of the HP strains isolated, the HA protein was cleaved in chicken embryo fibroblast cells in the absence of trypsin, and two alterations not found in earlier non-HP isolates were detected. In the HA protein, HP strains all had a glutamic acid replaced by lysine substitution at amino acid position 324 and an insertion of arginine and lysine as new residues 325 and 326. The insertion appears to be due to a duplication of the nucleotide sequence AAAGAA at nucleotide positions 965-970 of the HA1-coding region. Computer-assisted secondary structure analyses place the target for the insertion in a predicted RNA stem-loop structure. A mechanism is suggested by which the polymerase duplicates the sequence.
Descriptors: avian influenza virus, structural genes, viral hemagglutinins, nucleotide sequences, amino acid sequences, pathogenicity, phenotypes, heterogeneity, phylogeny, molecular conformation, Mexico, secondary structure, cleavage site sequence, molecular sequence data, GENBANK u37165, GENBANK u37166, GENBANK u37167, GENBANK u37168, GENBANK u37169, GENBANK u37170, GENBANK u37171, GENBANK u37172, GENBANK u37173, GENBANK u37174, GENBANK u37175, GENBANK u37176, GENBANK u37177, GENBANK u37178, GENBANK u37179, GENBANK u37180, GENBANK u37181, GENBANK u37182.

NAL Call Number: RC111.R4
Abstract: An analysis was made of 149 influenza A viruses isolated from ducks in Hong Kong during the period of November 1975 through October 1977. The viruses were isolated five times more frequently from ducks raised in the People's Republic of China than from those raised in Hong Kong. The isolation rate for viruses was higher from the cloaca than it was from the trachea, but this pattern varied over the two years of investigation. The large number of different combinations (30) of hemagglutinin and neuraminidase genes suggests that recombination of viruses was taking place. Analysis of these combinations showed that their distribution was not random and that certain combinations occurred more frequently, and others less frequently, than was expected. The recombination of influenza viruses and the excess or restriction of
certain combinations may have implications for the evolution of pandemic strains of influenza virus in humans.

Descriptors: ducks microbiology, influenza A virus avian genetics, recombination, genetic, China, cloaca microbiology, evolution, gene frequency, genotype, hemagglutinins viral genetics, Hong Kong, influenza A virus avian isolation and purification, neuraminidase genetics, paramyxoviridae isolation and purification, seasons, trachea microbiology.

NAL Call Number: 383 So1
Abstract: The spike glycoproteins of many enveloped viruses are proteolytically cleaved at the carboxytermini of sequences containing the basic motif R-X-K/R-R. Cleavage is often necessary for the fusion capacity of the glycoproteins and, thus, for virus infectivity. Among these viruses are pathogenic avian influenza viruses, human parainfluenza virus, human cytomegalovirus, and human immunodeficiency virus; it has been demonstrated that these viruses can be activated by furin. Indigenous furin has been identified in T-lymphocytes, which are host cells for HIV. Furin has been localized in the TGN and on the surface of cells after vectorial expression. Peptidylchloroalkylketones have been designed that inhibit with high specificity cleavage and fusion activity of viral glycoproteins, as well as virus replication.
Descriptors: blood and lymphatics, cell biology, enzymology, genetics, infection, membranes, metabolism, microbiology, molecular genetics, avian influenza viruses, cell surface, cleavage, fusion activity, glycoprotein fusion, human parainfluenza virus, T lymphocyte, trans Golgi network, viral infectivity, virus infectivity, virus replication.

NAL Call Number: 448.8 V81
Descriptors: hemagglutinins viral metabolism, influenza A virus avian metabolism, protein precursors metabolism, amino acid sequence, peptide fragments analysis, protein processing, post translational.

NAL Call Number: 448.8 V81
Abstract: Lysates of cultured cells have been analyzed for arginine-specific endoproteases using peptidyl-p-nitroanilides as chromogenic substrates. The enzymes present in MDBK, MDCK, VERO, BHK, and chick embryo cells required lysine-arginine or arginine-arginine pairs as cleavage sites, whereas chorioallantoic membrane cells contained, in addition, an activity that could cleave at a single arginine. The effect of peptidyl chloroalkyl ketones on the activation of the fowl plague virus hemagglutinin by the proteases specific for paired basic residues has been investigated. When virions containing uncleaved hemagglutinin were incubated with lysates of uninfected cells, cleavage was completely inhibited by peptidyl chloroalkyl ketones containing paired basic residues at a concentration of 1 mM. In contrast a compound containing a single arginine had no inhibitory activity. When dibasic peptidyl chloroalkyl ketones were added to infected cell cultures, cleavage of hemagglutinin and multiple cycles of virus replication were inhibited at 10 mM. However, a 100- to 200-fold increase of the inhibitory activity in intact cells could be achieved by N-terminal acylation. These studies suggest a potential role of peptidyl chloroalkyl ketones as antiviral agents.
Descriptors: amino acid chloromethyl ketones pharmacology, hemagglutinins viral metabolism, influenza A virus avian metabolism, protease inhibitors pharmacology, protein processing, post translational drug effects, cell membrane enzymology, cultured cells, dogs, molecular weight, protease inhibitors chemical synthesis, structure activity relationship, virus replication.

Abstract: Factors determining cleavability of influenza virus hemagglutinin which is activated by ubiquitous cellular endoproteases were analysed by carrying out site-directed mutagenesis on the cloned hemagglutinin genes of strains A/FPV/Rostock/34 (subtype H7) and A/Port Chalmers/1/73 (subtype H3). Substitutions at the cleavage site of the H7 hemagglutinin indicate that the tetrapeptide Arg-X-Lys/Arg-Arg is the minimal consensus sequence recognized by the ubiquitous proteases. The H3 hemagglutinin also became susceptible to these enzymes, when additional arginines were inserted at the cleavage site. Three arginines were sufficient, when the carbohydrate was removed, whereas four additional arginines are needed when this carbohydrate was present, indicating that the accessibility of the cleavage motif is important for the protease. The appropriate localization of the basic cleavage motif within the amino acid sequence and the spatial structure of the hemagglutinin precursor is an additional prerequisite for cleavage.

Descriptors: endopeptidases metabolism, genes viral, hemagglutinin viral genetics, influenza A virus avian genetics, mutagenesis, site directed, amino acid sequence, base sequence, cell fusion, cell line, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral metabolism, influenza A virus avian immunology, molecular sequence data, oligodeoxyribonucleotides, recombinant proteins metabolism, viral envelope proteins genetics.


Abstract: Five temperature-sensitive mutants of influenza virus A/FPV/Rostock/34 (H7N1), ts206, ts293, ts478, ts482, and ts651, displaying correct hemagglutinin (HA) insertion into the apical plasma membrane of MDCK cells at the permissive temperature but defective transport to the cell surface at the restrictive temperature, have been investigated. Nucleotide sequence analysis of the HA gene of the mutants and their revertants demonstrated that with each mutant a single amino acid change is responsible for the transport block. The amino acid substitutions were compared with those of mutants ts1 and ts227, which have been analyzed previously (W. Schuy, C. Will, K. Kuroda, C. Scholtissek, W. Garten, and H.-D. Klenk, EMBO J. 5:2831-2836, 1986). With the exception of ts206, the changed amino acids of all mutants and revertants accumulate in three distinct areas of the three-dimensional HA model: (i) at the tip of the 80-A (8-nm)-long alpha helix, (ii) at the connection between the globular region and stem, and (iii) in the basal domain of the stem. The concept that these areas are critical for HA assembly and hence for transport is supported by the finding that the mutations that are unable to leave the endoplasmic reticulum at the nonpermissive temperature do not correctly trimerize. Upon analysis by density gradient centrifugation, cross-linking, and digestion with trypsin and endoglucosaminidase H, two groups can be discriminated among these mutants: with ts1, ts227, and ts478, the HA forms large irreversible aggregates, whereas with ts206 and ts293, it is retained in the monomeric form in the endoplasmic reticulum. With a third group, comprising mutants ts482 and ts651 that enter the Golgi apparatus, trimerization was not impaired.

Descriptors: hemagglutinin viral metabolism, influenza A virus avian metabolism, membrane glycoproteins metabolism, amino acid sequence, base sequence, biological transport, cell membrane metabolism, cell polarity, hemagglutinins viral chemistry, hemagglutinin viral genetics, influenza A virus avian genetics, macromolecular systems, membrane glycoproteins chemistry, membrane glycoproteins genetics, molecular sequence data, protein binding, protein conformation, protein processing, post translational, RNA viral genetics.


Abstract: Differences of nucleoproteins of human and avian influenza A virus strains shown by polyacrylamide gel electrophoresis and by the peptide mapping.

Descriptors: influenza A virus avian genetics, influenza A virus human genetics, nucleoproteins analysis, birds, electrophoresis, polyacrylamide gel, peptide mapping.
Abstract: Electrophoretic mobility differences in polyacrylamide gels were detected between (35S)-methionine-labelled nucleoproteins (NPs) induced in monolayer cells by 15 human and 4 avian reference strains of influenza viruses. The (35S)-methionine-labelled tryptic peptides of nucleoproteins of these strains were also analyzed by peptide mapping technique. Based on several detectable hydrophilic peptides the NPs could be arranged in 7 clearly differentiable groups. After radioiodination of NPs from 4 human and 3 avian reference strains the tryptic peptide patterns showed one clear difference between human and avian strains.

Descriptors: influenza A virus analysis, nucleoproteins analysis, viral proteins analysis, electrophoresis, polyacrylamide gel, influenza A virus avian analysis, influenza A virus avian genetics, influenza A virus human analysis, influenza A virus human genetics, influenza A virus genetics, peptide fragments analysis, variation genetics.


Abstract: NP proteins of 19 reference and 42 epidemic strains of influenza A virus were analysed for their mobility in polyacrylamide gel electrophoresis and distribution of tryptic peptides. The strains could be divided into 4 groups by differences in their electrophoretic mobility, and into 9 groups according to reproducible differences of several hydrophilic peptides determined by peptide mapping.

Descriptors: influenza A virus avian analysis, influenza A virus human analysis, nucleoproteins analysis, variation genetics, viral proteins analysis, birds, electrophoresis, polyacrylamide gel methods, East Germany, peptide mapping methods, viral structural proteins.


Abstract: Treatment with neuraminidase (100 units/ml) of chick embryo fibroblasts in vitro only partially inhibits adsorption of fowl plague virus on these cells. Cultivation of chick embryo fibroblasts in the presence of 50 units/ml neuraminidase had no effect on the sensitivity of these cells to fowl plague virus and on the extent of virus reproductions. It is suggested that neuraminic acid which is a component of the external cell membrane is not only substance responsible for adsorption of orthomyxoviruses.

Descriptors: influenza A virus avian drug effects, neuraminidase pharmacology, virus replication drug effects, adsorption, chick embryo, dose response relationship, drug, fibroblasts drug effects, time factors, virus cultivation.


Abstract: Changes in RNA synthesis in tissue culture cells infected with myxoviruses were studied. Changes in RNA synthesis in tissue culture cells infected with myxoviruses were studied.

Descriptors: influenza A virus avian metabolism, Newcastle disease virus metabolism, RNA biosynthesis, radiation effects, carbon isotopes, chick embryo, cycloheximide pharmacology, fibroblasts metabolism, fowl plague metabolism, influenza A virus avian radiation effects, Newcastle disease metabolism, Newcastle disease virus radiation effects, RNA nucleotidyltransferases metabolism, tissue culture, ultraviolet rays, uridine metabolism.


**NAL Call Number:** QR360.A1J6

**Abstract:** The rate of incorporation of 5-fluorouracil into complementary strands of replicating RNA of fowl plague virus (FPV) has been studied. The efficiency of incorporation was estimated by determination of the reversion frequency in s-mutants with known types of base transitions in the RNA of the virus particle. It was established that maximum incorporation of 5-fluorouracil into progeny virus particle RNA took place between 2 and 4 h after infection. The maximum incorporation of the mutagen into complementary RNA (plus strands) occurred when the cells were exposed to 5-fluorouracil from 1 to 2 h after infection.

**Descriptors:** influenza A virus avian metabolism, mutation, RNA viral biosynthesis, base sequence, ethyl methanesulfonate pharmacology, fluorouracil metabolism, fluorouracil pharmacology, hydroxylamines pharmacology, influenza A virus avian growth and development, mutagens, nitrous acid pharmacology, virus replication.


**NAL Call Number:** 448.3 AC85

**Descriptors:** hydroxylamines pharmacology, influenza A virus avian drug effects, mutagens pharmacology, mutation drug effects, cultured cells, chick embryo, cytosine metabolism, hydrogen-ion concentration, influenza A virus avian metabolism, influenza A virus avian pathogenicity, plaque assay, RNA viral metabolism, time factors, uracil metabolism.


**NAL Call Number:** 448.3 Ar23

**Descriptors:** influenza A virus avian drug effects, influenza A virus avian radiation effects, mutation, centrifugation, density gradient, chick embryo, chromatography, DEAE-cellulose, fibroblasts, mutagens, protamines pharmacology, radiation effects, sodium chloride, temperature, tissue culture, ultraviolet rays, virus replication.


**NAL Call Number:** QR360.A1J6

**Descriptors:** chromatography, DEAE-cellulose, influenza A virus avian isolation and purification, mutation, chick embryo, culture media, evaluation studies, fibroblasts, genetics, microbial, hemagglutination tests, hydroxylamines, influenza A virus avian growth and development, mutagens, protamines, sodium chloride, tissue culture.


**Descriptors:** genetics, microbial, influenza A virus avian drug effects, mutagens, virus replication drug effects, acridines, azirines, mutation, nitroso compounds.


**NAL Call Number:** 41.8 C61
Descriptors: cell culture, cytopathogenicity, avian influenza virus, turkeys.


Descriptors: cell culture, cytopathogenicity, avian influenza virus, poultry.


NAL Call Number: 448.8 V81

Descriptors: influenza A virus avian analysis, poly A analysis, RNA viral analysis, adenine nucleotides analysis, base sequence, cell free system, influenza A virus avian metabolism, RNA viral biosynthesis, viral isolation and purification, tissue culture, viral proteins analysis, viral proteins biosynthesis.


NAL Call Number: QR360.A1J6

Descriptors: fibroblasts radiation effects, influenza A virus avian metabolism, RNA viral biosynthesis, ultraviolet rays, carbon isotopes, chick embryo, fibroblasts enzymology, RNA viral analysis, radiation effects, ribonucleases metabolism, thymidine biosynthesis, tissue culture, uridine biosynthesis, virus replication.


NAL Call Number: QR360.A1J6

Abstract: Recombinants of human influenza type A viruses, A/Krasnodar/101/1959 (H2N2) or A/Habarovsk/15/1976 (H3N2), and fowl plague virus (FPV), strain Weybridge (Hav1Neq1) were obtained. The genome of the recombinant obtained by recombination of influenza A/Habarovsk/15/1976 virus and FPV contained the genes 4 (HA) and 6 (NA) derived from the influenza A/Habarovsk virus and all the other genes [1, 2, 3, 5 (NP), 7 (M), 8 (NS)] from FPV. The genome of the recombinant of A/Krasnodar/101/1959 virus and FPV contained the genes 2, 4 (HA) and 6 (NA) derived from influenza A/Krasnodar virus and all the other genes [1, 3, 5, (NP), 7 (M), 8 (NS)] from FPV. The recombinants, like FPV, gave high virus yields in chick embryos and could multiply at high temperatures (40 and 42 degrees C), but, like human influenza viruses, were non-pathogenic for chickens and did not replicate in chick embryo fibroblast culture, but did replicate in a human conjunctiva cell line, clone 1-5C-4. The virion transcriptase of the recombinants, in a number of properties determined in vitro, was similar to FPV transcriptase but not to the human influenza virus enzyme.

Descriptors: influenza A virus avian genetics, influenza A virus human genetics, recombination, genetic, chick embryo, influenza A virus avian analysis, influenza A virus human analysis, peptides analysis, RNA viral analysis, viral proteins analysis, virus replication.


NAL Call Number: 448.3 Ar23

Abstract: A fowl plague virus (FPV) temperature-sensitive mutant ts 5 having mutation lesions in the gene coding for the neuraminidase has been obtained. The mutant induced synthesis of cRNA, vRNA and proteins in cells under non-permissive conditions, but formation of virions including non-infectious ones was defective. The neuraminidase and haemagglutinin synthesized under non-permissive conditions possessed functional activity and could migrate from the rough endoplasmic reticulum into plasma membranes; however, cleavage of the haemagglutinin was reduced. In ts 5-infected cells under non-permissive conditions the synthesis of segments 5 and 8 of cRNA and vRNA was predominant both early and late in the reproduction cycle, and the synthesis of P1, P2, P3, HA and M proteins was reduced after approximately 3 hours. The data obtained suggest that involvement of the neuraminidase in the formation of infectious virions may have no direct association with the enzymatic activity of this protein, and that the mutation in the neuraminidase may affect regulation of replication and transcription processes.

**Abstract:** The anticholinergic anti-parkinsonism drug Norakin is an inhibitor of influenza virus multiplication. By crossing a Norakin-resistant variant of fowl plague virus (FPV) strain Weybridge with the sensitive FPV/Rostock/34 wild-type virus, Norakin-resistant recombinants were obtained. Analyses of the gene composition showed that all Norakin-resistant recombinants had inherited their haemagglutinin gene from the Norakin-resistant parent strain. The majority of the recombinants had received all the other gene segments from the sensitive parent strain. Norakin was shown to inhibit red blood cell lysis induced either by purified virions or by the haemagglutinin of a sensitive FPV strain at low pH, but failed to affect the Norakin-resistant FPV variant. No aggregation of autoliposomes containing the haemagglutinin of a sensitive FPV strain or digestion of the HA1 subunit of haemagglutinin by trypsin occurred in the presence of Norakin at acid pH. The data suggest that the haemagglutinin of FPV is the target for the antiviral activity of Norakin, which acts by inhibiting the conformational change in the haemagglutinin at acid pH important for lysis.

**Descriptors:** hemagglutinin viral genetics, hemagglutinin viral metabolism, influenza A virus avian drug effects, piperidines pharmacology, cultured cells, chick embryo, drug resistance, microbial, genes viral, hemagglutination drug effects, hemolysis drug effects, hydrogen-ion concentration, liposomes, membrane fusion drug effects, recombination, genetic, trypsin metabolism, virus replication drug effects.


**Abstract:** Fowl plague virus (FPV) ts mutants belonging to six recombination groups and obtained from the Weybridge strain (in the U.S.S.R.) or the Rostock strain (in the U.K.) have been studied in a recombination test. Temperature-sensitive mutants obtained from different FPV strains were revealed which had a ts mutation in gene 1; however, their crossing resulted in ts+ recombinants which appeared with a high frequency. This phenomenon was due not to intragenic complementation but to extragenic suppression, when the expression of a ts phenotype of the Rostock strain mutant gene 1 is suppressed by gene 2 products of the Weybridge strain.

**Descriptors:** influenza A virus avian genetics, gene expression regulation, genes viral, mutation, recombination, genetic, suppression, genetic, temperature.


**Abstract:** The effects of edeine, hygromycin B and alpha-sarcin on the synthesis of virus-specific proteins and formation of infectious virions was studied in cells infected with fowl plague virus (FPV). The manifestation of the antiviral effect of edeine depended on the peculiarities of the FPV strains and the host-cell systems. Hygromycin B inhibited significantly the synthesis of virus-specific proteins and the formation of the infectious virions, but did not influence protein synthesis in uninfected cells. Alpha-Sarcin in the concentrations tested neither showed a marked antiviral activity nor affected protein synthesis in the uninfected cells.

**Descriptors:** anti bacterial agents pharmacology, edeine pharmacology, endoribonucleases, fungal proteins pharmacology, hygromycin B pharmacology, influenza A virus avian drug effects, virus replication drug effects, cell line, chick embryo, hamsters, influenza A virus avian growth and development, influenza A virus avian metabolism, kidney, tissue culture, viral proteins biosynthesis.

Ghendon, Y.U.Z. and T.A. Mikhailovskaya (1982). Effect of kanamycin on the reproduction of

**NAL Call Number:** 448.3 AC85

**Abstract:** Kanamycin sulphate at a concentration of 8 mmol/l had no effect on the protein synthesis in uninfected chick embryo cell (CEC) cultures, but caused a 2-fold decrease of virus-specific protein synthesis in CEC infected with fowl plague virus (FPV). Kanamycin at a concentration of 2 mmol/l decreased the yield of infectious FPV in one growth cycle experiments on CEC culture by 1.5 log10 units and when added into the agar overlay it decreased the plaque number by nearly 1 log10 unit. Inoculation of 10 mg of kanamycin into a chick embryo decreased the yield of virus by 1.0 log10. Administration of kanamycin to mice (5-10 mg for three days post infection) reduced mortality of the animals 2--3-fold. Antibiotics of the streptomycin group presumably may penetrate into orthomyxovirus-infected cells due to virus-induced impairment of leakiness of the cell membrane and inhibit both the virus protein synthesis and formation of infectious virions.

**Descriptors:** influenza A virus avian drug effects, influenza A virus human drug effects, kanamycin pharmacology, cultured cells, chick embryo, influenza A virus avian growth and development, influenza A virus human growth and development, influenza A virus human pathogenicity, mice, proteins biosynthesis.


**NAL Call Number:** QR360.J6

**Descriptors:** influenza A virus avian, Newcastle disease virus, RNA biosynthesis, carbon isotopes, chick embryo, cytosine nucleotides metabolism, fibroblasts, RNA nucleotidylyltransferases metabolism, tissue culture, uridine metabolism, virus replication.


**NAL Call Number:** 448.3 Ar23

**Descriptors:** influenza A virus avian pathogenicity, mutation, polioviruses pathogenicity, brain microbiology, chick embryo, chickens, cytopathogenic effect, viral, genetic complementation test, haplorhini, HeLa cells, influenza A virus avian growth and development, influenza A virus avian isolation and purification, Macaca, mutagens, phenotype, polioviruses growth and development, polioviruses isolation and purification, spinal cord microbiology, temperature, tissue culture, virus cultivation, virus replication.


**NAL Call Number:** 501 L84Pb

**Abstract:** Temperature-sensitive (ts) mutants of fowl plague virus (FPV) were divided into six complementation groups. Experiments with ts mutants having defects of transcription showed that in FPV strain Weybridge, protein P1 coded by gene N2 takes part in primary transcription, and protein P3 coded for by gene N1 takes part in secondary transcription. Ts mutants of FPV with lower pathogenicity were present in all six complementation groups under study. Simultaneous inoculation of chickens with two pathogenic ts mutants of FPV caused death of the chickens and a pathogenic virus with ts+ phenotype was isolated from their organs. By recombination of ts multimutant FPV with human influenza virus a recombinant was obtained that contained genes coding for the haemagglutinin and neuraminidase of human influenza virus; all other genes were derived from FPV. In experiments on volunteers this recombinant appeared to be non-reactogenic but capable of inducing antibody formation.

**Descriptors:** influenza A virus avian genetics, mutation, chickens, hemagglutinins viral genetics, influenza A virus avian pathogenicity, influenza A virus human genetics, RNA viral biosynthesis, recombination, genetic, transcription, genetic, translation, genetic, vaccination, virus replication.


**NAL Call Number:** 448.8 V81

**Descriptors:** influenza A virus avian metabolism, RNA viral biosynthesis, chick embryo, DNA directed RNA
polymerases metabolism, dactinomycin pharmacology, electrophoresis, polyacrylamide gel, fibroblasts, genetic complementation test, influenza A virus avian enzymology, mutation, phenotype, temperature, tissue culture, transcription, genetic, uridine metabolism, viral proteins biosynthesis.


Abstract: Two fowl plague virus temperature-sensitive (ts) mutants belonging to different complementation groups were studied. Both were defective in the synthesis of unpolyadenylated complementary RNA (A(-)cRNA) and virus RNA (vRNA) at non-permissive temperature whereas primary transcription was unaffected. In addition, ts 29, in which the ts mutation is in gene 1 coding for polypeptide P3, has a defect in ‘secondary’ synthesis of mRNA at non-permissive temperature whereas inhibition of mRNA synthesis by ts 131, in which the ts mutation is in gene 2 coding for polypeptide P1, appeared to result from a defect in vRNA synthesis. These results indicate, therefore, that different enzymes are responsible for the syntheses of virus mRNAs and A(-)cRNAs, which is consistent with the apparent differences in initiation and termination of transcription in the two reactions. The patterns of synthesis of the various types of virus RNA during infection are discussed.

Descriptors: genes viral, influenza A virus avian genetics, transcription, genetic, cycloheximide pharmacology, influenza A virus avian metabolism, mutation, RNA, messenger biosynthesis, RNA viral biosynthesis, temperature, viral proteins genetics.


Abstract: A fowl plague virus (FPV) temperature-sensitive mutant, ts 303/1 having a ts mutation in gene 7 coding for the matrix (M) protein has been obtained. The mutant induced synthesis of virus-specific RNA and polypeptides as well as ribonuclear protein (RNP) formation in cells under non-permissive conditions; however, haemagglutinin cleavage was reduced, functionally active haemagglutinin and neuraminidase were absent and virions were not formed. In mutant-infected cells at 36 degrees C haemagglutinin cleavage was also reduced and virions formed had an altered NP:M ratio as well as a decreased haemagglutinin content. A population of virions formed under these conditions was heterogeneous both in morphology and in buoyant density. The data obtained suggest that a mutation in the M proteins of orthomyxoviruses can affect processing of the haemagglutinin and impair final stages of virion morphogenesis.

Descriptors: genes viral, genetic code, influenza A virus avian genetics, viral proteins genetics, genetic complementation test, hemagglutinins viral genetics, microscopy, electron, mutation, neuraminidase genetics, RNA viral genetics, temperature, viral matrix proteins, virion genetics.


Abstract: On interaction of ts mutants of fowl plague virus (FPV) belonging to different complementation
groups and human influenza A viruses under conditions of abortive infection for both partners, complementation was marked and recombinants occurred with a high frequency. The level and degree of complementation as well as the frequency of recombinants depended on the stage at which the reproduction of the human influenza A viruses involved was blocked. On simultaneous inoculation of chicks with two apathogenic ts mutants of FPV belonging to different complementation groups, pathogenic ts+ recombinants appeared. On interaction of influenza B virus with ts mutants of FPV or ultraviolet-irradiated FPV, neither complementation nor recombination was observed. There was no complementation between influenza B virus and ts mutants of FPV even at the level of the formation of virus-specific substructures.

Descriptors: influenza A virus avian genetics, influenza A virus human genetics, mutation, orthomyxoviridae genetics, recombination, genetic, chick embryo, genetic complementation test, influenza A virus avian growth and development, influenza A virus avian pathogenicity, influenza A virus human growth and development, tissue culture.

NAL Call Number: QR375.V6

Abstract: Influenza A virus reassortants which are nonpathogenic for chickens are like mammalian influenza A viruses in that they are temperature sensitive for growth at 41 degrees C. We have investigated the mechanism of this temperature sensitivity using reassortants between the two highly pathogenic strains A/FPV/Rostock/34 (FPV, H7N1) and A/turkey/England/63 (TE, H7N3). These reassortants show a strict correlation between the pathogenicity for chickens and the constellation of the genes coding for the ribonucleoprotein complex, RNP. Evidence is presented which shows that all viral components are synthesized in sufficient amounts and that the block in the viral replication cycle at the nonpermissive temperature is a late one affecting virus maturation. It is suggested that the RNP, although still enzymatically functional, may lose its ability to interact normally with viral surface components, thus interfering with the process of virus maturation. Some of the nonpathogenic reassortants which possessed the neuraminidase of TE showed an interesting temperature-dependent phenomenon: the haemagglutinin synthesized at the elevated temperature could only agglutinate erythrocytes at 20 degrees C, when the neuraminidase was inhibited or the infected cells vigorously disrupted by ultrasonication. This phenomenon is possibly not directly related to the temperature-sensitive block.

Descriptors: influenza A virus avian growth and development, chick embryo, chickens microbiology, genes viral, hemagglutination, viral, influenza A virus avian genetics, influenza A virus avian pathogenicity, influenza A virus avian physiology, neuraminidase metabolism, RNA viral biosynthesis, recombination, genetic, ribonucleoproteins genetics, temperature, viral proteins biosynthesis, virus replication.

NAL Call Number: 448.8 P942

Abstract: A simple method for preparation of monospecific antiserum for the hemagglutinin of fowl plague virus has been developed. It is based on selective inactivation of the enzymatic and antigenic properties of neuraminidase by heating of the virus at 56 degrees for 3 hours followed by disruption of the preparation with detergent and removal of the inner proteins by ultracentrifugation. Immunization of animals with such preparations produced antiserum containing considerable amounts of antibody for the hemagglutinin in the absence of antibody for other proteins of fowl plague virus.

Descriptors: hemagglutininins viral, immune sera, immunologic techniques, influenza A virus avian immunology.

NAL Call Number: 448.3 AC85

Abstract: Some biological properties of recombinants obtained by crossing of fowl plague and human
influenza viruses were studied. The capacity of the recombinants to reproduce in chick embryo fibroblast cultures was in reverse correlation to the number of genes coding for P proteins derived from the human influenza virus. The genome composition was of importance for the expression of ts-phenotype of the recombinants in different systems. Substitution of at least one gene in the fowl plague virus genome by a corresponding human influenza virus gene resulted in the decrease of virulence for 1-day-old chickens. The presence of three P genes from human influenza virus genome in the genome of the recombinant proved to be insufficient for the capability of the recombinant to reproduce in organ cultures of human origin. Descriptors: genes viral, influenza A virus avian genetics, influenza A virus human genetics, recombination, genetic, cultured cells, chick embryo, chickens, influenza A virus avian pathogenicity, influenza A virus avian physiology, influenza A virus human pathogenicity, influenza A virus human physiology, nasal polyps microbiology, organ culture, plaque assay, temperature, virus replication.

Abstract: Organ cultures of human nasal polyps were shown to support the replication of five out of seven human influenza A viruses and three out of six avian strains with varying degrees of efficiency. The ability to replicate was independent of the antigenic formula of the virus. The structure of nasal polyps closely resembled that of normal nasal mucosa and infection with influenza A virus resulted in histological changes analogous to those seen in natural infections. This system provides an in vitro method for more detailed studies of influenza A virus and possibly other respiratory virus infections of man. Descriptors: influenza microbiology, influenza A virus physiology, nasal polyps microbiology, virus replication, influenza A virus avian physiology, influenza A virus human physiology, organ culture, species specificit.

Abstract: Human influenza virus strains were easily grown and passaged in human nasal polyp organ cultures causing marked damage of the epithelium. Unlike to human strains, the animal influenza virus strain could be propagated for no longer than 2 or 3 passages and even the 1st passage failed to cause significant morphological changes of the epithelium cells. Descriptors: influenza A virus avian growth and development, influenza A virus human growth and development, influenza A virus growth and development, nasal polyps microbiology, DNA replication, deer, influenza A virus genetics, nasal polyps pathology, organ culture, species specificity, virus replication.

Abstract: Non-infectious virus particles produced by influenza virus (classical fowl plague)-infected Ehrlich ascitic carcinoma cells have the same morphology, size and sedimentation rate as the standard virions. Their main difference from the allantoic virus is their extreme fragility. They remain intact upon a short-term centrifugation in sucrose solutions but desintegrate upon prolonged centrifugation. In isopicnic fractionation they are detected in two forms, with a density of 1.23 g/ml retaining the hemagglutinating but not the neuraminidase activity and with a density of 1.27 g/ml deprived of both hemagglutinating and neuraminidase activity. In the electron microscopic examination the 1.23 g/ml structure appears as virus particles with defective areas in the surface spikes layer whereas the 1.27 g/ml structure has no spike layer at all. The protein analysis by polyacryl amide gel electrophoresis revealed a sharply reduced amount of the membrane protein in the ascitic virus. A hypothesis is suggested according to which the reduced amount of the membrane protein is the cause of the unusual fragility of ascitic virus particle membranes as a result of which they readily lose glycoproteins which, in its turn, leads to their reduced infectious activity. Descriptors: carcinoma, Ehrlich tumor microbiology, influenza A virus avian isolation and purification,
influenza A virus avian metabolism, cultured cells, centrifugation, centrifugation, density gradient, centrifugation, isopycnic, hemagglutinins viral analysis, microscopy, electron, neuraminidase metabolism, viral proteins analysis.

NAL Call Number: 448.3 Ar23
Descriptors: influenza A virus avian analysis, nucleoproteins analysis, parainfluenza virus 1, human analysis, buffers, carbon isotopes, centrifugation, density gradient, cesium, chick embryo, chlorides, hemagglutination tests, influenza A virus avian isolation and purification, nucleoproteins isolation and purification, parainfluenza virus 1, human isolation and purification, phosphates, phosphorus isotopes, precipitation, RNA, viral, species specificity, sucrose, surface active agents, trichloroacetic acid, virus cultivation.

NAL Call Number: 448.3 AC85
Descriptors: nucleoproteins analysis, orthomyxoviridae analysis, viral proteins analysis, centrifugation, density gradient, cesium, chick embryo, chlorides, influenza A virus avian analysis, nucleoproteins isolation and purification, phosphorus isotopes, sucrose, tissue culture, tritium, viral proteins isolation and purification, virus cultivation.

NAL Call Number: QH301.A25
Abstract: The influence of acidic pH on the infectivity and neuraminidase activity of human, equine and avian type A influenza virus strains has been studied. Following exposure to pH 3 human and equine strains lost their infectivity completely, whereas all investigated strains of the subtypes Hav6N2 and Hav7Neq2 retained a certain amount of infectivity. In contrast to human and equine strains the avian strains retained also 38% of their original neuraminidase activity after acidic treatment. Partial retention of infectivity and the relative stability of the neuraminidase following exposure to acidic pH are supposed to be linked together in avian influenza virus strains implicating neuraminidases for their ability to prevent the aggregation of virions.
Descriptors: influenza A virus human enzymology, influenza A virus enzymology, neuraminidase metabolism, hydrogen-ion concentration, influenza A virus avian enzymology, influenza A virus human pathogenicity, influenza A virus pathogenicity.

NAL Call Number: QR360.J6
Abstract: The interferon-inducible gene (IFI-78K gene) that codes for a human protein, p78, of 78,000 Mr is the equivalent of the mouse Mx gene encoding Mx protein. The IFI-78K gene is located on chromosome 21 together with the alpha/beta interferon (IFN-alpha/beta) receptor. The p78 protein is important since it may be involved in resistance to influenza viruses. The regulation of the IFI-78K gene was studied in human diploid cells by using a cDNA probe to p78 mRNA and specific monoclonal antibodies to p78 protein. The IFI-78K gene, a normally quiescent gene, is transcriptionally regulated by IFN-alpha, and its induction does not require protein synthesis. The rate of transcription measured in a run-on assay increased rapidly but transiently. The level of p78 mRNA increased up to 8 h, declining slowly afterwards. The p78 protein, undetectable in untreated cells, accumulated up to 16 h, and its amount remained stable for at least 36 h after the addition of IFN-alpha. Cytokines such as tumor necrosis factor, interleukin-1 alpha, and interleukin-1 beta activated the IFI-78K gene at concentrations comparable to that of IFN-alpha. However, gene activation by these cytokines required protein synthesis. Poly(rI)-poly(rC) induced the IFI-78K gene directly
at the transcriptional level without requirement for protein synthesis. Newcastle disease virus, influenza virus, and to a lesser extent vesicular stomatitis virus also induced the IFI-78K gene in the absence of any protein synthesis. Induction of transcription by viruses was markedly enhanced by pretreatment of cells with IFN-gamma (which by itself is a poor inducer of the IFI-78K gene), resulting in accumulation of p78 protein during the course of infection; this suggests that IFN-gamma programs cells to full antiviral activity upon virus infection.

Descriptors: chromosomes, human, pair 21, GTP binding proteins, gene expression regulation, proteins genetics, blotting, northern, blotting, western, influenza A virus avian physiology, interferon type I, recombinant pharmacology, interferon gamma, recombinant pharmacology, interleukin 1 pharmacology, Newcastle disease virus physiology, RNA, double stranded pharmacology, recombinant proteins pharmacology, transcription, genetic, translation, genetic, tumor necrosis factor pharmacology, vesicular stomatitis Indiana virus physiology.

NAL Call Number: 396.8 An84
Abstract: The effect of antibiotic 6734-21 on the viruses of variolovaccine, Herpes simplex, influenza and classical avian plague was studied on various experimental models. Antibiotic 6734-21 inhibited development of the variolovaccine virus in the tissue culture, in chick embryos, in rabbits with variolovaccine infection, as well as the development of the viruses of Herpes simplex, Aueski, and Newcastle diseases in the tissue culture. It had a virulicidal effect on the viruses of variolovaccine, influenza and classical avian plague.
Descriptors: anti bacterial agents pharmacology, antiviral agents, anti bacterial agents therapeutic use, chick embryo, herpes simplex drug therapy, herpesvirus 1, suid drug effects, influenza A virus avian drug effects, influenza A virus drug effects, mice, Newcastle disease virus drug effects, rabbits, simplexvirus drug effects, smallpox drug therapy, variola virus drug effects.

NAL Call Number: 396.8 An84
Abstract: The effect of 9 analogues of distamycin A was studied in a tissue culture with respect to the virus of a smallpox vaccine and classical avian plague. Three analogues of distamycin A (I, VI, VII) were studied in chick embryos with respect to the smallpox and influenza viruses. The analogues were characterized by a loss or decrease of the activity against the smallpox vaccine virus as compared to distamycin A. In contrast to distamycin A analogue VII had an inhibitory effect on influenza infection in chick embryos.
Descriptors: antiviral agents, distamycins pharmacology, influenza A virus avian drug effects, orthomyxoviridae drug effects, pyrroles pharmacology, variola virus drug effects.

Abstract: El objetivo fue analizar mediante histopatologia e inmunohistoquimica (IH), el tipo de lesiones y el patron de infectividad que producen en el embrion de pollo y aves al inocular los aislamientos del virus de influenza aviar (IA), provenientes de diferentes zonas del pais. Como cepas de IA de alta patogenicidad, se utilizaron los aislamientos Queretaro y Puebla y como cepa de baja patogenicidad, la cepa vacunal.
Descriptors: avian influenza virus, infection, histopathology, disease transmission, influenza virus, orthomyxoviridae, pathogenesis, pathology, viruses.

Nucleotide sequences of 24 nucleoprotein (NP) genes isolated from a wide range of hosts, geographic regions, and influenza A virus serotypes and 18 published NP gene sequences were analyzed to determine evolutionary relationships. The phylogeny of NP genes was determined by a maximum-parsimony analysis of nucleotide sequences. Phylogenetic analysis showed that NP genes have evolved into five host-specific lineages, including (i) Equine/Prague/56 (EQPR56), (ii) recent equine strains, (iii) classic swine (H1N1 swine, e.g., A/Swine/Iowa/15/30) and human strains, (iv) gull H13 viruses, and (v) avian strains (including North American, Australian, and Old World subgroups). These NP lineages match the five RNA hybridization groups identified by W. J. Bean (Virology 133:438-442, 1984). Maximum nucleotide differences among the NPs was 18.5%, but maximum amino acid differences reached only 10.8%, reflecting the conservative nature of the NP protein. Evolutionary rates varied among lineages; the human lineage showed the highest rate (2.54 nucleotide changes per year), followed by the Old World avian lineage (2.17 changes per year) and the recent equine lineage (1.22 changes per year). The per-nucleotide rates of human and avian NP gene evolution (1.62 x 10(-3) to 1.39 x 10(-3) changes per year) are lower than that reported for human NS genes (2.0 x 10(-3) changes per year; D. A. Buonagurio, S. Nakada, J. D. Parvin, M. Krystal, P. Palese, and W. M. Fitch, Science 232:980-982, 1986). Of the five NP lineages, the human lineage showed the greatest evolution at the amino acid level; over a period of 50 years, human NPs have accumulated 39 amino acid changes. In contrast, the avian lineage showed remarkable conservatism; over the same period, avian NP proteins changed by 0 to 10 amino acids. The specificity of the H13 NP in gulls and its distinct evolutionary separation from the classic avian lineage suggests that H13 NPs may have a large degree of adaptation to gulls. The presence of avian and human NPs in some swine isolates demonstrates the susceptibility of swine to different virus strains and supports the hypothesis that swine may serve as intermediates for the introduction of avian influenza virus genes into the human virus gene pool. EQPR56 is relatively distantly related to all other NP lineages, which suggests that this NP is rooted closest to the ancestor of all contemporary NPs. On the basis of estimation of evolutionary rates from nucleotide branch distances, current NP lineages are at least 100 years old. (ABSTRACT TRUNCATED AT 400 WORDS)

Descriptors: evolution, genes viral, influenza A virus genetics, nucleoproteins genetics, viral proteins genetics, adaptation, biological, amino acid sequence, base sequence, cloning, molecular, DNA, viral analysis, influenza A virus classification, molecular sequence data, phylogeny, software, species specificity.


Abstract: Because cleavage of the hemagglutinin (HA) molecule by proteases is a prerequisite for infectivity of influenza A viruses, this molecule is a major determinant of viral pathogenicity. Although well documented in the pathogenicity of avian influenza viruses, the role of HA cleavage in the pathogenicity of mammalian viruses is not well understood. Therefore, we studied a mouse-adapted human isolate A/WSN/33 (WSN), a neurovirulent influenza virus strain that causes systemic infection when inoculated intranasally into mice. We found a novel mechanism of HA cleavage for WSN virus: the neuraminidase (NA) of WSN virus binds and sequesters plasminogen on the cell surface, leading to enhanced cleavage of the HA. The structural basis of this novel function of the NA molecule appears to be the presence of a carboxyl-terminal lysine and the absence of an oligosaccharide side chain at position 146. To obtain direct evidence that the plasminogen-binding activity of the NA enhances the pathogenicity of WSN virus, we generated mutant viruses that are deficient in plasminogen-binding activity by reverse genetics. The mutant viruses showed attenuated growth in mice and failed to grow at all in the brains of these animals. Therefore, we concluded that the novel function of plasminogen-binding activity of the NA determines the pathogenicity of WSN virus in mice.

Descriptors: influenza A virus enzymology, influenza A virus pathogenicity, neuraminidase metabolism, plasminogen metabolism, virulence, hemagglutinins metabolism, mice, neuraminidase chemistry, protein binding.


NAL Call Number: 448.3 AC85
Abstract: Mouse-adapted (MA) variants of human and avian influenza A (H2) viruses were generated and characterized with respect to acquisition of virulence in mice. From the nucleotide sequence the amino acid sequence was deduced. The HA1 subunit of the hemagglutinin (HA) contained three amino acid substitutions in the A/black duck/New Jersey/1580/78-MA variant (Glu216-->Asp, Lys307-->Arg, and Thr318-->Ile) and two substitutions in the A/JapanxBellamy/57-MA variant (Lys25-->Thr and Ser203-->Phe). In the M1 protein, there were two substitutions in the A/black duck/New Jersey/1580/78-MA variant (Asn30-->Asp and Gln214-->His) and a single substitution in the A/JapanxBellamy/57-MA variant (Met179-->Lys). The M2 protein amino acid sequences of the parental virus and the MA variants differed by a single identical mutation (Asn93-->Ser). The localization and atomic distances of the observed mutations on the three-dimensional (3D) structure of the HA protein were analyzed for influenza H2 viruses. The obtained results were similar to those published earlier on H1, H3 and H5 subtypes. The amino acid changes in the HA protein could be divided into two groups. In one group the substitutions were situated at the top of the molecule, while in the other group they were clustered in the stem area at the interface region between three HA monomers. The analysis revealed that the substitutions observed in the MA variants probably increase the flexibility of the HA molecule and/or weaken the interactions between monomers or subunits in the HA trimer. The relationships of the observed amino acid changes in the HA and M proteins to the biological properties of the respective viruses and possible mechanisms involved in the acquisition of viral virulence are discussed.

Descriptors: bacterial outer membrane proteins, hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian genetics, influenza A virus human genetics, viral matrix proteins genetics, amino acid substitution, bacterial proteins chemistry, bacterial proteins genetics, birds, carrier proteins chemistry, carrier proteins genetics, cell line, chick embryo, hemagglutinin glycoproteins, influenza virus chemistry, influenza A virus avian pathogenicity, influenza A virus human pathogenicity, lung virology, mice, viral matrix proteins chemistry.


NAL Call Number: 448.8 P942

Abstract: Mathematical methods were used to analyse the data on the antigenic specificity of H2 subtype hemagglutinin of human and avian influenza A viruses. This approach allowed the evaluation of possible evolutionary relationships in this little-studied group of viruses. Influenza A (H2) viruses isolated from birds in the USA were found to represent a sufficiently isolated group, whereas European avian strains (A/duck/Germany/1215/73, A/pintail duck/Primor'e/695/76, A/duck/Marseilles/46/76) were close to “human” viruses. The A/Leningrad/1468/65, A/laughing gull/New Jersey/75/85, and A/pintail duck/Alberta/2728/77 strains represent marked antigenic variants apparently rather far gone as a result of hemagglutinin drift.


NAL Call Number: QR360.J6

Abstract: The 2004 outbreaks of H5N1 influenza viruses in Vietnam and Thailand were highly lethal to humans and to poultry; therefore, newly emerging avian influenza A viruses pose a continued threat, not only to avian species but also to humans. We studied the pathogenicity of four human and nine avian H5N1/04 influenza viruses in ferrets (an excellent model for influenza studies). All four human isolates were fatal to intranasally inoculated ferrets. The human isolate A/Vietnam/1203/04 (H5N1) was the most pathogenic isolate; the severity of disease was associated with a broad tissue tropism and high virus titers in
multiple organs, including the brain. High fever, weight loss, anorexia, extreme lethargy, and diarrhea were observed. Two avian H5N1/04 isolates were as pathogenic as the human viruses, causing lethal systemic infections in ferrets. Seven of nine H5N1/04 viruses isolated from avian species caused mild infections, with virus replication restricted to the upper respiratory tract. All chicken isolates were nonlethal to ferrets. A sequence analysis revealed polybasic amino acids in the hemagglutinin connecting peptides of all H5N1/04 viruses, indicating that multiple molecular differences in other genes are important for a high level of virulence. Interestingly, the human A/Vietnam/1203/04 isolate had a lysine substitution at position 627 of PB2 and had one to eight amino acid changes in all gene products except that of the M1 gene, unlike the A/chicken/Vietnam/C58/04 and A/quail/Vietnam/36/04 viruses. Our results indicate that viruses that are lethal to mammals are circulating among birds in Asia and suggest that pathogenicity in ferrets, and perhaps humans, reflects a complex combination of different residues rather than a single amino acid difference.

Descriptors: influenza virus infection, respiratory system disease, viral disease complications, etiology, mortality, pathology, transmission, Vietnam, Thailand, ferrets, chickens, humans.


Abstract: Cross-protection of mice immunized with inactivated preparations of human and avian influenza A (H2) viruses was determined after lethal infection with mouse-adapted (MA) variants of human A/Jap x Bell/57 (H2N1) and avian A/NJers/78 (H2N3) viruses. The MA variants differed from the original strains by acquired virulence for mice and changes in the HA antigenicity. These studies indicated that mice vaccinated with human influenza A (H2) viruses were satisfactorily protected against challenge with A/Jap x Bell/57-MA variant; the survival rate was in the range of 61%-88.9%. Immunization of mice with the same viral preparations provided lower levels of protection against challenge with A/NJers/78-MA variant. Vaccination of mice with the avian influenza A (H2) viruses induced better protection than with human strains against challenge with both MA variants. Challenge with A/NJers/78-MA variant revealed that 76.2%-95.2% of animals were protected when vaccinated with avian influenza virus strains isolated before 1980, and that the protection reached only 52.4%-60.0% in animals vaccinated with strains isolated in 1980-1985. The present study revealed that cross-protection experiments in a mouse model could provide necessary information for the development of appropriate influenza A (H2) virus vaccines with a potential for these viruses to reappear in a human population.


Abstract: Mutations in the influenza M2 membrane protein which confer resistance to the antiviral drug amantadine are exclusively located within the transmembrane region of the molecule. The influence of specific amino acid substitutions on the activity of the M2 protein in influenza A virus-infected cells is assessed in this report by their effects upon haemagglutinin (HA) stability and virus growth. A number of amino acid substitutions, e.g., L26H, A30T, S31N and G34E reduced the activity of the M2 protein of A/chicken/Germany/34 (Rostock) and caused a substantial increase in expression of the low-pH form of HA. The adverse effects of the mutations on virus replication were evident from changes selected during subsequent passage of the mutant viruses in the presence or absence of amantadine: reversion to wt, the acquisition of a second suppressor mutation in M2, or the appearance of a complementary mutation in HA which increased its pH stability. In contrast, 127T and 127S, mutations which were most readily selected following passage of the wt virus in the presence of drug, caused an increase in M2 activity. Furthermore, in double mutants the 127T mutation suppressed the attenuating effects of the A30T and S31N mutations on M2 activity. The influence of primary structure on the consequences of particular amino acid changes was further emphasized by the contrasting effects of the G34E mutation on the activities of two closely related
proteins, causing an increase in the activity of the M2 of A/chicken/Germany/27 (Weybridge) as opposed to the decrease in activity of the Rostock protein. Estimates of differences in trans Golgi pH based on the degree of conversion of HA to the low-pH form, or complementation of differences in pH stability of mutant HAs, indicate that changes in M2 may influence pH within the transport pathway by as much as 0.6. The results thus provide further evidence that M2 regulates transmembrane pH gradients in the trans Golgi. Incompatibility between particular HA and M2 components and the selection of M2 mutants with suboptimal activity stresses the essential relationship between the structures and functions of these two virus proteins. **Descriptors:** amantadine pharmacology, influenza A virus avian metabolism, viral matrix proteins drug effects, viral matrix proteins genetics, water electrolyte balance genetics, amino acid sequence, drug resistance, microbial, genetic complementation test, hemagglutinins viral biosynthesis, hydrogen-ion concentration, influenza A virus avian growth and development, molecular sequence data, mutagenesis, mutation, structure activity relationship, variation genetics.

**NAL Call Number:** 448.3 Ar23
**Descriptors:** hemagglutinins viral, influenza A virus avian immunology, neuraminidase metabolism, Newcastle disease virus enzymology, Newcastle disease virus immunology, orthomyxoviridae immunology, chick embryo, cycloheximide pharmacology, drug stability, fetal membranes, influenza A virus avian enzymology, influenza A virus avian growth and development, Newcastle disease virus growth and development, orthomyxoviridae enzymology, orthomyxoviridae growth and development, tissue culture.

**NAL Call Number:** 448.3 AC85
**Abstract:** A resistant influenza virus has been obtained during successive passages of influenza A virus in 10 to 11-day-old chick embryos (CE) in the presence of 2-(1'-amino-ethyl)-bicyclo(2.2.1) heptane chlorohydrate possessing a high antiviral activity. The virus resistance to the inhibitor was not lost after one passage in the absence of the drug.
**Descriptors:** antiviral agents pharmacology, influenza A virus avian drug effects, norbornanes pharmacology, drug resistance, microbial, virus replication drug effects.

**NAL Call Number:** QD415.A1S62
**Abstract:** Complete nucleotide sequence of the cloned full-length DNA copy of the influenza virus A/FPV Weybridge (H7N7) neuraminidase gene has been determined.
**Descriptors:** base sequence, DNA, viral genetics, genes viral, influenza A virus avian genetics, neuraminidase genetics, sequence homology, nucleic acid, antigens, viral analysis, cloning, molecular, DNA genetics, influenza A virus avian classification, influenza A virus avian enzymology, molecular sequence data.

**NAL Call Number:** QR360.J6
**Abstract:** The transmission of H9N2 influenza viruses to humans and the realization that the A/Hong Kong/156/97-like (H5N1) (abbreviated HK/156/97) genome complex may be present in H9N2 viruses in southeastern China necessitated a study of the distribution and characterization of H9N2 viruses in poultry in the Hong Kong SAR in 1999. Serological studies indicated that H9N2 influenza viruses had infected a high proportion of chickens and other land-based birds (pigeon, pheasant, quail, guinea fowl, and chukka) from
southeastern China. Two lineages of H9N2 influenza viruses present in the live-poultry markets were represented by A/Quail/Hong Kong/G1/97 (Qa/HK/G1/97)-like and A/Duck/Hong Kong/Y280/97 (Dk/HK/Y280/97)-like viruses. Up to 16% of cages of quail in the poultry markets contained Qa/HK/G1/97-like viruses, while about 5% of cages of other land-based birds were infected with Dk/HK/Y280/97-like viruses. No reassortant between the two H9N2 virus lineages was detected despite their cocirculation in the poultry markets. Reassortant viruses represented by A/Chicken/Hong Kong/G9/97 (H9N2) were the major H9N2 influenza viruses circulating in the Hong Kong markets in 1997 but have not been detected since the chicken slaughter in 1997. The Qa/HK/G1/97-like viruses were frequently isolated from quail, while Dk/HK/Y280/97-like viruses were predominately associated with chickens. The Qa/HK/G1/97-like viruses were evolving relatively rapidly, especially in their PB2, HA, NP, and NA genes, suggesting that they are in the process of adapting to a new host. Experimental studies showed that both H9N2 lineages were primarily spread by the aerosol route and that neither quail nor chickens showed evidence of disease. The high prevalence of quail infected with Qa/HK/G1/97-like virus that contains six gene segments genetically highly related to HK/156/97 (H5N1) virus emphasizes the need for surveillance of mammals including humans.

Descriptors: genome, viral, influenza A virus avian isolation and purification, poultry virology, China, hemagglutination inhibition tests, influenza A virus avian genetics, phylogeny, temperature, virus replication.


NAL Call Number: QR360.J6

Abstract: The development of viral resistance to the neuraminidase (NA) inhibitor, 4-guanidino-Neu5Ac2en, of influenza viruses was studied by serial passage of A/Turkey/Minnesota/833/80 (H4N2) in Madin-Darby canine kidney cells in the presence of increasing concentrations of inhibitor. Resistant mutants selected after eight passages, had a 10,000-fold reduction in sensitivity to the inhibitor in plaque assays, but their affinity (1/Kd) to the inhibitor was similar to that of the parental virus. Electron microscopic analysis revealed aggregation of the mutant virus at the cell surface in the presence of the inhibitor. Sequence analysis established that a substitution had occurred in the NA (Arg-249 to Lys) and in the HA2 subunit of the hemagglutinin (Gly-75 to Glu), in the vicinity of the proposed second sialic acid binding site. The change of residue 249 appears to be a chance mutation, for we were unable to reisolate this mutant, whereas subsequent experiments indicate changes in the hemagglutinin. After 13 passages of the parental virus, mutants that were resistant to the high concentrations of inhibitor tested were obtained. These viruses retained their drug-resistant phenotype even after five passages without the inhibitor. Electron microscopic analysis revealed no aggregation of virus on the surface of infected cells in the presence of the inhibitor. Sequence analysis of the NA gene from these drug-resistant mutants revealed an additional substitution of Glu to Ala at the conserved amino acid residue 119. This substitution is responsible for reducing the affinity of the inhibitor to the NA. Our findings suggest that the emergence of mutants resistant to 4-guanidine-Neu5Ac2en is a multistep process requiring prolonged exposure to the inhibitor.

Descriptors: antiviral agents pharmacology, enzyme inhibitors pharmacology, influenza A virus avian drug effects, mutation, neuraminidase antagonists and inhibitors, sialic acids pharmacology, base sequence, cell line, DNA, viral, dogs, drug resistance, microbial genetics, influenza A virus avian enzymology, influenza A virus avian genetics, influenza A virus avian ultrastructure, molecular sequence data, neuraminidase chemistry, turkeys virology.


NAL Call Number: 448.8 J821

Abstract: A recent outbreak of influenza in Hong Kong was caused by a highly virulent virus of avian origin. Concern that the appearance of such a virus in the human population may be a harbinger of a new pandemic has brought increased attention to the issue of antivirals available for treatment of influenza. A/HongKong/156/97 (H5N1), the first virus of H5N1 subtype isolated from a human host, is highly virulent in the mouse model and can infect mouse lungs without requiring adaptation. High mortality and evidence of systemic disease, including spread to the brain after intranasal inoculation, are observed. Zanamivir, a novel
neuraminidase inhibitor, is effective at decreasing replication of the virus in vitro. In a model of lethal challenge in mice, Zanamivir reduces lung titers of the virus and decreases morbidity and mortality.

**Descriptors:** antiviral agents therapeutic use, influenza prevention and control, influenza A virus avian physiology, sialic acids therapeutic use, chick embryo, Hong Kong, influenza physiopathology, influenza A virus avian drug effects, influenza A virus avian isolation and purification, influenza A virus avian pathogenicity, influenza A virus human, lung virology, mice, mice inbred BALB c, organ specificity, virulence, virus replication drug effects.


**NAL Call Number:** 448.8 V81

**Abstract:** The sialidase inhibitor 4-guanidino-2,4-dideoxy-2,3-dehydro-N-acetylneuraminic acid (4-guanidino-Neu5Ac2en), designed with computer assistance and knowledge of the crystal structure of influenza virus neuraminidase, has shown antiviral effects in animal models of human influenza (M. von Itzstein et al., *Nature*, 363, 418-423, 1993). Here we demonstrate that the compound efficiently inhibits the enzyme activity of all nine subtypes of avian influenza A neuraminidase in vitro. When administered intranasally to chickens infected with lethal viruses, high doses of the compound (1000 microgram/kg) protected 85% of birds harboring A/Chick/Victoria/1/85 (H7N7), a fowl plague virus, but not chickens infected with other highly virulent viruses of the N1, N2, or N3 subtype. This differential inhibitory effect was also seen in a plaque reduction assay with Madin-Darby canine kidney cells (MDCK), where 4-guanidino-Neu5Ac2en was more effective against A/Chick/Vic/85 (H7N7) than A/FPV/Rostock/34 (H7N1). In contrast to the substantial plaque reduction observed in MDCK cells, the drug failed to inhibit plaque formation in chicken embryo fibroblasts infected with either A/Chick/Vic/85 or A/FPV/Rostock/34, regardless of its concentration. The different levels of drug efficacy seen in two cell systems most likely reflect the location of virus budding and release in polarized versus nonpolarized cells, as well as the compound’s mode of extracellular action.

**Descriptors:** avian influenza virus, glycosidases, enzyme inhibitors, enzymic activity, inhibition, animal models, influenza virus, mankind, antimetabolites, chemicophysical properties, enzymes, hydrolases, influenza virus, orthomyxoviridae, viruses, sialidase.


**NAL Call Number:** 385 J822

**Abstract:** From the aquatic bacterium *Rhodococcus equi* strain S(420), we isolated a substance that strongly binds to influenza viruses. Structural analyses revealed that it is a unique type of phosphatidylinositol (PtdIns) bearing a branched-chain fatty acid (14-methyloctadecanoic acid). In a TLC/virus-binding immunostaining assay, this PtdIns bound to all subtypes of hemagglutinin (HA) of influenza A viruses tested, isolated from humans, ducks and swine, and also to human influenza B viruses. Furthermore, the PtdIns significantly prevented the infection of MDCK cells by influenza viruses, and also inhibited the virus-mediated hemagglutination and low pH-induced hemolysis of human erythrocytes, which represents the fusogenic activities of the viral HA. We also used purified hemagglutinin instead of virions to examine the interaction between viral HA and PtdIns, showing that the PtdIns binds to hemagglutinin. These findings indicate that the inhibitory mechanism of PtdIns on the influenza virus infection may be through its binding to viral HA spikes and host cell endosomal/lysosomal membranes, which are mediated by the function of viral HA.

**Descriptors:** hemagglutinins viral metabolism, influenza prevention and control, influenza A virus human metabolism, phosphatidylinositol metabolism, phosphatidylinositol pharmacology, *Rhodococcus equi*, binding sites physiology, cultured cells, dogs, ducks, fatty acids chemistry, hemagglutination drug effects, hemolysis drug effects, influenza A virus avian metabolism, influenza A virus, porcine metabolism, influenza B virus chemistry, kidney cytology, orthomyxoviridae metabolism, phosphatidylinositols isolation and purification, swine.

**NAL Call Number:** 41.8 Av5

**Abstract:** The RNA of the hemagglutinin (HA) gene of A/Chicken/Guangdong/SS/1994 (H9N2) was reverse transcription-polymerase chain reaction amplified, and the cDNA was cloned into a plasmid vector. The complete coding sequence of the HA gene was sequenced and included 1683 nucleotides, which encoded for a protein of 560 amino acids. The potential glycosylation sites related to HA protein function were highly conserved. The amino acid sequence of the HA proteolytic cleavage was G-S-S-R/G. This cleavage site sequence is compatible with a low-pathogenic avian influenza virus. Sequence comparison of this HA gene with other H9 influenza virus sequences in the GenBank database showed a 82%-97% nucleotide and amino acid sequence similarity.

**Descriptors:** infection, virology, avian influenza, infectious disease, respiratory system disease, viral disease, cloning genetic techniques, laboratory techniques, reverse transcriptase polymerase chain reaction, RT PCR, genetic techniques, protein function sequence similarity.


**Abstract:** OBJECTIVE: To determine the nucleotide and amino acid sequences of PB2, PB1, PA and NP genes and compared them with sequences of A/HK/156/97(H5N1) virus for revealing the relationship between A/Googs/Guangdong/2/96(H5N1) and A/HK/156/97(H5N1) viruses. METHODS: Virion RNA was transcribed into cDNA by reverse transcriptase, cDNA amplified by PCR, the productions of PCR were purified. Afterward, RNA sequence analysis was performed by the dideoxynucleotide chain termination method, using synthetic oligodeoxynucleotide primers. RESULTS: The lengths of A/Goose/Guangdong/2/96(H5N1) virus RNA segment 1-3 and 5 contain 2,341, 2,341, 2,233 and 1,565 nucleotides, respectively. They encode for PB2 (759 amino acids), PB1 (757 amino acids), PA (716 amino acids) and NP (498 amino acids) proteins. The homologies of amino acid sequences of PB2, PB1, PA and NP proteins between A/Goose/Guangdong/2/96 (H5N1) and A/HK/156/97 (H5N1) virus are 96.4%, 97.2%, 97.3% and 97.0%, respectively. CONCLUSION: The lengths of RNA segment 1-3 and 5 of Goose strain are 2,341, 2,341, 2,233 and 1,565 nucleotides, respectively. The nucleotide sequences of these genes are distinguishable from those of Hong Kong virus.

**Descriptors:** geese virology, influenza A virus avian genetics, poultry diseases virology, RNA viral genetics, amino acid sequence, influenza A virus avian classification, influenza A virus avian isolation and purification, molecular sequence data, sequence analysis, RNA.


**Abstract:** OBJECTIVE: To determine the nucleotide sequences of M and NS genes of A/Goose/Guangdong/2/96(H5N1) virus and also to compare them with sequences of A/HK/156/97(H5N1) strain for revealing the relationship between the two viruses, as well as for setting up a solid basis for studying M and NS genes of influenza A viruses in the future. METHODS: Virion RNA was transcribed into cDNA by reverse transcriptase, cDNA was amplified by PCR, the productions of PCR were purified. Afterward, RNA sequence analysis was performed by the dideoxynucleotide chain termination method using synthetic oligodeoxynucleotide primers. RESULTS: The segment length of A/Goose/Guangdong/2/96(H5N1) virus RNA 7 is 1,027 nucleotides. It codes M1 (252 amino acids) and M2 (97 amino acids) proteins. However, the segment length of RNA 8 of A/Goose/Guangdong/2/96 (H5N1) and A/HK/156/97 (H5N1) virus are 96.4%, 97.2%, 97.3% and 97.0%, respectively. CONCLUSION: The lengths of RNA segment 1-3 and 5 of Goose strain are 2,341, 2,341, 2,233 and 1,565 nucleotides, respectively. The nucleotide sequences of these genes are distinguishable from those of Hong Kong virus.

NAL Call Number: QR360.A1J6

Abstract: In May 1993, a severe epidemic of respiratory disease began in horses in Inner Mongolia and spread throughout horses in China. The disease affected mules and donkeys as well as horses but did not spread to other species, including humans. The severity of the disease raised the question of whether the outbreak might have been caused by the new avian-like influenza viruses detected in horses in China in 1989 or by current variants of A/equine/Miami/1/63 (H3N8) (equine-2) or by a reassortant between these viruses. Antigenic and sequence analysis established that all gene segments of the influenza virus causing the epidemic were of recent equine-2 origin and that the virus was not a reassortant. Serological analysis of post-infection horse sera provided evidence for the continued circulation of the A/Equine/Jilin/1/89 (Eq/Jilin) (H3N8) avian-like viruses in horses in Heilongjiang province with original antigenic sin-like responses. It is noteworthy that prior infection with the avian-like Eq/Jilin strain did not afford cross-protection against a current equine-2 strain. Serological evidence for the continued circulation of the avian-like H3N8 influenza virus in horses indicates that this virus has probably established itself in horses in Asia.

Descriptors: horse diseases epidemiology, influenza veterinary, influenza A virus genetics, antibodies, viral blood, antigens, viral immunology, base sequence, China epidemiology, disease outbreaks veterinary, genome, viral, horse diseases virology, horses, influenza epidemiology, influenza virology, influenza A virus classification, influenza A virus immunology, molecular sequence data, phylogeny, sequence analysis, DNA, sequence homology, nucleic acid, seroepidemiologic studies, serotyping.


Abstract: Genetic analysis of viral HA gene showed that there were 22 nucleotide differences in HA gene between goose and human H5N1 viruses. The sequence analysis of amino acid on viral protein molecules indicated that there were 7 and 9 position differences between goose and human, chicken H5N1 viruses, respectively. All the three viruses share multiple basic amino acids (R-E-R-R-R-K-K-R) at the cleavage site between HA1 and HA2 domain, that is associated with highly pathogenic H5 avian viruses. Except one more glycosylation site located at 156 position in the chicken strain, there were 7 glycosylation sites at same positions in three virus HA protein molecules. The analysis of NA protein molecule indicated that the stalk region which extends from the viral membrane up to amino acid 85, human and chicken viruses had a 19 amino-acid deletion as compared with that of goose virus, while the goose NA gene was closely related to A/Parrot/Ulster/73 (H7N1) virus. Therefore, goose H5N1 virus HA and NA genes were avian in origin and were different from those of human and chicken H5N1 viruses. In our knowledge, this is the first time that the avian H5N1 virus was found causing influenza outbreak in goose. Why was A/Goose/Guangdong/2/96(H5N1) virus virulent for geese? It might be related to the substitution of amino acid located at 138 position near by RBS on HA protein molecule and 19 amino acids insertion on NA protein molecule as compared with those of human and chicken H5N1 viruses.

Descriptors: influenza virology, influenza A virus avian genetics, influenza A virus human genetics, poultry diseases virology, amino acid sequence, chick embryo, goose virology, influenza veterinary, influenza A virus avian isolation and purification, influenza A virus human isolation and purification, molecular sequence data, sequence homology, amino acid.


NAL Call Number: QH506.E46

Abstract: There are 15 subtypes of influenza A virus (H1-H15), all of which are found in avian species. Three caused pandemics in the last century: H1 in 1918 (and 1977), H2 in 1957 and H3 in 1968. In 1997, an
H5 avian virus and in 1999 an H9 virus caused outbreaks of respiratory disease in Hong Kong. We have determined the three-dimensional structures of the haemagglutinins (HAs) from H5 avian and H9 swine viruses closely related to the viruses isolated from humans in Hong Kong. We have compared them with known structures of the H3 HA from the virus that caused the 1968 H3 pandemic and of the HA--esterase--fusion (HEF) glycoprotein from an influenza C virus. Structure and sequence comparisons suggest that HA subtypes may have originated by diversification of properties that affected the metastability of HAs required for their membrane fusion activities in viral infection.

Descriptors: hemagglutinin glycoproteins, influenza virus chemistry, influenza A virus avian chemistry, porcine chemistry, orthomyxoviridae classification, amino acid motifs, amino acid sequence, amino acid substitution, crystallography, x-ray, evolution, molecular, hemagglutinin glycoproteins, influenza virus genetics, hemagglutinin glycoproteins, influenza virus physiology, hydrogen-ion concentration, avian classification, influenza A virus avian genetics, avian physiology, porcine classification, porcine genetics, porcine physiology, membrane fusion, models, molecular, molecular sequence data, protein conformation, protein structure, secondary, rotation, sequence alignment, sequence homology, amino acid, structure activity relationship.


NAL Call Number: 500 N21P

Abstract: The three-dimensional structures of avian H5 and swine H9 influenza hemagglutinins (HAs) from viruses closely related to those that caused outbreaks of human disease in Hong Kong in 1997 and 1999 were determined bound to avian and human cell receptor analogs. Emerging influenza pandemics have been accompanied by the evolution of receptor-binding specificity from the preference of avian viruses for sialic acid receptors in alpha2,3 linkage to the preference of human viruses for alpha2,6 linkages. The four new structures show that HA binding sites specific for human receptors appear to be wider than those preferring avian receptors and how avian and human receptors are distinguished by atomic contacts at the glycosidic linkage. alpha2,3-Linked sialosides bind the avian HA in a trans conformation to form an alpha2,3 linkage-specific motif, made by the glycosidic oxygen and 4-OH of the penultimate galactose, that is complementary to the hydrogen-bonding capacity of Gln-226, an avian-specific residue. alpha2,6-Linked sialosides bind in a cis conformation, exposing the glycosidic oxygen to solution and nonpolar atoms of the receptor to Leu-226, a human-specific residue. The new structures are compared with previously reported crystal structures of HA/sialoside complexes of the H3 subtype that caused the 1968 Hong Kong Influenza virus pandemic and analyzed in relation to HA sequences of all 15 subtypes and to receptor affinity data to make clearer how receptor-binding sites of HAs from avian viruses evolve as the virus adapts to humans.

Descriptors: hemagglutinin glycoproteins, influenza virus chemistry, hemagglutinin glycoproteins, influenza virus metabolism, influenza A virus avian physiology, porcine physiology, receptors, virus chemistry, receptors, virus physiology, amino acid sequence, binding sites, conserved sequence, crystallography, x-ray, ducks, hydrogen bonding, models, molecular, N-acetylneuraminic acid, protein conformation, swine.


NAL Call Number: QR189.A73

Descriptors: avian influenza virus, clinical aspects, experimental infections, histopathology, poultry.


NAL Call Number: 448.3 Ar23

Abstract: A hepatotropic variant of avian influenza virus A/Turkey/England 63 (Hav 1, Nav 3) was selected by serial passages in mouse liver. Adaptation to this organ was established after 13 in vivo passages and was found to improve during further passages as shown by increasing rates of replication in livers of ICR mice. The mutant virus finally selected was stable and differed from the original virus mainly in lethality upon intraperitoneal injection in mice, in its ability to grow to high titers in livers of susceptible animals and in
plaque morphology in chick embryo fibroblasts. No differences were detected in hemagglutination inhibition and neutralization by standard mouse antisera. Pathogenicity for the liver was independent of the route of inoculation, included other laboratory animals sensitive to influenza virus and could be inhibited by amantadine. Fatal hepatitis in 50 per cent of susceptible mice by the intraperitoneal route required from 10 to 20 EID50. Pathological changes consisted of severe necrosis of liver parenchyma accompanied by release of F antigen into the serum and were apparently due to virus replication in hepatic cells as evidenced by immunofluorescence. The main implications of this animal model for studies on experimental hepatitis and on myxovirus-host interactions in an organ not usually associated with influenza are discussed.

Descriptors: adaptation, physiological, hepatitis A microbiology, liver microbiology, mutation, orthomyxoviridae growth and development, amantadine therapeutic use, antigens, viral, disease models, animal, guinea pigs, hamsters, hepatitis A pathology, hepatitis A prevention and control, liver immunology, liver pathology, mice, mice inbred strains, orthomyxoviridae immunology, orthomyxoviridae pathogenicity, rats, virus replication.


NAL Call Number: QR1.I57

Abstract: Mice carrying the gene Mx were resistant to the lethal action of a hepatotropic line of avian influenza A virus. In resistant animals, foci of liver necrosis were self-limiting, and maximal virus titers reached were much below those in susceptible animals. Resistance could not be abrogated by immunosuppressive treatment with cyclophosphamide, methotrexate, or procarbazine, although such treatment prevented cellular infiltration at sites of virus replication and appeared to delay virus clearance. Silica and thorium dioxide, thought to inhibit macrophage function, likewise failed to abolish resistance. Regenerating liver tissue did not support more extensive virus replication than did intact adult liver.

Descriptors: immunosuppression, influenza prevention and control, liver microbiology, orthomyxoviridae pathogenicity, antigens viral analysis, cyclophosphamide pharmacology, hepatectomy, influenza genetics, liver pathology, liver regeneration, methotrexate pharmacology, mice, mice inbred A, mice inbred c57bl, mice inbred ICR, orthomyxoviridae growth and development, procarbazine pharmacology, reticuloendothelial system microbiology, silicon dioxide pharmacology, thorium dioxide pharmacology.


NAL Call Number: 448.8 J822

Abstract: Radiation chimeras produced by crosswise transfers of bone-marrow cell among histocompatible mice susceptible, or genetically resistant, to lethal challenge by a number of myxoviruses were used to test whether macrophage resistance (as assessed in vitro) and resistance of the animal (as measured in vivo), both previously shown to be brought about by the gene Mx, were causally related. 49 chimeras were tested individually, both of resistance of their macrophages to in vitro challenge with M-TUR (a strain of avian influenza virus A/Turkey/England/63 adapted to grow in cultured mouse peritoneal macrophages), and for resistance of the animal in vivo upon challenge with pneumotropic, neurotropic, or hepatotropic influenza viruses. Cultivated Kupffer cells and peritoneal macrophages harvested from chimeric mice expressed the resistance phenotype of the bone-marrow donor irrespective of the host environment in which they had differentiated. However, susceptibility or resistance in vivo was according to the genotype of the host. Thus, inborn resistance of radiation chimeras was found to be independent of Mx-gene expression in cells of the hemopoietic system.

Descriptors: hematopoietic stem cells immunology, immunity, natural, orthomyxoviridae immunology, phagocytes immunology, radiation chimera, genotype, hematopoietic stem cell transplantation, influenza immunology, mice, mice inbred strains genetics, homologous transplantation.


Abstract: The effects of selenocystamine, an inhibitor of influenza virus RNA-dependent RNA polymerase
in vitro activity, in the antibiotic rifampicin were studied on influenza A/PR/8/34 (HON1) infection in embryonated eggs. Both drugs completely inhibited hemagglutinating and infective virus yields when added at relatively early times postinfection. Maximal inhibition was produced by apparently noncytotoxic concentrations of 50 microgram of selenocystamine, or of 400 microgram of rifampicin, per egg.

Descriptors: cystamine analogs and derivatives, influenza A virus avian drug effects, organoselenium compounds, rifampin pharmacology, selenium pharmacology, virus replication drug effects, chick embryo, cystamine administration and dosage, cystamine pharmacology, avian growth and development, rifampin administration and dosage, selenium administration and dosage, time factors, tissue culture.


NAL Call Number: QR180.3.D4

Abstract: Attempts at virus isolation from cloacal swabs resulted in the recovery of 10 strains of hemagglutinating viruses from a total of 349 ducks, mainly shelducks (Tadorna tadorna) captured in the north of France. Four of these isolates were identified as influenza strains corresponding to the following antigenic composition: Hav6-N2, Hav6-Nav4 and Hav1-N2 (2 strains). Shelduck is known to be a partially migratory species, wintering in western Europe, some of them migrating northward to Scandinavia during the summer. The captures were made between November 1976 and February 1977: one of the birds was caught four times and was found to be negative for virus in November, positive in December (isolation of a strain Hav6-Nav4), negative again in January and February. Blood taken in February did not show the presence of HI antibodies to the homologous virus.

Descriptors: antigens, viral, ducks microbiology, influenza A virus avian isolation and purification, neuraminidase immunology, antibodies, viral, cloaca microbiology, France, hemagglutination inhibition tests, hemagglutinins viral, avian enzymology, avian immunology, human enzymology, seasons.


Descriptors: endoderm, fetal membranes, hemagglutination inhibition tests, influenza A virus avian immunology, antibodies, chick embryo, glycosaminoglycans, hemagglutination tests, orthomyxoviridae immunology, virus cultivation.


NAL Call Number: 448.3 Ar23

Abstract: The nucleoprotein (NP) gene from avian influenza strain A/Shearwater/Aust/1/72 (H6N5) was cloned, sequenced, and expressed in vaccinia virus for the production of potent sera in immunised rabbits. The NP gene is 1565 bp and shares greater than 95% amino acid sequence identity with other NPs of the avian subtype. The recombinant NP expressed by vaccinia virus comigrated with endogenous A/Shearwater/Aust/1/72 NP by Western blot analysis. Polyclonal rabbit sera raised against recombinant NP was evaluated in an antigen capture ELISA system as a potential diagnostic tool for the detection of avian influenza. All type A strains, comprising several HA and NA subtypes, but not type B nor other avian viruses, were detected.

Descriptors: fowl plague diagnosis, genes viral, influenza A virus avian genetics, nucleoproteins genetics, vaccinia virus genetics, viral core proteins, viral proteins genetics, amino acid sequence, antibodies, viral immunology, base sequence, blotting, southern, cloning, molecular, DNA, viral, enzyme linked immunosorbent assay, avian immunology, molecular sequence data, nucleoproteins immunology, predictive value of tests, thymidine kinase genetics, vaccinia virus immunology, viral proteins immunology.


NAL Call Number: 448.3 Ar23
Abstract: The nucleoprotein (NP) gene from influenza virus A/Shearwater/Australia/72 has been expressed intracellularly in both *E. coli* and insect cells. *E. coli*-derived NP was identified by Western blot analysis as a 56 kDa protein which co-migrates with virion-derived NP. This protein was purified by immunoaffinity chromatography and a nitrocellulose binding assay showed that NP formed complexes with positive- and negative-sense influenza neuraminidase RNA transcribed in vitro. ELISA and Western blot analysis revealed that recombinant NP of 56 kDa was produced in high yields in insect cells using a baculovirus vector. Immunofluorescence microscopy revealed that NP was localised to the nucleus of infected insect cells.


NAL Call Number: 448.8 V81

Abstract: The neuraminidase (NA) gene from the prototype N5 influenza virus, A/Shearwater/Australia/72, has been cloned and completely sequenced. An open reading frame of 1404 bp (468 amino acids) is flanked by 20-bp 5'- and 31-bp 3'-untranslated regions. The deduced amino acid sequence of the N5 gene was compared with sequences from N2, N1, N7, N8, and N9 subtypes. One hundred thirteen amino acid residues (24%) are completely conserved across subtypes and include active site residues, cysteines, potential glycosylation sites, and certain glycines which suggests that these subtypes share a common ancestor and adopt the same 3-D conformation. Three groups can be assigned from amino acid homologies: (i) N5, N8, N1; (ii) N7, N9; and (iii) N2 where the percentage identity within groups is 55-68% and between groups is 40-46%, the N5-N8 pair bearing the closest identity (68%). Phylogenetic analysis suggests that these groups diverged concurrently.

Descriptors: DNA, viral genetics, influenza A virus avian genetics, neuraminidase genetics, amino acid sequence, base sequence, cloning, molecular, DNA probes, deoxyribonuclease ecori, avian enzymology, molecular sequence data, phylogeny.


NAL Call Number: 448.8 V81

Descriptors: influenza A virus avian analysis, influenza A virus analysis, RNA viral analysis, genes viral, avian genetics, influenza A virus genetics, nucleic acid hybridization, peptides analysis, recombination, genetic, viral proteins analysis.


NAL Call Number: QR360.A1J6

Abstract: A nucleic acid fraction consisting of RNA and DNA sequences with an apparent mol. wt. of 1.4 to 1.5 x 10(6) is present in minor amounts in purified influenza virus. The RNA is virus-specific and in the case of fowl plague virus (FPV) contains sequences of genes 2 and 7 which code for one of the proteins constituting the polymerase complex and for the matrix protein respectively.

Descriptors: DNA analysis, influenza A virus avian analysis, RNA viral analysis, genes viral, avian genetics, molecular weight, nucleic acid hybridization, viral genetics, viral proteins biosynthesis.


NAL Call Number: QR360.J6

Abstract: The binding specificities of a panel of avian influenza virus subtype H5 hemagglutinin (HA) proteins bearing mutations at key residues in the receptor binding site were investigated. The results demonstrate that two simultaneous mutations in the receptor binding site resulted in H5 HA binding in a pattern similar to that shown by human viruses. Coexpression of the ion channel protein, M2, from most avian and human strains tested protected H5 HA conformation during trafficking, indicating that no genetic barrier to the reassortment of the H5 surface antigen gene with internal genes of human viruses existed at
NAL Call Number: QR360.J6
Descriptors: cell nucleus enzymology, DNA directed RNA polymerases metabolism, orthomyxoviridae enzymology, RNA metabolism, cell fractionation, centrifugation, density gradient, chick embryo, cytochrome reductases analysis, cytochrome C group, DNA, viral isolation and purification, dactinomycin pharmacology, enzyme induction, fibroblasts, hemagglutination tests, influenza A virus avian enzymology, magnesium pharmacology, manganese pharmacology, microsomes enzymology, NAD, nucleic acid hybridization, proteins metabolism, sucrose, time factors, tritium.

NAL Call Number: 470 Sci2
Abstract: In 1997, an H5N1 influenza A virus was transmitted from birds to humans in Hong Kong, killing 6 of the 18 people infected. When mice were infected with the human isolates, two virulence groups became apparent. Using reverse genetics, we showed that a mutation at position 627 in the PB2 protein influenced the outcome of infection in mice. Moreover, high cleavability of the hemagglutinin glycoprotein was an essential requirement for lethal infection.
Descriptors: influenza epidemiology, influenza virology, influenza A virus genetics, influenza A virus pathogenicity, amino acid sequence, birds virology, DNA, recombinant genetics, hemagglutinin glycoproteins, influenza virus chemistry, hemagglutinin glycoproteins, influenza virus genetics, hemagglutinin glycoproteins, influenza virus metabolism, Hong Kong epidemiology, influenza mortality, influenza transmission, influenza A virus avian genetics, avian pathogenicity, avian physiology, human genetics, human pathogenicity, human physiology, influenza A virus physiology, lung virology, mice, mutation, missense genetics, reassortant viruses genetics, reassortant viruses pathogenicity, reassortant viruses physiology, viral proteins chemistry, viral proteins genetics, viral proteins metabolism.

Abstract: We have previously shown that retroviral vector particles derived from Moloney murine leukemia virus (Mo-MuLV) can efficiently incorporate influenza hemagglutinin (HA) glycoproteins from fowl plague virus (FPV), thus conferring a broad tropism to the vectors. To modify its host range, we have engineered the FPV HA to display four different polypeptides on its N terminus: the epidermal growth factor, an anti-human MHC class I molecules scFv (single-chain antibody), an anti-melanoma antigen scFv, and an IgG Fc-binding polypeptide. All recombinant HA glycoproteins were correctly expressed and processed, and efficiently incorporated into Mo-MuLV retroviral particles, indicating that amino-terminal insertion of large polypeptides did not alter the conformation of HA chimeras. Virions carrying the different chimeras bound specifically to cells expressing the targeted cell surface molecules of each ligand. In addition, all virion types were infectious but exhibited various degrees of specificity regarding the use of the targeted cell surface molecule versus the wild-type FPV HA receptor for cell entry and infection. For some ligands tested, infectivity was significantly increased on cells that express the targeted receptor, compared with cells that express only the wild-type HA receptor. Furthermore, some polypeptides could abolish infectivity via the wild-type FPV HA receptor. Our data therefore indicate that it is possible to engineer the HA envelope glycoprotein by fusing ligands to its amino-terminal end without affecting its fusion activity.
Descriptors: genetic vectors, hemagglutinin glycoproteins, influenza virus genetics, moloney murine leukemia virus, peptides genetics, 3T3 cells, antibodies, neoplasm genetics, binding sites, epidermal growth
factor genetics, gene fusion, hemagglutinin glycoproteins, influenza virus metabolism, immunoglobulin fragments genetics, immunoglobulin variable region genetics, influenza A virus avian genetics, mice, peptides metabolism, recombinant fusion proteins genetics, tumor cultured cells, virion metabolism.


**Abstract:** We describe retrovirus particles carrying the fowl plague virus (FPV) hemagglutinin (HA). When expressed in cells providing Moloney murine leukemia virus (MoMLV) Gag and Pol proteins and a lacZ retroviral vector, FPV HA was found to be efficiently expressed, correctly processed, and stably incorporated into retroviral particles. HA-bearing retroviruses were infectious with a wide host range and were only 10-fold less infectious than retroviruses carrying wild-type MLV retroviral envelopes. We also coexpressed HA proteins in retroviral particles with chimeric MoMLV-derived envelope glycoproteins that efficiently retarget virus attachment but are only weakly fusogenic. Our results suggest that HA can in some cases enhance the fusion ability of these retroviral particles, depending on the cell surface molecule that is used as a receptor.

**Descriptors:** hemagglutinins genetics, influenza A virus avian genetics, leukemia virus, murine genetics, viral fusion proteins genetics, gene products, gag genetics, gene products, pol genetics, lac operon, mice, recombination, genetic, virion genetics.


**Abstract:** Intracellular transport, glycosylation, tetramerization and enzymatic activity of the neuraminidase (NA) of fowl plague virus (FPV) were analysed in vertebrate cells after expression from a vaccinia virus vector. Tetramerization occurred with a half-time of 15 min, whereas passage through the medial Golgi apparatus and transport to the plasma membrane occurred with half-times of 2 and 3 h, respectively, suggesting a step in NA maturation beyond tetramerization that limits the rate of transport to the medial Golgi. NA transport rates were about fourfold slower than those of haemagglutinin (HA). Slow transport and processing of FPV NA was not altered by coexpression of FPV HA, nor was the transport rate of HA influenced by NA. The slow transport kinetics of NA were also observed in FPV-infected CV-1 cells. As deduced from the coding sequence, FPV NA has the shortest stalk of all naturally occurring NAs described to date and contains only three potential N-glycosylation sites, which are all located in the globular head domain. Elimination of each of the three N-glycosylation sites revealed that the two oligosaccharides at positions 124 and 66 are of the complex type, whereas the one at Asn-213 remains in mannnose-rich form. The glycosylation mutants showed also that oligosaccharides at positions 124 and 213 of FPV NA modulate enzymatic activity. Transport of NA is not influenced by single elimination of any of the three oligosaccharide attachment sites. Mutational analysis of the three Cys residues not involved in intrachain disulfide pairing revealed that Cys-49 in the stalk of the NA molecule is responsible for the formation of disulfide-linked dimers. Analysis of cysteine mutants of FPV NA also demonstrated that disulfide-linked dimers are not absolutely necessary for the formation of enzymatically active tetramers but may stabilize the quaternary structure of NA.

**Descriptors:** birds virology, influenza A virus avian enzymology, neuraminidase metabolism, biological transport, cysteine, enzyme activation, glycosylation, oligosaccharides.


**Abstract:** We describe retrovirus particles carrying the fowl plague virus (FPV) hemagglutinin (HA). When expressed in cells providing Moloney murine leukemia virus (MoMLV) Gag and Pol proteins and a lacZ retroviral vector, FPV HA was found to be efficiently expressed, correctly processed, and stably incorporated into retroviral particles. HA-bearing retroviruses were infectious with a wide host range and were only 10-fold less infectious than retroviruses carrying wild-type MLV retroviral envelopes. We also coexpressed HA proteins in retroviral particles with chimeric MoMLV-derived envelope glycoproteins that efficiently retarget virus attachment but are only weakly fusogenic. Our results suggest that HA can in some cases enhance the fusion ability of these retroviral particles, depending on the cell surface molecule that is used as a receptor.

**Descriptors:** hemagglutinins genetics, influenza A virus avian genetics, leukemia virus, murine genetics, viral fusion proteins genetics, gene products, gag genetics, gene products, pol genetics, lac operon, mice, recombination, genetic, virion genetics.
analysis, nucleotidases analysis, orthomyxoviridae immunology, peptides analysis, sulfur radioisotopes.


**NAL Call Number:** 448.8 V81  
**Descriptors:** genes viral, influenza A virus avian genetics, RNA, messenger biosynthesis, viral biosynthesis, transcription, genetic, cell line, avian metabolism, poly A, viral analysis, virion metabolism.


**NAL Call Number:** QR360.A1J6  
**Abstract:** Polyadenylated transcripts synthesized in vitro by detergent-disrupted influenza virus resemble virus mRNAs in that they possess the complement of the 3' terminus of the genome RNAs but lack sequences corresponding to the same 5' terminal region, including the homologous sequence of nucleotides 1 to 22. Transcription is initiated at the 3' terminus by both ApG and GpG as well as in the absence of added primer.  
**Descriptors:** influenza A virus avian analysis, orthomyxoviridae analysis, RNA viral analysis, transcription, genetic, base sequence, cell free system, avian metabolism, nucleic acid hybridization, nucleotides analysis, poly A analysis, viral biosynthesis.


**NAL Call Number:** 448.8 V81  
**Descriptors:** influenza A virus avian genetics, RNA viral analysis, adenosine metabolism, base sequence, chromatography, DEAE-cellulose, chromatography, thin layer, phosphorylation, ribonucleases pharmacology, ribonucleotides analysis, transcription, genetic.


**NAL Call Number:** QH506.E46  
**Abstract:** Amantadine (1-aminoadamantane hydrochloride) is effective in the prophylaxis and treatment of influenza A infections. In tissue culture this selective, strain-specific antiviral activity occurs at relatively low concentrations (5 microM or less), which inhibit either the initiation of infection or virus assembly. The data reported here demonstrate that the basis of these actions is similar and resides in the virus-coded M2 membrane protein, the product of a spliced transcript of RNA segment 7. Mutations which confer resistance to amantadine are restricted to four amino acids within a hydrophobic sequence, indicating that the drug is targeted against the putative membrane-associated portion of the molecule. The influence of the virus haemagglutinin on the amantadine sensitivity of virus strains implies that the drug may interfere with interactions between these two virus proteins.  
**Descriptors:** amantadine pharmacology, influenza A virus avian drug effects, human drug effects, membrane proteins genetics, chick embryo, chickens, drug resistance, microbial, fibroblasts cytology, avian genetics, human genetics, mutation, RNA splicing, species specificity, transcription, genetic drug effects.


**NAL Call Number:** QD415.F4  
**Descriptors:** glycoproteins isolation and purification, mammary tumor virus, mouse analysis, orthomyxoviridae analysis, parainfluenza virus 1, human analysis, viral proteins isolation and purification, chromatography, affinity, electrophoresis, polyacrylamide gel, influenza A virus avian analysis, lectins, polysaccharides, sodium dodecyl sulfate.


**Abstract:** The ts lesion of the fowl plague virus (FPV) mutants ts 18 and ts 236 has been located in RNA segment 2 (Ptra gene, corresponding to P3). After double-infection with these mutants and ts 90 or ts 93, which also carry a ts lesion in segment 2, plaques were formed at the non-permissive temperature (40 degrees C). These plaques cannot be passaged at 40 degrees C and exhibit a morphology which differs from those formed by the wild-type virus. The yield of infectious particles after double-infection shows a non-linear correlation between the plaque number and dilution, indicating that at least two particles are needed for infection of a cell. All experimental evidence points to an intracistronic complementation within the P3 protein.

**Descriptors:** genes, structural, genes viral, influenza A virus avian genetics, recombination, genetic, cultured cells, chick embryo, genetic complementation test, avian growth and development, mutation, plaque assay, temperature.


**Abstract:** The function of acidification in protein sorting along the biosynthetic pathway has been difficult to elucidate, in part because reagents used to alter organelle pH affect all acidified compartments and are poorly reversible. We have used a novel approach to examine the role of acidification in protein sorting in polarized Madin-Darby canine kidney (MDCK) cells. We expressed the influenza virus M2 protein, an acid-activated ion channel that equilibrates lumenal and cytosolic pH, in polarized MDCK cells and examined the consequences on the targeting and delivery of apical and basolateral proteins. M2 activity affects the pH of only a subset of acidified organelles, and its activity can be rapidly reversed using ion channel blockers (Henkel, J.R., G. Apodaca, Y. Altschuler, S. Hardy, and O.A. Weisz. 1998. Mol. Biol. Cell. 8:2477-2490; Henkel, J.R., J.L. Popovich, G.A. Gibson, S.C. Watkins, and O.A. Weisz. 1999. J. Biol. Chem. 274:9854-9860). M2 expression significantly decreased the kinetics of cell surface delivery of the apical membrane protein influenza hemagglutinin, but not of the basolaterally delivered polymeric immunoglobulin receptor. Similarly, the kinetics of apical secretion of a soluble form of gamma-glutamyltranspeptidase were reduced with no effect on the basolaterally secreted fraction. Interestingly, M2 activity had no effect on the rate of secretion of a nonglycosylated protein (human growth hormone [hGH]) that was secreted equally from both surfaces. However, M2 slowed apical secretion of a glycosylated mutant of hGH that was secreted predominantly apically. Our results suggest a role for acidic trans-Golgi network pH in signal-mediated loading of apical cargo into forming vesicles.

**Descriptors:** Golgi apparatus metabolism, influenza A virus avian metabolism, ion channels metabolism, viral matrix proteins metabolism, cell line, cell membrane metabolism, cell polarity, dogs, gene expression, hemagglutinin glycoproteins, influenza virus biosynthesis, hemagglutinin glycoproteins, influenza virus genetics, protons, receptors, polymeric immunoglobulin biosynthesis, receptors, polymeric immunoglobulin genetics, viral matrix proteins genetics.


**Abstract:** M2, an acid-activated ion channel, is an influenza A virus membrane protein required for efficient nucleocapsid release after viral fusion with the endosomal membrane. Recombinant M2 slows protein traffic through the Golgi complex (Sakaguchi, T., Leser, G. P., and Lamb, R. A. (1996) J. Cell Biol. 133, 733-47). Despite its critical role in viral infection, little is known about the subcellular distribution of M2 or its fate.
following delivery to the plasma membrane (PM). We measured the kinetics of M2 transport in HeLa cells, and found that active M2 reached the PM considerably more slowly than inactive M2. In addition, M2 delayed intra-Golgi transport and cell surface delivery of influenza hemagglutinin (HA). We hypothesized that the effects of M2 on transport through non-acidified compartments are due to inefficient retrieval from the trans-Golgi of machinery required for intra-Golgi transport. In support of this, acutely activated M2 had no effect on intra-Golgi transport of HA, but still slowed HA delivery to the PM. Thus, M2 has an indirect effect on early transport steps, but a direct effect on late steps in PM delivery. These findings may help explain the conflicting and unexplained effects on protein traffic observed with other perturbants of intraorganelle pH such as weak bases and inhibitors of V-type ATPases.

Descriptors: Golgi apparatus metabolism, influenza A virus avian metabolism, ion channels secretion, viral matrix proteins secretion, amantadine pharmacology, antiviral agents pharmacology, biological transport drug effects, cell compartmentation, cell membrane metabolism, HeLa cells, hemagglutinin glycoproteins, influenza virus metabolism, hydrogen-ion concentration, imidazoles pharmacology, spiro compounds pharmacology.

NAL Call Number: QR360.A1J6

Abstract: The temperature-sensitive defect of mutant ts 263 of fowl plague virus (FPV) is located in the acidic polymerase (PA) gene and is due to a single base substitution (C2036T), which leads to an amino acid replacement (Ala671 to Val) in a highly conserved region of the protein. During passage at 33 degrees C ts 263 stably carries over a ninth RNA segment, which consists of a truncated PA gene. Although the deletion is in-frame and it is transcribed into mRNA, no corresponding protein is detected in vivo. After reversion to wild-type this extra RNA segment is immediately lost. At the non-permissive temperature of 40 degrees C no significant viral products of ts 263 are synthesized. Under semi-permissive conditions there is a relative, but very significant over-production of the M1 protein, which is not accompanied by a corresponding elevated M1 mRNA synthesis. These results are in agreement with the idea that the PA protein is involved in the regulation of viral protein synthesis at the level of expression of mRNA. Preinfection of chicken embryo cells with ts 263 at a semi-permissive temperature interferes with the replication of FPV wild-type indicating that premature availability of M1 might be detrimental for influenza virus replication.

Descriptors: DNA directed RNA polymerases genetics, gene expression regulation, viral, genes viral, influenza A virus avian genetics, avian metabolism, mutation, viral proteins biosynthesis, amino acid sequence, blotting, northern, cultured cells, chick embryo, cloning, molecular, conserved sequence, crosses, genetic, DNA directed RNA polymerases metabolism, avian physiology, polymerase chain reaction, RNA, messenger biosynthesis, messenger metabolism, viral isolation and purification, viral metabolism, temperature, virus replication.

Hernandez Magdaleno, A., M.T. Casaubon Hugening, and J. Garcia Garcia. (1998). Viremia durante la infeccion del virus de influenza aviar (h5n2) altamente patogeno en aves susceptibles y en aves inmunizadas. [Study of the viremia during the infection of a highly pathogenic avian influenza virus (h5n2) on susceptible and immunized chickens]. In: 34 Reunion Nacional de Investigacion Pecuaria, Queretaro, Qro. (Mexico), p. 250.

Abstract: El objetivo de la presente investigacion fue contribuir al estudio de la patogenia del virus de influenza aviar (H5N2) altamente patogeno, en aves susceptibles y en aves inmunizadas. Durante las primeras 72 horas post-inoculacion (hpi), a traves del estudio de la viremia. Se formaron dos grupos de 100 aves libres de patogenos especificos. A los 8 dias de edad, uno de los grupos fue inmunizado con una vacuna emulsionada contra influenza aviar (IA) y el otro grupo permanecio sin inmunizar. A las cuatro semanas de edad, ambos grupos de aves fueron inoculados via intranasal con 1 x 103 DLEP50 del virus A/Chicken/Queretaro/14588-19/95 (H5N2), altamente patogeno. Se tomaron aleatoriamente 3 aves de cada grupo a las 2, 4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68 y 72 hpi. De cada ave se tomo una muestra de sangre directamente del corazon para aislamiento y titulacion viral. A partir de las muestras de sangre se pudo identificar y cuantificar el virus de influenza aviar de alta patogenicidad, solo en las Av-Susc. El aislamiento e identificacion del virus se realizo a partir de las 28 hpi
en el 100% de las Av-Susc. El título del virus circulante en las Av-Susc a las 28 hpi fue de 106.12 DLEP50/ml de sangre; posteriormente el título de virus circulante se mantuvo en un rango de 105.69 a 108.06 DLEP50/ml, entre las 32 y 68 hpi. La mayor cantidad de virus circulante, fue detectado a las 72 hpi, con un título de 109.04 DLEP50/ml de sangre. La conversión del título viral a numeros naturales, indica que entre las 28 y 68 hpi, las Av-Susc, tuvieron menos de 200,000,000 DLEP50/ml de sangre. A las 72 hpi, el título de virus circulante fue de 109.04 DLEP50/ml de sangre, lo que al convertirse a numeros naturales equivale a 1,096,478,196 DLEP50/ml de sangre, siendo este el valor maximo que se identifico. La titulacion del virus circulante en sangre, sugiere que el virus tuvo varios ciclos de replicacion local, antes de diseminarlse. La replicacion viral fue muy eficiente, si se toma en cuenta que la dosis inoculada contenia 1,000 DLEP50 de virus y a las 72 hpi, la cantidad de virus circulante fue de 1,096,478,196 DLEP50/ml de sangre. Las Av-Inm no presentaron viremia, lo que sugiere que uno de los mecanismos por el cual la vacunacion previene la mortalidad es que evita la viremia.

Descriptors: broiler chickens, avian influenza virus, pathogenicity, immunity, Septicaemia, bacteriose, biological properties, birds, chickens, domestic animals, Galliformes, infectious diseases, influenza virus, livestock, meat animals, microbial properties, orthomyxoviridae, poultry, useful animals, viruses.


NAL Call Number: 448.3 Ar23
Descriptors: ducks, influenza A virus avian drug effects, acridines, biometry, chick embryo, chloroform pharmacology, enzymes pharmacology, ethyl ethers pharmacology, filtration, heat, hydrogen-ion concentration, staining and labeling.


NAL Call Number: 448.3 Ar23
Descriptors: influenza A virus avian growth and development, adaptation, biological, cell line, leukemia L1210, mice, virus cultivation, virus replication.


NAL Call Number: 448.3 Im6
Abstract: The capacity of the IgM-like bile immunoglobulin (IgX) of the duck (Anas platyrhynchos) to express antibody activity to H3N2 influenza A viruses, and the dependence of this activity on the co-existence of serum IgM antibodies were investigated. Ducklings infected orally and intranasally at 15-29 days of age with viruses isolated from different host species were examined for haemagglutination-inhibiting (HI) antibodies in biles and sera 16-29 days after infection (p.i.). All biles had antibodies associated with IgX; all sera had antibodies associated only with the 7.8S IgG. Following oral infection of birds 42-days-old with influenza A/duck/HK/7/75 virus, serum HI antibodies were an initial IgM response occurring from 5-12 days p.i., followed by the appearance of 7.8S IgG antibodies. Virus-neutralizing (VN) antibodies in serum were also biphasic; isotype classification was not attempted. Bile IgX developed HI and VN activity. HI antibodies reached peak titres 12 days p.i. and fell to low levels by 24 days p.i. VN antibodies also reached peak titres 12 days p.i., but thereafter persisted at quite high levels throughout the experiment. Development of high titres of antibody in bile coincided with the termination of virus excretion in faeces. These experiments confirm that bile IgX of the duck can function as antibody in response to influenza A viruses, and that its activity appears to be independent of serum IgM. Its possible relevance in determining survival of virus in the intestine is discussed.

Descriptors: antibodies, viral analysis, bile immunology, fowl plague immunology, immunoglobulins analysis, influenza A virus avian immunology, ducks, hemagglutination inhibition tests, immunoglobulin G analysis, immunoglobulin M analysis.

NAL Call Number: 448.8 V81
Descriptors: avian influenza virus, surveys, genetic reassortment, ducks.

NAL Call Number: QR360.J6
Abstract: In previous studies, we observed that the virulent avian influenza A virus A/Turkey/Ontario/7732/66 (Ty/Ont) induced severe lymphoid depletion in vivo and rapidly killed an avian lymphocyte cell line (RP9) in vitro. In examining the mechanism of cell killing by this virus, we found that Ty/Ont induced fragmentation of the RP9 cellular DNA into a 200-bp ladder and caused ultrastructural changes characteristic of apoptotic cell death by 5 h after infection. We next determined that the ability to induce apoptosis was not unique to Ty/Ont. In fact, a variety of influenza A viruses (avian, equine, swine, and human), as well as human influenza B viruses, induced DNA fragmentation in a permissive mammalian cell line, Madin-Darby canine kidney (MDCK), and this correlated with the development of cytopathic effect during viral infection. Since the proto-oncogene bcl-2 is a known inhibitor of apoptosis, we transfected MDCK cells with the human bcl-2 gene; these stably transfected cells (MDCKbcl-2) did not undergo DNA fragmentation after virus infection. In addition, cytotoxicity assays at 48 to 72 h after virus infection showed a high level of cell viability for MDCKbcl-2 compared with a markedly lower level of viability for MDCK cells. These studies indicate that influenza A and B viruses induce apoptosis in cell cultures: thus, apoptosis may represent a general mechanism of cell death in hosts infected with influenza viruses.
Descriptors: dogs, avian influenza virus, equine influenza virus, swine influenza virus, pathogenicity, DNA, pathogenesis, kidneys, cell culture, genes, mankind, toxicity, acids, animal morphology, biological properties, canidae, Carnivora, cell structure, chromosomes, culture techniques, in vitro culture, influenza virus, mammals, microbial properties, nucleic acids, nucleic compounds, nucleus, organic acids, urinary tract, urogenital system, viruses, cell death, DNA fragmentation, bcl-2 gene, cytopathogenicity, DNA modification, infections, cell lines, transfection, man, cytotoxicity.

NAL Call Number: 448.3 Ar23

NAL Call Number: QR360.J6
Abstract: To define the recognition site of cytotoxic T lymphocytes (CTLs) on influenza virus H5 hemagglutinin (HA), an H5 HA-specific CTL clone was examined for the ability to recognize monoclonal antibody-selected HA variants of influenza virus A/Turkey/Ontario/7732/66 (H5N9). On the basis of 51Cr release assays with the variants, a CTL epitope was located near residue 168 of H5 HA. To define the epitope more precisely, a series of overlapping peptides corresponding to this region was synthesized and tested for CTL recognition. The minimum peptide recognized by the CTL clone encompassed residues 158 to 169 of H5 HA. Relative to the H3 HA three-dimensional structure, this CTL epitope is located near the
distal tip of the HA molecule, also known as a major B-cell epitope on H3 HA. A single mutation at residue 168 (Lys to Glu) in the H5 HA variants abolished CTL recognition; this same amino acid was shown previously to be critical for B-cell recognition (M. Philpott, C. Hioe, M. Sheerar, and V. S. Hinshaw, J. Virol. 64:2941-2947, 1990). Additionally, mutations within this region of the HA molecule were associated with attenuation of the highly virulent A/Turkey/Ontario/7732/66 (H5N9) (M. Philpott, B. C. Easterday, and V.S. Hinshaw, J. Virol. 63:3453-3458, 1989). When tested for recognition of other H5 viruses, the CTL clone recognized the HA of A/Turkey/Ireland/1378/83 (H5N8) but not that of A/Chicken/Pennsylvania/1370/83 (H5N2), even though these viruses contain identical HA amino acid 158-to-169 sequences. These results suggest that differences outside the CTL epitope affected CTL recognition of the intact HA molecule. The H5 HA site defined in these studies is, therefore, important in both CTL and B-cell recognition, as well as the pathogenesis of the virus.

Descriptors: B lymphocytes immunology, epitopes immunology, hemagglutinins viral immunology, influenza A virus avian immunology, T lymphocytes, cytotoxic immunology, amino acid sequence, cell line, chickens, cytotoxicity, immunologic, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral genetics, avian genetics, mice, mice inbred BALB c, molecular models, molecular sequence data, mutagenesis, site directed, protein conformation, turkeys, variation genetics.

NAL Call Number: 450 P697
Abstract: We investigated the effect of ferulic acid (FA) and isoferulic acid (IFA), which are active components of the rhizoma of Cimicifuga species used frequently as anti-inflammatory drugs in Japanese Oriental medicines, on murine interleukin-8 (IL-8) production in response to influenza virus infections in vitro and in vivo by antibody-sandwich enzyme-linked immunosorbent assay. In the in vitro study, the murine macrophage cell line RAW 264.7 was infected with influenza virus at a dose of 10 plaque forming units (PFU)/cell and cultured in the presence or absence of drugs. Both FA and IFA reduced the IL-8 levels in the 20-h conditioned medium in comparison with control in a dose-dependent manner. The effect of IFA was greater than that of FA: IL-8 levels were reduced to 43% and 56% of the control in the presence of 100 micrograms/ml of IFA and FA, respectively. In the in vivo study, mice were infected with 1,000 PFU of virus and received daily oral administrations of Cimicifuga heracleifolia extract (5 mg/mouse/day), FA (0.5 mg/mouse/day), IFA (0.125 mg/mouse/day), or phosphate buffered saline. The three drugs showed a tendency to reduce IL-8 levels in bronchoalveolar lavage (BAL) obtained 2 days after infection. Moreover, both FA and IFA also significantly reduced the number of exuded neutrophils into BAL. However, the drug administrations did not affect the virus yields in BAL. These data suggest that FA and IFA are novel and potent inhibitors of murine IL-8 production and might act as one of the main components of anti-inflammatory rhizoma of Cimicifuga species.

Descriptors: cinnamates pharmacology, coumaric acids pharmacology, influenza immunology, influenza A virus avian immunology, interleukin 8 biosynthesis, antihypertensive agents pharmacology, cell line, chick embryo, lipopolysaccharides pharmacology, lung virology, macrophages drug effects, macrophages immunology, mice, mice inbred ICR, neutrophils drug effects, neutrophils physiology, medicinal plants, plants.

NAL Call Number: 448.8 V81
Descriptors: genes viral, hemagglutinins viral genetics, influenza A virus human immunology, amino acid sequence, base sequence, DNA, viral, avian immunology, human classification, human genetics.

NAL Call Number: 448.3 Ar23
Descriptors: hemagglutinins viral biosynthesis, orthomyxoviridae metabolism, chick embryo, cycloheximide
pharmacology, fibroblasts microbiology, hemadsorption, hemagglutination tests, influenza A virus avian growth and development, avian isolation and purification, avian metabolism, orthomyxoviridae growth and development, orthomyxoviridae isolation and purification, time factors, tissue culture, viral proteins biosynthesis.


NAL Call Number: QR189.V32

**Descriptors:** genetic vectors genetics, influenza A virus avian genetics, human genetics, influenza vaccine biosynthesis, reassortant viruses genetics, antigenic variation genetics, birds virology, cell line, chick embryo, China, Czechoslovakia, DNA, recombinant genetics, dogs, genes viral, avian immunology, avian isolation and purification, human immunology, human isolation and purification, influenza vaccine genetics, influenza vaccine immunology, influenza vaccine isolation and purification, New Caledonia, Panama, phenotype, reassortant viruses immunology, reassortant viruses isolation and purification, reproducibility of results, reverse transcriptase polymerase chain reaction, transfection, virus cultivation.


NAL Call Number: 500 N21P

**Abstract:** We have developed an eight-plasmid DNA transfection system for the rescue of infectious influenza A virus from cloned cDNA. In this plasmid-based expression system, viral cDNA is inserted between the RNA polymerase I (pol I) promoter and terminator sequences. This entire pol I transcription unit is flanked by an RNA polymerase II (pol II) promoter and a polyadenylation site. The orientation of the two transcription units allows the synthesis of negative-sense viral RNA and positive-sense mRNA from one viral cDNA template. This pol I-pol II system starts with the initiation of transcription of the two cellular RNA polymerase enzymes from their own promoters, presumably in different compartments of the nucleus. The interaction of all molecules derived from the cellular and viral transcription and translation machinery results in the generation of infectious influenza A virus. The utility of this system is proved by the recovery of the two influenza A viruses: A/WSN/33 (H1N1) and A/Teal/HK/W312/97 (H6N1). Seventy-two hours after the transfection of eight expression plasmids into cocultured 293T and MDCK cells, the virus yield in the supernatant of the transfected cells was between 2 x 10^5 and 2 x 10^7 infectious viruses per milliliter. We also used this eight-plasmid system for the generation of single and quadruple reassortant viruses between A/Teal/HK/W312/97 (H6N1) and A/WSN/33 (H1N1). Because the pol I-pol II system facilitates the design and recovery of both recombinant and reassortant influenza A viruses, it may also be applicable to the recovery of other RNA viruses entirely from cloned cDNA.

**Descriptors:** DNA, complementary genetics, viral genetics, influenza A virus avian genetics, human genetics, plasmids genetics, transfection methods, base sequence, cell line, dogs, avian growth and development, human growth and development, molecular sequence data, promoter regions genetics, RNA polymerase I genetics, polymerase II genetics, messenger biosynthesis, RNA viral biosynthesis, recombination, genetic, regulatory sequences nucleic acid, transcription, genetic.


NAL Call Number: QH301.F3

**Descriptors:** lymphocytes, avian influenza virus, chicken.


NAL Call Number: QR180.D4

**Abstract:** We had previously found that inactivated avian influenza virus (AIV) could enhance the response of chicken lymphocytes to mitogen or antigen activation. An investigation into the possible mechanisms of this enhancement was undertaken. Peripheral blood lymphocytes (PBL) were incubated with AIV expressing different hemagglutinin (HA) types (H1-H13) along with doses of concanavalin A (Con A) which induce
maximum (0.5 microgram) or submaximum (0.125 microgram) PBL activation. The lymphocyte activation was measured 72 h later. All of the HA types except H13 enhanced the Con A response. Diminished but significant enhancement could be observed when AIV administration was delayed by as much as 48 h of the 72-h incubation time. The AIV A/ck/Ala/75 (H4N8) was also examined for its effect on interleukin 2 (IL 2) synthesis by Con A-activated PBL and was found to modestly increase the synthesis of this lymphokine. All of the AIV hemagglutinin types agglutinated the PBL with titers slightly lower than that observed for the chicken erythrocyte agglutination. These results indicate that the AIV-induced enhancement of Con A responsiveness by chicken PBL is due, at least partly, to increased synthesis of IL 2 and that the effect may be due to some viral component other than the agglutinin.

Descriptors: influenza A virus avian immunology, interleukin 2 secretion, lymphocyte activation, agglutination, chickens, concanavalin a pharmacology, hemagglutination, viral, avian classification, lymphocytes immunology, species specificity.


NAL Call Number: 41.8 Av5

Abstract: A study was conducted to examine the effect of avian influenza virus (AIV) on chicken lymphocyte activation. Unprimed or Brucella abortus antigen (Ag)-primed lymphocytes were incubated with various doses of the T-cell mitogen concanavalin A (Con A) or Ag, respectively, plus serial dilutions of inactivated AIV for 72 hr, and cell proliferation was measured via uptake of tritiated thymidine. AIV enhanced the proliferative response to Con A or Ag by 150% or better, and the enhancement decreased in a viral dose-dependent manner. The effects were more readily observed in cells that had not been maximally activated by the Con A or Ag. The enhanced response was observed in lymphocytes from both white rock and white leghorn breeds of chicken and in mature peripheral blood lymphocytes or immature thymocytes. The viral activity could be abrogated by pre-treatment of the viral preparation with AIV-specific antisera or prior adsorption of the AIV with chicken erythrocytes. These results indicate that AIV can interact with and modify the in vitro activity of chicken lymphocytes and may exert modulatory effects on the avian immune system.

Descriptors: chickens immunology, lymphocyte activation immunology, lymphocytes immunology, orthomyxoviridae pathogenicity, chickens microbiology, concanavalin A, erythrocytes immunology, specific pathogen free organisms.


NAL Call Number: 41.8 Au72

Abstract: In groups receiving intranasal inoculations, 22 of 24 birds became affected. Illnesses were usually less than 2 d with clinical signs generally depression and dullness. Examination of lesions showed that this strain of virus produced in the laboratory a consistent, characteristic disease pattern, affecting predominantly the bursa of Fabricius, the pancreas and the brain.

Descriptors: chickens, avian influenza virus, wounds, pathology, birds, domestic animals, domesticated birds, Galliformes, influenza virus, lesions, livestock, poultry, useful animals, viruses.


NAL Call Number: 41.8 Av5

Abstract: Comparative histological and immunocytochemical studies were conducted on formalin-fixed tissues from chickens infected with avian influenza viruses of varying virulence. Results showed a distinct pattern of disease that depended on the virulence of the virus and the susceptibility of the birds. At 3 days post-intranasal inoculation with a highly virulent H7N7 virus, all 6-to-8-week-old specific-pathogen-free (SPF) birds were affected, and all developed pancreatic necrosis and encephalitis associated with specific immunoperoxidase staining. Other same-aged SPF birds were only occasionally affected 6 to 8 days after intravenous inoculation with almost avirulent H4N4, H6N2, or H3N8 virus. Specific lesions and immunoperoxidase staining were noted in the kidneys only. The H7N7 virus in older commercial birds and an H7N3 virus in young SPF and older commercial birds caused intermediate mortality rates at 4 to 11 days
postinoculation, and there was a broad range of lesions and specific immunoperoxidase staining in the pancreas, brain, kidney, heart, and skeletal muscle. Two exceptional birds had immunostaining of small blood vessels throughout their bodies with or without lesions or staining in the tissues, which may have represented a transitory pre-localizing phase occurring in many birds. There was necrosis without virus antigen detection in the bursae, thymuses, and cecal tonsils, possibly secondary to stress or only transitory infection of virus. These data indicate that rapid, retrospective diagnosis of avian influenza in fixed tissues is possible by using an immunoperoxidase test on pancreas, brain, and kidney.

Descriptors: chickens, avian influenza virus, pathogenicity, disease resistance, body parts, animal tissues, antigens, histopathology, immunology, biological properties, birds, body parts, domestic animals, domesticated birds, Galliformes, immunological factors, influenza virus, livestock, microbial properties, orthomyxoviridae, pathology, poultry, resistance to injurious factors, useful animals, viruses, susceptibility, viral antigens, immunocytochemistry.


**NAL Call Number:** SF604.J342

**Abstract:** An avian influenza virus, A/turkey/England/50-92/91 (H5N1), showed extremely high virulence in chickens, although its hemagglutinin (HA) cleavage site sequence (R-K-R-K-T-R), having a nonbasic (Thr) residue at the second position (P-2) from the carboxyl terminus of HA1, does not conform to the previously established consensus sequence motif, X-X-R/K-X-R/K-R (X = nonbasic residue), for highly virulent phenotype of the H5 virus. When we evaluated the HA cleavability of this strain in chicken embryo fibroblast culture, we observed that, unlike other HAs with a Thr residue at P-2, this HA was efficiently cleaved. These findings suggest that a nonbasic residue at the P-2 does not affect its recognition and catalyzation by cleavage enzymes that are otherwise influenced by steric structure around the cleavage site.

Descriptors: chickens virology, fowl plague virology, hemagglutinins viral metabolism, influenza A virus avian pathogenicity, turkeys virology, amino acid sequence, cultured cells, chick embryo, fibroblasts cytology, fibroblasts virology, hemagglutinins viral chemistry, molecular sequence data, virulence.


**NAL Call Number:** QR375.V6

**Abstract:** We mutated the virulent avian influenza virus A/turkey/Ontario/7732/66 (H5N9)[Q-R-R-R-K-K-R?G at the hemagglutinin (HA) cleavage site] to create a mutant, R(MO-0), with additional basic residues at this site (Q-R-R-R-R-R-K-K-R?G) by reverse genetics. When tested in chicken embryo fibroblast culture, this mutant showed reduced HA cleavability compared to that of the wild-type virus, but its plaque size was not appreciably altered. Virulence of the R(MO-0) virus in chickens was lower than that of the wild-type virus. These findings indicate that addition of excessive basic residues to an optimal recognition sequence for HA cleavage enzymes at the cleavage site is deleterious for HA cleavability. Previously, we showed that a mutant containing the suboptimal HA cleavage site sequence for cleavage enzyme recognition also had reduced HA cleavability and virulence compared to the wild-type virus. We conclude that the data presented here further substantiate our belief that the level of HA cleavability correlates with the degree of virulence when all other genetic characteristics are considered equal, irrespective of the mechanisms by which HA cleavability is reduced.

Descriptors: hemagglutinins viral metabolism, influenza A virus avian genetics, avian pathogenicity, administration, intranasal, chick embryo, chickens, fowl plague virology, hemagglutinins viral chemistry, hemagglutinins viral genetics, avian chemistry, injections, intramuscular, mutagenesis, site directed, plaque assay.


**NAL Call Number:** 448.8 V81
Abstract: Many viral membrane glycoproteins are post-translationally processed by intracellular endoproteases such as subtilisin-like proteases. These proteases recognize a cleavage site sequence comprising basic amino acids positioned upstream of the cleavage site of the viral proteins. Here, we mutated the glycine residue immediately downstream of the cleavage site (P1) of hemagglutinin (HA) from a virulent avian influenza virus, A/turkey/Ontario/7732/66 (H5N9) (R-R-R-K-K-R/G), to examine the effect of this mutation on its cleavability. Substitution of Gly with Ile, Leu, Val, or Pro, but not Ala, Asp, Phe, His, Ser, or Thr, resulted in substantial reduction of HA cleavage by endogenous endoproteases in CV-1 cells and by vaccinia-expressed PC6 and, albeit to a lesser extent, furin. We conclude that HA cleavage by subtilisin-like proteases is influenced by the downstream P1 amino acid in the absence of upstream cleavage site sequence alterations.

Descriptors: avian influenza virus, agglutinins, chemical composition, mutation, proteases, proteolysis, pathogenicity, biological properties, chemical reactions, enzymes, genetics, hydrolases, hydrolysis, influenza virus, microbial properties, orthomyxoviridae, proteins, viruses, viral hemagglutinins, amino acid sequences, proteinases, virulence.


NAL Call Number: 448.8 V81

Abstract: The emergence of virulent avian influenza viruses in poultry is unpredictable. To gain insight into the mechanism for this event, we sought to identify the molecular changes in virulent mutants that occur during replication in 14-day-old embryonated chicken eggs. After three passages in 14-day-old eggs, avirulent H5 viruses with the K/R-K-K/T-R sequence at the hemagglutinin (HA) cleavage site became virulent in chickens, concomitantly acquiring high HA cleavability, whereas those with the R-E-T-R sequence did not. None of the test viruses converted to a virulent phenotype when passaged in 10-day-old eggs. Nucleotide sequence analysis indicated that the virulent mutants either lost a glycosylation site near the HA cleavage site or acquired an additional arginine at the latter. Avirulent viruses that became virulent after passage in older eggs included an H5N2 avian strain with the R-K-T-R sequence that was isolated in 1993, indicating that viruses with this sequence motif, which are currently circulating in bird populations, should be considered potentially virulent. Failure to generate virulent mutants from viruses with R-E-T-R at the HA cleavage site underscores the pathogenic heterogeneity among avian influenza viruses.

Descriptors: chicks, avian influenza virus, pathogenicity, mutants, agglutinins, nucleotide sequence, chemical composition, biological properties, birds, chickens, domestic animals, domesticated birds, Galliformes, genomes, influenza virus, livestock, microbial properties, orthomyxoviridae, poultry, progeny, proteins, useful animals, viruses, young animals, virus replication, cleavage site, virulence, viral hemagglutinins, amino acid sequences.


NAL Call Number: SF604.J342

Abstract: The emergence of virulent avian influenza viruses in poultry is unpredictable. To gain insight into the mechanism of this event, we previously examined the possible role of older (14-day-old) embryonated eggs, in which virulent mutants were preferably selected (Horimoto and Kawaoka, *Virology* 206: 755-759, 1995). However, it is unknown why virulent mutants replicate predominantly in older eggs. In the present study, we compared protease activities responsible for cleavage activation of the hemagglutinin (HA) in allantoic fluids in 10-day and 14-day-old eggs. In vitro assays showed that the protease activities were stronger in the 14-day-old than 10-day-old eggs. The allantoic fluids with strong protease activity degraded HA. These results indicate that replication of avirulent viruses is hampered in older eggs, while that of virulent viruses whose HAs are activated by other intracellular proteases was not, possibly leading to a replicative advantage for virulent mutants in the older eggs.

Descriptors: influenza A virus avian pathogenicity, avian physiology, virulence, virus replication, allantois physiology, allantois virology, chick embryo, chickens, endopeptidases metabolism, glycosylation, hemagglutinins viral chemistry, hemagglutinins viral genetics, hemagglutinins viral physiology, avian

**Abstract:** To obtain direct evidence for a relationship between hemagglutinin (HA) cleavability and the virulence of avian influenza A viruses, we generated a series of HA cleavage mutants from a virulent virus, A/turkey/ Ontario/7732/66 (H5N9), by reverse genetics. A transfectant virus containing the wild-type HA with R-R-R-K-K-R at the cleavage site, which was readily cleaved by endogenous proteases in chicken embryo fibroblasts (CEF), was highly virulent in intramuscularly or intranasally/orally inoculated chickens. By contrast, a mutant containing the HA with an avirulent-like sequence (R-E-T-R) at the cleavage site, which was not cleaved by the proteases in CEF, was avirulent in chickens, indicating that a genetic alteration confined to the HA cleavage site can affect cleavability and virulence. Mutant viruses with HA cleavage site sequences of T-R-R-K-K-R or T-T-R-K-K-R were as virulent as viruses with the wild-type HA, whereas a mutant with a two-amino-acid deletion but retention of four consecutive basic residues (R-K-K-R) was as avirulent as a virus with the avirulent-type HA. Interestingly, although a mutant containing an HA with R-R-R-K-T-R, which has reduced cleavability in CEF, was as virulent as viruses with high HA cleavability when given intramuscularly, it was less virulent when given intranasally/orally. We conclude that the degree of HA cleavability in CEF predicts the virulence of avian influenza viruses.

**Descriptors:** chickens, avian influenza virus, agglutinins, proteolysis, mutants, induced mutation, pathogenicity, biological properties, birds, chemical reactions, domestic animals, domesticated birds, Galliformes, genetics, hydrolysis, influenza virus, livestock, microbial properties, mutation, poultry, progeny, proteins, useful animals, viruses, posttranslational proteolysis, viral hemagglutinins, amino acid sequences.


**Abstract:** Among the proprotein-processing subtilisin-related endoproteases, furin has been a leading candidate for the enzyme that activates the hemagglutinin (HA) of virulent avian influenza viruses. In the present study, we examined the cleavage activity of two other recently isolated ubiquitous subtilisin-related proteases, PACE4 and PC6, using wild-type HA of A/turkey/Ireland/1378/83 (H5N8) and a series of its mutant HAs. Vaccinia virus-expressed wild-type HA was not cleaved in human colon adenocarcinoma LoVo cells, which lack active furin. This processing defect was correlated by the expression of furin and PC6 but not of PACE4 and a control wild-type vaccinia virus. PC6 showed a sequence specificity similar to that with the endogenous proteases in cultured cells. When LoVo cells were infected with a virulent avian virus, A/turkey/Ontario/7732/66 (H5N9), only noninfectious virions were produced because of the lack of HA cleavage. However, when the cells were coinfected with vaccinia virus that expressed either furin or PC6, the avian virus underwent multiple cycles of replication, indicating that both furin and PC6 specifically cleave the virulent virus HA at the authentic site. These data suggest that PC6, as well as furin, can activate virulent avian influenza virus in vivo implying the presence of multiple HA cleavage enzymes in animals.

**Descriptors:** avian influenza virus, agglutinins, proteolysis, proteases, chemical reactions, enzymes, hydrolases, hydrolysis, influenza virus, proteins, viruses, proteolytic activation, proteolytic cleavage, viral hemagglutinins, precursors, proteinases.


**Abstract:** In October of 1993, there was decreased egg production and increased mortality among Mexican chickens, in association with serologic evidence of an H5N2 influenza virus. First isolated from chickens in May of 1994, after spreading widely in the country, the virus caused only a mild respiratory syndrome in specific pathogen-free chickens. Because eradication of the virus by destruction of infected birds posed
major obstacles to the poultry industry in Mexico, we were able to conduct a "field experiment" to determine the fate of an avirulent virus after repeated cycles of replication in millions of chickens. By the end of 1994, the virus had mutated to contain a highly cleavable hemagglutinin (HA), but remained only mildly pathogenic in chickens. Within months, however, it had become lethal in poultry. Nucleotide sequence analysis of the HA cleavage site of the original avirulent strain revealed R-E-T-R, typical of avirulent viruses and unlike the K-K-K-R sequence characterizing viruses responsible for the 1983 outbreak in poultry in the United States. Both mildly and highly pathogenic isolates contained insertions and a substitution of basic residues in the HA connecting peptide, R-K-R-K-T-R, which made the HA highly cleavable in trypsin-free chicken embryo fibroblasts. Phylogenetic analysis of the HA of H5 avian influenza viruses, including the Mexican isolates, indicated that the epidemic virus had originated from the introduction of a single virus of the North American lineage into Mexican chickens. This sequence of events demonstrates, apparently for the first time, the stepwise acquisition of virulence by an avian influenza virus in nature.

Descriptors: chickens, Mexico, United States, avian influenza virus, agglutinins, pathogenicity, chemical composition, phylogeny, America, biological properties, birds, domestic animals, domesticated birds, evolution, Galliformes, influenza virus, Latin America, livestock, microbial properties, North America, orthomyxoviridae, poultry, proteins, useful animals, viruses, cleavage site, viral hemagglutinins, virulence, amino acid sequences, outbreaks.

NAL Call Number: 448.8 V81
Descriptors: influenza A virus avian metabolism, RNA viral biosynthesis, viral proteins metabolism, base sequence, cytidine triphosphate metabolism, DNA directed RNA polymerases metabolism, guanosine triphosphate metabolism, kinetics, mutation, messenger biosynthesis, temperature.

NAL Call Number: QR360.J6
Abstract: The human protein p78 is induced and accumulated in cells treated with type I interferon or with some viruses. It is the human homolog of the mouse Mx protein involved in resistance to influenza virus. A full-length cDNA clone encoding the human p78 protein was cloned and sequenced. It contained an open reading frame of 662 amino acids, corresponding to a polypeptide with a predicted molecular weight of 75,500, in good agreement with the Mr of 78,000 determined on sodium dodecyl sulfate gels for the purified natural p78 protein. The cloned gene was expressed in vitro and corresponded in size, pl, antigenic determinant(s), and NH2 terminus sequence to the natural p78 protein. A second cDNA was cloned which encoded a 633-amino-acid protein sharing 63% homology with human p78. This p78-related protein was translated in reticulocyte lysates where it shared an antigenic determinant(s) with p78. A putative 5' regulatory region of 83 base pairs contained within the gene promoter region upstream of the presumed p78 mRNA cap site conferred human alpha interferon (IFN-alpha) inducibility to the cat reporter gene. The p78 protein accumulated to high levels in cells treated with IFN-alpha. In contrast, the p78-related protein was not expressed at detectable levels. The rate of decay of p78 levels in diploid cells after a 24-h treatment with IFN-alpha was much slower than the rate of decay of the antiviral state against influenza A virus and vesicular stomatitis virus, suggesting that the p78 protein is probably not involved in an antiviral mechanism. Furthermore, we showed that these proteins, as well as the homologous mouse Mx protein, possess three consensus elements in proper spacing, characteristic of GTP-binding proteins.
Descriptors: DNA genetics, gtp binding proteins, genes, structural, guanine nucleotides metabolism, influenza A virus genetics, interferon type I, recombinant pharmacology, promoter regions genetics, proteins genetics, vesicular stomatitis Indiana virus genetics, virus inhibitors genetics, amino acid sequence, base sequence, binding sites, cell line, cloning, molecular, DNA isolation and purification, *Escherichia coli* genetics, gene library, influenza A virus avian genetics, molecular sequence data, molecular weight, proteins biosynthesis, proteins metabolism, RNA, messenger genetics, sequence homology, nucleic acid, transcription, genetic.
Huang Jianwen, Jiang Yanfen, and He Weimin (2002). Effects of the transfer factor on artificial infected chickens by AIV. *Journal of Gansu Agricultural University (China). Gansu Nongye Daoxue Xuebao (China)* 37(2): 170-173. ISSN: 1003-4315.

**Descriptors:** transfer factor, avian influenza virus, chickens.


**Descriptors:** adsorption, influenza A virus avian immunology, anions, cations, divalent, cations, monovalent, erythrocytes, hemagglutination.


**Abstract:** A dansyl (diaminoaphthalenesulfonyl)-derivative of cerebroside was prepared which could be effectively incorporated into the plasma membranes of tissue culture cells and erythrocytes. The cells which had assimilated the glycolipid fluoresced intensely and could be observed under a fluorescent microscope. Cells were initially labeled rather homogeneously over the whole surface. With longer incubation time organization of the fluorescent glycolipid took place and patches of the lipid in the membrane were formed. The redistribution and organization of the membrane lipid could be demonstrated most clearly when cells labeled with this fluorescent glycolipid were infected with myxoviruses. After infection of MDBK and BHK cells with fowl plaque virus areas of dense fluorescence appeared at margins of neighboring cells. When BHK cells were infected with Newcastle disease virus fusion of the cells was accompanied by complete redistribution of the glycolipid. Erythrocytes could also easily incorporate dansyl cerebroside. Chicken erythrocytes which contain cytoplasmic and nuclear membranes incorporated the fluorescent glycolipid in both membranes.

**Descriptors:** cerebrosides blood, dansyl compounds, erythrocytes metabolism, binding sites, cell line, cell membrane metabolism, cell membrane ultrastructure, chickens, erythrocyte membrane metabolism, erythrocyte membrane ultrastructure, fluorescent dyes, influenza A virus avian, Newcastle disease virus, spectrometry, fluorescence.


**NAL Call Number:** QR180.B4

**Abstract:** The envelopes of influenza viruses contain in addition to lipids also two glycoproteins, the hemagglutinin and the neuraminidase, that are responsible for the adsorption, receptor splitting, penetration and budding processes of these viruses. In this article, hypotheses presented in the past with regard to the virus penetration are reconsidered. Based on results obtained with the fowl plaque virus (influenza A/FPV/Rostock/34, H7N1) and MDCK-cells, we conclude that a fusion between the viral envelope and the plasma membrane is the initial step of virus entry.

**Descriptors:** influenza A virus avian physiology, membrane fusion, cell line, cell membrane physiology, hemagglutination, viral envelope proteins metabolism.


**Abstract:** Structural features of the glycosyl chains of the influenza virus have been determined. It was found that fucose was solely terminal, whereas mannose and galactose were present at the terminal as well as subterminal and core positions. Mannose and glucose molecules were shown to be branching points in the glycosyl chains. Furthermore, linkage positions of carbohydrates within the chains were characterized.

**Descriptors:** carbohydrates analysis, influenza A virus avian analysis, orthomyxoviridae analysis, fucose analysis, galactose analysis, glucose analysis, mannose analysis.

NAL Call Number: QP751.L5

Abstract: Myxoviruses (influenza virus and paramyxovirus) enter host cells by two successive steps consisting of attachment and fusion between viral and cellular membranes. The initial attachment is known to occur through specific binding of the viruses with the neuraminic acid-containing receptors of cellular membranes. Evidence is presented here that, in the following step of membrane fusion, neutral glycolipids terminating in galactose and certain phospholipids (primarily lecithin and sphingomyelin) interact with the viral envelopes and that this interaction may be fundamental to the fusion process.

Descriptors: cell membrane physiology, glycolipids physiology, influenza A virus avian physiology, membrane lipids physiology, parainfluenza virus 1, human physiology, phospholipids physiology, receptors, virus physiology, chick embryo, glycolipids pharmacology, hemolysis drug effects, phospholipids pharmacology, receptors, virus drug effects.


NAL Call Number: 381 B522

Abstract: Total lipid of four egg grown influenza viruses (A2-Asia, A2-England, A2-Taiwan and fowl plague virus) were extracted with chloroform-methanol. After mild alkali treatment of the extracts, glycosphingolipids and sphingomyelin were separated by a silicic acid column, and finally purified by thin layer chromatography. Fatty acid, sphingosine and carbohydrate components of individual lipid classes were then analysed by gas-liquid chromatography. Nearly identical results were obtained with all viruses investigated. Approximately 20% of the total lipid was monohexosylceramide, distributed equally between glucosyl- and galactosyl-anallogues. Lactosylceramide and oligohexosylceramides were found in much smaller concentrations (approx. 2%). About 15% of the total lipid was attributed to sphingomyelin. A large proportion of fatty acids (around 25% in sphingomyelin and 60% in glycolipids) belonged to the long chain (C19-C26) normal- and 2-hydroxy series. C18-sphingosine was found to be the only base present in all lipid classes investigated.

Descriptors: influenza A virus avian analysis, orthomyxoviridae analysis, sphingolipids analysis, fatty acids analysis, hexoses analysis, oligosaccharides analysis, sphingomyelins analysis.


NAL Call Number: 448.8 N442

Descriptors: antiviral agents pharmacology, aspirin pharmacology, influenza A virus avian drug effects, human drug effects, cultured cells.


NAL Call Number: QR360.A1J6

Abstract: The role of neuraminidase and the mechanism of low pH dependence in influenza virus-induced membrane fusion have been studied further using fowl plague virus (FPV, H7N1). Two specific anti-FPV neuraminidase antisera obtained from chickens immunized with recombinant virus strains inhibited viral neuraminidase activity without influencing its haemagglutinating activity. These sera totally inhibited the FPV-induced fusion of erythrocytes and partially reduced haemolysis. But both fusion and haemolysis activities could be restored by external addition of Vibrio cholerae neuraminidase, indicating participation of neuraminidase in FPV-induced membrane fusion. With regard to low pH-dependent fusion by influenza virus, it was found that erythrocytes of various species showed different pH optima for haemolysis by FPV and that erythrocytes could be sensitized for fusion and haemolysis by FPV at neutral pH if they had been pretreated with a low pH buffer. These results demonstrated that surface properties of erythrocytes rather than that of the virus are critical in the low pH-dependent fusion and haemolysis by influenza viruses.

Descriptors: cell fusion, influenza A virus avian physiology, neuraminidase physiology, viral proteins physiology, bacterial proteins physiology, chick embryo, erythrocytes, hemagglutination, viral, hemolysis, hydrogen-ion concentration, rabbits, rats, Vibrio cholerae enzymology.

Huang, R.T., B. Lichtenberg, and O. Rick (1996). Involvement of annexin V in the entry of influenza viruses and
NAL Call Number: QD415.F4

Abstract: Influenza viruses bind to annexin V, a widely spread non-glycosylated phospholipid-binding protein. Externally added phospholipids as well as antiserum against this protein specifically inhibit infection of these viruses in cell cultures. We conclude that annexin V plays an important role in the entry of these viruses.

Descriptors: annexin V metabolism, influenza A virus avian metabolism, human metabolism, phospholipids metabolism, receptors, virus metabolism, antibodies, viral immunology, capsid metabolism, cell line, dogs, avian immunology, avian pathogenicity, human immunology, human pathogenicity, phosphatidylethanolamines metabolism, plaque assay, recombinant fusion proteins metabolism, time factors, viral core proteins metabolism.

NAL Call Number: 384 Z38

Descriptors: influenza A virus avian enzymology, neuraminidase, Newcastle disease virus enzymeology, chickens, colloids, enzyme tests, gangliosides, glycolipids, hydrolysis, macromolecular systems, milk, human, oligosaccharides, structure activity relationship.

NAL Call Number: QH301.Z4

Descriptors: glycoproteins metabolism, neuraminic acids metabolism, orthomyxoviridae metabolism, adsorption, binding sites, erythrocytes drug effects, hemagglutination, viral, hemagglutinins viral, influenza A virus avian metabolism, neuraminidase pharmacology, Newcastle disease virus metabolism, respirovirus metabolism, sindbis virus metabolism.

NAL Call Number: 448.8 V81

Descriptors: cell membrane physiology, glycoproteins physiology, influenza A virus avian immunology, neuraminidase physiology, Newcastle disease virus immunology, cultured cells, chick embryo, hemagglutinins viral metabolism, hemagglutinins viral physiology, liposomes metabolism, viral proteins metabolism, viral proteins physiology.

NAL Call Number: 448.8 V81

Descriptors: cell membrane physiology, hemagglutinins viral, influenza A virus avian physiology, human physiology, orthomyxoviridae physiology, cultured cells, chick embryo, glycoproteins, liposomes, microinjections, receptors, virus physiology, viral proteins.


Abstract: To test whether penetration of influenza viruses could occur at the plasma membrane of host cells, virus particles were tightly bound on Concanavalin A-coated substratum of plastic culture plates and then overlaid with embryo cells. Under these conditions, endocytosis of the viruses was prevented but the cells were found to be effectively infected. The results indicate, that infection by influenza viruses can occur through fusion between the viral membrane and the host cell plasma membrane.

Descriptors: cell membrane permeability, influenza A virus avian physiology, orthomyxoviridae physiology, cultured cells, chick embryo, endocytosis, avian ultrastructure, microscopy, electron, virus cultivation methods.

**NAL Call Number:** QR360.J6

**Descriptors:** influenza A virus, avian genetics, avian pathogenicity, viral matrix proteins genetics, base sequence, chickens, DNA, viral genetics, glycosylation, hemagglutinins, viral chemistry, viral genetics, avian classification, influenza, avian etiology, models, molecular, neuraminidase chemistry, neuraminidase genetics, viral matrix proteins chemistry, virulence genetics.


**NAL Call Number:** 448.8 P942

**Abstract:** Six different monoclonal antibodies to influenza A/Brazil/11/78 virus hemagglutinin were used for selection of antigenic variants of H1N1 viruses: A/USSR/090/77 and A/black-headed gull/ Kaz SSR/470/79. The group-specific monoclonal antibody completely neutralized the infective activity of the parental viruses (dilutions 1:5 to 1:640). Two antigenic variants of wild type viruses were obtained using cross-reactive antibody. A comparative study of the antigenic structure, biological properties, and peptide maps of the heavy chain of the original viruses, antigenic variants, and some epidemic H1N1 strains was carried out. The selected variants of A/black-headed gull/ Kaz. SSR/470/77 and A/USSR/090/79 viruses were shown to be similar to epidemic H1N1 strains isolated in 1953 and 1978.

**Descriptors:** antibodies, monoclonal analysis, antigens, viral isolation and purification, influenza A virus human immunology, selection genetics, variation genetics, antigens, viral analysis, birds, cross reactions, electrophoresis, polyacrylamide gel, hemagglutination inhibition tests, avian immunology, peptides analysis.


**NAL Call Number:** 448.8 P942

**Abstract:** The antigenic structure of influenza H13 viruses isolated from wild birds in the USSR in 1976-1985 was studied. Antiserum against the reference A/gull/Maryland/704/77 (H13N6) strain was used to demonstrate the antigenic variations among the viruses. The homology of nucleotide sequences in the region 99-215 for the two A/H13N6 strains, A/gull/Maryland/704/77 and A/great black-headed gull/Astrakhan/227/84, were 75% and 86%, respectively. The 9-base segment deletion in A/grey black-headed gull/Astrakhan/277/84 was observed. Comparison of the predicted amino acid sequences of the strains' hemagglutinin in the appropriate region (amino acids 2-40) revealed 5 replacements (86% homology). Two replacements of arginine by lysine and asparagine by serine in positions 15 and 16, respectively, are the most significant. The latter replacement is accompanied by a change in the glycosylation site and might alter its three-dimensional structure. Further studies of the isolate genome are under way.

**Descriptors:** antigenic variation, antigens, viral immunology, influenza A virus avian immunology, amino acid sequence, antigens, viral genetics, base sequence, hemagglutinins viral genetics, avian genetics, molecular sequence data, radioimmunoassay, sequence homology, nucleic acid, viral proteins analysis.


**NAL Call Number:** QH506.M65F2

**Abstract:** The analysis of escape mutants of the avian influenza virus of H5 subtype (strain A/Mallard/Pennsylvania/10218/84) revealed the location and structure of two antigenic sites in the hemagglutinin (HA) molecule. Several escape mutants exhibited unusual features in the reactions with
monoclonal antibodies (Mabs), being completely resistant in the infectivity neutralization test to the Mabs used for their selection, and retaining the ability to bind the Mabs as revealed by enzyme-linked immunosorbent assay. An enhancement of the binding by an amino acid change in a different antigenic site was demonstrated, as well as a complete abolishment of the binding by a mutation selected by passage in the presence of an excess of the non-neutralizing Mab of high binding ability. The observed effects did not result from the changes in the affinity of the mutant HA toward sialic receptors. The data suggest that one amino acid change in HA may prevent the virus neutralization by different mechanisms for different Mabs: either the binding of the Mab to HA is prevented, or the bound Mab is unable to block the receptor-binding pocket of HA. Different mechanisms of the acquisition of resistance to Mabs in the course of the selection of escape mutants are discussed.

Descriptors: immune system, infection, methods and techniques, molecular genetics, ELISA immunologic techniques, laboratory techniques, virus infectivity neutralization test bioassay techniques, laboratory techniques, gene mutations, methodology, viral genetics, viral neutralization, mechanisms, analysis.


Abstract: The hemagglutinin (HA) of six H5 influenza virus strains isolated from ducks in Japan and China in 1976 to 1996 were analyzed antigenically and genetically. Antigenic analysis using a panel of monoclonal antibodies revealed that the HA of H5 influenza viruses isolated from ducks are antigenically closely related to each other. Phylogenetic analysis indicates that the isolates from ducks in Hokkaido were derived from an ancestor common with the highly pathogenic isolates from chickens and humans in Hong Kong in 1997.

Descriptors: ducks virology, hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian classification, avian genetics, phylogeny, antibodies, monoclonal, antigens, viral genetics, viral immunology, chickens virology, China, genes viral, hemagglutinin glycoproteins, influenza virus immunology, Hong Kong, avian isolation and purification, Japan, RNA viral genetics, viral isolation and purification.


Descriptors: influenza A virus avian genetics, human genetics, mutation, ribavirin pharmacology, ribonucleosides pharmacology, drug resistance, fowl plague microbiology, influenza microbiology, phenotype.


Descriptors: amantadine pharmacology, influenza A virus avian metabolism, RNA viral biosynthesis, autoradiography, carbon radioisotopes, cultured cells, chick embryo, dactinomycin pharmacology, avian drug effects, avian growth and development, plaque assay, tissue culture, tritium, uridine metabolism, virus replication drug effects.


Descriptors: adamantane analogs and derivatives, influenza A virus avian drug effects, human drug effects, mutation, recombination, genetic drug effects, rimantadine antagonists and inhibitors, antigens, viral analysis, chick embryo, drug resistance, microbial genetics, genes viral drug effects, avian genetics, avian immunology, human genetics, human immunology, plaque assay.

Evidence is presented which confirms that the influenza virus genome specifies a polypeptide of molecular mass 11 000, in addition to the eight previously recognized gene products. A summary is included of results that show that this polypeptide is encoded by the smallest genome segment of the virus (segment 8) which also encodes a polypeptide of molecular mass 23 000 (NS1). The implications of these findings are considered.

Descriptors: genes viral, influenza A virus avian genetics, viral proteins genetics, cultured cells, chickens, genes, structural, molecular weight, species specificity.


Descriptors: fowl plague microbiology, influenza A virus avian genetics, RNA splicing, RNA viral genetics, chick embryo, DNA genetics, viral genetics, gene expression regulation, I cells cell line microbiology, mice, nucleic acid hybridization, peptides genetics, viral proteins biosynthesis, virus cultivation, virus replication.


Descriptors: DNA, viral genetics, influenza A virus avian genetics, poly A genetics, RNA genetics, chick embryo, cloning, molecular, DNA restriction enzymes, fibroblasts, RNA, messenger genetics, transcription, genetic, translation, genetic, viral proteins genetics.


Descriptors: influenza A virus avian metabolism, translation, genetic, viral proteins biosynthesis, cultured cells, hemagglutinins viral, influenza A virus avian enzymology, molecular weight, neuraminidase biosynthesis, nucleoproteins biosynthesis, peptide synthesis, peptides analysis, RNA replicase, viral proteins analysis.


Descriptors: 501 L84Pb
Abstract: The relationship of the mRNAs encoding the NS1 and NS2 polypeptides of influenza virus has been investigated through synthesis and characterisation of complementary DNA copies of the mRNAs. Previous work had shown that both mRNAs are encoded by virion RNA segment 8, and that the sequences comprising the smaller of the two mRNAs (the NS2 mRNA) were also present on the NS1 mRNA. Our results indicate that the mRNA encoding the NS2 polypeptide of the avian influenza, fowl plague virus, is approximately 400 ntds long, and that its sequences correspond largely with the 3'-terminal region of the NS1 mRNA.

Descriptors: DNA, viral metabolism, genes, structural, orthomyxoviridae metabolism, RNA, messenger biosynthesis, transcription, genetic, nucleic acid hybridization, peptide synthesis, translation, genetic, viral proteins biosynthesis.

NAL Call Number: 448.8 V81
Descriptors: influenza A virus avian metabolism, RNA, messenger biosynthesis, viral biosynthesis, viral proteins biosynthesis, cell line, cycloheximide pharmacology, genes viral, avian genetics, transcription, genetic, translation, genetic.

NAL Call Number: 448.8 V81
Descriptors: influenza A virus avian metabolism, peptide synthesis, RNA, messenger metabolism, RNA viral metabolism, translation, genetic, viral proteins biosynthesis, cell free system, genetic code, glycoproteins biosynthesis, hemagglutinins viral, triticum.

NAL Call Number: QR360.J6
Abstract: We determined the deduced amino acid sequences of two H1 duck influenza A virus hemagglutinins (HAs) and found that the consensus sequence of the HA, determined directly from virus recovered from the intestinal tract, remains unchanged through many generations of growth in MDCK cells and chicken embryos. These two duck viruses differ from each other by 5 amino acids and from A/Dk/Alberta/35/1976 (F. J. Austin, Y. Kawaoka, and R. G. Webster, J. Gen. Virol. 71:2471-2474, 1990) by 9 and 12 amino acids, most of which are in the HA1 subunit. They are antigenically similar to each other but different from the Alberta virus. We compared these H1 duck HAs with the HAs of human isolates to identify structural properties of this viral glycoprotein that are associated with host range. By comparison to the human H1 HAs, the duck virus HA sequences are highly conserved as judged by the small fraction of nucleotide differences between strains which result in amino acid substitutions. However, the most striking difference between these duck and human HAs is in the number and distribution of glycosylation sites. Whereas duck and swine viruses have four and five conserved glycosylation sites per HA1 subunit, none of which are on the tip of the HA, all human viruses have at least four additional sites, two or more of which are on the tip of the HA. These findings stress the role of glycosylation in the control of host range and suggest that oligosaccharides on the tip of the HA are important to the survival of H1 viruses in humans but not in ducks or swine.
Descriptors: consensus sequence genetics, ducks microbiology, hemagglutinins viral genetics, influenza A virus avian genetics, human genetics, amino acid sequence, antigens, viral genetics, antigens, viral immunology, cultured cells, consensus sequence immunology, feces microbiology, glycosylation, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral immunology, avian immunology, human immunology, models, molecular, molecular sequence data, protein processing, post translational, regulatory sequences, nucleic acid genetics, selection genetics, sequence homology, amino acid, variation genetics.

Inpanbutr, N. and R.D. Slemons (1993). Immunocytochemical localization of type A influenza virus

**NAL Call Number:** 41.8 Am3A

**Abstract:** Kidney tissues were removed from euthanatized mature White Leghorn chickens 4 days after IV inoculation with type A influenza virus. The kidney tissues were then fixed at -70 C, using a freeze substitution technique. Type A influenza virus nucleoprotein was readily detected in the nuclei and cytoplasm of the proximal and distal tubular epithelial cells by immunocytochemistry, and the sharpness of the immunomarker in the cells indicated minimal antigen migration during fixation and tissue section preparation. This tissue fixation technique also resulted in good preservation of cellular morphology. The freeze substitution technique of tissue fixation is an excellent alternative to cryostat-cut acetone-fixed tissue sections or conventional chemical fixation of paraffin-embedded tissues for in situ immunocytochemical localization of type A influenza virus nucleoprotein antigen.

**Descriptors:** influenza A virus avian isolation and purification, kidney microbiology, nucleoproteins analysis, chick embryo, chickens, epithelium microbiology, freezing, immunohistochemistry, kidney tubules microbiology.


**NAL Call Number:** 448.8 P942

**Abstract:** The interrelations between H3/73 hemagglutinin of human influenza virus and the other 16 mammalian and avian hemagglutinin subtypes (a total of 50 strains) were studied by the method of radioimmunologic analysis (RIA). The antigenic relations of H3, Hav7 and Heq2 were confirmed, certain common determinants were also found in H3/73 hemagglutinin and avian viral Hav6 and Hav9 hemagglutinins. No interrelations were revealed with previously circulating human influenza viruses H0, H1, H2 as well as with swine influenza virus and avian viruses Hav1-Hav5, Hav8. It has been shown that the H3/73 determinant in some avian viruses evolves similarly to drift-variants of human influenza virus. The method can be recommended for fine analysis of influenza virus antigenic structure as it allows detecting small antigenic quantities.

**Descriptors:** hemagglutinins viral immunology, influenza A virus immunology, ducks microbiology, avian immunology, human immunology, porcine immunology, species specificity, turkeys microbiology, radioimmunologic analysis.


**NAL Call Number:** 448.8 P942

**Abstract:** Comparative studies of the antigenic properties of hemagglutinin (HA) of animal and human viruses revealed both similarities between them and complete differences in the composition of antigenic determinants. Avian influenza viruses A/chicken/Kamchatka/12/71, A/pintail/Primorie/730/76, and A/bat/Alma-Ata/73/77 were completely identical with human strains of influenza virus. Influenza A/horse/Miami/63 contains one antigenic determinant H3.1.HA of A/tern/Turkmenia/18/73 (Hav7) viruses has a peculiar set of antigens. Apart from two antigenic determinants H3.1 and H3.3 inherent in human virus strains, HA of A/tern/Turkmenia/18/73 virus contains an antigenic determinant the population of antibodies to which shows no relation to HA of subtypes Hav2-Hav9.

**Descriptors:** epitopes isolation and purification, influenza A virus human immunology, orthomyxoviridae immunology, complement fixation tests, epitopes analysis, hemagglutination inhibition tests, hemagglutinins viral analysis, hemagglutinin viral isolation and purification, immunoelectrophoresis, orthomyxoviridae isolation and purification.

NAL Call Number: QR360.A1J6

Abstract: A mammalian cell-adapted mutant of the Dobson strain of fowl plague virus (FPV-B) was characterized. Genetic analyses of recombinants between a ts mutant of this virus and either the non-adapted Dobson strain or the Rostock strain of FPV showed that the gene coding for the P3 protein of the adapted Dobson strain was sufficient to enable any recombinant to grow in L cells. The abortive cycle of wild-type Dobson strain (FPV+) was compared to the productive cycle of the mutant. By using 100 p.f.u./cell, no quantitative difference could be detected in infected L cells between polypeptides and cRNAs induced by FPV+ and FPV-B. However, the maturation of virions at the plasma membrane did not proceed correctly. At a lower m.o.i. the amounts of virus polypeptides decreased with the m.o.i. This decrease was not the same for all polypeptides and cRNA segments: HA, M and NA and their mRNAs decreased to a greater extent than the others. These results are discussed in relation to a possible biological activity of polypeptide P3.

Descriptors: genes viral, influenza A virus avian genetics, virus replication, avian growth and development, avian metabolism, L cells cell line, mice, mutation, RNA viral biosynthesis, recombination, genetic, viral proteins biosynthesis.


NAL Call Number: 448.3 An75

Abstract: Particles produced during the abortive infection of L cells by fowl plague virus (Dobson strain) have been characterized and compared to the infectious particles produced by a mutant of this virus adapted to mammalian cells. The former are of apparently normal morphology but most of them are non-infectious. They have the same RNA/protein ratio as the infectious particles and the same polypeptide composition. They contain also the same RNA segments as those found in infectious particles. Possible reasons for the defectiveness of these particles are discussed.

Descriptors: influenza A virus avian analysis, L cells cell line microbiology, virion analysis, electrophoresis, polyacrylamide gel, hemagglutinins analysis, avian ultrastructure, peptides analysis, RNA viral analysis, viral proteins analysis, virion ultrastructure.


NAL Call Number: QR360.A1J6

Abstract: The abortive infection of L cells by the Dobson strain of fowl plague virus (FPV) and the productive infection by a mammalian cell-adapted mutant have been compared. The mRNA population during the abortive cycle is characterized by a lower production compared to the productive system of mRNA 7 (which codes for the M polypeptide) early in the cycle, and a lower production of mRNAs 4, 6 and 7 (which code for HA, NA and M) late in the cycle. Differences in the amounts of the corresponding polypeptides can also be detected when these mRNA populations are used to programme a wheat germ cell-free system. However, analysis of the polypeptides synthesized in vivo by the two viruses show that equivalent amounts of all virus polypeptides are synthesized during the productive and the abortive cycles. Possible reasons for differences between in vivo and in vitro translation of the virus mRNAs during the abortive cycle are discussed.

Descriptors: influenza A virus avian metabolism, RNA, messenger biosynthesis, RNA viral biosynthesis, viral proteins biosynthesis, avian growth and development, L cells cell line, mice, RNA, messenger genetics, viral genetics, translation, genetic, viral proteins analysis.


NAL Call Number: 448.8 V81

Descriptors: influenza A virus avian genetics, L cells cell line microbiology, chick embryo, dactinomycin pharmacology, electrophoresis, polyacrylamide gel, fluorouracil pharmacology, avian growth and development, mice, mutation, nucleic acid hybridization, peptide synthesis, plaque assay, RNA viral biosynthesis, temperature, viral proteins biosynthesis, virus cultivation, virus replication.

**NAL Call Number:** 448.3 Ar23

**Abstract:** Fetuin bound latex spheres do not adhere to the membranes of non-infected cells but adhere to those of cells productively infected by fowl plague virus (FPV Dobson strain). In contrast, asialo fetuin spheres do not attach to the membranes of productively infected cells. Moreover latex fetuin spheres incubated with extracts of productively infected cells and extensively washed are specifically enriched in neuraminidase activity without any trace of haemagglutinin. These observations suggest that viral neuraminidase in the membrane is the site of attachment of the sialic acid moieties of fetuin spheres. These neuraminidase sites are detectable when L cells are productively infected by a mammalian cell adapted mutant of the Dobson strain (FPV-B) but are not detectable on L cells abortively infected by wild type (FPV+). However, even in the abortive system, neuraminidase is synthesised de novo as shown by its labelling with 14C-glucosamine and by its isolation from labelled extracts of infected cells by latex fetuin spheres. These results show that misintegration of viral neuraminidase in the plasma membrane of L cells is a feature of abortive infection of these cells by the Dobson strain of FPV. However the relationship (if any) of this misintegration to abortive infection remains to be established.

**Descriptors:** cell membrane enzymology, influenza A virus avian enzymology, microbiological techniques, neuraminidase analysis, cell line, avian growth and development, L cells cell line, latex, microscopy, electron, scanning, microspheres, neuraminidase biosynthesis, alpha fetoproteins.


**NAL Call Number:** 448.8 V81

**Descriptors:** influenza A virus avian growth and development, mutation, RNA viral analysis, viral proteins analysis, cell line, chickens, glycoproteins analysis, hamsters, avian analysis, mice, molecular weight, nucleic acid conformation, peptides analysis, virus replication.


**Abstract:** Emergence of highly virulent influenza A/H5N1 viruses in Hong Kong in 1997 posed a threat of pandemic and brought an urgent need to develop a suitable seed virus for vaccine production. The virulence of the H5N1 viruses to chicken embryos should hamper the efficient production of the vaccine. In addition, potential virulence to humans raised safety issue in manufacturing vaccine. Toward vaccine development, one approach is to use an avirulent avian influenza virus antigenically similar to the virulent ones as a surrogate vaccine strain. The other approach is based on the attenuation of pathogenicity of virulent H5N1 virus by genetic engineering of the hemagglutinin gene and selection of a gene constellation. The reverse genetics technique can make the latter approach possible. Candidate strains suitable for vaccine production could be prepared by using either approach.

**Descriptors:** influenza transmission, influenza A virus human genetics, human immunology, influenza vaccine, chick embryo, genes viral, genetic engineering, hemagglutinins chemistry, hemagglutinins genetics, vaccines, attenuated, virulence.


**Descriptors:** proteins, avian influenza virus, electrophoresis.


**NAL Call Number:** 448.3 Ar23

**Abstract:** Three non-overlapping antigenic sites were defined on the hemagglutinin of avian influenza virus A/budgerigar/Hokkaido/1/77 (H4N6) by competitive binding assay of monoclonal antibodies to the virus and
comparative antigenic analysis of variants selected with monoclonal antibodies. Antigenic relationship among 25 H4 influenza viruses of different bird origin was examined by ELISA with the monoclonal antibodies to each of defined antigenic sites. Two of the three antigenic sites contained epitopes specific to the H4 influenza viruses of budgerigar and mynah origin, and the remaining site contained an epitope which was cross-reactive with almost all of the H4 influenza viruses.

Descriptors: hemagglutinins viral immunology, influenza A virus avian immunology, antibodies, monoclonal, antibodies, viral, birds microbiology, chickens microbiology, cross reactions, ducks microbiology, enzyme linked immunosorbent assay, epitopes immunology, species specificity.

NAL Call Number: QR375.V6

Abstract: Virulent avian influenza A viruses produce lethal disease in chickens. Since cell death can be caused by either necrosis or apoptosis, we investigated the types of cell death that occur in natural hosts, chickens, infected with virulent avian viruses. Using biochemical methods, we demonstrate that virulent avian influenza viruses induce apoptosis of vascular endothelial cells in liver, kidney, and brain. Viral antigens were also detected in these organs, suggesting that viral replication induces apoptosis in infected chickens. These results indicate that apoptosis does occur in virulent avian influenza virus infection in a natural host, and may contribute to the lethality of the virus.

Descriptors: apoptosis, influenza A virus avian pathogenicity, antigens, viral physiology, chickens, virulence.

NAL Call Number: 448.8 V81

Abstract: Despite their uniform ability to bind to oligosaccharide-containing terminal sialic acids, influenza A viruses show differences in receptor specificity. To test whether agglutination of erythrocytes from different animal species could be used to assess the receptor specificity of influenza A viruses, we determined the agglutinating activities of a range of virus strains, including those with known receptor specificities, using erythrocytes from seven animal species. All equine and avian viruses, including those known to recognize N-acetyl and N-glycolyl sialic acid linked to galactose by the alpha2,3 linkage (NeuAc alpha2,3Gal and NeuGc alpha2,3Gal), agglutinated erythrocytes from all of the animal species tested (chickens, ducks, guinea pigs, humans, sheep, horses, and cows). The human viruses, including those known to preferentially recognize NeuAc alpha2,6Gal, agglutinated all but the horse and cow erythrocytes. Fluorescence-activated cell sorting analysis of erythrocytes using linkage-specific lectins [Sambucus nigra agglutinin for sialic acid (SA) alpha2,6Gal and Maackia amurensis agglutinin for SA alpha2,3Gal] showed that both cow and horse erythrocytes contain a large amount of SA alpha2,3Gal-, but virtually no SA2,6Gal-specific lectin-reactive oligosaccharides on the cell surface, while human and chicken erythrocytes contained both types of oligosaccharides. Considering that the majority (>93%) of sialic acid in horse and cow erythrocytes is of the N-glycolyl type, our results suggest that viruses able to agglutinate these erythrocytes (i.e., avian and equine viruses) recognize NeuGc alpha2,3Gal. These findings also show that agglutinating assays with erythrocytes from different animal species would be useful in characterizing the receptor specificity of influenza A viruses.

Descriptors: erythrocytes physiology, erythrocytes virology, hemagglutination, influenza A virus physiology, receptors, virus physiology, carbohydrate sequence, cattle, chick embryo, chickens, guinea pigs, horses, influenza A virus avian physiology, human physiology, porcine, lectins, molecular sequence data, species specificity, substrate specificity, swine.

NAL Call Number: QR360.J6

Abstract: The hemagglutinin (HA) of H3 human influenza viruses does not support viral replication in duck...
intestine despite its avian origin. A Leu-to-Gln mutation at position 226 and a Ser-to-Gly mutation at position 228 in the HA of human A/Udorn/307/72 (H3N2) permit a reassortant virus [human Udorn HA, with all other genes from A/mallard/New York/6750/78 (H2N2)] to replicate in ducks. To understand the molecular basis of this change in host range restriction, we investigated the receptor specificity of duck influenza viruses as well as of human-duck virus reassortants. The results indicate that the recognition of a glycoconjugate moiety possessing N-glycolneuraminic acid (NeuGc) linked to galactose by the alpha2,3 linkage (NeuGcalpha2,3Gal) is associated with viral replication in duck intestine. Immunofluorescence assays with NeuGcalpha2,3Gal-specific antiserum detected this moiety primarily on the crypt epithelial cells of duck colon. Such recognition, together with biochemical evidence of NeuGc in crypt cells, correlated exactly with the ability of the virus to replicate in duck colon. These results suggest that recognition of the NeuGcalpha2,3-Gal moiety plays an important role in the enterotropism of avian influenza viruses.

Descriptors: ducks virology, hemagglutinins viral physiology, influenza virology, influenza A virus physiology, neuraminic acids, galactose, virus replication.


Abstract: Highly virulent avian influenza viruses can arise from avirulent strains maintained in poultry, but evidence to support their generation from viruses in wild birds is lacking. The most likely mechanism for the acquisition of virulence by benign avian viruses is the introduction of mutations by error-prone RNA polymerase, followed by the selection of virulent viruses. To investigate whether this mechanism could apply to wild waterfowl, we studied an avirulent wild-swan virus that replicates poorly in chickens. After 24 consecutive passages by air sac inoculation, followed by five passages in chicken brain, the avirulent virus became highly pathogenic in chickens, producing a 100% mortality rate. Sequence analysis at the hemagglutinin cleavage site of the original isolate revealed a typical avirulence type of sequence, R-E-T-R, which progressed incrementally to a typical virulence type of sequence, R-R-K-K-R, during repeated passages in chickens. These results demonstrate that avirulent viruses maintained in wild waterfowl in nature and bearing the consensus avirulence type sequence R-E-T-R have the potential to become highly pathogenic while circulating in chickens.

Descriptors: molecular genetics, infection, veterinary medicine.


Abstract: In order to determine the role of neuraminidase (NA) in host range restriction, we studied a reassortant virus that replicated with poor efficiency in ducks. The reassortant virus, in which NA of an avian virus, A/duck/Hong Kong/278/78 (H2N9), was replaced with that from a human virus, A/England/12/62 (H2N2), was rectally inoculated into ducks. The viruses recovered were then orally inoculated into new ducks and a variant that replicated efficiently in the intestinal tract was isolated. Sequence analysis showed that the variant virus NA contained two amino acid substitutions at positions 165 (Val to Ile) and 431 (Gln to Pro). Differences in low pH resistance of the NAs were also assessed to identify differences in the NAs possibly related to the restriction of viral growth in ducks. The NA activity of the parental reassortant virus almost disappeared after low pH treatment (pH 3.0), while that of the variant was conserved under the same conditions. These results indicate that the amino acids, at positions 165 and/or 431 on the NA molecule, correlate with the ability to support viral growth in ducks, contributing to the low pH stability of NA activity.

Descriptors: avian influenza, intestinal replication, low pH, neuraminidase, ducks, amino acids, influenza A virus.


Abstract: A polysaccharide from the green marine algae *Ulva lactuca* has been isolated. The substance
has been investigated after acid hydrolysis by thin-layer and gas chromatography. The following carbohydrate components have been found: arabinose-xylose-rhamnose-galactose-mannose-glucose in ratio 1:1:9:5:2.5:16 respectively. One unidentified sugar has been demonstrated too. The polysaccharide has been studied for antiviral activity in vitro against a number of human and avian influenza viruses. A considerable inhibition of the viral reproduction was found. The effect was dose-dependent, strain-specific and selective.

Descriptors: algae, chemical composition, polysaccharides, purification, monosaccharides, arabinose, xylose, rhamnose, galactose, mannose, glucose, aldoses, carbohydrates, monosaccharides, processing, reducing sugars, sugars, carbohydrate composition, composition.


NAL Call Number: 448.3 AC85

Abstract: The serum antibody titre to the nucleoprotein (NP) of the influenza virus recombinant MRC-11 was determined in virus strains A/USSA/5/80 (H3N2), A/Hong Kong/8/64 (H3N2), A/duck/Ukraine/63 (Hav7Neq2) and in a recombinant strain between A/tern/Frunse/334/78(Hav4Nav1) and A/PR/8/34(H0N1) using the enzyme-linked immunosorbent assay (ELISA). Significant differences between the NP of these strains were found proving the usefulness for ELISA for such investigations.

Descriptors: antigens, viral analysis, influenza A virus avian analysis, human analysis, nucleoproteins immunology, viral proteins immunology, enzyme linked immunosorbent assay, avian immunology, human genetics, human immunology, recombination, genetic.


NAL Call Number: 448.8 P942

Abstract: A comparative study of the electrophoretic mobility of polypeptides of avian influenza viruses was carried out; molecular weights of polypeptides and their percent content were determined. Strains isolated from one host and possessing different hemagglutinin serotypes were found to have different electrophoregrams due to differences in the position of the light or heavy chain of hemagglutinin. Hemagglutinins (Hav7, Heq2, H3) and (Hav1, Heq1) in virions isolated from different hosts had similar electrophoretic mobilities of the heavy and particular light chain. No significant variations in the molecular weights of NP and M proteins of all the viruses under study were found. No identity in the electrophoretic mobility and content of P1–P3 proteins in different strains of avian influenza virus was found.

Descriptors: influenza A virus avian analysis, peptides analysis, birds microbiology, chick embryo, electrophoresis, polyacrylamide gel, hemagglutinins viral analysis, molecular weight.


Abstract: The H5N1 type of influenza A virus isolated from human patients in 1997 has a characteristic hemagglutinin and was considered to be directly transmitted from birds. Although neuropathogenicity of this virus was not demonstrated in human autopsy cases, some experimental studies using mice have disclosed that this virus infects the central nervous system (CNS) after intranasal inoculation. In this study we focused on the topographical localization of virus-infected cells in the murine CNS after intranasal inoculation. We immunohistochemically examined virus-infected cells in mouse tissues using a rabbit antiserum recognizing the nucleoprotein of influenza A virus. The virus-infected cells appeared initially in the respiratory tract. Thereafter, the virus antigen-positive cells appeared in the olfactory system and the cranial nerve nuclei innervating the facial region. This suggests that this virus is principally transmitted from the nasal cavity to CNS through the cranial nerves. Neurons were frequently infected and glial and ependymal cells were also infected. Transneuronal transmission of the virus might play the important role of viral spread within the CNS.

**Abstract:** To gain insight into the events that occur when avian influenza viruses are transmitted to humans, the receptor-binding properties of the index H5N1 influenza virus isolated from a human in 1997 and the A/turkey/Ontario/7732/66 (H5N9) virus were compared, by using a haemadsorption assay. Cells expressing the haemagglutinin (HA) of the human isolate were adsorbed by both chicken red blood cells (RBCs) and human RBCs; those expressing the avian virus HA were only adsorbed by chicken RBCs. These results indicate that human and avian influenza virus H5 HAs differ in their recognition of sialyloligosaccharides on the RBCs of different animal species. Mutational analyses indicated that differences in both the oligosaccharide chains and in the amino acid sequences around the HA receptor-binding site were responsible for this difference in receptor binding. These data further support the concept that alteration in receptor recognition is important for replication of avian viruses in humans.


**Abstract:** The oligosaccharide sidechains attached to the major polypeptide, HA1 of the haemagglutinin of influenza virus were examined for antigenic activity using a solid-phase radioimmunoassay. Cross-reactivity between the HA1 of the different human subtypes was clearly demonstrable with IgG raised against purified virus but was abrogated if anti-carbohydrate antibodies were first removed by passage of the IgG through an immunoabsorbent column containing haemagglutinin (HA) from an unrelated avian influenza strain. Antibodies eluted from the column were found to cross-react with the HA1 of all subtypes tested. 'Host antigen' extracted from chick chorioallantoic membrane and coupled to Sepharose was also able to remove cross-reactive antibodies from antiviral sera, while antibodies raised against host antigen bound to the HA1 isolated from each subtype tested. It is concluded that, although there are qualitative and quantitative differences between the oligosaccharide sidechains of influenza haemagglutinins, the antigenically active sidechains are cross-reactive.


**Abstract:** Immunogold electron microscopy revealed that site-specific antibodies elicited by a synthetic peptide representing the N-terminal sequence (residues 2-10) of influenza virus M2 protein were capable of binding to the surface of virions. Antibody binding was observed with two human influenza virus strains but not with an avian virus strain which has amino acid substitutions in the appropriate sequence of M2. These results provide direct evidence for the presence of M2 in the influenza virion.
immunology, orthomyxoviridae ultrastructure, peptides chemical synthesis, peptides immunology, viral matrix proteins ultrastructure, virion ultrastructure.


NAL Call Number: 448.8 J8232

Abstract: Recently, an avian influenza A virus (A/Hong Kong/156/97, H5N1) was isolated from a young child who had a fatal influenza illness. All eight RNA segments were of avian origin. The H5 hemagglutinin is not recognized by neutralizing Abs present in humans as a result of infection with the human H1, H2, or H3 subtypes of influenza A viruses. Subsequently, five other deaths and several more human infections in Hong Kong were associated with this avian-derived virus. We investigated whether influenza A-specific human CD8+ and CD4+ T lymphocytes would recognize epitopes on influenza A virus strains derived from swine or avian species, including the 1997 H5N1 Hong Kong virus strains. Our results demonstrate that adults living in an urban area of the U.S. possess influenza A cross-serotype reactive CD8+ and CD4+ CTL that recognize multiple epitopes on influenza A viruses of other species. Bulk culture cytotoxicity was demonstrated against avian and human influenza A viruses. Enzyme-linked immunospot assays detected precursor CTL specific for both human CTL epitopes and the corresponding A/HK/97 viral sequences. We hypothesize that these cross-reactive CTL might provide partial protection to humans against novel influenza A virus strains introduced into humans from other species.

Descriptors: cd4 positive T lymphocytes immunology, CD4 positive T lymphocytes virology, CD8 positive T lymphocytes immunology, CD8 positive T lymphocytes virology, influenza A virus avian immunology, porcine immunology, cell line, chickens, cytotoxicity, immunologic genetics, ducks, enzyme linked immunosorbent assay, avian genetics, porcine genetics, leukocytes, mononuclear immunology, leukocytes, mononuclear virology, peptides genetics, peptides immunology, point mutation, stem cells immunology, stem cells virology, swine.


NAL Call Number: SF604.C58

Descriptors: antibodies, genetic stability, hemagglutinins, immunity, avian influenza virus, fowl pox virus, chickens.


NAL Call Number: S494.5.B563N86

Descriptors: immunity, immunization, inactivated vaccines, recombinant vaccines, interferon, maternal antibodies, potency, avian influenza virus, fowl pox virus, chickens.


NAL Call Number: SF604.C58

Descriptors: chicks, immune response, immunization, dosage, maternal antibodies, mortality, recombinant vaccines, avian influenza, fowl pox virus.


NAL Call Number: QR360.J6

Abstract: When presented together on the intact influenza virus particle, the external hemagglutinin (HA)
and neuraminidase (NA) antigens are competitive, with HA dominant over NA in both T- and B-cell priming (B. E. Johansson, T. M. Moran, and E. D. Kilbourne, Proc. Natl. Acad. Sci. USA 84:6869-6873, 1987). Dissociation and purification of HA and NA from virus and their injection separately or in combination into BALB/c mice eliminates their antigenic competition as measured by antibody response, confirming that it is their structural association that leads to what we have termed intravirionic antigenic competition. We discuss this phenomenon with respect to previously described intermolecular antigenic competition and with regard to its probable mechanism. Our findings are relevant to contemporary interest in viral vaccine vectors and multicomponent vaccines.

Descriptors: hemagglutinins viral immunology, influenza immunology, influenza A virus avian immunology, human immunology, neuraminidase immunology, antibodies, viral blood, antibody formation, enzyme linked immunosorbent assay, hemagglutination inhibition tests, hemagglutinin glycoproteins, influenza blood, avian pathogenicity, human pathogenicity, lung microbiology, mice, neutralization tests, viral envelope proteins immunology.

Descriptors: antigens analysis, influenza A virus avian analysis, proteins analysis, centrifugation, density gradient, electrophoresis, hemagglutinins viral analysis, tritium.

Abstract: The complete sequence of a hemagglutinin (HA) gene of a recent human influenza A strain, A/Victoria/3/75, is 1768 nucleotides long and contains the information for 567 amino acids. It codes for a signal peptide of 16 amino acids, the HA1 chain of the mature hemagglutinin of 329 amino acids, a connecting region between HA1 and HA2 consisting of a single arginine residue and the HA2 portion of 221 amino acids. The sequence is compared with the hemagglutinin of two members of other subtypes, the human H2 strain A/Jap/305/57 and the avian Hav1 strain A/FPV/Rostock/34, and with one of the same H3 subtype, A/Memphis/3/72. To align the HA1 chain of different major subtypes several deletions/insertions of single amino acids must be invoked, but two more extensive differences are found at both ends, one leading to an extension of the amino terminal sequence of HA1 and the other (four residues) occurring in the region processed away between HA1 and HA2. Comparison of the HA1 of two H3 strains suggests that drift probably depends on single base mutations, some of which change antigenic determinants. The HA2 region, which apparently is not involved in the immune response, is highly conserved even between different subtypes, and single base substitutions account for all the observed diversity. A hydrophobic segment of 24 residues is present in the same position close to the carboxyl terminus of HA2 in both Victoria and FPV, and presumably functions in implantation into the lipid bilayer. The many conserved features not only in HA2 but also in HA1 suggest a rather rigid architecture for the whole hemagglutinin molecule.
Descriptors: genes viral, hemagglutninins viral genetics, influenza A virus human genetics, RNA viral genetics, amino acid sequence, base sequence, carbohydrates analysis, cloning, molecular, codon, DNA, viral genetics, epitopes, hemagglutinins viral analysis, avian genetics.

Abstract: Immunization of mice with DNA encoding the influenza virus hemagglutinin (HA) affords complete protection against lethal influenza virus infection and the means to investigate the mechanisms of B-cell responsiveness to virus challenge. Using a single-cell enzyme-linked immunospot assay, we sought to determine the localization of HA-specific antibody-forming cells (AFCs) during the development of humoral immunity in mice given HA DNA vaccine by gene gun. At 33 days postvaccination, populations of AFCs were maintained in the spleen and bone marrow. In response to lethal challenge with influenza virus, the
AFCs became localized at the site of antigenic challenge, i.e., within the draining lymph nodes of the lung compartment. Immunoglobulin G (IgG)- and IgA-producing AFCs were detected in lymph nodes of the upper and lower respiratory tracts, underscoring their importance in clearing virus from the lungs. Response to challenge required competent CD4+ T cells, without which no AFCs were generated, even those producing IgM. By contrast, in mice vaccinated with an HA-containing subunit vaccine, fewer AFCs were generated in response to challenge, and these animals were less capable of resisting infection. Our findings demonstrate the comparable localization of AFCs in response to challenge in mice vaccinated with either HA DNA or live virus. Moreover, the former strategy generates both IgG- and IgA-producing plasma cells.

Descriptors: B lymphocytes immunology, DNA, viral immunology, hemagglutinin viral genetics, influenza A virus avian immunology, influenza vaccine toxicity, T lymphocytes, helper inducer immunology, antibody formation, bone marrow immunology, CD4 positive T lymphocytes, viral metabolism, viral toxicity, hemagglutinin glycoproteins, influenza virus, viral biosynthesis, hemagglutinins viral immunology, immunization, secondary, immunologic memory, lethal dose 50, lymph nodes immunology, lymphocyte depletion, mice, spleen immunology, time factors.


NAL Call Number: 41.8 D482
Abstract: A haemagglutinating virus was isolated in summer 1972 from a single free-living siskin (Carduelis spinus Linnaeus, 1758) in embryonated chicken eggs. Additional cases of morbidity or mortality were not observed in the area were the sick siskin was found. The virus was characterized as an avian influenza A virus of the subtype H7N1 and designated H7N1/Carduelis/Germany/72. The virus induced following experimental inoculation of chicken embryos a high rate mortality (mean death time approximately 24 hours), formed plaques in chicken embryo fibroblast cultures without addition of trypsin and has an intracerebral pathogenicity index (ICPI) of 1.80. Therefore, this virus is considered as a highly pathogenic avian influenza A virus. Canaries (Serinus canarius Linnaeus, 1758), that were housed in the same room with the siskin were accidentally exposed by contact to the sick siskin which resulted in virus transmission followed by conjunctivitis, apathy, anorexia and a high rate mortality.

Descriptors: canaries virology, disease transmission, horizontal veterinary, influenza A virus, avian pathogenicity, influenza, avian transmission, Passeriformes virology, retrospective studies.


NAL Call Number: 41.8 D482
Abstract: The scientific literature of the past century is reviewed on fowl plague (presently termed highly pathogenic avian influenza, HPAI) in pigeons. HPAI viruses cause epidemic disease outbreaks with high rates of losses in many avian species, particularly in chickens and turkeys. Also susceptible to disease are quails, guinea fowl, ducks, geese, ostriches, passerine birds, and birds of prey whereas conflicting reports on the susceptibility of the domestic pigeon exist. Based on literature reports and on own experiments, and applying as criteria for judgements clinically overt forms of disease, virus multiplication plus shedding and seroconversion, it is concluded that domestic pigeons are only partially susceptible to influenza A viruses of the haemagglutinin subtype H7. Infection of pigeons with H7 viruses results only in some of them in signs, virus shedding and seroconversion. Using the same criteria, pigeons appear to be even less susceptible to infection with influenza A viruses of the H5 subtype. Only one of five publications describe in 1/19 pigeons exposed to H5 influenza A virus depression one day before death, and only 2/19 multiplied and excreted virus, and 1/19 developed circulating antibodies. Consequently, pigeons play only a minor role in the epidemiology of H5 influenza viruses. In contrast, following infection with influenza A virus of the subtype H7 clinical signs in pigeons consist of conjunctivitis, tremor, paresis of wings and legs, and wet droppings. H7-infected pigeons multiply and excrete H7 viruses and develop circulating antibodies. Albeit of the status of infection, free-flying domestic pigeons can act as mechanical vectors and vehicles for long-distance
transmission of any influenza A virus if plumage or feet were contaminated.

**Descriptors:** Columbidae virology, influenza A virus, avian pathogenicity, avian influenza virology, chick embryo, chickens, disease susceptibility veterinary, ducks, avian classification, avian influenza pathology, avian influenza transmission, species specificity, virus shedding.


**NAL Call Number:** 448.3 AC85

**Abstract:** The effect of several adamantane derivatives on the activity of virion-associated RNA-dependent RNA polymerase of fowl plague virus (FPV) and influenza B virus was studied in vitro. Some of the derivatives inhibited the activity of the polymerase by 60 per cent. A correlation was established between the previously demonstrated capacity of these inhibitors to suppress orthomyxovirus reproduction in vivo and their ability to reduce the activity of virion-associated RNA-dependent RNA polymerase in vitro.

**Descriptors:** adamantane pharmacology, bridged compounds pharmacology, influenza A virus avian enzymology, orthomyxoviridae enzymology, RNA nucleotidyltransferases metabolism, RNA replicase metabolism, adamantane analogs and derivatives, avian growth and development, orthomyxoviridae growth and development, virus replication drug effects.


**NAL Call Number:** QR360.J6

**Abstract:** Cells preinfected with fowl plague virus followed by treatment with actinomycin D are a suitable system for studying early protein synthesis in cells infected with Semliki forest virus. One and one-half hours after superinfection, three new nonstructural proteins (NVP) were detected: NVP 145, NVP, 112, and NVP 65. They appeared in parallel with a low incorporation of mannose at the beginning of the infectious cycle. Behavior on chasing suggested a precursor relationship of NVP 112 to the envelope glycoproteins. Two kinds of NVP 65 are described, both of which are varieties of NVP 68 with an incomplete mannose content. One type, detected early after infection, was converted into NVP 68 by supplementary glycosylation. The second, late type was stable. It contains fucose and resembles the NVP 65 observed after impairment of glycosylation. The mechanism of NVP 68 glycosylation is discussed. The presence of the complete carbohydrate moiety is crucial for the cleavage of NVP 68 into the envelope proteins E2 and E3 and, thus, for virus maturation. Only the complete form of NVP 68 was precipitated by envelope-specific antisera. A large production of NVP 78 is a further feature of the early events in infected cells. It is not related to the structural proteins.

**Descriptors:** Semliki Forest virus metabolism, viral proteins biosynthesis, chick embryo, dactinomycin pharmacology, epitopes, glycoproteins biosynthesis, glycoproteins immunology, influenza A virus avian growth and development, mannose metabolism, molecular weight, peptide synthesis, protein precursors biosynthesis, Semliki Forest virus immunology, tissue culture, viral proteins immunology.


**NAL Call Number:** QR360.J6

**Abstract:** A method is described for analysis of viral protein synthesis early after infection when minute amounts of viral proteins are effectively concealed by large amounts of produced host-specific proteins. The method is superior to a radioimmune assay, since all virus-induced proteins can be measured independent of their immunological reactivity. Host-specific protein synthesis can be suppressed by infection with fowl plague virus. Addition of actinomycin C 1.25 h postinfection does not prevent this suppression, but it does block effectively the formation of fowl plague virus-specific proteins. Such cells synthesize only small amounts of cellular proteins, as revealed by polyacrylamide electrophoresis. They can be superinfected with several different enveloped viruses, however, without significant diminution of virus yields. In pretreated cells the eclipse is shortened for Semliki Forest virus, Sindbis virus, and vesicular stomatitis virus, but prolonged for Newcastle disease virus. The onset of protein synthesis, specific for the superinfecting virus, could be clearly demonstrated within 1 h after superinfection. At this time, in cells superinfected with Semliki Forest
virus, great amounts of NSP 75 (nonstructural protein; molecular weight, 75 X 10(3)) and reduced amounts of the core protein C could be demonstrated. The precursor glycoprotein NSP 68 is followed by a new polypeptide, NSP 65: three proteins with molecular weights exceeding 100 X 10(3) were observed which are missing later in the infectious cycle. Similar results were obtained after superinfection with Sindbis virus. The formation of a new polypeptide with a molecular weight of about 80 X 10(3) was detected. After superinfection with vesicular stomatitis virus or Newcastle disease virus the formation of new proteins, characteristic for the early stage of infection, was not observed.

Descriptors: dactinomycin pharmacology, influenza A virus avian growth and development, proteins metabolism, RNA viruses metabolism, viral proteins biosynthesis, cell line, glycoproteins biosynthesis, molecular weight, Newcastle disease virus growth and development, Newcastle disease virus metabolism, peptide synthesis, protein precursors biosynthesis, Semliki Forest virus growth and development, Semliki Forest virus metabolism, sindbis virus growth and development, sindbis virus metabolism, tissue culture, vesicular stomatitis Indiana virus growth and development, vesicular stomatitis Indiana virus metabolism, virus replication drug effects.


NAL Call Number: QR360.A1J6

Descriptors: glucosamine pharmacology, hexoses pharmacology, RNA viruses growth and development, virus inhibitors pharmacology, virus replication drug effects, agglutination tests, antigens, viral analysis, cell line, cultured cells microbiology, concanavalin a pharmacology, fluorescent antibody technique, HeLa cells, hemagglutinins viral analysis, influenza A virus avian drug effects, Newcastle disease virus drug effects, polioviruses drug effects, RNA nucleotidyltransferases biosynthesis, RNA viruses drug effects, RNA viruses enzymology, RNA viruses immunology, RNA viruses metabolism, RNA viral biosynthesis, Semliki Forest virus drug effects, sindbis virus drug effects, viral proteins biosynthesis.


NAL Call Number: 448.3 Ar23

Abstract: The nucleotide sequences of the HA1 domain of the H1 hemagglutinin genes of A/duck/Hong Kong/36/76, A/duck/Hong Kong/196/77, A/sw/North Ireland/38, A/sw/Cambridge/39 and A/Yamagata/120/86 viruses were determined, and their evolutionary relationships were compared with those of previously sequenced hemagglutinin (H1) genes from avian, swine and human influenza viruses. A pairwise comparison of the nucleotide sequences revealed that the genes can be segregated into three groups, the avian, swine and human virus groups. With the exception of two swine strains isolated in the 1930s, a high degree of nucleotide sequence homology exists within the group. Two phylogenetic trees constructed from the substitutions at the synonymous site and the third codon position showed that the H1 hemagglutinin genes can be divided into three host-specific lineages. Examination of 21 hemagglutinin genes from the human and swine viruses revealed that two distinct lineages are present in the swine population. The swine strains, sw/North Ireland/38 and sw/Cambridge/39, are clearly on the human lineage, suggesting that they originate from a human A/WSN/33-like variant. However, the classic swine strain, sw/Iowa/15/30, and the contemporary human viruses are not direct descendants of the 1918 human pandemic strain, but did diverge from a common ancestral virus around 1905. Furthermore, previous to this the above mammalian viruses diverged from the lineage containing the avian viruses at about 1880.

Descriptors: evolution, hemagglutinins viral genetics, influenza A virus avian genetics, human genetics, porcine genetics, amino acid sequence, chick embryo, genes viral, hemagglutinin glycoproteins, influenza virus, avian classification, human classification, porcine classification, molecular sequence data, phylogeny, sequence homology, amino acid.


Abstract: It was established that classical fowl plague virus Rostock (H7N1) propagated in culture to which 10-25 micrograms/ml of remantadine had been added differed from the original FPV and its remantadine-resistant variant by markedly reduced infectious and hemagglutinating activity and, to a lesser extent, neuraminidase activity, lower amounts of M protein and hemagglutinin, incomplete cleavage of hemagglutinin, and significant loss of spikes on the virion surface.

Descriptors: adamantane analogs and derivatives, influenza A virus avian drug effects, rimantadine pharmacology, drug resistance, microbial, electrophoresis, polyacrylamide gel, hemagglutination, viral drug effects, hemagglutinins viral analysis, influenza A virus avian physiology, influenza A virus avian ultrastructure, viral matrix proteins analysis, viral proteins analysis, virus replication drug effects.


Abstract: Since 1998, H3N2 viruses have caused epizootics of respiratory disease in pigs throughout the major swine production regions of the U.S. These outbreaks are remarkable because swine influenza in North America had previously been caused almost exclusively by H1N1 viruses. We sequenced the full-length protein coding regions of all eight RNA segments from four H3N2 viruses that we isolated from pigs in the Midwestern U.S. between March 1998 and March 1999, as well as from H3N2 viruses recovered from a piglet in Canada in January 1997 and from a pig in Colorado in 1977. Phylogenetic analyses demonstrated that the 1977 Colorado and 1997 Ontario isolates are wholly human influenza viruses. However, the viruses isolated since 1998 from pigs in the Midwestern U.S. are reassortant viruses containing hemagglutinin, neuraminidase and PB1 polymerase genes from human influenza viruses, matrix, non-structural and nucleoprotein genes from classical swine viruses, and PA and PB2 polymerase genes from avian viruses. The HA proteins of the Midwestern reassortant swine viruses can be differentiated from those of the 1995 lineage of human H3 viruses by 12 amino acid mutations in HA1. In contrast, the Sw/ONT/97 virus, which did not spread from pig-to-pig, lacks 11 of these changes.

Descriptors: influenza A virus avian genetics, human genetics, porcine classification, porcine genetics, reassortant viruses genetics, genotype, influenza veterinary, influenza virology, molecular sequence data, North America, phylogeny, swine, swine diseases virology.


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Descriptors: influenza A virus avian genetics, human genetics, porcine classification, porcine genetics, reassortant viruses genetics, genotype, influenza veterinary, influenza virology, molecular sequence data, North America, phylogeny, swine, swine diseases virology.

**NAL Call Number:** QR180.S88

**Abstract:** Influenza viruses cause annual epidemics and occasional pandemics of acute respiratory disease. Improved vaccines that can overcome the decline in immune function with aging and/or can induce broader immunity to novel pandemic strains are a high priority. To design improved vaccines for the elderly, we need to better understand the effects of age on both innate and adaptive immunity. In a murine model, we have determined that defects in antigen-presenting cell (APC) expression of pattern-recognition molecules, co-stimulatory molecules, and cytokine production may play an important role in the reduced clonal expansion of T cells in aging. The use of immunomodulators such as adjuvants may overcome some of the defects of aging immunity and may also be useful in the development of improved vaccines for avian influenza A subtypes that pose a pandemic threat. Several novel strategies including the use of ISCOM-formulated vaccines, mucosal delivery, or DNA vaccination provided cross-subtype protection that could provide an important component of immunity in the event of a pandemic.

**Descriptors:** aging immunology, disease outbreaks prevention and control, influenza prevention and control, influenza vaccines immunology, adjuvants, immunologic pharmacology, aged, immunity, active immunology, immunity, natural, influenza epidemiology, influenza immunology, influenza A virus, avian immunology, avian pathogenicity, membrane glycoproteins genetics, membrane glycoproteins metabolism, mice, orthomyxoviridae immunology, orthomyxoviridae pathogenicity, receptors, cell surface genetics, receptors, cell surface metabolism.


**NAL Call Number:** 448.3 Ar23

**Abstract:** In order to evaluate the efficiency of the removal of sialic acid residues from the influenza virus hemagglutinin by the viral neuraminidase in the course of the virus replication cycle, CV-1 cells expressing the hemagglutinin of H7 subtype from an SV40-based vector were superinfected with influenza virus strain A/Duck/Ukraine/63 (H3N8) or A/USSR/90/77 (H1N1). Vector-expressed hemagglutinin was immunoprecipitated from cell lysates and analyzed by polyacrylamide gel electrophoresis. The data indicate that the removal of sialic acid residues from the vector-expressed H7 hemagglutinin by N1 neuraminidase of A/USSR/90/77 virus in the course of the virus replication cycle is incomplete. The results are discussed in connection with previously published data showing that the low activity of NA in wild-type influenza virus results in incomplete removal of sialic acid residues from virion components.

**Descriptors:** hn protein genetics, influenza A virus avian physiology, neuraminidase metabolism, virus replication, cell line, *Cecopithecus aethiops*, ducks, genetic vectors, hn protein biosynthesis, avian enzymology, avian genetics, simian virus 40, species specificity.


**NAL Call Number:** QR360.A1J6

**Abstract:** When CV-1 cells expressing haemagglutinin (HA) of fowl plague virus A/FPV/34/Rostock(H7) (FPV) from an SV40-based recombinant vector were superinfected with the human influenza virus A/FM/1/47(H1N1)(FM1), phenotypically mixed progeny virus was observed. It contained cleaved FPV HA and uncleaved FM1 HA, was infectious without trypsin treatment and its infectivity was neutralizable by anti-FPV serum. When superinfection of H7 HA-expressing CV-1 cells was performed at a low multiplicity of infection, multi-cycle replication occurred. Control cells preinfected with an SV40-based recombinant not expressing FPV HA did not allow multi-cycle replication. Multi-cycle replication of FM1 virus was also observed when cells were preinfected with a vector expressing a highly cleavable mutant of influenza virus A/Port Chalmers/1/73(H3) HA carrying an insert of four arginine residues at the cleavage site. This was not the case when cells expressing uncleaved wild-type H3 HA were used. The results show that by phenotypic
mixing with recombinant HA of high cleavability, a human influenza virus can be obtained in infectious form from cells lacking a suitable protease to activate this virus.

Descriptors: hemagglutinins viral physiology, influenza A virus avian physiology, human physiology, reassortant viruses physiology, cell line, hemagglutinin glycoproteins, influenza virus, hemagglutinin viral genetics, avian genetics, human genetics, phenotype, reassortant viruses genetics, trypsin, virus replication.


NAL Call Number: QR360.A1J6

Abstract: To elucidate the structure of the antigenic sites of avian H5 influenza virus haemagglutinin (HA) we analysed escape mutants of a mouse-adapted variant of the H5N2 strain A/Mallard/Pennsylvania/10218/84. A panel of five anti-H5 monoclonal antibodies (mAbs) was used to select 16 escape mutants. The mutants were tested by ELISA and haemagglutination inhibition with this panel of anti-H5 mAbs and the HA genes of the mutants were sequenced. The sequencing demonstrated that the amino acid changes were grouped in two antigenic sites. One corresponded to site A in the H3 HA. The other contained areas that are separated in the amino acid sequence but are topographically close in the three-dimensional structure and partially overlap in the reactions with mAbs. This site corresponds in part to site B in the H3 structure; it also includes a region not involved in site B that partially overlaps site Sa in the H1 HA and an antigenic area in H2 HA. Mutants with the amino acid change K152N, as well as those with the change D126N, showed reduced lethality in mice. The substitution D126N, creating a new glycosylation site, was accompanied by an increase in the sensitivity of the mutants to normal mouse serum inhibitors. Several amino acid changes in the H5 escape mutants occurred at the positions of reported changes in H2 drift variants. This coincidence suggests that the antigenic sites described and analysed here may be important for drift variation if H5 influenza virus ever appears as a pathogen circulating in humans.

Descriptors: antigenic variation genetics, antigens, viral genetics, epitopes, B lymphocyte genetics, hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian genetics, antigens, viral chemistry, antigens, viral immunology, base sequence, binding sites, birds, DNA, viral, enzyme linked immunosorbert assay methods, epitope mapping, epitopes, B lymphocyte chemistry, epitopes, B lymphocyte immunology, hemagglutination inhibition tests, hemagglutinin glycoproteins, influenza virus chemistry, hemagglutinin glycoproteins, influenza virus immunology, avian immunology, avian pathogenicity, mice, molecular sequence data, mutagenesis, phenotype, protein structure, tertiary, sequence analysis, DNA, virulence.


NAL Call Number: 448.3 Ar23

Abstract: Human-avian influenza reassortants possessing the HA gene of the avian parent virus were tested for their ability to replicate in MDCK cells at 37 degrees C and 31 degrees C. Both avian parent viruses, A/Duck/Ukraine/1/63 (H3N8) and A/Duck/Hoshimin/014/78 (H5N3) induced an efficient multi-cycle infection at 37 degrees C, but replicated poorly at 31 degrees C, whereas the human parent virus, MDCK-adapted variant of A/USSR/90/77 (H1N1) strain, replicated efficiently at both temperatures. The reassortant clone possessing the HA gene of A/Duck/Ukraine/1/63 virus and the other 7 genes of A/USSR/90/77 virus replicated at both temperatures almost as efficiently as the human parent virus. Among the reassortants between A/Duck/Hoshimin/014/78 and A/USSR/90/77, the clones possessing the HA and NA genes of the avian strain, or the HA, NA, NP, and NS genes of the avian strain, and the other genes of the human parent virus, replicated poorly at both temperatures, especially at 31 degrees C, whereas the reassortant possessing the HA, NA, and M genes of the avian virus replicated at both temperatures fairly efficiently. The results are discussed in connection with the limitations imposed by different genes upon avian influenza viruses' ability to replicate in mammalian cells.

Descriptors: genes viral, hemagglutinin viral physiology, influenza A virus avian pathogenicity, human pathogenicity, virus replication, birds microbiology, chick embryo, hemagglutinins viral biosynthesis,
hemagglutinins viral genetics, avian genetics, human genetics, RNA viral analysis, temperature, transfection, viral proteins biosynthesis.

NAL Call Number: 448.3 Ar23
Abstract: In order to assess the degree of immune cross-protection among avian H2 influenza virus strains, mice were immunised with beta-propiolactone-inactivated virus preparations and infected intranasally with mouse-adapted variant of A/Black Duck/New Jersey/1580/78 (H2N3) strain. The experiments with 11 avian H2 strains revealed that both Eurasian and American H2 avian influenza viruses exhibit either high or moderate degree of cross-protection. The grouping of the strains in accordance with their cross-protection efficiency does not coincide with H2 phylogenetic branches. Several reassortant clones were obtained with the use of A/Pintail Duck/Primorie/695/76 (H2N3) strain and high-yield X-67 reassortant as parent viruses, among them a high-yield H2N3 reassortant. Taking into account the data on cross-protection among avian H2 strains, the high-yield H2N3 reassortant may be regarded as a prototype strain to be used for the preparation of killed vaccines in the case of a new appearance of avian H2 haemagglutinin in circulation in humans.
Descriptors: influenza prevention and control, influenza A virus avian genetics, avian immunology, influenza vaccine immunology, reassortant viruses immunology, chick embryo, cross reactions, immunization, influenza immunology, avian pathogenicity, mice, reassortant viruses genetics, vaccines, attenuated immunology.

NAL Call Number: 385 J822
Abstract: A systematic and comparative study was performed on the polypeptide composition and the RNA polymerase activity associated with virions of various strains of influenza A virus, including four human and two avian viruses. Significant differences were found in the molecular weights of not only hemagglutinin (HA) but also both nucleoprotein (NP) and membrane protein (M), as determined by polyacrylamide gel electrophoresis under denaturing conditions. The results indicate that, among viruses sharing the same serotype determined by the surface proteins HA and NA (neuraminidase), considerable variations exist in the structure of viral proteins, including inner proteins. The relative contents of viral proteins also varied among these strains grown under similar conditions. The total content of three P proteins, the putative RNA polymerase subunits, was within the range between 1.1 and 2.2% of total viral proteins and roughly paralleled the virion-associated RNA polymerase activity. The virion-associated RNA polymerase of all the strains tested were stimulated by the same dinucleotide primers, ApG or GpG, indicating that the specificity of transcription initiation is conserved among wide varieties of influenza virus.
Descriptors: DNA directed RNA polymerases metabolism, dinucleoside phosphates, influenza A virus avian enzymology, human enzymology, 5’ guanylic acid analogs and derivatives, 5’ guanylic acid pharmacology, adenosine monophosphate analogs and derivatives, adenosine monophosphate pharmacology, chemistry, guanosine analogs and derivatives, guanosine pharmacology, macromolecular systems, molecular weight, peptides, species specificity, virion enzymology.

NAL Call Number: 448.3 C33 (1)
Descriptors: influenza A virus avian growth and development, parrots microbiology, Psittacines microbiology, virus replication, hemagglutination inhibition tests, avian isolation and purification, organ specificity, respiratory system microbiology.

**NAL Call Number:** SF604.J342

**Descriptors:** chickens microbiology, influenza A virus avian physiology, porcine physiology, influenza A virus physiology, mice microbiology, cloaca microbiology, avian pathogenicity, porcine pathogenicity, influenza A virus pathogenicity, orthomyxoviridae infections microbiology, orthomyxoviridae infections veterinary, poultry diseases microbiology, rodent diseases microbiology, trachea microbiology, virus replication.


**NAL Call Number:** QR360.J6

**Abstract:** The cleavability of the hemagglutinin (HA) molecule is related to the virulence of avian influenza A viruses, but its influence on human influenza virus strains is unknown. Two structural features are involved in the cleavage of avian influenza A virus HAs: a series of basic amino acids at the cleavage site and an oligosaccharide side chain in the near vicinity. The importance of these properties in the cleavability of a human influenza A virus (A/Aichi/2/68) HA was investigated by using mutants that contained or lacked an oligosaccharide side chain and had either four or six basic amino acids. All mutants except the one that contains a single mutation at the glycosylation site were cleaved, although not completely, demonstrating that a series of basic amino acids confers susceptibility to cellular cleavage enzymes among human influenza virus HAs. The mutants containing six basic amino acids at the cleavage site showed limited polykaryon formation upon exposure to low pH, indicating that cleavage was adequate to impart fusion activity to the HA. Deletion of the potential glycosylation site had no effect on the cleavability of these mutants; hence, the oligosaccharide side chain appears to have no role in human influenza virus HA cleavage. The inability to induce high cleavability in a human influenza A virus HA by insertion of a series of basic amino acids at the cleavage site indicates that other, as yet unidentified structural features are needed to enhance the susceptibility of these HAs to cellular proteases.

**Descriptors:** genes viral, hemagglutinins viral genetics, influenza A virus human genetics, amino acid sequence, arginine, cell line, chick embryo, cloning, molecular, glycosylation, hemagglutinin glycoproteins, influenza virus, hydrolysis, human immunology, human ultrastructure, lysine, molecular sequence data, mutagenesis, site directed, recombination, genetic, simian virus 40 genetics, simian virus 40 ultrastructure, transfection, viral envelope proteins genetics.


**NAL Call Number:** 448.8 V81

**Abstract:** The A/Chick/Penn/83 (H5N2) influenza virus that appeared in chickens in Pennsylvania in April 1983 and subsequently became virulent in October 1983, was examined for plaque-forming ability and cleavability of the hemagglutinin (HA) molecule. The avirulent virus produced plaques and cleaved the HA only in the presence of trypsin. In contrast, the virulent virus produced plaques and cleaved the HA precursor into HA1 and HA2 in the presence or absence of trypsin. The apparent molecular weight of the HA1 from the avirulent virus was higher than that from the virulent virus, but when the viruses were grown in the presence of tunicamycin, the molecular weights of HA were indistinguishable. Two of nine monoclonal antibodies to the HA of the avirulent virus indicate that there is at least one epitope on the HA that is different between the virulent and avirulent viruses. The nucleotide sequence coding for the processed HA polypeptide contained 1641 nucleotides specifying a protein of 547 amino acids. The amino acid sequences of the virulent and avirulent viruses were indistinguishable through the connecting peptide region, indicating that the difference in cleavability of the H5 HA is not directly attributed to the amino acid sequence of the connecting peptide. Four of seven nucleotide changes resulted in amino acid changes at residues 13, 69, and 123 of HA1 and at residue 501 of the HA2 polypeptide. Since there were no deletions or insertions in the amino acid sequence of the virulent or avirulent viruses, the possibility exists that the difference in
molecular weight is due to loss of a carbohydrate side chain in the virulent strain. The amino acid change in the virulent strain at residue 13 is the only mutation that could affect a glycosylation site and this is in the vicinity of the connecting peptide. It is postulated that the loss of this carbohydrate may permit access of an enzyme that recognizes the basic amino acid sequences and results in cleavage activation of the HA in the virulent virus.

Descriptors: hemagglutinins viral genetics, influenza A virus avian pathogenicity, amino acid sequence, antibodies, monoclonal, base sequence, carbohydrates analysis, chick embryo, chickens, DNA, viral genetics, hemagglutinins viral isolation and purification, avian genetics, plaque assay, RNA viral isolation and purification, serotyping, species specificity, virulence.


NAL Call Number: 448.8 V81
Abstract: Comparative sequence analysis of the hemagglutinin (HA) genes of a highly virulent H5N8 virus isolated from turkeys in Ireland in 1983 and a virus of the same subtype detected simultaneously in healthy ducks showed only four amino acid differences between these strains. Partial sequencing of six of the other genes and antigenic similarity of the neuraminidases established the overall genetic similarity of these two viruses. Comparison of the complete sequence of two H5 gene sequences and partial sequences of other virulent and avirulent H5 viruses provides evidence for at least two different lineages of H5 influenza virus in the world, one in Europe and the other in North America, with virulent and avirulent members in each group. In vivo studies in domestic ducks showed that all of the H5 viruses that are virulent in chickens and turkeys replicate in the internal organs of ducks but did not produce any disease signs. Additionally, both viruses isolated from turkeys and ducks in Ireland were detected in the blood. These studies provide the first conclusive evidence for the possibility that fully virulent influenza viruses in domestic poultry can arise directly from viruses in wild aquatic birds. Studies on the cleavability of the HA of virulent and avirulent H5 viruses showed that the principles established for H7 viruses (F. X. Bosch, M. Orlich, H. D. Klenk, and R. Rott, 1979, Virology 95, 197-207; F. X. Bosch, W. Garten, H. D. Klenk, and R. Rott, 1981, Virology 113, 725-735) also apply to the H5 subtype. These are (1) only the HAs of virulent influenza viruses were cleaved in tissue culture in the absence of trypsin and (2) virulent H5 influenza viruses contain a series of basic amino acids at the cleavage site of the HA, whereas avirulent strains contain only a single arginine with the exception of the avirulent Chicken/Pennsylvania virus. Thus, a series of basic amino acids at the cleavage site probably forms a recognition site for the enzyme(s) responsible for cleavage.

Descriptors: genes viral, hemagglutinins viral genetics, influenza A virus avian genetics, amino acid sequence, base sequence, chickens microbiology, ducks microbiology, fowl plague microbiology, avian pathogenicity, avian physiology, turkeys microbiology, virulence, virus replication.


NAL Call Number: 448.8 V81
Abstract: The epidemiological features of the H5N2 outbreak of influenza in poultry were studied by sequencing the HA genes of several viruses isolated during the epidemic. Comparison of the nucleotide sequences of the HA genes indicated there was a single introduction of virulent virus. The variation rate (silent mutations) in the HA gene of the virulent Ck/Penn virus was 9.0 or 14.4% per 10 years depending on the viruses compared and was similar to that in H3 HA gene of human influenza A virus. The virulent and avirulent viruses isolated after October 1983 were derived from a common ancestral virus and the virulent virus did not supersede the avirulent virus, instead, the virulent and avirulent viruses coexisted and evolved separately during the course of the epidemic. The evolutionary changes in the HA of H5N2 viruses that occurred during the epidemic permitted us to establish that a virus (A/Chick/Washington/84) that was isolated 8 months after the last H5N2 virus had been isolated from poultry in Pennsylvania belonged to the family of potentially dangerous H5N2 viruses and was a direct descendent of the virus that spread to Maryland and Virginia. All of the virulent Ck/Penn viruses retained the amino acid changes at residues 13 and 69 in the HA.

Descriptors: fowl plague microbiology, hemagglutinins viral genetics, influenza A virus avian genetics,
amino acid sequence, base sequence, disease outbreaks veterinary, District of Columbia, evolution, fowl plague epidemiology, genes viral, hemagglutinins viral analysis, avian isolation and purification, avian pathogenicity, Maryland, mutation, Pennsylvania, poultry, virulence.


**NAL Call Number:** QR360.J6

**Abstract:** The ability of many viruses to replicate in host cells depends on cleavage of certain viral glycoproteins, including hemagglutinin (HA). By generating site-specific mutant HAs of two highly virulent influenza viruses, we established that the relationship between carbohydrate in the stalk and the length of the connecting peptide is a critical determinant of cleavability. HAs that lacked an oligosaccharide side chain in the stalk were cleaved regardless of the number of basic amino acids at the cleavage site, whereas those with the oligosaccharide side chain resisted cleavage unless additional basic amino acids were inserted. This finding suggests that the oligosaccharide side chain interferes with HA cleavage if the number of basic amino acids at the cleavage site is not adequate to nullify this effect. Similar interplay could influence cleavage of other viral glycoproteins, such as those of human and simian immunodeficiency viruses and paramyxoviruses.

**Descriptors:** carbohydrates metabolism, hemagglutinins viral metabolism, influenza A virus avian metabolism, oligosaccharides metabolism, amino acid sequence, amino acids, glycosylation, hemagglutinins viral genetics, avian genetics, molecular sequence data, mutation.


**NAL Call Number:** QR175.M53

**Descriptors:** influenza A virus avian pathogenicity, chickens, influenza epidemiology, influenza microbiology, avian genetics, orthomyxoviridae pathogenicity, virulence.


**NAL Call Number:** 500 N21P

**Abstract:** Cleavage of the hemagglutinin (HA) in tissue culture systems has been correlated with virulence of avian influenza viruses. To examine the structural requirements for cleavage of the HA, the HA gene from a virulent H5 influenza virus was expressed in mammalian cells (CV-1), and the cleavage site of the HA was explored by using site-specific mutagenesis. The expressed HA protein exhibited normal cleavage, transport to the cell membrane, and ability to adsorb and to fuse erythrocytes at pH 5. Site-specific mutagenesis of the HA directly established that (i) most of the basic amino acids at this site are critical for cleavage activation; (ii) besides the connecting peptide sequence, at least one other structural feature of the HA is required for enzyme recognition; and (iii) the length of the connecting peptide can abrogate the structural feature(s).

**Descriptors:** hemagglutinins viral genetics, influenza A virus human genetics, amino acid sequence, cell line, cloning, molecular, DNA restriction enzymes, hemadsorption, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral immunology, human immunology, human pathogenicity, plasmids, simian virus 40 genetics, species specificity, transfection, virulence.


**NAL Call Number:** RA648.5.E46

**Abstract:** Influenza virus is not known to affect wild felids. We demonstrate that avian influenza A (H5N1) virus caused severe pneumonia in tigers and leopards that fed on infected poultry carcasses. This finding extends the host range of influenza virus and has implications for influenza virus epidemiology and wildlife conservation.

NAL Call Number: QH506.E46

Abstract: The structures of the oligosaccharides of the hemagglutinin of fowl plague virus [influenza A/FPV/Rostock/34 (H7N1)] have been elucidated by one- and two-dimensional 1H n.m.r. spectroscopy at 500 MHz and by microscale methylation analysis. N-Glycosidic oligosaccharides of the oligomannosidic (OM) and of the N-acetyllactosaminic type have been found, the latter type comprising biantennary structures, without (A) or with (E) bisecting N-acetylglucosamine, and triantennary (C) structures. Analysis of the tryptic and thermolytic glycopeptides of the hemagglutinin allowed the allocation of these oligosaccharides to the individual glycosylation sites. Each attachment site contained a unique set of oligosaccharides. Asn12 contains predominantly structures C and E which are highly fucosylated. Asn28 contains OM and A structures that lack fucose and sulfate. Asn123 shows A that has incomplete antennae but is highly fucosylated and sulfated. Asn149 has fucosylated A and E. Asn231 shows fucosylated A and E with incomplete antennae. Asn406 has OM oligosaccharides. Asn478 has A and E with little fucose. Localization of the oligosaccharides on the three-dimensional structure of the hemagglutinin revealed that the oligomannosidic glycans are attached to glycosylation sites at which the enzymes responsible for carbohydrate processing do not have proper access. These observations demonstrate that an important structural determinant for the oligosaccharide side chains is the structure of the glycoprotein itself. In addition, evidence was obtained that the rate of glycoprotein synthesis also has an influence on carbohydrate structure.

Descriptors: glycoproteins, hemagglutinins viral, influenza A virus avian, glycopeptides analysis, magnetic resonance spectroscopy, methylation, oligosaccharides analysis, protein processing, post translational.


NAL Call Number: QR360.J6

Abstract: Four different glycopeptides can be distinguished after pronase digestion of influenza A virus glycoproteins: Ia and Ib, containing N-acetylglucosamine, mannose, galactose, and fucose, and IIa and IIb, containing mannose and N-acetylglucosamine. All glycopeptides yielded N-acetylglucosaminyl-asparagine after mild acid hydrolysis. There was no evidence for O-glycosidic bonds. Thus, the carbohydrate complement is linked to the polypeptide exclusively by N-glycosidic linkages between N-acetylglucosamine and asparagine.

Descriptors: glycoproteins analysis, influenza A virus analysis, viral proteins analysis, acetylglucosamine analysis, asparagine analysis, carbohydrate conformation, glycopeptides analysis, influenza A virus avian analysis, molecular weight, oligosaccharides analysis, protein conformation.


NAL Call Number: 448.8 V81

Abstract: The carbohydrate side chains of the hemagglutinin of fowl plague virus (A/FPV/Rostock/34 (H7N1) have been localized by a procedure involving fragmentation of the polypeptide with cyanogen bromide and various proteases. The positions of the fragments were determined by radioactive labeling of the sugars and of specific amino acids. Side chains of the complex type I are attached to asparagine residues 12, 28, 123, 149, and 478. A mannose-rich (type II) side chain is linked to asparagine 406. Asparagine 231 is not glycosylated. The side chains attached to asparagine residues 12, 123, 149, and 478 contain sulfate. Glycopeptides derived by Pronase digestion from the individual attachment sites have been analyzed by their affinity to concanavalin A and Lens culinaris agglutinin. The results indicate that each glycosylation site has a typical set of heterogeneous oligosaccharides. Comparison of the glycosylation
patterns of the hemagglutinins of FPV and other influenza A viruses reveals that the glycosylation sites at asparagine residues 12, 28, and 478, which are located at the base of the spike, are highly conserved.

Mannose-rich side chains appear to be located preferentially at interfaces between the three monomers of a spike or between the globular and fibrous domains of a monomer.

**Descriptors:** hemagglutinins viral isolation and purification, influenza A virus avian immunology, oligosaccharides analysis, serine endopeptidases, acetylglucosaminidase, amino acid sequence, chromatography, affinity, cyanogen bromide, endopeptidases, glycopeptides analysis, hemagglutinins viral genetics, mannosyl glycoprotein endo beta N-acetylglucosaminidase, pronase, trypsin.


**NAL Call Number:** QR360.J6

**Descriptors:** cell nucleus physiology, orthomyxoviridae growth and development, virus replication, antigens, viral analysis, cell line, electrophoresis, polyacrylamide gel, fluorescent antibody technique, hamsters, influenza A virus avian growth and development, kidney, methionine, Newcastle disease virus growth and development, nucleic acid hybridization, peptides analysis, sulfur radioisotopes, tritium, uridine, vaccinia virus growth and development.


**NAL Call Number:** 448.8 V81

**Descriptors:** cell nucleus microbiology, dactinomycin pharmacology, influenza A virus avian growth and development, ultraviolet rays, virus replication drug effects, virus replication radiation effects, antigens, viral analysis, autoradiography, cell fusion, cell line, cell nucleus immunology, cultured cells cytology, chick embryo, chickens, erythrocytes cytology, fluorescent antibody technique, hamsters, hemagglutinins viral, avian immunology, avian metabolism, kidney, l cells cell line, mice, neuraminidase biosynthesis, nucleoproteins biosynthesis, radiation effects, viral proteins biosynthesis.


**NAL Call Number:** 448.3 Ar23

**Abstract:** Analysis of the effects of amantadine during a single cycle of replication of A/FPV/Rostock virus in vitro showed that, as with other influenza A viruses, an M2 protein-dependent step early in infection was inhibited. No effect was observed on later steps in replication under the conditions used.

**Descriptors:** amantadine pharmacology, influenza A virus avian drug effects, viral matrix proteins biosynthesis, viral matrix proteins drug effects, viral matrix proteins genetics, base sequence, avian genetics, avian physiology, molecular sequence data, mutation, viral proteins biosynthesis, virus replication drug effects.


**NAL Call Number:** 41.8 V6468

**Descriptors:** brain metabolism, hemagglutinins viral metabolism, influenza A virus avian immunology, brain cytology, cultured cells, chick embryo, tissue culture metabolism.


**NAL Call Number:** 448.8 P942

**Descriptors:** influenza A virus avian analysis, lipids analysis, virion analysis, carcinoma, Ehrlich tumor

NAL Call Number: 448.8 P942

Descriptors: adamantane analogs and derivatives, orthomyxoviridae drug effects, rimantadine pharmacology, drug resistance, microbial, influenza A virus avian drug effects, influenza A virus drug effects, variation genetics.


NAL Call Number: 472 N21

Abstract: The haemagglutinin glycoprotein HA of influenza viruses is responsible for the attachment of the virus to neuraminic acid-containing receptors at the cell surface and subsequent penetration by triggering fusion of the viral envelope with cellular membranes. To express full activity of the newly synthesized precursor, HA has to be modified by post-translational proteolytic cleavage into the polypeptides HA1 and HA2 by cellular enzymes. If proteases suitable for cleavage are not present in the host cell, the resulting virus particles are non-infectious. During adaptation of the apathogenic influenza virus A/turkey/Oregon/71 to chicken embryo cells, which are not permissive for HA cleavage, we obtained an infectious virus variant with increased pathogenicity. Sequence analysis revealed that during adaptation 54 nucleotides were inserted into the HA gene; their sequence corresponds to a region of the 28S ribosomal RNA. This insertion is probably responsible for increased cleavability of HA, as well as for infectivity and pathogenicity of the adapted virus.

Descriptors: DNA transposable elements, hemagglutinins viral genetics, influenza A virus avian pathogenicity, RNA, ribosomal genetics, ribosomal, 28S genetics, base sequence, cloning, molecular, hemagglutinin glycoproteins, influenza virus, avian genetics, molecular sequence data, recombinant fusion proteins genetics, turkeys, viral fusion proteins metabolism, virulence.


NAL Call Number: 448.8 V81

Descriptors: hemagglutinins viral immunology, influenza A virus avian immunology, antibodies, monoclonal, antibodies, viral, antibody specificity, antigen antibody reactions, epitopes.


NAL Call Number: QR1.I57

Abstract: Influenza viruses A/duck/Hokkaido/5/77 (Hav7N2), A/budgerigar/Hokkaido/1/77 (Hav4Nav1), A/Kumamoto/22/76 (H3N2), A/Aichi/2/68 (H3N2), and A/New Jersey/8/76 (Hsw1N1) were experimentally inoculated into Pekin ducks. Of these, the influenza viruses of duck and budgerigar origin replicated in the intestinal tract of the ducks. The infected ducks shed the virus in the feces to high titers, but did not show clinical signs of disease and scarcely produced detectable serum antibodies. Using immunofluorescent staining, we demonstrated that the target cells of the duck virus in ducks were the simple columnar epithelial cells which form crypts in the large intestines, especially in the colon. After primary infection, the birds resisted reinfection with the duck virus at least for 28 days, but from 46 days onward they were susceptible to reinfection. These infections were quickly restricted by a brisk secondary immune response, reflected in the rapid appearance of high titers of antibody after reinoculation. In contrast to the avian influenza viruses, the remaining three influenza viruses of human origin did not replicate in the intestinal tract but did cause a serum antibody response.

Descriptors: ducks microbiology, influenza veterinary, influenza A virus avian growth and development,
antibody formation, digestive system microbiology, feces microbiology, influenza immunology, human growth and development, parakeets microbiology, virus replication.


**NAL Call Number:** 41.8 R312

**Abstract:** Experimental infection of domestic fowl, ducks and geese with an influenza A virus (H7N2) isolated from a domestic duck showed that this virus was apathogenic for these poultry. A second virus (H6N2), also apathogenic and more 'non-avid' than any such isolates previously recognised in surveillance of domestic poultry in Hong Kong, was isolated from one goose after H7N2 shedding had ceased. This goose, in effect, acted as a selective isolation system for the H6N2 virus whose presence in the field isolate could not be detected in spite of multiple passage in embryonated eggs.

**Descriptors:** chickens microbiology, ducks microbiology, fowl plague microbiology, geese microbiology, influenza A virus avian pathogenicity, poultry diseases microbiology.

Kishida, N., Y. Sakoda, M. Eto, Y. Sunaga, and H. Kida (2004). **Co-infection of Staphylococcus aureus or Haemophilus paragallinarum exacerbates H9N2 influenza A virus infection in chickens.** *Archives of Virology* 149(11): 2095-104. ISSN: 0304-8608.

**NAL Call Number:** 448.3 Ar23

**Abstract:** H9N2 influenza viruses are frequently isolated from chicken meat and bone marrow imported from China to Japan since 2001. These isolates were experimentally inoculated into specific pathogen-free chickens intranasally. Viruses were recovered from the meat and bone marrow of birds showing no overt signs. On the other hand, chickens co-infected with H9N2 virus and either *Staphylococcus aureus* or *Haemophilus paragallinarum* showed clinical signs severer than those shown by birds infected only with the virus alone or each of the bacteria alone. In addition, H9N2 viruses were more efficiently recovered from the chickens co-infected with *S. aureus* or *H. paragallinarum* than those from the birds infected with only the virus. The present results indicate that co-infection of H9N2 influenza virus with *S. aureus* or *H. paragallinarum* enhances the replication of the virus in chickens, resulting in exacerbation of the H9N2 virus infection.

**Descriptors:** chickens virology, haemophilus infections veterinary, *Haemophilus paragallinarum*, influenza A virus, avian, influenza, avian virology, poultry diseases virology, staphylococcal infections veterinary, chickens microbiology, haemophilus infections complications, poultry diseases microbiology, specific pathogen free organisms, staphylococcal infections complications, virus replication.


**NAL Call Number:** QR360.A1J6

**Abstract:** An analysis of the nucleoprotein (NP) of 29 different influenza A viruses by phosphopeptide fingerprinting revealed three prototype patterns. The first, which was a complex pattern consisting of six to seven phosphopeptides, another which was relatively simple consisted of two or three phosphopeptides, and a third one which was complex but was missing the main phosphopeptide shared by the two other patterns. Phosphoserine was the only labelled phosphamino acid detected. A tentative deduction of two of the phosphate attachment sites (serine residues at positions 3 and 473) could be made by comparison of the known amino acid sequences of the NPs of 25 strains. No correlation was found between species specificity or subtype or year of isolation of the strains. During the infectious cycle the fingerprint underwent significant changes, indicating subtle phosphorylation and dephosphorylation of the NP at various stages during viral multiplication. Most of the phosphopeptides were metabolically stable; however one major phosphopeptide, which was not found in the NP of mature virions, exhibited a high turnover (presumably serine at position 3). The phosphopeptide fingerprint could be significantly influenced in vivo by the specific stimulation of cellular protein kinase C by the phorbol ester 12-O-tetradecanoylphorbol 13-acetate or by its inhibition with the isoquinoline sulphonamide H7. H7 specifically inhibited the replication of influenza A viruses by deregulation of viral protein synthesis without interfering with the multiplication of a parainfluenza virus (Newcastle disease virus), an alphavirus (Semliki Forest virus) or a flavivirus (West Nile). Therefore the correct phosphorylation of the NP of influenza viruses appears to be essential for influenza virus replication.

**NAL Call Number:** 448.8 J273

**Abstract:** Neuraminidases of 18 strains of avian influenza A virus were examined by both colorimetric and fluorometric assays using fetuin and 4-methylumbelliferyl-N-Ac-alpha-D-neuraminide as substrates, respectively, to compare them with those of human influenza A and B viruses. The ratios of the neuraminidase activity of avian influenza virus measured by the colorimetric assay method to that measured by the fluorometric assay were distributed in the range of 2.4-20.3. The enzyme of avian influenza virus showed calcium-ion dependence in both assay methods. These results suggest that neuraminidase of avian influenza A virus is varies greatly from one strain to another in substrate specificity as compared with those of human influenza A and B viruses, and that some strains of avian influenza A virus have a neuraminidase with unique enzymological characteristics different from that of human influenza A virus as well as that of influenza B virus.

**Descriptors:** influenza A virus avian enzymology, neuraminidase metabolism, colorimetry, edetic acid pharmacology, epitopes, fluorometry, species specificity, substrate specificity.


**NAL Call Number:** 384 Z38

**Abstract:** 4-O-Acetylated, 7-O-acetylated, and 9-O-acetylated 4-methylumbelliferyl-alpha-N-acetylneuraminic acids (Neu4,5Ac2-MU, Neu5,7Ac2-MU, Neu5,9Ac2-MU) were tested as substrates of sialidases of *Vibrio cholerae* and of *Clostridium perfringens*. Both sialidases were unable to hydrolyse Neu4,5Ac2-MU. This compound at 1 mM concentration did not inhibit significantly the cleavage of Neu5Ac-MU, the best substrate tested. The 4-O-acetylated sialic acid glycoside is hydrolysed slowly by the sialidase from fowl plague virus. The relative substrate specificity, reflected in V/Km of the *Vibrio cholerae* sialidase is Neu5Ac-MU much greater than Neu5,7Ac2-MU approximately Neu5,9Ac2-MU and of the clostridial enzyme it is Neu5Ac-MU greater than Neu5,9Ac2-MU greater than Neu5,7Ac2-MU. The affinities of both enzymes for the side-chain O-acetylated sialic acid derivatives are higher than for Neu5Ac-MU. The artificial, well-defined substrates, described here, provide the opportunity to quantify the influence of sialic acid O-acetylation on the hydrolysis of sialoglycoconjugates without the side effects introduced by other parts of more complex glycans.

**Descriptors:** glycosides metabolism, hymecromone analogs and derivatives, neuraminidase metabolism, sialic acids metabolism, acetylation, *Clostridium perfringens* enzymology, hymecromone metabolism, influenza A virus avian enzymology, kinetics, species specificity, substrate specificity, *Vibrio cholerae* enzymology.


**NAL Call Number:** QP601.M49

**Descriptors:** glycoproteins genetics, influenza A virus avian genetics, mutation, viral proteins genetics, cell line, cell membrane metabolism, cell transformation, viral, cultured cells, chick embryo, dogs, glycoproteins isolation and purification, hamsters, kidney, Newcastle disease virus genetics, Newcastle disease virus isolation and purification, parainfluenza virus 1, human genetics, parainfluenza virus 1, human isolation and purification, viral proteins isolation and purification.
NAL Call Number: 500 N484
Descriptors: antigen antibody reactions, antigens, viral, cultured cells immunology, influenza A virus avian immunology, lectins, cell line, chick embryo, concanavalin A, fibroblasts, glycoproteins immunology, hamsters, HeLa cells, hemadsorption, hemadsorption inhibition tests, avian ultrastructure, kidney, I cells cell line, mice, viral proteins biosynthesis, viral proteins immunology, virus replication.

NAL Call Number: QH506.E46
Abstract: At calcium-specific ionophore A23187 concentrations of approximately 0.25 microM [which still allow assembly and release of fowl plague virus (FPV) particles] post-translational proteolytic cleavage of the viral hemagglutinin precursor HA into the fragments HA1 and HA2 is inhibited. The resulting virus particles with uncleaved hemagglutinin, that cannot be obtained under normal conditions, provide a suitable substrate for in vitro assays of the protease sensitivity of the FPV hemagglutinin. Proteolytic activation is accomplished with trypsin. Treatment with cathepsin B at low pH yields aberrant cleavage products suggesting that the cellular cleavage enzyme is not of lysosomal origin. A protease that cleaves the FPV hemagglutinin in the correct place can be detected in lysates of MDBK cells. This enzyme is calcium dependent and has a neutral pH optimum.
Descriptors: calcimycin pharmacology, influenza A virus avian genetics, thermolysin metabolism, viral envelope proteins analysis, viral matrix proteins, cattle, cell line, hamsters, hemagglutination tests, avian drug effects, kidney, plaque assay, virus replication drug effects.

NAL Call Number: QR1.C8
Descriptors: carbohydrates analysis, hemagglutinins viral analysis, influenza A virus avian analysis, influenza A virus analysis, chemistry, glycopeptides analysis, avian immunology, human analysis, porcine analysis, influenza A virus classification, influenza A virus immunology, serotyping, species specificity.

NAL Call Number: QR180.B4
Descriptors: hemagglutinins viral genetics, influenza A virus avian genetics, influenza A virus genetics, baculoviridae genetics, carbohydrate conformation, cell line, genetic vectors, hemadsorption, hemagglutinin glycoproteins, influenza virus, avian physiology, influenza A virus physiology, insects, larva, moths, oligosaccharides analysis, viral envelope proteins genetics.

NAL Call Number: QR360.J6
Descriptors: influenza A virus avian metabolism, viral proteins biosynthesis, amino acids metabolism, carbon isotopes, chick embryo, electrophoresis, polyacrylamide gel, fibroblasts, fluorine, glucosamine metabolism, glycoproteins biosynthesis, glycoproteins metabolism, hemagglutination tests, hemagglutinins viral, influenza A virus avian growth and development, isoarylphate pharmacology, peptide synthesis, phenylalanine pharmacology, plaque assay, protein precursors biosynthesis, temperature, tissue culture, tritium, viral proteins metabolism, virus replication.

NAL Call Number: 448.8 V81
Descriptors: carbohydrates analysis, influenza A virus avian analysis, lipids analysis, viral proteins
analysis, agglutination tests, antigens, viral analysis, bromelains, carbon isotopes, centrifugation, density gradient, chick embryo, concanavalin a, electrophoresis, disc, erythrocytes immunology, fibroblasts, glycoproteins analysis, avian immunology, microscopy, electron, molecular weight, peptides analysis, sucrose, tissue culture, tritium, virus cultivation.

NAL Call Number: QR360.A1J6
Descriptors: glycoproteins metabolism, hemagglutinins viral, influenza A virus avian growth and development, influenza A virus growth and development, viral proteins metabolism, chick embryo, glycosaminoglycans metabolism, avian metabolism, influenza A virus metabolism, peptide hydrolases metabolism, tissue culture, trypsin metabolism, virus replication.

NAL Call Number: 448.8 V81
Descriptors: orthomyxoviridae pathogenicity, trypsin pharmacology, adsorption, arteritis virus, equine analysis, arteritis virus, equine growth and development, arteritis virus, equine pathogenicity, chick embryo, fetal membranes, glycoproteins analysis, hemagglutinins viral analysis, influenza A virus avian analysis, avian growth and development, avian pathogenicity, human analysis, human growth and development, human pathogenicity, porcine analysis, porcine growth and development, porcine pathogenicity, peptides analysis, tissue culture, viral proteins analysis, virulence, virus replication.

NAL Call Number: 448.8 V81
Descriptors: glucosamine pharmacology, glucose pharmacology, glycoproteins biosynthesis, influenza A virus avian metabolism, viral proteins biosynthesis, amino acids metabolism, carbon isotopes, cultured cells metabolism, cultured cells microbiology, chick embryo, chromatography, electrophoresis, polyacrylamide gel, fibroblasts microbiology, fucose metabolism, galactose metabolism, hemagglutinins viral biosynthesis, avian enzymology, avian growth and development, molecular weight, neuraminidase biosynthesis, peptide synthesis, stereoisomerism, tritium, uridine metabolism.

NAL Call Number: 448.3 AC85
Abstract: Recombinants between H3N2 human influenza viruses (A/Victoria/3/75 and A/Bangkok/1/79, low-yielding parents in chick embryos) and fowl plague virus (FPV, a high-yielding parent in chick embryos) have been obtained. The high reproductive capacity of recombinants in chick embryos has been shown to be due to the gene coding for M proteins.
Descriptors: genes viral, influenza A virus avian genetics, human genetics, recombination, genetic, viral proteins genetics, virus replication, chick embryo, avian physiology, human physiology, viral matrix proteins.

**NAL Call Number:** 448.3 Ar23

**Abstract:** Antigenic analysis of the haemagglutinin and matrix protein with corresponding sets of monoclonal antibodies as well as sequence analysis of HA-, M-, and NS-genes were carried out to establish antigenic and genetic relationships between four fowl plague virus (FPV) strains of H7 subtype. The data obtained revealed close genetic relatedness between the oldest known influenza A virus, A/chicken/Brescia/1902 (H7N7), and two FPV strains, A/FPV/Dobson (H7N7) and A/FPV/Weybridge (H7N7). These three strains apparently differ in all genes investigated from the A/FPV/Rostock isolate.

**Descriptors:** capsid genetics, genes viral, hemagglutinins viral genetics, influenza A virus avian genetics, viral core proteins genetics, viral matrix proteins genetics, amino acid sequence, base sequence, capsid immunology, DNA, viral, deoxyribonucleotides, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral immunology, avian immunology, molecular sequence data, sequence homology, nucleic acid, species specificity, viral core proteins immunology, viral matrix proteins immunology, viral nonstructural proteins.

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**NAL Call Number:** 448.3 AC85

**Descriptors:** centrifugation, density gradient methods, DNA directed RNA polymerases metabolism, influenza A virus avian enzymology, nucleoproteins isolation and purification, viral proteins isolation and purification, cell free system, deoxycholic acid, mercaptoethanol, sucrose, tritium, uracil nucleotides metabolism, urea.

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**NAL Call Number:** 448.3 AC85

**Abstract:** Fowl plague virus (FPV) ribonucleoprotein (RNP) bands in sucrose density gradient in a heterogeneous peak with sedimentation coefficients from 45 to 70 S, whereas in cesium chloride gradient it has a homogeneous density of 1.33-1.34 g/cm3. FPV RNP contains 7.4-8% RNA. Upon inoculation of chick embryo cell cultures. FPV RNP shows no infectivity, does not induce virus-specific protein synthesis and does not participate in complementation or recombination interactions with ts mutants of FPV. The biological activity of FPV RNP demonstrable under certain experimental conditions is due to admixture of undestroyed virions and is completely eliminated by treatment of the preparation with gamma-globulin fraction of antiserum to FPV haemagglutinin, but not with antiserum to RNP proteins.

**Descriptors:** influenza A virus avian analysis, influenza A virus avian metabolism, RNA viral analysis, viral proteins analysis, viral proteins biosynthesis, centrifugation, density gradient, genetic complementation test, immune sera, peptides analysis, recombination, genetic, ribonucleases.

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**NAL Call Number:** 448.3 Ar23

**Abstract:** Norakin-resistant (NR) mutants of fowl plague virus (A/FPV/Weybridge, H7N7) have 1 to 2 (in one instance 3) amino acid substitutions in different positions of the heavy (HA 1) and/or light (HA 2) subunits of the haemagglutinin (HA) molecule. Investigation of NR mutants using the haemagglutination inhibition test with monoclonal antibodies (MAb) to the HA of A/seal/Massachusetts/80 (H7N7) virus revealed that one of the mutants (NR 1) differs antigenically from the wild-type fowl plaque virus: its haemagglutination was not inhibited by MAb 55/2 and 58/6. By contrast, MAb-resistant (escape) mutants, selected from the wild-type fowl plaque virus under pressure from MAb 55/2 or 58/6, showed reduced drug sensitivity. These findings suggest a possibility of correlation between alteration of influenza virus antigenicity and change of its sensitivity to drugs whose target is the haemagglutinin. This potential effect should be taken into account when antiviral substances directed to surface influenza virus antigens are being developed for use as antiviral drugs.

**Descriptors:** genome, viral, influenza A virus avian physiology, influenza B virus physiology, reassortant viruses physiology, virus replication physiology, cell line, influenza A virus avian genetics, influenza B virus genetics, reassortant viruses genetics, virus cultivation, virus replication genetics.


**Descriptors:** influenza A virus avian enzymology, intestines virology, neuraminidase metabolism, virus replication, amino acid substitution, base sequence, DNA primers, ducks, avian growth and development, avian physiology, models, molecular, mutagenesis, site directed, neuraminidase chemistry, neuraminidase genetics, reassortant viruses enzymology, reassortant viruses genetics, reassortant viruses growth and development, reassortant viruses physiology.

Abstract: The N1 and N9 neuraminidase (NA) subtypes of influenza A viruses exhibit significant hemadsorption activity that localizes to a site distinct from that of the enzymatic active site. To determine the conservation of hemadsorption activity among different NAs, we have examined most of the NA subtypes from avian, swine, equine, and human virus isolates. All subtypes of avian virus NAs examined and one equine virus N8 NA possessed high levels of hemadsorption activity. A swine virus N1 NA exhibited only weak hemadsorption activity, while in human virus N1 and N2 NAs, the activity was detected at a much lower level than in avian virus NAs. NAs which possessed hemadsorption activity for chicken erythrocytes (RBCs) were similarly able to adsorb human RBCs. However, none of the hemadsorption-positive NAs could bind equine, swine, or bovine RBCs, suggesting that RBCs from these species lack molecules, recognized by the NA hemadsorption site, present on human and chicken RBCs. Mutagenesis of the putative hemadsorption site of A/duck/Hong Kong/7/75 N2 NA abolished the high level of hemadsorption activity exhibited by the wild-type protein but also resulted in a 50% reduction of the NA enzymatic activity. A transfectant virus, generated by reverse genetics, containing this mutated NA replicated 10-fold less efficiently in chicken embryo fibroblast cultures than did a transfectant virus expressing the wild-type NA. However, both viruses replicated equally well in Peking ducks. Although conservation of NA hemadsorption activity among avian virus NAs suggests the maintenance of a required function of NA, loss of the activity does not preclude the replication of the virus in an avian host.

Descriptors: biochemistry and molecular biophysics, blood and lymphatics, cell biology, enzymology, genetics, infection, microbiology, skeletal system, A, duck, Hong Kong, 7, 75, blood and lymphatics, enzymology, erythrocyte fibroblasts, hemadsorption activity, host infection, influenza A viruses, N1 neuraminidase, N9 neuraminidase, Peking duck, viral replication, viral surface, glycoprotein.


NAL Call Number: 41.8 Av5

Abstract: Mallard duck tracheal organ cultures were used to study structural changes associated with infection with type-A influenza (A/Turkey/WIS/68) (H9N2) at the light-microscope and electron-microscope levels. Light-microscope changes in infected organ culture were cytoplasmic vacuolization, nuclear swelling, reduction in ciliated epithelium, and sloughing of epithelial cells. Ultrastructural changes included the loss of cilia and microvilli, distortion and swelling of cellular organelles, breakdown of intercellular junction, and apparent phagocytosis of the ciliated epithelium. Numerous budding virions were noted at the plasmalemma. Virus was detected by egg inoculation from all experimental cultures throughout the 192-hour experiment.

Descriptors: influenza A virus, avian growth and development, trachea ultrastructure, organ culture, trachea microbiology.


NAL Call Number: QR360.J6

Abstract: Inoculation of mice with hemagglutinin (HA)-expressing DNA affords reliable protection against lethal influenza virus infection, while in chickens the same strategy has yielded variable results. Here we show that gene gun delivery of DNA encoding an H5 HA protein confers complete immune protection to chickens challenged with lethal H5 viruses. In tests of the influence of promoter selection on vaccine efficacy, close correlations were obtained between immune responses and the dose of DNA administered, whether a cytomegalovirus (CMV) immediate-early promoter or a chicken beta-actin promoter was used. Perhaps most important, the HA-DNA vaccine conferred 95% cross-protection against challenge with lethal antigenic variants that differed from the primary antigen by 11 to 13% (HA1 amino acid sequence homology). Overall, the high levels of protection seen with gene gun delivery of HA-DNA were as good as, if not better than, those achieved with a conventional whole-virus vaccine, with fewer instances of morbidity and death. The absence of detectable antibody titers after primary immunization, together with the rapid appearance of high titers immediately after challenge, implicates efficient B-cell priming as the principal mechanism of DNA-mediated immune protection. Our results suggest that the efficacy of HA-DNA influenza
virus vaccine in mice extends to chickens and probably to other avian species as well. Indeed, the H5 preparation we describe offers an attractive means to protect the domestic poultry industry in the United States from lethal H5N2 viruses, which continue to circulate in Mexico.

Descriptors: hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian immunology, influenza vaccine immunology, vaccines, DNA immunology, antibodies, viral blood, biolistics, chickens, dose response relationship, immunologic, epitopes, fowl plague prevention and control, hemagglutinin glycoproteins, influenza virus immunology, promoter regions genetics, vaccination.


NAL Call Number: 41.8 Av5

Abstract: The effects of avian influenza virus (AIV) infection on systemic phagocytes and pulmonary macrophages of turkeys were studied. There was a significant increase (P < 0.0001) in oxidative burst in systemic phagocytes of AIV-inoculated turkeys on 2, 4, 6, and 8 days postinoculation (PI), as measured by chemiluminescence. There was also a significant increase (P < 0.02) in oxidative burst in pulmonary macrophages on day 4 PI. The chemiluminescence response was depressed on 6, 8, and 10 days PI in AIV-inoculated turkeys compared with controls. The increase in oxidative response in both systemic phagocytes and pulmonary macrophages correlated with the peak virus titer in the lungs and trachea of AIV-inoculated turkeys. Bacterial killing by pulmonary macrophages from AIV-inoculated turkeys was reduced on days 6 and 10 PI compared with uninoculated controls. Histopathological changes in trachea were more pronounced on day 6 PI in AIV-inoculated turkeys; no significant changes were detected in the lungs. These data indicate that compromised functional capacity of pulmonary macrophages predisposes turkeys to secondary bacterial infections.

Descriptors: turkeys, avian influenza virus, phagocytes, macrophages, immune response, histopathology, lungs, trachea, antimicrobial properties, animal morphology, antibody properties, birds, cells, Galliformes, immunity, influenza virus, pathology, phagocytes, respiratory system, viruses, oxidative burst, phagocytosis, immune competence, antibacterial properties.


Descriptors: influenza A virus avian drug effects, oxadiazoles pharmacology, virus replication drug effects, cultured cells, chick embryo, cytopathogenic effect, viral, fibroblasts.


NAL Call Number: 448.8 P942

Abstract: The process of influenza virus deproteinization was compared in two systems: chick fibroblasts infected with fowl plague virus (FPV) and MDCK cells infected with WSN virus. The cells were infected with 3H-uridine-labeled viruses. Deproteinization of virus structures was studied at 4 degrees C and after incubation of virus-infected cells at 37 degrees C. At 4 degrees C, the bulk of radioactivity of the original virus was found in the perinuclear cytoplasm (the fraction obtained by treatment of triton X-100-purified nuclei with 0.1 M citric acid) and much less radioactivity was found in the nucleus. After incubation at 37 degrees C the level of radioactivity in the nucleus increased and reached or even exceeded that in the perinuclear cytoplasm. A biophysical analysis of the structures showed the perinuclear cytoplasm to contain subviral particles (SVP) similar to nucleoids as well as RNP with a buoyant density of 1.35 g/ml in cesium chloride. The nuclear extract contained RNP with a buoyant density 1.39-1.41 m/ml. The experimental results indicate that the first stage of deproteinization of virus particles to SVP occurs at 4 degrees C. The second stage of deproteinization, to RNP with a buoyant density 1.35 g/ml, also occurs at a low temperature.

Descriptors: orthomyxoviridae metabolism, temperature, viral proteins metabolism, chick embryo, influenza A virus avian metabolism, ribonucleoproteins metabolism, time factors, tritium, virus cultivation.

NAL Call Number: 448.8 P942

Abstract: A comparative study of pH-dependence of hemolytic and neuraminidase activities of four remantadin-sensitive influenza A virus strains CAPV (classical avian plague virus) (H7N7), USSR/090/77 (H1N1), Ann Arbor (H2N2), and Texas (H3N2) and their remantadin-resistant variants was carried out. The original strains were shown to produce hemolysis in a narrow pH range (5.0 and 5.5) and to have maximal neuraminidase activity at the same pH values. In remantadin-resistant variants the optimal pH values for hemolytic and neuraminidase activities were higher by 0.5-1.0 than for the sensitive variants.

Descriptors: adamantane analogs and derivatives, hemolysis, influenza A virus enzymology, neuraminidase metabolism, rimantadine pharmacology, variation genetics drug effects, drug resistance, microbial, hydrogen-ion concentration, influenza A virus avian drug effects, avian enzymology, influenza A virus drug effects.


NAL Call Number: 448.8 P942

Abstract: A comparative study of receptors for influenza virus, fowl plague virus, and human parainfluenza type 3 virus was carried out. Natural receptors of guinea pig erythrocytes were destroyed with neuraminidase, and individual gangliosides GM1, GD1a, and GT1b were inserted into their membranes. The labeled virus was adsorbed on the erythrocytes modified in this manner, and the degree of restoration of the receptor activity of erythrocytes lost after neuraminidase treatment was determined. Two gangliosides, GD1a and GT1b, were found to be capable of functioning as specific receptors for influenza virus. Both gangliosides restored completely the virus adsorption on erythrocytes. In contrast, none of the three gangliosides used did not restore parainfluenza virus adsorption. It is concluded that the nature of influenza and parainfluenza virus receptors is different.

Descriptors: influenza A virus avian metabolism, orthomyxoviridae metabolism, parainfluenza virus 3, human metabolism, receptors, virus metabolism, respirovirus metabolism, adsorption, cell line, erythrocytes drug effects, erythrocytes metabolism, gangliosides metabolism, guinea pigs, neuraminidase pharmacology, receptors, virus drug effects, virus cultivation.


NAL Call Number: 381 An13

Descriptors: antibodies, monoclonal metabolism, biosensing techniques methods, immunoglobulin fragments immunology, immunoglobulins, fab immunology, influenza A virus avian enzymology, neuraminidase immunology, birds, avian immunology, kinetics, neuraminidase metabolism, protein binding, whales.


NAL Call Number: 448.8 P942

Abstract: Immunological analysis has shown hemagglutinins of avian viruses like hemagglutinins of human viruses to have a complex antigenic composition. Three antigenic determinants were discovered in hemagglutinin of A/Chicken/12/71 virus previously designated H3 and in hemagglutinin of A/Tern/18/73 virus previously designated Hav7. The H3 determinant and the second determinant are identical in avian and A/Hong Kong/1/68 human viruses. In addition, hemagglutinins of avian viruses have a determinant specific
for each virus which is lacking in human influenza virus hemagglutinin.

Descriptors: antigens, viral isolation and purification, birds microbiology, hemagglutinins viral isolation and purification, influenza A virus avian immunology, human immunology, adsorption, chick embryo, complement fixation tests, epitopes, hemagglutination inhibition tests.


NAL Call Number: QP501.E8

Descriptors: DNA directed RNA polymerases antagonists and inhibitors, DNA directed RNA polymerases blood, enzyme inhibitors isolation and purification, ribonucleases antagonists and inhibitors, centrifugation, density gradient, chick embryo, chromatography, affinity, cytoplasm enzymology, cytosol, electrophoresis, polyacrylamide gel, hydrogen-ion concentration, influenza A virus avian enzymology, kinetics, molecular weight, orthomyxoviridae enzymology.


NAL Call Number: QR360.A1J6

Abstract: In the present study we have investigated the role of the hydrophobic domains of the fowl plague virus (FPV) haemagglutinin (HA) on its intracellular transport and maturation in insect cells. To this end processing of full-length HA (A+) has been compared to that of two truncated forms lacking either the cytoplasmic domain and the transmembrane domain (A-) or lacking the entire HA2 subunit, i.e. the transmembrane domain and the fusion peptide (HA2-). All glycosylation sites present on A- and HA2- were glycosylated, indicating that both truncated forms were completely translocated in the endoplasmic reticulum. Unlike A+, A- and HA2- did not form trimers as indicated by cross-linking, gradient centrifugation and studies employing conformation-specific antibodies. Whereas HA2- was efficiently secreted, A- was retained in the cells in an apparently membrane-bound form. The data show that the carboxy-terminal transmembrane region is essential for the formation and stability of the trimers of the FPV HA. These observations also indicate that, under certain conditions, the fusion peptide of the FPV HA can serve as a membrane anchor.

Descriptors: hemagglutinins viral metabolism, influenza A virus avian metabolism, protein processing, post translational, viral envelope proteins secretion, base sequence, biological transport, active, cell fractionation, cultured cells, DNA mutational analysis, endopeptidases metabolism, glycosylation, hemagglutinin glycoproteins, influenza virus, avian genetics, insects, molecular sequence data, protein conformation, recombinant proteins biosynthesis, structure activity relationship.


NAL Call Number: 470 Sci2

Abstract: During the 2003 to 2004 outbreak of avian influenza A (H5N1) virus in Asia, there were anecdotal reports of fatal infection in domestic cats, although this species is considered resistant to influenza. We experimentally inoculated cats with H5N1 virus intratracheally and by feeding them virus-infected chickens. The cats excreted virus, developed severe diffuse alveolar damage, and transmitted virus to sentinel cats. These results show that domestic cats are at risk of disease or death from H5N1 virus, can be infected by horizontal transmission, and may play a role in the epidemiology of this virus.

Descriptors: cat diseases virology, influenza veterinary, influenza A virus, avian pathogenicity, cat diseases pathology, cat diseases transmission, cats, chickens virology, disease transmission, horizontal veterinary, feeding behavior, influenza pathology, influenza transmission, influenza virology, influenza A virus, avian isolation and purification, avian influenza virology, pulmonary alveoli pathology, pulmonary alveoli virology.


NAL Call Number: 448.8 P942
Abstract: The results of the studies on fowl plague virus (FPV, Rostok strain) reproduction in *Aedes aegypti* mosquitoes are presented. The virus-containing allantoic fluid was inoculated intrathoracically in volumes of 0.1 and 0.2 microliter. The virus was isolated in chick embryos and could be detected at 5–14 days after inoculation. After inoculation of 0.1 microliter of virus it could be detected in doses of 0.5, 2.0, 1.75 Ig2 ID50, after inoculation of 0.2 microliter—in doses of 5, 1.5, and 0.5 Ig2 ID50.

Descriptors: *Aedes* microbiology, influenza A virus avian physiology, time factors, virus replication.


NAL Call Number: RM265.A5125

Abstract: *Bacillus intermedius* ribonuclease modified by the residue of adamantane carboxylic acid was prepared. When the cells of chick embryo fibroblasts infected by the fowl plague virus were exposed to the modified ribonuclease, the antiviral activity proved to be higher by comparison to that of the native enzyme. The chemotherapeutic index of the RNAse after the modification increased 4 times.

Descriptors: adamantane analogs and derivatives, antiviral agents isolation and purification, Bacillus enzymology, ribonucleases isolation and purification, adamantane chemistry, antiviral agents pharmacology, chick embryo, fibroblasts drug effects, fowl plague drug therapy, influenza A virus avian drug effects, molecular structure, ribonucleases chemistry, ribonucleases pharmacology.


NAL Call Number: QR360.J6

Abstract: The hemagglutinin of influenza (fowl plague) virus was expressed in larvae of *Heliothis virescens* by using recombinant *Autographa californica nuclear polyhedrosis* virus (AcNPV) as a vector. Animals were infected with the recombinant virus either by parenteral injection or by feeding. For oral uptake, recombinant virus occluded in polyhedra obtained from cultured *Spodoptera frugiperda* cells after coinfection with authentic AcNPV was used. Immunohistological analyses of infected animals revealed that the hemagglutinin was expressed only in those tissues that are also permissive for the replication of authentic AcNPV. These tissues included hypodermis, fat body, and tracheal matrix. After oral infection, hemagglutinin was also detected in individual gut cells. The amount of hemagglutinin synthesized in larvae after parenteral infection was 0.3% of the total protein, compared with 5% obtained in cultured insect cells. The hemagglutinin was transported to the cell surface and expressed in polarized cells only at the apical plasma membrane. It was processed by posttranslational proteolysis into the cleavage products HA1 and HA2. Oligosaccharides were attached by N-glycosidic linkages and were smaller than those found on hemagglutinin obtained from vertebrate cells. Hemagglutinin from larvae expressed receptor binding and cell fusion activities, but quantitation of the hemolytic capacity revealed that it was only about half as active as hemagglutinin from vertebrate or insect cell cultures. Chickens immunized with larval tissues containing hemagglutinin were protected from infection with fowl plague virus. These observations demonstrate that live insects are able to produce a recombinant membrane protein of vertebrate origin in biologically active form.

Descriptors: hemagglutinins viral genetics, influenza A virus avian immunology, insect viruses genetics, administration, oral, blotting, western, cloning, molecular, DNA, recombinant, genetic vectors, hemolysis, avian genetics, larva, *Lepidoptera*, membrane glycoproteins genetics, recombinant proteins genetics.


NAL Call Number: 448.8 V81

Abstract: When expressed in *Spodoptera frugiperda* cells by a baculovirus vector, the hemagglutinin of fowl plague virus has been found to contain palmitic acid in covalent hydroxylamine-sensitive linkage, indicating that these cells have the capacity to acylate foreign proteins at cysteine residues. Centrifugation on sucrose density gradients and immune precipitation with conformation-specific antibodies were used to compare
Trimerization of the hemagglutinin in insect cells and in fowl plague virus-infected MDCK cells. Trimerization of the hemagglutinin was incomplete in insect cells, and the kinetics of this reaction were about three times slower than in vertebrate cells. Similarly, post-translational proteolytic cleavage occurred in insect cells with a half-time of 90 min, and a substantial fraction of the hemagglutinin persisted in uncleaved form. In contrast, hemagglutinin was almost completely cleaved in MDCK cells, and the half-time of cleavage was only 30 min. The data indicate that in insect cells trimerization and, as a result, the subsequent processing steps of the hemagglutinin, are retarded and less efficient. The possible roles of aberrant glycosylation, acidic milieu, and lack of other influenza virus proteins in hemagglutinin trimerization are discussed.

Descriptors: hemagglutinins viral metabolism, influenza A virus avian metabolism, acylation, antibodies, monoclonal, biological transport, cell line, centrifugation, density gradient, electrophoresis, polyacrylamide gel, eukaryotic cells, fatty acids metabolism, avian growth and development, kinetics, moths cytology, polymers, precipitin tests, protein processing, post translational.


NAL Call Number: 448.8 P942

Abstract: Recombination of a human influenza virus with an avian influenza virus produced a H2Nav2 recombinant with the antigenic properties analogous to those of avian influenza virus (H2Nav2) isolated from wild ducks in the Far East, USSR. Recombination of two avian influenza viruses yielded a recombinant H2N2, an antigenic analogues of influenza A/Singapore/1/57 (H2N2) virus which had started an epidemic of influenza in 1957.

Descriptors: antigens, viral genetics, influenza A virus genetics, recombination, genetic, animals, wild, crosses, genetic, ducks microbiology, hemagglutination inhibition tests, influenza A virus human genetics, neuraminidase antigens and inhibitors.


NAL Call Number: QR360.A1J6

Abstract: Nine rabbits were immunized with type A influenza virions and the epitope specificities of the secondary serum haemagglutination-inhibition (HI) antibody response were analysed with a panel of neutralizing monoclonal (MAb) antibody double escape mutants. Each of the latter was made by sequential selection using a MAb directed to an epitope of a discrete antigenic site, site A, site B or site D, of the haemagglutinin (HA). Thus the epitope reactivity of the escape mutants was represented as A+ B- D-, A- B+ D- and A- B- D+. The HI antibody response of all antisera was biased to the site B epitope. In 9/12 antisera, obtained from seven rabbits immunized with whole virions, the site B epitope was predominant, representing 65-82% of the total HI antibody. The restriction of HI antibody was unaffected by strain of rabbit, route of inoculation (intravenous or subcutaneous), use of Freund's adjuvant, and up to four immunizing injections. In 3/7 rabbits immunized with whole virus, there was a HI antibody response to the HC2 (site A) or HC10 (site D) epitope, but not both, of equal magnitude to the site B epitope. The HI antibody response in one of the rabbits (#40) became more biased to the site B epitope between the third and fourth immunizing doses. Two further rabbits were immunized with virions which had been partially digested with bromelain and then purified from free HA. Both of these made equal HI antibody responses to the site B epitope and the site D epitope, possibly because their remaining HA spikes were better exposed. Overall, these data demonstrate an unexpected degree of restriction in the production of biologically relevant antibody, such that some rabbits (e.g. #45) mount an HI antibody response which is essentially epitope-specific. Implications for epitope specificity of HI antibody stimulated by human influenza vaccines, and also for the generation of antigenic drift variants are discussed. The reason for the non-responsiveness of the immune system to the many other HI epitopes of the HA is not known.

Descriptors: antibodies, viral immunology, antibody specificity immunology, antigens, viral immunology, epitopes immunology, influenza A virus avian immunology, antibodies, viral blood, binding sites, cell line, chick embryo, dogs, hemagglutination inhibition tests, immunization, neutralization tests, rabbits, virion

NAL Call Number: QR360.A1J6

Abstract: It is not fully understood how antigenic drift of the haemagglutinin of type A influenza virus in man occurs in the presence of the expected polyclonal antibody response to the five antigenic sites, A to E. Here we show that 12% (11/92) of sera from mice which had mounted a secondary immune response to inactivated influenza virus were able to select escape mutants. No escape mutant was selected with serum from nonimmunized mice (0/65). Selection required only a single passage, and escape mutants were identified by their reaction with monoclonal antibodies (MAbs); all but one had altered reactivity at site A.

Most of the site A escape mutants (7/10) were conventional in character and did not react in haemagglutination-inhibition (HI) or neutralization assays with the identifying MAb. The HA genes of three of these were part sequenced and had a predicted single amino acid substitution (Gly-144-->Glu) in site A. The other escape mutants (3/10) had a small (2-fold) reduction in HI and neutralization to the site A MAb, but no amino acid substitution in site A. The final mutant was a conventional site B escape mutant. To model antiserum which selected escape mutants, we constructed 'pseudo-immune sera' using mixtures of two neutralizing MAbs in which the first MAb was held at a constant high concentration (1000 HIU/ml). Escape mutants could be selected to the first MAb when the titre of the second MAb was reduced to a low but still inhibiting concentration (1 to 3 HIU/ml). Mixtures of three MAbs also selected escape mutants with similar facility provided that the second and third MAbs were reduced to a similar low concentration. Thus it is possible that the ability of an antiserum to select escape mutants is due to the neutralizing antibody response being biased to an epitope/cross-reacting epitopes within a single antigenic site. However, when escape mutants were reacted in HI assay with their selecting antiserum, the maximum difference from the titre with wt virus was 75%. The findings of this study may be relevant to the understanding of antigenic drift in type A human influenza virus, and to immune-driven antigenic variation in other virus infections.

Descriptors: antibodies, monoclonal immunology, antigenic variation genetics, hemagglutinins viral genetics, immune sera, influenza A virus avian immunology, point mutation, antibodies, viral blood, DNA mutational analysis, epitopes analysis, gene frequency genetics, genes, structural, viral genetics, hemagglutination inhibition tests, hemagglutinin glycoproteins, influenza virus, hemagglutinin viral immunology, immunization, avian genetics, mice, mice inbred BALB c, mice, inbred c3h, neutralization tests, selection genetics, viral envelope proteins genetics, viral envelope proteins immunology.


NAL Call Number: 448.8 V81

Abstract: We have discovered a new type of abortive replication in Vero cells infected with fowl plague virus. In these cells there is an enhanced splicing of the colinear mRNAs of segment 7 and presumably also of segment 8, leading to an extreme overproduction of M2 and NS2 proteins. The cleavage of the hemagglutinin (HA) into HA1 and HA2 and the processing of its carbohydrate side chains are markedly retarded and incomplete. Although some of the HA is incorporated into the plasma membrane, leading to a positive hemadsorption, most of it accumulates in a discrete compartment close to the nuclear membrane, representing presumably the reticuloendothel and/or the Golgi network. Neuraminidase activity in Vero cells is extremely low. The nucleoprotein is normally released from nuclei late in infection. Very little infectious virus is released, and its spread is highly impeded.

Descriptors: gene expression regulation, viral, influenza A virus avian growth and development, vero cells microbiology, cultured cells, Cercopithecus aethiops, chick embryo, RNA, messenger metabolism, viral metabolism, time factors, viral proteins metabolism, virus replication.

Abstract: Ten avian type A influenza viruses consisting of seven waterfowl-origin, one pheasant-origin, and two turkey-origin viruses were evaluated for their pathogenicity potential after intravenous inoculation into domestic turkeys and mallard ducks (Anas platyrhynchos). The replicative abilities and tissue tropism properties of each virus isolate were examined in both species. The overall virus-isolation rate and histopathological lesion score were greater in the turkeys than in the ducks. The waterfowl-origin viruses caused more tissue damage in turkeys than in ducks but had a narrower tissue distribution range. The pheasant isolate was extremely pathogenic in turkeys but had limited distribution and little effect in ducks. The turkey isolates were more pathogenic in turkeys than in ducks. The pancreas was the most severely affected organ in turkeys, followed by kidney and liver. The spleen and bursa were the most commonly affected organs in ducks.

Descriptors: ducks microbiology, fowl plague microbiology, influenza A virus avian pathogenicity, turkeys microbiology, fowl plague pathology, avian isolation and purification, avian physiology, injections, intravenous, kidney microbiology, kidney pathology, organ specificity, pancreas microbiology, pancreas pathology, species specificity, spleen microbiology, spleen pathology, virus replication.


Abstract: Avian influenza virus (AIV) of waterfowl origin, A/Mallard/Ohio/184/86 (H5N1), was used to evaluate the effect of AIV infection on the functional capabilities of the immune system in mallard ducks. The three main arms of the immune system--humoral, cell-mediated, and cellular--were evaluated. The integrity of the humoral immune system after AIV infection was evaluated by measuring total immunoglobulin and IgG antibody production to sheep erythrocytes and Brucella abortus antigen using hemagglutination and microagglutination assays, respectively. Cell-mediated immunity was evaluated using mitogen/antigen stimulation assays, and by measuring the cutaneous basophilic hypersensitivity response to intradermal phytohemagglutinin-P inoculation. The cellular component of the immune response was evaluated using whole-blood chemiluminescence and bacterial clearance assays. Results showed that infection with this AIV isolate suppressed T-cell function and enhanced macrophage phagocytic activity.

Descriptors: bird diseases immunology, ducks, fowl plague immunology, basophils immunology, Escherichia coli infections complications, Escherichia coli infections immunology, Escherichia coli infections veterinary, fowl plague complications, fowl plague etiology, hypersensitivity, delayed, immunoglobulin g metabolism, immunoglobulins metabolism, influenza A virus avian immunology, avian isolation and purification, avian pathogenicity, lymphocyte activation, macrophages immunology, phagocytosis, T lymphocytes immunology.


Abstract: The pathogenicity potential of two H13N2 influenza viruses, one isolated from turkeys and the other isolated from surface water, was evaluated in turkeys, chickens, and mallard ducks (Anas platyrhynchos) after intracranial and oculonasal inoculation. Both isolates replicated in turkey pouls, causing depressed weight gain, morbidity and mortality; both also caused histopathological lesions, such as mild to severe pancreatitis, hepatitis, and nephritis in turkeys. These isolates replicated in mallard ducklings but not in chickens. There was depressed weight gain in ducklings given the H13N2 isolate from water. Neither isolate caused morbidity or mortality in ducklings or chicks after inoculation.

Descriptors: influenza A virus avian isolation and purification, turkeys microbiology, water microbiology, antibodies, monoclonal, chickens, cross reactions, ducks, fowl plague etiology, fowl plague pathology, avian immunology, avian pathogenicity, species specificity, virulence.

Abstract: Isolated intact influenza virus neuraminidase (NA) molecules of the N9 subtype have been found to possess hemagglutinin (HA) activity which, at equivalent protein concentration, was fourfold higher than that of isolated hemagglutinin molecules of the H3 subtype. The amino-terminal sequence of the N9 NA is the same as in neuraminidases of the eight other influenza A virus NA subtypes previously reported. Viruses possessing N9 NA therefore have two different HA activities and antibody to either HA or NA alone was incapable of inhibiting hemagglutination by the virus. However, antibody to the HA of an H1N9 virus neutralized its infectivity as effectively as it neutralized H1N1 or H1N2 viruses whose neuraminidases have no HA activity. (Antibodies to N9 NA did not neutralize the infectivity of viruses with N9 neuraminidase). 2-deoxy-2,3-dehydro-N-acetyl-neuraminic acid inhibited N9 NA activity but had no effect on the HA activity of the isolated N9 NA. One interpretation of this result would be that the HA and NA activities are located in separate sites. Pronase-released N9 NA heads form crystals suitable for X-ray diffraction studies and preliminary data to 2.9 A establish the space group as cubic, I432 with cell dimension a = 184 A. Data extend to beyond 1.9 A resolution, and these will be collected in the future.

Descriptors: hemagglutinins viral, influenza A virus avian enzymology, neuraminidase isolation and purification, antibodies, monoclonal, antigen antibody complex, birds, hemagglutination tests, neuraminidase immunology, x-ray diffraction.

NAL Call Number: 448.8 V81

NAL Call Number: 472 N21
Descriptors: amantadine pharmacology, interferons pharmacology, orthomyxoviridae drug effects, chick embryo, cytopathogenic effect, viral, ethionine pharmacology, fluorouracil pharmacology, hemagglutination tests, influenza A virus avian drug effects, tissue culture, virus cultivation, virus inhibitors.

NAL Call Number: 448.8 P942
Descriptors: amantadine pharmacology, influenza A virus avian drug effects, chickens, cytopathogenic effect, viral.

NAL Call Number: 448.8 P942
Abstract: Experimental studies of the influence of bis-(N,N'-uracil-1-yl)-selenoxomethane (I) and sodium selenite (II) on influenza virus reproduction on pieces of chorioallantoic membrane, both alone and in combination with remantadine and ribavirin, were carried out. The antiviral effects of both preparations were found to be enhanced in combination with effective and ineffective remantadine concentrations, whereas with ribavirin the additive effect was observed only in combination of the former preparation with ribavirin effective concentration. Combination of ribavirin with sodium selenite did not enhance the antiviral effect of the latter even when the effective concentration of nucleoside was used.
Descriptors: antimetabolites pharmacology, antiviral agents pharmacology, influenza A virus avian drug effects, organometallic compounds pharmacology, organoselenium compounds, uracil analogs and derivatives, chick embryo, drug synergism, fluorouracil pharmacology, avian physiology, ribavirin pharmacology, rimantadine pharmacology, selenious acid, selenium pharmacology, uracil pharmacology, virus replication drug effects.

**NAL Call Number:** QR360.A1J6

**Abstract:** Antigenic relationships among the matrix proteins of influenza A viruses were analysed using a competitive radioimmunoassay technique. There were at least two antigenic determinants on the M protein of A/PR/8/34 virus. One antigenic determinant was shared by several influenza A viruses of human, avian, swine or equine origin, while the second determinant was not necessarily shared by all influenza viruses since it was not detected on the M protein of A/chicken/Germany/N/49 virus. In addition, the cross-reactive determinant(s) of the M protein of N virus was not equally represented in other influenza A virus subtypes.

**Descriptors:** influenza A virus human immunology, influenza A virus immunology, viral proteins immunology, cross reactions, epitopes, avian immunology, porcine immunology, radioimmunoassay, viral matrix proteins.


**NAL Call Number:** QH506.A1M62

**Abstract:** The inhibitory effects of oligonucleotide derivatives on the transcription of virus RNA in an in vitro system and synthesis of virus proteins was studied. Oligonucleotide derivatives d(T)3, d(T)4, d(T)8, d(T)10, d(CCAAACA), d(TCACCTCT), d(TTCCATT), d(AAATACTCT) and d(TGACCCTCTTCCCATT), that bear residues of ethidium, deuteroporphyrin and its complexes with Fe3+, hemin, cholesterol, deuterocholesterol, estrone and naphthoquinone at the 5’-end phosphate and/or at the 3’-end phosphate were studied. Unmodified oligonucleotides and their derivatives had a negligible effect on the synthesis of cellular proteins, but did inhibit the synthesis of influenza virus proteins. The majority of structural modifications increased the inhibitory effect of oligonucleotides. It was shown that the oligonucleotide derivatives carrying residues of porphyrin, quinone, ethidium, cholesterol, deuteroestrogens and estrone at concentrations near 10 mM inhibit virus development to 50-80%. A clear inhibitory effect (20-25%) of deuteroporphyrin, cholesterol and ethidium derivatives was revealed even at concentration 0.1 mM. The obtained results testified that the inhibition of influenza virus development is dependent on the interaction of oligonucleotide derivatives with the transcription complex proteins.

**Descriptors:** influenza A virus avian genetics, oligonucleotides pharmacology, RNA viral genetics, transcription, genetic drug effects, autoradiography, base sequence, cultured cells, chick embryo, genes viral, molecular sequence data, oligonucleotides chemistry, viral drug effects, viral proteins metabolism.


**NAL Call Number:** 41.8 Av5

**Abstract:** Sequence analysis of the hemagglutinin (HA) gene of five Korean H9N2 avian influenza virus (AIV) isolates showed that these viruses were closely related and possibly came from the same source. Phylogenetic analysis of the HA1 subunit of H9 subtype isolates revealed that Korean AIV isolates were different from isolates from the poultry markets in Hong Kong in 1997. None of the Korean AIVs had multiple basic amino acids at the HA cleavage site that confer high pathogenicity to some H5 and H7 AIVs. Phylogenetic analysis of the nucleoprotein and matrix gene demonstrated that Korean isolates cluster with Eurasian origin AIVs. The pathogenic potential of one of the isolates (MS96) was assessed after several passages in 14-day-old embryonated chicken eggs (ECE). Fourteen-day-old ECE derivatives of MS96 showed increased HA titer and embryo mortality in eggs; this was apparent after the third passage in 14-day-old ECE. Sequence analysis of the cleavage site of MS96 after the third and tenth passages in 14-day-old ECE revealed no changes in the amino acid sequence. The pathogenicity of MS96 after the tenth passage in 14-day-old eggs (MS96p10(ECE14)) was tested with 4-wk-old specific-pathogen-free chickens. The 14-day-old derivative, MS96p10(ECE14), showed wider tissue tropism and induced more severe clinical signs than the parent virus. Furthermore, after intranasal inoculation of 86-wk-old broiler breeders and 30-
wk-old layers, the MS96p10(ECE14) derivative induced more severe signs of depression than the parent virus as well as a transient drop in egg production.

Descriptors: chick embryo virology, fowl plague physiopathology, hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian genetics, avian pathogenicity, amino acid sequence, Asia, chickens, disease progression, genes, structural, viral, avian classification, Korea, molecular sequence data, phylogeny, reverse transcriptase polymerase chain reaction, sequence alignment, specific pathogen free organisms, virulence genetics.


NAL Call Number: QR355.J6

Abstract: Avian influenza (AI) viruses are endemic in wild birds and if transmitted to poultry can cause serious economic losses. In the study of AI, the quantitation of virus shed from infected birds is valuable in pathogenesis studies and to determine the effectiveness of vaccines, and is performed routinely by cultivation of virus containing samples using embryonating chicken eggs (ECE) and expressed by 50% egg infectious dose (EID(50)). Although, this assay is accurate and is the standard test for infectious virus titration, the method is laborious, requires a large number of ECE, and takes at least 7 days to determine results. In this study, a one-tube hydrolysis fluorescent probe based real-time RT-PCR (RRT-PCR) was applied for the quantitation of AI virus and compared with conventional virus titration method. A strong positive correlation was observed between the amount of RNA determined by quantitative RRT-PCR and the EID(50)s determined by conventional methods. This RRT-PCR test was further applied in the study of competitive replication of co-infected H5 and H7 subtype viruses in chickens. Using hemagglutinin subtype specific probes, we were able to determine the amount of individual subtype virus, which could not have easily been done with conventional methods. This RRT-PCR based quantitation of AI virus, which is specific, sensitive, easy to perform, and rapid, will be useful for virological, pathogenesis, and protection studies.

Descriptors: influenza A virus, avian physiology, avian classification, avian genetics, avian isolation and purification, poultry, sensitivity and specificity, poultry diseases virology, reverse transcriptase polymerase chain reaction methods, virus replication, fluorescent dyes, hemagglutinin glycoproteins, influenza virus analysis.


NAL Call Number: 448.8 P942

Abstract: The extent of inhibition of transcription realized in vitro by fowl plague virus (FPV) ribonucleoprotein (RNP) upon the addition of M protein isolated from FPV virions does not depend on nonionic detergent concentration in the reaction medium but does depend greatly on NaCl concentration. The highest inhibition of transcription is observed at a low ionic strength (0.02 M NaCl); inhibition is completely eliminated by increasing NaCl concentration to 0.3 M. When M protein isolated from FPV virions with ts mutation of M protein is added to RNP, addition to the system of 0.3 M NaCl decreases transcription inhibition but does not eliminate it completely.

Descriptors: influenza A virus avian metabolism, mutation, ribonucleoproteins metabolism, viral proteins metabolism, DNA directed RNA polymerases metabolism, detergents pharmacology, dose response relationship, drug, drug interactions, avian drug effects, polyethylene glycols pharmacology, ribonucleoproteins antagonists and inhibitors, sodium chloride pharmacology, transcription, genetic drug effects, viral matrix proteins.


NAL Call Number: 448.3 AC85

Abstract: Acidic chloroform-methanol soluble proteins possessing hydrophobic properties and capable of
inhibiting in vitro transcriptase activity of influenza virus RNP were detected in native and partially purified human leukocyte interferon (IFN) preparations. Purification of IFN resulted in the removal of at least a portion of such proteins; however, no proteins have been found in highly-purified IFN preparations.

**Descriptors:** interferon type I analysis, proteins isolation and purification, chloroform, cytopathogenic effect, viral, DNA directed RNA polymerases antagonists and inhibitors, hydrogen-ion concentration, influenza A virus avian enzymology, interferon type I isolation and purification, methanol, proteins analysis, proteins pharmacology, ribonucleoproteins metabolism, solubility.


**Descriptors:** body fluids analysis, influenza A virus avian metabolism, viral proteins biosynthesis, body fluids metabolism, chick embryo, viral proteins analysis.


**NAL Call Number:** QR180.3.D4

**Abstract:** An influenza pandemic could arise unexpectedly with rapid spread across the world. The efficiency of production of a vaccine and the ability to administer it widely will be among the most important factors in the ability to protect public health. The current process for producing inactivated or live attenuated influenza vaccines requires six to nine months. That reduces considerably the likelihood that the vaccine will be available during the first wave of the pandemic. Therefore, a key element of preparedness is to optimize the production process and to reduce the vaccine development time. During the 1997 H5N1 outbreak in Hong Kong, seed viruses were prepared for production of inactivated and live-attenuated vaccines. We used the cold-adapted A/Ann Arbor/6/60 as the donor virus to generate live attenuated vaccines containing genetically modified HA and NA genes from H5N1 influenza viruses. These reassortants were shown to be safe and protective in animal models. This study indicates that production of live attenuated avian influenza vaccines is feasible and that development of a library of reassortants containing different subtype HA and NA genes may reduce the vaccine preparation time for future influenza pandemics.

**Descriptors:** antigens, viral immunology, influenza prevention and control, influenza A virus avian immunology, influenza epidemiology, influenza vaccine administration and dosage.


**Descriptors:** tissue distribution, brain, kidneys, liver, muscles, pancreas, spleen, avian influenza virus, fowl plague virus, experimental infection, virus shedding, chickens.


**NAL Call Number:** QR375.V6

**Abstract:** The hemagglutinin (HA) protein of influenza virus binds to terminal sialic acid residues present on cell surface glycoproteins and glycolipids. The specific amino acids involved in this interaction have been identified for a H3 subtype HA from the human non-pathogenic virus, A/Aichi/2/68, by both crystallographic and mutagenesis studies. We were interested to examine the receptor-binding pocket of a H7 subtype protein from the avian pathogenic virus A/FPV/Rostock/34. Accordingly, we made amino acid substitutions at six conserved residues (Y88, T126, H174, E181, L185, and G219), suggested by comparison with the receptor-binding pocket of the H3 protein, and analyzed the resulting proteins using pseudotyped retroviral vectors. The use of these vectors enabled us to quantitate both the ability of the mutant HA proteins to bind with receptor-expressing cells, and also to promote virus-cell fusion by measuring vector titer. Using this system, we identified a subset of mutants with impaired receptor-binding activity and a corresponding decrease in titer, but which retained the ability to induce syncytia in low pH cell-cell fusion assays. The most
severely affected mutants contained more than one substitution, with the triple mutant Y88F/E181Q/G219K being the most defective. These observations highlight the importance of multiple contact points for the interaction between sialic acid and HA.

Descriptors: hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian genetics, receptors, virus metabolism, 3T3 cells, amino acid sequence, amino acid substitution, binding sites, cell line, transformed, cell membrane metabolism, gene expression, genetic vectors, giant cells, hemagglutinin glycoproteins, influenza virus chemistry, hydrogen-ion concentration, avian metabolism, avian pathogenicity, avian physiology, membrane fusion, mice, molecular sequence data, mutagenesis, protein structure, tertiary, receptors, virus chemistry, retroviridae, sequence homology, amino acid, sialic acids chemistry, sialic acids metabolism, temperature.


Descriptors: antiviral agents pharmacology, influenza A virus avian drug effects, polyribosomes drug effects, RNA nucleotidyltransferases metabolism, RNA replicase metabolism, ribavirin pharmacology, ribonucleosides pharmacology, virus replication drug effects, cultured cells, chick embryo, depression, chemical, enzyme induction drug effects, RNA viral biosynthesis, viral proteins biosynthesis.


NAL Call Number: 448.8 P942

Abstract: Antigenic characteristics of influenza A virus M protein were studied by ELISA using a monospecific antiserum to M protein and monoclonal antibodies to the B4 and A7 antigenic determinants of M protein. The design of the test systems for M protein detection was based on the indirect and "sandwich" variants of ELISA as well as on the previously developed principle of blocking the indirect reaction. The latter variant of the test system had the highest specificity: 0.1–0.5 ng of specific protein. The high specificity of the method allows subtle antigenic differences of M protein within influenza A virus group to be detected. Comparative studies of remantadine-sensitive and resistant variants of the classic fowl plague virus showed the previously demonstrated significant differences in the physico-chemical properties of M protein of these variants to correlate with a marked antigenic divergence associated, in particular, with greater antigenicity of B4 epitope in M protein of remantadine-sensitive strains. The test system of ELISA blocking was found to be useful for M protein detection in virus-containing materials not subjected to purification and concentration (native allantoic fluids). The latter attests to the expedience of using ELISA in clinical diagnostic studies of influenza.

Descriptors: adamantane analogs and derivatives, antigens, viral analysis, glycoproteins analysis, influenza A virus analysis, rimantadine pharmacology, viral proteins analysis, enzyme linked immunosorbent assay, glycoproteins immunology, influenza A virus avian analysis, avian drug effects, avian immunology, influenza A virus drug effects, influenza A virus immunology, viral proteins immunology.


NAL Call Number: 448.8 P942

Abstract: Avian influenza A virus with H2 hemagglutinin has been adapted to mice for the first time. Alterations in the hemagglutinin of adapted variants of the virus as a result of adaptation to a new host are
described. Hemagglutinin of a highly virulent adapted variant differed from the parental avirulent strain by antigenic structure, electrophoretic mobility, and receptor activity during interactions with murine red cells.

Descriptors: adaptation, physiological, hemagglutinins viral metabolism, influenza A virus avian physiology, cultured cells, chick embryo, dogs, erythrocytes virology, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral chemistry, avian metabolism, avian pathogenicity, lethal dose 50, mice.


NAL Call Number: 448.3 AC85

Abstract: The protective properties of monoclonal antibody (MoAb) C179 directed to the stem region of haemagglutinin (HA) H2 that possessed fusion-inhibition and unique broad cross-neutralizing activities were examined in a mouse model. The MoAb efficiently protected mice against a lethal challenge with pneumovirulent human (H1) and avian (H2) strains of influenza A virus. Survival rates in mice that received intraperitoneally (i.p.) 1000 micrograms of the MoAb per mouse a day before the virus challenge were 90% for H1 and 100% for H2 strain. The dose of the MoAb of 100 micrograms per mouse significantly decreased mortality in mice. Moreover, the MoAb was also efficient in treatment of lethal bronchopneumonia caused by H2 influenza virus. The survival rate in mice that received 1000 micrograms of the MoAb per mouse 2 days after the virus challenge was 90%, while that in the control group was 30% only. These results indicate that the MoAb was effective in protection of animals against lethal influenza A infection without significant difference between H1 and H2 subtypes. The MoAb exerted significant effect in treatment of mice infected with H2 influenza virus. Thus, these data allow to suggest that the stem region of HA might be a potential target for prevention of influenza virus infection and antiviral therapy.

Descriptors: antibodies, monoclonal therapeutic use, bronchopneumonia therapy, hemagglutinins viral immunology, influenza therapy, influenza A virus avian immunology, human immunology, pneumonia, viral therapy, antibodies, monoclonal immunology, bronchopneumonia prevention and control, dose response relationship, immunologic, influenza prevention and control, mice, pneumonia, viral prevention and control, random allocation, time factors.


NAL Call Number: QR180.C62

Descriptors: hemagglutinins viral isolation and purification, influenza A virus avian isolation and purification, turkeys microbiology, hemagglutinins viral immunology, avian immunology, Israel.


NAL Call Number: 448.3 Ar23

Descriptors: hemagglutinins viral analysis, influenza A virus avian immunology, neuraminidase analysis, Newcastle disease virus immunology, surface active agents pharmacology, cell fractionation, cell nucleus, cultured cells, centrifugation, density gradient, chick embryo, avian enzymology, avian growth and development, microsomes, mitochondria, Newcastle disease virus enzymology, Newcastle disease virus growth and development, ribosomes, subcellular fractions analysis.

Lipkind, M., Y. Weisman, and E. Shihmanter (1987). The isolation of influenza virus from chickens in Israel and studies on its antigenic relationships with other native isolates of the same antigenicity by means of monoclonal antibodies. Comparative Immunology, Microbiology and Infectious Diseases 10(2): 133-9. ISSN: 0147-9571.

NAL Call Number: QR180.C62

Abstract: A hemagglutinating (HA) agent isolated from an outbreak of a respiratory disease in a kibbutz broiler farm was identified as influenza virus A/chicken/Degania, Israel/80(H7N2). Investigation using a panel of 5 monoclonal antibodies against H7 antigenic subtype has shown substantial difference of the isolate from
the other H7-containing influenza viruses isolated in Israel. Antigenic relationships between the native H7-containing strains revealed by means of the monoclonal antibodies led to re-evaluation of the suggested views on local epizootiology and interspecies transfer of avian influenza.

Descriptors: antigens, viral analysis, chickens, fowl plague microbiology, influenza A virus avian immunology, antibodies, monoclonal immunology, chick embryo, hemagglutination inhibition tests, avian isolation and purification, Israel.


NAL Call Number: QR180.3.D4

Abstract: Neuraminidase (Nase) thermostability and sensitivity to pH treatment as well as specific enzymatic activity (Nase activity per 1 HA unit) were determined in two groups of animal influenza virus strains containing equine 1 and equine 2 Nase subtypes, respectively (A/equine/Prague/56 (Heq1 Neq1), A/equine/Cambridge/63 (Heq1 Neq1), A/FPV/Dutch/34 (Hav1 Neq1), A/chicken/Germany "N" (Hav2 Neq1), in one group, and A/equine/Miami/1/63 (Heq2 Neq2), A/turkey/Canada/63 (Hav6 Neq2), A/duck/Ukraine/1/63 (Hav7 Neq2), in the other group). Nase of all the strains used was thermostable when heated at pH 4.5. Nase of Neq1 subtype irrespective of strain containing it was thermostable when heated both at pH 6.5 and 8.1 and sensitive to pH 4.5 treatment as such (without heating). Inversely, Nase of Neq2 antigenic subtype irrespective of the strain containing it, was thermostable when heated at pH 6.5 AND 8.1 and resistant to the treatment of pH 4.5. Specific enzymatic activity was considerably higher in all the strains containing Neq2 as compared to Neq1-containing strains (4-6 times as much). The results suggest that thermostability and pH sensitivity of equine Nases of both antigenic subtypes, as well as their specific activities, do not depend on the sort of HA which is coupled with enzyme subunits at viral envelope, but attributed rather to properties of the subunits themselves, such as glycoprotein entities. The data concerning specific activities may suggest that in the case of various combinations of Nase subunits with different HA subunits the amount of enzyme per virion is of the same order.

Descriptors: influenza A virus immunology, neuraminidase immunology, antigens, viral, heat, hemagglutinins viral, hydrogen-ion concentration, influenza A virus avian immunology, influenza A virus enzymology, influenza A virus genetics, recombination, genetic.


NAL Call Number: QR180.C62

Abstract: Twenty one N2 neuraminidase (NA)-containing viruses isolated in Israel from different avian hosts during 1971-1984 were studied comparatively by means of the panel of 7 monoclonal antibodies (MAB) against A/Guiyang/57(H2N2) virus. Fifteen from the 21 viruses were studied in comprehensive cross reaction NA inhibition (NI) tests with the corresponding polyclonal antisera. The principal result of the studies is that all the isolates can be distributed into two main groups. The 1st group includes the majority of the isolates whose NA shows close relatedness to the "early" (1957 type) N2 NA by NI tests with polyclonal antisera, and demonstrates remarkable stability in the NI tests by reacting with the same 6 from 7 MABs of the panel. The 2nd group does not show any special kinship to either "early" or "late" (1968 type) N2 when analyzed with polyclonal antisera and demonstrates heterogeneity by the analysis with the MABs. A hypothetical explanation of the phenomenon of co-circulation in the local avian reservoir of viral strains displaying either remarkable stability or wide heterogeneity of their NAs is suggested. In accordance with it, the viruses with "stable" ("conservative") N2 NA did not leave the avian reservoir and, hence, did not drift because of very low antibody "selection pressure". Contrary to it, the viruses with heterogeneous N2 NA had been circulating in the human (mammalian) reservoir during various periods before their transfer into the avian reservoir; they drifted accordingly and, being then isolated from birds and designated as "avian" viruses, demonstrate heterogeneity of their NAs which is typical for human viruses.

Descriptors: enzymology, immune system, infection, microbiology, nervous system, veterinary medicine, antigenicity viral ecology.

NAL Call Number: 448.3 AC85

**Abstract:** By recombination of ts mutants of fowl plague virus belonging to different complementation groups with two cold-adapted variants of human influenza virus, the number and gene localization of ts mutations occurring in these variants was determined. In the course of passaging of human influenza virus at lowered temperature, the number of genes with ts mutations increased.

**Descriptors:** genes viral, influenza A virus avian genetics, human genetics, cold, genetic complementation test, mutation, recombination, genetic.


NAL Call Number: 396.8 An84

**Descriptors:** antibody formation drug effects, interferons pharmacology, orthomyxoviridae infections immunology, poultry diseases immunology, chick embryo, hemagglutination inhibition tests, influenza A virus avian immunology.


NAL Call Number: 448.3 Ac83

**Abstract:** In order to explore the genetic mutations of the hemagglutinin(HA) gene and the law of molecular epidemiology of H9 subtype avian influenza viruses in China, 23 H9 subtype avian influenza viruses(AIVs) were isolated from 12 provinces of China in recent years. Their nucleotide sequences of cDNA of HA gene were determined by RT-PCR and sequencing. Their nucleotide and putative amino acid sequences homology was compared. The results showed that their nucleotide sequence homology was from 94.1% to 100% and that amino acid sequence homology was 95.4% to 100%. The sequences of the HA gene of these isolates were analyzed and compared with that of another 8 isolates from reference. The similarly indicated that HK170499 isolated from Hong Kong was close to the 2 isolates of Japan. And of the 31 isolates with complete HA gene sequences there were 5 isolates, HA gene of which were loss of one potelltial glycosylation site, which were CKGS199, CTKJ196, CTK296, CKSH300 and CKBJ197. Then 1098 nucleotide regions (bases 55 to 1,152) of HA gene of 23 isolates in this study were analyzed phylogenetically and compared with sequences from 31 H9 subtype viruses available in the GenBank database. Although considerable variation at the cleavage sites of the different viruses was observed, giving 10 different amino acid motifs, none had multiple basic amino acids that correlate with highly pathogenic avian influenza (HPAI) isolates. Examination of amino acid sequences involved in receptor binding site(RBS) revealed that the amino acid residue at position 191 characteristically distributed in the 54 isolates, that is, this amino acid residue of the isolates of mainland China and several Hong Kong strains was Asn(N) and that of the others was His(H). And the 141 143 amino acid residues, involved in forming the potential glycosylation sites, had the similiary characteristic distribution with the 191aa position. The isolates with Asn-191. excluding CKBJ197, had NVS in the position 141aa143aa, meanwhile those with His-191 had NVT. Twenty-six mainland China isolates was genetically in Eurasian lineage but did not show distinctly geographical and temporal relationship. It is concluded that in recent years H9N2 subtype AIV, circulating in chicken flocks of mainland China, may have a common origini. These findings provides importan basis for establishment of scientifically preventive measurements to control H9 subtype avian influenza.

**Descriptors:** genes viral, hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian genetics, phylogeny, amino acid sequence, base sequence, chickens, China, DNA, complementary genetics, fowl plague virology, avian classification, avian isolation and purification, sequence homology.


**Descriptors:** vaccination, avian influenza virus, genetic mutations, poultry.
NAL Call Number: 41.8 Av5  
**Abstract:** The complete coding region of hemagglutinin genes from 26 influenza A viruses of H9N2 subtype isolated from chicken flocks in China during 1996-2001 was amplified and sequenced. Sequence analysis and phylogenetic studies of H9N2 subtype viruses on the basis of data of 26 viruses in this study and 71 selected strains available in the GenBank were conducted. The results revealed that all the mainland China isolates showed high homology (94.1%-100%) and were assigned to a special sublineage in the major Eurasian lineage, in contrast to the high heterogeneity of Hong Kong SAR isolates. All the 29 mainland China isolates and six Hong Kong SAR strains also had the following common characteristics: sharing the same sequence of proteolytic cleavage site with one additional basic amino acid, RSSR, with only two exceptions; having the same amino acid motif of the receptor-binding site, YWTNV/ALY; 23 of 28 isolates bearing seven potential glycosylation sites and the remaining five having six; and sharing characteristic deduced amino acid residues Asn-183 at the receptor-binding site and Ser-130 at the potential glycosylation site. We concluded that the H9N2 subtype influenza viruses circulating in chicken flocks in China since the 1990s and Ck/HK/G9/97-like viruses isolated in Hong Kong SAR should have a common origin, whereas Qu/HK/G1/97-like viruses including human strains isolated in Hong Kong SAR might originate from other places. The available evidence also suggests that the H9N2 viruses of special lineage themselves and factors prone to secondary infections may contribute to the widespread and dominant distribution of viruses of this subtype in chicken flocks in China and other Asian countries.  
**Descriptors:** infection, molecular genetics, systematics and taxonomy, virology, phylogenetic analysis mathematical and computer techniques, reverse transcriptase polymerase chain reaction, genetic techniques, laboratory techniques, sequence analysis, sequence homology.

NAL Call Number: QH434.V57  
**Abstract:** Genetic analysis indicated that the pandemic influenza strains derived from wild aquatic birds harbor viruses of 15 hemagglutinin (HA) and 9 neuraminidase (NA) antigenic subtypes. Surveillance studies have shown that H9N2 subtype viruses are worldwide in domestic poultry and could infect mammalian species, including humans. Here, we genetically analyzed the HA and NA genes of five H9N2 viruses isolated from the migratory ducks in Hokkaido, Japan, the flyway of migration from Siberia during 1997-2000. The results showed that HA and NA genes of these viruses belong to the same lineages, respectively. Compared with those of A/quail/Hong Kong/G1/97-like and A/duck/Hong Kong/Y280/97-like viruses, HA and NA of the migratory duck isolates had a close relationship with those of H9N2 viruses isolated from the chicken in Korea, indicating that the Korea H9N2 viruses might be derived from the migratory ducks. The NA genes of the five isolates were located in the same cluster as those of N2 viruses, which had caused a human pandemic in 1968, indicating that the NA genes of the previous pandemic strains are still circulating in waterfowl reservoirs. The present results further emphasize the importance of carrying out molecular epidemiological surveillance of H9N2 viruses in wild ducks to obtain more information for the future human influenza pandemics preparedness.  
**Descriptors:** ducks virology, influenza A virus avian genetics, amino acid sequence, base sequence, binding sites genetics, DNA, viral genetics, disease reservoirs, epidemiology, molecular, genes viral, hemagglutinins viral genetics, avian enzymology, avian immunology, avian isolation and purification, Japan, neuraminidase genetics, phylogeny.

NAL Call Number: QR355.P5  
**Descriptors:** Western blot, cloning, influenza virus.

**internal protein genes of H2 influenza virus in migratory ducks from North America to Eurasia.** *Virus Genes* 29(1): 81-6. ISSN: 0920-8569.

**NAL Call Number:** QH434.V57

**Abstract:** H2 influenza virus caused a pandemic in 1957 and has the possibility to cause outbreaks in the future. To assess the evolutionary characteristics of H2 influenza viruses isolated from migratory ducks that congregate in Hokkaido, Japan, on their flyway of migration from Siberia in 2001, we investigated the phylogenetic relationships among these viruses and avian and human viruses described previously. Phylogenetic analysis showed that the PB2 gene of Dk/Hokkaido/107/01 (H2N3) and the PA gene of Dk/Hokkaido/95/01 (H2N2) belonged to the American lineage of avian virus and that the other genes of the isolates belonged to the Eurasian lineage. These results indicate that the internal protein genes might be transmitted from American to Eurasian avian host. Thus, it is further confirmed that interregional transmission of influenza viruses occurred between the North American and Eurasian birds. The fact that reassortants could be generated in the migratory ducks between North American and Eurasian avian virus lineage further stresses the importance of global surveillance among the migratory ducks.

**Descriptors:** ducks virology, emigration and immigration, influenza A virus, avian genetics, influenza, avian virology, viral proteins genetics, Asia, Europe, avian influenza A virus classification, molecular sequence data, North America, phylogeny, sequence analysis, DNA.


**NAL Call Number:** 442.8 B5242

**Abstract:** The redox properties of some myxoviruses [Fowl plaque virus strain Rostock (FPV), New Castle Disease virus strain Italy (NDV), B/Hong Kong, A/Port Chalmers, A/Victoria, A/Scotland, and A/Fort Dir] and electron microscopic studies as well as by the determination of the hemagglutination (HA) titer (antigen efficiency). The results have shown that viruses decrease the spin concentration of Cu2+ by acting as a reducing species (electron donor) which will result in the inactivation (oxidation) of the virus. Addition of an oxidizing substance, such as H2O2, to a virus suspension also leads to an oxidation of the viruses, and, thus, to their inability to reduce Cu2+. This result is confirmed by the decrease of the HA titer of viruses with increasing Cu2+ concentrations. H2O2 could not be applied for the HA titer test since it interacts with the erythrocytes of the chicken blood used for this determination. Therefore, another oxidizing substance (oxidized glutathione, GSS) was selected which exhibited a slightly less pronounced effect than Cu2+. Since reduced glutathione (GSH) exerts a similar but less pronounced effect than GSS, it might be concluded that viruses have a redox system of their own and act as reducing or oxidizing substance depending on the biological receptor system. Electron microscopic studies confirm this hypothesis. As can be seen by the electron micrographs, increasing concentrations of either Cu2+, GSS, H2O2, KMnO4, or GSH will, finally, result in a complete destruction of the virus. Because of structural similarities it might be assumed that other types of viruses behave very similarly.

**Descriptors:** influenza A virus metabolism, Newcastle disease virus metabolism, copper, electron spin resonance spectroscopy, glutathione, hemagglutination, viral, avian metabolism, avian ultrastructure, human metabolism, human ultrastructure, Newcastle disease virus ultrastructure, oxidation reduction, peroxides, potassium permanganate, time factors.


**NAL Call Number:** 448.8 V81

**Descriptors:** endoplasmic reticulum metabolism, hemagglutinin viral immunology, influenza A virus avian metabolism, viral proteins metabolism, carbohydrates metabolism, cell line, hemagglutination, viral, avian genetics, mutation, neuraminidase metabolism, temperature.


**NAL Call Number:** QR360.A1J6

**Abstract:** Synthesis and processing of the envelope proteins of influenza A virus (fowl plague virus) have been analysed in BHK, HeLa and L cells, in which the virus undergoes abortive replication and does not
form virus particles, and in the productive chick embryo fibroblast system. In abortive infection, synthesis of the M protein is specifically inhibited. The extent of this defect varies depending on the host cell and the amount of virus particles formed closely reflects the amount of M synthesized. Cell fractionation experiments demonstrated that the haemagglutinin glycoprotein HA is synthesized in abortive as well as in productive cells at the rough endoplasmic reticulum, that it migrates via smooth internal membranes to the plasma membrane and that it is cleaved by proteolysis into fragments HA1 and HA2 in the course of migration. Immune electron microscopy using monospecific antibodies against haemagglutinin and neuraminidase showed that both glycoproteins are exposed at the cell surface. Thus, synthesis and processing of the virus glycoproteins does not depend on the formation of the M protein. However, the M protein appears to be necessary for budding and thus for particle formation.

Descriptors: influenza A virus avian growth and development, viral proteins biosynthesis, cell line, cell membrane analysis, cultured cells, endoplasmic reticulum metabolism, glycoproteins biosynthesis, hemagglutinins viral analysis, neuraminidase biosynthesis, viral proteins analysis.

NAL Call Number: QR360.A1J6
Descriptors: cell line, influenza A virus avian growth and development, mutation, cell division, DNA biosynthesis, hamsters, avian metabolism, ovary, peptide synthesis, temperature, viral proteins biosynthesis, virus replication.

NAL Call Number: QP501.B64
Descriptors: chick embryo metabolism, influenza A virus avian metabolism, avian radiation effects, orthomyxoviridae infections metabolism, proteins biosynthesis, depression, chemical, interferons biosynthesis, RNA viral biosynthesis, ultraviolet rays, viral proteins biosynthesis, virus replication drug effects.

NAL Call Number: QR1.M54
Descriptors: cycloheximide pharmacology, dactinomycin pharmacology, influenza A virus avian radiation effects, interferons biosynthesis, poly I C pharmacology, puromycin pharmacology, reoviridae, chick embryo, radiation effects, tissue culture, ultraviolet rays.

NAL Call Number: QR360.A1J6
Descriptors: influenza A virus avian metabolism, proteins biosynthesis, carbon isotopes, chick embryo, cycloheximide pharmacology, dactinomycin pharmacology, avian drug effects, avian radiation effects, interferons pharmacology, phenylalanine pharmacology, puromycin pharmacology, RNA biosynthesis, RNA viral biosynthesis, radiation effects, time factors, tritium, ultraviolet rays, uridine metabolism, valine metabolism, virus cultivation.

NAL Call Number: 448.3 Ar23
Descriptors: amantadine pharmacology, influenza A virus avian drug effects, RNA viral antagonists and inhibitors, carbon isotopes, cultured cells drug effects, cultured cells metabolism, chick embryo, cycloheximide pharmacology, dactinomycin pharmacology, depression, chemical, electrophoresis, disc, avian growth and development, avian metabolism, avian radiation effects, interferons biosynthesis, proteins biosynthesis, RNA analysis, RNA biosynthesis, viral biosynthesis, radiation effects, time factors, tritium, ultraviolet rays, uridine metabolism, virus replication drug effects.

**NAL Call Number:** QR1.I57  
**Descriptors:** antibodies, viral analysis, hemagglutinins viral immunology, influenza A virus avian immunology, orthomyxoviridae infections immunology, ducks immunology, ferrets immunology, hemagglutination inhibition tests, avian physiology, mice, mice inbred BALB c immunology, T lymphocytes, cytotoxic immunology, virus replication.


**NAL Call Number:** 41.8 Av5  
**Abstract:** The H7N2 subtype of avian influenza virus (AIV) field isolate (H7N2/chicken/PA/3779-2/97), which caused the 1997-98 AIV outbreak in Pennsylvania, was evaluated for its infectivity, length of infection, and immune response in specific-pathogen-free (SPF) chickens. The composite findings of three clinical trials with various concentrations of virus indicated that this H7N2 subtype contained minimal pathogenicity for chickens. The concentration of the virus in the inoculum proved critical in the establishment of a productive infection in a chicken. Seven-day-old SPF chickens were not infected when inoculated with $10^{0.7-2.0}$ mean embryo lethal dose (ELD50) of the H7N2 virus per bird. At this dose level, the immune response to this virus was not detected by the hemagglutination-inhibition (HI) test. Nonetheless, chickens at ages of 5 and 23 wk old tested were successfully infected when exposed to $10^{4.7-5.7}$ ELD50 of H7N2 infectious doses per bird by various routes of administration and also by direct contact. Infected birds started shedding virus as early as 2 days postinoculation, and the period of virus shedding occurred mostly within 1 or 2 wk postinoculation (WPI). This H7N2 subtype of AIV induced a measurable immune response in all birds within 2 wk after virus exposure. Antibody titers were associated with AIV infectious doses and age of exposure of birds. Challenge of these infected birds with the same H7N2 virus at 5 and 10 WPI indicated the infective virus was recoverable from cloacal swabs at 3 days postchallenge and disappeared thereafter. In these challenged birds, the antibody levels as measured by the HI test spiked within 1-2 wk.

**Descriptors:** antibodies, viral analysis, chickens virology, influenza A virus, avian pathogenicity, avian virology, poultry diseases virology, antibody formation, cloaca virology, hemagglutination inhibition tests methods, hemagglutination inhibition tests veterinary, immunophenotyping, avian immunology, avian isolation and purification, avian immunology, poultry diseases immunology, specific pathogen free organisms, virus shedding.


**NAL Call Number:** S19.Y36  
**Descriptors:** amino acid, complementary DNA, hemagglutinins, strains, avian influenza virus, China.


**NAL Call Number:** 41.8 Av5  
**Abstract:** The virulent avian influenza virus A/Ty/Ont/7732/66 (H5N9) (Ty/Ont) causes a rapid destruction of lymphoid cells in infected birds. Avian macrophage cell lines, HD11 and MQ-NCSU, support productive replication of Ty/Ont and other influenza viruses. Therefore, the ability of these cell lines to produce nitric oxide (NO), a potentially cytotoxic mediator, in response to infection with Ty/Ont was examined. Although treatment with bacterial lipopolysaccharides (LPS) resulted in high NO levels, infection of macrophages with Ty/Ont resulted in NO levels lower than NO levels in untreated cells. Furthermore, Ty/Ont was able to inhibit the positive response to LPS in cultures simultaneously treated with LPS and virus. However, inactivated influenza virus did not exhibit this inhibitory effect. Different strains of influenza virus varied in their ability to inhibit NO production by the macrophages; this may be related to the level of virus replication in these cells. These data suggest that the ability of the avian macrophage to activate the NO synthesis pathway is
seriously impaired by infection with virulent influenza viruses such as Ty/Ont.

**Descriptors:** influenza A virus avian pathogenicity, macrophages metabolism, macrophages microbiology, nitric oxide biosynthesis, amino acid oxidoreductases antagonists and inhibitors, arginine analogs and derivatives, arginine pharmacology, cell line, chickens, fowl plague etiology, avian physiology, macrophages immunology, mice, nitric oxide synthase, orthomyxoviridae pathogenicity, orthomyxoviridae physiology, species specificity, virus replication, omega n methylarginine.


**NAL Call Number:** QR360.A1J6

**Abstract:** The virulent avian influenza virus A/Ty/Ont/7732/66 (H5N9) (Ty/Ont) causes severe destruction of the lymphoid cells in infected birds. Previous studies have suggested that viral infection of macrophages may be involved. However, Ty/Ont failed to replicate productively in primary cultures of chicken macrophages. Therefore, in an effort to develop an in vitro system for our studies, we examined the susceptibility of an avian macrophage cell line, HD11, to Ty/Ont. We found that Ty/Ont replicated in the HD11 cells to high titres, as measured by haemagglutination (HA) assays and infectivity yields. To determine whether this property was unique to Ty/Ont, we also examined the replication of influenza viruses representative of all 13 HA subtypes and an attenuated variant of Ty/Ont. All of the tested viruses replicated in HD11 cells; the avirulent strains required the presence of trypsin in the culture medium whereas virulent viruses and the attenuated variant of Ty/Ont did not. These results suggest that the HD11 cells can support the replication of a wide variety of influenza viruses and that this continuous avian cell line may prove useful for in vitro studies on these viruses.

**Descriptors:** influenza A virus avian physiology, macrophages microbiology, virus replication, cell line, chickens.


**NAL Call Number:** 41.8 V6426

**Descriptors:** fowl plague immunology, avian influenza virus, viral vaccines, aerosols, chickens.


**NAL Call Number:** QR360.A1J6

**Descriptors:** avian influenza A virus, strain comparisons, hemagglutinin, neuraminidase anitgens, chickens.


**NAL Call Number:** 501 L84Pb

**Abstract:** The replication of influenza virus is characterized by a unique dependence upon host cell nuclear function. In contrast to all other negative strand RNA viruses, transcription from host cellular DNA is a prerequisite for the synthesis of virus-specific messenger RNA; new DNA synthesis is not required. We have analysed the distribution of each of the nine virus-specified proteins between the nucleus and cytoplasm of virus-infected cells, and find that in addition of the NP and the NS1 proteins, two of the three P proteins show preferential migration into the nucleus. This subgroup of virus proteins may be involved in the early transcription of the viral genome which probably occurs in the nucleus. In non-permissive cell lines and in cells whose DNA function has been impaired by treatment with ultraviolet light, N-acetoxyacetaminofluorene or low doses of actinomycin D, production of some late virus proteins is inhibited. The specific host function required for this switch to late protein synthesis is unknown but in the cells treated with actinomycin D an abnormal accumulation of virus-specific mRNA occurs in the nucleus. In all cases studied, synthesis of new vRNA ceases when production of these late proteins has been blocked.

**Descriptors:** influenza A virus avian genetics, RNA viral biosynthesis, virus replication drug effects, biological transport drug effects, cell nucleus physiology, cultured cells, cytoplasm metabolism, dactinomycin
pharmacology, poly A metabolism, messenger metabolism, transcription, genetic, viral proteins metabolism.


**Descriptors:** influenza A virus avian, RNA biosynthesis, RNA nucleotidyltransferases metabolism, ribonucleases, chick embryo, fibroblasts metabolism, tissue culture, virus cultivation.


**Descriptors:** deoxyadenosines pharmacology, influenza A virus avian drug effects, Newcastle disease virus drug effects, RNA biosynthesis, virus replication drug effects, cell nucleolus metabolism, cell nucleus metabolism, cultured cells, chick embryo, depression, chemical, kinetics, tritium, uridine metabolism.


**Abstract:** Patterns of molecular evolution of the influenza virus proteins and genes are discussed. The subsets of all viral genes corresponding to statistically significant clusters on dendrogram were shown to fall into two distinct groups. The first group was characterized by the presence of an exact linear relationship between the year of the strain isolation and the evolutionary distance. The subsets of human influenza virus genes belong to this group. A method for eliminating the "frozen" strains from the subsets and for calculating the evolutionary rates without construction of phylogenetic trees has been elaborated. The substitution rates calculated according to this technique agreed with the data obtained previously. A linear relationship was not observed in the second group. This group was predominantly composed of avian influenza virus genes. The lack of linear correlation pointed to the cocirculation of a large amount of different influenza virus genomic segments in the avian population. An approach for an examination of the role of intragenic recombination in the development of the antigenic subtypes of hemagglutinin is suggested. Our results suggest that recombination did not play a considerable role in this process, and that all modern subtypes of this protein were probably formed before the introduction of the influenza viruses into the human population. These findings are consistent with the hypothesis that influenza viruses penetrated into human population from their pools in avian populations.

**Descriptors:** evolution and adaptation, genetics, influenza virus, human, avian.


**Abstract:** Influenza A virus of the H2 subtype caused a serious pandemic in 1957 and may cause similar outbreaks in the future. To assess the evolution and the antigenic relationships of avian influenza H2 viruses, we sequenced the haemagglutinin (HA) genes of H2 isolates from shorebirds, ducks and poultry in North America and derived a phylogenetic tree to establish their interrelationships. This analysis confirmed the divergence of H2 HA into two geographical lineages, American and Eurasian. One group of viruses isolated from shorebirds in North America had HA belonging to the Eurasian lineage, indicating an interregional transmission of the H2 gene. Characterization of HA with a monoclonal antibody panel revealed that the antigenicity of the Delaware strains differed from the other avian strains analysed. The data emphasizes the importance of avian influenza surveillance.

**Descriptors:** fowl plague transmission, fowl plague virology, hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian genetics, Asia, birds virology, Europe, genes viral, hemagglutination inhibition tests, avian isolation and purification, North America, phylogeny, poultry virology.


Abstract: ts19 is a temperature-sensitive (ts) mutant of the influenza A fowl plague virus with a defect in the nucleoprotein (NP). In ts19-infected chicken embryo cells all viral components are synthesized in normal yields at the nonpermissive temperature, but infectious virus is not formed. Under these conditions the migration of the NP and M of ts19 from the cell nucleus to the cytoplasm is affected. This ts defect is due to a single amino acid replacement (R162K) in a completely conserved region of the NP. Another mutant with a different defect in the NP is ts81. After infection with ts81 at 40 degrees no vRNA is being synthesized. By backcross of a revertant derived from ts81 many isolates with a ts defect in the PB2 protein were obtained. This ts defect seems to extragenically suppress the ts defect in the NP gene and to be dominant in a wild-type background.

Descriptors: genes viral, influenza A virus avian genetics, nucleoproteins genetics, suppression, genetic, viral core proteins genetics, amino acid sequence, chick embryo, crosses, genetic, avian growth and development, molecular sequence data, nucleoproteins chemistry, sensitivity and specificity, temperature, viral core proteins chemistry, virus replication genetics.


Abstract: The nucleotide sequences of the nucleoprotein (NP) genes of fowl plague virus (FPV) and of a temperature-sensitive (ts) mutant (ts81) derived therefrom have been determined. The ts81-NP nucleotide sequence possesses a single nucleotide substitution in comparison to the wild type. This causes an amino acid exchange at position 332 of the NP. An alanine in the wild type-NP is substituted by a threonine in ts81-NP. This substitution leads to a significant difference in the secondary structure prediction. Although this mutation is located within the karyophilic region of the NP, the accumulation of the NP in ts81-infected cells is not significantly affected at 40 degrees C. Therefore, we assume that the cooperation with one of the polymerase proteins (P) is interfered with at 40 degrees C, leading to the loss of viral vRNA or replicative cRNA synthesis. The comparison of the FPV-NP nucleotide sequence to a previously published sequence of the same strain (Tomley and Roditi, 1984) highlights ten nucleotide differences, four of them leading to amino acid substitutions.

Descriptors: influenza A virus avian genetics, nucleoproteins genetics, viral core proteins, viral proteins genetics, amino acid sequence, base sequence, cell nucleus metabolism, DNA, viral genetics, avian metabolism, avian ultrastructure, molecular sequence data, mutation, nucleoproteins biosynthesis, RNA viral genetics, temperature, viral proteins biosynthesis.


Abstract: Virus excretion, immune response, and, for chickens, deaths were recorded in 3-week-old ostriches and chickens inoculated by either the intramuscular or intranasal route with one of two influenza A viruses of subtype H5. One of the viruses, A/turkey/England/50-92/91 (H5N1) (50/92), was highly pathogenic for chickens causing 5/5 deaths by each route of inoculation. The other virus, A/ostrich/Denmark-Q/72420/96 (H5N2) (72420/96), isolated from ostriches in quarantine in Denmark during 1996, was of low pathogenicity for chickens, causing no clinical signs by either route of inoculation. No significant clinical signs were seen in any of the ostriches infected with either of the viruses by either route of infection. Both viruses were recoverable from both species up to 12 days post-infection, and low serological responses were detected in surviving infected ostriches and chickens at 21 days after inoculation.

Descriptors: ostriches, chickens, chicks, avian influenza virus, susceptibility, experimental infections, pathogenicity, clinical aspects, antibody formation, mortality, application methods, intramuscular injection, virus shedding, intranasal administration.

Markushin, S., H. Ghiasi, N. Sokolov, A. Shilov, B. Sinitsin, D. Brown, A. Klimov, and D. Nayak (1988). Nucleotide sequence of RNA segment 7 and the predicted amino sequence of M1 and M2 proteins of
FPV/Weybridge (H7N7) and WSN (H1N1) influenza viruses. Virus Research 10(2-3): 263-71. ISSN: 0168-1702.

NAL Call Number: QR375.V6

Abstract: Since the gene products (M1 and M2) of influenza virus RNA segment 7 have been implicated in host range restriction, sensitivity to the drug amantadine, virus yield in chicken embryos as well as in virus assembly and morphology, we have determined the nucleotide sequence of this RNA segment for an avian [A/FPV/Weybridge (H7N7)] and a human [A/WSN/33 (H1N1)] virus and compared it to that of the other influenza A virus strains. The results show that all ten strains of influenza A virus contain an identical number of nucleotides (1027 bases) in RNA segment 7 and an identical number of amino acids in M1 (252 aa) and M2 (97 aa) proteins. The observed amino acid changes are conservative in nature suggesting the requirement of a critical structure of both proteins in virus assembly. Furthermore, the presence of some consistent amino acid substitutions among different human and avian strains also supports the possible existence of host range and drug resistance determinants in M1 and M2 proteins.

Descriptors: influenza A virus avian genetics, human genetics, RNA viral genetics, viral matrix proteins genetics, amino acid sequence, base sequence, avian analysis, human analysis, molecular sequence data.


NAL Call Number: 448.8 P942

Abstract: The synthesis of virus-specific polypeptides in cells infected with a ts-mutant of fowl plague virus with disturbed process of secondary transcription was studied. Synthesis of all virus-specific proteins was shown to occur under conditions providing for synthesis of polyA+ cRNA at the stage of primary transcription but with disturbance of the secondary transcription and blocking of polyA- cRNA and vRNA synthesis. No time regulation of virus-specific polypeptide synthesis was in effect.

Descriptors: influenza A virus avian metabolism, peptide synthesis, transcription, genetic, viral proteins biosynthesis, avian genetics, mutation.


NAL Call Number: 448.3 AC85

Descriptors: influenza A virus avian classification, cultured cells, chick embryo, fluorouracil pharmacology, genetic complementation test, hydroxylamines pharmacology, avian pathogenicity, mutagens pharmacology, mutation drug effects, nitrites pharmacology, nitrosourea compounds pharmacology, plaque assay, recombination, genetic, temperature, virus replication drug effects.


NAL Call Number: QR360.A1J6

Abstract: Three different types of impairment in the synthesis of virion RNA (vRNA) were detected in three groups of temperature-sensitive (ts) mutants of fowl plague virus (FPV) having ts mutations in genes 1, 3 and 5 respectively. Normal synthesis of poly-(A+) cRNA, poly(A-) cRNA and vRNA was observed under non-permissive conditions early in infection in cells infected with the ts43 mutant having a ts mutation in gene 1 coding for the PB2 protein. However, 4 h after infection synthesis of vRNA ceased, synthesis of poly(A+) cRNA was reduced drastically, but the rate of poly(A-) cRNA synthesis was the same as that in cells infected with wild-type FPV. In cells infected with the ts 166 mutant having a ts mutation in gene 3, coding for the PA polypeptide, a drastic reduction was observed in poly(A+) cRNA synthesis under non-permissive conditions. Synthesis of poly(A-) cRNA was also reduced and synthesis of vRNA was not detected. The ts 60 mutant, having a ts mutation in gene 5 coding for the NP polypeptide, induced synthesis of all types of virus-specific RNA under non-permissive conditions, but the regulation of synthesis of vRNA and poly(A+) cRNA was affected, there being predominant syntheses of RNA segments 5 and 8 late in infection. In cells infected with mutants ts43 and ts 166 synthesis of virus-specific proteins was impaired, which reflected defects in the
synthesis of virus-specific RNAs. The data obtained suggest that the PB2 protein may be contained in an enzyme complex responsible for synthesis of vRNA, that different enzyme complexes may be involved in the synthesis of poly(A-) cRNA and vRNA, and that the NP protein plays a significant role in the regulation of vRNA synthesis.

Descriptors: influenza A virus avian genetics, mutation, RNA viral biosynthesis, cycloheximide pharmacology, avian metabolism, peptide synthesis, recombination, genetic, ribonucleoproteins biosynthesis, temperature.

NAL Call Number: 448.3 AC85

Abstract: The possibility of complementation between ts mutants of fowl plague virus (FPV) belonging to 5 different complementation groups was studied using various time intervals between inoculation of the cells with two complementation partners. The structural proteins of virions formed on complementation of individual ts mutants with wild virus were analysed by polyacrylamide gel electrophoresis after amino acid pulse label followed by pulse chase. The features of complementation interactions between the mutants are discussed.

Descriptors: influenza A virus avian growth and development, avian metabolism, mutation, genetic complementation test, peptide synthesis, temperature, viral proteins biosynthesis, virus replication.

NAL Call Number: 448.8 P942

Abstract: Crossing of norakin-resistant mutant NR1 of A/Waybridge (H7N7) strain of fowl plague virus (FPV) with human influenza virus strains produced recombinants inheriting the hemagglutinin (HA) gene of the NR1 mutant and neuraminidase (NA) genes of human influenza virus strains. The R120 recombinant produced by crossing of NR1 with A/Taiwan/1/86 (H1N1) strain, unlike other recombinants and NR1 mutant, lost the capacity of reacting in H1 test with two monoclonal antibodies (MCA) to HA7: 71/4 and 46/6. The ts mutant A/FPV/Rostok which has ts-mutation in HA-gene also had changes in the antigenic specificity of HA. The RA and RB recombinants produced by crossing R120 with the A/Krasnodar/101/59 strain and inheriting HA-gene from R120 and NA-gene from A/Krasnodar/101/59 strain recovered the initial HA antigenic structure. No changes in the antigenic properties of HA were observed in the recombinants produced by crossing the original A/FPV/Waybridge strain with A/Taiwan/1/86 strain and inheriting HA-gene from the original A/FPV/Waybridge strain and NA-gene from A/Taiwan/1/86 strain. It is concluded that ts mutations in influenza virus HA-gene may be accompanied by changes in the antigenic specificity of this virus HA. The possibilities of manifestation of phenotypic suppression at the level of influenza virus virion membrane proteins and the causes of changes in the HA antigenic structure in this virus recombinants are discussed.

Descriptors: hemagglutinins viral immunology, influenza A virus avian immunology, human immunology, antiviral agents antagonists and inhibitors, chick embryo, crosses, genetic, drug resistance, microbial, epitopes genetics, epitopes immunology, genes viral immunology, hemagglutinins viral genetics, avian genetics, human genetics, mutation immunology, piperidines antagonists and inhibitors, recombination, genetic genetics, recombination, genetic immunology, temperature.

NAL Call Number: 448.3 AC85

Abstract: Comparison of some avian influenza virus strains possessing haemagglutinin Havi revealed the greatest differences in strains A/FPV/Weybridge and A/FPV/Rostock/34. These strains differed in the degree of homology of eight genome fragments, electrophoretic mobility of the majority of proteins, size of plaques and rct42 marker and displayed significant differences in antigenic specificity of haemagglutinin. Strains A/FPV/Weybridge and A/FPV/Dobson proved to be more close in the degree of genome homology but
differed in three genes, electrophoretic mobility of some proteins, size of plaques, rct42 marker and antigenic specificity of haemagglutinin. The data obtained indicate that avian influenza virus strains of the Havl subtype may differ from each other in the degree of gene homology and some other properties including antigenic specificity of haemagglutinin like influenza viruses with other haemagglutinin subtypes.

Descriptors: genes viral, hemagglutinins viral immunology, influenza A virus avian genetics, electrophoresis, polyacrylamide gel, epitopes, avian immunology, avian physiology, neuraminidase immunology, nucleic acid hybridization, plaque assay, temperature, viral envelope proteins, viral proteins immunology.


NAL Call Number: 41.8 C162
Descriptors: Carnivora, influenza veterinary, monkey diseases microbiology, nose microbiology, orthomyxoviridae pathogenicity, respiratory tract infections microbiology, antigen antibody reactions, birds, cross reactions, haplorhini, hemagglutination inhibition tests, horses, immune sera, influenza immunology, orthomyxoviridae isolation and purification, respiratory tract infections immunology, turkeys, virus replication.


NAL Call Number: QR360.J6
Abstract: Human influenza A viruses replicate in the upper respiratory tract at a temperature of about 33 degrees C, whereas avian viruses replicate in the intestinal tract at a temperature close to 41 degrees C. In the present study, we analyzed the influence of low temperature (33 degrees C) on RNA replication of avian and human viruses in cultured cells. The kinetics of replication of the NP segment were similar at 33 and 37 degrees C for the human A/Puerto-Rico/8/34 and A/Sydney/5/97 viruses, whereas replication was delayed at 33 degrees C compared to 37 degrees C for the avian A/FPV/Rostock/34 and A/Mallard/NY/6750/78 viruses. Making use of a genetic system for the in vivo reconstitution of functional ribonucleoproteins, we observed that the polymerase complexes derived from avian viruses but not human viruses exhibited cold sensitivity in mammalian cells, which was determined mostly by residue 627 of PB2. Our results suggest that a reduced ability of the polymerase complex of avian viruses to ensure replication of the viral genome at 33 degrees C could contribute to their inability to grow efficiently in humans.
Descriptors: influenza A virus avian metabolism, human metabolism, RNA viral metabolism, viral proteins metabolism, cell line, mutation, viral genetics, temperature, time factors, transcription, genetic, viral proteins genetics, virus replication.


NAL Call Number: 448.8 V81
Descriptors: antibodies, viral, immunoglobulin G, influenza A virus avian enzymology, RNA replicate chemistry, base sequence, binding sites, antibody, chick embryo, enzyme linked immunosorbent assay, genome, viral, avian genetics, mutagenesis, site directed, oligodeoxyribonucleotides, RNA replicate metabolism, sequence deletion.


NAL Call Number: 442.8 J828
Abstract: The entry of fowl plague virus, and avian influenza A virus, into Madin-Darby canine kidney (MDCK) cells was examined both biochemically and morphologically. At low multiplicity and 0 degrees C, viruses bound to the cell surface but were not internalized. Binding was not greatly dependent on the pH of the medium and reached an equilibrium level in 60-90 min. Over 90% of the bound viruses were removed by neuraminidase but not by proteases. When cells with prebound virus were warmed to 37 degrees C, part of the virus became resistant to removal b neuraminidase, with a half-time of 10-15 min. After a brief lag period, degraded viral material was released into the medium. The neuraminidase-resistant virus was
capable of infecting the cells and probably did so by an intracellular route, since ammonium chloride, a
lysosomotropic agent, blocked both the infection and the degradation of viral protein. When the entry
process was observed by electron microscopy, viruses were seen bound primarily to microvilli on the cell
surface at 0 degrees C and, after warming at 37 degrees C, were endocytosed in coated pits, coated
vesicles, and large smooth-surfaced vacuoles. Viruses were also present in smooth-surfaced invaginations
and small smooth-surfaced vesicles at both temperatures. At physiological pH, no fusion of the virus with
the plasma membrane was observed. When prebound virus was incubated at a pH of 5.5 or below for 1 min at
37 degrees C, fusion was, however, detected by ferritin immunolabeling. t low multiplicity, 90% of the
prebound virus became neuraminidase-resistant and was presumably fused after only 30 s at low pH. These
experiments suggest that fowl plague virus enters MDCK cells by endocytosis in coated pits and coated
vesicles and is transported to the lysosome where the low pH initiates a fusion reaction ultimately resulting in
the transfer of the genome into the cytoplasm. The entry pathway of fowl plague virus thus resembles tht
earlier described for Semliki Forest virus.

Descriptors: kidney microbiology, cell line, dogs, endocytosis, hydrogen-ion concentration, lysosomes
microbiology, membrane fusion, microscopy, electron, temperature.

Matlin, K.S. and K. Simons (1983). Reduced temperature prevents transfer of a membrane glycoprotein to the
NAL Call Number: QH573.C42

Abstract: The transport kinetics of the influenza virus hemagglutinin from its site of synthesis to the apical
plasma membrane of Madin-Darby canine kidney cells, a polarized epithelial cell line, were studied by a
sensitive tryptic assay. Hemagglutinin acquired terminal sugars, as judged by sensitivity to endo-beta-N-
acetylglicosaminidase H, 10-15 min after synthesis, and first appeared on the apical domain 15 min later.
None of the pulse-labeled hemagglutinin accumulated on the basolateral domain. At 20 degrees C, terminal
glycosylation continued, but no hemagglutinin was detected on the cell surface within 2 hr. If the incubation
temperature was raised from 20 degrees C to 37 degrees C, hemagglutinin was quickly externalized,
demonstrating that the inhibition at low temperature was reversible.

Descriptors: cell membrane metabolism, hemagglutinins viral, influenza A virus avian metabolism,
oligosaccharides metabolism, viral proteins metabolism, biological transport, cell line, dogs, kinetics,
temperature, viral envelope proteins.

(2000). Early alterations of the receptor-binding properties of H1, H2, and H3 avian influenza virus
hemagglutinins after their introduction into mammals. Journal of Virology 74(18): 8502-12. ISSN: 0022-
538X.
NAL Call Number: QR360.J6

Abstract: Interspecies transmission of influenza A viruses circulating in wild aquatic birds occasionally
results in influenza outbreaks in mammals, including humans. To identify early changes in the receptor
binding properties of the avian virus hemagglutinin (HA) after interspecies transmission and to determine the
amino acid substitutions responsible for these alterations, we studied the HAs of the initial isolates from the
human pandemics of 1957 (H2N2) and 1968 (H3N2), the European swine epizootic of 1979 (H1N1), and the
seal epizootic of 1992 (H3N3), all of which were caused by the introduction of avian virus HAs into these
species. The viruses were assayed for their ability to bind the synthetic sialyglycopolymers 3'SL-PAA and
6'SLN-PAA, which contained, respectively, 3'-sialyllactose (the receptor determinant preferentially
recognized by avian influenza viruses) and 6'-sialyl(N-acetyllactosamine) (the receptor determinant for
human viruses). Avian and seal viruses bound 6'SLN-PAA very weakly, whereas the earliest available
human and swine epidemic viruses bound this polymer with a higher affinity. For the H2 and H3 strains, a
single mutation, 226Q-->L, increased binding to 6'SLN-PAA, while among H1 swine viruses, the 190E-->D
and 225G-->E mutations in the HA appeared important for the increased affinity of the viruses for 6'SLN-
PAA. Amino acid substitutions at positions 190 and 225 with respect to the avian virus consensus sequence
are also present in H1 human viruses, including those that circulated in 1918, suggesting that substitutions
at these positions are important for the generation of H1 human pandemic strains. These results show that
the receptor-binding specificity of the HA is altered early after the transmission of an avian virus to humans
and pigs and, therefore, may be a prerequisite for the highly effective replication and spread which
characterize epidemic strains.

Descriptors: hemagglutinin glycoproteins, influenza virus metabolism, influenza A virus avian metabolism, receptors, virus metabolism, amino acid sequence, amino acid substitution, disease outbreaks, ducks virology, hemagglutinin glycoproteins, influenza virus chemistry, avian isolation and purification, models, molecular, molecular sequence data, mutation, missense, phylogeny, protein binding, seals virology, sequence alignment, sialic acids metabolism, species specificity, swine virology.


NAL Call Number: QR360.J6

Abstract: In 1997, 18 confirmed cases of human influenza arising from multiple independent transmissions of H5N1 viruses from infected chickens were reported from Hong Kong. To identify possible phenotypic changes in the hemagglutinin (HA) and neuraminidase (NA) of the H5 viruses during interspecies transfer, we compared the receptor-binding properties and NA activities of the human and chicken H5N1 isolates from Hong Kong and of H5N3 and H5N1 viruses from wild aquatic birds. All H5N1 viruses, including the human isolate bound to Sia2-3Gal-containing receptors but not to Sia2-6Gal-containing receptors. This finding formally demonstrates for the first time that receptor specificity of avian influenza viruses may not restrict initial avian-to-human transmission. The H5N1 chicken viruses differed from H5 viruses of wild aquatic birds by a 19-amino-acid deletion in the stalk of the NA and the presence of a carbohydrate at the globular head of the HA. We found that a deletion in the NA decreased its ability to release the virus from cells, whereas carbohydrate at the HA head decreased the affinity of the virus for cell receptors. Comparison of amino acid sequences from GenBank of the HAs and NAs from different avian species revealed that additional glycosylation of the HA and a shortened NA stalk are characteristic features of the H5 and H7 chicken viruses. This finding indicates that changes in both HA and NA may be required for the adaptation of influenza viruses from wild aquatic birds to domestic chickens and raises the possibility that chickens may be a possible intermediate host in zoonotic transmission.

Descriptors: hemagglutinin glycoproteins, influenza virus metabolism, influenza A virus avian metabolism, human metabolism, alpha globulins metabolism, amino acid sequence, carbohydrates metabolism, chickens, fowl plaque virology, Hong Kong, horseradish peroxidase metabolism, influenza veterinary, influenza virology, avian classification, avian isolation and purification, human classification, human isolation and purification, molecular sequence data, neuraminidase metabolism, ovomucin metabolism, phenotype, receptors, virus metabolism, sequence homology, amino acid.


NAL Call Number: 448.8 V81

Descriptors: influenza A virus avian metabolism, poultry virology, receptors, virus metabolism, amino acid substitution, Asia, binding sites, fowl plague transmission, fowl plague virology, hemagglutinin glycoproteins, influenza virus genetics, hemagglutinin glycoproteins, influenza virus metabolism, avian classification, avian genetics, human classification, human genetics, human metabolism, mutation, neuraminidase genetics, neuraminidase metabolism, phylogeny, viral envelope proteins genetics, viral envelope proteins metabolism.


NAL Call Number: 500 N21P

Abstract: The recent human infections caused by H5N1, H9N2, and H7N7 avian influenza viruses highlighted the continuous threat of new pathogenic influenza viruses emerging from a natural reservoir in birds. It is generally believed that replication of avian influenza viruses in humans is restricted by a poor fit of these viruses to cellular receptors and extracellular inhibitors in the human respiratory tract. However, detailed mechanisms of this restriction remain obscure. Here, using cultures of differentiated human airway epithelial cells, we demonstrated that influenza viruses enter the airway epithelium through specific target cells and that there were striking differences in this respect between human and avian viruses. During the
course of a single-cycle infection, human viruses preferentially infected nonciliated cells, whereas avian viruses as well as the egg-adapted human virus variant with an avian virus-like receptor specificity mainly infected ciliated cells. This pattern correlated with the predominant localization of receptors for human viruses (2-6-linked sialic acids) on nonciliated cells and of receptors for avian viruses (2-3-linked sialic acids) on ciliated cells. These findings suggest that although avian influenza viruses can infect human airway epithelium, their replication may be limited by a nonoptimal cellular tropism. Our data throw light on the mechanisms of generation of pandemic viruses from their avian progenitors and open avenues for cell level-oriented studies on the replication and pathogenicity of influenza virus in humans.

Descriptors: influenza A virus, avian pathogenicity, human pathogenicity, respiratory mucosa microbiology, bronchi, cell line, dogs, avian isolation and purification, avian physiology, human isolation and purification, human physiology, kidney, lectins, microscopy, confocal, nasal mucosa microbiology, sialic acids analysis, trachea.


NAL Call Number: QR360.J6

Abstract: Influenza virus neuraminidase (NA) plays an essential role in release and spread of progeny virions, following the intracellular viral replication cycle. To test whether NA could also facilitate virus entry into cell, we infected cultures of human airway epithelium with human and avian influenza viruses in the presence of the NA inhibitor oseltamivir carboxylate. Twenty- to 500-fold less cells became infected in drug-treated versus nontreated cultures (P < 0.0001) 7 h after virus application, indicating that the drug suppressed the initiation of infection. These data demonstrate that viral NA plays a role early in infection, and they provide further rationale for the prophylactic use of NA inhibitors.

Descriptors: bronchi virology, nasal mucosa virology, neuraminidase physiology, orthomyxoviridae physiology, trachea virology, acetamides pharmacology, orthomyxoviridae enzymology.


NAL Call Number: 41.8 P27

Abstract: Intranasally inoculated neurotropic influenza viruses in mice infect not only the respiratory tract but also the central nervous system (CNS), mainly the brain stem. Previous studies suggested that the route of invasion of virus into the CNS was via the peripheral nervous system, especially the vagus nerve. To evaluate the transvagal transmission of the virus, we intranasally inoculated unilaterally vagectomized mice with a virulent influenza virus (strain 24a5b) and examined the distribution of the viral protein and genome by immunohistochemistry and in situ hybridization over time. An asymmetric distribution of viral antigens was observed between vagal (nodose) ganglia: viral antigen was detected in the vagal ganglion of the vagectomized side 2 days later than in the vagal ganglion of the intact side. The virus was apparently transported from the respiratory mucosa to the CNS directly and decussately via the vagus nerve and centrifugally to the vagal ganglion of the vagectomized side. The results of this study, thus, demonstrate that neurotropic influenza virus travels to the CNS mainly via the vagus nerve.

Descriptors: brain stem virology, influenza A virus, avian, orthomyxoviridae infections virology, vagus nerve virology, immunohistochemistry, in situ hybridization, lung virology, mice, nodose ganglion virology, respiratory mucosa virology.


NAL Call Number: 448.3 Ar23

Abstract: Mink were found to be susceptible to the intranasal inoculation of human, swine, equine and avian influenza A viruses. The viruses were recovered until the 7th post inoculation (p.i.) day from the respiratory tract. The inoculated mink showed antibody response against these viruses. Contact infection in mink with A/Kumamoto/22/77 (H3N2) was possible.

Descriptors: influenza A virus pathogenicity, orthomyxoviridae infections microbiology, antibodies, viral
biosynthesis, disease models, animal, hemagglutination inhibition tests, influenza A virus immunology, influenza A virus isolation and purification, orthomyxoviridae infections immunology, orthomyxoviridae infections transmission, respiratory system microbiology.


NAL Call Number: QR360.A1J6

Descriptors: genetics, microbial, influenza A virus avian pathogenicity, orthomyxoviridae pathogenicity, recombination, genetic, antigens, viral analysis, azirines pharmacology, chick embryo, fetal membranes, fibroblasts, heat, hemagglutination inhibition tests, hemagglutinins viral analysis, horses, immune sera, avian drug effects, avian immunology, avian radiation effects, neuraminidase analysis, orthomyxoviridae immunology, orthomyxoviridae radiation effects, quinones pharmacology, rabbits, radiation effects, tissue culture, ultraviolet rays, virus cultivation.


NAL Call Number: QR360.A1J6

Abstract: Nucleotide sequence analysis of a recombinant DNA clone of RNA segment 7 from FPV/Rostock/34 has shown it to be highly conserved in comparison with RNA segment 7 from two human strains (Allen et al., 1980; Winter & Fields, 1980; Lamb & Lai, 1981). FPV RNA segment 7 contains the coding capacity for two polypeptide chains. The sequence homology between RNA segment 7 of avian and human viruses was greater than 90%, and most of the changes did not result in amino acid substitutions.

Descriptors: influenza A virus avian genetics, RNA viral analysis, base sequence, cloning, molecular, DNA restriction enzymes, DNA, recombinant analysis, Escherichia coli genetics, plasmids.


NAL Call Number: QR375.V6

Abstract: We have measured the pathogenicity for 6-week-old chicks of infection by H7 avian influenza viruses. One virus, strain S3 from A/FPV/Rostock/34(H7N1) showed a temperature sensitive phenotype at 41.5 degrees C and reduced pathogenicity. By analysis of reassortants made between virus S3 and A/FPV/Dobson/27(H7N7), a fully pathogenic virus, two conclusions arise. (1) The critical cut-off temperature for avian influenza virus in 6-week-old chicks is 41.5 degrees. (2) RNA segment 1 of virus S3 is responsible for the lack of pathogenicity in reassortant viruses. Nucleotide sequencing of RNA segment 1 from S3 and its parent, A/FPV/Rostock/34 has revealed a single mutation at nucleotide 1561. This results in a substitution of isoleucine for leucine at amino acid position 512 in the cap-binding protein, PB2.

Descriptors: carrier proteins genetics, fowl plague microbiology, influenza A virus avian pathogenicity, RNA caps metabolism, amino acid sequence, base sequence, carrier proteins metabolism, chickens, avian genetics, avian growth and development, molecular sequence data, mutation, phenotype, plaque assay, RNA cap binding proteins, RNA viral genetics, temperature.


NAL Call Number: QP501,B64

Abstract: The effects of alpha-D-mannopyranosylmethyl-p-nitrophenyltriazene (MMNT) on mannosidases involved in asparagine-linked oligosaccharide processing were investigated. MMNT was found to inhibit the activity of rat liver Golgi alpha-mannosidase I in a concentration-dependent manner (50% inhibition with 0.18 mM-MMNT), whereas rat liver endoplasmic-reticulum alpha-mannosidase appeared to be resistant (less than 5% inhibition at 1 mM-MMNT). Jack-bean alpha-mannosidase was also sensitive to inhibition by MMNT (50% inhibition with 0.32 mM-MMNT). Treatment of influenza-virus-infected chick-embryo cells with 1 mM-MMNT led to a decrease in the formation of complex-type asparagine-linked oligosaccharides and an accumulation of high-mannose-type oligosaccharides with the composition Man8(GlcNAc)2 and Man7(GlcNAc)2 on the viral glycoproteins. The biological activities of influenza-virus haemagglutinin and
neuraminidase synthesized in the presence of 1 mM-MMNT remained unchanged, but the virus was less infectious than the control.

Descriptors: glycoproteins metabolism, mannosidases antagonists and inhibitors, oligosaccharides metabolism, triazenes pharmacology, chick embryo, endoplasmic reticulum drug effects, endoplasmic reticulum metabolism, fabaceae drug effects, fabaceae enzymology, Golgi apparatus drug effects, Golgi apparatus enzymology, influenza A virus avian physiology, liver drug effects, liver enzymology, mannans metabolism, plants, medicinal, rats, alpha mannosidase.

NAL Call Number: 500 N21P
Abstract: The genomic RNA of the avian influenza A virus, fowl plague, was fractionated into eight species by electrophoresis in polyacrylamide-agarose gels containing 6 M urea. The separated 32P-labeled RNA species were characterized by digestion with RNase T1 and fractionation of the resulting oligonucleotides by two-dimensional gel electrophoresis; this demonstrated that each species has a distinct nucleotide sequence. A tentative correlation of each genome RNA species with the virus protein that it encodes was made.
Descriptors: influenza A virus avian analysis, RNA viral analysis, base sequence, genes, structural, molecular weight, oligoribonucleotides analysis, viral isolation and purification, viral proteins biosynthesis.

NAL Call Number: QR360.J6
Abstract: The influenza virus neuraminidase (NA)-specific inhibitor zanamivir (4-guanidino-Neu5Ac2en) is effective in humans when administered topically within the respiratory tract. The search for compounds with altered pharmacological properties has led to the identification of a novel series of influenza virus NA inhibitors in which the triol group of zanamivir has been replaced by a hydrophobic group linked by a carboxamide at the 6 position (6-carboxamide). NWS/G70C variants generated in vitro, with decreased sensitivity to 6-carboxamide, contained hemagglutinin (HA) and/or NA mutations. HA mutants bound with a decreased efficiency to the cellular receptor and were cross-resistant to all the NA inhibitors tested. The NA mutation, an Arg-to-Lys mutation, was in a previously conserved site, Arg292, which forms part of a triarginyl cluster in the catalytic site. In enzyme assays, the NA was equally resistant to zanamivir and 4-amino-Neu5Ac2en but showed greater resistance to 6-carboxamide and was most resistant to a new carbocyclic NA inhibitor, GS4071, which also has a hydrophobic side chain at the 6 position. Consistent with enzyme assays, the lowest resistance in cell culture was seen to zanamivir, more resistance was seen to 6-carboxamide, and the greatest resistance was seen to GS4071. Substrate binding and enzyme activity were also decreased in the mutant, and consequently, virus replication in both plaque assays and liquid culture was compromised. Altered binding of the hydrophobic side chain at the 6 position or the triol group could account for the decreased binding of both the NA inhibitors and substrate.
Descriptors: conserved sequence, enzyme inhibitors pharmacology, influenza A virus human enzymology, mutation, N-acetylneuraminic acid analogs and derivatives, neuraminidase antagonists and inhibitors, neuraminidase genetics, acetamides chemistry, acetamides pharmacology, adsorption, binding sites, birds, cell line, dogs, drug resistance, microbial, enzyme inhibitors chemistry, heating, hemagglutinin glycoproteins, influenza virus genetics, avian enzymology, human growth and development, human metabolism, kinetics, molecular structure, N-acetylneuraminic acid chemistry, N-acetylenuraminic acid pharmacology, phenotype, plaque assay, sialic acids chemistry, sialic acids pharmacology, substrate specificity, virus replication.

NAL Call Number: 448.3 AC85
Abstract: The ts phenotype and location of ts mutations were studied in the genome of parent viruses and those obtained by recombination of cold-adapted strains A/Leningrad/134/17/57 or A/Leningrad/134/47/57 with epidemic H1N1 and H3N2 influenza A virus strains. The epidemic H1N1 and H3N2 strains under study possessed a ts phenotype and contained ts mutations in one or two genes. The ts phenotype was lost following three clonings at 40 degrees C, suggesting that influenza virus strains isolated from humans may be heterogeneous and contain virions either carrying or not carrying the ts mutations in their genomes. Two cold-adapted strains possessing a distinct ts phenotype contained ts mutations in three (A/Leningrad/134/17/57 virus after 17 passages at 25 degrees C) or in five (A/Leningrad/134/47/57 variant after 30 additional passages at 25 degrees C) genes coding for non-glycosylated proteins. When compared with cold-adapted donor strains, the recombinants had either the same set or additional ts mutations. However, no ts mutation was detected in a gene which had been inherited from the donor strain. It is suggested that, in addition to the analysis of the genome composition, in cold-adapted recombinant influenza virus strains recommended as vaccine candidates it is necessary to control the number of genes containing ts mutations.

Descriptors: genes viral, influenza A virus avian genetics, human genetics, mutation, vaccines, attenuated, acclimatization, adult, child, cold, avian immunology, avian pathogenicity, human immunology, human pathogenicity, phenotype, recombination, genetic, variation genetics, virulence.


Abstract: The effect of the neuraminidase inhibitors zanamivir and oseltamivir on the transmission of highly pathogenic avian influenza (HPAI) in chickens was studied. Per group, five chickens inoculated with HPAI A/Chicken/Pennsylvania/1370/83 H5N2 virus were placed 1 day post-inoculation (p.i.) in one cage with five contact chickens. Inoculated and contact chickens were treated twice daily from 1 day before inoculation up to day 7 p.i. All untreated inoculated and contact chickens became infected and four inoculated and two contact chickens died. Similarly, all of the zanamivir-treated inoculated and contact chickens became infected and all inoculated and four contact chickens died. Obviously, locally active zanamivir has no effect. In contrast, although oseltamivir could not prevent tracheal infection of the inoculated chickens, none had an infected cloaca and only one died. More important, only after stopping treatment three contact chickens became positive, suggesting limited transmission within or after the treatment period. In conclusion, treatment with systemically active oseltamivir limits to a large extent a severe outcome and chicken-to-chicken transmission of HPAI virus.

Descriptors: highly pathogenic avian influenza virus, chicken, transmission, antiviral treatment, antiviral prophylaxis, neuraminidase inhibitors, zanamivir, oseltamivir.


NAL Call Number: 448.3 Ar23

Abstract: A fraction of polysomes synthesizing fowl plague virus (FPV) haemagglutinin (HA) was isolated from an infected chick embryo fibroblast (CEF) culture using a double immunoprecipitation assay. In an immunoprecipitate of HA-synthesizing polysomes (HA precipitate) the content of the HA polypeptide was increased with respect to the M1 + NS1 polypeptides as compared to a preparation of unprecipitated polysomes. In the HA precipitate, besides mRNA coding for HA synthesis, we have detected mRNAs corresponding to genes 1, 2 and 3 coding for high molecular weight P proteins. Studies of a cytoplasmic extract (CE) from FPV-infected CEF cultures in a sucrose density gradient revealed a fraction of polysomes with a sedimentation value of about 500S; the composition of virus-specific polypeptides and mRNA of the fraction was similar to that of the HA precipitate. It is thought that P proteins are synthesized on membrane-bound polysomes located closely to HA-synthesizing polysomes.

Descriptors: hemagglutinins isolation and purification, influenza A virus avian metabolism, polyribosomes metabolism, viral proteins biosynthesis, cultured cells, chick embryo, fowl plague immunology, fowl plague metabolism, avian immunology, RNA, messenger metabolism.

The ability of the fowl plague virus (FPV) M protein to form a complex with FPV RNP and to inhibit the RNP transcriptase activity in vitro depended on NaCl concentration and did not depend on the concentration of nonionic detergents. The results obtained indicate that the M protein-RNP links formed were of an electrostatic rather than a hydrophobic nature. As demonstrated using individual RNP components, vRNA and RNA-free protein structures, M protein formed complexes only with vRNA, and the complex formation was salt-dependent. Analysis of products formed in the in vitro system containing RNP of FPV in the presence of the M protein showed impairment in the transcription of all RNA segments. The degree of inhibition correlated with the size of a segment, transcription of high molecular weight RNA segments being inhibited significantly more than that of low molecular weight RNA segments.

Descriptors: influenza A virus avian metabolism, ribonucleoproteins metabolism, viral proteins metabolism, cultured cells, chick embryo, avian genetics, RNA replicase metabolism, RNA viral isolation and purification, ribonucleoproteins isolation and purification, transcription, genetic, viral matrix proteins, viral proteins isolation and purification.
a stage of primary transcription.

Descriptors: influenza A virus avian physiology, orthomyxoviridae physiology, viral interference, cultured cells, chick embryo, cycloheximide pharmacology, RNA viral biosynthesis, transcription, genetic, viral proteins biosynthesis.

NAL Call Number: 448.3 AC85
Abstract: Rimantadine prevents the conformational changes of influenza virus haemagglutinin (HA) caused by acid pH and the acquisition of sensitivity to trypsin, protects the haemolytic activity from inactivation and prevents the morphological changes of HA spikes on the virus surface.
Descriptors: adamantane analogs and derivatives, hemagglutinins viral analysis, influenza A virus avian drug effects, membrane fusion drug effects, rimantadine pharmacology, chick embryo, hemagglutinin glycoproteins, influenza virus, hydrogen-ion concentration, avian immunology, avian physiology, protein conformation drug effects, trypsin, virion drug effects, virion ultrastructure.

NAL Call Number: QP552.G59G593
Abstract: A human strain of influenza virus (A, H1N1) was shown to bind in an unexpected way to leukocyte and other gangliosides when compared with avian virus (A, H4N6) as assayed on TLC plates. The human strain bound only to species with about 10 or more sugars, while the avian strain bound to a wide range of gangliosides including the 5-sugar gangliosides. By use of specific lectins, antibodies, and FAB and MALDI-TOF mass spectrometry an attempt was done to preliminary identify the sequences of leukocyte gangliosides recognized by the human strain. The virus binding pattern did not follow binding by VIM-2 monoclonal antibody and was not identical with binding by anti-sialyl Lewis x antibody. There was no binding by the virus of linear NeuAcalpha3- or NeuAcalpha6-containing gangliosides with up to seven monosaccharides per mol of ceramide. Active species were minor NeuAcalpha6-containing molecules with probably repeated HexHexNAc units and fucose branches. This investigation demonstrates marked distinctions in the recognition of gangliosides between avian and human influenza viruses. Our data emphasize the importance of structural factors associated with more distant parts of the binding epitope and the complexity of carbohydrate recognition by human influenza viruses.
Descriptors: gangliosides metabolism, influenza A virus human metabolism, carbohydrate sequence, chromatography, thin layer methods, avian metabolism, leukocytes chemistry, molecular sequence data, species specificity, spectrometry, mass, fast atom bombardment, spectrometry, mass, matrix assisted laser desorption ionization.

NAL Call Number: 385 AC85
Abstract: Receptor-active gangliosides with affinity for Helicobacter pylori and influenza virus were chemically modified and analyzed by negative ion fast atom bombardment mass spectrometry (FAB MS) or electron ionization mass spectrometry (EI MS) after permethylation. Derivatizations included mild periodate oxidation of the sialic acid glycerol tail or conversion of the carboxyl group to primary alcohol or amides. The modified gangliosides were then tested for binding affinity using thin-layer plates overlaid with labeled microbes or microbe-derived proteins. Mild periodate oxidation, which shortens sialic acid tail without destruction of sugar cores, abolished or drastically reduced binding of H. pylori and avian influenza virus to sialyl-3-paragloboside (S-3-PG). The same effect was observed in the case of binding of the human influenza virus to receptor-active gangliosides of human leukocytes. Conversion of S-3-PG or leukocyte gangliosides to primary alcohols or amides also abolished the binding. However, mild periodate oxidation had no effect on binding of NAP (neutrophil-activating protein of H. pylori) to the active ganglioside.
Descriptors: gangliosides metabolism, Helicobacter pylori metabolism, orthomyxoviridae metabolism,
binding sites, gangliosides chemistry, methylation, receptors, cell surface chemistry, receptors, cell surface metabolism, spectrum analysis.


NAL Call Number: 448.3 Ar23
Abstract: The optimum conditions for the coupling of fowl plague virus (FPV) transcription to an in vitro reticulocyte translation system have been established and shown to be close to those required for maximum RNA synthesis by purified FPV virions. Products have been characterized by the peptides they yield on limited proteolysis in SDS and it has been shown that virus nucleoprotein (NP) and matrix (M) protein are made. The smallest virus coded polypeptide, the non-structural protein (NS), is made in only small amounts in the coupled system although it is a major virus coded product of infected cells early in infection.
Descriptors: influenza A virus avian metabolism, RNA viral biosynthesis, viral proteins biosynthesis, cell free system, fluorometry, avian genetics, peptide synthesis, rabbits, reticulocytes metabolism, transcription, genetic, translation, genetic.


NAL Call Number: 448.8 V81
Descriptors: influenza A virus avian metabolism, viral proteins biosynthesis, virus replication, amanitins pharmacology, camptothecin pharmacology, cell line, cell nucleus metabolism, dactinomycin pharmacology, hemagglutinins viral analysis, avian growth and development, avian immunology, neuraminidase biosynthesis, RNA viral biosynthesis.


NAL Call Number: 448.8 V81
Descriptors: cell nucleus metabolism, influenza A virus avian growth and development, virus replication, antigens, viral analysis, cell fractionation, cell fusion, cycloheximide pharmacology, dactinomycin pharmacology, hemagglutinins viral, hybrid cells, neuraminidase biosynthesis, neuraminidase immunology, ribonucleoproteins biosynthesis, ribonucleoproteins immunology, viral proteins biosynthesis, viral proteins immunology.


NAL Call Number: 448.8 V81
Descriptors: influenza A virus avian drug effects, viral proteins biosynthesis, 4 nitroquinoline 1 oxide pharmacology, camptothecin pharmacology, cell line, dactinomycin pharmacology, daunorubicin pharmacology, echinomycin pharmacology, ethidium pharmacology, hemagglutinins viral, avian growth and development, avian metabolism, neuraminidase biosynthesis, Newcastle disease virus drug effects, Newcastle disease virus growth and development, Newcastle disease virus metabolism, nogalamycin pharmacology, plicamycin pharmacology, profлавine pharmacology, virus replication drug effects.


NAL Call Number: 41.8 Am3A
Abstract: Electrocardiograms of chickens infected with viscerotrophic velogenic Newcastle disease virus (NDV) or virulent avian influenza virus (AIV) were characterized and compared. The ECG were monitored by radiotelemetry and were recorded twice daily before virus infection and during the course of the infection. Thirteen lead II intervals, segments, and amplitudes were measured and analyzed. The ECG of NDV-infected chickens were characterized by lengthened (P less than or equal to 0.05) ST segments and increased (P less than or equal to 0.05) P amplitudes. The ECG of AIV-infected chickens were characterized by lengthened (P less than or equal to 0.05) RS intervals, ST segments, TP intervals, and PR segments and
by increased (P less than or equal to 0.05) P amplitudes. The TP intervals and PR segments of ECG of AIV-infected chickens were significantly (P less than or equal to 0.05) longer than those of NDV-infected chickens. The pronounced conduction delays indicated in the ECG of AIV-infected chickens may have diagnostic importance.

**Descriptors:** chickens, fowl plague physiopathology, heart physiopathology, Newcastle disease physiopathology, electrocardiography veterinary, influenza A virus avian pathogenicity, Newcastle disease virus pathogenicity, specific pathogen free organisms, virulence.


**NAL Call Number:** 41.8 Av5

**Abstract:** Design and performance information is presented on an automated embryo-monitoring system for intact eggs. The computer-based system has been used successfully for several months to characterize viral pathogenicity in embryonated eggs. Features include electronic sensing of embryo movement, automatic quantification of the amount of movement, and automatic recording of the results on electronic media. The system does not require that eggs be removed from the incubator or that the incubator be opened during the course of an experiment, as is necessary with the manual candling technique. It has greatly improved discrimination of viral pathogenicity effects in fertile eggs because of its sensitivity and reduced intervals between observations. One important potential application involves using the system to measure the effects on virulence of mixing closely related variants of the same strain of virus that differ in pathogenicity, which is the biological scenario most likely approximating a natural disease outbreak.

**Descriptors:** chick embryo microbiology, influenza A virus avian pathogenicity, microcomputers, chick embryo physiology, lethal dose 50, movement, software.


**NAL Call Number:** 448.8 P942

**Abstract:** Antineuraminidase antibody was determined in the subjects who had suffered influenza during the epidemics of 1970-1975 in the GDR. As early as 1970 the highest titers of antibody (greater than or equal to 1:60) were found not only to the prototype A/Hong Kong/1/68 strain but also to its subsequent drift variants A/England/42/72, A/Port Chalmers/1/73. Some subjects had antineuraminidase antibody to avian influenza virus.

**Descriptors:** antibodies, viral analysis, influenza immunology, influenza A virus human immunology, neuraminidase immunology, adult, child, child, preschool, convalescence, disease outbreaks epidemiology, Germany, East, influenza epidemiology, human enzymology, neuraminidase antagonists and inhibitors.


**NAL Call Number:** 448.8 P942

**Abstract:** Significant differences in the molecular organization of lipid bilayer in remantadin-resistant and remantadine-sensitive strains of influenza virus were demonstrated by means of fluorescent phospholipid probes, analogues of phosphatidylcholine and sphingomyelin. The data on fluorescence polarization and
transfer of excitation energy from protein tryptophanes on probe fluorophores showed phosphatidylcholine and sphingomyelin to be segregated in influenza virion membrane. Gradients of mobility of lipid chains in virion membrane and in phospholipid vesicles have opposite directions. The results indicate that M protein coming inside virion into contact with the lipid bilayer does not penetrate further than its middle. In virions of the resistant strain remantadin destroys the array of the entire bilayer whereas in the sensitive strain the addition of remantadin results in a marked decrease of mobility of the chains in the surface area. It is suggested that the molecular organization of lipids is one of the factors determining influenza virus sensitivity to remantadin.

Descriptors: adamantane analogs and derivatives, capsid analysis, influenza A virus avian ultrastructure, membrane proteins analysis, rimantadine pharmacology, viral proteins analysis, drug resistance, microbial, energy transfer, fluorescent dyes analysis, avian drug effects, lipid bilayers analysis, phosphatidylcholines analysis, spectrometry, fluorescence, sphingomyelins analysis.


NAL Call Number: RB37.A1C5

Abstract: Influenza is a virus that is capable of causing a pandemic of the human race. Influenza has the ability to infect humans by mutating and altering its pathogenic characteristics. Efforts must be made worldwide to educate people about the possibilities of a potential outbreak. Awareness of optimal conditions which could lead to viral mutation and human to human transmission of a neogenetic strain of influenza appears to be a key deterrent against future cases.

Descriptors: influenza genetics, influenza transmission, influenza A virus genetics, mutation, adolescent, adult, birds, child, preschool, disease outbreaks, Hong Kong epidemiology, infant, influenza physiopathology, influenza virology, influenza A virus avian genetics, middle aged, species specificity.


NAL Call Number: 448.8 J821

Abstract: Immunization with live influenza virus expands Th1 memory cells and facilitates more rapid recovery after heterosubtypic virus challenge. Immunization with inactivated virus generates a Th2 response and does not lead to heterosubtypic immunity. Creation of a Th1 priming environment by the inclusion of interleukin (IL)-12 with antibodies to IL-4 converted the response against inactivated virus to a Th1 response that was able to facilitate virus clearance upon heterosubtypic virus challenge. Evaluation of memory responses of mice immunized by the various protocols demonstrated that the type of immunization imprints T cell memory, dictating the nature of the response to subsequent infection. After live virus challenge, expansion of Th1 cells seems to facilitate the generation of cytotoxic T lymphocytes from naive precursors. This latter finding may be the mechanism by which inactivated virus immunization in a Th1 cytokine context mediates heterosubtypic immunity.

Descriptors: influenza immunology, influenza A virus avian physiology, human physiology, influenza vaccine, Th1 cells immunology, Th2 cells immunology, virus latency physiology, cell line, cytokines biosynthesis, dogs, immunologic memory, avian radiation effects, human radiation effects, mice, inbred BALB c, spleen immunology, T lymphocytes, cytotoxic immunology, Th1 cells virology, Th2 cells virology, ultraviolet rays.


NAL Call Number: 500 N21P

Abstract: Transgenic expression of the influenza virus hemagglutinin (HA) in the pancreatic islet beta cells of InsHA mice leads to peripheral tolerance of HA-specific T cells. To examine the onset of tolerance, InsHA mice were immunized with influenza virus A/PR/8 at different ages, and the presence of nontolerant T cells was determined by the induction of autoimmune diabetes. The data revealed a neonatal period wherein T
cells were not tolerant and influenza virus infection led to HA-specific beta cell destruction and autoimmune diabetes. The ability to induce autoimmunity gradually waned, such that adult mice were profoundly tolerant to viral HA and were protected from diabetes. Because cross-presentation of islet antigens by professional antigen-presenting cells had been reported to induce peripheral tolerance, the temporal relationship between tolerance induction and activation of HA-specific T cells in the lymph nodes draining the pancreas was examined. In tolerant adult mice, but not in 1-week-old neonates, activation and proliferation of HA-specific CD8(+) T cells occurred in the pancreatic lymph nodes. Thus, lack of tolerance in the perinatal period correlated with lack of activation of antigen-specific CD8(+) T cells. This work provides evidence for the developmental regulation of peripheral tolerance induction.

Descriptors: aging immunology, hemagglutinin glycoproteins, influenza virus immunology, influenza A virus immunology, islets of langerhans immunology, receptors, antigen, T cell immunology, T lymphocytes immunology, animals, newborn, diabetes mellitus, type I immunology, diabetes mellitus, type I pathology, hemagglutinin glycoproteins, influenza virus genetics, immune tolerance, influenza A virus avian immunology, islets of langerhans growth and development, islets of langerhans pathology, lymphocyte activation, mice, mice inbred BALB c, mice, transgenic, receptors, antigen, T cell genetics.


NAL Call Number: QR180.I52
Abstract: The immunomodulatory activity of Isoprinosine treatments have been experimentally verified on chicken infected by three different viruses: Newcastle disease, fowl plague and avian infectious bronchitis. In protection tests, positive variations in the mean day of death rather than in the mortality rate were found depending on the modality of treatment. A stimulatory influence on primary anti-Newcastle disease virus antibody response was observed. In the avian model the Isoprinosine antiviral effect appears as due mainly to the enhancement of interferon production and to a synergistic interferon-isoprinosine interaction.

Descriptors: adjuvants, immunologic pharmacology, inosine analogs and derivatives, inosine pranobex pharmacology, virus diseases immunology, antibodies, viral biosynthesis, chickens, hemagglutination inhibition tests, infectious bronchitis virus immunology, influenza A virus avian immunology, interferons therapeutic use, kinetics, Newcastle disease virus immunology, vesicular stomatitis Indiana virus immunology, virus diseases drug therapy.


NAL Call Number: 448.8 V81
Abstract: Cooperation of viral proteins, or functional domains within a protein, can be studied by analyzing temperature-sensitive (ts) mutants and revertants carrying suppressor mutations. Accordingly, we have sequenced the hemagglutinin (HA) genes of a ts mutant of fowl plague virus (FPV), with a transport defect in the HA, and of five independent ts+ revertants (R1, R3, R4, R5, and R9). The amino acid replacement in position 480 from Thr to Ile, leading to the loss of a complex carbohydrate side chain, is responsible for the ts phenotype. R3, R4, and R5 are true revertants in that they have Thr in position 480, while R1 and R9 have kept Ile. The sequence of the HA of R1 is exactly the same as that of the ts mutant, while the R9 HA has two additional amino acid replacements in positions 91 (Lys-Thr) and 104 (Gly-Val). By doing a backcross with wild-type virus, it was shown that R1 carries an extragenic suppressor mutation, while R9 is intragenically suppressed. We conclude that the HA is transported from the site of its synthesis in the rough endoplasmic reticulum (RER) to the plasma membrane along with another viral gene product, which by mutation can complement the ts defect. An alternative interpretation is that the ts mutation results from a change in HA which allows an interacting protein to bind HA too soon, holding it back in the RER. The suppressor mutation may remove this premature interaction.

Descriptors: genes viral, hemagglutinins viral genetics, influenza A virus avian genetics, suppression, genetic, base sequence, biological transport, cultured cells, crosses, genetic, avian immunology, avian metabolism, mutation, temperature.

**NAL Call Number:** QP552.G59G593

**Abstract:** Comparison of the haemagglutinins (HA) of the pathogenic avian influenza viruses A/FPV/Dutch/27 (H7N7) and A/FPV/Rostock/34 (H7N1) revealed 94.7% nucleotide and 93.8% amino acid sequence homologies. Six of the seven N-glycosidic oligosaccharides of the Rostock HA are at the same positions as the six carbohydrates of the Dutch strain. The additional oligosaccharide side chain of the Rostock strain, which is of the complex type, is attached to asparagine149 in antigenic epitope B. The accessibility of this antigenic epitope has been analysed by using rabbit antisera raised against synthetic peptides comprising amino acids 143-162. The carbohydrates of the HA of the Rostock strain have been modified (i) to truncated cores by expression in insect cells using a baculovirus vector, (ii) to oligomannosidic side chains by growth in the presence of the trimming inhibitor methyldeoxynojirimycin and (iii) to a single N-acetylglucosamine residue by removal of the oligomannosidic sugar with endo-beta-N-acetylglucosaminidase H. Neither the authentic nor the modified oligosaccharides allowed antibody binding, as indicated by enzyme-linked immunosorbent assay (ELISA) and Western blot analyses. Reactivity was observed, however, after complete removal of the carbohydrate from HA of the Rostock strain by digestion with peptide-N-glycosidase F. HA of the Dutch strain was reactive without prior peptide-N-glycosidase F treatment. These results demonstrate that a single N-acetyl-glucosamine at asparagine149 is sufficient to prevent recognition of the peptide epitope.

**Descriptors:** hemagglutinins viral chemistry, influenza A virus avian chemistry, avian immunology, oligosaccharides chemistry, oligosaccharides immunology, amino acid sequence, antigens, viral chemistry, epitopes chemistry, hemagglutinins viral immunology, models, molecular, molecular conformation, molecular sequence data, sequence homology, nucleic acid, species specificity.


**NAL Call Number:** QP501.E8

**Abstract:** Extracellular cleavage of virus envelope fusion glycoproteins by host cellular proteases is a prerequisite for the infectivity of mammalian and nonpathogenic avian influenza viruses, and Sendai virus. Here we report a protease present in the airway that, like tryptase Clara, can process influenza A virus haemagglutinin and Sendai virus envelope fusion glycoprotein. This protease was extracted from the membrane fraction of rat lungs, purified and then identified as a mini-plasmin. Mini-plasmin was distributed predominantly in the epithelial cells of the upward divisions of bronchioles and potentiated the replication of broad-spectrum influenza A viruses and Sendai virus, even that of the plasmin-insensitive influenza A virus strain. In comparison with plasmin, its increased hydrophobicity, leading to its higher local concentrations on membranes, and decreased molecular mass may enable mini-plasmin to gain ready access to the cleavage sites of various haemagglutinins and fusion glycoproteins after expression of these viral proteins on the cell surface. These findings suggest that mini-plasmin in the airway may play a pivotal role in the spread of viruses and their pathogenicity.

**Descriptors:** bronchi cytology, epithelial cells chemistry, infection, influenza A virus metabolism, peptide fragments chemistry, plasmin chemistry, respirovirus metabolism, amino acid sequence, blotting, western, bronchi metabolism, bronchi pathology, bronchi virology, cell membrane metabolism, dose response relationship, drug, electrophoresis, polyacrylamide gel, immunohistochemistry, isoﬂuorophate pharmacology, lung metabolism, lung pathology, lung virology, molecular sequence data, rats, rats, wistar, sequence analysis, protein, sequence homology, amino acid, substrate specificity, viral envelope proteins chemistry, viral envelope proteins metabolism.


**NAL Call Number:** 448.3 Ar23

**Abstract:** Growth characteristics of a wide range of influenza A viruses from different mammals and bird
species were examined in an established line of canine kidney (MDCK) cells at an ordinary (37 degrees C) and a high temperature (42 degrees C). Although all viruses employed in the present study possessed a capability of replicating at 37 degrees C, virus growth at 42 degrees C showed considerable variation and reflected differences in the natural hosts of the isolates. All reference strains and isolates from bird species grew well in the MDCK cells maintained at 42 degrees C, but human viruses did not, showing an asymmetrical growth behavior. In contrast to this, growth of swine and equine viruses showed growth characteristics intermediate between human and avian viruses. Of the two swine viruses examined, replication of one strain occurred equally well at both temperatures and another failed to grow at 42 degrees C. Similarly, two of the three equine viruses tested belonging to H3N8 antigenic subtypes grew at 42 degrees C. However, the results obtained from comparison of plaque sizes and growth curves indicated that the replication of the above swine and equine viruses was restricted under a stringent temperature when compared to avian viruses. The detailed analysis of cloned viruses revealed that some of the swine and equine viruses contained two variants which are readily distinguished by growth behavior at 42 degrees C. Genome analysis of parental and virus clones by oligonucleotide mapping and migration profiles of RNA segments did not detect any differences among the above variants exhibiting the asymmetrical growth characteristics at 42 degrees C.

Descriptors: influenza A virus avian growth and development, human growth and development, influenza A virus growth and development, cell line, genes viral, horses, avian genetics, human genetics, porcine genetics, porcine growth and development, influenza A virus genetics, plaque assay, RNA viral genetics, temperature.


NAL Call Number: 448.8 J821

Abstract: Reassortant influenza A viruses were produced by mating an avian virus (A/Mallard/NY/78, A/Mallard/Alberta/78, or A/Pintail/Alberta/79) with a wild-type human influenza A virus. From each mating a reassortant virus was obtained that contained the genes coding for the hemagglutinin and neuraminidase surface antigens of the human influenza A wild-type virus and the six other RNA segments (“internal genes”) of the avian influenza A virus parent. The avian-human reassortant influenza viruses produced resembled their avian virus parent in that they produced plaques on MDCK monolayers at 42 C, a temperature restrictive for the human influenza viruses. In the trachea of squirrel monkeys, each avian-human reassortant influenza virus was as restricted in its replication as was its avian influenza virus parent. Thus, one or more of the six internal genes of each avian parent virus was responsible for restriction of the reassortant virus in monkeys. The A/Washington/80 X A/Mallard/NY/78 reassortant virus retained its phenotype of restricted replication in monkeys after five serial passages in vivo. It also failed to transmit to cagemates or induce resistance to wild-type virus challenge, and it did not initiate a systemic or enteric infection. These findings form the basis for evaluation of these attenuated avian-human reassortant influenza A viruses as live attenuated vaccines for humans.

Descriptors: crosses, genetic, influenza A virus avian genetics, human genetics, neuraminidase genetics, chickens, child, ducks, hemagglutinins viral genetics, immunization, avian physiology, human physiology, saimiri, virus replication.


NAL Call Number: QR189.V32

Abstract: A reassortant virus possessing RNA segment 7, which codes for the M1 and M2 proteins, of the avian influenza A/Mallard/New York/6750/78 (H2N2) virus and the other seven RNA segments of the human influenza A/Udorn/307/72 (H3N2) virus had been shown previously to be markedly restricted in replication in the respiratory tract of squirrel monkeys. In contrast, a reassortant possessing segment 7 of another avian influenza virus, A/Pintail/Alberta/119/79 (H4N6), and the seven other RNA segments from the A/Udorn/72 virus was not restricted. The nucleotide and deduced amino acid sequence of the RNA segment 7 of each virus was determined to identify the structural basis for the attenuation phenotype specified by RNA segment
7 of the A/Mallard/78 virus. Analysis of the deduced amino acid sequences revealed only two amino acid differences in the M1 protein and one difference in the M2 protein, suggesting that the attenuation phenotype of a reassortant virus possessing segment 7 of the A/Mallard/78 virus may be specified by one to three amino acids. Reassortant viruses possessing RNA segment 6, which codes for the nucleoprotein, of either avian influenza virus and the other seven RNA segments of a human influenza virus were also restricted in replication in squirrel monkeys. A comparison of the deduced amino acid sequences of the two avian nucleoproteins demonstrated only three amino acid differences indicating that these two avian viruses possess NP genes that are highly related. The high degree of relatedness of both the NP and M proteins of these two avian viruses contrasts with their divergent surface antigens. (ABSTRACT TRUNCATED AT 250 WORDS)

Descriptors: genes viral, influenza A virus avian genetics, nucleoproteins genetics, viral core proteins, viral matrix proteins genetics, viral proteins genetics, amino acid sequence, base sequence, human genetics, RNA viral analysis, saimiri, virus replication.

NAL Call Number: 448.8 J821

NAL Call Number: 470 Sci2
Abstract: An influenza A reassortant virus that contained the hemagglutinin and neuraminidase genes of a virulent human virus, A/Udorn/72 (H3N2), and the six other influenza A virus genome segments from an avirulent avian virus, A/Mallard/New York/6750/78 (H2N2), was evaluated for its level of replication in squirrel monkeys and hamsters. In monkeys, the reassortant virus was as attenuated and as restricted in its level of replication in the upper and lower respiratory tract as its avian influenza virus parent. Nonetheless, infection with the reassortant induced significant resistant to challenge with virulent human influenza virus. In hamsters, the reassortant virus replicated to a level intermediate between that of its parents. These findings suggest that the nonsurface antigen genes of the avian parental virus are the primary determinants of restriction of replication of the reassortant virus in monkeys. Attenuation of the reassortant virus for primates is achieved by inefficient functioning of the avian influenza genes in primate cells, while antigenic specificity of the human influenza virus is provided by the neuraminidase and hemagglutinin genes derived from the human virus. This approach could lead to the development of a live influenza A virus vaccine that is attenuated for man if the avian influenza genes are similarly restricted in human cells.
Descriptors: influenza A virus avian genetics, human genetics, influenza vaccine immunology, antigens, surface genetics, epitopes genetics, epitopes immunology, hamsters, hemagglutinins genetics, hemagglutinins immunology, neuraminidase genetics, neuraminidase immunology, saimiri, vaccines, attenuated immunology.

NAL Call Number: QR360.J6
Abstract: Avian influenza virus reassortants containing human influenza virus hemagglutinins do not replicate in ducks. Two mutations in the receptor-binding site of a human hemagglutinin at residues 226 and 228 allowed replication in ducks. The mutations resulted in a receptor-binding-site sequence identical to the known avian influenza virus sequences.
Descriptors: influenza A virus avian genetics, human genetics, mutation, receptors, immunologic genetics,
A double-strand DNA copy of the influenza virus A/Seal/Mass/1/80 (H7N7) [seal] hemagglutinin (HA) gene was cloned into the plasmid pAT153/PvuII/8 and sequenced to deduce the primary amino acid sequence. The gene is 1731 nucleotides long and codes for a protein of 560 amino acids with a nonglycosylated molecular weight of 62098 Da. The deduced amino acid sequence displays similarities to all other sequenced hemagglutinins by retaining six of seven potential glycosylation sites, showing conservation in the number and position of cysteine residues, conservation in the fusion and anchor peptides, and conservation in the putative receptor site of the molecule. However, three features of the primary amino acid sequence could be distinguished from the H7 amino acid sequence of A/fowl plague/Rostock/34 (FPV), another avian H7 influenza virus which does not produce disease in mammals. First, the seal HA sequence has three fewer amino acids in the connecting peptide region of the HA than FPV. This lack of multiple basic amino acids in the connecting peptide is similar to that found in avirulent H7 avian strains and to mammalian serotypes H1, H2, and H3. Second, the seal HA has gained four additional proline residues, all in HA1, as compared to FPV. These residues may alter the tertiary structure of the HA and ultimately contribute to the biological features of this virus. Third, the seal HA has lost a potential carbohydrate attachment site at residue 149 which lies at the tip of the HA structure. The loss of this carbohydrate could alter the seal HAs interaction with host cell receptors.

Descriptors: genes viral, hemagglutinins viral genetics, influenza A virus genetics, amino acid sequence, base sequence, chemistry, DNA, hemagglutinins viral analysis, influenza A virus avian genetics, influenza A virus immunology, proline analysis, protein conformation, structure activity relationship.

To determine which gene segments of influenza A viruses are responsible for the property of tissue tropism, reassortants were produced between the avian influenza strain, A/Mal/NY/6750/78 [H2N2] (Mal/NY), and a human strain, A/Udorn/307/72 [H3N2] (Udorn). The avian strain replicates in the intestinal tract of ducks and the human strain does not. Eight reassortants were shown by hybridization analysis to have the same gene constellation, having received hemagglutinin gene segment 4 from Udorn and the remaining seven gene segments from Mal/NY. With one exception, all reassortants containing the Udorn HA were restricted in their ability to traverse the digestive tract of ducks and replicate therein. The exception, reassortant R2, replicated to high titers in the intestinal tract. The R2 virus was shown to possess a hemagglutinin molecule that was antigenically distinguishable from the Udorn parent with polyclonal and monoclonal antibodies. The virus was "nonavid" in reaction with antihemagglutinin antibodies and was phenotypically similar to avian influenza viruses. The results suggest that the R2 hemagglutinin has undergone mutation(s) altering tissue tropism and antigenic properties of the virus. These studies illustrate the importance of the hemagglutinin gene in determining tissue tropism and present an example of phenotypic variation in a virus population with the same gene constellation but do not exclude a requirement for other gene products.

Descriptors: ducks microbiology, genes viral, influenza A virus avian genetics, influenza A virus human genetics, virus replication, hemagglutinins viral genetics, hemagglutinins viral immunology, influenza A virus avian immunology, influenza A virus avian physiology, influenza A virus human immunology, influenza A virus human physiology, intestines microbiology, nucleic acid hybridization, recombination, genetic.
influenza A viruses can interact with each other in the context of a mammalian cell, a genetic system that allows the in vivo reconstitution of active ribonucleoproteins was used. The ability to achieve replication of a viral-like reporter RNA in COS-1 cells was examined with heterospecific mixtures of the core proteins (PB1, PB2, PA and NP) from two strains of human viruses (A/Puerto Rico/8/34 and A/Victoria/3/75), two strains of avian viruses (A/Mallard/NY/6750/78 and A/FPV/-Rostock/34), and a strain of avian origin (A/Hong Kong/156/97) that was isolated from the first human case of H5N1 influenza in Hong Kong in 1997. In accordance with published observations on reassortant viruses, PB2 amino acid 627 was identified as a major determinant of the replication efficiency of heterospecific complexes in COS-1 cells. Moreover, the results showed that replication of the viral-like reporter RNA was more efficient when PB2 and NP were both derived from the same avian or human virus or when PB1 was derived from an avian virus, whatever the origin of the other proteins. Furthermore, the PB1 and PB2 proteins from the A/Hong Kong/156/97 virus exhibited intermediate properties with respect to the corresponding proteins from avian or human influenza viruses, suggesting that some molecular characteristics of PB1 and PB2 proteins might at least partially account for the ability of the A/Hong Kong/156/97 virus to replicate in humans.

Descriptors: influenza A virus avian genetics, influenza A virus human genetics, nucleoproteins, RNA replicase, viral core proteins genetics, viral core proteins metabolism, cos cells, chloramphenicol o acetyltransferase, cloning, molecular, DNA, complementary, DNA directed RNA polymerases genetics, DNA directed RNA polymerases metabolism, influenza A virus avian metabolism, influenza A virus human metabolism, molecular sequence data, plasmids genetics, sequence analysis, DNA, transcription, genetic, transfection, viral proteins genetics, viral proteins metabolism, virus replication.

NAL Call Number: QH434.V57
Abstract: We compared the amino acid sequences of the NS1 proteins of human, equine, and avian influenza viruses. The ratios of the amino acid substitutions per nucleotide substitutions in the NS1 proteins were about 27-45%, suggesting the existence of constraints on the amino acid changes of the NS1 protein in evolution. As a measure of constraints exerted on the regions of a protein, a changeability index is proposed. There was a highly conserved region between amino acid residues 30 and 50. The C-terminal region of amino acid residue 165 was a continuously changeable region. We have either introduced several nucleotide substitutions to the NS cDNA of the A/Udorn/72 virus in vitro or constructed the recombinant NS cDNAs between the A/Udorn/72 and A/chick/Japan/24 viruses, and then expressed them in animal cells. We have found that the amino acid substitutions introduced to the low-conserved region of the NS1 protein affected the stability and nuclear localization of the NS1 protein. One of the chimeric proteins between the A/Udorn/72 and A/chick/Japan/24 viruses did not move to the nucleus of the cell and remained in the cytoplasm.
Descriptors: capsid genetics, evolution, genes viral, influenza A virus genetics, viral core proteins genetics, amino acid sequence, base sequence, birds, chimera, cytoplasm ultrastructure, DNA, viral analysis, fluorescent antibody technique, horses, molecular sequence data, mutation, structure activity relationship, viral nonstructural proteins.

NAL Call Number: 448.8 V81
Abstract: The nucleotide sequences of the M and NS1 genes of influenza virus A/Swine/Iowa/15/30 (A/SW/IW/30)(H1N1) were determined with cloned DNAs and compared with reported sequences of human and avian influenza viruses. A/SW/IW/30 virus was found to be closely similar to A/PR/8/34(H1N1) virus in the nucleotide sequences of the M and NS1 genes, the base differences between the two strains being 64 out of 1027 nucleotides in the M gene and 52 out of 740 in the NS1 gene. Based on the assumptions that these two viruses were derived from a common ancestor and that the rate of base changes per year was the same in man and in swine, it was estimated that the progenitor virus was in circulation during the period from 1915 to 1920. This estimation was compatible with the epidemiological findings suggesting that the progenitor of the swine influenza virus was the agent of the 1918 influenza pandemic. Furthermore, the M
and NS1 gene sequences of A/FPV/Rostock/34(H7N6) virus were much closer to those of A/SW/IW/30 and A/PR/8/34 viruses than to A/duck/Alberta/60/76(H12N5) virus, but not as close as the A/SW/IW/30 virus was to A/PR/8/34 virus.

Descriptors: influenza A virus human genetics, influenza A virus, porcine genetics, influenza A virus genetics, base sequence, evolution, genes viral.


NAL Call Number: QH434.V57

Abstract: We compared the nucleotide sequences of the NS genes of 13 animal influenza viruses belonging to human, swine, avian, and equine viruses for the study of the genetic relatedness of the NS genes in animal influenza viruses. The NS genes of three virus strains A/chicken/Brescia/02, A/equine/Prague/56, and A/equine/Miami/63 were newly sequenced. The base sequence homologies between the NS genes of avian, human, swine, and the A/equine/Miami/63 viruses were 87.8% or higher. On the other hand, the base sequence of the NS gene of the A/equine/Prague/56 virus differed widely from those of other viruses analyzed in the present study. We constructed a model of the genetic tree of the NS genes of avian and equine influenza viruses by a modified Farris method. For comparison of the NS genes between human and avian viruses, we estimated the speed of the nucleotide substitutions of the avian influenza NS genes. It was roughly constant, even though the substitutions did not occur sequentially. The nucleotide substitution rate of the NS genes of avian influenza viruses was one-third to one-fourth that of human influenza viruses. We deduced the time of separation between the NS genes of human and avian influenza viruses during evolution.

Descriptors: base sequence, capsid genetics, evolution, genes viral, influenza A virus genetics, sequence homology, nucleic acid, viral core proteins genetics, DNA, viral analysis, molecular sequence data, viral nonstructural proteins.


NAL Call Number: 448.8 V81

Abstract: The nucleotide sequences of the NS genes of avian influenza A viruses, A/Chicken/Japan/24, A/Duck/England/56, A/Tern/South Africa/61, A/Duck/Ukraine/1/63, and A/Mynah/Hanedo-Thai/76, were determined and compared among themselves and with two reported NS sequences of the avian viruses, A/FPV/Rostock/34 and A/Duck/Alberta/60/76. Thirty-six to two hundred forty base differences in the NS genes were found in pairwise comparisons among the viruses. The numbers of base differences in the NS genes increased with time, except A/Duck/Alberta/60/76 virus. However, the NS genes of the avian viruses did not change sequentially with time and were arranged in separate evolutionary lineages. When the NS genes of avian viruses employed in the present study were compared with those of human viruses, sequence similarity was confirmed (M. Baez, R. Taussig, J. J. Zarza, J. F. Young, P. Palese, A. Reisfield, and A. M. Skalka, 1980, Nucleic Acids Res. 8, 5845-5858). The numbers of base differences in the NS genes between avian viruses and the A/PR/8/34 virus were 61 to 83, and the NS gene of the oldest avian isolate, A/Chicken/Japan/24, was most closely related to that of the A/PR/8/34 virus. It was hypothesized that NS genes of human influenza viruses and those of some avian influenza viruses had been derived from a common ancestor gene.

Descriptors: antigens, viral genetics, influenza A virus immunology, viral proteins genetics, sequence homology, nucleic acid, viral core proteins genetics, DNA, viral analysis, molecular sequence data, viral nonstructural proteins.


NAL Call Number: QR375.V6

Abstract: Nine mutants of fowl plague virus with temperature-sensitive defects in the biosynthesis of the hemagglutinin have been characterized by analyzing the processing and the intracellular location of this glycoprotein in MDCK and chick embryo cells. It was found that with all of these mutants the transport of the
hemagglutinin to the cell surface was impeded at the non-permissive temperature. There were differences, however, in the site of the block. With mutants tsl, ts227, ts478 and ts658 the precursor HA was not cleaved and the oligosaccharide side chains remained sensitive to endoglucosaminidase H. When the hemagglutinin was analyzed in permeabilized cells by immunofluorescence, usually only cytoplasmic labeling was seen. Immunofluorescence of non-permeabilized cells and hemadsorption revealed that the hemagglutinin did not reach the cell surface. In contrast, the hemagglutinin of mutants ts79, ts482, ts532, ts546 and ts651 was cleaved and oligosaccharides were processed to the endoglucosaminidase H-resistant form at non-permissive temperature. In permeabilized cells, the cytoplasm and juxtanuclear regions typical for the Golgi apparatus were labeled by immunofluorescence. Except for ts482, ts532 and ts546 which were leaky, hemagglutinin could not be detected at the cell surface. These observations indicate that, with the first group of mutants, hemagglutinin transport is usually arrested already in the rough endoplasmic reticulum, whereas with the second group it is inhibited at a late stage between the Golgi apparatus and the plasma membrane.

Descriptors: defective viruses genetics, hemagglutinins viral, influenza A virus avian genetics, mutation, cell line, chick embryo, defective viruses growth and development, hemagglutination, influenza A virus avian growth and development, temperature.


NAL Call Number: 47.8 Am33P

Abstract: The effect of microaerosolized H2O2 on bacterial and viral poultry pathogens was investigated. Bacterial cultures and viruses were dried on sterile glass Petri dishes and subjected to direct and indirect 5% (H2O2) microaerosol mist. In the trials using Escherichia coli and Staphylococcus aureus, there was complete inactivation following exposure to H2O2. Using Salmonella typhimurium, indirect exposure resulted in only partial inactivation whereas direct exposure to H2O2 gave complete inactivation. For the viruses studied, 5% H2O2 microaerosol mist completely inactivated infectious laryngotracheitis virus. Newcastle disease virus, infectious bronchitis virus, and avian influenza virus showed reduced infectivity but were not completely inactivated. Avian reovirus susceptibility varied with the method of exposure and infectious bursal disease virus was highly resistant. The use of 10% H2O2 mist, however, resulted in total inactivation of infectious bursal disease virus. The effect of 10% H2O2 on equipment and selected materials representative of a hatcher or poultry house was investigated. A solar cell calculator, a thermostat containing a microswitch, and samples of uncoated steel, galvanized steel, and uncoated aluminum were subjected to 10 fumigation cycles. No damage was detected in the calculator and the thermostat. Both the uncoated steel and the galvanized steel showed signs of oxidation. The aluminum did not show signs of oxidation.


Nerome, K., Y. Yoshioka, S. Sakamoto, H. Yasuhara, and A. Oya (1985). Characterization of a 1980-swine recombinant influenza virus possessing H1 hemagglutinin and N2 neuraminidase similar to that of the earliest Hong Kong (H3N2) virus. Archives of Virology 86(3-4): 197-211. ISSN: 0304-8608.

NAL Call Number: 448.3 Ar23

Abstract: A recombinant (H1N2, formerly Hsw 1N2), A/swine/Ehime/1/80 was found to possess antigenic, biological and genomic characteristics different from those of a previous A/swine/Kanagawa/2/78 (H1N2) strain. Five monoclonal antibodies to A/NJ/8/76 definitely differentiated the hemagglutinin molecules of the former virus from the latter, showing that these viruses differed, at least, at two antigenic determinants. Neuraminidase-inhibition tests with monoclonal antibodies to different H2N2 and H3N2 viruses revealed that the A/swine/Ehime/1/80 strain contained a neuraminidase very similar to that of the late human Asian (H2N2) and the earliest Hong Kong (H3N2) viruses. Growth comparison of swine and human isolates indicated that A/swine/Ehime/1/80 and A/swine/Shizuoka/1/78 (H1N1) failed to grow at 42 degrees C, while
A/swine/Kanagawa/2/78 and its possible parental virus, A/swine/Kanagawa/4/78 (H1N1) replicated efficiently at this stringent temperature. These results revealed that the viruses having growth characteristics similar to those of avian influenza virus were present in the swine population. RNA analysis by oligonucleotide mapping suggested that A/swine/Ehime/1/80 may be a recombinant between A/swine/Shizuoka/1/78-like and A/Aichi/2/68 (H3N2)-like viruses. To further determine the gene constellation of this recombinant virus, DNA-RNA hybridization was performed by using DNA segments complementary for swine (H1N1) virus RNA and the entire RNAs of three viruses. The molecular hybridization could define the genomic composition of the recombinant, indicating that only the neuraminidase gene of this virus is derived from the earliest Hong Kong (H3N2)-like virus and remaining seven genes from swine (H1N1) virus.


NAL Call Number: 448.3 Ar23

Abstract: The characteristics of an avian influenza virus were compared in detail with those of human Asian (H2N2) influenza viruses. Antigenic analysis by different antisera against H2N2 viruses and monoclonal antibodies to both the hemagglutinin and neuraminidase antigens showed that an avian isolate, A/duck/Munchen/9/79 contained hemagglutinin and neuraminidase subunits closely related to those of the early human H2N2 viruses which had been prevalent in 1957. However, this avian virus gave low HI titers with absorbed and non-absorbed antisera to different human H2N2 viruses isolated in 1957. Like human Q phase variant such as A/RI/5-/57 (H2N2), hemagglutination of the above avian strain was not inhibited by the purified non-specific gamma-inhibitor from guinea pig serum. Growth behavior at restrictive temperature (42 degrees C) clearly differentiate the avian H2N2 virus from human influenza viruses, showing that the former virus grew well in MDCK cells at 42 degrees C but not the latters. Genomic analysis of these viruses revealed that the oligonucleotide map of H2N2 virus isolated from a duck was quite different from those of human H2N2 viruses from 1957 to 1967. The oligonucleotide mapping also indicated that different H2N2 influenza virus variants had co-circulated in humans in 1957.

Descriptors: influenza A virus avian immunology, influenza A virus human immunology, hemagglutinin viral immunology, influenza A virus avian genetics, influenza A virus human genetics, influenza A virus growth and development, neuraminidase immunology, RNA viral genetics.


NAL Call Number: 448.8 V81

Abstract: In 1985 a fowl plague-like disease occurred in chickens in Lockwood, Victoria, Australia and caused high mortality. An H7N7 influenza virus was isolated from the chickens (A/Chicken/Victoria/1/85); additionally, an antigenically similar virus was isolated from starlings (A/Starling/Victoria/5156/85) and serological evidence of H7N7 virus infection was found in sparrows. Antigenic analysis with monoclonal antibodies to H7, oligonucleotide mapping of total vRNA, and sequence analysis of the HA genes established that the chicken and starling influenza viruses were closely related and probably came from the same source. There was high nucleotide sequence homology (95.3%) between the HA genes of A/Chick/Vic/85 and a fowl plague-like virus isolated from chickens in Victoria 9 years earlier [A/Fowl/Vic/76 (H7N7)]. The sequence homologies indicated that the A/Chick/Vic/85 and A/Fowl/Vic/76 were derived from a common recent ancestor, while another recent H7N7 virus, Seal/Mass/1/80 originated from a different evolutionary lineage. Experimental infection of chickens and starlings with A/Chick/Vic/1/85 (H7N7) was associated with high mortality (100%), transmission to contact birds of the same species, and virus in all organs. In sparrows one-third of the birds died after infection and virus was isolated from most organs; transmission to contact sparrows did not occur. In contrast, the H7N7 virus replicated in ducks and spread to...
contact ducks but caused no mortality. These studies establish that the host species plays a role in determining the virulence of avian influenza viruses, and provide the first evidence for transmission of virulent influenza viruses between domestic poultry and passerine birds. They support the hypothesis that potentially virulent H7N7 influenza viruses could be maintained in ducks where they cause no apparent disease and may sometimes spread to other wild birds and domestic poultry.

Descriptors: birds microbiology, hemagglutinin viral genetics, influenza A virus avian genetics, amino acid sequence, animals, wild microbiology, Australia, base sequence, chickens microbiology, disease reservoirs, genes viral, molecular sequence data, nucleotide mapping, RNA viral genetics, species specificity, virus replication.


NAL Call Number: QH506.M65F2

Abstract: The complete primary structure of cDNA for hemagglutinin gene of influenza virus A/FPV/waynebridge/27 subtype H7 has been determined. Its comparison with the structures of analogous genes from other strains of the same subtype has shown 75% of base changes resulting in silent mutations. This suggests the weak immunological pressing in course of evolution of this subtype strains. The reason for apathogenicity of this avian strain is supposed to be elimination of a glycosylation site present in the strain A/FPV/Rostock/34. The possibility of using the obtained data for construction of the new generation of vaccines is discussed.

Descriptors: genes viral, hemagglutinin viral genetics, influenza A virus avian genetics, amino acid sequence, base sequence, molecular sequence data.


NAL Call Number: 41.8 Av5

Abstract: Avian influenza viruses are major contributors to viral disease in poultry as well as humans. Outbreaks of high-pathogenicity avian influenza viruses cause high mortality in poultry, resulting in significant economic losses. The potential of avian influenza viruses to reassort with human strains resulted in global pandemics in 1957 and 1968, while the introduction of an entirely avian virus into humans claimed several lives in Hong Kong in 1997. Despite considerable research, the mechanisms that determine the pathogenic potential of a virus or its ability to cross the species barrier are poorly understood. Reverse genetics methods, i.e., methods that allow the generation of an influenza virus entirely from cloned cDNAs, have provided us with one means to address these issues. In addition, reverse genetics is an excellent tool for vaccine production and development. This technology should increase our preparedness for future influenza virus outbreaks.

Descriptors: epidemiology, infection, molecular genetics, avian influenza, genetics, infectious disease, prevention and control, respiratory system disease, viral disease, disease control, economic losses, global pandemics, reverse genetics, viral outbreaks, viral pathogenicity.


NAL Call Number: 500 N21P

Abstract: We describe a new reverse-genetics system that allows one to efficiently generate influenza A viruses entirely from cloned cDNAs. Human embryonic kidney cells (293T) were transfected with eight plasmids, each encoding a viral RNA of the A/WSN/33 (H1N1) or A/PR/8/34 (H1N1) virus, flanked by the human RNA polymerase I promoter and the mouse RNA polymerase I terminator-together with plasmids encoding viral nucleoprotein and the PB2, PB1, and PA viral polymerases. This strategy yielded >1 x 10(3) plaque-forming units (pfu) of virus per ml of supernatant at 48 hr posttransfection. The addition of plasmids expressing all of the remaining viral structural proteins led to a substantial increase in virus production, 3 x
We also used reverse genetics to generate a reassortant virus containing the PB1 gene of the A/PR/8/34 virus, with all other genes representing A/WSN/33. Additional viruses produced by this method had mutations in the PA gene or possessed a foreign epitope in the head of the neuraminidase protein. This efficient system, which does not require helper virus infection, should be useful in viral mutagenesis studies and in the production of vaccines and gene therapy vectors.

**Descriptors:** DNA, complementary, DNA, viral genetics, influenza A virus genetics, RNA viral genetics, cell line, chick embryo, dogs, hn protein genetics, influenza A virus avian genetics, influenza A virus human genetics, influenza A virus physiology, kidney, mice, plasmids, RNA polymerase I metabolism, reverse transcriptase polymerase chain reaction, transfection, viral structural proteins genetics, virus replication.


**NAL Call Number:** RS1.A7

**Abstract:** benzoxazolone-5-(2'-nitro)-sulphonanilides were synthesized by acylation of o-nitroanilines with benzoxazolone-5-sulphochloride or 3-methylbenzoxazolone-5-sulphochloride. The nitro group in these compounds was subjected to reduction and the resulting amino derivatives were cyclised to yield the corresponding 1-(benzoxazolone-5'-sulphonyl)-benzotriazoles. Decyclization of the oxazolone cycle of benzoxazolone-5-(2'-amino)-sulphonanilides resulted in 4-hydroxy-3,2'-diaminobenzenesulphonanilides. In vitro testing of the antiviral activity of the compounds obtained during successive synthetic steps revealed that some of them exhibited marked antiviral effect against toga, orthomixo, oncorna and herpes viruses.

**Descriptors:** antiviral agents chemical synthesis, benzoxazoles chemical synthesis, sulfanilamides chemical synthesis, antiviral agents pharmacology, benzoxazoles pharmacology, chemistry, cytopathogenic effect, viral drug effects, herpesvirus 1, suid drug effects, influenza A virus avian drug effects, mice, mice inbred BALB c, moloney murine leukemia virus drug effects, Semliki Forest virus drug effects, sulfanilamides pharmacology, triazoles chemical synthesis, triazoles pharmacology.


**NAL Call Number:** QR360.A1J6

**Abstract:** Eleven temperature-sensitive (ts) mutants of influenza A (fowl plague, Rostock) virus were analysed for in vitro RNA transcriptase activity in reactions primed by ApG or globin mRNA at 31 degrees C or at 40.5 degrees C, the restrictive temperature for ts mutant growth. Only those ts mutants studied which were defective in RNA segment 1, coding for the virion P2 protein, were defective in RNA transcriptase activity when compared to wild-type virus. Mutants having a defect in the P2 protein had no significant RNA transcriptase activity in reactions at 40.5 degrees C primed by globin mRNA. However, one mutant showed RNA transcriptase activity similar to wild-type virus at 40.5 degrees C when ApG (0.3 mM) was used as primer. The results suggest that influenza (fowl plague, Rostock) P2 protein is directly involved in the mRNA priming reaction, as well as in the RNA transcription reaction in vitro.

**Descriptors:** dinucleoside phosphates, influenza A virus avian metabolism, RNA nucleotidyltransferases metabolism, RNA replicase metabolism, RNA viral biosynthesis, viral proteins physiology, adenosine monophosphate analogs and derivatives, adenosine monophosphate physiology, globins, guanosine analogs and derivatives, guanosine physiology, influenza A virus avian genetics, mutation, RNA, messenger physiology, transcription, genetic.


**NAL Call Number:** 381 B522

**Descriptors:** cell membrane physiology, cell transformation, viral, influenza A virus avian, influenza A virus, Newcastle disease virus, sarcoma viruses, avian, cell membrane ultrastructure, chick embryo, fibroblasts physiology, magnetic resonance spectroscopy.

NAL Call Number: QP501.E8

Abstract: The N-glycosidically linked glycans in the large subunit (HA1) of the hemagglutinin from fowl plague virus, strain Dutch (containing about 15%, w/w, of carbohydrates), were liberated by alkaline hydrolysis, and were filtrated through Bio-Gel as the re-N-acetylated oligosaccharide alditols. One major fraction (90%, mol/mol) was obtained. It was subfractionated by concanavalin A affinity chromatography and was analyzed by methylation/capillary gas chromatography/mass fragmentography and especially by one-dimensional and two-dimensional 1H nuclear magnetic resonance. The major HA1 glycans, which are not sialylated, were thus found to comprise about 40%, 30% and 20% (mol/mol), respectively, of biantennary intersected, biantennary, and triantennary N-acetyllactosaminic ('complex') oligosaccharides. About two thirds of the internal GlcNAc residues in these glycans are substituted by Fuc(alpha 1----6), all the triantennary species carry the third Gal(beta 1----4)GlcNAc(beta 1----unit at the Man(alpha 1----6)-branch, and roughly one fourth of the N-acetyllactosamine units in the non-intersected biantennary oligosaccharides are incomplete.

Descriptors: hemagglutinins viral, influenza A virus avian analysis, oligosaccharides analysis, amino acids analysis, chemistry, hemagglutination tests, hemagglutinin glycoproteins, influenza virus, hexosamines analysis, magnetic resonance spectroscopy methods, mass fragmentography, methylation, polysaccharides analysis.


NAL Call Number: 381 J824

Abstract: We have fluorescently labeled one of the eight genomic segments of influenza virus RNA and a recombinant influenza viral protein, the nucleoprotein (NP), to investigate the requirement for their uptake into nuclei of digitonin-permeabilized cells. We found that the influenza viral NP behaves like a nuclear localization sequence (NLS) containing protein. Thus, at 0 degrees C it docks at the nuclear envelope only in the presence of the heterodimeric karyopherin (either karyopherin alpha 1 beta or karyopherin alpha 2 beta), and docking is competitively inhibited by an unlabeled NLS containing substrate. Like other NLS-containing proteins, at 20 degrees C NP is imported into the nucleus after further addition of the GTPase Ran and of p10. In contrast, the fluorescently labeled, 890-nucleotide-long viral RNA segment does not dock to the nuclear envelope or enter the nucleus either in the presence of exogenous cytosol or of karyopherin heterodimer, Ran, and p10. However, in the presence of NP the RNA is able to dock and enter the nucleus with transport requirements indistinguishable from those for docking and entry of NP. These data indicate that uptake of the influenza virus RNA segment is not via a signal in the RNA but via an NLS of a viral protein such as NP.

Descriptors: cell nucleus metabolism, influenza A virus avian physiology, nuclear proteins metabolism, RNA viral metabolism, binding, competitive, cell nucleus virology, digitonin, kinetics, liver virology, macromolecular systems, nuclear envelope metabolism, rats, rats, inbred buf.


NAL Call Number: 448.8 P942

Descriptors: amantadine analogs and derivatives, antiviral agents, influenza prevention and control, influenza A virus avian drug effects, amantadine pharmacology, amantadine therapeutic use, mice, virus replication drug effects.


**Abstract:** The hemagglutinin of the Rostock strain of fowl plague virus was expressed in CV-1 cells by a simian virus 40 vector, and its stability in the exocytotic transport process was examined by a fusion assay. A 50-fold increase in the fusion activity of the hemagglutinin was observed when expression occurred in the presence of ammonium chloride, Tris-HCl, or high doses of amantadine. When chloroquine, another acidotropic agent, was used, the hemagglutinin exposed at the cell surface had to be activated by trypsin, because intracellular cleavage was inhibited by this compound. Hemagglutinin mutants resistant to intracellular cleavage did not require acidotropic agents for full expression of fusion activity, when treated with trypsin after arrival at the cell surface. These results indicate that fowl plague virus hemagglutinin expressed by a simian virus 40 vector is denatured in the acidic milieu of the exocytotic pathway and that cleavage is a major factor responsible for the pH instability. Coexpression with the M2 protein also markedly enhanced the fusion activity of the hemagglutinin, and this effect was inhibited by low doses of amantadine. These results support the concept that M2, known to have ion channel function, protects the hemagglutinin from denaturation by raising the pH in the exocytotic transport system. The data also stress the importance of acidotropic agents or coexpressed M2 for the structural and functional integrity of vector-expressed hemagglutinin.

**Descriptors:** hemagglutinin, viral biosynthesis, influenza A virus avian metabolism, viral matrix proteins, pharmacology, ammonium chloride pharmacology, base sequence, biological transport, cell fusion drug effects, cultured cells, *Cercopithecus aethiops*, fluorescent antibody technique, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral genetics, hemagglutinin viral isolation and purification, hydrogen-ion concentration, influenza A virus avian genetics, membrane proteins biosynthesis, molecular sequence data, recombinant proteins biosynthesis, simian virus 40 genetics, viral fusion proteins biosynthesis, viral fusion proteins genetics, viral matrix proteins biosynthesis, viral matrix proteins genetics.


**Abstract:** When hemagglutinin (HA) of fowl plague virus (FPV) was expressed in CV-1 cells by a simian virus 40 vector, hemadsorption was barely detectable, although HA was exposed at the cell surface. However, treatment of HA-expressing cells with *Vibrio cholerae* neuraminidase (VCNA) resulted in extensive hemadsorption. VCNA treatment enhanced the electrophoretic mobility of the HA1 subunit of HA, indicating the removal of sialic acid. When two oligosaccharides in the vicinity of the receptor binding site of FPV HA were deleted by site-specific mutagenesis, VCNA treatment was not required for hemadsorption. Mutants which retained one of these oligosaccharides and mutants in which oligosaccharides not adjacent to the receptor binding site were deleted needed VCNA treatment to show hemadsorption. VCNA treatment also enhanced hemadsorption of vector-expressed HA of the WSN strain, which had a complex-type oligosaccharide in the vicinity of the receptor binding site, but had no effect on hemadsorption of Hong Kong type HA, which has a high-mannose type oligosaccharide adjacent to the receptor binding site. These results indicate that sialic acid on oligosaccharides near the receptor binding site interferes with hemadsorption. Thus, the neuraminidase is essential for FPV HA to show hemagglutinating activity.

**Descriptors:** hemagglutination, hemagglutinins viral metabolism, influenza A virus avian immunology, neuraminidase pharmacology, glucosaminidase, glycosylation, hemagglutinins viral chemistry, N-acetylneuraminic acid, sialic acids chemistry.


**NAL Call Number:** QR360.J6

**Abstract:** The hemagglutinin (HA) of fowl plague virus was lengthened and shortened by site-specific mutagenesis at the cytoplasmic tail, and the effects of these modifications on HA functions were analyzed after expression from a simian virus 40 vector. Elongation of the tail by the addition of one to six histidine (His) residues did not interfere with intracellular transport, glycosylation, proteolytic cleavage, acylation, cell surface expression, and hemadsorption. However, the ability to induce syncytia at a low pH decreased dramatically depending on the number of His residues added. Partial fusion (hemifusion), assayed by fluorescence transfer from octadecylrhodamine-labeled erythrocyte membranes, was also reduced, but even with the mutant carrying six His residues, significant transfer was observed. However, when the formation of fusion pores was examined with hydrophilic fluorescent calcein, transfer from erythrocytes to HA-expressing cells was not observed with the mutant carrying six histidine residues. The addition of different amino acids to the cytoplasmic tail of HA caused an inhibitory effect similar to that caused by the addition of His. On the other hand, a mutant lacking the cytoplasmic tail was still able to fuse at a reduced level. These results demonstrate that elongation of the cytoplasmic tail interferes with the formation and enlargement of fusion pores. Thus, the length of the cytoplasmic tail plays a critical role in the fusion process.

**Descriptors:** hemagglutinin glycoproteins, influenza virus metabolism, histidine metabolism, influenza A virus avian metabolism, membrane fusion physiology, amino acids, biological transport, cell line, cell membrane metabolism, *Cercopithecus aethiops*, cytoplasm metabolism, hemagglutinin glycoproteins, influenza virus chemistry, hemagglutinin glycoproteins, influenza virus genetics, histidine genetics, influenza A virus avian genetics, intracellular fluid, mutagenesis.


**NAL Call Number:** QR360.J6

**Abstract:** The hemagglutinin (HA) of the fowl plague virus (FPV) strain of influenza A virus has two N-linked oligosaccharides attached to Asn123 and Asn149 in the vicinity of the receptor binding site. The effect of these carbohydrate side chains on the binding of HA to neuraminic acid-containing receptors has been analyzed. When the oligosaccharides were deleted by site-specific mutagenesis, HA expressed from a simian virus 40 vector showed enhanced hemadsorbing activity. Binding was so strong under these conditions that erythrocytes were no longer released by viral neuraminidase and that release was significantly reduced when neuraminidase from Vibrio cholerae was used. Similarly, when these oligosaccharides were removed selectively from purified viruses by N-glycosidase F, such virions were unable to elute from receptors, although they retained neuraminidase activity. Thus, release of FPV from cell receptors depends on the presence of the HA glycans at Asn123 and Asn149. On the other hand, receptor binding was abolished when these oligosaccharides were sialylated after expression in the absence of neuraminidase (M. Ohuchi, A. Feldmann, R. Ohuchi, and H.-D. Klenk, Virology 212:77-83, 1995). These observations indicate that the receptor affinity of FPV HA is controlled by oligosaccharides adjacent to the receptor binding site.

**Descriptors:** hemagglutinin glycoproteins, influenza virus chemistry, influenza A virus avian metabolism, neuraminidase chemistry, receptors, virus metabolism, binding sites, cell line, cultured cells, dogs, erythrocytes virology, glycosylation, hemagglutinin glycoproteins, influenza virus metabolism, neuraminidase metabolism, structure activity relationship, virion metabolism.


**NAL Call Number:** 448.8 V81

**Abstract:** Six variants that form plaques in chick embryo cells in the absence of trypsin have been isolated from the apathogenic avian influenza virus A/chick/Pennsylvania/1/83 (H5N2). Unlike the wild-type, the plaque variants contain a hemagglutinin that is cleaved in chick embryo cells and MDCK cells. The variants differ also from the wild-type in their pathogenicity for chickens. Nucleotide sequence and oligosaccharide analysis of the hemagglutinin have revealed that, unlike natural isolates with increased pathogenicity (Y.
Kawaoka et al., 1984, Virology 139, 303-316; Y. Kawaoka and R. G. Webster, 1985, Virology 146, 130-137), the variants obtained in vitro have retained an oligosaccharide at asparagine 11 that is believed to interfere with the cleavage site of the wild-type. However, all variants showed mutations in the hemagglutinin resulting in an increased number of basic groups at the cleavage site. These observations demonstrate that masking of the cleavage site by an oligosaccharide is overcome by an enhancement of the basic charge at the cleavage site.

Descriptors: hemagglutinins, viral genetics, influenza A virus, avian pathogenicity, amino acid sequence, base sequence, cultured cells, chick embryo, chickens, fowl plague, microbiology, genes viral, hemagglutinins, viral analysis, influenza A virus, avian genetics, influenza A virus, avian growth and development, molecular sequence data, mutation, oligosaccharides analysis, plaque assay, trypsin pharmacology.


NAL Call Number: QR360.J6

Abstract: To examine the prerequisites for cleavage activation of the hemagglutinin of human influenza viruses, a cDNA clone obtained from strain A/Port Chalmers/1/73 (serotype H3) was subjected to site-directed mutagenesis and expressed in CV-1 cells by using a simian virus 40 vector. The number of basic residues at the cleavage site, which consists of a single arginine with wild-type hemagglutinin, was increased by inserting two, three, or four additional arginines. Like wild-type hemagglutinin, mutants with up to three additional arginines were not cleaved in CV-1 cells, but insertion of four arginines resulted in activation. When the oligosaccharide at asparagine 22 of the HA1 subunit of the hemagglutinin was removed by site-directed mutagenesis of the respective glycosylation site, only three inserted arginines were required to obtain cleavage. Mutants containing a series of four basic residues were also generated by substituting arginine for uncharged amino acids immediately preceding the cleavage site. The observation that these mutants were not cleaved, even when the carbohydrate at asparagine 22 of HA1 was absent, underscores the fact that the basic peptide had to be generated by insertion to obtain cleavage. The data show that the hemagglutinin of a human influenza virus can acquire high cleavability, a property known to be an important determinant for the pathogenicity of avian influenza viruses. Factors important for cleavability are the number of basic residues at the cleavage site, the oligosaccharide at asparagine 22, and the length of the carboxy terminus of HA1.

Descriptors: hemagglutinins, viral metabolism, influenza A virus, human metabolism, amino acid sequence, arginine chemistry, base sequence, cloning, molecular, DNA mutational analysis, endopeptidases, metabolism, glycoproteins metabolism, hemagglutinins, viral chemistry, hemagglutinins, viral genetics, molecular sequence data, oligonucleotides chemistry, protein processing, post translational, structure activity relationship.


NAL Call Number: 448.8 V81

Abstract: Nucleotide sequences of the PA genes of influenza A viruses, isolated from a variety of host species, were analyzed to determine the evolutionary pathways of these genes and the host specificity of the genes. Results of maximum parsimony analysis of the nucleotide sequences indicate at least five lineages for the PA genes. Those from human strains represent a single lineage, whereas the avian genes appear to have evolved as two lineages—one comprising genes from many kinds of birds (e.g., chickens, turkeys, shorebirds, and ducks) and the other comprising only genes from gulls. H3N2 swine influenza virus PA genes are closely related to the currently circulating duck virus PA gene. By contrast, the H1N1 swine and equine virus PA genes appear to have evolved along independent lineages. Comparison of predicted amino acid sequences disclosed 10 amino acid substitutions in the PA proteins of all avian and H3N2 swine viruses that distinguished them from human viruses. The H1N1 swine viruses seem to be chimeras between human and avian viruses and they contain 8 amino acids not shared by other viruses. The equine viruses also appear to show their own amino acid substitutions. These findings indicate that the PA genes of influenza A viruses have evolved in different pathways defined by apparently unique amino acid substitutions and host specificities. They also indicate that influenza A viruses have been transmitted from
avian to mammalian species.

Descriptors: genes viral, influenza A virus genetics, RNA replicase, RNA viral genetics, viral proteins genetics, amino acid sequence, base sequence, birds, cloning, molecular, ducks, evolution, horses, influenza A virus avian genetics, influenza A virus human genetics, influenza A virus, porcine genetics, molecular sequence data, poultry, sequence homology, nucleic acid, species specificity, swine.


Abstract: Given our recent discoveries that the ocular human pathogens adenovirus serotype 37 and enterovirus serotype 70 use sialic acid linked to galactose via alpha2,3 glycosidic bonds as a cellular receptor, we propose that the presence of this receptor in the eye also explains the ocular tropism exhibited by zoonotic avian influenza A viruses such as subtype H5N1 in Hong Kong in 1997, H7N7 in the Netherlands in 2003, H7N2 in the USA in 2003, and H7N3 in Canada in 2004. We also draw attention to the implications this hypothesis may have for epizootic and zoonotic influenza, and the initiation of future pandemics.

Descriptors: Adenoviridae classification, eye diseases virology, avian influenza pathology, cell surface physiology receptors, zoonoses virology, Adenoviridae pathology, birds, avian influenza epidemiology, avian influenza transmission, serotyping, zoonoses transmission, sialic acid.


NAL Call Number: 448.8 V81

Abstract: The influenza virus A/turkey/Oregon/71 (H7N3) has been adapted to grow in MDCK or chicken embryo cells (CEC) in the absence of trypsin. Changes occurred in the biological properties of the virus variants selected, depending on the cell type used for adaptation. They coincided with enhanced hemagglutinin (HA) activation by intracellular proteolytic cleavage. In the case of MDCK cell selected variants growth, plaque formation, and HA cleavability were restricted to this cell type, whereas the CEC-derived variants displayed altered activities in a broad range of host cells. Unlike the wild-type virus and its MDCK cell-derived variants, CEC variants had acquired pathogenic properties for chickens. By nucleotide sequence analysis of the HA genes of the MDCK cell variants several point mutations were found, which were localized predominantly at the distal, globular part of the HA molecule. The mechanism by which these point mutations increased HA cleavability has not been defined. In the CEC-derived variants besides point mutations, an insertion of 54 nucleotides adjacent to the cleavage site was observed, which corresponds in its sequence to a region in the 28 S ribosomal RNA. This insertion is probably responsible for the altered cleavability of the CEC variants' HA, leading to increased growth potential and pathogenicity.

Descriptors: hemagglutinins viral genetics, influenza A virus avian genetics, RNA viral genetics, adaptation, physiological, amino acid sequence, base sequence, cell line, DNA, viral genetics, electrophoresis, polyacrylamide gel, glycosylation, hemagglutinins viral metabolism, influenza A virus avian growth and development, influenza A virus avian metabolism, molecular sequence data, mutation, plaque assay.


Descriptors: avian influenza virus, cell culture, attenuation, fowl.


NAL Call Number: 41.8 Av5

Abstract: We isolated 24 Hav1 Neq1 and 18 Hav6 Nav3 influenza viruses from such free-living wild waterfowl as whistling swans, black-tailed gulls, and tufted ducks in western Japan in 1980. Two Hav1 Neq1 viruses isolated from a whistling swan and a black-tailed gull and a Hav6 Nav3 virus from a whistling swan were examined for their pathogenicity for chickens. Five-week-old specific-pathogen-free chickens were inoculated with the viruses intratracheally or intraperitoneally. Virus was recovered successfully from all the
organs, including the brain, despite the absence of signs of disease. The intracerebral pathogenicity index scores obtained for the Hav1 Neq1 viruses were 0.43 and 0.87; the score for the Hav6 Nav3 virus was 0.43. No virus produced plaques in cultivated chick embryo fibroblast cells in the absence of trypsin.

Descriptors: animal population groups microbiology, animals, wild microbiology, birds microbiology, chickens microbiology, ducks microbiology, influenza A virus avian pathogenicity, chick embryo, Japan, specific pathogen free organisms, terminology.


Abstract: Influenza A viruses are the cause of annual epidemics of human disease with occasional outbreaks of pandemic proportions. The zoonotic nature of the disease and the vast viral reservoirs in the aquatic birds of the world mean that influenza will not easily be eradicated and that vaccines will continue to be needed. Recent technological advances in reverse genetics methods and limitations of the conventional production of vaccines by using eggs have led to a push to develop cell-based strategies to produce influenza vaccine. Although cell-based systems are being developed, barriers remain that need to be overcome if the potential of these systems is to be fully realized. These barriers include, but are not limited to, potentially poor reproducibility of viral rescue with reverse genetics systems and poor growth kinetics and yields. In this study we present a modified A/Puerto Rico/8/34 (PR8) influenza virus master strain that has improved viral rescue and growth properties in the African green monkey kidney cell line, Vero. The improved properties were mediated by the substitution of the PR8 NS gene for that of a Vero-adapted reassortant virus. The Vero growth kinetics of viruses with H1N1, H3N2, H6N1, and H9N2 hemagglutinin and neuraminidase combinations rescued on the new master strain were significantly enhanced in comparison to those of viruses with the same combinations rescued on the standard PR8 master strain. These improvements pave the way for the reproducible generation of high-yielding human and animal influenza vaccines by reverse genetics methods. Such a means of production has particular relevance to epidemic and pandemic use.

Descriptors: influenza A virus avian growth and development, influenza A virus human growth and development, influenza vaccine, reassortant viruses growth and development, vero cells virology, *Cercopithecus aethiops*, influenza A virus avian genetics, influenza A virus human genetics, reassortant viruses genetics, viral nonstructural proteins genetics, virus cultivation, virus replication.


Descriptors: infection, acute renal tubular necrosis, avian influenza, non suppurative encephalitis, vasculitis, reverse transcription polymerase chain reaction, clinical techniques, diagnostic techniques, viral replication, chickens.


Descriptors: influenza A virus avian enzymology, DNA directed RNA polymerases biosynthesis, temperature, templates, genetic, virulence.


Descriptors: fowl plague prevention and control, viral vaccines, influenza A virus avian, vaccination.

**NAL Call Number:** QR1.A37

**Descriptors:** calcimycin pharmacology, virus replication drug effects, viruses drug effects, chick embryo, dose response relationship, drug, herpesvirus 1, suid drug effects, influenza A virus avian drug effects, Newcastle disease virus drug effects, vaccinia virus drug effects, virus cultivation, viruses growth and development.


**NAL Call Number:** SF601.V44

**Abstract:** One-hundred thirty-seven BALB/c mice were intranasally inoculated with neurotropic avian influenza A virus (H5N3). Thirty-nine of these mice died within 16 days post-inoculation (PID) and 98 of the mice recovered from the infection. To investigate whether viral antigens and genomes persist in the central nervous system (CNS) of recovered mice, immunohistochemistry and reverse transcription-polymerase chain reaction (RT-PCR) methods were performed. Histopathologically, mild interstitial pneumonia and non-suppurative encephalomyelitis restricted to the basal part of the frontal lobe of the cerebrum, brain stem and thoracic spinal cord were observed in BALB/c mice until 40 PID. Small amounts of viral antigens were detected in the brain and spinal cord and some viral RNA segments (NA, NP, M, PA, HA, NS, PB1) were intermittently detected in the CNS until 48 PID. Immunosuppression of these mice by dexamethazone (DEX) treatment did not increase the frequency of detection of the lesions, viral antigens or genomes. These findings suggest that viral genomes of neurovirulent influenza virus persist with restricted transcriptive activity in the CNS of the mice even after clinical recovery from the infection.

**Descriptors:** central nervous system virology, fowl plague virology, influenza A virus avian isolation and purification, RNA viral analysis, brain pathology, brain virology, central nervous system pathology, disease models, animal, fowl plague mortality, fowl plague pathology, immunohistochemistry veterinary, influenza A virus avian genetics, mice, mice inbred BALB c, random allocation, reverse transcriptase polymerase chain reaction veterinary, specific pathogen free organisms.


**NAL Call Number:** QR375.V6

**Abstract:** A temperature sensitive mutant, ts C47, derived from A/FPV/Rostock/34 and with a ts mutation in RNA segment 8, fails to form plaques in MDCK cells. From data obtained with reassortant viruses using the human influenza isolate A/FM/1/47 it was apparent that more than one mutation contributed to the temperature-sensitive (ts) and host range (hr) phenotypes of ts C47, and the phenotype of reassortants containing RNA segment 1 from A/FM/1/47 indicated that this segment was involved. A single nucleotide substitution at nucleotide 1961, resulting in valine instead of methionine in the predicted amino acid sequence of polypeptide PB2, was found in RNA segment 1 of ts C47, but this mutation did not segregate with the attenuated phenotype on gene reassortment. The following conclusions are drawn: (a) that ts C47 has at least two mutations in addition to that already known to exist in RNA segment 8, one of which (that in RNA segment 1) does not contribute to the observed ts hr phenotypes and (b) that the hr phenotype can be suppressed by substitution of RNA segment 1 by that of another strain.

**Descriptors:** influenza A virus avian genetics, RNA viral physiology, amino acid sequence, base sequence, cultured cells, chick embryo, dogs, influenza A virus avian growth and development, influenza A virus human genetics, kidney, phenotype, plaque assay, RNA viral genetics, recombination, genetic, temperature.


**NAL Call Number:** QR360.A1J6

**Abstract:** We have identified the cap-recognizing protein of two strains of influenza A fowl plague virus (FPV) by photoaffinity labelling of virion proteins with a photoreactive analogue of the 5’-methyl cap structure.
of messenger RNA. The cap-recognizing protein of influenza A/FPV/Rostock/34 is the P2 polypeptide, and that of influenza A/FPV/Dutch/27 (Dobson) is the P3 polypeptide. In each case the cap-recognizing protein is the product of RNA segment 1.

Descriptors: carrier proteins analysis, influenza A virus avian analysis, viral proteins analysis, affinity labels, carrier proteins genetics, influenza A virus avian genetics, RNA cap binding proteins, RNA viral genetics, viral proteins genetics.


NAL Call Number: QR375.V6

Abstract: The A/Turkey/Wisconsin/68 (H5N9) isolate of avian influenza (AI) consists of two virus populations which have different NS genes and differ in their biological responses in chicken embryos. They were classified as being either rapidly embryo-lethal (REL) or slowly embryo-lethal (SEL), (Avian Dis., 33 (1989) 695-706). In this study, sequence analysis identified only two nucleotide differences between the two NS genes, creating single amino acid differences in both the NS1 and the NS2 protein. The difference in the NS1 protein appears to be neutral, while the differences in the NS2 places a phenylalanine at position 48. This amino acid has not been previously demonstrated at this position in an NS2 sequence and its presence results in a distinct hydrophobic shift in the region. The sequence specifying the phenylalanine also creates an EcoRI site in the cDNA of the REL NS gene. Analysis of several clones showed that this site appears to co-segregate with the REL characteristic. Molecular differences between the two NS gene variants were reflected by differences in the kinetics of early protein synthesis in infected cells. In particular, the NS2 protein is in higher concentration (relative to the NS1) in SEL-infected cells than in REL-infected cells. No differences were detectable, however, in the rates of viral replication, either in cell culture or in embryos. Also, the REL or SEL rate was established early during infection of the embryo and could not be competed out by the other variant population 3 h after inoculation. Thus, these two natural NS gene variants appear to specify early differences which influence the time of death of an infected embryo but the differences do not appear to influence virus replication.

Descriptors: capsid genetics, influenza A virus avian genetics, viral core proteins genetics, amino acid sequence, base sequence, capsid metabolism, chick embryo, cloning, molecular, DNA restriction enzymes, embryo, nonmammalian microbiology, gene expression regulation, viral, genetic vectors, influenza A virus avian classification, influenza A virus avian pathogenicity, molecular sequence data, polymerase chain reaction, RNA viral isolation and purification, sequence homology, nucleic acid, variation genetics genetics, viral core proteins metabolism, viral nonstructural proteins, virus replication.


NAL Call Number: QH434.V57

Abstract: Recent isolations of H5N2 subtype avian influenza (AI) viruses in North America have raised questions concerning their origin, transmission to commercial poultry, and potential for virulence. One ratite-origin isolate of low pathogenicity, A/emu/TX/39924/93 (H5N2), was subjected to a procedure that rapidly selects and/or amplifies highly pathogenic (HP) strains. The resulting highly virulent derivative had an altered hemagglutinin (HA) gene containing an additional six nucleotides at position 970-975 in the HA1 coding region. This resulted in an arg-lys insertion near the proteolytic cleavage site of the HA protein. The remainder of the HA sequence differed by an additional seven amino acids from the parent. The HA precursor of the derivative, but not the parent, was readily cleaved during replication in cell culture without addition of trypsin. In experimentally infected chickens, the derivative produced lesions typical of highly pathogenic avian influenza. A reverse transcriptase-polymerase chain reaction (RT-PCR) primer set was designed to amplify exclusively from molecules with the inserted six nucleotides. The set yielded product only from the selected derivative samples and not the parent. Thus, the levels of the HP variants in the parent stock were undetectable, or the insertion occurred rapidly during the selection process.

Descriptors: hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian genetics, arginine, base sequence, chickens, fowl plague genetics, fowl plague virology, lysine, molecular sequence data, mutation, phylogeny, polymerase chain reaction, RNA viral genetics.

**NAL Call Number:** SF995.W4  
**Descriptors:** avian influenza virus, Mexico, America, influenza virus, Latin America, North America, orthomyxoviridae, viruses.


**NAL Call Number:** QR375.V6  
**Abstract:** Recent highly pathogenic (HP) field isolates of avian influenza (AI) virus from Mexico all possess an insertion of at least two basic amino acids (arg-lys) at the cleavage site of the hemagglutinin (HA) glycoprotein. One HP isolate has additional information which yields a 4 amino acid insert (arg-lys-arg-lys). We present here the nucleotide sequence of the HA gene of this unique isolate and compare it to recent H5N2 and other avian influenza isolates. The complete HA nucleotide sequence of the isolate and phylogenetic relationship suggest that it was derived in direct succession from a non-pathogenic strain isolated about 1 month earlier. The unique insertion sequence is a direct duplication of part of the purine-rich region preceding the arginine codon at the HA cleavage site. This evidence along with other data in this report provide compelling support for a proposed model explaining the mechanism of spontaneous, virulence-related insertions in type A influenza viruses.

**Descriptors:** hemagglutinins chemistry, hemagglutinins genetics, influenza A virus avian genetics, influenza A virus avian pathogenicity, repetitive sequences, nucleic acid, amino acid sequence, base sequence, chick embryo, chickens, endopeptidases, fowl plague virology, hydrolysis, influenza A virus avian chemistry, models, molecular, molecular sequence data, nucleic acid conformation, protein structure, secondary, sequence alignment, structure activity relationship, virulence.


**NAL Call Number:** QR375.V6  
**Abstract:** Several field isolates of avian influenza virus of the H7 subtype were analyzed for the presence of hemagglutinin variants by labeling proteins in cells infected with virus clones, and reacting with monoclonal antibodies. Each strain was shown to contain two distinct electrophoretic variants of the uncleaved hemagglutinin. In the A/Tk/Ore/71 (H7N3) isolate, two variants remained in the population through 35 laboratory passages, indicating both are stable and may be important to expression of the viral phenotype. Nucleotide sequence analysis of the HA gene of these two variants demonstrated differences at several amino acid positions in the HA1 subunit including one glycosylation site. Three additional recent North American isolates were also each found to contain two electrophoretic variants occurring within populations as few as one embryo passage away from the original clinical specimen. Pulse-chase assays indicated none of the variant HA molecules were cleavable in chick embryo fibroblasts. In the highly pathogenic Australian isolate; A/Ck/Victoria/75, both HA variants are cleavable in fibroblasts, without added trypsin, and the differences are localized within the HA1 region. With all the strains tested, the slower migrating HA variant was associated with a consistently higher hemagglutinin titer in embryos. Finally, recent H7 isolates from imported birds (A/Soft Bill/III/92) also exhibit similar variants, indicating their occurrence is not limited to domestic poultry. This consistent presence of two distinct electrophoretic variants in several avian H7 isolates suggests multiple allelic forms of the H7 hemagglutinin.

**Descriptors:** antigenic variation genetics, hemagglutinins viral genetics, influenza A virus avian genetics, antibodies, monoclonal immunology, antibodies, viral immunology, chick embryo, chickens virology, electrophoresis, polyacrylamide gel, genes, structural, viral, glycosylation, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral immunology, influenza A virus avian classification, influenza A virus avian immunology, mice, mice inbred BALB c, protein processing, post translational, RNA viral genetics, sequence analysis, RNA.


NAL Call Number: 448.8 V81

Abstract: The highly pathogenic (HP) avian influenza isolate, A/Fowl/Victoria/76 (H7N7), contains two naturally occurring hemagglutinin (HA) variants. The two hemagglutinin proteins differ only in the possession of a potential asparagine-linked glycosylation site at amino acid position 188-190, which is near the proposed receptor binding region of the HA. Expanded virus plaques which possess the addition site exhibit more slowly migrating HA, subunits and are significantly more lethal in chickens than those which lack the site. When artificial mixtures of the two variants were inoculated in birds, as few as 1 in 1000 particles containing the glycosylation site was sufficient to exhibit 100% lethality in birds. The data raise the possibility that presence of carbohydrate near the receptor site on the H7 avian influenza virus hemagglutinin may influence virulence.

Descriptors: chickens, avian influenza virus, agglutinins, chemical composition, pathogenicity, mortality, biological properties, birds, domestic animals, domesticated birds, Galliformes, influenza virus, livestock, microbial properties, orthomyxoviridae, poultry, proteins, useful animals, viruses, glycosylation site, GENBANK z47199, molecular sequence data, viral hemagglutinins, binding site, amino acid sequences, virulence.


NAL Call Number: SF601.V44

Abstract: Analysis of the structure of the avian influenza (AI) virus hemagglutinin (HA) gene and protein has yielded a wealth of information on the virulence mechanisms of influenza viruses. The AI hemagglutinin appears to be unique in its capacity to accept basic amino acids at its proteolytic cleavage site (PCS). The association of multiple basic (MB) amino acids, HA cleavage, tissue spread and virulence by AI strains first proposed in the late 1970s and early 1980s [Klenk, H.D., Rott, R., Orlich, M., 1977. J. Gen. Virol. 36, 151-161; Bosch, F.X., Garten, W., Klenk, H.D., Rott, R., 1981. Virology 113, 725-735] has held fast for two decades now. While other structural characteristics and other genes can certainly influence virulence, the presence of MB amino acids at the PCS has provided a hallmark structural feature which justifies continuing sequence analysis of emerging field isolates of AI strains. In addition to this structural feature, the distal tip of the HA is prone to appearance and disappearance of glycosylation sites, some of which have been associated with virulence. The recent outbreaks of highly pathogenic AI in Mexico, Australia, Pakistan, Hong Kong and in the ongoing outbreak of moderately pathogenic H7 avian influenza in the northeast US have all provided new and useful information regarding the role of HA RNA and protein structure in both virulence and host adaptation. We have previously noted that stable RNA secondary structure near the PCS is related to the acquisition of virulence and have proposed that the secondary structure may promote the insertion of basic amino acids. In this report we evaluate the phylogenetic relationships for three recent isolates of highly pathogenic avian influenza viruses and the possible virulence factors associated with their primary and secondary structure.

Descriptors: hemagglutinin glycoproteins, influenza virus chemistry, influenza A virus avian pathogenicity, glycosylation, hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian classification, numerical analysis, computer assisted, peptide library, phylogeny, protein structure, secondary, structure activity relationship.


NAL Call Number: 41.8 Av5

Abstract: Embryo lethality patterns induced by an avian influenza virus isolate (A/Tk/Ws/68/H5N9) suggested that it contained more than one genetic form. Two different virus populations were recovered from the isolate by plaque isolation and limit-dilution cloning and were characterized with respect to their biological and molecular properties. They were very closely related but exhibited strikingly different mean death times (MDT) in 10-day-old chick embryos. One was rapidly embryo lethal (REL), while the other was slowly embryo lethal (SEL). The REL isolate demonstrated a small but measurable mortality rate in 4-week-old chicks, as did the parental isolate. The SEL isolate, however, was nonlethal to 4-week-old chicks. The
embryo MDT induced by the parental isolate revealed a biphasic death pattern reflecting expression of both REL and SEL populations. Mixing experiments, using different amounts of the two cloned populations, demonstrated that expression of their unique phenotypic property (either REL or SEL) was competitive. The number of early or late embryo deaths was directly related to the input levels of each respective virus. The only molecular difference thus far detected between the two populations is in the nonstructural (NS) gene, with the REL clone possessing a faster migrating electrophoretic form of that RNA than the SEL clone. Both forms of the NS gene were present in the original parental isolate. This study thus demonstrates the competitive coexistence of two closely related virus populations within a single natural isolate.

Descriptors: orthomyxoviridae growth and development, RNA viral analysis, viral proteins analysis, chick embryo, clone cells, influenza etiology, influenza mortality, influenza veterinary, orthomyxoviridae isolation and purification, orthomyxoviridae pathogenicity, phenotype, plaque assay, virulence.


NAL Call Number: QR375.V6

Abstract: When white leghorn (WL) chick embryos ranging in age from 8 to 13 days were inoculated with a variety of avian influenza virus (AIV) isolates, strain-specific differences in embryo mean death times (MDT) were observed. Non-highly pathogenic (nHP) strains killed 8 or 9 day-old embryos much more rapidly than 12 or 13 day-old embryos. Highly pathogenic (HP) strains, however, were less sensitive to embryo age resulting in similar MDTs in both older and younger embryos. These observations were consistent over a broad range of virus doses for both HP and nHP strains. When a HP derivative of H5N2 AIV was compared to its nHP parent, the derivative killed older embryos more rapidly than the parent virus, while MDTs in younger embryos were the same for both parent and derivative. The two strains further exhibited clear differences in the structure of their respective hemagglutinin, a previously described pathogenicity determinant for this virus. Thus it may be possible to readily demonstrate the HP phenotype in AIV strains based on MDT measurements in WL embryos.

Descriptors: chick embryo microbiology, orthomyxoviridae pathogenicity, orthomyxoviridae infections veterinary, poultry diseases mortality, antibodies, monoclonal immunology, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral immunology, orthomyxoviridae infections mortality, specific pathogen free organisms, time factors, viral envelope proteins immunology.


NAL Call Number: 449.9 W892B

Descriptors: orthomyxoviridae classification, antigens, complement fixation tests, Italy, poultry, serotyping.


NAL Call Number: QR360.A1J6

Abstract: Two-dimensional analysis of polypeptides from A/FPV/Rostock/34 (FP/R)-infected chick embryos fibroblast cells using non-equilibrium pH gradient gel electrophoresis followed by polyacrylamide gel electrophoresis, showed that nucleoprotein (NP) was the only detectable virus phosphoprotein and was present in both the nucleus and cytoplasm. The kinetics of accumulation of phosphorylated NP in the nucleus and cytoplasm were similar, suggesting that the presence or absence of phosphate groups did not control the entry of NP into the nucleus. In the course of this study, two-dimensional analysis of [35S]methionine-labelled FP/R-infected cells revealed some major differences from previously published work which are discussed.

Descriptors: cell nucleus metabolism, cytoplasm metabolism, influenza A virus avian metabolism, nucleoproteins metabolism, viral proteins metabolism, cultured cells, chick embryo, fibroblasts, nucleoproteins analysis, phosphoproteins analysis, phosphoproteins metabolism, phosphorylation, viral proteins analysis.

Abstract: The type-specific non-structural protein 1 (NS1) of influenza A viruses was found to be heterogeneous with respect to charge, varying in pl by more than two orders of magnitude, and to phosphorylation. Phosphorylation was strain-specific, variable in extent between strains, and in some strains NS1 proteins were not detectably phosphorylated. Phosphorylation was not responsible for the major variations in charge as, paradoxically, the most acidic NS1 proteins were not phosphorylated. Cytoplasmic inclusions, which are formed between NS1 proteins and cellular RNA in infections with a number of human strains, were absent from A/FP/Rostock-infected cells and do not, therefore, appear to be essential in virus multiplication. We suggest that the acidic nature of the NS1 of A/FP/Rostock may prevent it from binding RNA and hence from forming inclusions. The variation in charge of NS1 proteins which we determined experimentally correlates with the overall differences in charge adduced from published amino acid sequence and implications of this variability to the biological role of NS1 are discussed.

Descriptors: influenza A virus avian analysis, influenza A virus human analysis, influenza A virus analysis, viral proteins analysis, cell line, chick embryo, dogs, electrophoresis, polyacrylamide gel, inclusion bodies, viral analysis, influenza A virus growth and development, isoelectric point, phosphoproteins analysis, phosphorylation, species specificity, viral matrix proteins, viral nonstructural proteins, viral proteins metabolism.


Abstract: The complete nucleotide sequence of the cloned full-length DNA copy of the avian influenza virus A/FPV Weybridge PB2 gene has been determined.

Descriptors: genes viral, influenza A virus avian genetics, viral proteins genetics, amino acid sequence, base sequence, molecular sequence data.


Abstract: To define and characterize the major neutralizing epitopes of the H5 hemagglutinin, a panel of monoclonal antibodies specific for the H5 hemagglutinin of the virulent avian influenza virus A/Turkey/Ontario/7732/66 (H5N9) was prepared. Antibodies which neutralized infectivity of the virus were used to select a panel of escape mutants. Reactivity patterns of the panel of monoclonal antibodies against the panel of mutants by both enzyme-linked immunosorbent assay serology and hemagglutination inhibition operationally defined five distinct epitopes on the H5 molecule. The mutants were analyzed in vivo for virulence in chickens, and the findings indicate that viruses with mutations in four of five epitopes were no less virulent than the wild type, producing a rapidly fatal disease, while all viruses with mutations in the fifth epitope (group 1 mutants) were attenuated. These group 1 mutants were unaltered in the cleavage properties of the hemagglutinin, suggesting that the mechanism of attenuation is unrelated to processing of the hemagglutinin. One of the group 1 mutants, 77B1v, was characterized for its ability to produce necrosis of the spleen and was found to produce none of the lesions in the spleen which are characteristic of the wild-type virus, although virus was present in this organ. The results suggest an altered tissue tropism, perhaps sparing a population of cells critical to an effective immune response.

Descriptors: epitopes analysis, hemagglutinins viral immunology, influenza A virus avian immunology, antibody specificity, chickens, cross reactions, enzyme linked immunosorbent assay, epitopes genetics, epitopes immunology, fowl plague microbiology, hemagglutination inhibition tests, hemagglutination tests, influenza A virus avian genetics, influenza A virus avian pathogenicity, mutation, neutralization tests, virulence.

Abstract: The H5 hemagglutinin (HA) of a highly virulent avian influenza virus, A/Turkey Ontario/7732/66 (H5N9), was previously shown to have five neutralizing epitopes, and escape mutants within one epitope (group 1) were markedly attenuated (M. Philpott, B. C. Easterday, and V. S. Hinshaw, J. Virol. 63:3453-3458, 1989). To define the genetic changes related to these antigenic and biologic properties, the HA genes of mutants within each of the epitope groups were sequenced by using the polymerase chain reaction. The mutations in the attenuated group 1 mutants were located near the distal tip of the HA molecule in close proximity to the receptor-binding site, on the basis of alignment with the three-dimensional structure of the H3 HA. All group 1 mutations involved charged amino acids. The group 1 mutants, similar to the wild-type virus, spread systemically and were recovered from the spleens of infected chickens but, unlike the wild-type virus, failed to produce severe necrosis in the spleens. Viral replication in the spleens was investigated by in situ hybridization of spleen sections from chickens infected with the wild-type or attenuated mutants. Wild-type virus replication was demonstrated in large, mononuclear, macrophagelike cells; however, group 1 mutant virus was detected attached only to erythrocytes within the red pulp. These results suggest that the attenuated mutants differ in their cell tropism within the spleen.

Descriptors: hemagglutinins viral genetics, influenza A virus avian genetics, mutation, amino acid sequence, base sequence, chick embryo, chickens, cloning, molecular, DNA, viral genetics, influenza A virus avian pathogenicity, influenza A virus avian physiology, molecular sequence data, spleen microbiology, virulence genetics, virus replication.


Podchernyaeva, R.J., R.G. Webster, V.V. Skovorodka, A.I. Klimov, and V.M. Zhdanov (1989). Molecular and biological properties of a variant of avian influenza A/Seal/Massachusetts/1/80 (H7N7) virus that is pathogenic for mice. Acta Viroligica 33(1): 38-42. ISSN: 0001-723X.

Podchernyaeva, R.J., R.G. Webster, V.V. Skovorodka, A.I. Klimov, and V.M. Zhdanov (1989). Molecular and biological properties of a variant of avian influenza A/Seal/Massachusetts/1/80 (H7N7) virus that is pathogenic for mice. Acta Viroligica 33(1): 38-42. ISSN: 0001-723X.

**NAL Call Number**: 448.3 AC85

**Abstract**: Some biological properties and the genome composition of antigenic recombinants obtained by crossing of human and animal influenza viruses were studied. Analysis of the recombinants has shown that upon heating of virions in vitro thermostability of the haemagglutinin (HA) does not necessarily correlate with the properties of parent HA; apparently it depended not only on the properties of the HA itself, but also on the peculiarities of other virion proteins. All recombinants obtained by crossing of pathogenic and apathogenic for mice parents either had a reduced pathogenicity for mice or were apathogenic. In some instances, reduction or loss of pathogenicity was observed in recombinants which inherited only one gene from the apathogenic parent; however, the data obtained suggest that pathogenicity involves functions of a number of genes. Human and animal influenza virus strains under study proved to be capable of replication in human embryo tracheal and kidney organ cultures. The degree of reproduction of the recombinants was either lower or higher as compared to the parent strains.

**Descriptors**: genes viral, influenza A virus avian genetics, influenza A virus human genetics, recombination, genetic, chick embryo, hemagglutinins viral immunology, influenza A virus avian immunology, influenza A virus avian physiology, influenza A virus human immunology, influenza A virus human physiology, organ culture, virus replication.


**NAL Call Number**: 448.3 AC85

**Abstract**: Two groups of antigenic recombinants Hav4N1 were obtained by recombination of human influenza virus H0N1 with two avian influenza viruses isolated from ducks in 1956 and terns in 1978 and possessing the same surface antigen Hav4 Nav1. Recombinants obtained by crossing A/PR/8/34 and A/duck/CSSR/56 viruses showed a lower ability to reproduce at optimal and lowered temperatures and differed in the thermosensitivity of haemagglutinin and neuraminidase. An analysis of virus-specific proteins of the recombinants revealed different combinations of genes coding for internal (PI, NP) and nonstructural (NS1) proteins. Recombinants obtained by crossing A/PR/8/34 and A/tern/Frunze/334/78 viruses possessed a thermostable haemagglutinin; they produced plaques of a size characteristic of avian influenza but, as distinct from the latter, they were practically not eluted from fowl erythrocytes. Polypeptide analysis of these recombinants showed that the genes coding for NP, M and NS1 proteins were inherited from the A/tern/Frunze/334/78 strain.

**Descriptors**: antigens, viral genetics, influenza A virus avian genetics, influenza A virus human genetics, recombination, genetic, antigens, viral analysis, hemagglutinins viral analysis, influenza A virus avian immunology, influenza A virus human immunology, neuraminidase immunology, viral proteins analysis.


**NAL Call Number**: QR360.J6

**Abstract**: The poly(A) tail of influenza virus mRNA is synthesized by reiterative copying of a U track near the 5’ end of the virion RNA (vRNA) template by the viral RNA polymerase. We have engineered a novel influenza A/WSN/33 virus which contains a neuraminidase (NA) vRNA with its U track mutated into an A track. Instead of synthesizing poly(A)-tailed NA mRNA, this novel virus synthesizes poly(U)-tailed NA mRNA. In infected cells, most poly(U)-tailed NA mRNA was retained in the nucleus, while most control polyadenylated NA mRNA was transported to the cytoplasm. These results suggest that the poly(A) tail is important for efficient nuclear export of NA mRNA. The mutant virus produced a reduced amount of NA and showed an attenuated phenotype, suggesting that poly(A) signal mutants of this type might be useful as potential live attenuated virus vaccines. In addition, this virus mutant might provide a useful model to further elucidate the basic mechanisms of mRNA nuclear export.

**Descriptors**: cell nucleus metabolism, influenza A virus avian genetics, poly U metabolism, RNA,
messenger biosynthesis, recombination, genetic, base sequence, biological transport, chick embryo, DNA primers, mutation, neuraminidase genetics, nucleic acid conformation, RNA, messenger chemistry, RNA, messenger metabolism.


NAL Call Number: 472 N21

Abstract: A synthetic fowl plague virus (FPV) haemagglutinin gene has been cloned in bacteria and the complete sequence of the RNA gene deduced. It is 1,742 nucleotides long and the mRNA codes for 56.3 amino acids in an uninterrupted sequence. The nature of some of the important domains in the haemagglutinin has been established, and their structure is discussed in relation to their function. Extensive amino acid sequence homologies exist between FPV and human influenza haemagglutinins.

Descriptors: genes, structural, genes viral, hemagglutinins viral genetics, influenza A virus avian genetics, viral proteins genetics, amino acid sequence, codon, DNA repair, DNA, recombinant, RNA, messenger genetics.


NAL Call Number: 500 N21P

Abstract: The smallest RNA segment of influenza A viruses (vRNA segment 8) has recently been shown to code for two unrelated nonstructural proteins (NS1 and NS2) translated from separate mRNAs. Molecular weight considerations indicated that there might not be enough space on vRNA segment 8 for the two coding regions unless they overlap. We have recently cloned in bacterial plasmids several genes of an avian influenza A virus, fowl plague virus (EPV), and now present the complete nucleotide sequence of FPV RNA segment 8 largely determined from the cloned DNA. The DNA sequence predicts two open protein synthesis reading frames that can be translated into polypeptides of sizes similar to those of NS1 and NS2. The coding regions for these polypeptides overlap by the equivalent of 43-60 amino acids, the exact amount depending on which of several possible methionines initiates the synthesis of NS2.

Descriptors: genes, structural, genes viral, influenza A virus avian genetics, viral proteins genetics, amino acid sequence, base sequence, cloning, molecular, codon genetics, DNA restriction enzymes, genes, synthetic, molecular weight, plasmids, RNA viral genetics.


NAL Call Number: QR375.V6

Abstract: Several experimental data support the idea that certain mammalian cells are unable to replicate influenza viruses type A, although these viruses can efficiently penetrate the cells. This cannot be attributed to a lack of specific receptors on the cell surface, but depends upon the failure of specific step(s) to occur during viral growth. Here we report a study of abortiveness of human and avian type A influenza viruses in HeLa 229 cells. Viral polypeptide synthesis was monitored by [35S]methionine pulse labelling at several time points after infection, showing that normal amounts of virus-induced components were synthesized. Cellular fractionation of HeLa 229 cells infected by influenza viruses showed that the distribution of viral proteins into nuclear and cytoplasmic compartments was comparable to that seen in the permissive host, chick embryo fibroblasts. Viral HA glycoprotein, produced during the infectious cycle, was entirely found in the cytoplasm of infected HeLa 229 cells. The polypeptide was able to agglutinate red blood cells but did not show positive haemadsorption even at late times of infection. Therefore it seems that during the maturation of viral particles there is a failure of the haemagglutinin to perform a correct insertion into the plasma membrane of infected HeLa 229 cells.

Descriptors: fibroblasts microbiology, hemagglutinins viral metabolism, influenza A virus avian growth and development, influenza A virus human growth and development, cell membrane metabolism, chick embryo, HeLa cells, hemadsorption, hemagglutinin glycoproteins, influenza virus, influenza A virus avian metabolism, influenza A virus human metabolism, methionine metabolism, virus replication.

**NAL Call Number:** QR1.M57

**Abstract:** A number of experimental data demonstrate that certain mammalian cells are unable to replicate Influenza viruses type A. In these cellular hosts the viruses can efficiently perform their biological as well as biochemical activities but the production of mature viral particles is greatly restricted. Here we report a study of abortiveness of human and avian type A Influenza viruses in HeLa 229 cells in which the final stages of maturation of viral particles seem to be affected. We show that the incorrect insertion of virus-coded haemagglutinin into the plasma membrane might be the cause of the unpermissive condition of infection exhibited by this cellular host.

**Descriptors:** hemagglutinins viral metabolism, influenza A virus avian physiology, influenza A virus human physiology, virus replication, cultured cells, chick embryo, HeLa cells, hemadsorption.


**NAL Call Number:** 448.8 J821

**Descriptors:** fluorenes therapeutic use, influenza drug therapy, influenza A virus avian drug effects, interferons therapeutic use, polynucleotides therapeutic use, polysaccharides therapeutic use, cultured cells drug effects, chick embryo, chickens, disease models, animal, ethylamines therapeutic use, injections, intravenous, interferons biosynthesis, interferons blood, poly I C pharmacology, poly I C therapeutic use, polysaccharides pharmacology, temperature, virus replication drug effects.


**NAL Call Number:** QR360.A1J6

**Abstract:** Influenza viruses, which had lost up to 99.999% infectivity by incubation with antibody (a) specific for the haemagglutinin (HA) or with monoclonal alpha-HA, attached on to and penetrated chick embryo fibroblast (CEF) cells to the same extent as non-neutralized virus. Neutralized virus was also uncoated efficiently as shown by the accumulation of virion RNA in the nucleus and virion envelope in the cytoplasm. Polyacrylamide gel electrophoresis of virion RNA segments recovered from the nucleus or cytoplasm of cells inoculated with neutralized or non-neutralized virus showed that antibody did not potentiate degradation of RNA. However, these RNAs were not expressed since virus-induced proteins were not detected in cells to which neutralized virus had been added. Assay of virion transcriptase of neutralized virus in vitro showed that its activity was reduced up to sevenfold compared with non-neutralized virus, and annealing studies showed that no detectable transcription took place in vivo with neutralized virus. These studies support the conclusion that antibody directed specifically against the HA protein on the outer surface of the influenza virus particle neutralizes infectivity by inactivating virion transcriptase activity and it is suggested that antibody to HA brings about allosteric rearrangements in the HA molecule which are transmitted across the virus envelope to the interior of the particle.

**Descriptors:** antibodies, viral physiology, DNA directed RNA polymerases antagonists and inhibitors, hemagglutinins viral immunology, influenza A virus avian immunology, influenza A virus human immunology, cultured cells, chick embryo, influenza A virus avian enzymology, influenza A virus avian growth and development, influenza A virus human enzymology, influenza A virus human growth and development, neutralization tests, viral proteins biosynthesis.


**Descriptors:** electrophoresis, polyacrylamide gel methods, orthomyxoviridae analysis, paramyxoviridae
analysis, viral proteins analysis, influenza A virus avian analysis, influenza A virus avian isolation and purification, molecular weight, Newcastle disease virus analysis, Newcastle disease virus isolation and purification, orthomyxoviridae isolation and purification, paramyxoviridae isolation and purification.


Abstract: Deoxyadenylguanosine (dAdG, 0.2-0.4 mM), affecting the RNA polymerase activity, caused inhibition of transcription of the influenza A virus in presence of precursor AdG by 50-60% and a 80-85% inhibition in absence of the precursor. The inhibitor exhibited its effect independently on the time of addition into an incubation mixture. Addition of 0.5 mM inhibitor into a cultural medium inhibited reproduction of the influenza A virus in a culture of chicken embryonal fibroblasts.

Descriptors: DNA directed RNA polymerases antagonists and inhibitors, deoxyadenine nucleotides, deoxyguanosine, influenza A virus avian enzymology, oligodeoxyribonucleotides pharmacology, virus replication drug effects, cultured cells, chickens, influenza A virus avian physiology.


NAL Call Number: QR375.V6

Abstract: It has been previously shown that influenza virus nucleocapsid protein (NP) forms homooligomers in vivo. Our analyses revealed that the reducing agent dithiothreitol (DTT) introduced in pulse labeling period prevented further formation of native NP-oligomers. The shortly pulse-labeled non-reduced newly synthesized NP possessed a relatively faster mobility in non-reducing PAGE and a higher resistance to protease than the reduced one. These data suggest that there is an early disulfide-dependent step in NP maturation and that the newly synthesized NP possesses the intrachain disulfide bonds. In contrast to the newly synthesized NP, the non-reduced chased NP possessed the same mobility in non-reducing PAGE and the same sensitivity to protease as the reduced NP. DTT introduced in the chase period did not prevent NP-oligomers formation and did not destabilize already formed NP-oligomers. This suggests that the chased NP monomers and NP-oligomers do not contain intrachain nor interchain disulfide bonds. It was also shown that the non-reduced newly synthesized NP could not form NP-NP complexes in vitro, and acquired such ability only after reducing. The possibility is discussed that there are several stages in the maturation of NP: the initial formation of intrachain disulfide-linked NP and conversion into disulfide-free NP, which forms non-covalently stabilized NP-oligomers. Early intrachain disulfide bonds may be necessary for the prevention of early spontaneous NP-NP association.

Descriptors: avian influenza A virus chemistry, nucleoproteins chemistry, RNA binding proteins, viral core proteins chemistry, cell line, disulfides chemistry, dithiothreitol metabolism, dogs, electrophoresis, polyacrylamide gel, immunoblotting, avian influenza A virus growth and development, nucleoproteins isolation and purification, oxidation reduction, protein binding, protein conformation, viral core proteins isolation and purification.


NAL Call Number: QR375.V6

Abstract: In the culture medium of MDCK cells infected with influenza A/Duck/Ukraine/1/63(H3N8) virus two kinds of virus nucleoprotein (NP) are detected: full-length 56 kDa NP and truncated 53 kDa NP. However, in infected cells 53 kDa NP may be detected only at short pulse and after 10 min chase it becomes nondetectable. The extracellular truncated 53 kDa NP is detected in free RNP, and not in the virions. Both extracellular free 53 and 56 kDa NP in the virions are completely oligomerized. Several data argue against the possibility of extracellular 53 kDa NP formation being a result of extracellular 56 kDa NP proteolytic degradation. Thus, the accumulation of extracellular 53 kDa NP takes place only in the course of infection, and the amount of 53 kDa NP is not increased during prolonged storage of cell-free culture medium at +37 degrees C. Moreover, all extracellular 56 kDa NP of A/Duck/Ukraine/1/63 influenza virus is present in the
oligomeric form, and the latter, in contrast to the monomeric form, is highly resistant to proteases. The possibility is discussed that in the course of A/Duck/Ukraine/1/63 (H3N8) influenza virus infection a fraction of the synthesized 56 kDa monomeric NP undergoes the proteolytic cleavage in the infected cells before oligomerization and forms the 53 kDa NP. This 53 kDa NP is then oligomerized, enters the RNP and is quickly secreted from the cells.

Descriptors: influenza A virus avian metabolism, nucleoproteins metabolism, viral core proteins metabolism, cell line, culture media, dogs, ducks, fowl plague virology, influenza A virus avian pathogenicity, nucleoproteins chemistry, viral core proteins chemistry.


NAL Call Number: 448.8 V81

Abstract: It has previously been shown that the purified influenza virus nucleoprotein (NP) forms the oligomers in vitro in NP preparations obtained from virions (Wiley et al., 1977, Virology, 79, 446-448; Ruigrok and Baudin, 1995, J. Gen. Virol., 76, 1009-1014) and infected cells (Becht and Weiss, 1991, Behring Inst Mitt., Justus-Liebig Universitat, Giessen, 89, 1-11). We have shown in this report that boiling-sensitive NP oligomers (di- and trimers) are formed in vivo in the course of intracellular influenza virus replication. They are detected by PAGE about 10 min after monomeric 56-kDa NP molecules are synthesized. NP oligomers are formed by different strains of influenza virus in different cell lines. Some influenza virus strains are characterized by complete conversion of NP monomers into oligomers and others by only partial conversion. In the Triton X-114 phase partitioning system NP oligomers show more hydrophobicity than NP monomers. NP oligomers are detected in the sedimentable and soluble fractions of both cell lysate and extracellular medium. The possibility is discussed that oligomeric NP is a native and functionally significant form of influenza virus NP.

Descriptors: influenza A virus metabolism, nucleoproteins metabolism, viral core proteins metabolism, cell line, chick embryo, dogs, ducks, influenza A virus avian metabolism, influenza A virus human metabolism, swine.


NAL Call Number: 381 B523

Abstract: Antibody NC41 binds to the subtype N9 neuraminidase (NA) of influenza virus A/tern/Australia/G70c/75 and inhibits its enzyme activity. To address the molecular mechanisms by which antibodies interact with neuraminidase and the requirements for successful escape from antibody inhibition, we made amino acid substitutions in heavy chain CDRs of NC41. Antibody proteins expressed as a single-chain Fv (scFv) fused with maltose-binding protein were assayed for binding to NA by ELISA. Association constants (Ka) for wild-type and mutant scFvs are as follows: wild type, 2 x 10(7) M-1; Asn31-->Gln, 2 x 10(7) M-1; Glu96-->Asp, 1 x 10(7) M-1; Asp97-->Lys, 6 x 10(6) M-1; and Asn98-->Gln, 8 x 10(6) M-1. The Ka for intact NC41 antibody was 4 x 10(8) M-1 in the same assay, reflecting increased stability compared to that of the scFv. Mutations in the scFv antibody had less of an effect on binding than mutations in their partners on the NA, and modeling studies suggest that interactions involving the mutant antibody side chains occur, even without taking increased flexibility into account. Asp97 forms a salt link with NA critical contact Lys434; of the four mutants, D97K shows the largest reduction in binding to NA. Substitution N31Q had no effect on Ka. NC41 residue Glu96 interacts with NA critical contact Ser368, yet E96D showed only a 2-fold reduction in binding to NA, apparently because the H bond can still form. Asp97 and Asn98 provide the most important interactions, but some binding is maintained when they are mutated, in contrast to their partners on the NA. The results are consistent with maturation of the immune response, when the protein epitope is fixed while variation in the antibody paratope allows increasing affinity. Influenza viruses may exploit this general mechanism since single amino acid changes in the epitope allow the virus to escape from the antibody.

Descriptors: amino acids metabolism, antibodies, monoclonal metabolism, binding sites, antibody, immunoglobulins, heavy chain metabolism, influenza A virus avian immunology, neuraminidase immunology, amino acid sequence, amino acid substitution genetics, amino acids genetics, amino acids immunology, antibodies, monoclonal biosynthesis, antibodies, monoclonal chemistry, base sequence,

NAL Call Number: 442.8 J828

Abstract: The MAL (MAL/VIP17) proteolipid is a nonglycosylated integral membrane protein expressed in a restricted pattern of cell types, including T lymphocytes, myelin-forming cells, and polarized epithelial cells. Transport of the influenza virus hemagglutinin (HA) to the apical surface of epithelial Madin-Darby canine kidney (MDCK) cells appears to be mediated by a pathway involving glycolipid- and cholesterol-enriched membranes (GEMs). In MDCK cells, MAL has been proposed previously as being an element of the protein machinery for the GEM-dependent apical transport pathway. Using an antisense oligonucleotide-based strategy and a newly generated monoclonal antibody to canine MAL, herein we have approached the effect of MAL depletion on HA transport in MDCK cells. We have found that MAL depletion diminishes the presence of HA in GEMs, reduces the rate of HA transport to the cell surface, inhibits the delivery of HA to the apical surface, and produces partial missorting of HA to the basolateral membrane. These effects were corrected by ectopic expression of MAL in MDCK cells whose endogenous MAL protein was depleted. Our results indicate that MAL is necessary for both normal apical transport and accurate sorting of HA.

Descriptors: hemagglutinin glycoproteins, influenza virus metabolism, proteolipids physiology, antibodies, monoclonal pharmacology, biological transport drug effects, cell polarity, detergents pharmacology, dogs, epithelial cells metabolism, kidney, membrane lipids metabolism, membrane proteins metabolism, oligonucleotides, antisense pharmacology, proteolipids antagonists and inhibitors, proteolipids genetics, proteolipids immunology, rats, rats, wistar, transfection.


NAL Call Number: 41.8 Av5

Abstract: A workshop in which 17 practicing scientists participated was intended to address primarily people who use or could use biotechnology in their work and was confined to five techniques. Endonuclease fingerprinting and mapping involved cleaving nucleic acid with a specific restriction enzyme and separating the nucleic acid fragments by electrophoresis. Field and vaccine isolates of Pasteurella multocida could be distinguished; Salmonella enteritidis could be divided into three groups; chlamydia could be grouped into seven groups; and vaccinia, quail pox, and fowl pox could be clearly distinguished. Preparation of nucleic acid probes involved producing large amounts of labeled oligonucleotides, usually of unknown sequence. Successful probes had been made for infectious bursal disease virus, avian influenza virus, Newcastle disease virus, and infectious bronchitis virus. In Southern, Northern, and dot blotting, either DNA or RNA fragments were placed on or transferred to a solid substrate and probed. The procedure was able to detect infectious bursal disease virus, infectious bronchitis virus, Mycoplasma gallisepticum, and Marek's disease virus. In situ hybridization involved applying a labeled probe to frozen or fixed sections or to intact cells. In Polymerase chain reaction, two primers, some distance apart, were annealed to a denatured target DNA. Repeated cycles of DNA synthesis with a thermostable polymerase, denaturing, and reannealing resulted in great amplification of a rare sequence. After 30 cycles, a rare gene sequence could be amplified more than 10(6) times. It was used successfully to detect minute quantities of influenza virus and infectious bursal disease virus, and the process was used to facilitate DNA sequencing of coccidiosis gene segments.

Descriptors: poultry diseases diagnosis, blotting, northern, blotting, Southern, DNA restriction enzymes genetics, nucleic acid hybridization, nucleic acid probes, peptide mapping, polymerase chain reaction.


Descriptor: amantadine pharmacology, ethionine pharmacology, influenza A virus avian drug effects, antiviral agents pharmacology, chickens, fibroblasts, tissue culture, virus replication drug effects.


Descriptor: antibodies, experimental infections, gene expression, immunity, potency, recombinant vaccines, vaccine development, viral hemagglutinins, avian influenza virus, fowl pox virus, chickens, poultry, fowl, mortality.


Descriptor: complementary DNA, DNA cloning, genes, nucleotide sequences, avian influenza virus, fowl pox virus, poultry, geese, China, Guangdong.


Descriptor: influenza A virus avian physiology, chick embryo, hydrogen-ion concentration, kinetics, mathematics, membrane fusion, PC-12 cells, rats, temperature.


Descriptor: antiviral agents therapeutic use, chlorides administration and dosage, DNA viruses drug effects, hydroquinones administration and dosage, quinones administration and dosage, RNA viruses drug effects, virus diseases prevention and control, aphthovirus drug effects, chick embryo, cytopathogenic effect, viral drug effects, depression, chemical, herpesviridae drug effects, hydroquinones therapeutic use, influenza A virus avian drug effects, mice, quinones therapeutic use, tissue culture, viruses pathogenicity.

The synthesis of influenza virus ribonucleoprotein structures (RNPs) in infected chick embryo cells was analysed by polyacrylamide gel electrophoresis (PAGE) in the presence of sodium deoxycholate which resolves the RNPs into five size classes. A relatively small proportion of total RNPs accumulated in the nucleus but free NP protein was found there in large amounts over the period 1.5 to 4 h post-infection. In contrast, by 4 h post-infection, all cytoplasmic NP was complexed into RNP structures. At early times, during an 15 min pulse of (35S)methionine, nearly all the newly synthesized NP was incorporated into RNPs but by 4 h the majority of pulse-labelled NP was present as free protein. However, the proportion of free NP: NP in RNPs remained constant over the 1.5 to 4 h post-infection period, indicating that there was a delay before the NP synthesized later in infection was assembled into RNP structures. Individual RNP size classes were predominantly cytoplasmic and accumulated at similar rates but were not produced in equimolar amounts. The rates of synthesis of individual RNPs were in general agreement with their rates of accumulation with the remarkable exception of RNP d (containing RNA 7, the matrix protein gene). This was synthesized nearly 10-fold faster but accumulated at the same rate as the other RNPs. Possibly RNP d is more rapidly degraded than the other RNPs.

Descriptors: bacterial proteins biosynthesis, influenza A virus avian metabolism, nucleoproteins biosynthesis, ribonucleoproteins biosynthesis, cell nucleus metabolism, cultured cells, chick embryo, cytoplasm metabolism, influenza A virus avian growth and development, kinetics.


The nucleoprotein (NP) gene of the 1918 pandemic influenza A virus has been amplified and sequenced from archival material. The NP gene is known to be involved in many aspects of viral function and to interact with host proteins, thereby playing a role in host specificity. The 1918 NP amino acid sequence differs at only six amino acids from avian consensus sequences, consistent with reassortment from an avian source shortly before 1918. However, the nucleotide sequence of the 1918 NP gene has more than 170 differences from avian strain consensus sequences, suggesting substantial evolutionary distance from known avian strain sequences. Both the gene and protein sequences of the 1918 NP fall within the mammalian clade upon phylogenetic analysis. The evolutionary distance of the 1918 NP sequences from avian and mammalian strain sequences is examined, using several different parameters. The results suggest that the 1918 strain did not retain the previously circulating human NP. Nor is it likely to have obtained its NP by reassortment with an avian strain similar to those now characterized. The results are consistent with the existence of a currently unknown host for influenza, with an NP similar to current avian strain NPs at the amino acid level but with many synonymous nucleotide differences, suggesting evolutionary isolation from the currently characterized avian influenza virus gene pool.

Descriptors: nucleoproteins genetics, RNA binding proteins genetics, viral core proteins genetics, amino acid sequence, base sequence, influenza epidemiology, molecular sequence data, nucleoproteins chemistry, orthomyxoviridae classification, phylogeny, RNA binding proteins chemistry, regression analysis, swine, time factors, viral core proteins chemistry.

Reina, J. (2002). Factores de virulencia y patogenicidad en las cepas gripales (virus influenza tipo A) aviares y humanas. [Factors affecting the virulence and pathogenicity of avian and human viral strains (influenza virus type A)]. Enfermedades Infecciosas y Microbiologia Clinica 20(7): 346-53. ISSN: 0213-005X.

Most studies performed in avian viral strains seem to indicate that virulence is a polygenic phenomenon. However, hemagglutinin and neuraminidase and the genes codifying these substances (genes 4 and 6) play an essential role in viral pathogenesis. Avian strains can be classified as avirulent or virulent according to the ability of hemagglutinin to be activated by endoproteases of the respiratory tract only or by proteases from other tissues. This ability is based on the progressive development of mutations that lead to the substitution of the normal amino acids at the point of hemagglutinin hydrolysis by the other basic amino acids that determine the amplification of the spectrum of hydrolysis and activation. Neuraminidase participates in the acquisition of virulence through its capacity to bind to plasminogen and by increasing the concentration of activating proteases. Adaptation to the host, through recognition of the cell
receptor, is another factor determining the virulence and interspecies transmission of avian strains. From an epidemiological point of view, viral strains should be subtyped and the activating capacity of hemagglutinin should be determined to identify their degree of virulence.

Descriptors: influenza A virus avian pathogenicity, influenza A virus human pathogenicity, hemagglutinins, neuraminidase, peptide hydrolases, virulence.


NAL Call Number: 474 N213

Descriptors: influenza A virus avian growth and development, cell membrane, chick embryo, microscopy, electron, virus cultivation.


NAL Call Number: 448.8 L11

Abstract: Coinfection of a cell culture with a human and avian influenza A virus had yielded a recombinant virus with high neurovirulence for mice. This study reports on the comparative pathogenesis of central nervous system infection in mice between the parental human and the recombinant virus using the immunohistologic peroxidase-antiperoxidase method and virus assay of tissue suspensions. The human virus replicated poorly in mice and did not replicate in the brain even after intracerebral inoculation. In contrast, the recombinant virus replicated to high titer in the lung and brain with resulting viremia after inoculation of young mice by the intracerebral, intraperitoneal, or intranasal routes. Different populations of cells in the brain became infected after inoculation by each of the three routes: choroid plexus, and ependymal and subependymal cells after intracerebral inoculation; cells in perivenous areas, neurons in the olfactory bulbs and trigeminal ganglia and nuclear groups in the brainstem and midbrain after intranasal inoculation. Intraperitoneal inoculation resulted almost exclusively in the perivenous spread of the virus. The intranasal inoculation suggested that virus entry into the brain both by spread along nerve cell processes from the nasal mucosa to the brain and trigeminal ganglia and subsequent perivenous spread after viremia developed following virus replication in the lung. To dissect these two mechanisms we inoculated neonatal mice that had acquired high levels of serum antibody by nursing from actively immunized mothers. Intraperitoneal inoculation of these mice failed to cause infection, whereas intranasal inoculation resulted in the same pattern of cellular spread through the olfactory and trigeminal pathways as noted previously. This proved that this recombinant influenza virus could invade the central nervous system after infection via a natural route of infection. This highly neuroinvasive agent provides one example of the extent of virulence which can be acquired by recombination of apathogenic influenza viruses and raises a note of caution for adequate control of those agents generated in the laboratory.


NAL Call Number: 448.3 Ar23

Abstract: Cellular uptake of fowl plague virus occurs 10-30 minutes after inoculation of chick embryo cells. The penetration of the virions is by pinocytosis (viropexis); fusion with the cellular membrane has not been observed. After pinocytosis the virions become gradually disintegrated. Budding of newly formed virions from the cellular membrane starts 3 hours post inoculation (p.i.) and reaches its maximum 8 hours p.i. At the same time budding takes place into electron microscopically empty and autophagic vacuoles. Eight hours p.i. about 3 per cent of the infected cells show budding of virions from the surface and into cytoplasmic
Labelling of the cellular membrane with ruthenium red demonstrated that these cytoplasmic vacuoles are not simple cross-sections of invaginations of the cellular membrane. Cluster-like structures were found at 6 hours p.i. in the nuclei of infected cells; however, the suggestion that the clusters develop from nucleoli could not be confirmed.

Descriptors: influenza A virus avian ultrastructure, virus replication, cell membrane microbiology, cell membrane ultrastructure, chick embryo, influenza A virus avian growth and development, pinocytosis, time factors, tissue culture, vacuoles microbiology, vacuoles ultrastructure.

Reinhardt, J. and T. Wolff (2000). The influenza A virus M1 protein interacts with the cellular receptor of activated C kinase (RACK) 1 and can be phosphorylated by protein kinase C. *Veterinary Microbiology* 74(1-2): 87-100. ISSN: 0378-1135.

NAL Call Number: SF601.V44

Abstract: The M1 protein of influenza A virus has multiple regulatory functions during the infectious cycle, which include mediation of nuclear export of viral ribonucleoproteins, inhibition of viral transcription and a crucial role in virus assembly and budding. The only known modification of the M1 protein is by phosphorylation through yet-to-be-identified kinases. We postulated that at least some of the M1 functions are exerted or regulated through interactions with cellular components. In a screen for such cellular mediators, the protein receptor of the activated C-kinase (RACK 1) was identified by its interaction with the viral M1 protein in the yeast two hybrid system. The physical M1-RACK 1 interaction was confirmed in glutathione-S-transferase-based coprecipitation assays for the diverged M1 proteins of avian, swine and human influenza A virus strains. This conservation suggests that the M1-RACK 1 interaction is of general importance during influenza A virus infections. RACK 1 has previously been identified to specifically bind the activated form of protein kinase C (PKC) and is assumed to anchor the kinase at membranes in the vicinity of its substrates. Since the M1 protein becomes phosphorylated during influenza virus infection, we examined if PKC could catalyze the phosphate transfer. We demonstrate that virion-derived and recombinant M1 protein can indeed be efficiently phosphorylated by purified PKC. Moreover, in cell extracts, we detected M1 phosphorylation activity that was strongly reduced in the presence of the PKC-specific inhibitor compound GF109203X. These data suggest that PKC is the main M1-phosphorylating activity in the cell. Since both, the M1 protein and PKC have been shown to interact with RACK 1, we suggest that the M1-RACK 1 interaction is involved in M1 phosphorylation.

Descriptors: ion channels metabolism, peptides metabolism, protein kinase c metabolism, viral matrix proteins metabolism, binding sites, chick embryo, electrophoresis, polyacrylamide gel, enzyme inhibitors pharmacology, indoles pharmacology, influenza A virus avian, influenza A virus human, influenza A virus, porcine, maleimides pharmacology, phosphorylation, recombinant proteins metabolism, serine metabolism, software, structure activity relationship, threonine metabolism.


NAL Call Number: 41.8 Av5

Abstract: Cynomolgus macaques (*Macaca fascicularis*) infected with influenza virus A/HongKong/156/97 (H5N1) developed acute respiratory distress syndrome (ARDS) with fever. Reverse transcriptase/polymerase chain reaction (RT/PCR) and virus isolation showed that the respiratory tract is the major target of the virus. The main lesion observed upon necropsy, performed 4 or 7 days postinfection, was a necrotizing bronchointerstitial pneumonia, similar to that found in primary influenza pneumonia in human beings. By immunohistochemistry, influenza virus antigen proved to be limited to pulmonary tissue and tonsils. The data indicate that ARDS and multiple organ dysfunction syndrome (MODS), observed in both humans and monkeys infected with this virus, are caused by diffuse alveolar damage from virus replication in the lungs alone.

Descriptors: infection, acute respiratory distress syndrome (ARDS), respiratory system disease, avian influenza, infectious disease, respiratory system disease, viral disease, bronchointerstitial pneumonia, respiratory system disease, multiple organ dysfunction syndrome (MODS), disease miscellaneous, immunohistochemistry immunologic techniques, laboratory techniques, necropsy clinical techniques, reverse transcriptase polymerase chain reaction (RT PCR) genetic techniques, laboratory techniques, viral isolation

**NAL Call Number:** QD341.A2N8

**Abstract:** Extensive nucleotide sequence analysis of the 5' and the 3' terminal of the RNA segments of the genome of fowl plague virus, an avian strain of influenza virus, confirms the presence of a common sequence at the 5' terminus of each segment and a common sequence at the 3' terminus of each segment. Between the ends of each individual segment there is a complementary sequence which may be important in the control of transcription and replication of the genome. In addition, the probable sites of initiation of translation of fowl plague virus mRNA are indicated along with the corresponding NH2-terminal amino acid sequences of the virus polypeptides.

**Descriptors:** influenza A virus avian analysis, RNA viral analysis, base sequence, electrophoresis, polyacrylamide gel, genes viral.


**NAL Call Number:** 501 L84Pb

**Descriptors:** influenza A virus, RNA viral genetics, base sequence.


**NAL Call Number:** 448.8 V81

**Abstract:** A mutant of fowl plague virus, ts47, induces the synthesis in infected cells of a truncated NS1 polypeptide at both permissive and restrictive temperatures. Nucleotide sequence analysis of the segment coding for the NS1 polypeptide, segment 8, indicates that this aberration is due to a nonsense mutation. This mutation occurs in the region of the NS1 gene which overlaps with the NS2 gene and there is a corresponding amino acid substitution in the NS2 polypeptide. While it is not clear which polypeptide is responsible for the thermal instability of ts47, the loss of the COOH-terminal 28 amino acid residues from the NS1 polypeptide does not affect replication of the virus at permissive temperatures.

**Descriptors:** genes viral, influenza A virus avian genetics, RNA viral genetics, viral proteins genetics, base sequence, codon, mutation, RNA, messenger, temperature, viral nonstructural proteins.


**NAL Call Number:** QR375.V6

**Descriptors:** avian influenza virus, nucleotide sequence, RNA, polypeptide.


**NAL Call Number:** QR355.J6

**Abstract:** Cross-linked, poly(N-isopropylacrylamide) gel was used to concentrate avian influenza virus from allantoic fluid. Placing the gel in virus-infected allantoic fluid at 4 degrees C caused the gel to swell and absorb small molecular weight solutes, while excluding avian influenza virus and other large particles. Warming the gel to 37 degrees C or more caused the gel to collapse. The gel remained functional after sterilization in an autoclave and could be reused to concentrate other samples of allantoic fluid. Using a combined concentration and elution technique, we were able to achieve an average of 84.2% virus recovery, while reducing the fluid volume from 90 ml to 7.6 ml.

**Descriptors:** allantois microbiology, fetal membranes microbiology, influenza A virus avian isolation and purification, acrylic resins, chick embryo, hydrogen-ion concentration, temperature.

**NAL Call Number:** 448.8 V81

**Abstract:** It has been previously reported that several human H1 influenza viruses isolated prior to 1956, in contrast to human H3 isolates which are quite specific for SA alpha 2,6Gal sequences, apparently recognize both SA alpha 2,3Gal and SA alpha 2,6Gal sequences (Rogers, G.N., and Paulson, J.C., *Virology* 127, 361-373, 1983). In this report human H1 isolates representative of two epidemic periods, from 1934 to 1957 and from 1977 to 1986, and H1 influenza isolated from pigs, ducks, and turkeys were compared for their ability to utilize sialyloligosaccharide structures containing terminal SA alpha 2,3Gal or SA alpha 2,6Gal sequences as receptor determinants. Five of the eight human isolates from the first epidemic period recognize both SA alpha 2,3Gal and SA alpha 2,6Gal linkages, in agreement with our previous results. Of the remaining three strains, all isolated towards the end of the first epidemic, two appear to prefer SA alpha 2,6Gal sequences while the third preferentially binds SA alpha 2,3Gal sequences. In contrast to the early isolates, 11 of 13 human strains isolated during the second epidemic period preferentially bind SA alpha 2,6Gal containing oligosaccharides. On the basis of changes in receptor binding associated with continued passage in the laboratory for some of these later strains, it seems likely that human H1 isolates preferentially bind SA alpha 2,6Gal sequences in nature, and that acquisition of SA alpha 2,3Gal-binding is associated with laboratory passage. Influenza H1 viruses isolated from pigs were predominantly SA alpha 2,6Gal-specific while those isolated from ducks were primarily SA alpha 2,3Gal-specific. Thus, as has been previously reported for H3 influenza isolates, receptor specificity for influenza H1 viruses appears to be influenced by the species from which they were isolated, human isolates binding preferentially to SA alpha 2,6Gal-containing oligosaccharides while those isolated from ducks prefer SA alpha 2,3Gal-containing oligosaccharides. However, unlike the SA alpha 2,6Gal-specific H3 isolates, binding to cell surface receptors by the H1 influenza viruses is not sensitive to inhibition by horse serum glycoproteins, regardless of their receptor specificity. These results suggest that, while the H1 and H3 hemagglutinins appear to be subject to similar host-derived selective pressures, there appear to be certain fundamental differences in the detailed molecular interaction of the two hemagglutinins with their sialyloligosaccharide receptor determinants.

**Descriptors:** influenza A virus avian metabolism, influenza A virus human metabolism, influenza A virus, porcine metabolism, influenza A virus metabolism, orthomyxoviridae metabolism, receptors, virus metabolism, ducks, hemagglutination inhibition tests, hemagglutination tests, species specificity, swine, turkeys.


**NAL Call Number:** 448.8 V81

**Abstract:** The binding of influenza virus to erythrocytes and host cells is mediated by the interaction of the viral hemagglutinin (H) with cell surface receptors containing sialic acid (SA). The specificity of this interaction for 19 human and animal influenza isolates was examined using human erythrocytes enzymatically modified to contain cell surface sialyloligosaccharides with the sequence SA alpha 2,6Gal beta 1,4GlcNAc; SA alpha 2,3Gal beta 1,4(3)GlcNAc; SA alpha 2,3Gal beta 1,3GalNAc; or SA alpha 2,6GalNAc. Although none of the viruses agglutinated cells containing the SA alpha 2,6GalNAc linkage, differential agglutination of cells containing the other three sequences revealed at least three distinct receptor binding types. Several virus isolates exhibited marked receptor specificity, binding only to cells containing the SA alpha 2,6Gal or the SA alpha 2,3Gal linkage, while others bound equally well to cells containing either linkage. Moreover, some viruses could distinguish between two oligosaccharide receptor determinants containing the terminal SA alpha 2,3Gal linkage when present in the SA alpha 2,3Gal beta 1,4(3)GlcNAc sequence or the SA alpha 2,3Gal beta 1,3GalNAc sequence binding cells containing only the former. The observed receptor specificities were not significantly influenced by the viral neuraminidases as shown by the use of the potent neuraminidase inhibitor 2-deoxy-2,3-dehydro-N-acetylneuraminic acid. Receptor specificity appeared, to some extent, to be dependent on the species from which the virus was isolated. In particular, human isolates of the H3 serotype all agglutinated cells containing the SA alpha 2,6Gal linkage, but not cells bearing the SA alpha 2,3Gal beta 1,3GalNAc sequence. In contrast,
antigenically similar (H3) isolates from avian and equine species preferentially bound erythrocytes containing the SA alpha 2,3Gal linkage. This is of particular interest in view of the identification of the avian virus H3 hemagglutinin as the progenitor of the H3 hemagglutinin present on the current human Hong Kong viruses. 


NAL Call Number: 448.8 V81

Abstract: Human and animal (avian and equine) influenza A virus isolates of the H3 serotype exhibit marked differences in their ability to bind specific sialyloligosaccharide sequences that serve as cell surface receptor determinants (G. Rogers and J. Paulson, 1983, Virology 127, 361-373). Whereas human isolates of this subtype strongly agglutinate enzymatically modified human erythrocytes containing the terminal SA alpha 2,6Gal sequence, avian and equine isolates preferentially agglutinate erythrocytes bearing the SA alpha 2,3Gal sequence. As shown in this report, a glycoprotein found in horse serum, alpha 2-macroglobulin, is a potent inhibitor of viral adsorption to the cell surface for human H3 isolates. In contrast, avian and equine isolates are poorly inhibited suggesting a correlation between receptor specificity and inhibitor sensitivity. Growth of a human H3 isolate (A/Memphis/102/72) on MDCK cells in the presence of horse serum resulted in an overall shift in the virus receptor specificity from preferential binding of the SA alpha 2,6Gal linkage to preferential binding of the SA alpha 2,3Gal linkage characteristic of avian and equine isolates. Clonally isolated variants of A/Memphis/102/72 grown in the presence or absence of horse serum exhibited binding properties that account for those observed in the field isolates. Clones which preferentially bound the SA alpha 2,6Gal linkage, like the parent human virus, were very sensitive to inhibition of hemagglutination by horse serum and equine alpha 2-macroglobulin. In contrast, receptor variants which preferentially bound the SA alpha 2,3Gal linkage, like the avian and equine isolate, were insensitive to such inhibitors. None of the variants was very sensitive to inhibition of hemagglutination by human alpha 2-macroglobulin. These results suggest that the presence, in vivo, of a glycoprotein inhibitor such as equine alpha 2-macroglobulin could suppress infection of influenza viruses bearing an H3 hemagglutinin with a SA alpha 2,6Gal specific, inhibitor sensitive phenotype, allowing growth to predominance of a virus which is SA alpha 2,3Gal specific and inhibitor insensitive as found in avian and equine isolates.

Descriptors: glycoproteins antagonists and inhibitors, influenza A virus avian drug effects, influenza A virus human drug effects, influenza A virus drug effects, receptors, virus drug effects, viral proteins antagonists and inhibitors, adsorption, chick embryo, ducks, erythrocytes immunology, erythrocytes microbiology, hemagglutination inhibition tests, hemagglutination tests, hemagglutinins viral analysis, horses, alpha macroglobulins pharmacology.


NAL Call Number: 448.3 Ar23

Abstract: The influenza strain 413 1,1 segregated as a stable recombinant during passage of the isolate 19/N which was obtained after double infection of chick embryo fibroblasts by virus N and the fowl plague virus (FPV) mutant ts 19. Its gene constellation was determined by molecular hybridization. Upon infection of chick embryo cells by this recombinant strain, two particle populations of high (H) and low (L) buoyant densities were produced. By biological and biochemical parameters, the H-population (delta = 1.22 g/cm3) cannot be distinguished from standard infectious influenza virus. In contrast, the noninfectious L-particles (delta = 1.14 g/cm3) lack all virus-specific glycoproteins (HA, NA) as well as the matrix protein M and are visualized by electron microscopy as spikeless particles. Significant changes in the quantitative composition of the phospholipid bilayer are evident as compared to the H-particles. In addition to the previously characterized eight genes both populations contain a variety of smaller RNA fragments which hybridize with complementary RNA and presumably represent degradation products of full-length genes.

Descriptors: influenza A virus avian ultrastructure, phospholipids analysis, RNA viral analysis, viral proteins
analyses, virion ultrastructure, chick embryo, fibroblasts, genes viral, influenza A virus avian genetics, influenza A virus avian growth and development, mutation, recombination, genetic, tissue culture, virus replication.


NAL Call Number: 448.8 V81
Descriptors: influenza A virus analysis, RNA viral analysis, translation, genetic, base sequence, electrophoresis, polyacrylamide gel, horses, influenza A virus avian, influenza A virus isolation and purification, nucleic acid hybridization, recombination, genetic, viral proteins analysis.


NAL Call Number: 448.3 Ar23
Abstract: The gene coding for the nucleocapsid protein NP of the influenza A virus recombinant strain 413 1,1 was characterized biochemically by molecular hybridization and fingerprint analysis. The data presented suggest that this NP gene has evolved by intracistronic recombination between NP genes of virus N and the fowl plague virus temperature-sensitive mutants ts 19.
Descriptors: capsid genetics, genes viral, influenza A virus avian genetics, RNA viral genetics, viral proteins genetics, avian analysis, mutation, nucleic acid hybridization, oligonucleotides analysis, peptides analysis, viral analysis, recombination, genetic, temperature, viral proteins analysis.


NAL Call Number: 448.8 V81
Abstract: Avian influenza A viruses of the H5 and H7 subtypes periodically cause severe outbreaks of disease in poultry. The question we wished to address in this study is whether these highly pathogenic strains constitute unique lineages or whether they and related nonpathogenic viruses are derived from common ancestors in the wild bird reservoir. We therefore compared the nucleotide and amino acid sequences of the hemagglutinin (HA) genes of 15 H5 and 26 H7 influenza A viruses isolated over 91 years from a variety of host species in Eurasia, Africa, Australia, and North America. Phylogenetic analysis indicated that the HA genes of H5 and H7 viruses that cause severe disease in domestic birds do not form unique lineages but share common ancestors with nonpathogenic H5 and H7 viruses. These findings predict that highly pathogenic avian H5 and H7 influenza A viruses will continue to emerge from wild bird reservoirs. Another important question is whether H7 influenza viruses found in mammalian species are derived from avian strains. We included eight equine influenza viruses and one seal isolate in the phylogenetic analysis of H7 HA genes. We could show that the HA genes of both, the equine and the seal viruses, shared ancestors with avian H7 HA genes. This indicates that currently circulating H7 viruses with an avian HA gene may have the potential to adapt to mammalian species and to cause an influenza outbreak in the new host.
Descriptors: avian influenza virus, agglutinins, genes, pathogenicity, phylogeny, nucleotide sequence, chemical composition, biological properties, cell structure, chromosomes, evolution, genomes, influenza virus, microbial properties, nucleus, orthomyxoviridae, proteins, viruses, viral hemagglutinins, structural genes, amino acid sequences.


NAL Call Number: 448.8 V81
Abstract: The hemagglutinin (HA) genes from four avian H7N7 influenza A isolates, from a single outbreak, were shown to possess different cleavage sites that contain varying numbers of basic amino acid residues (KKKKR, KRKKR, KKRKKR, KKKKKKR). All four variants are highly pathogenic in chickens and share an immediate common ancestral HA with A/tern/Potsdam/342-6/79 (H7N7) and A/swan/Potsdam/63-6/81 (H7N7). These viruses are nonpathogenic and contain no extra basic amino acids at the cleavage site of
During evolution a common precursor virus acquired different sequences at the cleavage site of the HA and became highly pathogenic in chickens. In vitro assays revealed that the HA from A/chicken/Leipzig/79 with KKKKR at the cleavage site was only partially cleaved (41%), compared to 93-100% cleavage of the other HAs. Since all four viruses were highly pathogenic in chickens, these findings confirm that the degree of pathogenicity in vivo is not exclusively determined by the degree of HA cleavability.

Descriptors: chickens, disease outbreaks veterinary, fowl plague virology, hemagglutinins viral metabolism, influenza A virus avian metabolism, amino acid sequence, base sequence, DNA, viral, fowl plague epidemiology, geese, Germany epidemiology, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral genetics, avian genetics, molecular sequence data, phylogeny.


Abstract: Two viruses with a novel hemagglutinin (HA), A/duck/Australia/341/83 and A/shearwater/West Australia/2576/79, have been isolated from a duck and a shorebird in Australia. Hemagglutination inhibition and double immunodiffusion assays failed to reveal cross-reactivity with any of the known subtypes (H1 to H14). We therefore propose that these viruses constitute a new HA subtype, H15. Sequence analysis of the HA genes confirmed the serologic findings. When compared at the amino acid level, the HA1 region of the H15 subtype differs from those of the other subtypes by 30% and more. This degree of heterogeneity is also found among HA genes of other subtypes. Thus we propose that amino acid sequence data should be evaluated when determining the HA subtypes of influenza A viruses. Sequence comparison and phylogenetic analysis suggested that the HA subtype H15 is most closely related to the H7. Compared to the H7 HA, the H15 acquired a 30-nucleotide insertion within HA1 at position 253 which is located in the globular head of the molecule. This finding suggests that RNA recombination, although a rare event in nature, may play an important role in the evolution of influenza viruses.

Descriptors: hemagglutinins viral immunology, influenza A virus avian classification, influenza A virus classification, amino acid sequence, antigens, viral genetics, genes, structural, viral, hemagglutinins viral genetics, avian immunology, influenza A virus immunology, molecular sequence data, phylogeny, RNA viral genetics, sequence homology, amino acid, sequence homology, nucleic acid.


Abstract: Pyridoxal 5'-phosphate (PLP), a reversible inhibitor of in vitro transcription by fowl plague virus, has been used to identify the transcriptase. Kinetic analyses showed that PLP competitively inhibits the addition of each nucleoside triphosphate in ApG-primed reactions, suggesting that both initiation and elongation are affected. The irreversible inhibition by PLP following reduction with borohydride was prevented by preincubation with the first substrate: GTP in unprimed reactions or CTP in the presence of ApG. On reaction of FPV proteins with PLP and [3H]borohydride the core protein PB1 was preferentially labeled and the labeling was selectively blocked by GTP or ApG + CTP. These data suggest that PB1 has the nucleotide-binding site of the transcriptase, is responsible for both initiation and elongation, and is apparently associated with the 3' ends of template RNAs in virions.

Descriptors: influenza A virus avian enzymology, pyridoxal phosphate pharmacology, reverse transcriptase inhibitors, affinity labels, chick embryo, kinetics, transcription, genetic, viral core proteins, viral proteins metabolism.


Abstract: The glucose analogue N-methyl-1-deoxynojirimycin was found to be a specific inhibitor of the trimming of the outermost glucose residue of the N-linked precursor-oligosaccharide Glc3Man9GlcNAc2,
and therefore of oligosaccharide processing, in fowl plague virus-infected chicken-embryo cells. The fowl plague virus glycoproteins in N-methyl-1-deoxynojirimycin-treated cells contain oligosaccharides of the composition Glc3ManxGlcNAc2 (x = 7, 8, and 9). Inhibition of trimming of the outermost glucose residues does not prevent release of infectious virus with oligosaccharides of the composition Glc3Man7(GlcNAc)2. On the other hand inhibition of the trimming of the innermost glucose residue does inhibit release of infectious virus (Datema, R., Romero, P. A., Legler, G., and Schwarz, R. T. Proc. Nat. Acad. Sci. USA 79, 6787-6791 (1982)).

Descriptors: 1 deoxynojirimycin analogs and derivatives, anti bacterial agents pharmacology, antiviral agents pharmacology, glucosamine analogs and derivatives, glycoproteins antagonists and inhibitors, influenza A virus avian drug effects, viral proteins antagonists and inhibitors, chick embryo, glucosamine pharmacology, avian metabolism, oligosaccharides antagonists and inhibitors, virion drug effects, virion metabolism.

NAL Call Number: 448.3 M583
Descriptors: influenza A virus avian, viral vaccines, virus cultivation, chick embryo, chickens, HeLa cells, orthomyxoviridae infections immunology, tissue culture, vaccination.

NAL Call Number: 448.3 AC85
Descriptors: influenza A virus avian enzymology, Newcastle disease virus enzymology, orthomyxoviridae enzymology, parainfluenza virus 1, human enzymology, centrifugation, density gradient, chick embryo, chlorides, hydrogen-ion concentration, avian metabolism, magnesium, Newcastle disease virus metabolism, orthomyxoviridae metabolism, parainfluenza virus 1, human metabolism, perchloric acid, phosphorus isotopes, precipitation, RNA, ribosomal analysis, ribosomal metabolism, ribonucleases metabolism, solubility, sucrose, temperature.

NAL Call Number: 448.3 AC85
Descriptors: leukosis virus, avian enzymology, orthomyxoviridae enzymology, ribonucleases metabolism, carcinoma, ehrlich tumor, cattle, chick embryo, DNA metabolism, deoxyribonucleases metabolism, influenza A virus avian enzymology, leukosis virus, avian isolation and purification, Newcastle disease virus enzymology, nucleic acid denaturation, orthomyxoviridae isolation and purification, parainfluenza virus 1, human enzymology, paramyxoviridae enzymology, paramyxoviridae isolation and purification, polynucleotides metabolism, RNA, neoplasm isolation and purification, neoplasm metabolism, species specificity, temperature, thymus gland, tissue culture, virus cultivation.

NAL Call Number: 501 L84Pb
Abstract: The objective of the studies presented was to define a molecular basis for infectivity and pathogenicity of influenza virus. It is demonstrated that activation of the HA glycoprotein by post-translational proteolytic cleavage is indispensable for the formation of infectious influenza virus. There are two preconditions for influenza virus to be pathogenic: (1) the presence on the virus particle of a cleaved HA molecule essential for the infectivity, and (2) an optimal genome composition. In naturally occurring avian influenza viruses there is a direct correlation between the cleavability of the haemagglutinin, the potential of the virus to be produced in infectious form in a wide range of host cells, and the viruses’ pathogenicity for chicken. It is concluded that Nature selects an optimal gene constellation for each individual field strain. In these viruses the structure of the haemagglutinin is the determining factor for pathogenicity.
Descriptors: hemagglutininis viral genetics, influenza A virus avian genetics, avian pathogenicity, protein

**Descriptors:** influenza A virus avian classification, microbiological techniques veterinary, chick embryo, fibroblasts, hemagglutination tests, avian pathogenicity, plaque assay veterinary, tissue culture, virulence, virus cultivation.


**Abstract:** Influenza viruses, like other viruses, must exhibit a genome constellation, which permits optimal virus reproduction in a given host. Besides this prerequisite the influenza virus haemagglutinin glycoprotein (HA) has been shown to be an essential determinant for pathogenicity. HA, which is synthesized as a precursor molecule, is activated by posttranslational cleavage by host proteases to obtain its full biological properties. Proteolytic activation is therefore indispensable for effective virus spread in the infected host and thus for pathogenicity. HA of the highly pathogenic avian influenza viruses inducing a systemic infection in birds is cleaved in a broad range of different host cells. On the other hand, HA of all mammalian viruses and the nonpathogenic avian strains, which cause local infection, exhibit a restricted cleavability. The prime determinant for these differences has been found to be the structure of the cleavage site. This concept was corroborated on virus mutants adapted in vitro to a new host.

**Descriptors:** hemagglutinins viral immunology, orthomyxoviridae pathogenicity, viral envelope proteins immunology, amino acid sequence, base sequence, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral chemistry, hemagglutinins viral genetics, molecular sequence data, mutagenesis, insertional, orthomyxoviridae genetics, orthomyxoviridae immunology, RNA, ribosomal, 28S chemistry, viral envelope proteins chemistry, viral envelope proteins genetics.


**Descriptors:** hemagglutinins viral analysis, neuraminidase analysis, neuraminidase immunology, orthomyxoviridae enzymology, glycopeptides analysis, influenza A virus avian enzymology, avian immunology, avian ultrastructure.


**Abstract:** Influenza virus Equine 1 (A/equine/Prague/56) has a hemagglutinin which is antigenically related to the hemagglutinin of fowl plague virus strain Rostock (FPV) and a neuraminidase which cross-reacts with the enzyme of virus N (A/chick/Germany/49). After a single injection of chickens with Equine 1 virus no hemagglutination inhibiting (HI) and neutralizing antibodies against FPV can be demonstrated, although the birds are fully protected against a lethal dose of FPV. HI and neutralizing antibodies against FPV appear after a second injection of Equine 1 virus several weeks after the first one. Liberation of newly synthesized FPV from the host cell is inhibited by antibodies cross-reacting with any antigen of virus surface.

**Descriptors:** antigens, viral administration and dosage, arteritis virus, equine immunology, influenza A virus avian immunology, RNA viruses immunology, binding sites, antibody, epitopes, fluorescent antibody technique, hemadsorption, hemagglutination inhibition tests, hemagglutination tests, hemagglutinin viral isolation and purification, injections, intravenous, neuraminidase analysis, neutralization tests, plaque assay.


**NAL Call Number:** QR360.A1J6

**Descriptors:** antibody formation, antigens, viral, fowl plague immunology, influenza A virus avian immunology, neuraminidase analysis, orthomyxoviridae immunology, chickens immunology,
hemagglutination inhibition tests, hemagglutinins viral analysis, immune sera, immunization, influenza veterinary, avian enzymology, neutralization tests, orthomyxoviridae enzymology, rabbits immunology, swine, swine diseases microbiology.


**NAL Call Number:** 41.8 Z52

**Descriptors:** antibodies, viral biosynthesis, hemagglutination tests, influenza A virus avian immunology, chickens, tissue culture, virus cultivation.


**NAL Call Number:** 448.3 C33 (1)

**Abstract:** In addition to acute viral diseases, persistent infections have attained considerable interest in recent years. Such persistent infections are characterized by extended time periods in which the infecting virus remains within the organism before the eventual appearance of manifest symptoms. These infections may be evoked by a variety of virus species resulting in a diversity of pathogenic reactions and clinical manifestations. The mechanisms of viral persistence, where known, also appear to be quite diverse. As far as space permits, some examples of persistent infections will be presented and the mechanisms of the pathogenesis of the resulting diseases will be discussed.

**Descriptors:** hemagglutinins viral analysis, hemagglutinins viral genetics, hemagglutinins viral immunology, influenza A virus avian pathogenicity, amino acid sequence, cell membrane microbiology, chick embryo, fetal membranes microbiology, genes viral, avian genetics, avian growth and development, avian ultrastructure, models, molecular, mutation, virulence.


**NAL Call Number:** QR360.J6

**Abstract:** A number of antigenic hybrids of influenza A viruses were produced possessing either the hemagglutinin or the neuraminidase of fowl plague virus and the corresponding antigen derived from another influenza A virus. Other recombinants were obtained carrying both surface antigens of fowl plague virus but differing from the parent in certain biological properties. None of the recombinants isolated were pathogenic for adult chickens. Most recombinants obtained after crosses between reciprocal recombinants carrying both fowl plague virus surface antigens were also apathogenic for chickens. Using the same parent recombinants for double infection some of the progeny "back-recombinants" were pathogenic, whereas others were not. From these results it is concluded that the surface components do not by themselves determine the pathogenicity of influenza A viruses.

**Descriptors:** hemagglutinins viral analysis, influenza A virus avian pathogenicity, neuraminidase immunology, orthomyxoviridae pathogenicity, recombination, genetic, chick embryo, crosses, genetic, avian enzymology, avian immunology, neuraminidase analysis, orthomyxoviridae enzymology, orthomyxoviridae immunology.


**NAL Call Number:** QR360.A1J6

**Abstract:** We have demonstrated by recombination of two highly pathogenic avian influenza viruses [A/FPV/Rostock (Hav1N1) x A/turkey/England/63 (Hav1Nav3)] that recombinants can be isolated which are pathogenic as well as non-pathogenic for chickens. They carried the glycoproteins of either parent strains,
and all are produced in infectious form in chick embryo cells. Genetic analysis revealed that the non-pathogenic recombinants possess a mixed RNA polymerase complex, consisting of pol 1, pol 2, ptra and NP gene products, while, with one exception, the pathogenic recombinants have the genes coding for the polymerase activity from one or other parent virus. The biological properties of the recombinant viruses did not correlate with their pathogenicity for chickens.

Descriptors: genes viral, influenza A virus avian genetics, recombination, genetic, chickens, DNA directed RNA polymerases genetics, fowl plague microbiology, avian pathogenicity, neuraminidase genetics, turkeys.

NAL Call Number: 448.8 V81
Descriptors: chickens microbiology, influenza A virus avian pathogenicity, recombination, genetic, cell line, chick embryo, DNA directed RNA polymerases genetics, genes viral, avian genetics, avian growth and development, plaque assay, temperature.

NAL Call Number: 448.3 Ar23
Abstract: The spread of infection in the chorioallantoic membrane (CAM) has been analysed with pathogenic and non-pathogenic avian influenza A viruses. After allantoic inoculation of pathogenic strains, high titers of infectious virus were found in the allantoic fluid, and virus growth could be demonstrated by immunohistology and electron microscopy in the allantoic epithelium, the mesenchyma, and in the chorionic epithelium. By the same route of inoculation, non-pathogenic strains yielded also higher titers of infectious virus in the allantoic fluid, but virus replication was restricted to the allantoic epithelium and did not occur in the other cell layers. After chorionic inoculation of pathogenic strains, replication occurred in all layers of the CAM, and infectious virus was released into the allantoic fluid. However, when the chorionic epithelium was infected with a non-pathogenic strain, infection did not spread beyond the site of inoculation. These differences in virus spread are based on differential activation of the hemagglutinin by proteolytic cleavage. The hemagglutinin of pathogenic strains is cleaved in cells of each layer, whereas the hemagglutinin of non-pathogenic strains is cleaved only in the allantoic epithelium. In epithelial cells, virus budding occurred nearly exclusively at the apical side of the cell surface, but this polarization of virus maturation was found with both pathogenic and nonpathogenic strains, indicating that it does not account for the differences in virus spread and, thus, in pathogenicity.
Descriptors: fetal membranes microbiology, hemagglutinin viral, influenza A virus avian growth and development, virus replication, allantois microbiology, chick embryo, chorion microbiology, epithelium microbiology, avian immunology, avian pathogenicity, tissue culture, virus replication.

NAL Call Number: QR360.A1J6
Descriptors: influenza A virus avian, virus replication, carbon isotopes, complement fixation tests, cycloheximide pharmacology, cytopathogenic effect, viral, neuraminidase metabolism, RNA biosynthesis, temperature, tissue culture, uridine metabolism.

Descriptors: orthomyxoviridae growth and development, virus replication, antigens, viral, chick embryo, DNA biosynthesis, dactinomycin pharmacology, defective viruses, hemagglutinins viral, inclusion bodies, viral, influenza A virus avian growth and development, neuraminidase biosynthesis, neuraminidase pharmacology, Newcastle disease virus growth and development, phagocytosis, RNA viral biosynthesis, viral proteins biosynthesis.

NAL Call Number: 472 N21
Descriptors: mycotoxins pharmacology, orthomyxoviridae drug effects, virus replication drug effects, depression, chemical, influenza A virus avian, leucine metabolism, Newcastle disease virus, orthomyxoviridae metabolism, RNA viral biosynthesis, tritium, uridine metabolism, viral proteins biosynthesis.

NAL Call Number: 47.8 B77
Descriptors: avian influenza virus, low pathogenic H7N1, experimental challenge, model, protection.

NAL Call Number: 448.8 P942
Abstract: A comparative immunological analysis of the composition of antigenic determinants (AGD) in hemagglutinins of human influenza A virus (HIAV) of the serosubtypes H1, H2, H3, and in hemagglutinins of animal influenza viruses (AIV) of the serosubtypes H1, H3-H6, H8-H11 with 25 polyclonal highly active sera was demonstrated. Using original monospecific mon AGD in HIAV and AIV hemagglutinins was demonstrated. Using original monospecific antibodies to individual AGD, those AGD contributing to similarity and differences between HIAV and AIV were determined. It was found that influenza A. virus strains isolated from man in the USSR in 1986 were identical in the antigenic structure of hemagglutinin with that isolated from a tern in 1973 (A/tern/Turkmenistan/18/73).
Descriptors: epitopes, genes viral, influenza A virus avian immunology, human immunology, antigens, viral immunology, cross reactions, hemagglutination tests, hemagglutinins viral genetics, hemagglutinins viral immunology, avian genetics, human genetics, neuraminidase genetics, neuraminidase immunology, species specificity.

NAL Call Number: 448.3 Ar23
Abstract: A series of 33 human-avian and human-mammalian influenza virus reassortant clones possessing either HA or both HA and NA genes of the avian or mammalian virus was obtained by crosses of A/USSR/90/77 (H1N1) human virus with 5 avian and 1 mammalian influenza virus strains. All of the reassortants possessing NA genes of the H1N1 human parent virus and HA gene of an avian or mammalian parent virus had high values of infectivity/HA activity ratio. Since this feature could result from a limited virion
aggregation, several reassortants were analyzed by velocity sucrose gradient centrifugation. In all cases tested, the reassortants of H3N1, H4N1, H10N1 and H13N1 composition were shown to be aggregated, whereas the preparations of the parent H1N1 virus and the reassortants possessing both HA and NA genes from the avian parents were represented mostly by single virions. The aggregates were formed at 4 degrees C and dissociated at 37 degrees C. The dissociation was blocked by an inhibitor of neuraminidase activity (2-deoxy-2,3-dehydro-N-acetyl-neuraminic acid). The dissociation was reversible since the virions reaggregated at 4 degrees C; however, treatment with bacterial neuraminidase led to an irreversible dissociation of the aggregates. The tendency of the reassortants to aggregate correlates with an increased infectivity/HA ratio. No regular decrease in the neuraminidase activity in the virions of reassortants as compared to the parent H1N1 virus was revealed. The most likely explanation of the observed phenomenon seems to be an inefficient removal of sialic acid residues from the avian virus hemagglutinin by the human virus N1 neuraminidase.

Descriptors: influenza A virus genetics, membrane glycoproteins genetics, reassortant viruses genetics, viral proteins genetics, chick embryo, chickens, ducks, electrophoresis, polyacrylamide gel, genes viral, hemagglutination, viral, hemagglutinins viral genetics, avian genetics, avian physiology, human genetics, human physiology, influenza A virus physiology, neuraminidase genetics, neuraminidase pharmacology, RNA viral analysis, reassortant viruses physiology, recombination, genetic drug effects, temperature, whales.

NAL Call Number: 448.8 P942
Abstract: A series of reassortant clones with antigenic formulae H2N1 and H2N3 were produced by genetic reassortment performed with the use of an avian influenza virus, A/Pintail Duck/Primorie/695/76 (H2N3) and a high-yield reassortant strain X-67. Preliminary identification of the parent origin of NP and NS genes for 5 reassortants was performed by comparison of the mobilities of virus-specific proteins in polyacrylamide gel electrophoresis. The parent origin of genes of internal and nonstructural proteins for 3 reassortants was identified by partial sequencing. Although the genes of internal and nonstructural proteins of the reassortants originated from high-yield X-67 virus, only H2N3 reassortants were similar to the high-yield parent virus as concerns the level of the virus accumulation evaluated by hemagglutination titration and measurement of the virus protein content.
Descriptors: hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian genetics, reassortant viruses genetics, birds, electrophoresis, polyacrylamide gel, phenotype.

NAL Call Number: 448.8 P942
Abstract: A series of reassortant clones with antigenic formulae H2N1 and H2N3 were produced by genetic reassortment performed with the use of an avian influenza virus, A/Pintail Duck/Primorie/695/76 (H2N3) and a high-yield reassortant strain X-67. Preliminary identification of the parent origin of NP and NS genes for 5 reassortants was performed by comparison of the mobilities of virus-specific proteins in polyacrylamide gel electrophoresis. The parent origin of genes of internal and nonstructural proteins for 3 reassortants was identified by partial sequencing. Although the genes of internal and nonstructural proteins of the reassortants originated from high-yield X-67 virus, only H2N3 reassortants were similar to the high-yield parent virus as concerns the level of the virus accumulation evaluated by hemagglutination titration and measurement of the virus protein content.
Descriptors: molecular genetics, gene analysis analytical method, genetic reassortment phenotypes, viral genetics.

Comparing the structures of H3, H5 and H9 subtype haemagglutinins, we deduced a structural basis for including all 15 influenza subtypes in four clades. H3, H5 and H9 represent three of these clades; we now report the structure of an H7 HA as a representative of the fourth clade. We confirm the structure of the turn at the N-terminus of the conserved central alpha-helix of HA2, and the combination of ionisable residues near the "fusion peptide" as clade-specific features. We compare the structures of three H1 HAs with H5 HA in the same clade, to refine our previous classification and we confirm the division of the clades into two groups of two. We also show the roles of carbohydrate side chains in the esterase-fusion domain boundaries in the formation of clade-specific structural markers.

Descriptors: hemagglutinin glycoproteins, influenza virus chemistry, hemagglutinin glycoproteins, influenza virus classification, influenza A virus chemistry, influenza A virus classification, amino acid sequence, carbohydrates chemistry, crystallography, x-ray, hemagglutinin glycoproteins, influenza virus genetics, influenza A virus genetics, models, molecular, molecular sequence data, phylogeny, protein structure, quaternary, protein structure, tertiary, sequence homology, amino acid.
Phylogenetic analysis of the N8 neuraminidase (NA) genes from 18 influenza A viruses, representing equine and avian hosts in different geographic locations, revealed three major lineages: (i) currently circulating equine 2 viruses; (ii) avian viruses isolated in the Eurasian region, including A/Equine/Jilin/1/89, a recent avian-like N8 isolate found in horses in China; and (iii) avian viruses isolated in North America. Comparison of mutation rates indicated that avian N8 genes have evolved more slowly than their equine counterparts. That is, in both avian lineages, 72% of the nucleotide changes were silent in the terminal branches of the phylogenetic tree, whereas in equine 2 viruses, 59% of the nucleotide changes were silent. This suggests greater selective pressure on the NA gene from the mammalian immune system, leading to progressive evolution. Alternatively, the slower mutation rate for avian N8 genes could reflect a selective advantage gained from a longer, continuous span of evolution. The shape of the phylogenetic tree, the evolutionary rate, and the calculated date of origin for the N8 equine 2 virus lineage were comparable to findings for the equine 2 virus hemagglutinin (HA) gene (Bean et al., J. Virol. 66, 1129-1138, 1992). This suggests that both viral membrane glycoproteins of equine 2 viruses have evolved together and have been subjected to similar levels of selective pressure. Several amino acid residues were found to differ among the three host-specific lineages, but they may not be involved in host restriction of the NA, as they are shared by EQ/Jilin/1/89 and viruses of avian origin. The present findings complement detailed structural information on the N2 and N9 subtypes and should prove valuable in understanding future X-ray diffraction studies of N8 crystals.

In order to develop a surrogate virus strain for production of an inactivated influenza vaccine against a human H9N2 virus, A/Hong Kong/1073/99 (HK1073: H9N2) was co-infected in embryonated chicken eggs with an apathogenic avian influenza virus, A/Duck/Czechoslovakia/56 (Dk/Cz: H4N6), for gene segment reassortment. Multiple-gene reassortants obtained were examined for replication in mammalian hosts in vitro and in vivo by infecting MDCK cells and by intranasal administration to hamsters, respectively. A 2-6 gene reassortant with both surface glycoproteins of HK1073 origin and the rest of Dk/Cz origin, HK/CZ-13, was shown to replicate poorly in the mammalian hosts both in vivo and in vitro comparing with HK1073, although this reassortant replicated as efficiently as each parental strain in embryonated eggs. No sequence difference was observed in the HA1 region between HK1073 and HK/CZ-13, indicating that the reassortant would be equivalent in its immunogenicity to the parental HK1073 strain when it is used as an inactivated vaccine. A virus strain with attenuation in mammalian hosts is preferable for production of an H9 vaccine, since it should reduce the risk of manufacturing-related infections of employees during the vaccine production. HK/CZ-13 can therefore be a surrogate strain for production of an inactivated vaccine as well as diagnostic antigens in case of a possible future pandemic caused by an HK1073-like H9 influenza virus.

Abstract: To locate antigenic epitopes on the N8 neuraminidase (NA), we generated a panel of 97 monoclonal antibodies (MAbs), 66 of which inhibited NA activity (NI antibodies). Three groups of NI MAbs were identified from their different reactivities with escape mutants. Group 1 antibodies recognized the peptide loop containing residues 344 to 346, which appears to be an immunodominant region on the rim of the enzyme center of the N8 NA. Group 2 antibodies recognized a novel epitope containing residues 150, 199, 367, 399, and 400 (N2 numbering). From the location of these residues on the three-dimensional structure of the N8 NA, the epitope appears to be located at the interface of two adjacent monomers in the tetrameric NA, one contributing residues 150 and 199 and the other contributing residues 367 and 399 to 400. The available evidence indicates that the MAbs of this group react with the NA only after it is fully assembled. The third group of antibodies recognized the peptide loops containing residues 367 and 399 to 400. All of the amino acid substitutions in N8 escape mutants which affect the NI activity of antibodies were located in the peptide loops known to form epitopes in the N2 and N9 subtypes, indicating that antigenic regions in the NA head inducing NI antibodies appear to be similar among different subtypes of influenza A viruses. The MAbs used in this study will be valuable in studying the role of each N8 NA epitope in host immune defense systems and in the kinetics analysis of the biosynthesis of the enzyme.

Descriptors: antibodies, viral immunology, epitopes immunology, influenza A virus avian immunology, neuraminidase immunology, amidohydrolases metabolism, antibodies, monoclonal, antibodies, viral classification, base sequence, avian enzymology, avian genetics, models, molecular, molecular sequence data, mutation genetics, precipitin tests, sequence analysis, structure activity relationship.

**NAL Call Number:** 448.3 Ar23

**Abstract:** Monoclonal antibodies raised against the separated hemagglutinin subunits (HA1 and HA2) of influenza A/Vic/3/75 (H3N2) virus were tested against a large panel of human and avian strains. The epitopes recognized by most antibodies were conserved among subtype H3 viruses, but reactivity of some antibodies with members of other subtypes was also observed. Particularly, the H4 virus reacted with most antibodies directed against the HA2 subunit. These results are discussed in terms of sequence similarities between subtypes and application of these antibodies as subtyping reagents.

**Descriptors:** antibodies, viral immunology, epitopes immunology, hemagglutinins viral immunology, influenza A virus immunology, antibodies, monoclonal immunology, cross reactions immunology, electrophoresis, polyacrylamide gel, hemagglutinin glycoproteins, influenza virus, avian classification, avian immunology, human classification, human immunology, influenza A virus classification.


**NAL Call Number:** 448.3 AC85

**Descriptors:** bacteria enzymology, gm1 ganglioside metabolism, gangliosides metabolism, influenza A virus avian enzymology, neuraminidase metabolism, paramyxoviridae enzymology, sialic acids metabolism, acetylation, species specificity, substrate specificity, time factors.


**NAL Call Number:** QR355.J6

**Abstract:** Expression of glycoproteins has been carried out successfully using recombinant vaccinia virus vectors. Especially attractive is the use of recombinant vaccinia viruses which express the DNA-dependent RNA polymerase of the phage T7 (T7-polymerase). The T7-polymerase drives the transcription of plasmid-based genes under the control of the T7 RNA polymerase promoter transfected into the infected cell. Comparison of two different recombinant vaccinia viruses, vTF7-3 and MVA-T7, revealed that post-translational processing of Marburg virus surface glycoprotein (GP) is impaired in the MVA-T7 but not in the vTF7-3 system. Influenza virus hemagglutinin, however, was transported and processed like the authentic protein in both systems. It is shown that transport of GP in the MVA-T7 system is not completely blocked, but the vast majority of molecules remained Endo H-sensitive. Only trace amounts evaded the endoplasmatic reticulum and reached the plasma membrane. Thus, the adverse effects of MVA-T7 on the processing of recombinant glycoproteins cannot be predicted, and correct processing has to be investigated for every expressed glycoprotein.

**Descriptors:** genetic vectors, vaccinia virus genetics, viral envelope proteins metabolism, cell membrane metabolism, endoplasmic reticulum metabolism, HeLa cells, hemagglutinins viral genetics, hemagglutinins viral metabolism, influenza A virus avian genetics, avian metabolism, protein processing, post translational, protein transport, viral envelope proteins genetics.


**NAL Call Number:** TP248.P77P763

**Abstract:** The influenza A M2 protein forms cation-selective ion channels which are blocked by the anti-influenza drug amantadine. A molecular model of the M2 channel is presented in which a bundle of four parallel M2 transbilayer helices surrounds a central ion-permeable pore. Analysis of helix amphipathicity was used to aid determination of the orientation of the helices about their long axes. The helices are tilted such that the N-terminal mouth of the pore is wider than the C-terminal mouth. The channel is lined by residues V27, S31 and I42. Residues D24 and D44 are located at opposite mouths of the pore, which is narrowest in
the vicinity of I42. Energy profiles for interaction of the channel with Na+, amantadine-H+ and cyclopentylamine-H+ are evaluated. The interaction profile for Na+ exhibits three minima, one at each mouth of the pore, and one in the region of residue S31. The amantadine-H+ profile exhibits a minimum close to S31 and a barrier near residue I42. This provides a molecular model for amantadine-H+ block of M2 channels. The profile for cyclopentylamine-H+ does not exhibit such a barrier. It is predicted that cyclopentylamine-H+ will not act as an M2 channel blocker.

Descriptors: influenza A virus avian chemistry, ion channels chemistry, protein structure, tertiary, viral matrix proteins chemistry, amantadine chemistry, amantadine metabolism, computer simulation, cyclopentanes chemistry, cyclopentanes metabolism, ion channels metabolism, models, molecular, protein structure, secondary, protons, receptors, nicotinic chemistry, receptors, nicotinic metabolism, sodium chemistry, sodium metabolism, viral matrix proteins metabolism.

NAL Call Number: 448.8 C16

Descriptors: carcinoembryonic antigen, hemagglutinins viral, influenza A virus avian immunology, bronchial neoplasms immunology, cell line, cell membrane immunology, virus replication.

NAL Call Number: 448.3 AC85
Abstract: Proteins and RNAs of influenza A (H2N2) viruses isolated from birds in 1983 in East Germany were compared antigenically with those of H2N2 human strains. The electrophoretic mobility of the viral proteins and of the S1-treated double-stranded RNAs from two human and six avian strains, as well as the results of EIA-tests using monoclonal antibodies to their matrix protein and nucleoproteins indicate an antigenic relationship between the avian isolates and human strains of H2N2 subtype. One of the avian strains had a reduced amount of matrix protein.
Descriptors: antigens, viral analysis, epitopes analysis, influenza A virus avian chemistry, human chemistry, RNA viral analysis, viral matrix proteins analysis, antibodies, monoclonal, ducks, enzyme linked immunosorbent assay, East Germany.

NAL Call Number: 448.8 P942
Abstract: The influence of the conditions of adsorption and virion destruction by freezing-thawing and detergents on the detection of M1 and NP proteins of different influenza virus strains by solid-phase enzyme immunoassay with direct virion adsorption on polystyrene was studied. It was found that for the detection of M1 protein the optimal conditions included virion disruption with detergent and adsorption to polystyrene at 4 degrees C, and for NP protein disruption by freezing-thawing at adsorption to polystyrene at 37 degrees C. In the study of the antigenic properties of protein M1 of different influenza virus strains using monoclonal antibodies it was shown to be necessary, first, to achieve maximum detection of proteins and, second, to standardize the amount of the adsorbed antigen with polyclonal antibodies.
Descriptors: antigens, viral analysis, capsid analysis, influenza A virus avian analysis, human analysis, viral core proteins analysis, viral matrix proteins analysis, adsorption, antibodies, monoclonal diagnostic use, antigens, viral immunology, capsid immunology, enzyme linked immunosorbent assay methods, enzyme

**NAL Call Number:** 381 J824

**Abstract:** During the budding of enveloped viruses from the plasma membrane, the lipids are not randomly incorporated into the envelope, but virions seem to have a lipid composition different from the host membrane. Here, we have analyzed lipid assemblies in three different viruses: fowl plague virus (FPV) from the influenza virus family, vesicular stomatitis virus (VSV), and Semliki Forest virus (SFV). Analysis of detergent extractability of proteins, cholesterol, phosphoglycerolipids, and sphingomyelin in virions showed that FPV contains high amounts of detergent-insoluble complexes, whereas such complexes are largely absent from VSV or SFV. Cholesterol depletion from the viral envelope by methyl-beta-cyclodextrin results in increased solubility of sphingomyelin and of the glycoproteins in the FPV envelope. This biochemical behavior suggests that so-called raft-lipid domains are selectively incorporated into the influenza virus envelope. The "fluidity" of the FPV envelope, as measured by the fluorescence polarization of diphenylhexatriene, was significantly lower than compared with VSV or SFV. Furthermore, influenza virus hemagglutinin incorporated into the envelope of recombinant VSV was largely detergent-soluble, indicating the depletion of raft-lipid assemblies from this membrane. The results provide a model for lipid selectivity during virus budding and support the view of lipid rafts as cholesterol-dependent, ordered domains in biological membranes.

**Descriptors:** influenza A virus avian physiology, membrane lipids metabolism, Semliki Forest virus physiology, vesicular stomatitis Indiana virus physiology, cell line, cell membrane virology, detergents, fluorescence polarization, hamsters, solubility.


**NAL Call Number:** 41.8 T445

**Descriptors:** avian influenza, strains, vaccines, immunology, ducks.
neuraminidase antagonists and inhibitors, orthomyxoviridae drug effects.


Descriptors: central nervous system diseases virology, influenza A virus avian pathogenicity, human pathogenicity, influenza B virus pathogenicity, peripheral nervous system diseases virology, central nervous system diseases pathology, peripheral nervous system diseases pathology.


Abstract: Both 2-deoxy-2-fluoro-D-glucose and 2-deoxy-2-fluoro-D-mannose were found to be potent inhibitors of the synthesis of infectious Semliki forest and fowl plague virus in chicken embryo cells and also of pseudorabies virus grown in rabbit kidney cells. It was found that the pseudorabies virus-mediated cell fusion and the synthesis of functional hemagglutinin of fowl plague virus were blocked. In all cases the 2-deoxy-2-fluoro-D-mannose-caused inhibition was stronger than the 2-deoxy-2-fluoro-D-glucose- or 2-deoxy-D-glucose-mediated blocks. Studies on the virus-specified proteins from Semliki forest virus-infected cells grown in the presence of the inhibitors show that the target of the fluorosugar action, parallel to the well-studied effects of 2-deoxy-D-glucose, is the glycoprotein biosynthesis.

Descriptors: deoxy sugars analogs and derivatives, deoxyglucose analogs and derivatives, herpesviridae drug effects, herpesvirus 1, suid drug effects, influenza A virus avian drug effects, rhamnose analogs and derivatives, Semliki Forest virus drug effects, cell fusion drug effects, cell line, deoxyglucose pharmacology, fluorine, glycoproteins biosynthesis, hemagglutentin viral, herpesvirus 1, suid growth and development, herpesvirus 1, suid metabolism, avian growth and development, avian metabolism, rhamnose pharmacology, Semliki Forest virus growth and development, Semliki Forest virus metabolism, viral proteins biosynthesis, virus replication drug effects.


Descriptors: influenza A virus, tracheal tissue culture, pathogenesis, human, swine, equine, chicken, ferret.


Descriptors: influenza A virus, tracheal tissue culture, pathogenesis, human, swine, equine, chicken, ferret.
Descriptors: antibodies, viral immunology, antigens, viral immunology, hemagglutinin glycoproteins, influenza virus immunology, influenza A virus avian immunology, antibodies, monoclonal immunology, antibody affinity, antigen antibody reactions, chickens, epitope mapping, kinetics, neutralization tests.

NAL Call Number: QR360.A1J6

Abstract: Neutralization and haemagglutination-inhibition (HI) of a type A influenza virus by a panel of five monoclonal IgGs, their F(ab')2s, Fabs and Fabs+ anti-mouse Fab were compared. The MAbs were specific for antigenic sites A, B and D of the haemagglutinin. Activities of the IgGs varied by up to 6-fold on a molar basis, apart from the HI activity of HC58 which was > 100-fold lower. This was not due to low functional affinity as HC58 had the second highest value (nM) as determined by an equilibrium method with whole virions. Conversion to the F(ab')2 reduced neutralization and HI by only 2- to 6-fold, indicating that the Fc region had little involvement in these processes. However, all Fabs had low neutralization and HI activity compared with their IgGs, neutralization being reduced by 86 to > 1912-fold, and HI by 13 to > 69-fold. Although decreased, their affinities remained high, in the nM range. Neutralization and HI by three of the Fabs (HC2, HC3W and HC61) were restored by the addition of anti-Fab IgG; however, HC10 Fab+anti-Fab IgG still had no detectable neutralization activity but gave HI, and HC58 Fab+anti-Fab IgG had no detectable HI activity but neutralized to the same extent as its IgG. The different properties of the antibodies are discussed in the light of their known mechanisms of action: HI by steric blocking of attachment of virus to the red cell receptor, and neutralization by the inhibition of post-attachment events (HC2, HC10 and HC61). The data demonstrate just how variable are the antiviral properties of individual IgGs.

Descriptors: antibodies, monoclonal immunology, antibodies, viral immunology, hemagglutinin glycoproteins, influenza virus immunology, influenza A virus avian immunology, adult, antibodies, anti idiotypic immunology, antigen antibody reactions, cell membrane immunology, chickens, dose response relationship, immunologic, hemagglutination inhibition tests, immunoglobulin g immunology, immunoglobulins, Fab immunology, membrane glycoproteins immunology, neutralization tests.

NAL Call Number: 448.8 V81

Descriptors: genes, structural, genes viral, glycoproteins genetics, influenza A virus genetics, viral proteins genetics, base sequence, hemagglutinins viral genetics, influenza A virus avian genetics, neuraminidase genetics, nucleic acid hybridization, RNA viral genetics.

NAL Call Number: 448.3 Ar23

Abstract: Virazole (ribavirin) inhibits the RNA synthesis of an influenza A virus (fowl plague). Neither virion RNA nor complementary RNA are produced. Although the effect of virazole can be counteracted by guanosine the inhibitor does not interfere with the uptake or incorporation of labelled guanosine into chick embryo cells, nor does replacement of glucose by mannose amplify the effect of virazole. Thus virazole seems not to act via an interference with the GTP pool. Synthesis of Semliki Forest virus RNA is not affected by virazole.

Descriptors: influenza A virus avian metabolism, RNA viral biosynthesis, ribavirin pharmacology, ribonucleosides pharmacology, DNA directed RNA polymerases biosynthesis, depression, chemical, hemagglutinins viral, avian drug effects, neuraminidase biosynthesis, Semliki Forest virus metabolism, tissue culture, viral proteins biosynthesis.

NAL Call Number: QR189.V32
Abstract: After treatment of different strains of influenza A at low pH, the threshold pH, at which the infectivity was lost, depended on the haemagglutinin (HA) subtype of the virus strain. Strains with noncleaved HA were much more stable when compared to strains with cleaved HA. These observations might explain why duck influenza viruses spread well by lake water, while highly pathogenic strains with cleaved HA do not. There were also significant differences in heat stability of infectivity among influenza A strains, which do not correlate with differences in stability at low pH.

Descriptors: influenza A virus pathogenicity, chick embryo, heat, hemagglutinins viral, hydrogen-ion concentration, influenza A virus avian pathogenicity, human pathogenicity, species specificity.


NAL Call Number: 448.3 Ar23

Abstract: We have measured the infectivity of influenza A virus strains grown either in embryonated eggs or in chick embryo cells in culture after treatment at low pH. At pH values at which hemolysis occurs there was an irreversible loss of infectivity. The threshold pH, at which the infectivity was lost, depended on the hemagglutinin subtype of the virus strain. All H5 and H7 strains tested were extremely labile at low pH. In contrast, all H3 strains were relatively stable, independent of the species from which the viruses were isolated. With several H1 viruses the hemagglutination (HA) activity was irreversibly lost at intermediate pH values causing inactivation of infectivity. Strains with noncleaved hemagglutinins were much more stable. These observations might explain why duck influenza viruses can easily survive in lake water and wet faeces, and multiply in the intestinal tract, where trypsin is present. There are also significant differences in heat stability exhibited by influenza A strains. In contrast to pH stability this is not a specific trait of the hemagglutinin, since it can be influenced by reassortment. There is no correlation between the stability of infectivity at low pH and heat.

Descriptors: heat, influenza A virus pathogenicity, cultured cells, chick embryo, hemagglutination, viral, hydrogen-ion concentration, influenza A virus avian growth and development, influenza A virus classification, influenza A virus growth and development.


NAL Call Number: QR360.A1J6

Descriptors: antiviral agents pharmacology, cytopathogenic effect, viral, influenza A virus avian drug effects, avian pathogenicity, carbon isotopes, ethylenes pharmacology, imines pharmacology, leucine metabolism, quinones pharmacology, RNA viral metabolism, tritium, uridine metabolism, virus cultivation.


NAL Call Number: QR360.A1J6

Descriptors: antibiotics, antineoplastic pharmacology, influenza A virus avian drug effects, Newcastle disease virus drug effects, virus inhibitors, virus replication drug effects, antigens metabolism, chick embryo, dactinomycin pharmacology, fibroblasts, hemagglutination inhibition tests, hemagglutination tests, avian enzymology, avian growth and development, avian immunology, avian metabolism, leucine metabolism, neuraminidase metabolism, Newcastle disease virus growth and development, proteins biosynthesis, RNA biosynthesis, RNA nucleotidyldtransferases metabolism, RNA viral biosynthesis, tritium, uridine metabolism.


NAL Call Number: 448.8 V81

Abstract: The hemagglutinin (HA) gene of the influenza virus subtype H1N1 isolated from pigs and birds has been analyzed by the hybridization technique. According to the RNase protection data the HA genes of recent isolates from pigs in Northern Europe are genetically more closely related to those of isolates from birds in Europe and North America than to those of isolates from pigs in the United States, Taiwan, and Italy. Thus, two different H1N1 subtypes are circulating in the pig population. The results are consistent with the
view that H1N1 viruses can be transmitted from birds to pigs and/or vice versa.

Descriptors: hemagglutinins viral genetics, influenza A virus avian genetics, porcine genetics, genetics, birds microbiology, genes viral, avian immunology, avian isolation and purification, porcine classification, porcine immunology, porcine isolation and purification, nucleic acid hybridization, swine microbiology.


Abstract: In an attempt to assess the importance of the nucleoprotein (NP) in the determination of host specificity, a series of experiments was performed on influenza A viruses of the H3N2 subtype. We have examined rescue of mutants of A/FPV/Rostock/34 with temperature-sensitive (ts) lesions in the nucleoprotein (NP) gene by double infection of chick embryo cells with H3N2 strains isolated from different species. The ts mutants could be rescued by all avian H3N2 strains but not by any of the human H3N2 isolates. Only two of the swine H3N2 strains tested were able to rescue our mutants. The NP gene of these two swine isolates resembled the NP gene of the avian strains genetically in the hybridization test. However, their NPs reacted differently with a set of monoclonal antibodies when compared with NPs of avian H3N2 strains. Concerning multiplication in ducks they behaved like the other swine and human strains. The phosphopeptide fingerprints of all swine isolates tested were alike and were different from those of human or avian origin. Our observations are compatible with the idea that human H3N2 strains might not be able to cross the species barrier to birds directly, and possibly also not the other way around, without prior reassortment in pigs, which seem to have a broader host range concerning the compatibility of the NP gene in reassortants.

Descriptors: capsid physiology, influenza A virus avian physiology, human physiology, porcine physiology, influenza A virus physiology, viral core proteins physiology, antibodies, viral analysis, capsid analysis, capsid genetics, capsid immunology, cultured cells, chick embryo, ducks, electrophoresis, polyacrylamide gel, epitopes, fowl plague immunology, fowl plague microbiology, avian genetics, avian immunology, human genetics, human immunology, porcine genetics, porcine immunology, mutation, nucleic acid hybridization, phosphopeptides analysis, recombination, genetic, temperature, viral core proteins analysis, viral core proteins genetics, viral core proteins immunology.


NAL Call Number: 384 Z38

Descriptors: glucosamine pharmacology, influenza A virus avian metabolism, RNA viral biosynthesis, Semliki Forest virus metabolism, chick embryo, depression, chemical.


NAL Call Number: QR360.A1J6

Abstract: Several influenza A strains and recombinants of fowl plague virus (FPV) with a known gene constellation were tested for amantadine sensitivity under two different experimental conditions. In a haemagglutinin yield analysis of a single growth cycle experiment FPV was found to be highly sensitive to amantadine, while in the plaque reduction and inhibition test it was highly resistant. With the A3 Hong Kong and equi 2 strains the opposite observation was made. The A2 Singapore strain was sensitive while Ao PR8 was resistant in both tests. In the haemagglutinin yield analysis of a single growth cycle all recombinants carrying segment 4 (HA) of the resistant strain were resistant against amantadine, independent of the derivation of the other genes. In the plaque reduction and inhibition test recombinants carrying the haemagglutinin of the sensitive strain were either resistant or sensitive depending on the gene constellation. Drug sensitivity was transferred by the combination of segments 5 (NP) and 6 (NA). Segment 7 (M) of certain sensitive strains seems to counteract this effect. The results are compatible with the concept that amantadine resistance or sensitivity is not confined to a single gene product or a single mechanism.

Descriptors: amantadine pharmacology, influenza A virus drug effects, recombination, genetic, drug resistance, microbial, hemagglutinin viral analysis, influenza A virus avian drug effects, human drug effects,

**NAL Call Number**: 448.8 V81

**Descriptors**: genes, influenza A virus avian metabolism, RNA viral metabolism, base sequence, nucleic acid denaturation, nucleic acid hybridization, plaque assay, recombination, genetic.


**NAL Call Number**: QR360.A1J6

**Descriptors**: influenza A virus avian metabolism, Newcastle disease virus metabolism, protein precursors, RNA viral metabolism, chick embryo, culture media, daicitoxinomycin pharmacology, fibroblasts, glucosamine pharmacology, hemagglutination tests, avian growth and development, Newcastle disease virus growth and development, nucleic acid hybridization, plaque assay, RNA biosynthesis, viral biosynthesis, Semliki Forest virus growth and development, tissue culture, tritium, uracil nucleotides metabolism, uridine metabolism, virus replication.


**NAL Call Number**: 448.8 V81

**Descriptors**: influenza A virus avian genetics, recombination, genetic, cell line, chickens microbiology, genes viral, hemagglutinins viral analysis, avian growth and development, avian pathogenicity, human genetics, influenza A virus genetics, RNA viral biosynthesis.


**NAL Call Number**: 448.8 V81

**Descriptors**: influenza A virus avian metabolism, mutation, RNA viral biosynthesis, temperature, amino acids metabolism, antigens, viral analysis, chick embryo, DNA directed RNA polymerases metabolism, electrophoresis, polyacrylamide gel, fibroblasts, fluorouracil, hemagglutinins viral analysis, avian enzymology, avian growth and development, avian immunology, mutagens, neuraminidase analysis, peptide synthesis, tissue culture, tritium, uridine metabolism, viral proteins biosynthesis, virus replication.


**NAL Call Number**: 448.3 Ar23

**Abstract**: The nucleoprotein (NP) gene of influenza A viruses is decisive for separating two large individually evolving reservoirs in birds and humans. A phylogenetic analysis of the NP gene revealed that all mammalian influenza viruses originated--directly or indirectly--from an avian ancestor. The stable introduction of an avian influenza A virus into a mammalian species seems to be a relatively rare event, the latest one occurred in 1979 when such an avian virus was introduced into pigs in Northern Europe which gave rise to a new lineage. At least two concomitant events are required for such a new and stable introduction: (1) The new species has to become infected, and (2) a mutation in the polymerase complex has to establish a labile variant, which is prone to provide a large number of different variants, from which some can adapt rapidly to the new host (or to any unusual environments). Since such mutator mutations might be advantageous only during stress periods, variants with a less error prone polymerase might emerge again after adaptation. Examples for such fluctuations in terms of mutational and evolutionary rates are discussed in this brief review.

**Descriptors**: influenza A virus genetics, nucleoproteins chemistry, phylogeny, viral core proteins chemistry, genes viral, influenza A virus chemistry, mutation, nucleoproteins genetics, sequence homology, amino acid, viral core proteins genetics.

**Abstract:** At intermediate concentrations of DMSO the yields of infectious virus and biologically active hemagglutinin and neuraminidase of an influenza A virus (fowl plague virus) and of reassortants therefrom are enhanced severalfold, even though viral protein synthesis is not significantly affected. A corresponding enhancing effect was also found with Newcastle disease and Semliki Forest viruses. At elevated concentrations of DMSO virus yield decreases, and under these conditions the synthesis of the late influenza virus proteins is specifically inhibited. The results indicate that DMSO can facilitate the assembly of virus particles, and viral components, which are normally produced in surplus amounts, now contribute to the maturation of infectious particles.

**Descriptors:** dimethyl sulfoxide pharmacology, virus replication drug effects, hemagglutination, viral drug effects, influenza A virus avian drug effects, avian growth and development, Newcastle disease virus drug effects, Newcastle disease virus growth and development, plaque assay, Semliki Forest virus drug effects, Semliki Forest virus growth and development, viral proteins biosynthesis, virus cultivation.


**Abstract:** 3-Deazaadenosine and H7 specifically inhibit influenza virus replication under conditions at which they have no effect on other tested RNA viruses. This effect can be significantly potentiated by concomitant application of both compounds. Even under the most stringent conditions we failed to obtain any drug resistant variants. A possible explanation for this failure is that these compounds presumably do not act on a viral component like amantadine which was used as a control, but they interfere with cellular enzymes (factors) absolutely essential for influenza virus replication but more or less dispensable for the survival of the cell.

**Descriptors:** influenza A virus avian drug effects, isoquinolines pharmacology, piperazines pharmacology, tubercidin pharmacology, 1 5 isoquinolinesulfonyl 2 methylpiperazine, cultured cells, chick embryo, drug combinations, drug resistance, microbial, virus replication drug effects.


**Abstract:** The infectivity of influenza A viruses like fowl plague virus (FPV) with a cleaved hemagglutinin (HA) is highly sensitive to treatment at pH 5, while strains like PR 8 or virus N with a noncleaved HA survive under this condition. After double infection of chick embryo cells with FPV and PR 8 or virus N, the yield of virus with the HA gene of FPV is greatly reduced. However, it can now survive treatment at pH 5, and the surviving FPV particles form plaques only in the presence of trypsin, indicating that they were coated by the HA of PR 8 or virus N, depending on the coinfecting virus. The results are discussed with respect to the build-up and maintenance of a large reservoir of nonpathogenic influenza A viruses with noncleavable HA in water fowl.

**Descriptors:** fowl plague microbiology, hemagglutinins viral physiology, influenza A virus avian pathogenicity, cultured cells, fibroblasts microbiology, fowl plague enzymology, hemagglutinins viral metabolism, hydrogen-ion concentration, avian enzymology, plaque assay, trypsin physiology, viral interference, water microbiology.


**Abstract:** Temperature-sensitive (ts) mutants obtained by undiluted passages of fowl plague virus at 33 degrees C have their defects located mainly in RNA segments 3, 4 and 8 as determined by rescue to wild-
type with standard ts mutants. This result is different from that obtained after treatment of virus with mutagens, where the frequency of mutations follows roughly the target size of the RNA segments. Many isolates generated after undiluted passages at 33 degrees C, which seem to have mutations in RNA segments 3 and 4, can be rescued to wild-type. This occurs, however, with certain defined standard ts mutants having a defect in RNA segment 4, but not by other segment 4 mutants. One such mutant, ts 1/93 (ts defect in segment 3), interferes with the multiplication of ts 227 (ts defect in segment 4) at the permissive temperature, presumably at the level of vRNA synthesis, preventing reassortment to wild-type. Similarly, ts 263 (ts defect in segment 3) interferes with the multiplication of ts 1/1 (ts defect in segment 4). For other such interfering mutants, the mechanism preventing reassortment to wild-type is different from that of ts 1/93 or ts 1/1, but is not yet understood. Thus, the number of mutations as determined by rescue with standard ts mutants in isolates obtained by undiluted passages is overestimated due to intrinsic interference.

Descriptors: genes viral, influenza A virus avian genetics, cultured cells, chick embryo, fluorouracil pharmacology, avian growth and development, mutation, plaque assay, RNA viral genetics, temperature, viral interference.

NAL Call Number: QR375.V6
Abstract: Insulin and 12-O-tetradecanoylphorbol-13-acetate (TPA) interfere with the multiplication of fowl plague virus, an influenza A virus, in primary chick embryo cells. Specifically the production of the viral glycoproteins hemagglutinin and neuraminidase are affected by the drugs. A decrease or omission of glucose from the culture medium enhances this effect, which is in agreement with the idea that these drugs act on virus replication via a shortage of glucose in the host cell. Virus replication in cells of different organs is affected to different extents by insulin and TPA.
Descriptors: glucose metabolism, influenza A virus avian drug effects, insulin pharmacology, tetradecanoylphorbol acetate pharmacology, virus replication drug effects, cell line, cultured cells, chick embryo, electrophoresis, polyacrylamide gel, avian physiology.

NAL Call Number: 448.3 Ar23
Abstract: Temperature-sensitive (ts) mutants of fowl plague virus with a ts-lesion in segment 1 (ts 3, polymerase 1 gene) or segment 2 (ts 90, transport gene) do not form plaques on MDCK cells at the permissive temperature, while the wild type and ts-mutants of other groups are able to do so. This property is correlated with the ts-lesion, since revertants for the ts-lesion of ts 3 and ts 90 again form plaques on MDCK cells. The block on MDCK cells—at least for ts3—may be located in a late function, since viral RNA polymerase and hemagglutinin are formed in almost normal yields. MDCK cells infected with ts 3 or ts 90 exhibit a retarded cytopathic effect at 33 degrees C, but no cytopathic effect at 39 degrees C, at which temperature the infected cells can be passaged and super-infected with the wild type strain. Cells surviving the infection with ts 90 at 33 degrees C sometimes grow out again to a normal monolayer. It is suggested that the spread of virus is inhibited under these conditions.
Descriptors: genes viral, influenza A virus avian growth and development, cell line, cytopathogenic effect, viral, DNA directed RNA polymerases biosynthesis, hemagglutinins viral, avian genetics, mutation, plaque assay, temperature.

NAL Call Number: 448.8 V81
Descriptors: base sequence, biochemistry, hemagglutinins viral analysis, influenza A virus analysis, influenza A virus immunology, RNA viral analysis, influenza A virus avian analysis, avian immunology, human analysis, human immunology, porcine analysis, porcine immunology, nucleic acid hybridization.


**NAL Call Number:** 448.8 V81

**Descriptors:** genes viral, influenza A virus avian genetics, influenza A virus genetics, recombination, genetic, base sequence, heterozygote, avian analysis, influenza A virus analysis, mutation, neuraminidase analysis, nucleic acid conformation, RNA viral analysis.


**NAL Call Number:** QR375.V6

**Abstract:** The reversion of temperature-sensitive (ts) mutants of fowl plague virus to the ts+ phenotype was correlated with pathogenicity for chicken. Two types of ts mutants were investigated: those obtained by mutagenesis with 5-fluorouracil and those obtained by undiluted passages at 33 degrees C. The reversion frequency of the former mutants depended on the RNA segment in which the ts defect was located, mutations in RNA segments 1 and 2 having the highest reversion frequency, those in the RNA segments coding for the glycoproteins the lowest. ts mutants obtained by undiluted passages behaved differently in this respect. There was an approximate correlation between frequency of reversion and pathogenicity for chicken. Double mutants induced by 5-fluorouracil, having one tight and one leaky mutation, reverted easily without loss of the leaky mutation. These double mutants were still to a limited extent pathogenic for the chicken. Only one double mutant with two tight mutations (ts 293) was completely nonpathogenic after intramuscular inoculation. Two ts mutants with multiple tight defects (ts 1/1 and ts 3/18) obtained by undiluted passage did not revert to wild-type after injection into embryonated eggs and incubation at 33 degrees C, but they were still slightly pathogenic for the chicken. There was no obvious correlation between the shut-off temperature and pathogenicity of mutants carrying a single ts defect. However, for mutants with multiple tight mutations a high shut-off temperature seemed to be essential for reversion during serial passages as well as for pathogenicity in the chicken, when different routes of inoculation were examined. ts mutants seem to be safe as live vaccines only, (1) if they carry at least two tight ts defects, (2) if they have a relatively low shut-off temperature, and (3) if they could be administered other than via the respiratory tract.

**Descriptors:** influenza A virus avian genetics, mutation, temperature, chickens microbiology, fluorouracil pharmacology, avian pathogenicity.


**NAL Call Number:** QR360.A1J6

**Descriptors:** influenza A virus avian growth and development, fibroblasts, hemagglutination, viral, avian enzymology, leucine, neuraminidase metabolism, nucleosides, RNA nucleotidyltransferases metabolism, temperature, tissue culture, tritium.


**NAL Call Number:** 472 N21

**Descriptors:** dactinomycin pharmacology, influenza A virus avian, Newcastle disease virus, phenylalanine pharmacology, proteins, RNA viral biosynthesis, uridine metabolism, carbon isotopes, chick embryo.


**NAL Call Number:** QR360.A1J6

**Descriptors:** influenza A virus avian, RNA nucleotidyltransferases, tissue culture, chickens, dactinomycin pharmacology, dextrans pharmacology, enzyme induction, fibroblasts, guanine nucleotides metabolism, magnesium pharmacology, nucleotides pharmacology, phenylalanine pharmacology, protamines pharmacology, RNA pharmacology, ribonucleases pharmacology, tritium.


**Descriptors:** antiviral agents pharmacology, glucosamine pharmacology, influenza A virus avian drug effects, Newcastle disease virus drug effects, Semliki Forest virus drug effects, vesicular stomatitis Indiana virus drug effects, virus replication drug effects, culture media, cytidine pharmacology, DNA directed RNA polymerases metabolism, dose response relationship, drug, fructose metabolism, glucose metabolism, glycoproteins biosynthesis, guanosine pharmacology, avian growth and development, Newcastle disease virus growth and development, RNA viral biosynthesis, Semliki Forest virus growth and development, tritium, uracil nucleotides metabolism, uridine pharmacology, vesicular stomatitis Indiana virus growth and development, virus cultivation.


**Abstract:** By molecular hybridization and by neuraminidase inhibition tests it is shown that all influenza A strains tested carrying an Nav3 or Nav2 neuraminidase (NA) are genetically highly related in their NA genes and cross-react serologically with specific antineuraminidase sera. The Nav6 strains exhibit a very low RNase protection after hybridization and do not cross-react serologically with Nav2 or Nav3 strains. Thus, the Nav2 and Nav3 strains comprise one group which is distinct from that of Nav6 strains.

**Descriptors:** genes viral, influenza A virus genetics, neuraminidase genetics, cross reactions, influenza A virus avian enzymology, avian genetics, influenza A virus enzymology, neuraminidase immunology, nucleic acid hybridization.


**Descriptors:** genes, influenza A virus avian pathogenicity, recombination, genetic, antibodies, viral biosynthesis, chickens, fluorouracil, avian analysis, avian immunology, influenza A virus pathogenicity, mutagens, mutation, RNA viral analysis.


**Abstract:** A temperature-sensitive mutant (ts 1/1) with a defect in the hemagglutinin (HA) gene, which was obtained by undiluted passage of fowl plague virus (FPV) at 33 degrees, is described. At 33 degrees proteolytic cleavage of the abnormal HA yielded an altered HA2 (XHA2) which migrated ahead of the NS1 protein and lacked the complex oligosaccharide side chain. At the nonpermissive temperature of 40 degrees, the migration of the HA of ts 1/1 from the rough endoplasmic reticulum (RER) via the Golgi apparatus to the cell surface was rate limiting for virus maturation. The HA was only slowly cleaved and migrated during polyacrylamide gel electrophoresis ahead of the HA of wild type FPV. Some revertants of ts 1/1 exhibited the same protein pattern as the mutant, others resembled wild type FPV, while one revertant gave rise to a mixture of HA2 and XHA2 at 40 degrees. These results suggest that (1) the loss of the complex oligosaccharide side chain is not responsible for the ts phenotype, (2) the mutation is presumably not at the site where the oligosaccharide side chain is linked to the protein backbone, and (3) ts 1/1 presumably carries a mutation located in RNA segment 4, which by pseudoreversion (suppressor mutation) in the same gene leads to different ts+ phenotypes.

**Descriptors:** influenza A virus avian genetics, mutation, RNA viral genetics, suppression, genetic, crosses, genetic, genes viral, genetic markers, recombination, genetic, virus activation.


**Abstract:** To analyze the compatibility of avian influenza A virus hemagglutinins (HAs) and human influenza A virus matrix (M) proteins M1 and M2, we doubly infected Madin-Darby canine kidney cells with amantadine (1-aminoadamantane hydrochloride)-resistant human viruses and amantadine-sensitive avian strains. By using antisera against the human virus HAs and amantadine, we selected reassortants containing the human virus M gene and the avian virus HA gene. In our system, high virus yields and large, well-defined plaques indicated that the avian HAs and the human M gene products could cooperate effectively; low virus yields and small, turbid plaques indicated that cooperation was poor. The M gene products are among the primary components that determine the species specificities of influenza A viruses. Therefore, our system also indicated whether the avian HA genes effectively reassorted into the genome and replaced the HA gene of the prevailing human influenza A virus. Most of the avian HAs that we tested efficiently cooperated with the M gene products of the early human A/PR/8/34 (H1N1) virus; however, the avian HAs did not effectively cooperate with the most recently isolated human virus that we tested, A/Nanchang/933/95 (H3N2). Cooperation between the avian HAs and the M proteins of the human A/Singapore/57 (H2N2) virus was moderate. These results suggest that the currently prevailing human influenza A viruses might have lost their ability to undergo antigenic shift and therefore are unable to form new pandemic viruses that contain an avian HA, a finding that is of great interest for pandemic planning.

**Descriptors:** hemagglutinin glycoproteins, influenza virus metabolism, influenza A virus avian genetics, human genetics, reassortant viruses, viral matrix proteins metabolism, amantadine pharmacology, antiviral agents pharmacology, cell line, dogs, drug resistance, viral, fowl plague virology, hemagglutinin glycoproteins, influenza virus genetics, influenza virology, avian drug effects, avian growth and development, avian metabolism, human drug effects, human growth and development, human metabolism, kidney cytology, kidney virology, plaque assay, poultry, viral matrix proteins genetics.

**NAL Call Number:** QR355.A5

**Descriptors:** antiviral agents, biperiden pharmacology, influenza A virus avian drug effects, human drug effects, piperidines pharmacology, amantadine pharmacology, cell line, chick embryo, drug interactions, drug resistance, microbial, genes viral drug effects, hemagglutination, viral drug effects, hemolysis drug effects, avian physiology, human growth and development, human physiology, interferon type I biosynthesis, interferons pharmacology, measles virus drug effects, mutation, virus replication drug effects.


**NAL Call Number:** 41.8 Av5

**Abstract:** Apoptosis is essential in many physiological processes including wound healing and development of the immune response. Apoptosis also plays an important role in the pathogenesis of many infectious diseases including those caused by viruses. Influenza viruses induce apoptosis in cells that are permissive for viral replication and cells that do not support viral replication. The cellular pathways involved in influenza virus induced apoptosis are currently ill defined. Previous studies suggest that influenza virus infection increased the expression of the Fas antigen in HeLa cells, and that Fas antigen is partially involved in apoptosis. In these studies we examined the cellular pathways involved in avian influenza virus induced apoptosis in two cell lines that support productive viral replication: Madin-Darby canine kidney cells (MDCK) and mink lung epithelial (Mv1Lu) cells.

**Descriptors:** cell biology, infection, cellular pathways, immune response, physiological processes, viral replication, virally induced apoptosis, wound healing.


**NAL Call Number:** 448.8 V81

**Abstract:** There is evidence that the nucleoprotein (NP) gene of the classical swine virus (A/Swine/1976/31) clusters with the early human strains at the nucleotide sequence level, while at the level of the amino acid sequence, as defined by consensus amino acids and in functional tests, its NP is clearly "avian like." Therefore it was suggested that the Sw/31 NP had been recently under strong selection pressure, possibly caused by reassortment with other avian influenza genes, whose gene products have to cooperate intimately with NP (Gammelin et al., 1989. Virology 170, 71-80). This suggestion has been investigated by sequencing the genes of internal and nonstructural proteins of Sw/31. The data on these sequences and on the phylogenetic trees are not in accordance with that suggestion: all these genes cluster with the early human strains at the nucleotide level while, at the level of the amino acid sequence, most of them are more closely related to the avian strains, thus resembling NP in this respect. This indicates that these genes rather evolved concomitantly with the NP gene. Our data are in agreement with the suggestion that, at about the time of the Spanish Flu (1918/19), a human influenza A (H1N1) virus entered the pig population. Furthermore, it is known that the NP of the human influenza A viruses—in contrast to that of the avian and swine strains—has been under strong selection pressure to change (Gammelin et al., 1990. Mol. Biol. Evol. 7, 194-200. Gorman et al., 1990a. J. Virol. 64, 1487-1497). Thus, after transfer of a human strain into pigs, the selection pressure might be released, enabling the NP and the other genes of the swine virus to evolve back to the optimal avian sequences, especially at the functionally important consensus positions. The swine influenza viruses circulating since 1979 in Northern Europe—represented by A/Swine/Germany/2/81 (H1N1)-have all genes, so far examined, derived from an avian influenza virus pool and are different from the classical swine viruses.

**Descriptors:** influenza A virus, porcine genetics, phylogeny, RNA replicase, viral proteins genetics, chick embryo, consensus sequence, genes viral, nucleoproteins genetics, swine, viral core proteins genetics.

Mutants ts1 and ts227 of fowl plague virus have a temperature-sensitive defect in the transport of the hemagglutinin from the rough endoplasmic reticulum to the Golgi apparatus. The primary structure of the hemagglutinin of the mutants and of a number of revertants derived from them has been analysed by nucleotide sequencing. The transport block of the hemagglutinin of ts227 can be attributed to a single amino acid exchange. It involves the replacement of aspartic acid at position 457 by asparagine thereby introducing a new glycosylation site which appears to be located in a cryptic position in the lower part of the hemagglutinin stalk. Attachment of carbohydrate to this site is temperature-dependent. At permissive temperature only a small fraction of the monomers (approximately 30%) is glycosylated in this position, whereas at nonpermissive temperature this is the case with all subunits. The data suggest that under the latter conditions the new oligosaccharide interferes by steric hindrance with the trimerization of the hemagglutinin. The hemagglutinin of ts1 has an essential amino acid exchange at position 275 where serine is replaced by glycine. This substitution may increase the flexibility of the molecule in the hinge region between the globular domain and the stalk. The exchange of a conserved glutamic acid residue at position 398 that is involved in the interaction between different monomers contributes also to the structural instability of the ts1 hemagglutinin. These observations support the notion that the transport of the hemagglutinin from the rough endoplasmic reticulum to the Golgi apparatus depends on trimer assembly.
Abstract: Tunicamycin, a new antibiotic, halts the formation of physical particles of Semliki forest and fowl plague virus, whereas avian oncornavirus particles which show a reduction in infectivity and do not contain detectable labeled glycoprotein are released in the presence of the drug. In Semliki forest virus-infected cells only the protein moieties of the glycoproteins could be labeled. In cells infected with fowl plague and avian sarcoma virus neither intact glycoproteins nor their protein moieties could be detected. By using a protease inhibitor (N-alpha-p-tosyl-L-lysin chloromethyl ketone, TLCK) it could be shown, however, that the carbohydrate-free hemagglutinin precursor of influenza virus is synthesized but is presumably degraded by intracellular proteases in the absence of TLCK as a consequence of the lack of carbohydrate.

Descriptors: anti bacterial agents pharmacology, glycoproteins biosynthesis, influenza A virus avian drug effects, sarcoma viruses, avian drug effects, Semliki Forest virus drug effects, viral proteins biosynthesis, chick embryo, glucosamine analogs and derivatives, glucosamine metabolism, glucosamine pharmacology, hemagglutinins viral analysis, avian metabolism, mannose metabolism, sarcoma viruses, avian metabolism, Semliki Forest virus metabolism, tissue culture, tosyllysine chloromethyl ketone pharmacology.


NAL Call Number: QH301.Z4

Descriptors: DNA directed RNA polymerases analysis, influenza A virus avian enzymology, adenosine triphosphate, chick embryo, RNA viral biosynthesis, templates, genetic.


NAL Call Number: 448.8 J821

Abstract: The infectivity, immunogenicity, and efficacy of live, attenuated influenza A/Texas/1/85 (H1N1) and A/Bethesda/1/85 (H3N2) avian-human (ah) and cold-adapted (ca) reassortant vaccines were compared in 252 seronegative adult volunteers. The immunogenicity and efficacy of the H1N1 reassortant vaccine were also compared with those of the trivalent inactivated virus vaccine. Each reassortant vaccine was satisfactorily attenuated. The 50% human infectious dose was 10(4.9) for ca H1N1, 10(5.4) for ah H1N1, 10(6.4) for ca H3N2, and 10(6.5) TCID50 for ah H3N2 reassortant virus. Within a subtype, the immunogenicities of ah and ca vaccines were comparable. Five to seven weeks after vaccination, volunteers were challenged with homologous wild-type influenza A virus. The magnitude of shedding of virus after challenge was greater than 100-fold less in H1N1 vaccinees and greater than 10-fold less in H3N2 vaccinees compared with unimmunized controls. The vaccines were equally efficacious, as indicated by an 86%-100% reduction in illness. Thus, the ah A/Mallard/New York/6750/78 and the ca A/Ann Arbor/6/60 reassortant viruses are comparable.

Descriptors: influenza prevention and control, influenza A virus avian immunology, human immunology, influenza vaccine, adult, antibodies, viral biosynthesis, cold, double blind method, enzyme linked immunosorbent assay, hemagglutination inhibition tests, avian pathogenicity, avian physiology, human pathogenicity, human physiology, random allocation, vaccines, attenuated, vaccines, synthetic, virus replication.


Abstract: Interferon (IFN) action survival curves for an avian influenza virus (AIV) in chicken or quail cells showed that 40-60% of the virions in a stock of virus were highly sensitive to the inhibitory effects of chicken IFN-alpha (ChIFN-alpha), whereas the rest were up to 100 times less sensitive. This greater resistance to IFN was transient, that is, was not a stable characteristic, in that virus stocks grown from plaques that formed in the presence of 50-800 U/ml IFN gave rise to virus populations that contained both sensitive and resistant virions. If AIV was serially passaged several times in the presence of IFN, the proportion of transiently IFN-resistant virus was greater. We propose a model to account for this transient resistance of
AIV to IFN action based on the reported inactivation of the dsRNA-dependent protein kinase (PKR) and its activator dsRNA by the NS1 protein of influenza virus and also on the increase in the survival of AIV in IFN-treated cells exposed to 2-aminopurine, a known inhibitor of PKR. We suggest that IFN-resistant AIV is generated from a random packaging event that results in virions that contain two or more copies of RNA segment 8, the gene segment that encodes the NS1 protein of AIV, and that these virions will produce correspondingly elevated levels of NS1. The experimental data fit well to theoretical curves based on this model and constructed from the fraction of virus in the population expected by chance to contain one, two, or three copies of the NS gene when packaging an average of 12 influenza gene segments that include the 8 segments essential for infectivity.

Descriptors: influenza A virus avian genetics, avian physiology, interferon alpha pharmacology, viral nonstructural proteins genetics, virus assembly, 2-aminopurine pharmacology, chick embryo, genes viral, half-life, avian growth and development, interferon alpha administration and dosage, plaque assay, serial passage, viral nonstructural proteins metabolism, EIF 2 kinase antagonists and inhibitors.


Descriptors: endocrine system, infection, avian influenza, viral disease, interferon resistance interferon sensitivity (IFN sensitivity) viral sensitivity, meeting abstract, meeting poster.


NAL Call Number: 448.8 P942

Abstract: The paper describes a simple and convenient method for qualitative and quantitative evaluation of the capacity of influenza virus for autointerference consisting in the lack or considerable reduction of the cytolytic effect of the virus under agar overlay at a high multiplicity of infection. Some experimental and theoretical arguments assuming the role of defective interfering particles in the formation of the observed phenomenon. It is assumed that the detection of autointerference under agar may be used as an additional criterion for detection of non-plaque-forming strains of influenza virus, tentative determination of their interfering capacity as well as for the establishment of biological relationships of viruses.

Descriptors: influenza A virus physiology, viral interference, defective viruses, influenza A virus avian, plaque assay.


NAL Call Number: 448.8 P942

Abstract: Comparison of human and avian influenza virus nucleoprotein (NP) oligomerization showed that the efficiency of NP oligomerization is different in influenza viruses of different origin. NP oligomerization is virtually complete in avian influenza viruses, while in human influenza viruses only part of monomeric NP is oligomerized. The authors discuss the utilization of NP oligomerization efficiency as a sign for identification of the origin of influenza virus.

Descriptors: influenza A virus metabolism, nucleoproteins metabolism, biopolymers, birds virology, cell line, dogs, influenza A virus classification, species specificity.


NAL Call Number: 448.8 P942

Abstract: Comparison of human and avian influenza virus nucleoprotein (NP) oligomerization showed that the efficiency of NP oligomerization is different in influenza viruses of different origin. NP oligomerization is
virtually complete in avian influenza viruses, while in human influenza viruses only part of monomeric NP is oligomerized. The authors discuss the utilization of NP oligomerization efficiency as a sign for identification of the origin of influenza virus.

Descriptors: biochemistry and molecular biophysics, infection, virology.


Abstract: The deduced amino acid sequence at the hemagglutinin (HA) cleavage site of 76 avian influenza (AI) viruses, subtypes H5 and H7, was determined by reverse transcription-polymerase chain reaction and cycle sequencing techniques to assess pathogenicity. Eighteen of the 76 viruses were isolated in 1993 and 1994 from various sources in the United States. In addition, 34 H5 (4 highly pathogenic [HP] and 30 non-highly pathogenic [nonHP]) and 24 H7 (3 HP and 21 non-HP) repository viruses, isolated between 1927 and 1992, were sequenced and the sequences compared to those in recent isolates. All repository HP H5 and H7 viruses studied had multiple basic amino acids adjacent to the HA cleavage site and most had basic amino acids in excess of the proposed minimum motif B-X-B-R (B = basic amino acids arginine or lysine, X = nonbasic amino acid, R = arginine) that has been associated with high pathogenicity. Of the non-HP viruses studied, 35 of 38 for H5 and 30 of 31 for H7 conformed to the motif B-X-X-R and B-X-R, respectively. Two nonHP HS viruses had the motif X-X-X-R at the cleavage site and a third had the motif B-X-X-K (K = basic amino acid lysine). One non-HP H7 (A/Pekin robin/CA/30412-5/94) had four basic amino acids (K-R R-R) adjacent to the cleavage site. Although the Pekin robin isolate did not produce disease in chickens under the conditions of the study it did have the amino acid sequence compatible with that in HP AI viruses and, therefore, is considered potentially HP. This is the first account of an H7 virus that is non-HP in chickens but meets the molecular criterion to be classified as HP.

Descriptors: United States, avian influenza virus, chemical composition, nucleotide sequence, agglutinins, pathogenicity, PCR, DNA, acids, America, biological properties, genomes, influenza virus, microbial properties, North America, nucleic acids, nucleic compounds, organic acids, orthomyxoviridae, proteins, viruses, molecular sequence data, characterization, DNA sequencing.


Abstract: The H5N1 influenza viruses transmitted to humans in 1997 were highly virulent, but the mechanism of their virulence in humans is largely unknown. Here we show that lethal H5N1 influenza viruses, unlike other human, avian, and swine influenza viruses, are resistant to the anti-viral effects of interferons and tumor necrosis factor alpha The nonstructural (NS) gene of H5N1 viruses is associated with this resistance. Pigs infected with recombinant human H1N1 influenza virus that carried the H5N1 NS gene experienced significantly greater and more prolonged viremia, fever, and weight loss than did pigs infected with wild-type human H1N1 influenza virus. These effects required the presence of glutamic acid at position 92 of the NS1 molecule. These findings may explain the mechanism of the high virulence of H5N1 influenza viruses in humans and provide insight into the virulence of 1918 Spanish influenza.

Descriptors: cytokines pharmacology, drug resistance, multiple, viral genetics, influenza immunology, avian influenza A virus pathogenicity, human influenza A virus pathogenicity, viral nonstructural proteins genetics, cell line, cytokines metabolism, influenza physiopathology, influenza virology, avian influenza A virus genetics, interferons metabolism, interferons pharmacology, mutation, recombination, genetic, swine virology, tumor necrosis factor alpha metabolism, tumor necrosis factor alpha pharmacology.


Abstract: In 1997, avian H5N1 influenza virus transmitted from chickens to humans resulted in 18
confirmed infections. Despite harboring lethal H5N1 influenza viruses, most chickens in the Hong Kong poultry markets showed no disease signs. At this time, H9N2 influenza viruses were cocirculating in the markets. We investigated the role of H9N2 influenza viruses in protecting chickens from lethal H5N1 influenza virus infections. Sera from chickens infected with an H9N2 influenza virus did not cross-react with an H5N1 influenza virus in neutralization or hemagglutination inhibition assays. Most chickens primed with an H9N2 influenza virus 3 to 70 days earlier survived the lethal challenge of an H5N1 influenza virus, but infected birds shed H5N1 influenza virus in their feces. Adoptive transfer of T lymphocytes or CD8(+) T cells from inbred chickens (B(2)/B(2)) infected with an H9N2 influenza virus to naive inbred chickens (B(2)/B(2)) protected them from lethal H5N1 influenza virus. In vitro cytotoxicity assays showed that T lymphocytes or CD8(+) T cells from chickens infected with an H9N2 influenza virus recognized target cells infected with either an H5N1 or H9N2 influenza virus in a dose-dependent manner. Our findings indicate that cross-reactive cellular immunity induced by H9N2 influenza viruses protected chickens from lethal infection with H5N1 influenza viruses in the Hong Kong markets in 1997 but permitted virus shedding in the feces. Our findings are the first to suggest that cross-reactive cellular immunity can change the outcome of avian influenza virus infection in birds in live markets and create a situation for the perpetuation of H5N1 influenza viruses.

Descriptors: chickens, fowl plague immunology, fowl plague virology, influenza A virus avian immunology, T lymphocytes, cytotoxic immunology, adoptive transfer, cross reactions, fowl plague prevention and control, hemagglutination inhibition tests, Hong Kong, immunity, cellular, immunization, avian classification, avian pathogenicity.


NAL Call Number: QR360.J6

Abstract: Previous studies have associated influenza virus-induced expression of inflammatory cytokines, including tumor necrosis factor alpha (TNF-alpha), with influenza pathogenesis in the human respiratory tract and have suggested that alpha and beta interferons are the first cytokines recruited to counteract such infection. However, we report here that TNF-alpha has powerful anti-influenza virus activity. When infected with influenza virus, cultured porcine lung epithelial cells expressed TNF-alpha in a dose-dependent manner. Expression of TNF-alpha was induced only by replicating virus. TNF-alpha showed strong antiviral activity against avian, swine, and human influenza viruses, and the antiviral effect of TNF-alpha was greater than that of gamma or alpha interferon. These findings suggest that TNF-alpha serves as the first line of defense against influenza virus infection in the natural host.


NAL Call Number: RS164.P59

Descriptors: amantadine pharmacology, antiviral agents pharmacology, influenza A virus avian drug effects, plant extracts pharmacology, amantadine administration and dosage, amantadine analogs and derivatives, antiviral agents administration and dosage, cultured cells, chick embryo, drug therapy, combination, fibroblasts drug effects, hemagglutination, influenza prevention and control, avian classification, phytotherapy, plants, medicinal therapeutic use.


NAL Call Number: 448.3 AC85
Abstract: A polyphenolic complex (PC) with antiviral properties has been isolated from the Bulgarian medicinal plant *Geranium sanguineum* L. A study was undertaken to investigate the effect of PC on virus-specific protein synthesis in influenza virus-infected cells. The expression of viral glycoproteins on the surface of chick embryo fibroblasts infected with virus A/FPV, strain Rostock (H7N1) was suppressed. Virus protein synthesis was selectively inhibited as shown by SDS polyacrylamide gel electrophoresis of 35S-methionine-labelled proteins and proteins immunoprecipitated with monoclonal antibodies. The inhibitory effect was dose-dependent and better pronounced when PC was applied after virus infection. Two variants of influenza virus FPV/Rostock with reduced drug susceptibility were selected. PC affected to a lesser extent the synthesis of viral proteins in cells infected with the variants as compared to the sensitive parental virus.

Descriptors: antiviral agents pharmacology, influenza A virus avian drug effects, phenols pharmacology, plants medicinal chemistry, viral proteins biosynthesis, cultured cells, chick embryo, plant roots chemistry, protein synthesis inhibitors pharmacology.


NAL Call Number: QH301.Z4

Abstract: Sixty products, derived from marine organisms, typical of the Bulgarian Black Sea coast, were examined for inhibitory activity on the reproduction of influenza viruses in tissue cultures. The antiviral effect was investigated by the reduction of virus infectivity. Using representative strains of influenza virus it was shown that apparently the inhibitory effect was strain-specific. The most effective products were further studied in fertile hen's eggs and in experimental influenza infection in white mice.

Descriptors: algae chemistry, antiviral agents pharmacology, influenza drug therapy, influenza A virus avian drug effects, human drug effects, plant extracts pharmacology, tissue extracts pharmacology, antiviral agents isolation and purification, chick embryo, hemagglutination inhibition tests, invertebrates, mice, seawater, species specificity.


Abstract: The pavine alkaloid (-)-thalimonine (Thl), isolated from the Mongolian plant *Thalictrum simplex* inhibited markedly the reproduction of influenza virus A/Germany/27, str. Weybridge (H7N7) and A/Germany/34, str. Rostock (H7N1) in cell cultures of chicken embryo fibroblasts. In a number of assays at a non-toxic concentration range of 0.1-6.4 microM the alkaloid inhibited viral reproduction in a selective and specific way (selectivity index = 640, 106.6, respectively). Expression of viral glycoproteins haemagglutinin (HA), neuraminidase (NA) and nucleoprotein (NP) on the surface of infected cells, virus-induced cytopathic effect, infectious virus yields, HA production and virus-specific protein synthesis were all reduced. The inhibition was dose-related and depended on virus inoculum. The time of addition experiments indicated that viral reproduction was markedly inhibited when Thl was added at 4-5 h of infection. No inactivating effect on extracellular virus was found.

Descriptors: alkaloids pharmacology, antiviral agents pharmacology, benzylisoquinolines pharmacology, influenza A virus avian drug effects, Thalictrum chemistry, alkaloids isolation and purification, benzylisoquinolines isolation and purification, chick embryo, dose response relationship, drug, enzyme linked immunosorbent assay, fibroblasts cytology, fibroblasts drug effects, fibroblasts virology, hemagglutinin glycoproteins, influenza virus drug effects, hemagglutinin glycoproteins, influenza virus metabolism, avian metabolism, neuraminidase antagonists and inhibitors, neuraminidase metabolism, nucleoproteins drug effects, nucleoproteins metabolism, plant extracts pharmacology, time factors.


NAL Call Number: QR1.A37

Descriptors: influenza A virus avian drug effects, interferon inducers pharmacology, pyrimidines pharmacology.

NAL Call Number: QR1.A3
Descriptors: interferon inducers, interferons biosynthesis, pyrimidines pharmacology, chick embryo, fibroblasts, influenza A virus avian drug effects, avian growth and development, interferons pharmacology, tissue culture, virus replication drug effects.


NAL Call Number: QR1.A3
Descriptors: antiviral agents pharmacology, influenza A virus avian drug effects, pyrimidines pharmacology, cytopathogenic effect, viral drug effects, avian growth and development, tissue culture, virus replication drug effects.


NAL Call Number: QR360.J6
Descriptors: influenza A virus avian enzymology, neuraminidase, orthomyxoviridae enzymology, virus replication, cell line, chick embryo, conjunctiva, immune sera, microscopy, electron, tissue culture.


NAL Call Number: 448.8 V81
Descriptors: influenza A virus avian enzymology, avian growth and development, neuraminidase metabolism, adsorption, chick embryo, complement fixation tests, immune sera, neutralization tests.


Abstract: Matrix protein (M1) of influenza virus is a bifunctional protein that mediates the encapsidation of RNA-nucleoprotein cores into the membrane envelope. It is therefore required that M1 binds both membrane and RNA simultaneously. The X-ray crystal structure of the N-terminal portion of type A influenza virus M1-amino acid residues 2-158-has been determined at 2.08 A resolution at pH 4.0. The protein forms a dimer. A highly positively charged region on the dimer surface is suitably positioned to bind RNA while the hydrophobic surface opposite the RNA binding region may be involved in interactions with the membrane. The membrane-binding hydrophobic surface could be buried or exposed after a conformational change.

Descriptors: protein structure, secondary, RNA binding proteins chemistry, viral matrix proteins chemistry, amino acid sequence, crystallography, x-ray, dimerization, influenza A virus avian, human, macromolecular systems, models, molecular, models, structural, molecular sequence data, RNA binding proteins isolation and purification, sequence homology, amino acid, software, viral matrix proteins isolation and purification.


NAL Call Number: 41.8 Av5
Abstract: Specific-pathogen-free laying hens were inoculated with avian influenza virus (AIV) A/chicken/Alabama/7395/75 (H4N8) either intratracheally (IT) or intravenously (IV). IT inoculation produced a localized infection of the upper and lower respiratory tracts with lesions of tracheitis, bronchitis, airsacculitis, and pneumonia around the secondary bronchi. IV inoculation produced a systemic infection with major lesions of nephritis, interstitial pneumonia, salpingitis, and splenic and hepatic necrosis. In IV-inoculated hens, AIV nucleo-protein was demonstrated within renal tubule epithelium, in luminal surface and
glandular oviduct epithelium, and in mononuclear cells within pulmonary blood capillaries. However, no virus was recovered from internal contents of eggs laid between days 1.5 and 5 postinfection. These data indicate that A/chicken/Alabama/7395/75 has tissue tropism and pathogenicity for the respiratory and urogenital systems of reproductively active laying hens. Site and severity of lesion development are determined by the localized or systemic nature of AIV infection.

Descriptors: fowl plague pathology, influenza A virus avian isolation and purification, chickens, kidney microbiology, kidney pathology, lung microbiology, lung pathology, ovary microbiology, ovary pathology, oviducts microbiology, oviducts pathology, oviposition, specific pathogen free organisms.


Descriptors: amantadine therapeutic use, antibodies, viral therapeutic use, antiviral agents therapeutic use, encephalitis, viral drug therapy, encephalitis, viral prevention and control, influenza A virus avian pathogenicity, influenza vaccine therapeutic use, antibodies, viral blood, brain pathology, brain virology, disease models, animal, dogs, encephalitis, viral mortality, encephalitis, viral pathology, avian immunology, influenza vaccine administration and dosage, lung pathology, lung virology, mice, treatment outcome, vaccines, inactivated administration and dosage, vaccines, inactivated therapeutic use.


NAL Call Number: 448.8 V81

Abstract: A single amino acid substitution, from glutamic acid to lysine at position 627 of the PB2 protein, converts a nonlethal H5N1 influenza A virus isolated from a human to a lethal virus in mice. In contrast to the nonlethal virus, which replicates only in respiratory organs, the lethal isolate replicates in a variety of organs, producing systemic infection. Despite a clear difference in virulence and organ tropism between the two viruses, it remains unknown whether the dissimilarity is a result of differences in cell tropism or the reduced replicative ability of the nonlethal virus in mouse cells in general. To determine how this single amino acid change affects virulence and organ tropism in mice, we investigated the growth kinetics of the two H5N1 viruses both in vitro and in vivo. The identity of the PB2 amino acid at position 627 did not appreciably affect viral replicative efficiency in chicken embryo fibroblasts and a quail cell line; however, viruses with lysine at this position instead of glutamic acid grew better in the different mouse cells tested. When the effect of this substitution was investigated in mice, all of the test viruses showed the same cell tropism, but infection by viruses containing lysine at position 627 spread more rapidly than those viruses containing glutamic acid at this position. Further analysis showed a difference in local immune responses: neutrophil infiltration in lungs infected with viruses containing lysine at position 627 persisted longer than that associated with viruses lacking a glutamic acid substitution. Our data indicate that the amino acid at position 627 of the PB2 protein determines the efficiency of viral replication in mouse (not avian) cells, but not tropism among cells in different mouse organs. The presence of lysine leads to more aggressive viral replication, overwhelming the host's defense mechanisms and resulting in high mortality rates in mice.

Descriptors: amino acid substitution, avian influenza A virus pathogenicity, avian influenza A virus physiology, viral proteins genetics, virus replication, brain virology, cell line, chick embryo, influenza physiopathology, influenza virology, avian influenza A virus genetics, mice, viral proteins chemistry, viral proteins metabolism, virulence.


NAL Call Number: 448.3 Ar23

Abstract: To define the route of influenza virus invasion into the central nervous system (CNS), an avian influenza A (H5N3) virus was inoculated into mice intranasally or intravenously. Only the intranasal infection group mice showed depression and retention of gas in the digestive system. Pathological findings in the animals were bronchiointerstitial pneumonia and non-suppurative encephalitis restricted to the brain stem.
The nerve nucleus primarily affected was the nucleus of solitary tract. Prior to the development of the CNS lesions, viral antigen was detected in vagal and trigeminal ganglia. These results suggest that the primarily replicated virus in the respiratory mucosa ascended to the CNS via sensory nerve routes, inducing lesions in the brain stem, and then spread trans-synaptically in the CNS.

Descriptors: encephalitis, viral virology, influenza A virus avian pathogenicity, orthomyxoviridae infections virology, visceral afferents virology, antigens, viral analysis, brain pathology, brain virology, brain stem pathology, brain stem virology, encephalitis, viral pathology, ganglia virology, avian isolation and purification, lung virology, mice inbred BALB c, orthomyxoviridae infections pathology, respiratory mucosa virology.


NAL Call Number: SF604.J342

Abstract: Five-week-old ddY mice were inoculated intranasally with a low virulent (4e) or highly virulent (24a5b) avian influenza virus strain originated from a water bird. None of mice in the 4e group showed clinical signs and brain lesions. Of the 24a5b group, two mice died and one mouse was killed at a moribund state at day 7 post-inoculation (PI). Four mice of the 24a5b group necropsied at day 5 or 7 PI had mild to severe encephalitis in the brain stem and the cerebellar white matter. Influenza virus antigen was detected in neurons, glial cells and vascular endothelium in the lesions. The distribution of the lesions seems to indicate the transneuronal invasion of the virus via cranial nerve fibers into the brain.

Descriptors: birds virology, brain pathology, encephalitis, viral pathology, influenza pathology, influenza A virus avian pathogenicity, antigens, viral analysis, brain virology, brain stem pathology, cerebellum pathology, encephalitis, viral virology, immunohistochemistry, avian isolation and purification, mice, necrosis, virulence.


NAL Call Number: 500 N21P

Abstract: Intact influenza A virions were bombarded with thermally activated tritium atoms, and the intramolecular distribution of the label in the matrix protein M1 was analyzed to determine the in situ accessibility of its tryptic fragments. These data were combined with the previously reported x-ray crystal structure of the M1 fragment 2-158 [Sha, B. & Luo, M. (1997) Nat. Struct. Biol. 4, 239-244] and the predicted topology of the C domain (159-252) to propose a model of M1 arrangement in the virus particle.

Descriptors: influenza A virus avian physiology, protein structure, secondary, viral matrix proteins chemistry, chick embryo, crystallography, x-ray, avian ultrastructure, models, molecular, tritium, viral matrix proteins isolation and purification.


NAL Call Number: 448.8 P942

Descriptors: amphotericin B analogs and derivatives, influenza drug therapy, multiple sclerosis drug therapy, amphotericin B pharmacology, amphotericin B therapeutic use, amphotericin B toxicity, chick embryo, drug evaluation, drug evaluation, preclinical, drug therapy, combination, influenza A virus avian drug effects, mice, rimantadine therapeutic use, tilorone therapeutic use, virus replication drug effects.


NAL Call Number: 448.8 J821

Descriptors: antigens, viral immunology, influenza A virus, porcine immunology, influenza A virus immunology, swine microbiology, viral core proteins, antibodies, monoclonal immunology, antibodies, viral
immunology, antigens, viral analysis, China, cross reactions, epitopes, hemagglutinins viral immunology, Hong Kong, avian immunology, human immunology, neuraminidase immunology, nucleoproteins immunology, Taiwan, viral proteins immunology.

**NAL Call Number:** 448.3 Ar23  
**Abstract:** An antigenic analysis was carried out on 145 duck influenza virus isolates of the H3 haemagglutinin subtype obtained over five years continuous surveillance from the region of southern China, a hypothetical influenza epicentre. This was done using a panel of twelve monoclonal antibodies raised to an early human strain of the H3 subtype. We demonstrate the existence of an extensive range of antigenic profiles, broadly similar but not identical to the human H3 strain, which persisted over the five year period. This variability was as great during discrete twelve month periods as over the whole five years. Hierarchic progression (observed with human strains) was not evident and no correlation of antigenic drift, in either positive or negative direction, was observed with the domestic duck isolates over time. Changing dominant antigenic profiles were, however, observed in faecal isolates with time within a single farm. The much broader range of profiles detected in pond water samples from the same farm suggested the existence of a heterogeneous antigenic reservoir. Local switching of dominant profiles may occur due to changes of cohorts as birds are taken to market. In vitro and in vivo passage experiments revealed a high degree of heterogeneity in antigenic profiles in progeny of uncloned isolates, whereas the profiles of cloned isolates were largely conserved. These results suggested that particular antigenic profiles in primary isolates may result from mixtures of subpopulations of the wild type virus in natural duck infections. Switching between reactivity profiles of different progeny is likely to be largely a result of regrouping of these subpopulations with lesser effects due to mutation. Hypervariability in some of the cloned isolates was observed with a few monoclonal antibodies recognising a region of HA reported to be hypervariable in swine influenza virus. Reactivity with one particular antibody was correlated with passage in chicken eggs. The ability of this enormously varied pool of duck influenza H3 strains to cross the species barrier to man and give rise to viruses with hierarchic capabilities was considered.  
**Descriptors:** antigens, viral immunology, ducks microbiology, hemagglutinins viral immunology, influenza A virus avian immunology, human immunology, antibodies, monoclonal immunology, antibodies, viral immunology, CHI square distribution, China, hemagglutination inhibition tests, serial passage.

**NAL Call Number:** SF604.J342  
**Abstract:** Two-day-old specific-pathogen free chicks were inoculated with type A influenza virus (A/whistling swan/Shimane/499/83 (H5N3) through the air sac. Inoculated chicks showed mild to severe diarrhea and lesions of pancreatitis and atrophy of the pancreas, thymus and bursa of Fabricius. One chick died on each of days 4, 6 and 14 postinoculation (PI). Reduced weight gain was conspicuous from day 22 PI. Positive immunoreaction to the virus antigen was detected in the pancreas, kidneys, liver, lungs and air sacs, and cecal lamina propria. Virus recovery persisted longer in the pancreas. Some of these findings conformed to those of stunting syndrome.  
**Descriptors:** chickens, growth disorders veterinary, influenza A virus avian physiology, poultry diseases virology, air sacs immunology, air sacs virology, antigens, viral analysis, antigens, viral immunology, atrophy, bursa of fabricius pathology, growth disorders pathology, growth disorders virology, avian immunology, kidney immunology, kidney virology, liver immunology, liver virology, lung immunology, lung virology, pancreas pathology, pancreatitis etiology, pancreatitis pathology, pancreatitis veterinary, poultry diseases pathology, poultry diseases physiopathology, regression analysis, syndrome, thymus gland pathology, weight gain physiology.

NAL Call Number: SF604.J342
Abstract: Three-day-old, specific-pathogen-free (SPF) chicks were inoculated with the strains of influenza A/whistling swan/Shimane/499/83 (H5N3) via the air sac route. The strains had been passaged through airsacs or air sacs and brains of SPF chicks. Two experiments were undertaken to examine the pathogenicity of these strains and the development of brain lesions based on time-interval changes. In experiment 1, original strain (4e) showed low pathogenicity with mild respiratory signs and zero mortality. Air sac passaged strains (18a and 24a) of 4e demonstrated mortalities of 50% and 67%, respectively, and inoculated chicks showed hemorrhages and necrotic lesions in major organs. Air sac-brain passaged strain (24a5b) of 4e produced 100% mortality and severe nervous signs. Severe circulatory disturbance with multiple foci of necrosis in major organs including the brain was found in chicks inoculated with 24a5b. The 24a5b was analogous to highly pathogenic avian influenza virus in regard to its pathogenicity to chicks. Hence, low pathogenic influenza virus (4e) gradually aggravated its pathogenicity to highly pathogenic virus (24a5b) by air sac and brain passages. In experiment 2, chicks were inoculated with 24a5b, and the earliest histological lesion was the enlargement of the vascular endothelial cells at 18 hr post-inoculation (PI) followed by necrotizing encephalitis at 24 to 48 hr PI. Immunohistological staining revealed avian influenza virus antigen initially in the vascular endothelial cells and then in the astrocytes, neurons and ependyma.

Descriptors: air sacs virology, brain virology, chickens, fowl plague pathology, influenza A virus pathogenicity, air sacs pathology, antigens, viral analysis, brain immunology, brain pathology, endothelium, vascular pathology, influenza A virus immunology, microscopy, electron methods, microscopy, electron veterinary, necrosis, neurons ultrastructure, serial passage, specific pathogen free organisms, time factors.


NAL Call Number: 41.8 R312
Abstract: The effect of avian influenza virus (AIV) infection on the ability of turkeys to eliminate Pasteurella multocida from the respiratory tract was evaluated. Four-week-old turkeys were experimentally infected with an apathogenic AIV subtype (H5N2) by the oculonasal route and subsequently superinfected with P. multocida (Urbach strain) by the intranasal route three days after infection with AIV. Quantitative clearance of P. multocida from the trachea and lung was determined using a pour plate technique on samples collected at intervals after infection. Samples from turkeys which had been infected with AIV were found to yield more P. multocida than those from turkeys which had not been infected with the virus. The numbers of P. multocida increased in infected birds to a greater extent than in birds which had not been infected with the virus. The present study suggests that AIV infection may contribute to the increased numbers and a decreased clearance of P. multocida in turkeys.

Descriptors: fowl plague microbiology, influenza A virus avian physiology, Pasteurella infections veterinary, Pasteurella multocida physiology, poultry diseases microbiology, turkeys, fowl plague complications, Pasteurella infections complications, Pasteurella infections microbiology, respiratory system microbiology.


NAL Call Number: 448.8 V81
Descriptors: influenza A virus avian metabolism, peptide synthesis, viral proteins biosynthesis, autoradiography, chick embryo, cycloheximide pharmacology, dactinomycin pharmacology, densitometry, electrophoresis, polyacrylamide gel, fibroblasts, avian growth and development, methionine metabolism, sulfur radioisotopes, time factors, tissue culture, transcription, genetic, virus replication.


NAL Call Number: 448.8 V81
Descriptors: cultured cells metabolism, influenza A virus avian growth and development, peptide synthesis, viral proteins biosynthesis, amino acids metabolism, carbon isotopes, cattle, cell line microbiology, chick embryo, electrophoresis, disc, fibroblasts microbiology, fucose metabolism, glycopeptides biosynthesis, hamsters, haplorhini, HeLa cells microbiology, avian analysis, avian metabolism, kidney embryology,
methionine metabolism, molecular weight, neoplasms, experimental, peptides analysis, sulfur isotopes, virus replication.


**NAL Call Number:** QR360.J6

**Descriptors:** influenza A virus avian metabolism, RNA nucleotidyltransferases metabolism, RNA viral biosynthesis, carbon isotopes, cell nucleus, centrifugation, density gradient, chick embryo, dactinomycin pharmacology, edetic acid pharmacology, electrophoresis, disc, hydrogen-ion concentration, avian isolation and purification, magnesium pharmacology, manganese pharmacology, nucleotides metabolism, ribosomes, tissue culture, tritium, uracil nucleotides metabolism, uridine metabolism, valine metabolism.


**NAL Call Number:** QP501,B64

**Descriptors:** chick embryo, influenza A virus avian, orthomyxoviridae infections enzymology, RNA viral biosynthesis, centrifugation, density gradient, RNA nucleotidyltransferases metabolism, ribosomes enzymology.


**NAL Call Number:** QD341.A2N8

**Abstract:** The results of analyses of the 5'-terminal sequences of Fowl Plague virus RNAs are presented. The first 13 residues of each of the eight RNA molecules which constitute the genome are in the identical sequence 5'AGUAGAAAUUAGG- and this conservation of sequence is shown to extend to other influenza viruses. The 5'-terminal sequences of virion RNA transcripts produced in vitro are also reported and again the first 12 nucleotides of these are identical for all influenza type A transcripts examined in the sequence 5'AGCAAAAGCAGG-. In addition the results of attempts to determine the sequence relationship between vRNAs and the two classes of complementary RNA synthesized in influenza infected cells are described which support the conclusion that influenza messenger RNAs are incomplete transcripts.

**Descriptors:** influenza A virus avian, RNA viral analysis, base sequence, RNA, messenger metabolism, ribonucleotides analysis, templates, genetic, transcription, genetic.


**NAL Call Number:** QR360.A1J6

**Abstract:** The results of analyses of fowl plague virus-specific RNA and protein synthesis in infected chick embryo fibroblasts incubated in amantadine hydrochloride are reported. They indicate that provided amantadine is present from the time of virus addition no expression of the virus genome occurs and that the synthesis of even the first detectable transcripts catalysed by the polymerase of the infecting virus particles is prevented. In agreement with previous reports it is concluded that amantadine prevents an unknown event which occurs immediately following virus infection.

**Descriptors:** amantadine pharmacology, influenza A virus avian drug effects, virus replication drug effects, chick embryo, DNA directed RNA polymerases metabolism, hemagglutinins viral analysis, avian growth and development, avian metabolism, peptide synthesis, RNA viral biosynthesis, tissue culture, viral proteins biosynthesis.


**NAL Call Number:** 41.8 Av5

**Abstract:** Enteric infection and cloacal shedding of influenza virus was demonstrated in ducks exposed experimentally to an aerosol of an avirulent type-A influenza virus. The fluorescent-antibody technique was used to identify sites of virus replication in the epithelial cells of the digestive tract and the bursa.

**Descriptors:** ducks microbiology, influenza A virus avian growth and development, intestines microbiology,
aerosols, antigens, viral analysis, bursa of fabricius microbiology, cloaca microbiology, fluorescent antibody technique, avian immunology, avian isolation and purification, trachea microbiology, virus replication.


**NAL Call Number:** 41.8 Av5

**Abstract:** Seventy-six type A influenza viruses recovered from waterfowl in Wisconsin, California, South Dakota, Florida, Texas, Alabama, and Nebraska were tested for virulence in chickens. The challenge to chickens was intravenous inoculation of first-, second-, or third-egg-passage virus. Each of the virus strains was tested separately in three or four chickens. Eighteen of the 76 viruses caused the death of one or more chickens following inoculation. Postmortem lesions were similar in all dead birds. In decreasing order of frequency, gross lesions included: swollen kidneys evident as accentuated lobular patterns, urates in the pericardial sac, and urates on the surface of the liver. Microscopic lesions present in kidneys were consistent with visceral gout. Mortality was associated with inoculations having higher concentrations of infectious virus. These results indicate that the influenza A viruses circulating in duck populations may include strains potentially pathogenic for chickens.

**Descriptors:** chickens, fowl plague pathology, influenza A virus avian pathogenicity, kidney pathology, animals, wild, antibodies, viral biosynthesis, birds, ducks, fowl plague microbiology, fowl plague mortality, geese, avian immunology, avian isolation and purification, virulence.


**NAL Call Number:** 41.8 Av5

**Abstract:** Tissue tropism properties of A/chicken/Alabama/75 (H4N8) were examined after intravenous inoculation of 5-week-old specific-pathogen-free chickens. From 14 clinically normal chickens euthanatized on days 1-20 postinoculation, the frequencies of virus recovery were highest for cloacal swabs (86%), bursal swabs (64%), and kidney tissues (64%) and lowest for tracheal swabs (14%), thymus tissues (14%), bone-marrow swabs (7%), and brain tissues (0%). Evidence that the high frequency of virus recovery from kidney tissues was associated with virus replication in the kidney tissues was provided by high virus titers, ranging up to 10(9.5) mean embryo infectious dose per gram of kidney tissue, and by identification of intranuclear and intracytoplasmic type A influenza nucleoprotein in kidney cells using immunohistochemistry. Virus-recovery and virus titer results from three chickens that died on days 4 and 5 postinoculation paralleled the results from the clinically normal chickens. These findings indicate that A/chicken/Alabama/75 has nephrotropic properties similar to nephrotropic properties previously reported for waterfowl-origin type A influenza viruses and provide evidence that kidney lesions could be manifestations of systemic influenza infections in commercial laying chickens.

**Descriptors:** chickens microbiology, fowl plague pathology, influenza A virus avian isolation and purification, kidney microbiology, poultry diseases microbiology, fowl plague microbiology, injections, intravenous veterinary, kidney pathology, nucleoproteins analysis, poultry diseases pathology, viral core proteins analysis.


**NAL Call Number:** 41.8 Av5

**Abstract:** Intravenous inoculation of chickens with a waterfowl-origin type A influenza virus resulted in high titers of virus in kidney tissues and viral nucleoprotein in renal tubular epithelial cells and in intestinal mucosal epithelial cells. Virus titers in kidneys of four of eight clinically normal chickens sampled on days 3 and 5 postinoculation (PI), one dead chicken on day 3 PI, and one dead chicken on day 7 PI exceeded 10(6) mean embryo infectious dose per gram of tissue. Using immunofluorescent and immunoperoxidase staining, viral nucleoprotein was identified in the cytoplasm and nucleus of tubular epithelial cells in kidneys and in nucleus of mucosal epithelial cells lining villi in the lower small intestine. Based on the low intravenous pathogenicity index for this virus (0.3) along with the high virus titers in kidney tissues and localization of viral antigen in kidney important site for replication of avian influenza (AI) virus of low pathogenicity. Recovery of
type A influenza viruses from cloacal swabs could result from viral replication in kidneys as well as in the lower intestine and/or the bursa of Fabricius.

Descriptors: chickens microbiology, fowl plague microbiology, influenza A virus avian physiology, intestine, small microbiology, kidney microbiology, fluorescent antibody technique, immunoenzyme techniques, immunohistochemistry, virus replication.


NAL Call Number: 448.8 P942

Abstract: Endocytic vacuoles (receptosomes) containing influenza virus were isolated from the cytoplasm of Ehrlich ascitic carcinoma cells and characterized. In the sucrose density gradient, the virus-containing material was detected in two peaks with a buoyant density of 1.175-1.16 and 1.155-1.135 g/cm3 with which the activity of marker enzymes of cell plasma membranes was associated. The virus was present in receptosomes in morphologically and electrophoretically intact condition. Examinations for the lipid composition of endocytic vacuoles showed the presence in their membranes of large amounts of cholesterol and glycolipids, particularly asialo-GM1 which, according to some authors may enhance the fusion of viral and cell membranes.

Descriptors: endocytosis, influenza A virus avian pathogenicity, organoids microbiology, vacuoles microbiology, carcinoma, Ehrlich tumor enzymology, carcinoma, Ehrlich tumor microbiology, carcinoma, Ehrlich tumor ultrastructure, cell fractionation, cell membrane analysis, cell membrane enzymology, cell membrane microbiology, chick embryo, chromatography, thin layer, electrophoresis, polyacrylamide gel, endosomes analysis, endosomes enzymology, endosomes microbiology, glycolipids analysis, lipids analysis, microscopy, electron, vacuoles analysis, vacuoles enzymology, virus cultivation.


NAL Call Number: 448.8 P942

Abstract: Avian influenza A viruses belonging to hemagglutinin (HA) subtypes H5 and H6 were studied in the infectivity neutralization test and radioimmunoprecipitation assay (RIPA) with monoclonal antibody MAb C179. This MAb recognizes a conformational antigenic epitope in the stem region of HA formed by two regions (amino acid positions 318-322 in HA1 subunit and 47-58 in HA2), conserved in all H1 and H2 influenza viruses. MAb C179 reacts with HA of H5 viruses in RIPA and neutralizes these strains as efficiently as H2 viruses. C179 precipitates H6 subtype HA but does not neutralize the infectivity of these viruses. Comparison of amino acid sequences of H2, H5, and H6 strains showed identical epitope recognized by MAb C179 in H5 and H6 HAs, which differs from epitopes of H1 and H2 by two amino acids in the HA2 subunit. Causes of disagreement between immunoprecipitation of H6 HA by MAb C179 and neutralization of this serosubtype by this MAb are discussed.

Descriptors: antigens, viral immunology, epitopes immunology, hemagglutinins viral immunology, influenza A virus immunology, antibodies, monoclonal immunology, birds, cell line, chick embryo, dogs, influenza A virus pathogenicity, neutralization tests, radioimmunoprecipitation assay.


NAL Call Number: QR375.V6

Abstract: Avian H5N1 influenza A viruses are considered to be of high pandemic potential as they are able to cross the avian-human species barrier and cause disease in humans. In the present study we assessed the impact of amino acid substitutions in the hemagglutinin (HA) of antigenic escape mutants of influenza A/Mallard/Pennsylvania/10218/84 (H5N2) (Mld/PA/84-MA) virus on the level of neutralizing antibodies and the ability to protect mice against challenge with the wild type H5 influenza virus. beta-Propiolactone-inactivated vaccines prepared from eight different H5 escape mutants could be separated into two groups
based on levels of protection. One group of escape mutants [m46(7), m46(7)-24B9, m46(7)-55, and m46(7)-55-24B9] was characterized by providing high levels of protection (90.0-95.4% survival) to mice against subsequent challenge with 5 LD(50) of wild type Mld/PA/84-MA virus. The other group of escape mutants [m176/26, m55(2), m55(2)-24B9, and m24B9-176/26] provided moderate level of protection (57.1-66.6% survival) in mice. Analysis of the amino acid substitutions in the HA revealed that two amino acid changes in antigenic site B of the HA molecule (D(126)->N and K(152)->N) were associated for decreases in the levels of antibody and the immune protection afforded by vaccination with these H5 virus escape mutants. The phenotypic effects of mutations in HA gene of H5 virus may be of importance to appraise the extent and direction of H5 influenza viruses antigenic evolution.

Descriptors: antibodies, viral blood, hemagglutinin glycoproteins, influenza virus genetics, hemagglutinin glycoproteins, influenza virus immunology, influenza prevention and control, avian influenza A virus genetics, avian influenza A virus immunology, influenza vaccines immunology, amino acid substitution, antigens, viral genetics, antigens, viral immunology, genes, viral, influenza virology, avian influenza A virus growth and development, mice, mutation, missense, neutralization tests, vaccines, inactivated immunology, virus inactivation.


**NAL Call Number:** 448.3 AC85

**Abstract:** The membrane-inserted hemagglutinin (HA) is the most variable protein of influenza viruses. Here we describe the characterization of a shared epitope in the HA of influenza A virus H1, H2, and H5 subtypes which were completely neutralized by a monoclonal antibody (MAb), directed against this epitope. This MAb (C179) also efficiently precipitated the HAs of these viruses. In addition, MAb C179 did not neutralize H6 subtype strains despite complete amino acid homology of the epitope regions. Furthermore, only the non-glycosylated form of the HA of one of the H6 subtype strains could be precipitated by the MAb. The conformational epitope may be masked by glycosylation, although it could not be excluded that differences in the primary amino acid sequence may cause the decreased accessibility of the epitope in H6 subtype strains.

**Descriptors:** epitopes immunology, hemagglutinin glycoproteins, influenza virus immunology, influenza A virus avian immunology, human immunology, amino acid sequence, antibodies, monoclonal immunology, antibodies, viral immunology, electrophoresis, polyacrylamide gel, avian classification, human classification, molecular sequence data, neutralization tests, radioimmunoprecipitation assay, sequence analysis, DNA.


**NAL Call Number:** 448.8 P942

**Abstract:** Avian influenza A viruses belonging to hemagglutinin (HA) subtypes H5 and H6 were studied in the infectivity neutralization test and radioimmunoprecipitation assay (RIPA) with monoclonal antibody MAb C179. This MAb recognizes a conformational antigenic epitope in the stem region of HA formed by two regions (amino acid positions 318-322 in HA1 subunit and 47-58 in HA2), conserved in all H1 and H2 influenza viruses. MAb C179 reacts with HA of H5 viruses in RIPA and neutralizes these strains as efficiently as H2 viruses. C179 precipitates H6 subtype HA but does not neutralize the infectivity of these viruses. Comparison of amino acid sequences of H2, H5, and H6 strains showed identical epitope recognized by MAb C179 in H5 and H6 HAs, which differs from epitopes of H1 and H2 by two amino acids in the HA2 subunit. Causes of disagreement between immunoprecipitation of H6 HA by MAb C179 and neutralization of this serosubtype by this MAb are discussed.

**Descriptors:** immune system, infection, virology virus neutralization.


**NAL Call Number:** QH506.E46

**Abstract:** The influenza virus NS2 mRNA is generated through processing by cellular enzymes of a transcript (the NS1 mRNA) of virion RNA segment 8. Production of this mRNA is altered in cells infected with
a mutant of influenza A (fowl plague) virus. The proportion of segment 8 transcripts which accumulated in a spliced form was found to be considerably lower in mutant virus-infected cells than in cells infected with wild-type virus, and the amplification in production of NS2 mRNA relative to that of the NS1 mRNA, which normally occurs during infection with wild-type virus, was not observed with the mutant. The NS1 mRNA specified by the mutant virus has unaltered splice recognition sites and was apparently processed normally during a mixed infection with a strain of virus which is wild-type for production of NS2 mRNA. These results suggest that the production of NS2 mRNA is regulated by virus-specific products; these products may act by increasing the efficiency of splicing of NS1 mRNA.

Descriptors: influenza A virus avian genetics, RNA, messenger genetics, RNA viral genetics, base sequence, chick embryo, DNA metabolism, fibroblasts, mutation, nucleic acid hybridization, species specificity, transcription, genetic, virion genetics.


NAL Call Number: 448.8 V81

Descriptors: DNA directed RNA polymerases antagonists and inhibitors, influenza A virus human enzymology, polynucleotides pharmacology, avian enzymology, orthomyxoviridae enzymology, poly A pharmacology, poly I pharmacology, poly U pharmacology, structure activity relationship, virion enzymology.


NAL Call Number: 41.8 R312

Abstract: An avian influenza A virus (Hav7 Neq2) isolated from a feral duck in Western Australia was transmitted to groups of broiler chickens by cloaca, mouth, eye drop or spray. No disease or deaths occurred. Serum samples were examined by haemagglutination inhibition test and enzyme linked immunosorbent assays and the results gave reasonable correlation. Chickens infected by cloaca or spray gave the best overall seroconversions.

Descriptors: chickens immunology, influenza A virus avian immunology, antibodies, viral analysis, beak, cloaca, enzyme linked immunosorbent assay, eye, hemagglutination inhibition tests, injections, viral vaccines administration and dosage.


NAL Call Number: 41.8 V6426

Descriptors: chickens, fowl plague microbiology, influenza A virus avian isolation and purification, variation genetics, antigens, viral analysis, avian immunology, serotyping.


NAL Call Number: QR46.J6

Abstract: We evaluated the abilities of three different avian influenza A viruses to attenuate the wild-type human influenza A/Korea/1/82 (H3N2) virus in squirrel monkeys, chimpanzees, and adult seronegative human volunteers. Two of these, avian influenza A/Mallard/NY/78 and A/Mallard/Alberta/76 viruses, appeared to be satisfactory donors of attenuating genes for the production of live influenza A reassortant virus vaccines for human use because the reassortants exhibited an acceptable balance between attenuation and immunogenicity.

Descriptors: influenza A virus avian immunology, human immunology, influenza vaccine immunology, antibodies, viral biosynthesis, avian genetics, avian physiology, human genetics, human physiology, Pan troglodytes, recombination, genetic, saimiri, vaccines, attenuated, virus replication.

**NAL Call Number:** 448.8 J821

**Descriptors:** antibodies, viral biosynthesis, influenza A virus avian immunology, human immunology, influenza vaccine immunology, administration, intranasal, aerosols, immunization, avian pathogenicity, human pathogenicity, saimiri, vaccines, attenuated, virulence.


**NAL Call Number:** 448.8 P942

**Abstract:** Oligopeptide maps of M proteins of "wild" fowl plague virus (FPV) and a temperature-sensitive mutant of FPV were compared with respect of gene. In maps of M proteins labeled with 14C-chlorella hydrolysate and 35S-methionine the mutant virus was found to lack one of oligopeptides present in maps of M proteins of the "wild" virus. The electrophoretic mobility of M proteins of ts 303 and FPV in 25% polyacrylamide gel was similar.

**Descriptors:** influenza A virus avian analysis, mutation, oligopeptides analysis, temperature, viral proteins analysis, electrophoresis, polyacrylamide gel, viral matrix proteins.


**NAL Call Number:** 448.3 Ar23

**Abstract:** Oligopeptide mapping of 35S-methionine labeled non-structural (NS1) proteins of 23 influenza virus strains showed the presence of both common and variable oligopeptides. Analysis of the oligopeptide maps revealed at least four groups of NS1 proteins. The first group includes NS1 proteins of several human H1N1 influenza viruses (that were designated as H0N1 according to the old classification). The second group is composed of NS1 proteins of H1N1 and H2N2 viruses. The third group includes NS1 proteins of H3N2 human influenza viruses. The fourth group is composed of NS1 proteins of five avian influenza viruses and an equine (H3N8) influenza virus. Two animal influenza viruses A/equi/Prague/56 (H7N7) and A/duck/England/56 (H11N6) contain NS1 proteins that belong to the second group.

**Descriptors:** influenza A virus human classification, influenza A virus classification, oligopeptides analysis, viral proteins classification, avian analysis, avian classification, human analysis, influenza A virus analysis, trypsin, viral nonstructural proteins, viral proteins analysis.


**NAL Call Number:** 448.8 P942

**Abstract:** Peptide mapping was used for comparative analysis of nonstructural proteins (NS1) of 21 strains of human and animal influenza A viruses. At least 4 groups of NS1 proteins could be distinguished by the analysis of the peptide maps; we designated these groups as 0, 1, 2, and 3. Group O includes NS1 proteins of human influenza virus serotype H0N1, group 1 - NS1 proteins of viruses of serotypes H1N1 and H2N2, group 2 - NS1 proteins of viruses of serotype H3N2. NS1 proteins of avian influenza viruses A/duck Czechoslovakia/63, A/turkey Massachusetts/65, A/petrel Australia/1/71, A/duck Ukraine/63, and A/turkey Ontario/68 have been included into group 3.

**Descriptors:** influenza A virus classification, viral proteins classification, electrophoresis methods, electrophoresis, polyacrylamide gel, influenza A virus analysis, peptides analysis, peptides classification, viral proteins analysis.

Descriptors: orthomyxoviridae radiation effects, genetics, microbial, influenza A virus avian radiation effects, mutation, nucleic acid hybridization, RNA, viral, radiation genetics, recombination, genetic, ultraviolet rays, virulence, virus replication.

NAL Call Number: 448.8 P942
Descriptors: influenza A virus avian radiation effects, mutation radiation effects, ultraviolet rays, chick embryo, fibroblasts, genetics, microbial, avian isolation and purification, plaque assay, radiation effects, tissue culture, virus cultivation.

Descriptors: avian influenza virus, hemagglutination, chick embryos, strains, pathogenicity.

NAL Call Number: 472 N21
Descriptors: amanitins pharmacology, DNA directed RNA polymerases metabolism, influenza A virus avian growth and development, RNA polymerase ii metabolism, virus replication drug effects, cell line, drug resistance, avian metabolism, RNA polymerase ii antagonists and inhibitors, RNA viral biosynthesis, time factors, viral proteins biosynthesis.

NAL Call Number: 448.3 Ar23
Descriptors: enterovirus growth and development, RNA viruses growth and development, RNA viral biosynthesis, adenine metabolism, antimetabolites pharmacology, chick embryo, culture media, dactinomycin pharmacology, fibroblasts, formates metabolism, histones pharmacology, influenza A virus avian growth and development, methotrexate pharmacology, nucleosides metabolism, orotic acid metabolism, phenylalanine pharmacology, puromycin pharmacology, radiation effects, thymidine metabolism, ultraviolet rays, uridine metabolism.

NAL Call Number: 448.39 SO12A
Descriptors: avian influenza virus, heterogeneity, RNA.

NAL Call Number: 41.8 Av5
Abstract: The combined effects of water temperature, salinity, and pH on persistence of avian influenza virus (AIV) were evaluated in a model distilled-water system using three isolates from ducks sampled in Cameron Parish, Louisiana. Variables were tested within the ranges normally associated with surface water. Differences were detected between temperature (17 C and 28 C), pH (6.2, 7.2, 8.2), and salinity (0 ppt and 20 ppt), with a strong interactive effect observed between pH and salinity. Estimated persistence of infectivity for 1 x 10(6) mean tissue-culture infective dose of A/mottled duck/LA/38M/87 (H6N2) was longest at 17 C/0 ppt/pH 8.2 (100 days) and shortest at 28 C/20 ppt/pH 8.2 (9 days). Differences in the response to these variables were apparent between viruses. The ability of AIV to persist in surface water was also evaluated using samples collected from varied waterfowl habitats in coastal Louisiana. Observations were
consistent with the model system, with duration of infectivity decreasing with increased salinity and pH. This suggests that experimental results may have application to field conditions.

Descriptors: influenza A virus avian growth and development, water microbiology, chick embryo, ducks, fresh water, hydrogen-ion concentration, linear models, Louisiana, regression analysis, sodium chloride, specific pathogen free organisms, temperature.


NAL Call Number: QH301.Z4

Abstract: New 3'-, 5'-, 5-bromo-2'-deoxyuridine (3a-g) and 3'-, 5'-thymidine (4a-i) analogues with amino acid and peptide residues were synthesized and evaluated for antiviral activity. The influence of long peptide chains, essential amino acids and the effect of this structural modification on the antiviral activity has been also reported. Three 5-bromo-2'-deoxyuridine derivatives containing glycyl-, glycyl-glycyl- and glycyl-glycyl-glycyl- residues (3a, 3b, 3c) showed a strong activity against the herpes virus PsRV and a moderate one vs. HSV-1. The corresponding thymidine analogues were considerably less effective, and only compounds 4d and 4h showed a borderline effect against PsRV.

Descriptors: anti-HIV agents chemical synthesis, antiviral agents chemical synthesis, bromodeoxyuridine analogs and derivatives, bromodeoxyuridine chemical synthesis, thymidine analogs and derivatives, thymidine chemical synthesis, amino acids, anti-HIV agents chemistry, anti-HIV agents pharmacology, antiviral agents chemistry, antiviral agents pharmacology, bromodeoxyuridine chemistry, bromodeoxyuridine pharmacology, cultured cells, chick embryo, chickens, drug design, fibroblasts cytology, fibroblasts virology, HIV drug effects, herpesvirus 1, human drug effects, herpesvirus 1, suid drug effects, influenza A virus avian drug effects, microbial sensitivity tests, peptides, structure activity relationship, thymidine chemistry, thymidine pharmacology.


NAL Call Number: QH506.A1M62

Abstract: The synthesis of the complete and incomplete transcripts (the templates in genome replication and mRNA, respectively) of influenza A WSN virus in chicken fibroblasts was analyzed by gel electrophoresis analysis of the duplexes formed between virion RNA and complementary RNA. Three steps in the transcription could be defined: 1) primary transcription when similar amounts of mRNA of all the genes are accumulated; 2) early secondary transcription when mRNA of NS gene is synthesized in larger amounts than that of other genes and 3) late secondary transcription when the amplification of transcription from all the genes is performed. The synthesis of complete transcripts starts during or after primary transcription. When actinomycin D was added to infected cells, the synthesis of incomplete transcripts was inhibited to a larger degree then that of complete transcripts. Most of incomplete transcripts was observed within the cell nuclei while the complete transcripts were found in the nuclei and cytoplasm, suggesting that the synthesis of incomplete transcripts is located in the nuclei. alpha-Amanitin blocked the synthesis of incomplete transcripts without interfering with that of complete transcripts. These data suggest that the synthesis of complete transcripts does not require the synthesis of cell mRNA as primers in transcription.

Descriptors: cell nucleus metabolism, genes, structural drug effects, genes viral drug effects, influenza A virus avian genetics, transcription, genetic drug effects, amanitins pharmacology, chickens, dactinomycin pharmacology, fibroblasts, RNA, messenger genetics.


NAL Call Number: 448.8 J821

Abstract: Randomized, placebo-controlled studies with 10(3)-10(7) 50% tissue-culture infectious dose (TCID50) of avian-human (ah) and cold-adapted (ca) influenza A/Bethesda/85 (H3N2) reassortant viruses...
were completed in 106 seronegative young children 6-48 months of age. Although the reassortants differed in six of eight RNA segments, they exhibited similar properties in level of attenuation, infectivity, immunogenicity, and efficacy. The 50% human infectious dose was $10^{4.6}$ TCID$_{50}$ for ah and $10^{4.4}$ for ca vaccines. Both reassortants were satisfactorily attenuated with restricted replication and were no more reactogenic than placebo. The mean peak titer of virus shed was $10^{1.5}$ (ah) to $10^{2.0}$ (ca) TCID$_{50}$/ml, and each of 37 isolates tested retained their characteristic vaccine phenotypes. Infection with ah or ca virus conferred immunity to experimental challenge with homologous virus. These findings indicate that both ah and ca influenza A/Bethesda/85 (H3N2) reassortants should be suitable vaccine candidates for use in healthy infants and young children.

Descriptors: influenza prevention and control, influenza A virus avian immunology, human immunology, influenza vaccine immunology, antibodies, viral biosynthesis, child, preschool, cold, dose response relationship, immunologic, double blind method, enzyme linked immunosorbent assay, immunoglobulin G biosynthesis, infant, avian isolation and purification, human isolation and purification, randomized controlled trials, vaccines, attenuated immunology, vaccines, synthetic immunology.


NAL Call Number: 381 B522

Descriptors: cell nucleus metabolism, cytoplasm metabolism, fibroblasts metabolism, influenza A virus avian, RNA, ribosomal biosynthesis, carbon radioisotopes, chick embryo, electrophoresis, polyacrylamide gel, fibroblasts cytology, hemagglutinins viral, methylation, molecular weight, RNA, ribosomal isolation and purification, RNA, ribosomal metabolism, RNA viral biosynthesis, tritium, uridine metabolism, virus replication.


NAL Call Number: QR360.A1J6

Abstract: In cell-free protein synthesizing systems from wheat embryos, messenger RNAs extracted from chick embryo fibroblasts infected with fowl plague virus direct the synthesis of nine virus-specific polypeptides, two of which may be related to the virus-specific glycopolypeptides. All of the mRNAs are complementary in sequence to virion RNA, and RNAs which do not contain poly A appear to be translated as efficiently as their polyadenylated counterparts. Under certain conditions of incubation, virion RNA also directs the synthesis of discrete polypeptides but these products are not detected in infected cells.

Descriptors: influenza A virus avian analysis, RNA, messenger analysis, RNA viral analysis, cell free system, chick embryo, fibroblasts, avian metabolism, peptide synthesis, RNA, messenger metabolism, RNA viral metabolism, tissue culture, translation, genetic, viral proteins biosynthesis.


NAL Call Number: QR180.C4

Abstract: Influenza-specific human-T-cell clones, proliferating in the presence of virus-infected cells with restriction by class II molecules and displaying class II-restricted CTL activity or specific helper activity in antibody synthesis, have been analyzed for antigenic specificities. All of them were obtained by in vitro stimulation against influenza A/Texas virus. In all cases the virus specificity appeared identical in cytolytic and proliferative responses. Three of the clones were broadly cross-reactive, recognizing all or almost all type A influenza strains. The three remaining clones were subtype specific when tested with human strains and recognized the surface glycoproteins of influenza virus. One of these lines reacted with an epitope of the neuraminidase N2 while the other two recognized the hemagglutinin H3. By using a large panel of mammalian and avian influenza strains, it can be demonstrated that hemagglutinin-specific human T cells can recognize a cross-reacting determinant shared by H3 and H4 subtypes of hemagglutinin which has never been detected with antibodies.

Descriptors: influenza A virus immunology, T lymphocytes immunology, antigens, viral immunology, cell line, clone cells, cytotoxicity, immunologic, ducks immunology, epitopes immunology, horses immunology.

Descriptors: blood platelets microbiology, influenza A virus avian immunology, adsorption, chickens, microscopy, electron, phagocytosis, time factors.


NAL Call Number: 41.8 Z52

Descriptors: fowl plague microbiology, influenza A virus avian growth and development, phagocytosis, virus replication, blood platelets microbiology, chickens, fowl plague blood, microscopy, electron.


NAL Call Number: 448.3 C33 (1)

Descriptors: avian influenza virus, DNA, molecular conformation, neuraminidase sequence.


NAL Call Number: 448.8 V81

Abstract: The complete sequence of the neuraminidase (NA) gene of the influenza A strain A/parrot/ Ulster/73 (H7N1 ) has been determined after reverse transcribing and cloning it into the pBR322 plasmid, followed by subcloning into M13 vectors and sequencing with dideoxynucleotide chain terminators. The gene consists of 1458 nucleotides and codes for a protein of 469 amino acids. The neuraminidase has seven potential glycosylation sites. According to the molecular weight as determined by electrophoretic migration in polyacrylamide gel all of these sites might carry a carbohydrate side chain. When the parrot Ulster NA was compared with two other N1 neuraminidases, those of the human PR8 and WSN strains, deletions in the stalk region of 15 amino acids for PR8 NA and of 16 amino acids for WSN NA were apparent. No further rearrangements were found within N1 neuraminidases. Although the parrot Ulster strain was isolated 40 years after the two human strains, the base sequence homology of their NA genes is still 83 or 82%, respectively.

Descriptors: genes, structural, genes viral, influenza A virus avian enzymology, neuraminidase genetics, allantoin, amino acid sequence, base sequence, chick embryo, DNA restriction enzymes, avian genetics.


NAL Call Number: QR375.V6

Abstract: The nucleotide sequence of the nucleoprotein (NP) gene of the avian influenza A virus strain A/parrot/Ulster/73 (H7N1) has been determined. The gene (RNA segment 5) consists of 1565 bases. The only large open reading frame of the complementary RNA codes for a protein of 498 amino acids. A comparison of its sequence with that of three other influenza virus NPs shows that the NP of the parrot Ulster strain, although closely related to the NP of the other avian strain (A/FPV/Rostock/34), is definitely more closely related genetically to the NPs of the two human influenza strains, A/PR/8/34 and A/NT/60/68 than that of FPV. This raises the question how far the NP gene can cross the species barrier by reassortment and become adapted by mutation to the new host.

Descriptors: influenza A virus avian genetics, nucleoproteins genetics, RNA viral genetics, viral proteins genetics, amino acid sequence, base sequence, cloning, molecular, genes, structural, genes viral, human genetics.

uncleaved human H1 hemagglutinin from the extinct 1918 influenza virus. Science 303(5665): 1866-70. ISSN: 1095-9203.

NAL Call Number: 470 Sci2

Abstract: The 1918 "Spanish" influenza pandemic represents the largest recorded outbreak of any infectious disease. The crystal structure of the uncleaved precursor of the major surface antigen of the extinct 1918 virus was determined at 3.0 angstrom resolution after reassembly of the hemagglutinin gene from viral RNA fragments preserved in 1918 formalin-fixed lung tissues. A narrow avian-like receptor-binding site, two previously unobserved histidine patches, and a less exposed surface loop at the cleavage site that activates viral membrane fusion reveal structural features primarily found in avian viruses, which may have contributed to the extraordinarily high infectivity and mortality rates observed during 1918.


NAL Call Number: QH506.E46

Abstract: Many viruses have membrane glycoproteins that are activated at cleavage sites containing multiple arginine and lysine residues by cellular proteases so far not identified. The proteases responsible for cleavage of the hemagglutinin of fowl plague virus, a prototype of these glycoproteins, has now been isolated from Madin-Darby bovine kidney cells. The enzyme has a mol. wt of 85,000, a pH optimum ranging from 6.5 to 7.5, is calcium dependent and recognizes the consensus sequence R-X-K/R-R at the cleavage site of the hemagglutinin. Using a specific antiserum it has been identified as furin, a subtilisin-like eukaryotic protease. The fowl plague virus hemagglutinin was also cleaved after coexpression with human furin from cDNA by vaccinia virus vectors. Peptidyl chloroalkylketones containing the R-X-K/R-R motif specifically bind to the catalytic site of furin and are therefore potent inhibitors of hemagglutinin cleavage and fusion activity.

Descriptors: hemagglutinins viral metabolism, influenza A virus avian enzymology, membrane proteins metabolism, subtilisins metabolism, viral envelope proteins metabolism, affinity labels, amino acid chloromethyl ketones pharmacology, amino acid sequence, blotting, western, cattle, cultured cells, chick embryo, chromatography, liquid, DNA, dogs, furin, hemagglutinin glycoproteins, influenza virus, hydrogen-ion concentration, avian metabolism, molecular sequence data, vaccinia virus genetics.


NAL Call Number: QR360.A1J6

Abstract: The lytic activity of secondary cytotoxic lymphocytes against influenza A virus was tested on cells which had been fused with liposomes containing the haemagglutinin and the neuraminidase of an avian influenza A virus (fowl plague virus, FPV). Fusion was obtained solely by the activity of the haemagglutinin and neuraminidase incorporated into the liposomes, without the need for any additional fusion factor. Highly reproducible lysis of these FPV-liposome target cells by influenza A-specific cytotoxic cells was found. In contrast, target cells containing the glycoproteins HN and F of Newcastle disease virus (NDV) were not lysed. In almost all experiments effector cell populations capable of lysing target cells also lysed the natural killer cell (NK)-sensitive cell line YAC-1. However, high NK activity alone was not sufficient to lyse target cells fused with liposomes containing the viral surface glycoproteins. To our knowledge this is the first report where after artificial introduction of viral surface components into cell membranes (either by fusion or by transfection) lysis of target cells was monitored also for non-specific lysis mediated by NK-like cells. Both the H-2 restriction and the virus specificity of lysis of FPV-liposome target cells indicate that influenza virus haemagglutinin and possibly neuraminidase do function as target antigens for influenza-specific T cells.

NAL Call Number: QR360.A1J6

Abstract: Lectins of different specificities do not interfere with the maturation of myxo-viruses; their inhibitory effect on virus replication is mainly due to prevention of the detachment of infectious virus particles from the host cell. In chick embryo fibroblasts infected with an influenza virus and treated with concanavalin A, budding occurs into intracytoplasmic vacuoles, but this phenomenon is not observed with a parainfluenza virus and with different cells.

Descriptors: influenza A virus avian growth and development, lectins pharmacology, Newcastle disease virus growth and development, virus replication drug effects, chick embryo, concanavalin A pharmacology, avian isolation and purification, methylmannosides pharmacology, Newcastle disease virus isolation and purification, sonication, tissue culture, vacuoles microbiology.


NAL Call Number: 448.8 J8292

Descriptors: cell biology, immune system, molecular genetics, gene transfer, gene transfer method, meeting abstract, meeting poster.


Abstract: Dendritic cells (DCs) are the most potent inducers of immune reactions. Genetically modified DCs, which express tumor-associated antigens (TAA), can efficiently induce antitumor immunity and thus have a high potential as tools in cancer therapy. The gene delivery is most efficiently achieved by viral vectors. Here, we explored the capacity of influenza virus vectors to transduce TAA genes. These viruses abortively infect DCs without interfering with their antigen-presenting capacity. In contrast to other viruses used for DC transduction, influenza viruses can be efficiently controlled by antiviral pharmaceuticals, lack the ability to integrate into host chromosomes, and fail to establish persistent infections. Genes encoding a melanoma-derived TAA (MAGE-3), or the green fluorescence protein (GFP), were introduced into a high-expression avian influenza virus vector. Monocyte-derived mature DCs infected by these recombinants efficiently produced GFP or MAGE-3. More than 90% of the infected DCs can express a transduced gene. Importantly, these transduced DCs retained their characteristic phenotype and their potent allogeneic T cell stimulatory capacity, and were able to stimulate MAGE-3-specific CD8(+) cytotoxic T cells. Thus influenza virus vectors provide a highly efficient gene delivery system in order to transduce human DCs with TAA, which consequently stimulate TAA-specific T cells.

Descriptors: antigens, neoplasm genetics, dendritic cells metabolism, gene transfer techniques, influenza A virus avian genetics, neoplasm proteins genetics, neoplasm proteins metabolism, antigens, neoplasm metabolism, CD8 positive T lymphocytes metabolism, cell line, cell separation, dogs, flow cytometry, genetic vectors, immunoblotting, immunophenotyping, luminescent proteins genetics, luminescent proteins metabolism, microscopy, phase contrast, phenotype, plasmids metabolism, reverse transcriptase polymerase chain reaction, T lymphocytes, cytotoxic metabolism, transduction, genetic, tumor cultured cells.


NAL Call Number: QH506.M684

Abstract: Replication of the influenza virus strains Influenza Ao/WSN (H0N1), fowl plague (Hav1N1) and B-
Lee/40 (ATCC) and the paramyxovirus, New Castle disease virus (Victoria) are highly sensitive to human interferon type alpha in Madin Darby bovine kidney cells. Pretreatment of cells with human interferon type alpha resulted in protection of the cells against viral cytopathic effect. The inhibition of the orthomyxovirus strains used in this study and New Castle disease virus replication is mediated by an inhibition of viral protein synthesis. Residual WSN virus particles released from interferon treated cells showed the same structural protein pattern as virus particles isolated from control cells. Glycosylation of the viral structural components appeared to be unaffected by interferon.

Descriptors: DNA replication drug effects, interferon type I pharmacology, Newcastle disease virus drug effects, orthomyxoviridae drug effects, virus replication drug effects, cattle, dogs, influenza A virus avian drug effects, human drug effects, influenza B virus drug effects, kinetics, mice, Newcastle disease virus genetics, orthomyxoviridae genetics, species specificity, structure activity relationship.


**Abstract:** Live attenuated influenza A virus vaccines are currently produced by the transfer of attenuating genes from a donor virus to new epidemic variants of influenza A virus, with the selection of reassortant viruses that possess the protective antigens (i.e., the two surface glycoproteins) of the epidemic virus and the attenuating genes from the donor virus. The previously studied attenuated donor viruses were produced by conventional methods such as passage of virus at low temperature or chemical mutagenesis. The present paper describes a new strategy for the generation of a donor virus bearing an attenuating, non-surface-glycoprotein gene. This strategy involves the introduction of attenuating mutations into the cDNA copy of the PB2 polymerase gene by site-directed mutagenesis, transfection of in vitro RNA transcripts of PB2 cDNA, and recovery of the transfected PB2 gene into an infectious virus. An avian-human influenza A virus PB2 single-gene reassortant virus (with an avian influenza A virus PB2 gene) that replicates efficiently in avian tissue but poorly in mammalian cells was used as a helper virus to rescue a transfected synthetic RNA derived from a human influenza A virus PB2 gene. The desired human influenza A virus mutant PB2 transfectant was favored in this situation because the avian influenza A virus PB2 gene restricts viral replication in mammalian cells in culture, the system used for rescue, thereby providing strong selection for the virus bearing the human influenza A virus PB2 gene. We validated the feasibility of this approach by rescuing the PB2 gene of the wild-type influenza A/Ann Arbor/6/60 virus and a mutant derivative that had a single amino acid substitution introduced at position 265 by site-directed mutagenesis. Previously, this amino acid substitution had been shown to specify both a temperature-sensitive (ts) and an attenuation (att) phenotype. The rescued mutant 265 PB2 transfectant virus exhibited the ts and att phenotypes, which confirms that these phenotypes were specified by this single amino acid substitution. The transfectant virus was immunogenic and protected hamsters from subsequent challenge with wild-type virus. The cDNA copy of this influenza A/Ann Arbor/6/60 virus mutant 265 PB2 gene will be used as a substrate for the introduction of additional attenuating mutations by site-directed mutagenesis.

Descriptors: genetics, immune system, microbiology, pharmacology, avian influenza A virus, challenge protection, hamster immunogenicity, host range, restriction, exploitation, human influenza A virus, vaccine donor, virus generation method.


**NAL Call Number:** 448.8 P942

**Descriptors:** hemolysis, influenza A virus avian pathogenicity, chick embryo, hydrogen-ion concentration, kinetics, light, scattering, radiation, time factors, virus cultivation.


**NAL Call Number:** SF604.J342
Abstract: The susceptibilities of culture cells to twelve avian influenza virus strains were determined with ten established cell lines including MDCK and ESK cells and three primary culture cells. The established cell lines derived from embryonic swine kidney (ESK) and chicken kidney (CK) primary culture cells were more sensitive to the avian influenza viruses than the other eleven cells. The ESK cell had a particularly higher infective titer than the MDCK cell with and without trypsin supplement in culture medium, and dispersion of the infective titers was narrower than that of the MDCK cell. The ESK cell is a suitable candidate for routine work on avian influenza viruses in laboratories.

Descriptors: fowl plague immunology, influenza A virus avian immunology, cell line immunology, chick embryo, chickens, cytopathogenic effect, viral immunology, fowl plague virology, hemagglutination, avian pathogenicity, poultry, swine, trypsin chemistry.

NAL Call Number: 41.9 T5750
Descriptors: antigens, viral analysis, influenza A virus avian immunology, cross reactions, hemagglutination inhibition tests, Japan.

NAL Call Number: 448.8 V81
Abstract: The M2 proteins of a variety of influenza A viruses of different subtypes were shown to possess associated palmitate. Susceptibility to removal by reduction or treatment with hydroxylamine is consistent with attachment via a thioester linkage to cysteine. The absence of the acyl group from the M2 proteins of several equine viruses of the H3N8 subtype correlates with the replacement of cysteine 50 with phenylalanine and points to this as the site of palmitate attachment.
Descriptors: influenza A virus metabolism, palmitic acids metabolism, viral matrix proteins metabolism, amino acid sequence, chick embryo, avian metabolism, human metabolism, molecular sequence data, molecular weight, palmitic acid, sequence homology, nucleic acid, viral matrix proteins isolation and purification.

NAL Call Number: 448.8 V81
Abstract: The evidence presented shows that the M2 protein of influenza A viruses exists in infected cells as a homotetramer composed of two disulfide-linked dimers held together by noncovalent interactions. The amphipathic nature of the transmembrane alpha-helical domain is consistent with the protein forming a transmembrane channel with which amantadine, the specific anti-influenza A drug, interacts. Together these features provide a structural basis for the hypothesis that M2 has a proton translocation function capable of regulating the pH of vesicles of the trans-Golgi network, a role important in promoting the correct maturation of the hemagglutinin glycoprotein.
Descriptors: influenza A virus avian physiology, viral matrix proteins isolation and purification, cultured cells, centrifugation, density gradient, chick embryo, chickens, ducks, electrophoresis, gel, two dimensional, electrophoresis, polyacrylamide gel, macromolecular systems, models, structural, molecular weight, protein conformation, viral matrix proteins metabolism.

NAL Call Number: 41.8 V6426
Descriptors: influenza A virus avian isolation and purification, phosphorus isotopes, bacteriological techniques.

Abstract: All types of the hemagglutinin (HA) of human, pig, horse and aq. bird influenza A viruses, recognize sialyl lacto-series type I and II sugar chains (Sialic acid (SA) alpha 2-3(6) Gal beta 1-3(4) GlcNAc beta 1-) in glycoproteins and glycolipids in the target cells as common receptor molecules. Avian and equine influenza viruses preferentially binds the terminal sialic acid alpha 2-3 Gal(SA2-3Gal) linkage, while human influenza viruses preferentially bind the SA2-6Gal linkage. SA distribution in animal species influence influenza virus host range. Swine trachea has both receptors for avian influenza viruses (SA2-3Gal specific) and for human influenza viruses(SA2-6Gal specific). In the case of horses, a virus with an HA recognizing Neu5Ac2-6Gal, but not Neu5Ac2-3Gal, failed to replicate in horses, while one with an HA recognizing the Neu5Gc2-3Gal moiety replicated in horses. The abundance of the Neu5Gc2-3Gal moiety in epithelial cells of horse trachea supports that recognition of Neu5Gc2-3Gal moiety is critical for viral replication in horses. The Neu5Gc2-3Gal is also associated with viral replication in duck intestine, primarily in the crypt epithelial cells. Such recognition, together with biochemical evidence of Neu5Gc in crypt cells, correlated exactly with the ability of the virus to replicate in duck colon. These results indicate the evidence of biologic effect of different sialic acid species in different animals.

Descriptors: orthomyxoviridae physiology, receptors, virus chemistry, sialic acids analysis, glycolipids analysis, glycoproteins analysis.


NAL Call Number: 41.8 P27

Abstract: To determine the association between specific structural changes in the hemagglutinin gene and pathogenicity of avian influenza viruses (AIVs), groups of 4-week-old White Plymouth Rock chickens were inoculated intravenously or intranasally with AIVs of varying pathogenicities isolated from chickens in central Mexico during 1994-1995. Mildly pathogenic (MP) viruses had a common hemagglutinin-connecting peptide sequence of Pro-Gln-Arg-Glu-Thr-Arg decreases Gly and had restricted capability for replication and production of lesions in tissues. The principle targets for virus replication or lesion production were the lungs, lymphoid organs, and visceral organs containing epithelial cells, such as kidney and pancreas. Death was associated with respiratory and/or renal failure. By contrast, highly pathogenic (HP) AIVs had one substitution and the addition of two basic amino acids in the hemagglutinin connecting peptide, for a sequence of Pro-Gln-Arg-Lys-Arg-Lys-Thr-Arg decreases Gly. The HP AIVs were pantropic in virus replication and lesion production ability. However, the most severe histologic lesions were produced in the brain, heart, adrenal glands, and pancreas, and failure of multiple critical organs was responsible for disease pathogenesis and death. No differences in lesion distribution patterns or in sites of AIV replication were evident to explain the variation in mortality rates for different HP AIVs, but HP AIVs that produced the highest mortality rates had more severe necrosis in heart and pancreas. The ability of individual HP AIVs to produce low or high mortality rates could not be explained by changes in sequence of the hemagglutinin-connecting peptide alone, but probably required the addition of other undetermined genomic changes.

Descriptors: chickens, fowl plague pathology, influenza A virus avian genetics, avian pathogenicity, avian physiology, adrenal glands chemistry, adrenal glands pathology, adrenal glands virology, brain pathology, brain virology, brain chemistry, fowl plague epidemiology, fowl plague mortality, hemagglutinins viral chemistry, hemagglutinins viral genetics, immunohistochemistry, kidney chemistry, kidney pathology, kidney virology, Mexico epidemiology, myocardium chemistry, myocardium pathology, pancreas chemistry, pancreas pathology, pancreas virology, specific pathogen free organisms, spleen chemistry, spleen pathology, spleen virology, viral proteins analysis, viral proteins metabolism, virus replication.


NAL Call Number: SF995.A1A9

Abstract: Avian influenza (AI) and Newcastle disease (ND) viruses are heat labile viruses, but exact parameters for heat inactivation at egg pasteurization temperatures have not been established. In this study we artificially infected four egg products with two AI (one low [LP] and one high pathogenicity [HP]) and three ND (two low and one highly virulent) viruses, and determined inactivation curves at 55, 57, 59, 61 and 63 degrees C. Based on D(t) values, the time to inactivation of the viruses was dependent on virus strain and egg product, and was directly related to virus titre, but inversely related to temperature. For all temperatures,
the five viruses had the most rapid and complete inactivation in 10% salt yolk, while the most resistant to inactivation was HPAI virus in dried egg white. This study demonstrated that the LPAI and all ND viruses were inactivated in all egg products when treated using industry standard pasteurization protocols. By contrast, the HPAI virus was inactivated in liquid egg products but not in dried egg whites when using the low-temperature industry pasteurization protocol.

Descriptors: chickens virology, eggs virology, heat, influenza A virus, avian pathogenicity, Newcastle disease virus pathogenicity, virus inactivation, time factors.


NAL Call Number: 41.8 Av5

Abstract: One-day-old and 5-week-old commercial leghorn, specific-pathogen-free leghorn, and broiler chickens were inoculated intravenously with either avian influenza virus isolate A/chicken/Alabama/7395/75 (H4N8) (Ck/AL) or sterile diluent. Ck/AL infection resulted in a 44% mortality rate, reduced weight gains, and necrosis of proximal renal tubules and/or tubulointerstitial nephritis. The renal tubule necrosis was more severe and widespread in chickens that died than in chickens that were euthanatized. Hyperuricemia, hypercalcemia, and hyperphosphatemia were present in 5-week-old chickens at day 5 postinfection. Influenza virus isolate Ck/AL was nephropathogenic, and death was associated with acute severe renal damage and failure. Some data suggested that the pathogenicity of Ck/AL may be more severe in leghorns than broilers.

Descriptors: chickens, avian influenza virus, kidney diseases, biological differences, age, experimental infection, in vivo experimentation, pathogenicity, kidneys, histopathology, symptoms, animal morphology, biological properties, birds, disease transmission, domestic animals, domesticated birds, experimentation, Galliformes, infection, influenza virus, livestock, microbial properties, organic diseases, pathogenesis, pathology, poultry, urinary tract, urinary tract diseases, urogenital system, useful animals, viruses, age differences.


NAL Call Number: 41.8 P27

Abstract: Forty-nine 5-week-old chickens were inoculated by the intravenous (i.v.), intratracheal (IT), or intranasal (IN) routes with either a chicken-origin or one of two duck-origin type A influenza virus isolates. Twelve control chickens were inoculated with sterile chorioallantoic fluid. For all viruses, i.v. inoculation produced predominately lesions of renal tubule necrosis (nephrosis) and nephritis, and influenza virus nucleoprotein was localized in nuclei and cytoplasm of necrotic renal tubule epithelium. Chickens inoculated by the IT route, and to a lesser extent the IN route, had mild to severe tracheitis, bronchitis, and ventromedial pneumonia associated with secondary bronchi but lacked renal tubule necrosis and nephritis. These data indicate low-virulence avian-origin influenza viruses were nephrotropic during simulated systemic infection (i.v. inoculation) and pneumotropic during simulated local infection (IT and IN inoculation). Gross and histologic kidney lesions produced by i.v. inoculation of the chicken-origin influenza virus were similar to changes reported in outbreaks of low-virulence influenza virus in laying chickens.

Descriptors: chickens microbiology, ducks microbiology, fowl plague pathology, influenza A virus avian pathogenicity, poultry diseases pathology, acute disease, administration, intranasal, immunohistochemistry, infections, intravenous, intubation, intratracheal, virulence.

Swayne, D.E. and D.L. Suarez (2003). *Additional glycosylation at the receptor binding site of the hemagglutinin (HA) for H5 and H7 viruses may be an adaptation to poultry hosts, but does it influence pathogenicity?* *Avian Diseases* 47(Special Issue): 942-950. ISSN: 0005-2086.

NAL Call Number: 41.8 Av5

Descriptors: binding sites, genes, hemagglutinins, pathogenicity, phylogenetics, poultry, viral proteins, avian influenza virus, Italy, United Kingdom, Galliformes.
NAL Call Number: TD899.P65.T3 2004
Abstract: Comprehensive guidelines were developed and used to train poultry company personnel on in-house composting procedures. Results to date suggest in-house composting of avian influenza infected flocks is a biosecure, cost effective and efficient means of disposal of broiler carcasses in clear-span houses.
Descriptors: poultry, avian influenza, composting, in-house composting, infected flocks.

ISSN: 0068-3957.
NAL Call Number: 448.39 B87
Descriptors: ammonium chloride pharmacology, influenza A virus avian drug effects, orthomyxoviridae drug effects, virus replication drug effects, ammonium sulfate pharmacology, cattle immunology, kidney, tissue culture, virus cultivation.

NAL Call Number: 385 J822
Abstract: The majority of influenza A viruses isolated from wild birds, but not humans, can replicate in the duck intestinal tract. Here we demonstrate that all duck isolates tested universally retain sialidase activities under low pH conditions independent of their neuraminidase (NA) subtypes. In contrast, the sialidase activities of most isolates from humans and pigs practically disappear below pH 4.5, with the exception of four human pandemic viruses isolated in 1957 and 1968. Sequence comparisons among duck, human, and swine N2 NA subtypes indicate that amino acids at positions 153, 253, 307, 329, 344, 347, 356, 368, 390, and 431 may be associated with the low pH stability of duck and human pandemic N2 NAs. This finding suggests that the low pH stability of duck influenza A virus NA may be a critical factor for replication in the intestinal tract through the digestive tract of ducks, and that the properties of NAs are important for understanding the epidemiology of the influenza virus.
Descriptors: influenza virology, influenza A virus avian enzymology, human enzymology, neuraminidase metabolism, ducks, enzyme stability, hydrogen-ion concentration, influenza transmission, avian physiology, human physiology, porcine enzymology, phylogeny, sequence analysis, swine.

ISSN: 0022-538X.
NAL Call Number: QR360.J6
Abstract: The influenza A/fowl plague virus/Rostock/34 hemagglutinin (HA), which is cleaved intracellularly and has a high pH threshold (pH 5.9) for undergoing its conformational change to the low-pH form, was expressed from cDNA in CV-1 and HeLa T4 cells in the absence of other influenza virus proteins. It was found, by biochemical assays, that the majority of the HA molecules were in a form indistinguishable from the low-pH form of HA. The acidotropic agent, ammonium chloride, stabilized the accumulation of HA in its native form. Coexpression of HA and the homotypic influenza virus M2 protein, which has ion channel activity, stabilized the accumulation of HA in its pH neutral (native) form, and the M2 protein ion channel blocker, amantadine, prevented the rescue of HA in its native form. These data provide direct evidence that the influenza virus M2 protein ion channel activity can affect the status of the conformational form of cleaved HA during intracellular transport.
Descriptors: hemagglutinins viral metabolism, influenza A virus metabolism, ion channels, viral matrix proteins metabolism, amantadine pharmacology, ammonium chloride pharmacology, biological transport, cultured cells, cercopithecus aethiops, endopeptidases pharmacology, glucosaminidase pharmacology, HeLa cells, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral drug effects, hemagglutinins
viral genetics, hydrogen-ion concentration, influenza A virus avian metabolism, oxidation reduction, protein conformation, recombinant proteins metabolism, viral matrix proteins genetics.


**NAL Call Number:** 448.8 V81

**Abstract:** The equine-1 influenza virus A/Cornell/74 (H7N7) hemagglutinin (HA) is cleaved to HA1 and HA2 in the trans Golgi network (TGN) of infected cells. The avian influenza virus A/chicken/Germany/34 (fowl plague virus Rostock) H7 HA is also cleaved to HA1 and HA2 intracellularly in the TGN. To maintain the fowl plague virus Rostock HA in its native form during transport through the TGN, a functioning M2 ion channel activity is required, otherwise the HA undergoes its transition to the low-pH form (Sugrue et al., 1990, EMBO J. 9, 3469-3476). Studies were initiated to investigate if the equine H7 HA has intracellular requirements different from those of the fowl plague virus Rostock HA. We report here that the pH of transition to the low-pH form of the equine-1 HA is approximately pH 5.3 and that the M2 protein ion channel blocker, amantadine, does not have a discernable effect on the native conformation of equine-1 HA during transport through the TGN. Moreover, the equine-1 HA expressed from cDNA does not require coexpression of a functional M2 protein to maintain HA in its native conformation.

**Descriptors:** hemagglutinins viral metabolism, influenza A virus metabolism, ion channels physiology, viral matrix proteins physiology, amantadine pharmacology, biological transport, Golgi apparatus metabolism, hydrogen-ion concentration, protein processing, post translational, virus replication drug effects.


**NAL Call Number:** 448.8 V81

**Abstract:** In this quantitative study of the interaction of influenza virus with neutralizing antibody we have determined the maximum number of antibody molecules which can bind to the haemagglutinin (HA) of native influenza A/FPV/Rostock/34 (H7N1) particles in aqueous suspension and the minimum number which is required to cause neutralization. Using radiolabelled immunoglobulins approximately one IgG molecule, whether of monoclonal or polyclonal origin, binds per HA spike under conditions of antibody saturation. In the same manner, we have determined that when infectivity is neutralized by 63% (1/e) about 70 molecules of monoclonal IgGs HC2 and HC10 were bound per virus particle and this is supported by independent evidence from electron microscopy. However, the kinetics of neutralization were single-hit or at most, under critical conditions of low temperature (4 degrees) and minimal neutralizing concentrations of antibody, two-hit. This apparent conflict is reconciled by a hypothesis which proposes that neutralization occurs only when antibody binds to certain "neutralization relevant" HA spikes which are in the minority. It is suggested that these only differ from the majority of "neutralization irrelevant" HA spikes by their transmembrane interaction with the core of the virion.

**Descriptors:** antibodies, viral immunology, hemagglutinin viral immunology, influenza A virus avian immunology, antibodies, monoclonal immunology, hemagglutination inhibition tests, hemagglutinin glycoproteins, influenza virus, immunoglobulin G immunology, neutralization tests, radioimmunoassay.


**NAL Call Number:** 448.8 V81

**Abstract:** Two-step solution competition assays were performed in solution with influenza type A virions and hemagglutinin (HA)-specific neutralizing monoclonal antibodies (mabs). These demonstrated that the binding of one molecule of IgG mab per HA trimer prevented the binding of mabs directed against other antigenic sites on the HA (site A, site B, or site D), even though these are topographically separate and antigenically independent. Furthermore the same procedures showed that one molecule of mab per trimer prevented the binding of polyclonal HA-specific IgG obtained from the serum of rabbits immunized with whole virus. This restricted binding is clearly a property of the intact virion, since others using purified HA have shown that up to four IgG molecules of different specificities can bind per trimer. Since the surface area
of the globular head of the trimer is equivalent to approximately 10 nonoverlapping antibody footprints, it is not understood how one prebound IgG molecule prevents the binding of other IgG molecules.

Descriptors: hemagglutinin viral immunology, immunoglobulin G immunology, influenza A virus avian immunology, viral envelope proteins immunology, antibodies, monoclonal immunology, antibody specificity, binding sites, antibody, binding, competitive, chick embryo, hemagglutinin glycoproteins, influenza virus, neutralization tests, solutions, virion immunology.


Abstract: The intracellular influenza virus-containing structures involved in RNA synthesis in the cytoplasm and in the nucleoplasm of infected chicken fibroblasts were studied. Two approaches were used: (1) short pulse labeling of infected cell with [3H]uridine; (2) determination in vitro of polymerase activity of intracellular virus-specific structures. Both methods revealed functionally active virus-specific structures in the nucleoplasm and showed that a functionally active virus-specific structure was localized in the nucleoplasm of infected cells. This structure contained proteins of the viral ribonucleoprotein, but sedimented somewhat faster (at 60--90S in velocity sucrose and glycerol gradients). Meanwhile, polymerase-containing structures in the cytoplasm of infected cells sedimented in the position of viral ribonucleoproteins (25--60S).

Descriptors: influenza A virus avian ultrastructure, viral proteins analysis, cell nucleus enzymology, cell nucleus microbiology, cultured cells, cytoplasm microbiology, DNA directed RNA polymerases metabolism, electrophoresis, polyacrylamide gel, avian analysis, avian enzymology, uridine metabolism.


NAL Call Number: QR360.A1J6

Descriptors: amino acids metabolism, anti bacterial agents pharmacology, RNA, messenger antagonists and inhibitors, viruses drug effects, arginine metabolism, asparagine metabolism, carbon isotopes, encephalitis viruses drug effects, glycine metabolism, herpesviridae drug effects, influenza A virus avian drug effects, leucine metabolism, lysine metabolism, molecular biology, Newcastle disease virus drug effects, phenylalanine metabolism, proline metabolism, vaccinia virus drug effects, virus replication drug effects.


NAL Call Number: 448.3 Ap5

Abstract: Several animal viruses were treated with gamma radiation from a 60Co source under conditions which might be found in effluent from an animal disease laboratory. Swine vesicular disease virus, vesicular stomatitis virus, and blue-tongue virus were irradiated in tissues from experimentally infected animals. Pseudorabies virus, fowl plague virus, swine vesicular disease virus, and vesicular stomatitis virus were irradiated in liquid animal feces. All were tested in animals and in vitro. The D10 values, that is, the doses required to reduce infectivity by 1 log10, were not apparently different from those expected from predictions based on other data and theoretical considerations. The existence of the viruses in pieces of tissue or in liquid feces made no difference in the efficacy of the gamma radiation for inactivating them. Under the "worst case" conditions (most protective for virus) simulated in this study, no infectious agents would survive 4.0 Mrads.

Descriptors: feces microbiology, sewage, viruses radiation effects, bluetongue virus radiation effects, enteroviruses, porcine radiation effects, gamma rays, herpesvirus 1, suid radiation effects, influenza A virus avian radiation effects, vesicular stomatitis Indiana virus radiation effects.


NAL Call Number: QR355.A5

Abstract: The sialidase inhibitor 4-guanidino-2,4-dideoxy-2,3-dehydro-N-acetylneuraminic acid was tested
for growth inhibitory effects against a panel of avian influenza A viruses encompassing all nine neuraminidase subtypes. Growth in tissue culture of viruses from each subtype was inhibited by this compound at concentrations within a range previously found effective against human N1 and N2 viruses. This compound may prove a selective agent for the treatment (and prevention) of influenza virus infections. **Descriptors:** enzymology, microbiology, pharmacology, antiviral drug avian influenza viruses human influenza viruses neuraminidase inhibition pharmacodynamics 4-guanidino-2,4-dideoxy-N-acetylneuraminic acid.


**NAL Call Number:** 396.8 J824

**Abstract:** A new antibiotic complex has been isolated from cultures of *Streptomyces* strain No. JA 10124. On the basis of taxonomic studies, the producing microorganism is described as *Streptomyces griseoflavus* (Krainsky, 1914) Waksman et Henrici, 1948, subsp. thuringiensis subsp. nov., type strain JA 10124. The antibiotic complex, designated as streptovirudin, was isolated from extracts of both mycelium and culture filtrate. It is a white amorphous material which consists of ten closely related components including streptovirudins A, B, C, D and E. The streptovirudin complex exhibits antibiotic activity against Gram-positive bacteria, *Mycoplasma*, and various DNA- and RNA-viruses.

**Descriptors:** anti bacterial agents isolation and purification, antiviral agents isolation and purification, administration, oral, anti bacterial agents administration and dosage, anti bacterial agents pharmacology, antiviral agents pharmacology, *Chlamydia* drug effects, fermentation, herpesvirus 1, suid drug effects, influenza A virus avian drug effects, injections, intraperitoneal, injections, intravenous, injections, subcutaneous, mice, *Mycoplasma* drug effects, Newcastle disease virus drug effects, sheep, sindbis virus drug effects, *Streptomyces* analysis, *Streptomyces* classification, vaccinia virus drug effects.


**NAL Call Number:** QR360.J6

**Abstract:** An avian influenza A virus, A/Mallard/NY/6750/78(H2N2), was restricted in in replication in the respiratory tract of squirrel monkeys. Avian-human influenza A reassortant viruses possessing the six RNA segments coding for nonsurface proteins (i.e., internal genes) of this avian virus were as restricted in replication in squirrel monkeys as their avian influenza parent. These findings indicated that restriction of replication of the avian influenza virus is a function of one or more of its internal genes. For an investigation of which of the avian influenza genes was responsible for restricted replication in the respiratory tract of primates, reassortant viruses were produced that contained human influenza virus surface antigens from the A/Udorn/72(H3N2) virus and one or more of the internal genes derived from the avian influenza virus parent. Avian-human reassortant influenza A viruses containing only the nucleoprotein or matrix protein RNA segment from the avian influenza virus parent were as restricted in their growth as an avian-human influenza reassortant virus containing each of the six avian influenza internal genes. In addition, an avian-human influenza reassortant virus possessing only the avian RNA 1 and nonstructural genes (which by themselves do not specify restricted replication) manifested a significant reduction of virus replication in squirrel monkey tracheas. Thus, the avian nucleoprotein and matrix genes appear to play a major role in the host range restriction exhibited by the A/Mallard/78 virus and its reassortants, but the combination of RNA 1 and nonstructural genes also contributes to restriction of replication.

**Descriptors:** genes viral, influenza A virus genetics, nucleoproteins genetics, viral proteins genetics, virus replication, birds microbiology, heat, influenza A virus physiology, RNA viral analysis, saimiri microbiology, trachea microbiology, viral matrix proteins.

Abstract: Influenza A viruses have been isolated from humans, from several other mammalian species and a wide variety of avian species, among which, wild aquatic birds represent the natural hosts of influenza viruses. The majority of the possible combinations of the 15 haemagglutinin (HA) and nine neuraminidase (NA) subtypes recognized have been identified in isolates from domestic and wild birds. Infection of birds can cause a wide range of clinical signs, which may vary according to the host, the virus strain, the host's immune status, the presence of any secondary exacerbating microorganisms and environmental factors. Most infections are inapparent, especially in waterfowl and other wild birds. In contrast, infections caused by viruses of H5 and H7 subtypes can be responsible for devastating epidemics in poultry. Despite the warnings to the poultry industry about these viruses, in 1997 an avian H5N1 influenza virus was directly transmitted from birds to humans in Hong Kong and resulted in 18 confirmed infections, thus strengthening the pandemic threat posed by avian influenza (AI). Indeed, reassortant viruses, harbouring a combination of avian and human viral genomes, have been responsible for major pandemics of human influenza. These considerations warrant the need to continue and broaden efforts in the surveillance of AI. Control programmes have varied from no intervention, as in the case of the occurrence of low pathogenic (LP) AI (LPAI) viruses, to extreme, expensive total quarantine-slaughter programmes carried out to eradicate highly pathogenic (HP) AI (HPAI) viruses. The adoption of a vaccination policy, targeted either to control or to prevent infection in poultry, is generally banned or discouraged. Nevertheless, the need to boost eradication efforts in order to limit further spread of infection and avoid heavy economic losses, and advances in modern vaccine technologies, have prompted a re-evaluation of the potential use of vaccination in poultry as an additional tool in comprehensive disease control strategies. This review presents a synthesis of the most recent research on AI that has contributed to a better understanding of the ecology of the virus and to the development of safe and efficacious vaccines for poultry.

Descriptors: animal husbandry, epidemiology, immune system, infection, veterinary medicine, virology, avian influenza, respiratory system disease, viral disease, avian influenza research: epidemiology, immunoprophylaxis, recent developments avian influenza vaccine development immunoprophylaxis poultry vaccine development: efficacy, safety.
Abstract: Influenza virus infection is responsible for hundreds of thousands of deaths annually. Current vaccination strategies and antiviral drugs provide limited protection; therefore, new strategies are needed. RNA interference is an effective means of suppressing virus replication in vitro. Here we demonstrate that treatment with small interfering RNAs (siRNAs) specific for highly conserved regions of the nucleoprotein or acidic polymerase inhibits influenza A virus replication in vivo. Delivery of these siRNAs significantly reduced lung virus titers in infected mice and protected animals from lethal challenge. This protection was specific and not mediated by an antiviral IFN response. Moreover, influenza-specific siRNA treatment was broadly effective and protected animals against lethal challenge with highly pathogenic avian influenza A viruses of the H5 and H7 subtypes. These results indicate that RNA interference is promising for control of influenza virus infection, as well as other viral infections.

Descriptors: influenza prevention and control, RNA interference, base sequence, influenza A virus, avian genetics, avian physiology, mice, inbred balb c, RNA, small interfering administration and dosage, small interfering genetics, viral genetics, virus replication.


NAL Call Number: QR1.A32
Descriptors: amantadine pharmacology, influenza A virus avian drug effects, spectrophotometry, benzyl compounds pharmacology, chick embryo, cytopathogenic effect, viral drug effects, fibroblasts, nitrosamines pharmacology, time factors, tissue culture, virus replication drug effects.


NAL Call Number: QR1.Z4
Descriptors: anti bacterial agents pharmacology, antiviral agents pharmacology, influenza A virus avian drug effects, anti bacterial agents biosynthesis, antiviral agents biosynthesis, chick embryo, cytopathogenic effect, viral, fibroblasts, hemadsorption, hemagglutination tests, avian growth and development, streptomyces metabolism, tissue culture, virus cultivation, virus replication.


NAL Call Number: 448.3 AC85
Abstract: Dipyridamole proved to be active against influenza viruses A/England 42/72, A/Bangkok 1/79 and A/fowl plague (FPV). The antiviral activities assayed by various methods varied from 90-99 per cent. No inhibition was found against influenza virus B/Leningrad 235/74 in vitro. Three dipyridamole derivatives were significantly active in tissue cultures against influenza virus A/England 42/72 and A/FPV. In white mice infected with influenza virus A/England 42/72 dipyridamole administered orally showed a protection rate of 62.5 per cent.

Descriptors: antiviral agents pharmacology, dipyridamole pharmacology, influenza A virus drug effects, dipyridamole analogs and derivatives, dipyridamole therapeutic use, influenza drug therapy, influenza A virus avian drug effects, mice, rimantadine therapeutic use.


NAL Call Number: 448.3 AC85
Abstract: Antibiotics of the streptovirudin complex (SV) inhibited the growth of influenza A and B viruses such as influenza A/fowl plague virus (FPV), strain Weybridge (Hav1 Neq1), influenza A/England 42/72 (H3N2), influenza A/Port Chalmers 1/73 (H3N2), influenza B/Leningrad 235/74, influenza B/Tokyo 7/66, and
influenza B/Jamagata in chick embryo cell (CEC) cultures, in permanent canine kidney cells (MDCK), and in suspended fragments of chick embryo chorioallantoic membranes (CAM). As revealed by spectrophotometric turbidity measurements, SV completely inhibited the FPV-induced cytopathic effect (CPE). A 99.99% reduction of infectious virus yield was obtained in one-step growth cycle experiments and in the plaque reduction test. The haemagglutination inhibition titres of influenza viruses in suspended CAM fragment cultures in the presence of SV drugs were also substantially reduced. The incorporation assays indicated that SV exhibited no effect on virus-induced RNA synthesis, but influenced virus maturation by inhibition of lipid-linked oligosaccharide synthesis. A partial protection from infection was found in influenza virus A/England infected mice.

Descriptors: anti bacterial agents pharmacology, influenza A virus avian drug effects, human drug effects, oligosaccharides biosynthesis, orthomyxoviridae drug effects, cell line, cytopathogenic effect, viral drug effects, dogs, dose response relationship, drug, glucose metabolism, avian metabolism, mice, RNA viral biosynthesis, virus replication drug effects.

NAL Call Number: RM260.C5
Descriptors: antiviral agents pharmacology, mengovirus drug effects, thiadiazoles pharmacology, virus replication drug effects, cultured cells, culture media, cytopathogenic effect, viral, depression, chemical, influenza A virus avian drug effects, microbial sensitivity tests, plaque assay, thiazoles, time factors, vaccinia virus drug effects.

NAL Call Number: 448.3 AC85
Abstract: Among 46 novel pyrimido [5.4-d] pyrimidine derivatives, 26 compounds were found to exhibit antiviral activity as revealed in a test programme against Mengo, Coxsackie B1, fowl plague, vaccinia and pseudorabies viruses, as concerns inhibition of plaque formation and of infectious virus yield. Attempts to disclose structure-activity relationships by discriminant analysis pointed to a possible importance of hydrophobic substitution for the antiviral effectiveness against Mengo virus of the derivatives investigated.
Descriptors: antiviral agents, dipyridamole analogs and derivatives, cell line, chemistry, dipyridamole pharmacology, enterovirus B, human drug effects, herpesvirus 1, suid drug effects, influenza A virus avian drug effects, mengovirus drug effects, Newcastle disease virus drug effects, vaccinia virus drug effects, virus replication drug effects.

NAL Call Number: QR375.V6
Abstract: The avian influenza A/Mallard/NY/6750/78 virus is currently being evaluated as a donor of attenuating genes in the construction of live avian-human influenza A reassortant virus vaccines for use in humans. We determined the nucleotide sequences of the three polymerase gene segments of this virus. This completes the nucleotide sequence of the six transferrable genes of the avian donor virus. Comparison of the nucleotide and deduced amino acid sequences of the non-glycoprotein genes of the avian A/Mallard/78 virus with representative avian and human influenza A viruses suggests that the PB1 gene of H2N2 subtype human influenza A viruses may have been derived from a non-human, possibly avian influenza A virus by genetic reassortment. In addition, several regions of conserved amino acids with potential functional significance were identified in the deduced amino acid sequences of the polymerase proteins.
Descriptors: influenza A virus avian genetics, amino acid sequence, base sequence, DNA, viral genetics, genes viral, avian enzymology, molecular sequence data, RNA directed DNA polymerase genetics, sequence homology, nucleic acid.


**NAL Call Number:** 448.8 V81

**Abstract:** The nonstructural (NS) genes of avian influenza A viruses have been divided into two groups on the basis of nucleotide sequence homology, which we have referred to here as alleles A and B. We sequenced the NS genes of eight additional avian influenza A viruses in order to define the differences between these two alleles more thoroughly. Four of the viruses had NS gene sequences which resembled that of A/FPV/Rostock/34 and belonged to allele A while the other four viruses had NS gene sequences more similar to that of A/Duck/Alberta/76 and belonged to allele B. There was approximately 90% sequence homology within alleles and 72% homology between alleles. As previously reported the NS genes of human influenza A viruses belong to allele A. We constructed single gene avian-human reassortant influenza A viruses containing an allele A or B NS gene segment from an avian influenza A virus and all other genes from a human influenza A virus and tested these reassortants for their ability to grow in the respiratory tract of a nonhuman primate. Reassortants containing an avian NS gene segment of allele B were significantly restricted in growth in the respiratory tract of squirrel monkeys while reassortants with an allele A NS gene segment were not. The divergent evolution of the B NS allele in birds may have resulted in gene products which do not function optimally in cooperation with genes from a human virus in viral replication in primate respiratory epithelium.

**Descriptors:** capsid genetics, influenza A virus avian genetics, human growth and development, viral core proteins genetics, alleles, amino acid sequence, base sequence, genes viral, human genetics, molecular sequence data, nasopharynx microbiology, saimiri microbiology, sequence homology, nucleic acid, trachea microbiology, viral nonstructural proteins, virus replication.


**NAL Call Number:** QR189.V32

**Abstract:** A unique requirement for live attenuated reassortant influenza vaccines is the need to generate new reassortant vaccine viruses with the appearance of each new antigenic variant. Thus, the attenuation phenotype conferred by the attenuated donor influenza virus must remain genetically stable during the generation of each new reassortant vaccine virus. In this study we used nucleotide sequence analysis to evaluate the genetic stability of the attenuating M and NP genes of the avian influenza A/Mallard/NY/6750/78 attenuated donor virus during the in vitro generation and subsequent in vivo replication of avian-human (AH) influenza A reassortant vaccine viruses in monkeys and humans. Nucleotide sequence changes in the M and NP genes occurred at a rate of approximately 0.61 substitutions/1000 nt/reassortant during in vitro generation of four AH reassortant viruses. Only two nucleotide sequence changes occurred in the M and NP gene segments of four isolates of H1N1 or H3N2 AH vaccine viruses following 6-8 days of replication in seronegative children, and neither change affected amino acids previously identified as playing a potential role in attenuation. In addition, there were no changes in the nucleotide sequence of the M and NP genes of single gene AH reassortant viruses following five serial passages in squirrel monkeys. Finally, there was no change in the level or duration of replication of the single gene reassortant viruses in the upper or lower respiratory tract of monkeys following serial passage. (ABSTRACT TRUNCATED AT 250 WORDS)

**Descriptors:** influenza A virus avian genetics, influenza vaccine genetics, nucleoproteins, viral core proteins genetics, viral matrix proteins genetics, base sequence, cloning, molecular, avian pathogenicity, avian physiology, human genetics, human pathogenicity, human physiology, molecular sequence data, mutation genetics, polymerase chain reaction, recombination, genetic physiology, saimiri, vaccines, attenuated genetics, vaccines, synthetic genetics, virus replication genetics.


**NAL Call Number:** QR375.V6

**Abstract:** The protein kinase activity associated with purified influenza virus has been examined. By use of
a radiolabelled photoreactive ATP analogue (3'-O-(4-benzoyl) benzoyl adenosine triphosphate) a 47 kD polypeptide has been identified that binds ATP. A comparison of the sensitivity of the kinase activity and the 47 kDa polypeptide labelling to inhibitors indicate that the 47 kDa polypeptide is likely to represent the major protein kinase activity of the virus. The virus associated protein kinase phosphorylates the synthetic peptide RREEEEEE, a peptide substrate for casein kinase II. Antiserum directed against casein kinase II revealed a positive signal in immunoblots of purified virus. We propose that the major protein kinase activity associated with purified virus preparations is host cell casein kinase II.


NAL Call Number: 448.3 AC85
Descriptors: diploidy, orthomyxoviridae growth and development, tissue culture, virus cultivation, chick embryo, hemagglutination tests, influenza A virus avian growth and development, orthomyxoviridae immunology, orthomyxoviridae pathogenicity, virulence.

NAL Call Number: 448.8 V81
Descriptors: orthomyxoviridae, ultraviolet rays, antigens, birds, complement fixation tests, genetics, hemagglutination inhibition tests, horses, influenza, influenza A virus avian, radiation effects, swine.

NAL Call Number: 448.8 J826
Descriptors: antibodies analysis, antigens analysis, orthomyxoviridae immunology, adult, age factors, aged, antigen antibody reactions, depression, chemical, ducks, hemagglutination inhibition tests, influenza A virus avian immunology, middle aged, neutralization tests, periodic acid pharmacology, potassium pharmacology, turkeys.

NAL Call Number: QR360.J6
Abstract: Influenza vaccines that induce greater cross-reactive or heterosubtypic immunity (Het-I) may overcome limitations in vaccine efficacy imposed by the antigenic variability of influenza A viruses. We have compared mucosal versus traditional parenteral administration of inactivated influenza vaccine for the ability to induce Het-I in BALB/c mice and evaluated a modified Escherichia coli heat-labile enterotoxin adjuvant, LT(R192G), for augmentation of Het-I. Mice that received three intranasal (i.n.) immunizations of H3N2 vaccine in the presence of LT(R192G) were completely protected against lethal challenge with a highly pathogenic human H5N1 virus and had nasal and lung viral titers that were at least 2,500-fold lower than those of control mice receiving LT(R192G) alone. In contrast, mice that received three vaccinations of H3N2 vaccine subcutaneously in the presence or absence of LT(R192G) or incomplete Freund's adjuvant were not protected against lethal challenge and had no significant reductions in tissue virus titers observed on day 5 post-H5N1 virus challenge. Mice that were i.n. administered H3N2 vaccine alone, without LT(R192G),
displayed partial protection against heterosubtypic challenge. The immune mediators of Het-I were investigated. The functional role of B and CD8+ T cells in Het-I were evaluated by using gene-targeted B-cell (IgH-6(-/-))- or beta2-microglobulin (beta2m(-/-))-deficient mice, respectively. beta2m(-/-) but not IgH-6(-/-) vaccinated mice were protected by Het-I and survived a lethal infection with H5N1, suggesting that B cells, but not CD8+ T cells, were vital for protection of mice against heterosubtypic challenge. Nevertheless, CD8+ T cells contributed to viral clearance in the lungs and brain tissues of heterotypically immune mice. Mucosal but not parenteral vaccination induced subtype cross-reactive lung immunoglobulin G (IgG), IgA, and serum IgG anti-hemagglutinin antibodies, suggesting the presence of a common cross-reactive epitope in the hemagglutinins of H3 and H5. These results suggest a strategy of mucosal vaccination that stimulates cross-protection against multiple influenza virus subtypes, including viruses with pandemic potential.

**Descriptors:** B lymphocytes immunology, fowl plague prevention and control, influenza A virus avian immunology, influenza vaccine immunology, adjuvants, immunologic administration and dosage, administration, cutaneous, administration, intranasal, antibodies, viral analysis, antibodies, viral blood, bacterial toxins administration and dosage, CD8 positive T lymphocytes immunology, cross reactions, enterotoxins administration and dosage, *Escherichia coli* immunology, fowl plague immunology, fowl plague virology, Freund's adjuvant administration and dosage, hemagglutinin viral immunology, immunoglobulin A analysis, immunoglobulin A blood, immunoglobulin G analysis, immunoglobulin G blood, influenza A virus avian isolation and purification, lung immunology, lung virology, mice inbred BALB c, mice, inbred c57bl, mice, knockout, species specificity, vaccines, inactivated immunology.


**NAL Call Number:** SF604.P32

**Abstract:** Two hundred intestines pieces (100 each of broilers and layers) of about 8 cm length were collected from the poultry sale shops in Faisalabad city, Pakistan. These pieces were opened, scratched and vigorously shaken into sterilized normal saline, the suspension was centrifuged and supernatants were subjected to spot haemagglutination with 2% chicken RBC's. Out of 200 samples, 95% samples of layers and 75% of the broilers showed positive spot haemagglutination. Micro haemagglutination inhibition with Newcastle disease (ND) antiserum revealed 85 and 66 samples positive in layers and broilers, respectively. A total of 10% samples of the layers and 9% of the broilers were not inhibited by ND antiserum suggesting other HA viruses. A total of 20 samples were used to isolate the virus in embryonated eggs (allantoic route). These isolates were confirmed as NDV by haemagglutination inhibition test. Five isolates were tested for intracerebral pathogenicity index (ICPI) in day old chicks. The ICPI values obtained were 0.28, 0.31, 0.37, 0.38 and 0.46. The isolates were found to be lentogenic.

**Descriptors:** broiler chickens, layer chickens, intestines, Newcastle disease virus, identification, hemagglutination tests, agglutination tests, Galliformes, immunological techniques.


**NAL Call Number:** 41.8 V6446

**Descriptors:** avian influenza virus, antiserum, antigenc varients, studies.


**NAL Call Number:** QR1.A3

**Descriptors:** influenza A virus avian growth and development, orthomyxoviridae growth and development, recombination, genetic, virus replication, amantadine pharmacology, cell line, cytopathogenic effect, viral, drug resistance, microbial, orthomyxoviridae drug effects, variation genetics.


**Abstract:** Recombinants from two influenza A strains that lacked mouse neurovirulence were tested, along with their parent strains, for mouse neurovirulence and for the ability to propagate in dissociated mouse embryo brain cells. The parents used were (i) strain A/Rostock/34 (FPV) (Hav1N1), with a high chicken neurovirulence, and (ii) the mouse-lung-adapted human strain Engl/1/61 (H2N2), lacking neurovirulence. In some of the recombinants high mouse neurovirulence could be detected after intracerebral inoculation of low virus doses. There was neither a correlation between surface antigen and neurovirulence nor between neurovirulence and mouse lung virulence in our system, although neurovirulence was only found in strains with Hav1 hemagglutinin. There was an association between replication in mouse embryo brain cells in culture and high mouse neurovirulence.

**Descriptors:** influenza A virus avian pathogenicity, human pathogenicity, recombination, genetic, brain microbiology, avian genetics, avian growth and development, human genetics, human growth and development, mice, virulence, virus replication.


**Descriptors:** influenza A virus avian genetics, human genetics, recombination, genetic, administration, intranasal, brain microbiology, cultured cells, genes viral, human pathogenicity, injections, intraperitoneal, mice, orthomyxoviridae infections etiology, orthomyxoviridae infections pathology, pneumonia microbiology, trypsin pharmacology, viremia, virulence, virus replication drug effects.


**Descriptors:** viian influenza virus, virulence, *Gallus gallus*, chickens, pathogenesis.


**Abstract:** Infection of chickens by a virulent avian influenza A virus, A/turkey/Ont/7732/66 (H5N9), was associated with a severe lymphopenia. High titres of infectious virus were found in lymphoid tissues early in infection and were accompanied by severe damage to the lymphocyte populations as demonstrated by histopathological examination. Non-lymphoid cell populations in these tissues were unaffected, as were other organs examined. The viral nucleoprotein was localized by immunoperoxidase staining to lymphocytes in affected tissues early in infection.

**Descriptors:** influenza A virus avian pathogenicity, lymphopenia veterinary, chickens, fowl plague microbiology, fowl plague pathology, avian isolation and purification, lymphocytes microbiology, lymphocytes pathology, lymphoid tissue microbiology, lymphoid tissue pathology, lymphopenia microbiology, lymphopenia pathology, necrosis, time factors, virulence.


**Abstract:** To investigate the pathogenesis of virulent avian influenza A viruses, the effect of A/turkey/Ont/7732/66 (H5N9) (Ty/Ont), A/tern/South Africa/1961 (H5N3) (Tern/S.A.) and A/chicken/Pennsylvania/1370/83 (H5N2) (Ck/Penn) on avian lymphoid cell populations was examined in vivo. Previous studies have shown that infection of chickens with Ty/Ont resulted in the extensive destruction of lymphoid tissues. In this study, other virulent avian H5 influenza viruses, Tern/S.A. or Ck/Penn, had little or no effect on lymphoid tissues of infected chickens. Therefore the effect of Ty/Ont on lymphoid tissue is a specific activity of this virus only and not of other virulent avian H5 influenza strains. To
examine the role of viral replication in the destruction of lymphocytes, in vitro cultures of avian macrophages and lymphocytes were inoculated with Ty/Ont. Macrophages supported the synthesis of viral proteins whereas lymphocytes produced small, but detectable amounts of viral protein; however, infectious virus was not produced by either cell type. Furthermore inoculation of chicken spleen cells with Ty/Ont in vivo and in vitro had a profound effect on the proliferative response of lymphocytes to concanavalin A. These results suggest that Ty/Ont infects macrophages as well as lymphocytes in the chicken, and the effects of the virus on both cell types may well contribute to lymphoid necrosis.

Descriptors: influenza veterinary, influenza A virus avian immunology, lymphocytes immunology, macrophages immunology, poultry diseases immunology, chickens microbiology, immunoenzyme techniques, influenza immunology, avian pathogenicity, lymphocyte activation, lymphocytes microbiology, macrophages microbiology, poultry diseases microbiology, RNA viral biosynthesis, viral proteins biosynthesis, virus replication.


NAL Call Number: RA651.A1E74

Descriptors: influenza virus A and B, characteristics, comparisons, disease transmission, pathogenicity.


Abstract: Pigs can be infected with both human and avian influenza A virus (IAV) strains and are therefore considered to be important intermediates in the emergence of new IAV strains due to mixing of viral genes derived from human, avian, or porcine influenza viruses. These reassortant strains may have potential to cause pandemic influenza outbreaks in humans. The innate immune response against IAV plays a significant role in containment of IAV in the airways. We studied the interactions of IAV with porcine surfactant protein D (pSP-D), an important component of this first line defense system. Hemagglutination inhibition analysis shows that the distinct interactions of pSP-D with IAV mediated by the N-linked carbohydrate moiety in the carbohydrate recognition domain of pSP-D depend on the terminal sialic acids (SAs) present on this carbohydrate. Analysis by both lectin staining and by cleavage with linkage-specific sialidases shows that the carbohydrate of pSP-D is exclusively sialylated with alpha(2,6)-linked SAs, in contrast to surfactant protein A, which contains both alpha(2,3)- and alpha(2,6)-linked SAs on its N-linked carbohydrate. Enzymatic modification of the SA-linkages present on pSP-D demonstrates that the type of SA-linkage is important for its hemagglutination-inhibitory activity, and correlates with receptor-binding specificity of the IAV strains. The SAs present on pSP-D appear especially important for interactions with poorly glycosylated IAV strains. It remains to be elucidated to what extent the unique sialylation profile of pSP-D is involved in host range control of IAV in pigs, and whether it facilitates adaptation of avian or human IAV strains that can contribute to the production of reassortant strains in pigs.

Descriptors: influenza A virus metabolism, pulmonary surfactant associated protein D chemistry, sialic acids metabolism, swine, carbohydrate conformation, carbohydrate sequence, chickens, hemagglutination inhibition tests, molecular sequence data, molecular structure, neuraminidase metabolism, pulmonary surfactant associated protein A chemistry, pulmonary surfactant associated protein A metabolism, pulmonary surfactant associated protein D metabolism, pulmonary surfactants chemistry, receptors, cell surface, sialic acids chemistry.


NAL Call Number: 381 B523

Abstract: Unilamellar liposomes can be fused at low pH with the plasma membrane of cells that express the hemagglutinin glycoprotein of influenza virus on their surface [van Meer, G., & Simons, K. (1983) J. Cell Biol. 97, 1365-1374]. Here, we have resolved this fusion process into two kinetically distinct steps. The first and more rapid step converts the bound liposome to a form that can no longer be released by
neuraminidase. The second step is the actual membrane fusion as measured by the loss of resonance energy transfer between two liposomal fluorescent phospholipids, N-(7-nitro-2,1,3-benzoxadiazol-4-yl)dioleoylphosphatidylethanolamine (N-NBD-PE) and N-(lissamine rhodamine B sulfonfonyl)dioleoylphosphatidylethanolamine (N-Rh-PE). In contrast to the first step, the rate of the second one was highly dependent on the liposomal lipid composition and the cell type used. The replacement of 50% of the phosphatidylcholine (PC) in egg PC-cholesterol liposomes by unsaturated phosphatidylethanolamine (PE) species increased the rate of fusion at least 2-fold. Of the PE-containing liposomes that were associated with Madin-Darby canine kidney (MDCK) cells after 30 s of fusion, 80% had actually fused with the plasma membrane. Fringe pattern fluorescence photobleaching experiments showed that after fusion a fraction of the cell-associated N-Rh-PE diffused laterally in the plasma membrane. Without fusion, the N-Rh-PE was completely immobile. Under optimal conditions, the mobile fractions were 65% on MDCK cells and 78% on baby hamster kidney cells. The mobility was acquired simultaneously with the dilution of the fluorescent phospholipids as measured from the loss of resonance energy transfer. The mobile fraction of N-Rh-PE on the cell surface can therefore be used as a second independent measure of actual membrane fusion. Finally, we observed that upon fusion up to 80% of the nonexchangeable liposome markers cholesterol [14C]oleate and glycerol tri[14C]oleate became accessible to cellular hydrolases. The results showed that this hydrolysis assay can also be used to monitor the second step of the fusion process.

Descriptors: cell membrane physiology, influenza A virus avian physiology, liposomes, cell line, cell transformation, viral, cholesterol esters metabolism, dogs, energy transfer, hamsters, hydrogen-ion concentration, kidney, kinetics, neuraminidase, spectrometry, fluorescence.

van Meer, G. and K. Simons (1982). Viruses budding from either the apical or the basolateral plasma membrane domain of MDCK cells have unique phospholipid compositions. EMBO Journal 1(7): 847-52. ISSN: 0261-4189.

NAL Call Number: QH506.E46

Abstract: Influenza virus and vesicular stomatitis virus (VSV) obtain their lipid envelope by budding through the plasma membrane of infected cells. When monolayers of Madin-Darby canine kidney (MDCK) cells, a polarized epithelial cell line, are infected with fowl plague virus (FPV), an avian influenza virus, or with VSV, new FPV buds through the apical plasma membrane whereas VSV progeny is formed by budding through the basolateral plasma membrane. FPV and VSV were isolated from MDCK host cells prelabeled with [32P]orthophosphate and their phospholipid compositions were compared. Infection was carried out at 31 degrees C to delay cytopathic effects of the virus infection, which lead to depolarization of the cell surface. 32P-labeled FPV was isolated from the culture medium, whereas 32P-labeled VSV was released from below the cell monolayer by scraping the cells from the culture dish 8 h after infection. At this time little VSV was found in the culture medium, indicating that the cells were still polarized. The phospholipid composition of the two viruses was distinctly different. FPV was enriched in phosphatidylethanolamine and phosphatidylserine and VSV in phosphatidylcholine, sphingomyelin, and phosphatidylinositol. When MDCK cells were trypsinized after infection and replated, non-infected control cells attached to reform a confluent monolayer within 4 h, whereas infected cells remained in suspension. FPV and VSV could be isolated from the cells in suspension and under these conditions the phospholipid composition of the two viruses was very similar. We conclude that the two viruses obtain their lipids from the plasma membrane in the same way and that the different phospholipid compositions of the viruses from polarized cells reflect differences in the phospholipid composition of the two plasma membrane domains.

Descriptors: influenza A virus avian physiology, phospholipids analysis, vesicular stomatitis Indiana virus physiology, cell line, cell membrane microbiology, dogs, avian analysis, kidney, trypsin, vesicular stomatitis Indiana virus analysis.


NAL Call Number: 500 N21P

Abstract: The x-ray structure of a complex of sialic acid (Neu5Ac) with neuraminidase N9 subtype from A/tern/Australia/G70C/75 influenza virus at 4 degrees C has revealed the location of a second Neu5Ac
binding site on the surface of the enzyme. At 18 degrees C, only the enzyme active site contains bound Neu5Ac. Neu5Ac binds in the second site in the chair conformation in a similar way to which it binds to hemagglutinin. The residues that interact with Neu5Ac at this second site are mostly conserved in avian strains, but not in human and swine strains, indicating that it has some as-yet-unknown biological function in birds.

Descriptors: influenza A virus avian enzymology, n acetylneuraminic acid metabolism, neuraminidase chemistry, viral proteins chemistry, binding sites, computer simulation, crystallography, x-ray, models, molecular, molecular sequence data, neuraminidase metabolism, protein conformation, sequence homology, amino acid, surface properties, viral proteins metabolism.

NAL Call Number: 448.8 P942
Descriptors: influenza A virus avian, tissue culture, cell division, chromosome aberrations etiology, chromosome disorders, cytopathogenic effect, viral, embryo, virus cultivation.

NAL Call Number: QR360.A1J6
Descriptors: infection, fowl plague, infectious laryngotracheitis virus infection, immunofluorescence, immunologic techniques, western blot, genetic techniques.

NAL Call Number: 448.8 V81
Abstract: The hemagglutinin of influenza virus A/FPV/Rostock/34 (H7) was altered at its multibasic cleavage site by site-directed mutagenesis and assayed for proteolytic activation after expression in CV-1 cells. The results indicated that the cellular protease responsible for activation recognizes the tetrapeptide motif R-X-K/R-R that must be presented in the correct sequence position. Studies on plaque variants of influenza virus A/fowl/Victoria/75 (H7N7) showed that alteration of the consensus sequence resulted in a loss of pathogenicity for chickens.
Descriptors: fowls, avian influenza virus, viral hemagglutinins, proteinases, proteolysis, amino acid sequences, mutants, clones, pathogenicity, cleavae site.

NAL Call Number: 448.8 P942
Descriptors: antibodies, monoclonal isolation and purification, immunoenzyme techniques, antibodies, monoclonal analysis, antibody specificity, chick embryo, hybridomas immunology, influenza A virus avian immunology, isoelectric focusing, mice, rabbits.

NAL Call Number: QH506.A1M62
Abstract: Effect of antisense oligonucleotides on the in vitro translation of the influenza virus M1 protein mRNA was investigated. The most efficient arrest of mRNA translation was achieved by simultaneous action
of two or three oligonucleotides (14-16-mers) complementary to the juxtaposed sequences in the 5'-terminus of the molecule around and upstream of the initiation codon.

**Descriptors:** RNA, messenger genetics, RNA viral genetics, translation, genetic drug effects, viral matrix proteins genetics, autoradiography, base sequence, electrophoresis, polyacrylamide gel, influenza A virus avian metabolism, molecular sequence data, oligonucleotides, antisense pharmacology, rabbits.


**NAL Call Number:** 448.8 V81

**Abstract:** The synthesis of influenza A virus RNA and proteins represents a highly regulated process whereby variable amounts of early and late viral RNAs and proteins may be produced. This regulation is upset by the presence of the methyltransferase inhibitor 3-deazaadenosine (3DA-Ado) or the protein kinase inhibitor H7, resulting in complete or partial inhibition of synthesis of late proteins but normal production of early proteins. Although the total yield of viral mRNAs is somewhat reduced by treatment with 3DA-Ado, the mRNAs that are produced can still be translated in vitro. Both 3DA-Ado and H7 interfere specifically with the transport of the late viral mRNAs from the nucleus to the cytoplasm, but do not affect transport of early mRNA. From these results we conclude that during influenza virus replication, posttranscriptional regulation takes place on the level of mRNA transport. Since hemagglutinin mRNA migrates to the cytoplasm in the presence of 3DA-Ado plus cycloheximide, we assume that a viral protein is involved in the regulation mechanism.

**Descriptors:** cell nucleus metabolism, influenza A virus avian genetics, methyltransferases antagonists and inhibitors, protein kinases antagonists and inhibitors, RNA, messenger metabolism, RNA viral metabolism, 15 isoquinolinesulfonyl 2 methylpiperazine, biological transport drug effects, cell nucleus drug effects, chick embryo, avian enzymology, isoquinolines pharmacology, piperazines pharmacology, RNA, messenger drug effects, RNA viral drug effects, translation, genetic drug effects, tubercidin pharmacology.


**NAL Call Number:** 448.3 Ar23

**Abstract:** In primary chicken embryo cells infected with fowl plague virus addition of actinomycin D at defined times during the infection cycle has different consequences on viral replication. If actinomycin D is added immediately after infection with a concentration which inhibits viral RNA synthesis only partially, it interferes with the nucleo-cytoplasmic transport of all viral RNA species (mRNA and vRNA) so far tested. If actinomycin D is present during infection (adsorption, penetration and uncoating) no viral RNA is synthesized, and the nucleocapsid of the infecting virus does not reach the nucleus, as shown by fluorescent antibodies. Therefore the primary effect of actinomycin D on influenza virus replication is on the transport of the incoming vRNPs from the cytoplasm to the cell nucleus, which is the cell compartment where transcription takes place.

**Descriptors:** dactinomycin pharmacology, hemagglutinins viral genetics, influenza A virus avian genetics, RNA viral metabolism, biological transport drug effects, capsid metabolism, cell compartmentation, cell nucleus metabolism, cultured cells, chick embryo, cytoplasm metabolism, nucleoproteins metabolism, RNA, heterogeneous nuclear metabolism, RNA, messenger metabolism, tubercidin pharmacology, viral proteins biosynthesis, virus replication drug effects.


**NAL Call Number:** 448.3 Ar23

**Abstract:** The degree of genetic relatedness of vRNA segments 1, 2, and 3 of avian influenza A viruses was investigated by molecular hybridization. The results indicate that avian influenza A viruses isolated within a given geographic region are genetically more closely related than strains from different regions, irrespective of the year of isolation and the species from which the virus was isolated. Studies on RNA segment 4 of viruses within the subtype H7 isolated in different regions gave similar results. Thus the genetic composition of avian influenza A viruses appears to be maintained to a rather high degree within a
given geographic region and the intrusion of genes from "foreign regions" appears to be taking place with low frequency. The results are discussed with respect to the worldwide distribution of influenza virus genes by migrating birds.

Descriptors: genes viral, influenza A virus avian genetics, RNA viral genetics, recombination, genetic, Europe, Great Britain, avian classification, North America, nucleic acid hybridization.


NAL Call Number: QH301.Z4


NAL Call Number: 448.8 P942

Descriptors: influenza A virus avian drug effects, mutagens pharmacology, ethylenes pharmacology, ethylenes toxicity, genetics, microbial, imines pharmacology, imines toxicity, mathematics.


NAL Call Number: 448.8 P942

Abstract: The effect of remantadine in tissue culture of primary chick embryo fibroblasts (CEF) infected with classical fowl plague virus (FRV) was found to be dual. On the one hand, in low concentrations remantadine effectively inhibited in CEF reproduction of the virus sensitive to it. On the other, in high (subtoxic) concentrations in CEF infected with either sensitive or remantadine-resistant FPV variants it induced virus reproduction. The latter became noninfectious for normal CEF but retained its capacity for multiplication in cells treated with high concentrations of remantadine.


NAL Call Number: QR360.A1J6

Abstract: The haemagglutinin (HA) protein of fowl plague virus A/FPV/Rostock/34 (H7N1) contains three N-linked oligosaccharide side chains in its stem domain. These stem glycans, which are attached to the Asn residues at positions 12, 28 and 478, are highly conserved throughout all HA protein sequences analysed to date. In a previous study, in which mutant HA proteins lacking individual stem glycosylation sites had been expressed from an SV-40 vector, it was shown that these glycans maintain the HA protein in the metastable form required for fusion activity. In the present study, the functional role of the stem N-glycans for virus replication was investigated using recombinant influenza viruses generated by an RNA polymerase I-based system. Studies in Madin-Darby canine kidney cells and embryonated chickens’ eggs revealed that the N-glycan at Asn(12) is crucial for virus replication. In both culture systems, growth of virus lacking this glycan (mutant cg1) was completely blocked at 37 degrees C and inhibited at 33 degrees C. Loss of the glycan from Asn(478) (mutant cg3) caused less striking, but still measurable, effects. Interestingly, it was not
possible to generate mutant viruses containing the HA protein lacking the N-glycan at Asn(28). It is concluded from this that the N-glycan at Asn(28) is indispensable for the formation of replication-competent influenza viruses. When compared to viruses containing wild-type HA protein, mutants cg1 and cg3 showed a significantly decreased pH stability. Taken together, these data show that the HA stem glycans are potent regulators of influenza virus replication.

Descriptors: hemagglutinin glycoproteins, influenza virus chemistry, hemagglutinin glycoproteins, influenza virus metabolism, influenza A virus avian chemistry, avian physiology, polysaccharides metabolism, virus replication, asparagine metabolism, cell line, chick embryo, dogs, flow cytometry, genetic engineering, glycosylation, hemagglutinin glycoproteins, influenza virus genetics, hydrogen-ion concentration, avian genetics, models, molecular, mutation, oligosaccharides metabolism, protein conformation, RNA genetics, temperature.


NAL Call Number: QP552.G59G593

Abstract: Spodoptera frugiperda (Sf9)-cells differ markedly in their protein glycosylation capacities from vertebrate cells in that they are not able to generate complex type oligosaccharide side chains. In order to improve the oligosaccharide processing properties of these cells we have used baculovirus vectors for expression of human (beta 1,2-N-acetylglucosaminyltransferase I (hGNT-I), the enzyme catalysing the crucial step in the pathway leading to complex type N-glycans in vertebrate cells. One vector (Bac/GNT) was designed to express unmodified GNT-I protein, the second vector (Bac/tagGNT) to express GNT-I protein with a tag epitope fused to its N-terminus. In Sf9-cells infected with Bac/tagGNT-virus a protein of about 50 kDa representing hGNT-I was detected with an antiserum directed against the tag epitope. HGNT-I activity was increased at least threefold in lysates of infected cells when N-acetylglucosamine (GlcNAc)-free ovalbumine was used as substrate. To monitor hGNT-I activity in intact Sf9-cells, the glycosylation of coexpressed fowl plague virus hemagglutinin (HA) was investigated employing a galactosylation assay and chromatographic analysis of isolated HA N-glycans. Coexpression of hGNT-I resulted in an at least fourfold increase of HA carrying terminal GlcNAc-residues. The only structure detectable in this fraction was GlcNAcMan3GlcNAc2. These results show that hGNT-I is functionally active in Sf9-cells and that the N-glycans of proteins expressed in the baculovirus/insect cell system are elongated by coexpression of glycosyltransferases of vertebrate origin. Complete complex type oligosaccharide side chains were not observed when hGNT-I was overexpressed, thus supporting the concept that Sf9-cells do not contain glycosyltransferases acting after hGNT-I.

Descriptors: hemagglutinin viral biosynthesis, influenza A virus avian genetics, N-acetylglucosaminyltransferases genetics, polysaccharides biosynthesis, base sequence, carbohydrate conformation, carbohydrate sequence, cell line, cloning, molecular, DNA primers, hemagglutinins viral genetics, avian metabolism, molecular sequence data, N-acetylglucosaminyltransferases metabolism, recombinant proteins, Spodoptera.


NAL Call Number: QR360.J6

Abstract: The hemagglutinin (HA) of fowl plague virus A/FPV/Rostock/34 (H7N1) carries two N-linked oligosaccharides attached to Asn123 and Asn149 in close vicinity to the receptor-binding pocket. In previous studies in which HA mutants lacking either one (mutants G1 and G2) or both (mutant G1,2) glycosylation sites had been expressed from a simian virus 40 vector, we showed that these glycans regulate receptor binding affinity (M. Ohuchi, R. Ohuchi, A. Feldmann, and H. D. Klenk, J. Virol. 71:8377-8384, 1997). We have now investigated the effect of these mutations on virus growth using recombinant viruses generated by an RNA polymerase I-based reverse genetics system. Two reassortants of influenza virus strain A/WSN/33 were used as helper viruses to obtain two series of HA mutant viruses differing only in the neuraminidase (NA). Studies using N1 NA viruses revealed that loss of the oligosaccharide from Asn149 (mutant G2) or loss of both oligosaccharides (mutant G1,2) has a pronounced effect on virus growth in MDCK cells. Growth
of virus lacking both oligosaccharides from infected cells was retarded, and virus yields in the medium were decreased about 20-fold. Likewise, there was a reduction in plaque size that was distinct with G1,2 and less pronounced with G2. These effects could be attributed to a highly impaired release of mutant progeny viruses from host cells. In contrast, with recombinant viruses containing N2 NA, these restrictions were much less apparent. N1 recombinants showed lower neuraminidase activity than N2 recombinants, indicating that N2 NA is able to partly overrule the high-affinity binding of mutant HA to the receptor. These results demonstrate that N-glycans flanking the receptor-binding site of the HA molecule are potent regulators of influenza virus growth, with the glycan at Asn149 being dominant and that at Asn123 being less effective. In addition, we show here that HA and NA activities need to be highly balanced in order to allow productive influenza virus infection.

Descriptors: hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian growth and development, neuraminidase genetics, cattle, cell line, chickens, erythrocytes virology, glycosylation, hemagglutinin glycoproteins, influenza virus metabolism, avian genetics, avian metabolism, mutagenesis, site directed, neuraminidase metabolism, plaque assay, receptors, virus genetics, receptors, virus metabolism, recombination, genetic.


NAL Call Number: QR360.A1J6

Abstract: The virulence of avian influenza A viruses depends on the cleavability of the haemagglutinin (HA) by an intracellular protease at multiple basic amino acids. Although previous studies have demonstrated the importance of these amino acids for processing by the cellular protease, with emphasis on conserved residues near the cleavage site, the minimal requirements for cleavage remain unknown. By expressing site-specific mutants of the HA of a virulent avian influenza virus, A/turkey/Ireland/1378/85 (H5N8), in the simian virus 40 system and testing for their cleavability by an endogenous protease in CV-1 cells, and their fusion activity in a polykaryon formation assay, we were able to show that glycine at the amino terminus of HA2 is not essential for cleavage and that maximal cleavage requires at least five basic residues at the cleavage site, when carbohydrate is nearby. Moreover, we confirmed, that a conserved proline upstream of the cleavage site is not essential for HA cleavage or fusion activity, and that lysine replacement of the carboxyl-terminal arginine of HA1 abolishes cleavability. These findings should help identify the proteases responsible for intracellular cleavage of the HA of virulent avian influenza viruses.

Descriptors: conserved sequence genetics, hemagglutinins viral chemistry, influenza A virus avian chemistry, amino acid sequence, conserved sequence physiology, hemagglutinins viral genetics, hemagglutinins viral metabolism, avian metabolism, avian pathogenicity, molecular sequence data, mutation, virulence genetics.


NAL Call Number: QR360.J6

Abstract: The virulence of avian influenza viruses correlates with the sensitivity of their hemagglutinin (HA) to cellular proteases. Furin, a proprotein-processing subtilisin-related endoprotease, is a leading candidate for the enzyme that cleaves the HA of virulent avian viruses. We therefore compared the specificity of furin with those of proteases in a variety of cultured cells and in a rat Golgi fraction, using the HA cleavage mutants of a virulent avian influenza virus, A/Turkey/Ireland/1378/85 (H5N8). The results indicated similar sequence specificities among the endoproteases when purified furin was used. In experiments with the vaccinia virus expression system, overexpressed furin cleaved mutant HAs that were not recognized by the endogenous proteases, resulting in an apparent broader specificity of furin. These findings authenticate the proposed role of furin as an HA-activating protease in vivo and caution against the use of expression vectors to study protease sequence specificity.

Descriptors: hemagglutinins viral metabolism, influenza A virus avian metabolism, protein precursors metabolism, protein processing, post translational, subtilisins metabolism, amino acid sequence, cultured cells, Furin, Golgi apparatus enzymology, hemagglutinin glycoproteins, influenza virus, liver enzymology,

**NAL Call Number:** 448.8 V81

**Abstract:** H.-D. Klenk, W. Garten, and R. Rott (1984, EMBO J. 3, 2911-2915) have reported that hemagglutinin (HA) cleavage of virulent avian influenza viruses occurs in later steps of its intracellular transport and that the cleavage enzyme is calcium dependent and has a neutral pH optimum. The precise intracellular location of the HA cleavage, however, has never been established. Furthermore, because Klenk et al. used the whole cell lysate to examine the cleavage activity and the amino acid sequencing of the cleaved product was not done, the identity of the cleavage enzyme remains to be established. We therefore attempted to systematically characterize the HA cleavage of the virulent avian virus A/tern/South Africa/61 (H5N3). Using an inhibitor of glycoprotein transport (Brefeldin A) and temporal markers of glycoprotein processing, we found that the endoprotease responsible for the HA cleavage acts after the acquisition of endo-N-acetylglucosaminidase H resistance but before the addition of galactose to the molecule, and thus is located in the medial and/or trans Golgi. This observation was directly confirmed by in vitro experiments using rat liver subcellular membrane fractions containing Golgi complex. A fraction rich in galactosyltransferase (a trans Golgi marker) demonstrated the highest HA cleavage activity. The endoprotease in this fraction cleaved only the HA of the virulent avian influenza virus but not that of an avirulent virus. Through amino-terminal sequencing of the HA2 produced by digestion with the endoprotease in the rat Golgi fraction, we established that HA cleavage by the protease occurs at the authentic site. Further studies using the rat Golgi fraction showed that the HA cleavage enzyme is calcium dependent and has a low pH (6.0) optimum. Thus, the pH optimum of the enzyme in the Golgi fraction differs from that in whole cell lysate reported previously.

**Descriptors:** endopeptidases metabolism, hemagglutinins viral metabolism, influenza A virus avian metabolism, biological transport, cattle, cell line, cell membrane enzymology, electrophoresis, polyacrylamide gel, glycosylation, Golgi apparatus enzymology, hydrogen-ion concentration, avian physiology, liver enzymology, monensin pharmacology, protein precursors metabolism, rats, inbred strains, virus replication.


**NAL Call Number:** QR360.J6

**Abstract:** The influenza A virus M2 integral membrane protein has ion channel activity which can be blocked by the antiviral drug amantadine. The M2 protein transmembrane domain is highly conserved in amino acid sequence for all the human, swine, equine, and avian strains of influenza A virus, and thus, known amino acid differences could lead to altered properties of the M2 ion channel. We have expressed in oocytes of *Xenopus laevis* the M2 protein of human influenza virus A/Udorn/72 and the avian virus A/chicken/Germany/34 (fowl plague virus, Rostock) and derivatives of the Rostock ion channel altered in the presumed pore region. The pH of activation of the M2 ion channels and amantadine block of the M2 ion channels were investigated. The channels were found to be activated by pH in a similar manner but differed in their apparent Kis for amantadine block.

**Descriptors:** amantadine pharmacology, influenza A virus avian physiology, human physiology, ion channels drug effects, viral matrix proteins metabolism, amino acid sequence, fluorescent antibody technique, hydrogen-ion concentration, kinetics, mathematics, membrane potentials drug effects, models, biological, molecular sequence data, mutagenesis, site directed, oocytes drug effects, oocytes physiology, RNA, messenger metabolism, viral matrix proteins biosynthesis, viral matrix proteins drug effects, *Xenopus laevis*.


**NAL Call Number:** 41.8 Av5

**Descriptors:** antibodies, antigens, disease control, disease prevention, dosage, immune response, inactivated vaccines, vaccination, vaccine development, avian influenza virus, fowl, embryos.


**Abstract:** Clearance of infectious virus and RNA occurred concurrently after oral infection of ducks with influenza virus. There was no evidence from polymerase chain reaction (PCR) analysis of the hemagglutinin (HA) gene for persistence of viral genetic information. No detectable RNA was found in the spleen indicating processing of antigen near the site of replication.

**Descriptors:** ducks microbiology, fowl plague microbiology, influenza A virus avian genetics, RNA viral genetics, chronic disease, DNA probes, fowl plague genetics, avian isolation and purification, molecular sequence data, polymerase chain reaction, RNA viral isolation and purification, virus replication.


**Abstract:** To enhance the rapidity in diagnosing the spread of avian influenza virus (AIV) in chicken layer flocks, studies were initiated to develop more sensitive and specific immunological and molecular methods for the detection of AIV. In this study, the purification of the hemagglutinin protein (H) from field isolates of H7N2, the production of monoclonal antibodies (MAbs), and their evaluation as diagnostic reagents are reported. Hybridomas were generated by fusion of SP2/0-Ag14 myelomas and spleen cells from immunized mice. Hybridomas secreting antibodies specific for the H protein were assayed by an ELISA and cloned using limiting dilution. The MAbs produced were characterized by hemagglutination inhibition (HI), immunohistochemistry (IHC), indirect fluorescent antibody assay (IFA), Western blots, and IFA flow cytometry using various AIV subtypes (i.e., H4N2, H5N3, H7N2). Of the various MAbs assayed, 6 had consistent and reproducible results in each of the assays used. The results obtained in this investigation enhanced the usage of the MAbs to viral H protein in the surveillance of AIV in chickens.

**Descriptors:** antibodies, monoclonal diagnostic use, fowl plague diagnosis, hemagglutinin glycoproteins, influenza virus immunology, influenza A virus avian isolation and purification, poultry diseases diagnosis, antibodies, monoclonal biosynthesis, blotting, western, chickens, fluorescent antibody technique, indirect, hemagglutination inhibition tests, hybridomas, immunohistochemistry, avian immunology, mice, poultry diseases virology.


**NAL Call Number:** QR1.C8

**Descriptors:** hemagglutinins viral analysis, hemagglutinins viral immunology, influenza A virus avian immunology, human immunology, amino acid sequence, base sequence, epitopes, genes viral, avian genetics, human genetics, macromolecular systems, protein conformation, variation genetics.


**NAL Call Number:** QR360.A1J6

**Abstract:** The haemagglutinin chains HA1 and HA2 from the avian influenza virus A/duck/Ukraine/1/63
(Hav7, Neq2) have been subjected to amino acid analysis and N-terminal sequencing. Automated sequenator analysis of HA1 (40 cycles), after enzymic removal of the N-terminal pyroglutamic acid blocking group, and HA2 (43 cycles) showed that the Hav7 haemagglutinin closely resembled the human Hong Kong (H3) haemagglutinins including the presence of the characteristic extended 10 residue sequence at the N-terminus of HA1. These findings, together with the amino acid compositions for both chains, demonstrate that the Hav7 haemagglutinin is structurally similar to the Hong Kong (H3) haemagglutinins.

Descriptors: hemagglutinins viral classification, influenza A virus avian immunology, human immunology, amino acid sequence, amino acids analysis, hemagglutinins viral analysis.


NAL Call Number: SF995.W4
Descriptors: Newcastle disease virus, nucleoproteins, chickens, immune response.


NAL Call Number: 381 J824
Abstract: Fusion of influenza virus with target membranes is induced by acid and involves complex changes in the viral fusion protein hemagglutinin. At 0 degree C, in a first kinetically resolvable step, the hemagglutinin polypeptide 2 (HA2) N-terminal segment (fusion peptide) is exposed and inserts into the target membrane (Tsurudome, M., Gluck, R., Graf, R., Falchetto, R., Schaller, U., and Brunner, J. (1992) J. Biol. Chem. 267, 20225-20232). We now report studies of the changes taking place at pH 5.0 and 37 degrees C, conditions that result in fusion or, in the absence of a target membrane, in inactivation of the virus' fusion capacity. To this end, we synthesized the new photosensitive phospholipid, 1-palmitoyl-2-[decanediol mono-[2-(125I)iodo-4-(3-trifluoromethyl-3H-diazirin-3-yl)-benzyl]ester]-sn-glycero-3-phosphocholine (specific radioactivity, > 2000 Ci/mmol), and worked out a protocol to incorporate this lipid into the viral membrane. Subsequent photoactivation of the reagent resulted in selective labeling of the C-terminal portion of the HA2 polypeptide chain, in agreement with the membrane topology of hemagglutinin. When, however, prior to reagent activation, the viruses were exposed at pH 5.0, 37 degrees C, both the HA2 C-terminal and the N-terminal regions were labeled, suggesting that the HA2 N-terminal segment (fusion peptide) inserted into the viral membrane. Possible implications for fusion and virus inactivation are discussed.

Descriptors: hemagglutinins viral metabolism, hydrogen-ion concentration, influenza A virus avian physiology, membrane fusion, azirines chemical synthesis, chick embryo, hemagglutinin glycoproteins, influenza virus, iodine radioisotopes, kinetics, liposomes, peptide fragments metabolism, phosphatidylcholines chemical synthesis, radioisotope dilution technique, temperature, viral envelope proteins metabolism.


NAL Call Number: 448.8 V81
Descriptors: orthomyxoviridae isolation and purification, recombination, genetic, antigens, heterophile, chickens, epitopes, genetics, microbial, hemagglutination inhibition tests, hemagglutinins viral analysis, hybridization, genetic, immunization, influenza A virus avian enzymology, avian immunology, lung, neuraminidase, neutralization tests, orthomyxoviridae enzymology, orthomyxoviridae immunology, tissue extracts, turkeys, viral vaccines.


NAL Call Number: 448.8 V81
Descriptors: orthomyxoviridae immunology, recombination, genetic, selection genetics, antibody formation, antigens, viral, chickens, hemagglutinins viral immunology, immunization, immunization, secondary,
influenza A virus avian immunology, neuraminidase immunology, turkeys.


**Descriptors:** orthomyxoviridae enzymology, orthomyxoviridae growth and development, orthomyxoviridae immunology, orthomyxoviridae isolation and purification, orthomyxoviridae pathogenicity, recombination, genetic, antigens analysis, centrifugation, density gradient, chick embryo, fetal membranes, fibroblasts, hemagglutination inhibition tests, hemagglutination tests, hemagglutinins viral analysis, hybridization, genetic, immune sera, influenza microbiology, influenza A virus avian enzymology, avian growth and development, avian immunology, avian pathogenicity, lung microbiology, neuraminidase analysis, rabbits, sucrose, swine, tissue culture, turkeys, virulence, virus replication.


**Descriptors:** influenza A virus physiology, orthomyxoviridae infections veterinary, pinnipedia microbiology, seals microbiology, antigens, viral analysis, birds microbiology, conjunctivitis etiology, genes viral, influenza A virus avian immunology, influenza A virus isolation and purification, mammals microbiology, orthomyxoviridae infections microbiology, RNA viral genetics, virus replication.


**Abstract:** One of the unresolved questions concerning the acquisition of virulence by the A/Chicken/Pennsylvania/83 (H5N2) influenza virus is which gene segments other than the hemagglutinin (HA) showed changes that were relevant. To answer this question, reassortants were made possessing the hemagglutinin gene of the virulent virus and the seven other genes from the avirulent parent. Since both the virulent and avirulent H5N2 strains are antigenically almost indistinguishable, it was necessary to transfer the genes of interest to a "carrier" virus before the appropriate reassortment could be selected. The gene compositions of the reassortants was established by a combination of sequence analysis and migration on polyacrylamide gels. These analyses established that the avirulent influenza virus present in April 1983 possessed seven of the eight gene segments necessary for virulence; mutation(s) in the HA gene were required for acquisition of virulence. Other viruses such as A/Seal/Mass/1/80 (H7N7) could provide the other genes necessary for virulence. Two changes in the HA have been associated with the acquisition of virulence; these are at amino acid residues 23 and 78 (H3 numbering) (Y. Kawaoka and R.G. Webster, Virology, 146, 130-137 (1985). Isolation of an amantadine-resistant avirulent revertant virus provided the opportunity to determine which of the two amino acid changes in HA is critical. Sequence analysis of the revertant virus revealed amino acid changes at residues 23 in HA1 and 40 in HA2 (H3 numbering). The change at residue 23 of HA1 is probably associated with reversion to avirulence, of cleavability of HA, and inability to plaque in tissue culture without trypsin; while the change at residue 40 of HA2 may be associated with the amantadine-resistant phenotype. These studies establish that a single critical point mutation in the hemagglutinin gene of the avirulent A/Chicken/Pennsylvania/1/83 (H5N2) was probably all that was required to produce the highly virulent Chicken/Pennsylvania virus; the avirulent virus already possessed the other genes necessary for virulence.

**Descriptors:** hemagglutinins viral genetics, influenza A virus avian pathogenicity, amino acid sequence,
culturated cells, chick embryo, chickens, genes viral, avian enzymology, avian genetics, avian immunology, mutation, neuraminidase genetics, plaque assay, recombination, genetic, virulence.


**Abstract:** Fowlpox virus (FPV) recombinants expressing influenza virus H5 haemagglutinin (HA), nucleoprotein (NP) or co-expressing both of these antigens were tested for vaccine efficacy in chickens. Immunization with the recombinant FPV-HA was highly efficacious but provided no cross protection between subtypes. Bursectomy established that immunity against the H5 subtype was antibody-mediated despite the presence of very low levels of antibody in the vaccinated birds. Immunization with the recombinant FPV expressing the cross-reactive NP antigen did not provide protective immunity despite hyperimmunization and provided no benefit above HA expressed alone. The results suggest that the kinetics of viral replication outpaces immunity induced by NP.

**Descriptors:** antigens, viral administration and dosage, fowl plague prevention and control, fowlpox virus immunology, viral vaccines administration and dosage, chickens, cross reactions, fowlpox virus genetics, hemagglutinins viral immunology, immunity, cellular, influenza A virus avian genetics, avian immunology, nucleoproteins immunology, vaccines, synthetic administration and dosage, viral proteins immunology.


**Descriptors:** agglutinins, hemagglutinins, orthomyxoviridae immunology, birds microbiology, turkeys microbiology.


**Descriptors:** Newcastle disease, fowlpox, avian influenza virus, prevention, control, Southern blot, gene sequence analysis, indirect immunofluorescence assay, polymerase chain reaction, PCR.


**Descriptors:** antiviral agents chemical synthesis, quinoxalines chemical synthesis, enterovirus drug effects, herpesvirus 1, suid drug effects, influenza A virus avian drug effects, quinoxalines pharmacology, sindbis virus drug effects, vaccinia virus drug effects.


**Abstract:** A simple assay is described to monitor fusion between fowl plague virus (FPV, an avian influenza A virus) and liposomes which allows the simultaneous quantitation of both lytic and non-lytic fusion events. As in fusion between viruses and the plasma membrane and in FPV-induced cell-cell fusion, the reaction only occurs at pH 5.5 or below, and it is fast, highly efficient, and essentially non-lytic when fresh virus and liposomes are used. The fusion occurs over a broad temperature range, and has no requirement for divalent cations. The fusion factor of influenza virus is a hemagglutinin (HA) spike which protrudes from the virus membrane and which is also responsible for virus binding to the host cell. The finding that fusion occurs as efficiently with liposomes containing or lacking virus receptor structures, further emphasizes the remarkable division of labor in the HA molecule: the receptor-binding sites are located in the globular HA1 domains and the fusion activation peptide is found at the N-terminal of HA2 in the stem region of the protein. The mechanism of fusion is discussed in terms of the three-dimensional structure of the HA and the
conformational change which the protein undergoes at the fusion pH optimum.

**Descriptors:** influenza A virus avian physiology, liposomes, membrane fusion, chick embryo, hemagglutinins viral, hydrogen-ion concentration, microscopy, electron, temperature, time factors, trypsin metabolism, trypsin inhibitor, kunitz soybean pharmacology.


**NAL Call Number:** 442.8 J828

**Abstract:** Representatives of three families of enveloped viruses were shown to fuse tissue culture cells together. These were: Semliki Forest virus (SFV, a togavirus), vesicular stomatitis virus (a rhabdovirus), and two myxoviruses, fowl plaque virus and Japan influenza virus (Japan)/A/305/57). Unlike paramyxoviruses, whose fusion activity is known to occur over a broad pH range, fusion by these viruses was restricted to mildly acidic pH. The pH thresholds for the four viruses were 6.0, 6.1, 5.5, and 5.1, respectively. The precursor form of Japan influenza, which is not infectious and which contains the uncleaved hemagglutinin, had no fusion activity. This result suggested a role for the influenza hemagglutinin in the low-pH-dependent membrane fusion activity. Taken together, our results show that low-pH-induced fusion is a widespread property of enveloped animal viruses and that it may play a role in the infective process. The fusion reactions with all four viruses were fast, efficient, and easy to induce. With UV-inactivated SFV, the fusion was shown to be nonlytic and the polykaryons were viable for at least 12 h. 30 ng of SFV/1 x 10(6) BHK-21 cells were required for 50% fusion, and 250 ng sufficed to fuse the entire culture into a single polykaryon.

**Descriptors:** cell fusion, influenza A virus avian physiology, human physiology, Semliki Forest virus physiology, vesicular stomatitis Indiana virus physiology, cell line, cell survival, hamsters, hemagglutinin viral, hydrogen-ion concentration.


**NAL Call Number:** QR360.J6

**Abstract:** Wild aquatic birds are the primary reservoir of influenza A viruses, but little is known about the viruses' gene pool in wild birds. Therefore, we investigated the ecology and emergence of influenza viruses by conducting phylogenetic analysis of 70 matrix (M) genes of influenza viruses isolated from shorebirds and gulls in the Delaware Bay region and from ducks in Alberta, Canada, during >18 years of surveillance. In our analysis, we included 61 published M genes of isolates from various hosts. We showed that M genes of Canadian duck viruses and those of shorebird and gull viruses in the Delaware Bay shared ancestors with the M genes of North American poultry viruses. We found that North American and Eurasian avian-like lineages are divided into sublineages, indicating that multiple branches of virus evolution may be maintained in wild aquatic birds. The presence of non-H13 gull viruses in the gull-like lineage and of H13 gull viruses in other avian lineages suggested that gulls' M genes do not preferentially associate with the H13 subtype or segregate into a distinct lineage. Some North American avian influenza viruses contained M genes closely related to those of Eurasian avian viruses. Therefore, there may be interregional mixing of the two clades. Reassortment of shorebird M and HA genes was evident, but there was no correlation among the HA or NA subtype, M gene sequence, and isolation time. Overall, these results support the hypothesis that influenza viruses in wild waterfowl contain distinguishable lineages of M genes.

**Descriptors:** animals, wild virology, birds virology, ecology, evolution, molecular, influenza A virus, avian genetics, viral matrix proteins genetics, ducks virology, avian classification, avian isolation and purification, molecular sequence data, phylogeny, sequence analysis, DNA.


**NAL Call Number:** QH301.Z4

**Descriptors:** orthomyxoviridae enzymology, ribonucleases analysis, deoxyribonucleases metabolism, hemagglutination, influenza A virus avian enzymology, Newcastle disease virus enzymology, polioviruses enzymology, ribonucleases metabolism.

**NAL Call Number:** 442.8 J828

**Descriptors:** cell transformation, neoplastic drug effects, actinomycin pharmacology, cell line, cell nucleus metabolism, clone cells, actinomycin metabolism, hamsters, influenza A virus avian growth and development, kidney, RNA antagonists and inhibitors, RNA biosynthesis, RNA, neoplasm biosynthesis, tritium, uridine metabolism, virus replication drug effects.


**NAL Call Number:** QR360.J6

**Abstract:** Virus-specific protein and RNA syntheses have been analyzed in chicken embryo fibroblast cells infected with two group IV temperature-sensitive (ts) mutants of influenza A (fowl plague) virus in which the ts lesion maps in RNA segment 8 (J. W. Almond, D. McGeoch, and R. D. Barry, Virology 92:416-427, 1979), known to code to code for two nonstructural proteins, NS1 and NS2. Both mutants induced the synthesis of similar amounts of all the early virus-specific proteins (P1, P2, P3, NP, and NS1) at temperatures that were either permissive (34 degrees C) or nonpermissive (40.5 degrees C) for replication. However, the synthesis of M protein, which normally accumulates late in infection, was greatly reduced in ts mutant-infected cells at 40.5 degrees C compared to 34 degrees C. The NS2 protein was not detected at either temperature in cells infected with one mutant (mN3), and was detected only at the permissive temperature in cells infected with mutant ts47. There was no overall reduction in polyadenylated (A+) complementary RNA, which functions as mRNA, in cells infected with these mutants at 40.5 degrees C compared to 34 degrees C, nor was there any evidence of selective accumulation of this type of RNA within the nucleus at the nonpermissive temperature. No significant differences in ts mutant virion RNA transcriptase activity were detected by assays in vitro at 31 and 40.5 degrees C compared to wild-type virus. Virus-specific non-polyadenylated (A-) complementary RNA, which is believed to act as the template for new virion RNA production, accumulated normally in cells at both 34 and 40.5 degrees C, but at 40.5 degrees C accumulation of new virion RNA was reduced by greater than 90% when compared to accumulation at 34 degrees C.

**Descriptors:** influenza A virus avian metabolism, RNA viral biosynthesis, viral proteins biosynthesis, chick embryo, chromosome mapping, DNA directed RNA polymerases metabolism, fibroblasts, avian genetics, mutation, temperature, viral nonstructural proteins.


**NAL Call Number:** 448.3 Ar23

**Abstract:** The deduced amino acid sequences of the haemagglutinins of avian influenza viruses, isolated from an outbreak in turkeys in Norfolk, England in 1991/92, were determined by PCR amplification and cycle sequencing. Both the highly pathogenic and avirulent isolates had the same cleavage site sequence with multiple-basic amino acids, which normally would be expected only for the former. Clones derived by plaque picking from the highly pathogenic isolate ranged from low to very high pathogenicity in vivo and these, and the original isolates, showed nucleotide and amino acid variation at one or more of five possible sites, none of which were at the cleavage site. None of these site variations correlated with pathogenicity, suggesting that the factor responsible for the suppression of the expected effects of the multiple-basic amino acid haemagglutinin cleavage site in the avirulent isolate may not have been part of the haemagglutinin amino acid sequence.

**Descriptors:** disease outbreaks veterinary, fowl plague microbiology, hemagglutinins viral genetics, influenza A virus avian genetics, poultry diseases microbiology, turkeys microbiology, amino acid sequence, base sequence, DNA, viral, England epidemiology, fowl plague epidemiology, hemagglutinin glycoproteins, influenza virus, molecular sequence data, poultry diseases epidemiology, RNA.

Wood, G.W., J. Banks, I. Strong, G. Parsons, and D.J. Alexander (1996). An avian influenza of H10 subtype that is highly pathogenic for chickens, but lacks multiple basic amino acids at the haemagglutinin
Abstract: Avian influenza virus isolate A/mandarin duck/Singapore/805/F-72/7/93 was found to be consistently highly pathogenic by recognised in vivo testing procedures although it was of a subtype (H10) not usually associated with high pathogenicity. The virus was also not typical of highly pathogenic influenza viruses in that it was not pathogenic when administered intra-nasally, did not possess a haemagglutinin cleavage site with multiple basic amino acids and did not replicate in the brains of chickens after intravenous inoculation. A re-examination of the earlier H10 isolate A/turkey/England/384/79 suggested that it was similarly pathogenic. The pathogenicity may have been associated with replication in the kidney.

Descriptors: chickens, avian influenza virus, pathogenicity, amino acids, nucleotide sequences, amino acid sequences, viral replication, animal tissues, molecular sequence data.


Abstract: The amino acid sequences at the haemagglutinin cleavage sites of 9 avian influenza A viruses of H5 subtype (5 high and 4 low pathogenicity for chickens) and 21 of H7 subtype (13 high and 8 low pathogenicity for chickens) were determined by direct RNA sequencing, PCR amplification sequencing or both. None of the viruses of low pathogenicity had multiple basic amino acids at the cleavage site. All highly pathogenic viruses had an insert of basic amino acids at the cleavage site, except A/chicken/Scotland/59 (H5N1) for which the multiple basic amino acids appeared as substitutions and not insertions. All highly pathogenic viruses examined conformed to the amino acid motif of R-X-R/K-R at the cleavage site which is considered to be essential for high pathogenicity in chickens, with the notable exception of highly pathogenic virus A/turkey/England/50-92/91 (H5N1) which had the sequence R-K-R-K-T-R adjacent to the cleavage site.

Descriptors: hemagglutinins viral genetics, influenza A virus avian genetics, amino acid sequence, base sequence, birds, chick embryo, chickens, hemagglutinin glycoproteins, influenza virus, avian classification, molecular sequence data, oligodeoxyribonucleotides, polymerase chain reaction, sequence homology, amino acid, sequence homology, nucleic acid, turkeys, viral envelope proteins genetics.


Abstract: Ten specific pathogen free light breed chickens and 10 commercial layer ducks were inoculated intranasally with one of five avian influenza A viruses which had been characterised as showing high or low pathogenicity for chickens. Recovery of the two viruses of low pathogenicity was restricted to the respiratory tract and gut of both species. Highly pathogenic viruses were recovered from all organs sampled. With two of the highly pathogenic viruses, A/duck/Ireland/113/83 (H5N8) and A/chicken/Victoria/85 (H7N7), the sites of recovery in ducks were similar to those seen in chickens except that virus was absent from the brain, apart from low levels detected in brain samples taken on day 5 from ducks infected with A/duck/Ireland/113/83. The levels recovered from organs of ducks for these two viruses were also similar to those in chickens, except for lower levels in kidney and liver for ducks infected with A/chicken/Victoria/85, and a delayed peak of recovery of both viruses in ducks. The third highly pathogenic virus, A/turkey/England/50-92/91 (H5N1), could not be recovered from any site in ducks. For all three highly pathogenic viruses mortality and morbidity were rapid and complete in chickens but absent in ducks.

Descriptors: animal husbandry, digestive system, infection, methods and techniques, nervous system, respiratory system, urinary system, veterinary medicine, brain gut kidney liver morbidity mortality pathogenicity respiratory tract.

Abstract: Neplanocin A (NeplA) and 3-deazaadenosine (3DA-Ado) are both inhibitors of methyltransferases, and both interfere with influenza virus replication. Their modes of action, however, are different. In chicken embryo cells NeplA inhibits only in media depleted of or low in methionine, while 3DA-Ado acts independently of the concentration of methionine. While homocysteine partially reverses the effect of NeplA, it strongly potentiates the effect of 3DA-Ado. While NeplA inhibits the synthesis of all viral proteins to nearly the same extent, 3DA-Ado interferes only with the production of late proteins (Fischer et al. (1990) Virology 177, 523-531). In NeplA-pretreated cells there is an extreme accumulation of S-adenosylhomocysteine, independent of the concentration of methionine in the medium, although NeplA inhibits influenza virus replication only in methionine-depleted medium. Therefore an accumulation of this intermediate by NeplA cannot account for the inhibitory effect, as has been implicated in the inhibition of the replication of other viruses. Our results indicate that at least two different methyltransferases are involved in influenza virus replication.

Descriptors: adenosine analogs and derivatives, influenza A virus avian drug effects, human drug effects, methyltransferases antagonists and inhibitors, tubercidin pharmacology, virus replication drug effects, adenosine antagonists and inhibitors, adenosine pharmacology, adenosylhomocysteinase, chick embryo, drug synergism, homocysteine pharmacology, hydraslamises antagonists and inhibitors, avian physiology, human physiology, methionine metabolism, RNA caps metabolism, RNA viral metabolism, S-adenosylhomocysteine metabolism, viral proteins biosynthesis, viral proteins genetics.
Ten influenza virus isolates were obtained from infected pigs from different places in Shandong province showing clinical symptoms from October 2002 to January 2003. All 10 isolates were identified in China's National Influenza Research Center as influenza A virus of H9N2 subtype. The complete genome of one isolate, designated A/Swine/Shandong/1/2003(H9N2), was sequenced and compared with sequences available in GenBank. The results of analyses indicated that the sequence of A/Swine/Shandong/1/2003(H9N2) was similar to those of several chicken influenza viruses and duck influenza viruses recently prevalent in South China. According to phylogenetic analysis of the complete gene sequences, A/Swine/Shandong/1/2003(H9N2) possibly originated from the reassortment of chicken influenza viruses and duck influenza viruses. It was found that the amino acid sequence at the HA cleavage site in Sw/SD/1/2003 is R-S-L-R-G, differing clearly from that of other H9N2 subtype isolates of swine influenza and avian influenza, which is R-S-S-R-G.

Descriptors: influenza veterinary, influenza A virus, porcine genetics, swine diseases virology, amino acid sequence, base sequence, chick embryo, guinea pigs, influenza virology, porcine chemistry, porcine isolation and purification, molecular sequence data, phylogeny, RNA, viral chemistry, viral genetics, rats, reverse transcriptase polymerase chain reaction veterinary, sequence analysis, DNA, sequence homology, nucleic acid, swine.


Descriptors: geese virology, hemagglutinin glycoproteins, influenza virus genetics, influenza virology, influenza A virus avian genetics, human genetics, chickens virology, DNA, viral chemistry, DNA, viral genetics, disease outbreaks, fowl plague epidemiology, fowl plague virology, genes viral, Hong Kong epidemiology, influenza epidemiology, avian classification, avian isolation and purification, human classification, molecular sequence data, neuraminidase genetics, phylogeny, sequence analysis, DNA, viral nonstructural proteins genetics.


Descriptors: antigens, viral immunology, hemagglutinins viral immunology, influenza A virus avian
immunology, human immunology, antibodies, monoclonal immunology, antigens, viral genetics, genes viral, hemagglutinins viral genetics, avian genetics, human genetics, variation genetics.


**Abstract:** The reversed single-radial-immunodiffusion (r-SRD) test using the avian-origin influenza A virus, A/chicken/Germany "N'/49 (Hav2Neql) disrupted with 1.0% sarkosyl, was established as the quantitative method for the assay of a type-specific antibody, particularly of an anti-nucleoprotein antibody, in human sera. Under the test conditions, human sera produced a definite opalescent zone around the well and the annulus area was found to have a high correlation to the antibody level of type A influenza nucleoprotein. The specificity of the opalescent zone produced in the test plate was confirmed with the specific antisera to each viral polypeptide and the adsorption procedures with the purified nucleoprotein. During an epidemic of H3N2 and H1N1 viruses, the r-SRD test was employed to estimate the infection ratio in junior high school students. The results demonstrated its convenience and high sensitivity in detecting the antibody rise to influenza A nucleoprotein. In addition, the age-distribution of the antibody level to influenza A nucleoprotein was examined and discussed. The results obtained strongly suggested that the r-SRD technique using the avian-origin influenza A virus provided a simple and reproducible method for the assay of the antibody level to influenza A nucleoprotein in a large scale seroepidemiology and in the serodiagnosis of influenza A virus infection.

**Descriptors:** antibodies, viral analysis, immunodiffusion methods, influenza A virus immunology, nucleoproteins immunology, viral proteins immunology, adolescent, adult, age factors, aged, child, complement fixation tests, hemagglutination inhibition tests, influenza immunology, middle aged.


**NAL Call Number:** 41.8 Av5

**Abstract:** A comparative study of the hemagglutinin (HA) receptor binding site (RBS) of a number of H13 influenza viruses isolated from Laridae family of birds (gulls) and other influenza viruses obtained from the Anatidae family (ducks) was conducted. The affinity of all viruses to alpha N-acetylneuraminic acid (Neu5Acalpha), 3'sialyllactose (3'SL), and sialylglycopolymers bearing 3'-sialyl(N-acetyllactosamine) (3'SLN-PAA), (Neu5Acalpha(2-3)Galbeta(1-4))(Fucalpha(1-3))GlcNAcbeta (SLex-PAA), and (Neu5Acalpha(2-3)Galbeta(1-3))(Fucalpha(1-4))GlcNAcbeta (SLea-PAA), was determined. The last three polymer glycoconjugates were synthesized for determining the contribution of carbohydrate chains after the galactose link to the binding with the receptor. The difference in affinity between 3'SL and Neu5Acalpha in all studied H13 viruses is small, which indicates a less significant role of the galactose moiety in the binding to the receptor. The results of virus binding with polymer sialylglycoconjugates indicates that the method of linking, the third monosaccharide moiety, and the presence of an extra fucose substitute in this moiety may influence the binding considerably. For viruses isolated from ducks, the suitable polymer is SLea-PAA (i.e., a 1-3 linkage between galactose and glucosamine is optimal). This finding is in accord with the data that H13 viruses isolated from the gulls differ based on their ability to interact with polymer sialylglycoconjugates. The affinity to all three polymers is uniform, and the presence of GlcNAc-linked fucose does not prevent the binding. A comparative analysis of six sequenced HA H13 viruses and other subtype viruses showed presence of substantial differences in the composition of amino acids of this region in H13 viruses.

**Descriptors:** biochemistry and molecular biophysics, infection, virology, avian influenza, infectious disease, respiratory system disease, viral disease, viral binding affinity.


**NAL Call Number:** QR360.J6

**Abstract:** Reverse genetics was used to analyze the host range of two avian influenza viruses which differ
in their ability to replicate in mouse and human cells in culture. Engineered viruses carrying sequences encoding amino acids 362 to 581 of PB2 from a host range variant productively infect mouse and human cells.

Descriptors: influenza A virus avian genetics, viral proteins genetics, cell line, genes viral, avian chemistry, avian pathogenicity, mice, sequence analysis, protein, species specificity, transfection.


NAL Call Number: 47.8 Ar2

Descriptors: avian influenza virus, disinfectants, formaldehyde, formic acid, potency, temperature, poultry.


NAL Call Number: 41.8 V6446

Descriptors: avian influenza virus, immune serum, hemagglutination, inhibition, antisera.


NAL Call Number: 448.8 P942

Abstract: A combination of electrophoresis in a single plate of polyacrylamide gel with preparative production of subunits upon electrophoresis in acetate cellulose was used for the analysis of the polypeptide composition of the A/turkey/Wisconsin/66 strain. Seven classes of proteins with certain functional significance and 4 minor components were detected. A preparation of neuraminidase could be obtained which has enzymatic and antigenic activity, and a molecular mass of 68,000 daltons. Some features of the polypeptide composition were revealed, including the presence of uncleaved hemagglutinin under reducing conditions and a decreased content of the light chain of hemagglutinin.

Descriptors: influenza A virus avian analysis, neuraminidase isolation and purification, viral proteins analysis, electrophoresis, cellulose acetate, electrophoresis, polyacrylamide gel, hemagglutination, viral, avian enzymology, molecular weight, peptides analysis.


NAL Call Number: 448.8 P942

Abstract: Nine strains having neuraminidase of subtype N1 and two strains in which the appurtenance of neuraminidase to subtype N1 was determined in the course of the study were examined for the antigenic specificity of the functional center of the enzyme in the cross neuraminidase activity inhibition test. Neuraminidase of the strains A/Swine/Tatarstan/64 and A/Swine/Iskshurmsk was shown to belong to the subtype N1 but to differ from neuraminidase of the strain A/Swine/Iowa/15/30. Neuraminidase of the strain A/Chicken/USSR/314/67 differs from neuraminidases of A/PR8/34, A/WS/33, and A/Swine/Iowa/15/30 but is related to neuraminidases of the strains A/New Jersey/8/76, A/duck/Germany/1868/68 and A/Chicken/Scotland/59. The A/New Jersey/8/76 neuraminidase is not related to neuraminidases of the strains A/PR8/34 and A/WS/33 but is related to neuraminidases of strains isolated from swine and domestic fowl. The disclosed considerable strain variations in the antigenic specificity of neuraminidases attest to heterogeneity of the subtype N1 and the possibility of its subdivision into groups.

Descriptors: antigens, viral, influenza A virus enzymology, binding sites, antibody, epitopes, avian enzymology, human enzymology, influenza A virus, porcine enzymology, influenza A virus immunology, species specificity.
ISSN: 0507-4088. NAL Call Number: 448.8 P942

**Abstract:** Antigenic relationships between human influenza A viruses containing hemagglutinins of HO and H1 subtypes and animal and avian influenza viruses Hsw1 and Hav5 were studied by immunoadsorption using inorganic base of the sorbent. Direct and indirect relations due to the presence in hemagglutinin of common antigenic determinants and hapten groups were revealed. The strains representing drift variations within one subtype differed by the spectrum of hapten determinants typical of other subtypes. No common determinant typical for all members of this group was isolated.

**Descriptors:** antigens, viral analysis, hemagglutinins viral analysis, influenza A virus avian immunology, human immunology, porcine immunology, influenza A virus immunology, epitopes analysis, hemagglutination inhibition tests, immunosorbent techniques.

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NAL Call Number: QR360.A1J6

**Descriptors:** alpharetrovirus, DNA, viral biosynthesis, influenza A virus avian drug effects, avian radiation effects, sarcoma viruses, avian, cell line metabolism, cell line radiation effects, cell transformation, neoplastic, chick embryo, DNA metabolism, dactinomycin pharmacology, hamsters, kidney, virus replication.

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NAL Call Number: 448.3 AC85

**Descriptors:** hybridization, genetic, influenza A virus avian immunology, phenotype, vesicular stomatitis Indiana virus immunology, antigens, viral analysis, cattle, centrifugation, density gradient, chick embryo, genetics, microbial, heat, hemolytic plaque technique, immune sera, avian growth and development, avian isolation and purification, neutralization tests, rabbits, sucrose, tissue culture, vesicular stomatitis Indiana virus growth and development, vesicular stomatitis Indiana virus isolation and purification, virus cultivation.

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**Abstract:** AIM: To prepare monoclonal antibodies (mAb) against the hemagglutinin(HA) of H9 subtype of avian influenza virus (AIV). METHODS: 8 week-old female BALB/c mice were immunized with the inactivated vaccine of H9 subtype of AIV. Splenocytes from the immunized mice were fused with Sp2/0 myeloma cells, and positive hybridoma clones were screened by indirect ELISA and hemagglutination inhibition test (HI). The specificity of the mAb was characterized by ELISA, HI test, indirect immunofluorescence (IF) staining and Western blot. RESULTS: Three hybridoma cell lines named 2H1, 2A3 and 1C8 against HA of AIV H9 were obtained. The HI titers of 3 mAbs were 1 x 10(-7), 1 x 10(-5) and 5 x 10(-6), respectively. The immunoglobulin subclass of all 3 mAbs was IgG1. Western blot analysis confirmed that mAb 2H1 could recognize HA and reacted to 31 out of 32 isolates of H9 subtype of AIV. CONCLUSION: Three mAbs recognizing HA of H9 subtype of AIV were obtained, which may provide an useful tool for the antigenic analysis, the serological diagnosis, the epidemiological survey and the evaluation of AIV vaccine.

**Descriptors:** characterization, H9, avian influenza, virus, monoclonal antibodies, mAb, HA, AIV, subtype,

**NAL Call Number:** QR355.P5  
**Descriptors:** SDS polyacrylamide gel electrophoresis analysis, SDS page analysis, Western blot analysis, affinity chromatography, prokaryotic expression vector construction, reverse transcription polymerase chain reaction, RT PCR, scan analysis, sequence analysis, pGEX-4T-3 vector, pGEX-4T-3, NS1 cDNA plasmid.


**NAL Call Number:** 448.8 L22  
**Descriptors:** nucleic acids biosynthesis, nucleoproteins biosynthesis, orthomyxoviridae metabolism, RNA viral biosynthesis, carbon isotopes, dactinomycin pharmacology, influenza A virus avian metabolism, Newcastle disease virus metabolism, nucleosides, parainfluenza virus 1, human metabolism, tissue culture, tritium, uridine.


**NAL Call Number:** QR360.A1J6  
**Abstract:** We previously reported that nucleoproteins (NPs) of human influenza viruses are cleaved in infected cells and, as a result, two forms of NP, uncleaved (mol. wt. 56000) and cleaved (mol. wt. 53000) were accumulated late in infection. Here, we report that NPs of animal influenza viruses of non-human origin (isolated from pigs, equids, seals, whales, birds) exhibited proteolytic resistance in infected cells and did not undergo a change in mol. wt. in the course of infection. The resistance of the animal virus NPs to proteolytic cleavage was shown to be a virus-specific property and not the consequence of a low level of proteolysis in infected cells. Influenza A/H3N2 viruses isolated from swine in Hong Kong in 1976 were found to have a cleavable NP like that of 'human' viruses, supporting the hypothesis concerning the 'human' origin of these strains. The NP of human influenza virus (A/Aichi/2/68) adapted to an animal host (mouse) retained susceptibility to limited intracellular proteolysis. Thus, NP resistance to cleavage seems to be a stable viral characteristic enabling the NP56 ---- NP53 modification to be used as an indication of the origin of influenza viruses.  

**Descriptors:** influenza microbiology, influenza A virus human metabolism, nucleoproteins metabolism, orthomyxoviridae metabolism, viral proteins metabolism, chick embryo, influenza metabolism, avian metabolism, porcine metabolism, peptide hydrolases metabolism, peptides analysis, peptides metabolism, virus cultivation.


**NAL Call Number:** 448.8 P942  
**Abstract:** Proteolytic cleavage of NP56 leads to NP53 protein of various influenza virus strains of human, avian, and animal origin in tissue culture was studied. A considerable portion of NP virus protein synthesized in human influenza virus-infected cells was modified by cellular proteases, and as early as 10 hours postinfection both intact (NP56) and cleaved (NP53) protein could be found in the cells. No proteolytic modification of NP protein was demonstrated in cells infected with 11 avian and animal influenza virus strains under study. Even 24 hours postinfection the cells contained intact (NP56) protein alone. Different resistance of NP protein of virus strains to cellular proteases allows the phenomenon of proteolytic modification of the nucleocapsid protein NP56 leads to NP53 to be used as a genetic marker of influenza virus strains.  

**Descriptors:** capsid metabolism, influenza enzymology, influenza A virus metabolism, peptide hydrolases

**Abstract:** The nucleocapsid protein (NP) (56 kDa) of human influenza A viruses is cleaved in infected cells into a 53-kDa form. Likewise, influenza B virus NP (64 kDa) is cleaved into a 55-kDa protein with a 62-kDa intermediate (O. P. Zhirnov and A. G. Bukrinskaya, Virology 109:174-179, 1981). We show now that an antibody specific for the N terminus of influenza A virus NP reacted with the uncleaved 56-kDa form but not with the truncated NP53 form, indicating the removal of a 3-kDa peptide from the N terminus. Amino acid sequencing revealed the cleavage sites ETD16*G for A/Aichi/68 NP and sites DID7*G and EAD61*V for B/Hong Kong/72 NP. With D at position -1, acidic amino acids at position -3, and aliphatic ones at positions -2 and +1, the NP cleavage sites show a recognition motif typical for caspases, key enzymes of apoptosis. These caspase cleavage sites demonstrated evolutionary stability and were retained in NPs of all human influenza A and B viruses. NP of avian influenza viruses, which is not cleaved in infected cells, contains G instead of D at position 16. Oligopeptide DEVD derivatives, specific caspase inhibitors, were shown to prevent the intracellular cleavage of NP. All three events, the NP cleavage, the increase of caspase activity, and the development of apoptosis, coincide in cells infected with human influenza A and B viruses. The data suggest that intracellular cleavage of NP is exerted by host caspases and is associated with the development of apoptosis at the late stages of infection.

**Descriptors:** caspases metabolism, influenza A virus human metabolism, influenza B virus metabolism, nucleocapsid proteins metabolism, amino acid sequence, apoptosis, caspases antagonists and inhibitors, cell line, dogs, molecular sequence data, oligopeptides pharmacology, swine.


**Abstract:** Chickens, fowl plague drug therapy, influenza A virus avian drug effects, protease inhibitors therapeutic use, chick embryo, drug evaluation, preclinical, fowl plague microbiology, avian growth and development, time factors, virus activation drug effects.

**Descriptors:** chickens, fowl plague drug therapy, influenza A virus avian drug effects, protease inhibitors therapeutic use, chick embryo, drug evaluation, preclinical, fowl plague microbiology, avian growth and development, time factors, virus activation drug effects.


**Abstract:** In late summer through early winter of 1998, there were several outbreaks of respiratory disease in the swine herds of North Carolina, Texas, Minnesota, and Iowa. Four viral isolates from outbreaks in different states were analyzed genetically. Genotyping and phylogenetic analyses demonstrated that the four swine viruses had emerged through two different pathways. The North Carolina isolate is the product of genetic reassortment between H3N2 human and classic swine H1N1 influenza viruses, while the others arose from reassortment of human H3N2, classic swine H1N1, and avian viral genes. The hemagglutinin genes of the four isolates were all derived from the human H3N2 virus circulating in 1995. It remains to be determined if either of these recently emerged viruses will become established in the pigs in North America and whether they will become an economic burden.

**Descriptors:** genome, viral, influenza A virus avian genetics, human genetics, porcine genetics, reassortant viruses, amino acid sequence, birds virology, molecular sequence data, swine virology.

Zilske, E., R. Sinnecker, and H. Sinnecker (1981). Neuraminidasehemmende Antikorper gegen aviare Influenzabirus- Subtypen in Humanseren. [Neuraminidase-Inhibiting Antibodies to Avian Influenza Virus Subtypes in Human Sera (author's transl)]. Zentralblatt Fur Bakteriologie, Mikrobiologie Und...
Abstract: 400 human sera were tested both in hemagglutination inhibition (HI) and neuraminidase inhibition (NI) tests for antibodies to avian and animal influenza virus subtypes. In the H1 test we only found antibodies to the avian subtype Hav 7 and the animal subtypes Hsw 1 and Heq 2 whereby the latter was mainly demonstrated in elderly persons 60 to 100 years old. The findings of Hav 7 are due to H 3 antibodies and reflect the relationship between both antigens. In the NI test we obtained positive results in 21.8% of the human sera with the neuraminidase subtype N 3 (Nav 2/3) with a peak in persons who were 60 to 70 years old. 11.0% of the sera contained antibodies to the neuraminidase subtype N 8 (Neq 2) and were found exclusively in people 60 to 100 years old, and 9.3% of sera showed positive reactions with the subtype N5 (Nav 5). Until now an immunological relationship between the neuraminidase subtypes N 1, N 2, and N 3 is not known, and couldn't be found in our own studies. Contaminations of antigens can also be excluded. The possible origin of these antibodies to avian neuraminidase subtypes is discussed.

Descriptors: antibodies, viral analysis, influenza A virus avian immunology, neuraminidase immunology, adolescent, adult, aged, child, preschool, Germany, East, hemagglutination inhibition tests, infant, porcine immunology, middle aged, serologic tests methods.


Abstract: The adamantanamine derivative 1-[p-(methylamino)-benzylidenamino]-adamantan (MBAA) at a concentration of 40 microgram/ml demonstrated no effect on adsorption of fowl plague virus (FPV) on chick embryonal cells. The penetration of the virions took place by means of pinocytosis. In the final stages of penetration the virions became gradually disintegrated. Under the influence of MBAA, after break-down of the membrane of pinocytic vesicles a swollen part of the virus core remained in cytoplasm. The morphologically visible replication stages were completely blocked by MBAA. From these results it was concluded that the antiviral action of MBAA most probably depends on a block of virus replication between the final stages of the penetration process and the beginning of production of virus specific structural antigens.

Descriptors: adamantan pharmacology, bridged compounds pharmacology, influenza A virus avian drug effects, nitrosamines pharmacology, adamantan analogs and derivatives, adsorption, cell membrane microbiology, cell nucleus microbiology, chick embryo, cytoplasm microbiology, avian growth and development, avian ultrastructure, pinocytosis, tissue culture, virus replication drug effects.


Abstract: cultured cells microbiology, influenza A virus avian pathogenicity, centrifugation, density gradient, chick embryo, clone cells microbiology, fibroblasts microbiology, fluorescent antibody technique, avian isolation and purification, interferons analysis, I cells cell line microbiology, nucleoproteins analysis, RNA viral analysis, time factors, virus cultivation, virus replication.

Descriptors: cultured cells microbiology, influenza A virus avian pathogenicity, centrifugation, density gradient, chick embryo, clone cells microbiology, fibroblasts microbiology, fluorescent antibody technique, avian isolation and purification, interferons analysis, I cells cell line microbiology, nucleoproteins analysis, RNA viral analysis, time factors, virus cultivation, virus replication.
Tests, Detection and Diagnosis


**NAL Call Number:** 41.8 Am3A

**Abstract:** The signal-to-noise ratio was useful in determining the optimal dilution of rabbit anti-turkey conjugate. Optimum dilution for rabbit anti-turkey conjugate to be used in the enzyme-linked immunosorbent assay (ELISA) was 1:1,000. The avian influenza virus antigen concentration was 128 hemagglutinating units (0.3 microgram of protein) per well, as determined by checkerboard titration. Bovine serum albumin fraction V increased nonspecific binding of conjugate and was not used to coat the plates in subsequent tests. Using ELISA, nonspecific binding to avian influenza virus-coated plates were not found with antibodies to Newcastle disease virus, infectious bursal disease, *Salmonella*, or *Escherichia coli*. Chromogens o-phenenediamine, and 2,2'-azino-di-(3-ethyl-benz-thiazoline sulfonic acid) were almost equal in sensitivity for detecting released oxygen from the H2O2. The substrate plate was more sensitive than was the polystyrene plate. Dual wavelength was reliable in reading ELISA results.

**Descriptors:** antibodies, viral analysis, fowl plague immunology, influenza A virus avian immunology, enzyme linked immunosorbent assay, hemagglutination inhibition tests, turkeys.


**NAL Call Number:** 41.8 Am3A

**Abstract:** A rapid and easy purification method was developed to obtain avian influenza antigen for use in immunochemical assays. This was achieved by rapid concentration of virus from infective allantoic fluid, using 8% (w/v) polyethylene glycol 8000, and later, by purification on gel-permeation chromatography through controlled-pore glass beads. Rabbit anti-turkey globulins were made specific for turkey globulins, using affinity chromatography, conjugated to horseradish peroxidase and used in enzyme-linked immunosorbent assay. A significant increase in specificity and sensitivity of the enzyme-linked immunosorbent assay was observed when purified antigen was used in place of a crude antigen preparation. This purified antigen eliminated the false-positives obtained as a result of the turkeys being previously vaccinated with egg-grown virus vaccines (Newcastle disease virus). The details of the technique and the importance of antigen preparation are discussed.

**Descriptors:** antigens, viral isolation and purification, enzyme linked immunosorbent assay, immunoenzyme techniques, influenza A virus avian isolation and purification, antibodies, anti idiotypic isolation and purification, chick embryo, chromatography, affinity, chromatography, gel, fowl plague diagnosis, horseradish peroxidase, avian immunology, rabbits immunology, turkeys immunology.


**NAL Call Number:** SF995.A1A9

**Descriptors:** avian influenza virus, screening techniques, ELISA, *Mycoplasma synoviae*, *Mycoplasma gallisepticum*, Gallus gallus, chickens.


**NAL Call Number:** 41.8 C162

**Abstract:** The application of the soluble antigen fluorescent test as a tool for serological investigation of influenza type A infection in wild birds was studied. The soluble antigen fluorescent antibody test is basically an indirect fluorescent antibody test except that an artificial matrix of cellulose acetate discs is used as a
substrate for antigen and the test results are scanned and recorded by a fluorometer. The influenza type A soluble antigen fluorescent antibody was obtained from concentrated and detergent disrupted virus particles, absorbed onto cellulose acetate discs. Anti-influenza sera were prepared in pheasants and ducks to A/turkey/Ontario/6118/67 and in pigeons to A/turkey/Ontario/6213/68. The antigen-antibody complex was detected by specific staining with monovalent or polyvalent fluorescein isothiocyanate conjugated rabbit anti-avian immunoglobulins. The soluble antigen fluorescent antibody test is a sensitive technique for the detection of specific influenza A antibodies in several avian species, and could be adapted for use in large scale surveys.

Descriptors: antibodies, viral analysis, fluorescent antibody technique, fowl plague diagnosis, influenza A virus avian immunology, antigens, viral, birds, hemagglutination inhibition tests veterinary, poultry, solubility.


NAL Call Number: SF601.P7

Abstract: Thirty blood samples were collected randomly from each of the 38 breeder-broiler farms in Jordan. Serum samples were examined using indirect ELISA for specific antibodies to avian influenza virus. The overall true flock-level sero-prevalence of avian influenza was 71% (95% CI: 55,83). Positive flocks had 2-30 sero-positive chickens and half of flocks had >20 sero-positive birds. The number of sero-positive flocks varied in the studied localities with more sero-positives in farms located within the migratory route of migratory wild fowl. The examined broiler-breeder flocks had no clinical signs, or noticeable decrease in egg production; mortalities were within the normal range (0.1-1%). The number of positive sera/flock correlated with flock size. There were a no significant (Pearsons r = 0.21, p = 0.21) correlation between positive flocks and age. A non-pathogenic AI virus infects broiler-breeder farms in Jordan. Wild local and migrating birds might promote the further spread of this virus in Jordan and other countries.

Descriptors: avian influenza, poultry, viral diseases, broiler-breeder, ELISA, age influence, Jordan.


NAL Call Number: SF771.M36 2000


NAL Call Number: SF995.A1A9

Descriptors: immunofluorescent test, avian influenza virus, diagnosis, techniques, detection, poultry.


NAL Call Number: aSF995.6.l6l5 1981a

Descriptors: avian influenza virus, diagnostic procedures.


NAL Call Number: 41.8 Av5

Abstract: The intravenous and intracerebral pathogenicity index tests normally used for Newcastle disease virus isolates were used to measure the virulence of 13 avian influenza viruses. The tests allowed quantitative measurements of the virulence of the avian influenza viruses, and the results confirmed the range in virulence, between the two extremes, of the avian influenza viruses and demonstrated the lack of correlation between virulence and antigenic type.

Descriptors: chickens, fowl plague etiology, influenza A virus avian pathogenicity, antigens, viral analysis, brain, chick embryo, fowl plague mortality, avian immunology, injections, intravenous, methods, virulence.

**NAL Call Number:** RA648.5.E46

**Abstract:** We report the first case of avian influenza in a patient with fever and diarrhea but no respiratory symptoms. Avian influenza should be included in the differential diagnosis for patients with predominantly gastrointestinal symptoms, particularly if they have a history of exposure to poultry.

**Descriptors:** gastrointestinal diseases physiopathology, influenza physiopathology, influenza A virus, avian pathogenicity, adult, chickens virology, fatal outcome, gastrointestinal diseases virology, health personnel, influenza virology, influenza, avian transmission, influenza, avian virology, poultry diseases transmission, poultry diseases virology.


**NAL Call Number:** SF995.A1A9

**Abstract:** The indirect ELISA was used to detect antibodies to influenzavirus A in the sera of wildfowl from the Donana National Park. Of the 712 birds examined, 44 (6.2%) were seropositive. Positive birds belonged to 10 of the 13 species studied. Infection rates varied widely: spoonbill (*Platalea leucorodia*, 32.2%), mallard (*Anas platyrhynchos*, 9.9%), gadwall (*Anas strepera*, 8.6%), red-crested pochard (*Netta rufina*, 8.1%), pochard (*Aythya ferina*, 6.4%), shoveler (*Anas clypeata*, 5%), great crested grebe (*Podiceps cristatus*, 4.3%), avocet (*Recurrostra avosetta*, 3.1%), grey heron (*Ardea cinerea*, 3.1%) and coot (*Fulica atra*, 0.8%). Although infection rates were not high, the wide range of avian species susceptible to influenzavirus A suggests circulation of the virus amongst wildfowl at Donana.

**Descriptors:** enzymology, immune system, infection, methods and techniques, pathology, veterinary medicine, diagnostic method ELISA epidemiology.


**Descriptors:** standard diagnostic techniques, animal diseases, Australia, booklet series.


**Abstract:** In the last two decades, various molecular biological methods were introduced in diagnostic virology. They are used for the rapid detection of viral nucleic acids, genetic characterization of the pathogens responsible for many viral infections and tracking of the origin and spread of viruses. In this review, the application of molecular biology methods, particularly the combined approach of amplifying defined fragments of viral genomes, using the polymerase chain reaction and subsequent nucleotide sequencing analysis, is described. Emphasis is placed on some of the few important viruses causing economically important diseases in poultry, like Newcastle disease virus, avian influenza virus, infectious bursal disease virus and chicken anaemia virus.

**Descriptors:** avian infectious bursitis, diagnosis, diagnostic techniques, DNA sequencing, fowl diseases, genomes, influenza, methodology, molecular biology, Newcastle disease, polymerase chain reaction, poultry, reviews, avian influenza virus, chicken anaemia virus, fowls, infectious bursal disease virus, Newcastle disease virus.


**NAL Call Number:** SF772.6.A97 1993

**Descriptors:** standard diagnostic techniques, avian influenza virus, *Gallus gallus*, Australia.

**NAL Call Number**: SF771.A8A97 no.51
**Descriptors**: avian influenza virus, standard diagnostic techniques, Australia.


**NAL Call Number**: 41.8 Av5
**Descriptors**: antibodies analysis, immunodiffusion, influenza diagnosis, poultry diseases diagnosis, antigens isolation and purification, chickens, hemagglutination inhibition tests, influenza immunology, orthomyxoviridae immunology, orthomyxoviridae isolation and purification, poultry diseases immunology, turkeys.


**Descriptors**: avian influenza virus, diagnosis, fowl plague virus, identification, isolation.


**NAL Call Number**: 41.8 Av5
**Descriptors**: hemagglutinins viral, influenza A virus avian immunology, orthomyxoviridae immunology, antibodies, viral analysis, chickens, fowl plague immunology, fowl plague microbiology, hemagglutination inhibition tests, immunization, influenza immunology, influenza microbiology, influenza veterinary, avian enzymology, avian isolation and purification, neuraminidase analysis, neutralization tests, orthomyxoviridae enzymology, orthomyxoviridae isolation and purification, poultry diseases immunology, poultry diseases microbiology, virulence.


**NAL Call Number**: 448.8 J8232
**Descriptors**: antigens, erythrocytes, hemagglutination tests, indicators and reagents, orthomyxoviridae, salicylic acids, sulfonic acids, complement fixation tests, immune sera, influenza A virus avian, nucleoproteins, sheep.

Becht, H. and B. Malole (1975). **Comparative evaluation of different fixation procedures and different coupling reagents for the demonstration of influenza virus-specific antibodies by the indirect hemagglutination test.** *Medical Microbiology and Immunology* 162(1): 43-53. ISSN: 0300-8584.

**Abstract**: The indirect hemagglutination technique has been improved by fixing the carrier erythrocytes successively with glutaraldehyde and sulfosalicylic acid. Sensitization by covalent conjugation of influenza virus antigens to the erythrocytes with various coupling reagents, which resulted in stable and highly sensitive test cells, has been defined. An economical affinity chromatography procedure using antibody-coated agarose has been developed to prepare sufficiently pure antigens from fowl plague virus-infected choriollantoic membranes.

**Descriptors**: antibodies, viral analysis, erythrocytes immunology, hemagglutination tests methods, antibody specificity, blood preservation, chromatography, affinity, cytological techniques, glutaral, hemagglutinin viral isolation and purification, influenza A virus avian immunology, salicylic acids.


**NAL Call Number**: 41.8 Av5
Abstract: Determination of the avian influenza (AI) status of a flock has traditionally been done by detection of serum antibodies. However, for many diseases, detection of antibodies in egg yolk has been effective in monitoring the disease status of laying flocks. This study compared the utility of egg yolk vs. serum for determining AI status in laying hen flocks. Specific-pathogen-free white leghorn hens were inoculated via the respiratory tract with a low-pathogenic H7N2 AI virus or sterile allantoic fluid or subcutaneously with an inactivated oil emulsion vaccine produced from the same AI virus or normal allantoic fluid. Antibody levels were determined by the agar gel immunodiffusion (AGID) test, the hemagglutination-inhibition (HI) test, and the enzyme-linked immunosorbent assay (ELISA). Anti-influenza antibodies were detected in sera of all live virus-inoculated hens by day 7 postinoculation (PI) (AGID and ELISA tests), but detection of antibodies in egg yolk was delayed by a few days, with all being positive by day 14 PI. Sera from all vaccinated hens were positive by day 14 PI (AGID and ELISA tests), and egg yolk was positive by day 18 PI. The HI test was less sensitive than the ELISA and AGID tests in detecting anti-influenza antibodies in both sera and yolk. Serum and yolk from all control birds remained negative throughout the study. These studies show that currently used serologic tests can detect antibodies in serum and yolk samples from hens exposed to live AI virus or from those that have been vaccinated. Antibody is detected earlier in the serum than in the yolk and antibody is detected earlier from birds exposed to a live infection compared to birds vaccinated with an inactivated oil emulsion vaccine.

Descriptors: animal husbandry, immune system, infection, avian influenza, infectious disease, viral disease, ELISA immunologic techniques, laboratory techniques, agar gel immunodiffusion test, agid test, egg yolk antibody testing, hemagglutination inhibition test, influenza status, laying flock disease status.


NAL Call Number: 41.8 Av5

Abstract: Highly pathogenic avian influenza (HPAI) in poultry causes high morbidity and mortality, and it is a List A disease of the Office International des Epizooties. An outbreak of HPAI in commercial poultry not only causes direct disease losses but often results in trade restrictions for the affected country. Because HPAI viruses can mutate from H5 and H7 low pathogenic avian influenza viruses, it is necessary to monitor and control even the low pathogenic form of the virus. We report a practical approach for screening large numbers of isolates that uses amplification by reverse transcriptase-polymerase chain reaction of a segment of the hemagglutinin (HA) gene (536-560 bp) of H7 avian influenza viruses followed by the heteroduplex mobility assay (HMA). The HMA test compares the amplified polymerase chain reaction product from unknown samples with reference isolates, which allows the identification of new variants. The HMA test results were compared with sequence analysis of the isolates used in the study. On the basis of the HMA, we could identify several new variant viruses present in the live bird markets in the northeastern United States. New strains gave a distinct pattern of bands in the gels in accordance with the different heteroduplexes formed when their HA region amplification products were incubated together with the same amplification product of a reference strain. These differences correlate with phylogenetic analysis from sequence data.

Descriptors: animal husbandry, infection, molecular genetics, avian influenza virus infection, infectious disease, viral disease, gene sequencing cycle DNA sequencing, sequencing method, heteroduplex mobility assay bioassay method, phylogenetic analysis genetic method, reverse transcriptase polymerase chain reaction genetic method, polymerase chain reaction, morbidity mortality.


NAL Call Number: 41.8 Am3A

Abstract: A practical method for collection and processing of dried whole blood samples on filter paper was developed to facilitate large-scale testing programs for Newcastle disease virus and avian influenza virus antibodies. A modified paper punch was used to cut and place dried blood samples simultaneously in a standard 96-well microlate for elution of antibody. Twelve eluted samples were simultaneously transferred to another microplate for the hemagglutination-inhibition (HI) microtest. Similar HI titers were obtained with simultaneously collected serum and dried blood samples. Minor differences were not considered of practical
importance in diagnostic serologic studies. Dried blood titers were not markedly affected by method of drying (37 °C for 2 hours or 26 °C for 4 hours), by storage for 24 hours before drying, or by storage of dried samples at 4 °C for 28 days or 30 °C for 14 days. Blood dried on paper was a satisfactory sample for assay of HI antibodies to Newcastle disease virus and avian influenza virus.

Descriptors: antibodies, viral analysis, blood specimen collection veterinary, chickens immunology, influenza A virus avian immunology, Newcastle disease virus disease immunology, blood specimen collection instrumentation, hemagglutination inhibition tests, paper.


Abstract: The present paper reports on the development, validation and field application of a control strategy for avian influenza infections in poultry. The "DIVA" (Differentiating Infected from Vaccinated Animals) strategy is based on the use of an inactivated oil emulsion vaccine containing the same haemagglutinin (H) subtype as the challenge virus, but a different neuraminidase (N). The possibility of using the heterologous N subtype, to differentiate between vaccinated and naturally infected birds, was investigated through the development of an "ad hoc" serological test based on the detection of specific anti-N antibodies. This test is based on an indirect fluorescent antibody assay, using as an antigen a baculovirus expressing recombinant N proteins. The vaccination strategy has been tested in the laboratory and shown to be efficacious both against challenge with highly pathogenic AI viruses and with low pathogenicity AI viruses, ensuring clinical protection, reduction of duration and titre of shedding. In addition, vaccination resulted in an increased resistance to infection. The companion diagnostic tests directed to the detection of anti-N1 and anti-N3 antibodies have been validated in the laboratory and using field samples. The serological assay showed an "almost perfect agreement" (Kappa value) with the HI test, with relative sensitivity and specificity values of 98.1 and 95.7, respectively. The results of the present investigation suggest that the "DIVA" control strategy may represent a tool to support the eradication of avian influenza infections in poultry.

Descriptors: animals, viral blood antibodies, viral immunology antibodies, genetic engineering, avian influenza A virus enzymology, avian influenza diagnosis, avian influenza prevention and control, neuraminidase genetics, poultry, sensitivity and specificity, veterinary serologic tests, marker vaccines, viral vaccines immunology, virus shedding.


NAL Call Number: SF995.A1A9

Descriptors: influenza A virus, avian isolation and purification, avian diagnosis, poultry diseases diagnosis, poultry diseases virology, immunoenzyme techniques methods, avian classification, avian genetics, reverse transcriptase polymerase chain reaction methods, sensitivity and specificity, trachea virology, turkeys.


NAL Call Number: 41.8 Av5

Abstract: The development of a discriminatory test, based on the differentiation between N1 and N3 antibodies, to be used in the framework of a vaccination program, based on vaccination with a heterologous H7N3 inactivated vaccine against the Italian H7N1 field virus, is reported. The indirect immunofluorescence antibody (iIFA) assay was based on the expression of the N1 protein in a baculovirus system. HighFive(R) insect cells were transfected with the recombinant virus and used as an antigen in the iIFA test. Preliminary validation on 608 turkey sera yielded relative sensitivity and specificity of 98.1% and 95.7%, respectively, when compared to the HI test with an almost perfect agreement between the two methods (Kappa value = 0.93). It is concluded that the iIFA test is a valid tool for monitoring avian influenza infection in a vaccinated population.

Descriptors: animal husbandry, immune system, infection, antibody differentiation test, immunologic techniques, immunofluorescence antibody assay, bioassay techniques, laboratory techniques, vaccination,
clinical techniques, influenza control.

NAL Call Number: SF995.W4
Descriptors: avian influenza virus, basic studies, challenge, pathogenicity test.

Descriptors: diagnosis, hemagglutination inhibition test, Newcastle disease, avian influenza, egg yolk, poultry.

NAL Call Number: 41.8 Av5
Abstract: Nucleic acid sequence-based amplification (NASBA) allows the rapid amplification of specific regions of nucleic acid obtained from a diverse range of sources. It is especially suitable for amplifying RNA sequences. A NASBA technique was developed that allows the detection of avian influenza A subtype H5 from allantoic fluid harvested from inoculated chick embryos. The amplified viral RNA is detected by electrochemiluminescence. The described NASBA technique is a specific, rapid, and sensitive method of detection of influenza A subtype H5 viruses. More importantly, it can be used to distinguish high- and low-pathogenicity strains of the H5 subtype.
Descriptors: immune system, infection, molecular genetics, electrochemiluminescence, immunologic techniques, laboratory techniques, nucleic acid amplification, genetic techniques, nucleic acid sequence based amplification, NASBA.

NAL Call Number: 442.8 B5236
Abstract: Nucleic acid sequence-based amplification with electrochemiluminescent detection (NASBA/ECL) is an isothermal technique allowing rapid amplification and detection of specific regions of nucleic acid from a diverse range of sources. It is especially suitable for amplifying RNA. A NASBA/ECL technique has been developed allowing the detection of RNA from avian influenza virus subtype H7 derived from allantoic fluid harvested from inoculated chick embryos and from cell cultures. Degenerate amplification primers and amplicon capture probes were designed enabling the detection of low and highly pathogenic avian influenza of the H7 subtype from the Eurasian and North American lineages and the Australian sub-lineage. The NASBA/ECL technique is specific for subtype H7 and does not cross-react with other influenza subtypes or with viruses containing haemagglutinin-like genes. The assay is 10- to 100-fold more sensitive than a commercially available antigen capture immunoassay system. The NASBA/ECL assay could be used in high throughput poultry screening programmes.
Descriptors: molecular genetics, influenza, diagnosis, respiratory system disease, viral disease, nucleic acid based amplification with electrochemiluminescent detection genetic techniques, laboratory techniques.

NAL Call Number: QR355.J6
Abstract: Nucleic acid sequence-based amplification (NASBA) is a technique that allows the rapid amplification of specific regions of nucleic acid obtained from a diverse range of sources. It is especially
suitable for amplifying RNA sequences. A NASBA technique has been developed that allows the detection of avian influenza A subtype H5 from allantoic fluid harvested from inoculated chick embryos. The amplified viral RNA is detected by electrochemiluminescence. The NASBA technique described below is rapid and specific for the identification of influenza A subtype H5 viruses of the Eurasian lineage. More importantly, it can be used to distinguish highly pathogenic and low pathogenic strains of the H5 subtype.

Descriptors: human medicine, infection, methods and techniques, molecular genetics, DNA sequencing analytical method, recombinant DNA technology, sequencing techniques, electrochemiluminescence technique analytical method, applications, description, molecular method, nucleic acid sequence based amplification technique molecular biology techniques and chemical characterization, applications, description, molecular method, reverse transcriptase polymerase chain reaction molecular method, polymerase chain reaction, diagnostics, pathogenicity, viral genetics, virological methodologies applications, virulence.

NAL Call Number: 41.8 Av5
Abstract: The standard tests used to detect avian influenza (AI) viral infection include virus isolation from tissues of the infected birds and the detection of AI antibody in blood or egg yolk. A new application of an existing human test to rapidly detect the presence of any influenza A virus is now possible. A commercially available antigen-capture enzyme immunoassay (AC-EIA), developed for the detection of influenza A in humans, was tested for relative sensitivity and specificity and for speed of use in diagnosing nonpathogenic H7N2 AI in naturally infected poultry. During the recent nonpathogenic H7N2 AI epornitic, the AC-EIA was used for rapid diagnosis and quarantine decisions. Between February and August 1997, 1524 samples from 295 commercial layer, pullet, and broiler flocks were submitted to the Laboratory of Avian Medicine and Pathology, New Bolton Center, for AI virus isolation and testing by AC-EIA. The relative specificity of the AC-EIA was 100% and the relative sensitivity was 79%. We believe that the AC-EIA will be a useful adjunct to standard AI diagnostic tests.
Descriptors: infection, methods and techniques, veterinary medicine, avian influenza, detection, respiratory system disease, viral disease, antigen capture enzyme immunoassay comparison, diagnostic method, virus isolation comparison, diagnostic method.

NAL Call Number: 448.3 Ar23
Abstract: A double antibody sandwich blocking ELISA, using a monoclonal antibody (MAb) against influenza A nucleoprotein (NP) was developed to detect antibodies against influenza. Collections of serum samples were obtained from human and various animal species. All influenza A subtypes induced antibodies against hemagglutinins and NP. A close correlation between titers of the hemagglutination inhibition (HI) test and the NP-ELISA was seen. Antibodies against influenza NP were demonstrated in serum samples from humans, ferrets, swine, horses, chickens, ducks, guinea pigs, mice, and seals. The serum samples were collected at intervals during prospective epidemiological studies, from experimental and natural infections, and vaccination studies. The decline of maternal antibodies was studied in swine and horses. The NP-ELISA enables rapid serological diagnosis and is suited for influenza A antibody screening, especially in species which harbor several influenza subtypes. The HI and neuraminidase inhibition tests, however, must still be used for subtyping.
Descriptors: antibodies, viral analysis, enzyme linked immunosorbent assay, influenza A virus immunology, nucleoproteins immunology, orthomyxoviridae infections immunology, viral core proteins immunology, ferrets, hemagglutination inhibition tests, horses, avian immunology, human immunology, porcine immunology, orthomyxoviridae infections veterinary, poultry, prospective studies, Rodentia, seals, species specificity, specific pathogen free organisms, swine, vaccination.

NAL Call Number: SF774.J68
Abstract: Three 1-tube Reverse Transcriptase Polymerase Chain Reactions (RT-PCR) directed against the genes encoding the nucleoprotein (NP) and the H5 and H7 hemagglutinin (HA) gene, respectively, were used for detection of avian influenza virus (AIV) in various specimens. A total of 1,040 samples originating from chickens experimentally infected with 2 different low pathogenic avian influenza viruses, from domestic ducks and from wild aquatic birds were examined. The outcome of 1) the universal AIV RT-PCR including a PCR-enzyme-linked immunosorbent assay (ELISA) procedure directed against NP (NP RT-PCR-ELISA) and 2) the subtype specific RT-PCR for H5 and H7 were compared to the results obtained by inoculation of the same specimens into the allantoic cavity of embryonated specific pathogen free (SPF) hen’s eggs. Using inoculation in SPF fowl eggs as standard the sensitivity of the NP RT-PCR-ELISA and the RT-PCR for H5 or H7 was 91% and 94%, and the corresponding specificity 98% and 96%. In comparison with inoculation into eggs an additional of 9 samples were positive by NP RT-PCR-ELISA and 13 samples were positive by RT-PCR for one of the HA subtypes. Hence, the 3 RT-PCR procedures described are fast, sensitive and specific for detecting AIV and subtyping H5 and H7 and they are obvious alternatives when testing large numbers of samples.
Descriptors: enzyme linked immunosorbent assay veterinary, hemagglutinins genetics, influenza veterinary, influenza A virus, avian classification, avian genetics, avian pathogenicity, nucleoproteins chemistry, avian isolation and purification, nucleoproteins genetics, poultry diseases virology, reverse transcriptase polymerase chain reaction veterinary, antibodies, viral blood, chick embryo, chickens, ducks, enzyme linked immunosorbent assay methods, hemagglutination inhibition tests veterinary, influenza diagnosis, influenza virology, RNA, viral chemistry, viral genetics, reverse transcriptase polymerase chain reaction methods, sequence analysis, DNA, virulence.

NAL Call Number: 41.8 Av5
Abstract: A one-tube reverse transcriptase/polymerase chain reaction coupled with an enzyme-linked immunosorbent assay (RT-PCR-ELISA) was developed for the rapid detection of avian influenza virus (AIV) in clinical specimens. A total of 419 swab pools were analyzed from chickens experimentally infected with low-pathogenicity AIV, from wild aquatic birds, and from domestic ducks. The AIV was detected in 32 swab pools by RT-PCR-ELISA compared to 23 by virus isolation (VI) in embryonated specific pathogen free (SPF) hen’s eggs. Thus, 39% more specimens were positive by RT-PCR-ELISA than by VI. Two of the twenty-three VI-positive specimens were negative when tested by RT-PCR-ELISA. The diagnostic sensitivity and specificity of the RT-PCR-ELISA was 91% and 97%, respectively, using VI in SPF eggs as the gold reference standard.
Descriptors: infection, molecular genetics, reverse transcriptase polymerase chain reaction ELISA clinical techniques, diagnostic techniques, genetic techniques, immunologic techniques, laboratory techniques, clinical specimens.

NAL Call Number: 41.8 T431

**NAL Call Number:** SF995.A1A9

**Descriptors:** disease outbreaks veterinary, avian influenza epidemiology, avian influenza diagnosis, avian influenza pathology, Netherlands epidemiology, poultry.


**NAL Call Number:** 448.8 P942

**Abstract:** Examinations of blood sera from different species of birds trapped in the Ukrainian and Azerbaijan SSRs using diagnostic preparations from the influenza A/sea gull/Maryland/704/77 virus strain and a recombinant R117 derived from it revealed the presence of antibodies to hemagglutinin H13. The diagnostic preparation produced from the recombinant strain was found to be more active in the detection of antibodies in avian sera.

**Descriptors:** antibodies, viral analysis, birds immunology, influenza A virus avian immunology, recombination, genetic, Azerbaijan, hemagglutination inhibition tests veterinary, avian genetics, Ukraine.


**NAL Call Number:** 41.8 Au72

**Descriptors:** chickens, avian influenza virus, antigens, diagnosis, birds, domestic animals, domesticated birds, Galliformes, immunological factors, immunology, influenza virus, livestock, poultry, useful animals, viruses.


**NAL Call Number:** 41.8 Av5

**Abstract:** A broad-spectrum viral antigen for the detection of avian-influenza-virus-specific antibodies, using the indirect enzyme-linked immunosorbent assay (ELISA), was identified. Purified and disrupted antigens were used, which helped to increase the sensitivity of the assay. All of the antigens tested were able to detect antibodies to homologous and heterologous viruses to varying degrees. The H9N2 antigen was the best single antigen to use in the ELISA to screen for avian influenza virus antibodies. It detected antibodies against six viruses as early as day 4 postinfection.

**Descriptors:** antibodies, viral analysis, antigens, viral immunology, enzyme linked immunosorbent assay, fowl plague immunology, influenza A virus avian immunology, antigens, viral analysis, turkeys immunology.


**NAL Call Number:** SF995.A1A9

**Descriptors:** disease control, adjuvants, avian influenza virus antigens, vaccines, turkeys.


**Abstract:** Type-specific antigens from horioallantoic membranes (HAM) and allanto-amnionic fluids (AAF) of chicken embryos (CE), infected with a referent avian influenza virus strain (AlV) subtype H2, as well as corresponding hyperimmune rabbit and guinea pig sera were prepared. The latter, being highly specific and with a high sensitivity, were used as ingredients in an indirect double-sandwich ELISA procedure for detection of type-specific antigen of AlV and antibodies against it in a blockade double sandwich ELISA procedure. The results of blockade ELISA, applied to 916 hen sera from different farms from different regions of the country and to 11 sera from wild birds revealed no antibodies against AlV. Seven hundred and sixty eight of these sera were parallely studied in agar gel immunodiffusion (AGID) test and the results were negative as well. The studies, performed in the period 1993-1998 for isolation of AlV in CE from viscera of 212 carcasses from 13 domestic and wild avian species, gave negative results.

**Descriptors:** avian influenza virus, antigens, antibodies, serotypes, ELISA, immunodiffusion tests, biological differences, immunoenzyme techniques, immunological factors, immunological techniques, immunoprecipitation tests, influenza virus, orthomyxoviridae, viruses.


**Abstract:** Inactivated antigens from the allantoamnionic fluids (AAF) and chorioallantoic membranes (CAM) of chicken embryos (CE) infected with the avian influenza A virus (grippe) were prepared. Referent viral strains from the subtypes H-2, H-5, H-6 and H-8 were used for that purpose. The titres for the 50% endpoint infection dose (EID50) of strains for HE were within the range 5.52-8.26 lg/ml and their haemagglutination titers - from 1:256 to 1:512. The antigens were predominantly used for screening studies of avian sera with the tests: agar gel immunodiffusion (AGID), haemagglutination inhibition (HI), complement fixation reaction (CFR) (with informative purpose) and the indirect immunofluorescence reaction (IIFR). With the AGID test, positive seroreagents were detected among samples from 2 farms. Using RHI in a previous period in other 2 farms, there were positive samples against the H-5 subtype.

**Descriptors:** avian influenza virus, antigens, immune serum, immunodiffusion tests, hemagglutination tests, complement fixation tests, immunofluorescence, agglutination tests, immunological factors, immunological techniques, immunoprecipitation tests, influenza virus, orthomyxoviridae, viruses.


**NAL Call Number:** 448.3 Ar23

**Abstract:** The nucleoprotein (NP) gene from avian influenza strain A/Shearwater/Aust/1/72 (H6N5) was cloned, sequenced, and expressed in vaccinia virus for the production of potent sera in immunised rabbits. The NP gene is 1565 bp and shares greater than 95% amino acid sequence identity with other NPs of the avian subtype. The recombinant NP expressed by vaccinia virus comigrated with endogenous A/Shearwater/Aust/1/72 NP by Western blot analysis. Polyclonal rabbit sera raised against recombinant NP was evaluated in an antigen capture ELISA system as a potential diagnostic tool for the detection of avian influenza. All type A strains, comprising several HA and NA subtypes, but not type B nor other avian viruses, were detected.

**Descriptors:** fowl plague diagnosis, genes viral, influenza A virus avian genetics, nucleoproteins genetics, vaccinia virus genetics, viral core proteins, viral proteins genetics, amino acid sequence, antibodies, viral

**Abstract:** A reverse transcriptase PCR (RT-PCR) was used for rapid determination of the hemagglutinin (HA) cleavage site sequence, a marker for the virulence potential of avian influenza viruses. When applied to specimens from chickens experimentally infected with either a virulent or an avirulent virus, RT-PCR uniformly detected the HA gene, even in specimens that were negative for virus by standard testing in eggs. This technique, combined with sequencing of the HA cleavage site, offers a rapid and sensitive way to assess the virulence potential of avian influenza viruses. Early detection of field isolates with virulence-associated structural motifs at the HA cleavage site would allow better control of influenza among large poultry populations.

**Descriptors:** chickens, avian influenza virus, pathogenicity, PCR, experimental infection, in vivo experimentation, agglutinins, genes, biological properties, birds, cell structure, chromosomes, disease transmission, domestic animals, domesticated birds, experimentation, Galliformes, infection, influenza virus, livestock, microbial properties, nucleus, orthomyxoviridae, pathogenesis, poultry, proteins, useful animals, viruses, hemagglutinins.


**Descriptors:** disease control, diagnosis, avian influenza virus, China.


**Abstract:** During the avian influenza outbreak of 2003-04 in Southeast Asia, two avian influenza viruses (AIV), one of H5N1 subtype and the other H9N2 subtype, were isolated and identified from local farms. The nucleoprotein (NP) gene of the H5N1 AI isolate was cloned, and the segment encoding amino acid 47-384, which covers its major antigenic domains, was subcloned and expressed in E. coli. Subsequently, the NP (47-384) expression product was purified and used as the diagnostic antigen to develop a NP-based type-specific indirect enzyme-linked immunosorbent assay (ELISA) for detecting antibodies to AI from chicken sera. The ELISA is shown to be specific for AIV and does not cross-react with chicken sera that has antibodies to other avian viruses. The NP(47-384)-ELISA was compared with a hemagglutination inhibition test and a commercial AIV ELISA kit in evaluating 150 sera samples from experimentally AIV-infected or vaccinated specific-pathogen-free (SPF) chickens. Our NP(47-384)-ELISA was more sensitive than the two tests and showed an 82% agreement ratio with the HI test and an 80.67% agreement ratio with the commercial kit. The NP(47-384)-ELISA and the commercial AIV ELISA were used to evaluate 448 field sera samples from diseased chickens or vaccinated chickens during the 2003-04 AI outbreak in China. The two ELISA tests had a 95% agreement ratio. We conclude that the NP(47-384)-ELISA developed in our laboratory was specific and sensitive and it has great application potential in China's long-term prevention and control of AI.

**Descriptors:** antibodies, viral blood, enzyme linked immunosorbent assay methods, influenza A virus, avian isolation and purification, nucleoproteins immunology, viral proteins immunology, amino acid sequence, chick embryo, chickens, avian immunology, avian influenza diagnosis, molecular sequence data, nucleoproteins chemistry, reagent kits, diagnostic, reproducibility of results, specific pathogen free organisms, viral proteins chemistry.


**NAL Call Number:** SF481.M54
Abstract: The most important virus-induced diseases associated with heavy losses in the domestic goose are Derzsy's disease which is caused by a goose parvovirus and duck plague (duck viral enteritis) which is caused by an avian herpesvirus. Both diseases still occur but can be prevented by timely vaccinations. Antibodies against Influenza A viruses of the subtypes H1, H5, and H7 as well as against avian paramyxoviruses of the serogroups 4, 6, and 8, respectively, were not detected in any of the examined sera. However, antibodies against paramyxovirus type 1 were detected in sera of one source. Haemagglutination inhibition or neutralizing antibodies against avian adenoviruses (ED76 virus and goose adenovirus of the serotypes 1, 2, and 3) were quite often detected. Based on the present knowledge their pathogenic potential is minor. Neutralizing antibodies against a reovirus originating from Muscovy ducks and against a chicken reovirus (strain U Con S 1133) were quite frequently detected. In 35 of 564 examined geese sera hepatitis B virus was found.

Descriptors: antibodies, viral blood, geese, poultry diseases diagnosis, virus diseases veterinary, avianadenovirus immunology, avulavirus immunology, hepatitis B virus, duck immunology, hepatitis virus, duck immunology, influenza A virus avian immunology, parvovirus immunology, poultry diseases prevention and control, reoviridae immunology, virus diseases diagnosis, virus diseases prevention and control.

**Descriptors:** avian influenza, diagnosis, control, turkeys.


**NAL Call Number:** SF605.C59

**Descriptors:** hemagglutinins, avian influenza virus, diagnosis, monoclonal antibodies, turkeys, ducks.


**NAL Call Number:** 41.8 V6426

**Descriptors:** laboratory diagnosis, Newcastle disease, avian influenza virus.


**NAL Call Number:** SF995.W4

**Descriptors:** ELISA, detection, antibodies, avian influenza, chicken, sera, type A virus.


**NAL Call Number:** SF995.W4

**Descriptors:** chickens, turkeys, avian influenza virus, birds, domestic animals, domesticated birds, Galliformes, influenza virus, livestock, orthomyxoviridae, poultry, useful animals, viruses.


**NAL Call Number:** SF995.W4

**Descriptors:** laboratory diagnosis, avian influenza virus.


**NAL Call Number:** 442.8 B5236

**Abstract:** Infection of poultry with highly pathogenic avian influenza virus (AIV) can be devastating in terms of flock morbidity and mortality, economic loss, and social disruption. The causative agent is confined to certain isolates of influenza A virus subtypes H5 and H7. Due to the potential of direct transfer of avian influenza to humans, continued research into rapid diagnostic tests for influenza is therefore necessary. A nucleic acid sequence-based amplification (NASBA) method was developed to detect a portion of the haemagglutinin gene of avian influenza A virus subtypes H5 and H7 irrespective of lineage. A further NASBA assay, based on the matrix gene, was able to detect examples of all known subtypes (H1-H15) of avian influenza virus. The entire nucleic acid isolation, amplification, and detection procedure was completed within 6h. The dynamic range of the three AIV assays was five to seven orders of magnitude. The assays were sensitive and highly specific, with no cross-reactivity to phylogenetically or clinically relevant viruses. The results of the three AIV NASBA assays correlated with those obtained by viral culture in embryonated fowl's eggs.

**Descriptors:** influenza A virus, genetics, isolation and purification, self sustained sequence replication methods, base sequence, birds, chick embryo, DNA primers genetics, DNA probes genetics, diagnosis, virology, sensitivity and specificity, species specificity, swine.

Avian influenza (AI) viruses are endemic in wild birds and if transmitted to poultry can cause serious economic losses. In the study of AI, the quantitation of virus shed from infected birds is valuable in pathogenesis studies and to determine the effectiveness of vaccines, and is performed routinely by cultivation of virus containing samples using embryonating chicken eggs (ECE) and expressed by 50% egg infectious dose (EID(50)). Although, this assay is accurate and is the standard test for infectious virus titration, the method is laborious, requires a large number of ECE, and takes at least 7 days to determine results. In this study, a one-tube hydrolysis fluorescent probe based real-time RT-PCR (RRT-PCR) was applied for the quantitation of AI virus and compared with conventional virus titration method. A strong positive correlation was observed between the amount of RNA determined by quantitative RRT-PCR and the EID(50)s determined by conventional methods. This RRT-PCR test was further applied in the study of competitive replication of co-infected H5 and H7 subtype viruses in chickens. Using hemagglutinin subtype specific probes, we were able to determine the amount of individual subtype virus, which could not have easily been done with conventional methods. This RRT-PCR based quantitation of AI virus, which is specific, sensitive, easy to perform, and rapid, will be useful for virological, pathogenesis, and protection studies.
ultracentrifugation and sedimentation through a sucrose gradient (10-50% sucrose). ELISA was carried out in 96-well microplates coated with purified AIV antigens. Conjugated rabbit-anti-chicken peroxidase and substrate of o-Phenylenediamine dihydrochloride (OPD) were used in this study. The results of Box Titration of ELISA showed that the most proper concentration of coating antigen, conjugate and OPD were 1.0 μg/well, 3,000X dilution and 0.4 mg/mL, respectively. Sera of 16X dilution were used. The high specificity of ELISA were conducted by using 40 AVI negative sera from specific-pathogen-free chickens, 5 positive sera of AIV, 5 positive sera of chicken anemia agent (CAA), 12 positive sera of Marek's disease virus (MDV), totally 62 tested sera.

Descriptors: enzymology, immune system, infection, microbiology, pathology, veterinary medicine, diagnosis.

NAL Call Number: SF604.C58
Descriptors: avian influenza virus, isolation, kidneys, strains, chickens, China.

NAL Call Number: SF604.C58
Descriptors: antibodies, ELISA, immunodiagnosis, influenza virus A and B, chickens.

NAL Call Number: 49 T222
Abstract: The purpose of this study was to develop a microimmunodiffusion test in gel (MIDG), to detect antibodies against type A of avian influenza virus in chicken serum. An antigen was prepared from chorioallantonic membranes infected with the avian influenza virus strain (A/Ck/Puebla/14585-622/94H5N2). Microimmunodiffusion test in gel (MIDG) was compared with immunodiffusion test in agar (IDA), and Hemagglutination inhibition test (HI) which is the reference technique. Seventy five serum samples were obtained from specific pathogen free chicken, which resulted negative by the three assays. 163 serum samples were obtained from vaccinated poultry with HI titers from 1:10 to 1:1280. The sensitivity of these 2 agar gel precipitin tests was relatively low (43%) in comparison with HI. It was found that sensitivity of MIDG was identical to IDG (98%), and both were positives from HI titers of 1:320 and above. We conclude that IDA and MIDG are very useful in detecting infected poultry with virus that produce HI titers from 1:320 to 1:1280. Both, can be used in laboratories with a reduced infrastructure, besides, MIDG has the advantage of making possible the analysis a great quantity of samples at low cost.
Descriptors: broiler chickens, avian influenza virus, immunodiagnosis, birds, chickens, diagnosis, domestic animals, Galliformes, immunological techniques, influenza virus, livestock, meat animals, orthomyxoviridae, poultry, useful animals, viruses.

NAL Call Number: 41.8 Av5
Abstract: A monoclonal antibody (MAb)-based dot-enzyme-linked immunosorbent assay (ELISA) has been developed that detected the epitopes specifically associated with avian influenza virus (AIV). The dot-ELISA detected the antigens of AIV directly from clinical and field specimens. Data obtained from experimentally AIV-infected specific-pathogen-free chickens and also the 2001/02 AIV outbreak of serotype H7N2 positive flocks in Pennsylvania indicated that the mean sensitivity (Se) of the dot-ELISA ranged between 45% and
68% and the mean specificity (Sp), between 85% and 90%. The values were derived from various clinical and field specimens when compared with virus isolation with embryonating chicken eggs. On routine AIV surveillance samples, the dot-ELISA achieved a 92%-100% Sp on the basis of testing over 1500 AIV surveillance samples that were confirmed negative by virus isolation. The dot-ELISA detected AIV antigens with a 5-mul allantoic fluid sample that contained a concentration of 0.4 hemagglutinating units. Furthermore, the dot-ELISA retained its specificity for AIV because no cross-reactions were obtained with various other avian viruses. The findings in this study indicated that the dot-ELISA was highly sensitive and specific and comparable with the commercial Directigen(R) test in the detection of AIV obtained from clinical and field specimens.

Descriptors: immune system, infection, avian influenza, diagnosis, infectious disease, respiratory system disease, viral disease, monoclonal antibody based dot ELISA, mab dot ELISA, immunologic techniques, laboratory techniques.


NAL Call Number: SF774.J68

Abstract: Acute respiratory tract infections are leading causes of morbidity in poultry farms throughout the world. Avian pneumovirus (APV), avian influenza virus (AIV), and Newcastle disease virus (NDV) have been recognized as the most important pathogens of both chicken and turkeys. Single-virus reverse transcription-polymerase chain reaction (sRT-PCR) assays are used extensively to detect these viruses in clinical samples. This study reports the development and evaluation of a single-tube multiplex RT-PCR (mRT-PCR) assay for simultaneous and specific detection of APV, AIV, and NDV. Specific primers for each virus were selected that amplified products of predicted sizes from each virus in the mRT-PCR as well as in the sRT-PCR assays (438, 218, and 532 bp for APV, AIV, and NDV, respectively). The sensitivity and specificity of mRT-PCR assay were compared with those of the sRT-PCR. The mRT-PCR assay was as sensitive as the sRT-PCR assays because virus detection limits were similar in both assays. The detection limits of mRT-PCR assay were 10(0.5) tissue culture infective dose (50%) (TCID50)/ml, 10(1.2) TCID50/ml, and 10(0.7) TCID50/ml for APV, AIV, and NDV, respectively. Overall, there was an excellent correlation between mRT-PCR and sRT-PCR assays. No product amplification was obtained with nucleic acid from infectious bronchitis virus and reovirus using these primer sets. In summary, mRT-PCR assay holds potential to be an economical and rapid diagnostic method for the simultaneous detection of 3 avian respiratory viruses in chickens and turkeys.

Descriptors: influenza A virus, avian growth and development, metapneumovirus growth and development, Newcastle disease virus growth and development, poultry diseases virology, respiratory tract infections veterinary, reverse transcriptase polymerase chain reaction veterinary, turkeys, avian genetics, metapneumovirus genetics, Newcastle disease virus genetics, RNA, viral chemistry, viral genetics, respiratory tract infections diagnosis, respiratory tract infections virology, reverse transcriptase polymerase chain reaction methods, sensitivity and specificity.


NAL Call Number: 241.71 B75

Descriptors: chickens, laboratory diagnosis, avian influenza virus, viroses, animal diseases, immunological techniques, pathogenicity, identification, enzyme inhibitors, nucleotide sequence, antimitabolites, biological properties, birds, diagnosis, domestic animals, Galliformes, genomes, infectious diseases, influenza virus, livestock, microbial properties, orthomyxoviridae, poultry, useful animals, viruses.


NAL Call Number: SF600.C82

**Descriptors**: avian influenza virus, diagnosis, vaccination.


**Abstract**: Avian influenza and Newcastle disease share many common clinical symptoms. A method for rapid identification and differentiation of these two diseases comes to be necessary. A pair of primers was designed based on the nucleotide sequences of the highly conserved region of nucleoprotein of avian influenza virus. By reverse transcription-polymerase chain reaction (RT-PCR), this pair of primers could amplify a 330 bp fragment from 13 reference strains (H1-H13) and 77 field isolates of avian influenza virus with a high sensitivity and specificity. A multiplex RT-PCR procedure was then developed by using the above AIV primers and primers for the detection of Newcastle disease virus (NDV) developed in the previous study. This multiplex RT-PCR procedure could detect both AIV and NDV in a single reaction tube, and could differentiate vaccine strains from field isolates of NDV. Since the one tube multiplex RT-PCR could significantly reduce the time and cost of AIV and NDV, it is suitable for rapid identification and differentiation of AIV and NDV.

**Descriptors**: molecular genetics, multiplex reverse transcriptase polymerase chain reaction (multiplex RT-PCR) DNA amplification method, polymerase chain reaction, nucleotide sequencing sequencing method.


**Abstract**: Electrocardiograms of chickens infected with viscerotropic velogenic Newcastle disease virus (NDV) or virulent avian influenza virus (AIV) were characterized and compared. The ECG were monitored by radiotelemetry and were recorded twice daily before virus infection and during the course of the infection. Thirteen lead II intervals, segments, and amplitudes were measured and analyzed. The ECG of NDV-infected chickens were characterized by lengthened (P less than or equal to 0.05) ST segments and increased (P less than or equal to 0.05) P amplitudes. The ECG of AIV-infected chickens were characterized by lengthened (P less than or equal to 0.05) RS intervals, ST segments, TP intervals, and PR segments and by increased (P less than or equal to 0.05) P amplitudes. The TP intervals and PR segments of ECG of AIV-infected chickens were significantly (P less than or equal to 0.05) longer than those of NDV-infected chickens. The pronounced conduction delays indicated in the ECG of AIV-infected chickens may have diagnostic importance.

**Descriptors**: chickens, fowl plague physiopathology, heart physiopathology, Newcastle disease physiopathology, electrocardiography veterinary, influenza A virus avian pathogenicity, Newcastle disease virus pathogenicity, specific pathogen free organisms, virulence.


**NAL Call Number**: SF481.A9

**Descriptors**: reviews, avian influenza virus, epidemiology, diagnosis, control.
Abstract: Avian influenza virus infections are a major cause of morbidity and rapid identification of the virus has important clinical, economical and epidemiological implications. We have developed a one-tube Reverse Transcriptase Polymerase Chain Reaction (RT-PCR) for the rapid diagnosis of avian influenza A. A panel of reference influenza strains from various hosts including avian species, human, swine and horse were evaluated in a one tube RT-PCR using primers designed for the amplification of a 218 bp fragment of the NP gene. The PCR products were detected by PCR-ELISA by use of an internal catching probe confirming the NP influenza A origin. The PCR-ELISA was about 100 times more sensitive than detection of PCR products by agarose gel electrophoresis. RT-PCR and detection by PCR-ELISA is comparable in sensitivity to virus propagation in eggs. We also designed primers for the detection of the influenza. A subtypes H5 and H7 shown to have pathogenic potential in poultry. The H5 primers cover the cleavage site of the HA gene and specifically amplify influenza A subtype H5. The H7 primers also cover the HA cleavage site and detected all H7 reference strains investigated. In addition, the H7 primers also amplified very weak and/or additional bands on an agarose gel from other subtypes. However, the H7 origin and the pathogenic potential defined by the presence or absence of basic amino acids at the cleavage site can be determined by sequencing of the PCR product. As far as we know this is the first demonstration of RT-PCR detection on a panel of H7 strains using only one primer set.

Descriptors: influenza A virus avian isolation and purification, polymerase chain reaction methods, birds, DNA primers genetics, enzyme linked immunosorbent assay, fowl plague virology, hemagglutinins viral genetics, horses, avian classification, avian genetics, nucleoproteins analysis, nucleoproteins genetics, RNA viral analysis, reverse transcriptase polymerase chain reaction, sensitivity and specificity, swine.
be isolated in those of bovine origin. Serum antibodies are demonstrated by virus neutralization and ELISA tests. Immunofluorescent investigation of tissue samples and virus isolation methods are used for the diagnosis of classical swine fever (CSF). Monoclonal antibodies are used to differentiate among CSF, BVD virus and Suvac vaccine virus strains. Different ELISA and virus neutralization test are used for the demonstration of serum antibodies. In case of a suspected African Swine Fever case, haemadsorption and immunofluorescent tests are used for the demonstration of the virus and also pigs are inoculated with the suspected material. ELISA is used for the serological diagnosis of EBL. Cultivation of avian influenza viruses is carried out in embryonated eggs. The type of virus is determined by immuno-diffusion test and the type of haemagglutinin and neuraminidase - and occasionally - the virulence have also been determined. Haemagglutination inhibition test is used for the demonstration of serum antibodies. Practically the same methods are used for the diagnosis of Newcastle disease.

Descriptors: animal husbandry, infection, methods and techniques, infectious disease, swine fever, virus neutralization test diagnostic method, ELISA diagnostic method.


Abstract: A multiplex polymerase chain reaction (PCR) was developed and optimized to simultaneously detect 6 avian respiratory pathogens. Six sets of specific oligonucleotide primers for infectious bronchitis virus (IBV), avian influenza virus (AIV), infectious laryngotracheitis virus (ILTV), Newcastle disease virus (NDV), Mycoplasma gallisepticum (MG), and Mycoplasma synoviae (MS) were used respectively in the test. With the use of agarose gel electrophoresis for detection of the PCR-amplified DNA products, the sensitivity of detection was between 10 pg for IBV, AIV, MG, and ILTV and 100 pg for NDV and MS after 35 cycles of PCR. Similar sensitivity of these primers was achieved with chickens experimentally infected with respiratory pathogens. In experimental infections, the multiplex PCR was able to detect all the infected chickens in each group at 1 and 2 wk postinfection as compared with serologic tests at 2 wk postinfection that confirmed the presence of specific antibodies. The multiplex PCR was also able to detect and differentiate infections with two or more pathogens. No specific DNA amplification for respiratory avian pathogens was observed among noninoculated birds kept separately as a negative control group.

Descriptors: bird diseases diagnosis, Mycoplasma infections veterinary, polymerase chain reaction veterinary, virus diseases veterinary, bird diseases microbiology, bird diseases virology, birds, chick embryo, chickens, DNA, bacterial isolation and purification, DNA, viral isolation and purification, diagnosis, differential, electrophoresis, agar gel veterinary, Mycoplasma genetics, Mycoplasma isolation and purification, Mycoplasma infections diagnosis, polymerase chain reaction methods, RNA viral isolation and purification, reverse transcriptase polymerase chain reaction methods, reverse transcriptase polymerase chain reaction veterinary, sensitivity and specificity, species specificity, specific pathogen free organisms, virus diseases diagnosis.


Descriptors: avian influenza virus, infectious bronchitis virus, infectious laryngotracheitis virus, Mycoplasma gallisepticum, Mycoplasma synoviae, Newcastle disease virus, diagnostic techniques, experimental infections, polymerase chain reaction, poultry, chicks.


NAL Call Number: 500 N21P

Abstract: We report direct, real-time electrical detection of single virus particles with high selectivity by using nanowire field effect transistors. Measurements made with nanowire arrays modified with antibodies for influenza A showed discrete conductance changes characteristic of binding and unbinding in the presence of influenza A but not paramyxovirus or adenovirus. Simultaneous electrical and optical measurements using fluorescently labeled influenza A were used to demonstrate conclusively that the
conductance changes correspond to binding/unbinding of single viruses at the surface of nanowire devices. pH-dependent studies further show that the detection mechanism is caused by a field effect, and that the nanowire devices can be used to determine rapidly isoelectric points and variations in receptor-virus binding kinetics for different conditions. Lastly, studies of nanowire devices modified with antibodies specific for either influenza or adenovirus show that multiple viruses can be selectively detected in parallel. The possibility of large-scale integration of these nanowire devices suggests potential for simultaneous detection of a large number of distinct viral threats at the single virus level.

Descriptors: influenza A virus, avian isolation and purification, nanotechnology methods, paramyxoviridae isolation and purification, birds, electric conductivity, immunochemistry, avian chemistry, avian immunology, avian metabolism, microscopy, electron, transmission, microscopy, fluorescence, nanotechnology instrumentation, paramyxoviridae chemistry, paramyxoviridae immunology, paramyxoviridae metabolism, silicon chemistry.


Abstract: Influenza A virus subtype H5N1 causes a rapidly fatal systemic disease in domestic poultry and spreads directly from poultry to humans. The aim of this study was to develop a rapid, cost-saving and effective method for influenza A virus subtype H5N1 detection. The selected primer set was used in single-step RT-PCR for simultaneous detection in multiplex format of the 276-, 189-, and 131-bp fragments, corresponding to sequences specific for M, H5 and N1. The amplified DNA fragments were clearly separated by agarose gel electrophoresis. The sensitivity of this assay was about 10(3) copies/μL. Moreover, this method can be applied to detect not only avian but also human influenza A virus subtype H5N1. In conclusion, the highlights of this particular method are its rapidity and cost-effectiveness, thus rendering it feasible and attractive for large-scale screening at times of influenza A virus subtype H5N1 outbreak.

Descriptors: influenza virology, influenza A virus, avian isolation and purification, avian influenza virology, reverse transcriptase polymerase chain reaction methods, birds virology, chickens virology, influenza diagnosis, avian genetics, avian influenza diagnosis, sensitivity and specificity.


NAL Call Number: aSF995.6.1615 1981a

Descriptors: avian influenza virus, tests, assays, diagnostic procedures, symposium.


NAL Call Number: SF771.I5 1986

Descriptors: avian influenza virus, diagnosis, turkeys, United States, symposium.


NAL Call Number: QR375.V6

Abstract: When white leghorn (WL) chick embryos ranging in age from 8 to 13 days were inoculated with a variety of avian influenza virus (AIV) isolates, strain-specific differences in embryo mean death times (MDT) were observed. Non-highly pathogenic (nHP) strains killed 8 or 9 day-old embryos much more rapidly than 12 or 13 day-old embryos. Highly pathogenic (HP) strains, however, were less sensitive to embryo age resulting in similar MDTs in both older and younger embryos. These observations were consistent over a broad range of virus doses for both HP and nHP strains. When a HP derivative of H5N2 AIV was compared to its nHP parent, the derivative killed older embryos more rapidly than the parent virus, while MDTs in younger embryos were the same for both parent and derivative. The two strains further exhibited clear differences in the structure of their respective hemagglutinin, a previously described pathogenicity
determinant for this virus. Thus it may be possible to readily demonstrate the HP phenotype in AIV strains based on MDT measurements in WL embryos.

Descriptors: chick embryo microbiology, orthomyxoviridae pathogenicity, orthomyxoviridae infections veterinary, poultry diseases mortality, antibodies, monoclonal immunology, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral immunology, orthomyxoviridae infections mortality, specific pathogen free organisms, time factors, viral envelope proteins immunology.

NAL Call Number: QR189.A73
Descriptors: ELISA, hemagglutination inhibition test, immunodiagnosis, antibody testing, diagnostic techniques, poultry, influenza virus.

NAL Call Number: 41.8 Av5
Abstract: A workshop in which 17 practicing scientists participated was intended to address primarily people who use or could use biotechnology in their work and was confined to five techniques. Endonuclease fingerprinting and mapping involved cleaving nucleic acid with a specific restriction enzyme and separating the nucleic acid fragments by electrophoresis. Field and vaccine isolates of Pasteurella multocida could be distinguished; Salmonella enteritidis could be divided into three groups; chlamydia could be grouped into seven groups; and vaccinia, quail pox, and fowl pox could be clearly distinguished. Preparation of nucleic acid probes involved producing large amounts of labeled oligonucleotides, usually of unknown sequence. Successful probes had been made for infectious bursal disease virus, avian influenza virus, Newcastle disease virus, and infectious bronchitis virus. In Southern, Northern, and dot blotting, either DNA or RNA fragments were placed on or transferred to a solid substrate and probed. The procedure was able to detect infectious bursal disease virus, infectious bronchitis virus, Mycoplasma gallisepticum, and Marek's disease virus. In situ hybridization involved applying a labeled probe to frozen or fixed sections or to intact cells. In Polymerase chain reaction, two primers, some distance apart, were annealed to a denatured target DNA. Repeated cycles of DNA synthesis with a thermostable polymerase, denaturing, and reannealing resulted in great amplification of a rare sequence. After 30 cycles, a rare gene sequence could be amplified more than 10(6) times. It was used successfully to detect minute quantities of influenza virus and infectious bursal disease virus, and the process was used to facilitate DNA sequencing of coccidiosis gene segments.
Descriptors: poultry diseases diagnosis, blotting, northern, blotting, Southern, DNA restriction enzymes genetics, nucleic acid hybridization, nucleic acid probes, peptide mapping, polymerase chain reaction.

NAL Call Number: 448.3 AC85
Abstract: The plaque inhibition method was modified in order to evaluate the effectiveness of various combinations of antiviral substances. One substance (A) diffuses from the centre of cell culture, the other (B) is incorporated into the agar overlay at subinhibitory concentration. The inhibitory effect of the combination (A + B) is demonstrated by the increase in size of the inhibitory zone in comparison with the control inhibitory zone produced by the substance A alone. The ratio of the diameter of the inhibitory zone with substance combination (A + B) to the diameter of single drug control zone (substance A) serves as index DI (degree of interaction). Quantitative evaluation of the degree of potentiation using isobolograms showed that DI greater than 1.5 indicate a synergistic effect of the respective combinations. This inexpensive method can serve for rapid selection of suitable combinations out of number of substances. Model experiments were performed with combinations of selected inhibitors of virus replication.
Descriptors: antiviral agents pharmacology, influenza A virus avian drug effects, vaccinia virus drug effects, chick embryo, cycloheximide pharmacology, drug synergism, drug therapy, combination, microbial sensitivity tests, models, biological, plaque assay, ribavirin pharmacology, rimantadine pharmacology.


Abstract: This article is the second part of a series of review articles dedicated to immunohistochemical detection of infectious agents in domestic animals and covers infectious diseases of horses and birds. Immunohistochemistry is heavily used in these species for certain infectious diseases and until recently was the only quick and reliable diagnostic technique for some diseases (e.g., West Nile virus). A discussion of the immunohistochemical detection of the following infectious diseases of horses (Borna disease, eastern equine encephalitis virus, equine herpesvirus 1, equine protozoal myelitis, equine viral arteritis, leishmaniasis, viral papillomatosis, rabies, and West Nile fever) and birds (avian adenovirus, avian influenza virus, avian pneumovirus, budgerigar fledgling disease, chlamydiosis, Newcastle disease virus, Tyzzer's disease, and West Nile fever) is presented. In addition, references of selected equine and avian infectious diseases in which immunohistochemistry has been used and immunohistochemical protocols from the authors' laboratories are tabulated.

Descriptors: infection, veterinary medicine, borna disease, diagnosis, infectious disease, viral disease, Newcastle disease, infectious disease, viral disease, west nile fever, infectious disease, nervous system disease, viral disease, abortion, reproductive system disease, female, infectious disease, infectious disease, formalin fixation histology and cytology techniques, laboratory techniques, immunohistochemistry clinical techniques, diagnostic techniques, immunologic techniques, laboratory techniques, paraffin embedding histology and cytology techniques, laboratory techniques.


NAL Call Number: QR46.J6

Abstract: From May to December 1997, 18 cases of mild to severe respiratory illness caused by avian influenza A (H5N1) viruses were identified in Hong Kong. The emergence of an avian virus in the human population prompted an epidemiological investigation to determine the extent of human-to-human transmission of the virus and risk factors associated with infection. The hemagglutination inhibition (HI) assay, the standard method for serologic detection of influenza virus infection in humans, has been shown to be less sensitive for the detection of antibodies induced by avian influenza viruses. Therefore, we developed a more sensitive microneutralization assay to detect antibodies to avian influenza in humans. Direct comparison of an HI assay and the microneutralization assay demonstrated that the latter was substantially more sensitive in detecting human antibodies to H5N1 virus in infected individuals. An H5-specific indirect enzyme-linked immunosorbent assay (ELISA) was also established to test children's sera. The sensitivity and specificity of the microneutralization assay were compared with those of an H5-specific indirect ELISA. When combined with a confirmatory H5-specific Western blot test, the specificities of both assays were improved. Maximum sensitivity (80%) and specificity (96%) for the detection of anti-H5 antibody in adults aged 18 to 59 years were achieved by using the microneutralization assay combined with Western blotting. Maximum sensitivity (100%) and specificity (100%) in detecting anti-H5 antibody in sera obtained from children less than 15 years of age were achieved by using ELISA combined with Western blotting. This new test algorithm is being used for the seroepidemiologic investigations of the avian H5N1 influenza outbreak.

Descriptors: antibodies, viral blood, influenza A virus avian immunology, serologic tests methods, adolescent, adult, blotting, western methods, blotting, western statistics and numerical data, child, preschool, cross reactions, enzyme linked immunosorbent assay methods, enzyme linked immunosorbent assay statistics and numerical data, hemagglutination inhibition tests methods, hemagglutination inhibition tests statistics and numerical data, Hong Kong epidemiology, influenza epidemiology, influenza immunology, influenza transmission, avian classification, avian pathogenicity, middle aged, neutralization tests methods, neutralization tests statistics and numerical data, sensitivity and specificity, seroepidemiologic studies, serologic tests statistics and numerical data.

Avian plague virus was used as antigen in a counterimmunoelectrophoresis technique. This virus was selected because it detects only type-specific influenza A antibodies in human sera, avoiding the possible interference of other antigens with anodic migration. The results with reference sera, as well as the correlation of positive sera found by counterimmunoelectrophoresis and complement fixation with the proposed antigen, in the absence of other types of antibodies to fowl plague virus antigen, support the conclusion that the counterimmunoelectrophoresis technique reveals type-specific antibodies. The test is more sensitive than immunodiffusion but less sensitive than complement fixation. Its sensitivity, simplicity, and rapidity make it suitable for serologic surveys of human influenza A.

Descriptors: antibodies, viral analysis, antigens, viral, immuno-electrophoresis, influenza immunology, influenza A virus avian immunology, antibody specificity, chick embryo, complement fixation tests, guinea pigs immunology, immune sera, immunodiffusion.


Using a monoclonal antibody (MAb) specific for the H7 influenza surface glycoproteins, a serological enzyme-linked immunosorbent assay (ELISA) test has been developed. This MAb was made using the low-pathogenicity (LP) avian influenza (AI) strain (BS2676/99) isolated in Italy during a recent outbreak. The test is able to detect H7 antibodies in avian sera. The H7 ELISA has a 99% concordance of results with the classical hemagglutination inhibition (HI) test.

Descriptors: immune system, infection, ELISA, immunologic techniques, laboratory techniques, hemagglutination inhibition test.


NAL Call Number: 41.8 Av5

Abstract: The 1985 outbreak of high-pathogenicity avian influenza (HPAI) in Victoria, Australia, took 5 days to confirm by standard laboratory tests, during which time infected chickens continued excreting virus, thus creating the opportunity for transmission to other farms. An immunofluorescence test for the detection of viral antigen in tissue impression smears was evaluated as a rapid diagnostic test for HPAI virus infections of poultry. Several test configurations were compared for background reactions and strength of fluorescence, with the optimum combination found to be an influenza A group-specific monoclonal antibody, detected by an anti-mouse fluorescein isothiocyanate conjugate. Immunohistochemical examination of tissues from chickens experimentally infected with low-pathogenicity and HPAI viruses identified the pancreas as the organ most consistently containing high concentrations of HPAI viral antigen. This test has since been used in Australia in the rapid laboratory confirmation of three avian influenza outbreaks and in showing that numerous other suspect cases were not caused by avian influenza.

Descriptors: epidemiology, infection, avian influenza, diagnosis, infectious disease, transmission, viral disease, immunofluorescence, immunologic techniques, laboratory techniques, immunohistochemistry, pancreatic impression smears, clinical techniques, diagnostic techniques, pathogenicity.


NAL Call Number: 448.8 P942

Abstract: The paper describes a simple and convenient method for qualitative and quantitative evaluation of the capacity of influenza virus for autointerference consisting in the lack or considerable reduction of the cytolytic effect of the virus under agar overlay at a high multiplicity of infection. Some experimental and theoretical arguments assuming the role of defective interfering particles in the formation of the observed phenomenon. It is assumed that the detection of autointerference under agar may be used as an additional criterion for detection of non-plaque-forming strains of influenza virus, tentative determination of their interfering capacity as well as for the establishment of biological relationships of viruses.

Descriptors: influenza A virus physiology, viral interference, defective viruses, influenza A virus avian, plaque assay.


NAL Call Number: 41.8 Av5

Abstract: Serologic screening of avian sera for group-specific antibodies to type A influenza is currently accomplished by using the avian influenza (AI) agar gel immunodiffusion (AGID) test. A competitive enzyme-linked immunosorbent assay (CELISA) was developed using a baculovirus vector, Autographa californica nuclear polyhedrosis virus, expressing the nucleoprotein (NP) gene of A/Ann Arbor/6/60 influenza virus. The recombinant NP was obtained by inoculation of Spodoptera frugiperda (Sf9) insect cells or Trichoplusia ni insect larvae with the recombinant baculovirus. A hybridoma cell line producing monoclonal antibody against influenza virus A nucleoprotein was used to generate mouse ascitic fluid for the CELISA. The nucleoprotein and the monoclonal antibody were used without further purification in a CELISA for detection of avian-origin serum antibodies to type A influenza. The AI AGID and CELISA tests were compared for sensitivity and specificity using 1651 experimental and reference antisera. Samples discrepant in AGID and CELISA test results were further evaluated by the AI indirect fluorescent antibody (IFA), hemagglutination-inhibition (HI), and neuraminidase-inhibition (NI) tests. The results demonstrated a high degree of correlation between the AGID and CELISA test results, with the IFA, HI, and NI tests offering additional support of CELISA test specificity. The CELISA is a rapid, economical, sensitive, and specific serodiagnostic method for screening large numbers of avian sera for antibodies to avian influenza virus.

Descriptors: birds, avian influenza virus, ELISA, antibodies, body fluids, immunology, immunodiagnosis,
testing, recombinant antigens, microbial proteins, animal viruses, gene expression, cell culture, monoclonal antibodies, evaluation, immunological techniques, antibodies, antigens, body parts, culture techniques, diagnosis, immunoenzyme techniques, immunological factors, immunological techniques, in vitro culture, influenza virus, orthomyxoviridae, viruses, serum, serology, screening, cell lines, comparisons.


Descriptors: animal tissues, staining techniques, immunoperoxidase technique, diagnosis, experimental infection, immune response, avian influenza virus, broilers, poultry.


Abstract: Nucleic acid sequence-based amplification with electrochemiluminescent detection (NASBA/ECL) of avian influenza virus was compared with viral culture in embryonated chicken eggs. Virus was isolated from blood or anal swabs of chickens artificially infected with highly pathogenic avian influenza A/Chicken/Hong Kong/1000/97 (H5N1). Viral nucleic acid was detected in blood samples by NASBA/ECL immediately prior to death, whilst nucleic acid extracted from anal swabs was detected from the day following artificial infection until death. Thus, blood and/or anal swabs are a suitable source of material for the detection of avian influenza in dead birds, but anal swabs are more suitable for detection of viral genetic material in live birds. Dilution of a known viral standard was used to determine the limit of sensitivity for both NASBA/ECL and egg culture detection methods. The NASBA/ECL method was equivalent in sensitivity to egg culture. The NASBA/ECL results agreed with egg culture data in 71/94 (75.5%) tissue samples obtained from artificially infected birds.

Descriptors: infection, molecular genetics, avian influenza virus infection, viral disease, electrochemiluminescence laboratory techniques, nucleic acid sequence based amplification genetic techniques, laboratory techniques, virus isolation.


Descriptors: avian influenza virus, diagnosis, hemagglutinins, monoclonal antibodies, poultry.


NAL Call Number: SF995.W4

Descriptors: diagnostic techniques, avian influenza virus, turkeys, phagocytosis assay.


NAL Call Number: SF995.W4

Descriptors: ELISA, avian influenza virus, immunoenzyme techniques, immunological techniques, influenza virus, orthomyxoviridae, viruses.


Descriptors: avian influenza virus, immunofluorescence, poultry, antibody.

An enzyme-linked immunosorbent assay (ELISA) was developed for detecting antibody to type A avian influenza (AI) virus. The sensitivity and group specificity of the AI-ELISA were compared with those of the agar-gel-precipitin test (AGPT) and the hemagglutination-inhibition (HI) test under conditions of both controlled and field exposure. During the course of temporal experimental infection (0-76 days) of specific-pathogen-free (SPF) chickens with AI subtype Hav9N2, the AI-ELISA was able to detect specific AI antibody as early as 8 days postinoculation (PI), and it measured rising levels of antibody through 35 days PI, at which time the chickens were re-exposed to AI virus. Conversely, AGP tests were negative through 35 days PI, and HI tests began to detect low levels of AI antibody only at 21 days PI. Following a secondary infection at 35 days PI with the same AI subtype, all tests measured rising levels of AI-specific antibody (35-76 days PI). However, the AGP test was positive at only the 7- and 14-day samplings postsecondary immunization. Under field conditions, the AI-ELISA was able to detect serum AI antibody in flocks from which highly pathogenic AI was isolated, but the AGP tests of these sera were negative.

Descriptors: antibodies, viral analysis, chickens, fowl plague immunology, influenza A virus avian immunology, enzyme linked immunosorbent assay, hemagglutination inhibition tests veterinary, precipitin tests veterinary.


A real-time reverse transcriptase/polymerase chain reaction (RRT-PCR) assay was developed using hydrolysis probes for the detection of avian influenza virus (AIV) and the H5 and H7 subtypes. The AIV specific primers and probes were directed to regions of the AIV matrix gene that are conserved among most type A influenza viruses. The H5 and H7 primers and probes are directed to H5 and H7 hemagglutinin gene regions that are conserved among North American avian influenza viruses. The sensitivity and specificity of this RRT-PCR assay was compared to virus isolation (VI) in chicken embryos with 1550 clinical swab samples from 109 live-bird markets (LBMs) in New York and New Jersey. RRT-PCR detected influenza in samples from 61 of 65 (93.8%) of the LBMs that were the sources of VI positive samples. Of the 58 markets that were positive for H7 influenza by hemagglutination inhibition assay, RRT-PCR detected H7 influenza in 56 markets (96.5%). Too few H5 positive samples were obtained to validate the H5 RRT-PCR assay in this study. Although RRT-PCR was less sensitive than VI on an individual sample basis, this study demonstrated that the AIV and H7 RRT-PCR assays are good tools for the rapid screening of flocks and LBMs.

Descriptors: infection, molecular genetics, avian influenza, infectious disease, respiratory system disease, viral disease, hemagglutination inhibition assay bioassay techniques, immunologic techniques, laboratory techniques, real time reverse transcriptase polymerase chain reaction, real time RT PCR, clinical techniques, diagnostic techniques, genetic techniques, viral isolation, diagnostic techniques, live bird markets.

reproducible detection limit for H7 of approximately 104 HA gene copies and approximately 104-105 HA gene copies of H5. A direct comparison of H5-H7 multiplex RRT-PCR with hemagglutination inhibition (HI) was performed with 83 AI RRT-PCR and virus isolation positive tracheal and cloacal swab samples obtained from various avian species and environmental swabs from live-bird markets in New York and New Jersey. Both multiplex RRT-PCR and HI agreed on the subtype determination of 79 (95.2%) of the 83 samples, of which 77 were positive for H7 and two were determined to be non-H5/non-H7 subtypes. No samples were determined to be the H5 subtype by either assay.

Descriptors: immune system, infection, molecular genetics, avian influenza, infectious disease, respiratory system disease, viral disease, hemagglutination inhibition clinical techniques, diagnostic techniques, immunologic techniques, laboratory techniques, multiplex real time reverse transcriptase polymerase chain reaction, multiplex RT PCR, clinical techniques, genetic techniques.


NAL Call Number: QR46.J6

Abstract: A real-time reverse transcriptase PCR (RRT-PCR) assay based on the avian influenza virus matrix gene was developed for the rapid detection of type A influenza virus. Additionally, H5 and H7 hemagglutinin subtype-specific probe sets were developed based on North American avian influenza virus sequences. The RRT-PCR assay utilizes a one-step RT-PCR protocol and fluorogenic hydrolysis type probes. The matrix gene RRT-PCR assay has a detection limit of 10 fg or approximately 1,000 copies of target RNA and can detect 0.1 50% egg infective dose of virus. The H5- and H7-specific probe sets each have a detection limit of 100 fg of target RNA or approximately 10(3) to 10(4) gene copies. The sensitivity and specificity of the real-time PCR assay were directly compared with those of the current standard for detection of influenza virus: virus isolation (VI) in embryonated chicken eggs and hemagglutinin subtyping by hemagglutination inhibition (HI) assay. The comparison was performed with 1,550 tracheal and cloacal swabs from various avian species and environmental swabs obtained from live-bird markets in New York and New Jersey. Influenza virus-specific RRT-PCR results correlated with VI results for 89% of the samples. The remaining samples were positive with only one detection method. Overall the sensitivity and specificity of the H7- and H5-specific RRT-PCR were similar to those of VI and HI.

Descriptors: fowl plague virology, hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian isolation and purification, poultry diseases virology, reverse transcriptase polymerase chain reaction, chick embryo, fluorescent dyes, hemagglutination inhibition tests, avian classification, avian genetics, poultry, sensitivity and specificity.


NAL Call Number: SF774.J68

Abstract: Proficiency assessments are important elements in quality control for diagnostic laboratories. Traditionally, proficiency testing for polymerase chain reaction (PCR)-based assays has involved the use of clinical samples, samples "spiked" with live agents or DNA plasmids. Because of government regulations and biosecurity concerns, distribution of live high-consequence pathogens of livestock and poultry, such as avian influenza, is not possible, and DNA plasmids are not technically suitable for evaluating RNA virus detection. Therefore, a proficiency testing panel using whole avian influenza in a diluent containing a phenolic disinfectant that inactivates the virus while preserving the RNA for at least 8 weeks at -70 C was developed and used in a multicenter proficiency assessment for a type A influenza real-time reverse transcriptase (RT)-PCR test. The test, which was highly standardized, except for variation in the real-time RT-PCR equipment used, was shown to be highly reproducible by proficiency testing in 12 laboratories in the United States, Canada, and Hong Kong. Variation in cycle threshold values among 35 data sets and 490 samples was minimal (CV = 5.19%), and sample identifications were highly accurate (96.7% correct identifications) regardless of real-time PCR instrumentation.

**NAL Call Number:** 41.8 Z52

**Abstract:** Reverse transcriptase (RT) PCR assays have been developed to improve the diagnosis of avian influenza A. RT-PCR using primers complementary to a conserved region of the matrix protein was assessed as being suitable for the detection of influenza A virus RNA from poultry as well as from pigs, horses and humans, regardless of the haemagglutinin (HA) and neuraminidase (NA) subtype. Therefore, this RT-PCR is a valuable tool to confirm the initial diagnosis of any influenza A infection. As a second approach, experiments were performed to identify the HA gene encoding the post-translational cleavage site of potentially highly pathogenic AIV isolates by RT-PCR. The principal aim was to design one universal primer pair for each virus subtype, H5 and H7, respectively, which allows the detection of all strain variants using only one consistent method. To realize this objective, it was necessary to develop 'wobble' primers. AIV RNAs from seven H5 and 11 H7 subtype viruses included in the investigations were specifically recognized by RT-PCR using these primers. This method therefore provides a rapid, subtype-specific diagnosis and subsequent sequencing of H5 and H7 avian influenza viruses.

**Descriptors:** animal husbandry, infection, methods and techniques, influenza A virus infection, avian, diagnosis, viral disease, reverse transcriptase polymerase chain reaction diagnostic method, polymerase chain reaction.


**NAL Call Number:** 41.8 Avv5

**Abstract:** Using clinical materials from experimentally infected poultry, we established an effective method for the preparation of viral RNA directly from tissue samples and eggs. Furthermore, our type A-specific matrix reverse transcription-polymerase chain reaction (RT-PCR) test was improved, and an H7 subtype-specific nested RT-PCR, which includes the hemagglutinin cleavage site, was designed. Both RT-PCR systems proved to be as sensitive as virus isolation. In addition, the labeled H7 HA-nested PCR primers were suitable for sequencing of the PCR products. The RT-PCR amplification of viral RNA and sequencing of the PCR product allows for the sensitive and rapid differentiation between low-pathogenic and highly pathogenic avian influenza viruses.

**Descriptors:** immune system, infection, molecular genetics, avian influenza, infectious disease, respiratory system disease, viral disease, H7 subtype, specific nester, reverse transcriptase polymerase chain reaction, clinical techniques, RT-PCR, diagnostic techniques, genetic techniques, laboratory techniques, genetic techniques, type A specific matrix.


**Abstract:** Haemagglutination-inhibition tests (HI) are used to detect increases in influenza antibody in serum. However, they are relatively insensitive for the detection of human antibody responses to avian haemagglutinin, even in the presence of high titres of neutralising antibody after confirmed infection or vaccination. Human influenza viruses bind preferentially sialic acid containing N-acetyleneuraminic acid alpha2,6-galactose (SAalpha2,6Gal) linkages while avian and equine viruses bind preferentially those containing N-acetyleneuraminic acid alpha2,3-galactose (SAalpha2,3Gal) linkages. Increasing the proportion of SAalpha2,3Gal linkages on the erythrocytes used, by enzymatic modification or change of species, improves the ability of erythrocytes to bind to avian influenza strains and thereby improves the sensitivity of detection of antibody to avian and equine HA in a range of mammalian and human sera using HI tests.

**Descriptors:** clinical chemistry, hematology, infection, methods and techniques, serology, veterinary medicine, hemagglutinin inhibition test clinical techniques, diagnostic techniques, immunologic techniques,

**Abstract:** An avian influenza (AI) real time reverse transcriptase-polymerase chain reaction (RRT-PCR) test was previously shown to be a rapid and sensitive method to identify AI virus-infected birds in live-bird markets (LBMs). The test can also be used to identify avian influenza virus (AIV) from environmental samples. Consequently, the use of RRT-PCR was being considered as a component of the influenza eradication program in the LBMs to assure that each market was properly cleaned and disinfected before allowing the markets to be restocked. However, the RRT-PCR test cannot differentiate between live and inactivated virus, particularly in environmental samples where the RRT-PCR test potentially could amplify virus that had been inactivated by commonly used disinfectants, resulting in a false positive test result. To determine whether this is a valid concern, a study was conducted in three New Jersey LBMs that were previously shown to be positive for the H7N2 AIV. Environmental samples were collected from all three markets following thorough cleaning and disinfection with a phenolic disinfectant. Influenza virus RNA was detected in at least one environmental sample from two of the three markets when tested by RRT-PCR; however, all samples were negative by virus isolation using the standard egg inoculation procedure. As a result of these findings, laboratory experiments were designed to evaluate several commonly used disinfectants for their ability to inactivate influenza as well as disrupt the RNA so that it could not be detected by the RRT-PCR test. Five disinfectants were tested: phenolic disinfectants (Tek-trol and one-stroke environ), a quaternary ammonia compound (Lysol no-rinse sanitizer), a peroxygen compound (Virkon-S), and sodium hypochlorite (household bleach). All five disinfectants were effective at inactivating AIV at the recommended concentrations, but AIV RNA in samples inactivated with phenolic and quaternary ammonia compounds could still be detected by RRT-PCR. The peroxygen and chlorine compounds were effective at some concentrations for both inactivating virus and preventing amplification by RRT-PCR. Therefore, the RRT-PCR test can potentially be used to assure proper cleaning and disinfection when certain disinfectants are used.

**Descriptors:** animal husbandry, infection, avian influenza, infectious disease, respiratory system disease, viral disease, environmental disinfection clinical techniques, therapeutic and prophylactic techniques, real time reverse transcriptase polymerase chain reaction clinical techniques, diagnostic techniques, genetic techniques, laboratory techniques, influenza eradication program, live bird markets.


**Descriptors:** avian influenza virus, vaccines, influenza virus, orthomyxoviridae, viruses.


**Descriptors:** virology, laboratory diagnosis, farm animals, identification.


**Abstract:** Vaccination programs for the control of avian influenza (AI) in poultry have limitations due to the problem of differentiating between vaccinated and virus-infected birds. We have used NS1, the conserved nonstructural protein of influenza A virus, as a differential diagnostic marker for influenza virus infection. Experimentally infected poultry were evaluated for the ability to induce antibodies reactive to NS1 recombinant protein produced in Escherichia coli or to chemically synthesized NS1 peptides. Immune sera were obtained from chickens and turkeys inoculated with live AI virus, inactivated purified vaccines, or
inactivated commercial vaccines. Seroconversion to positivity for antibodies to the NS1 protein was achieved in birds experimentally infected with multiple subtypes of influenza A virus, as determined by enzyme-linked immunosorbent assay (ELISA) and Western blot analysis. In contrast, animals inoculated with inactivated gradient-purified vaccines had no seroconversion to positivity for antibodies to the NS1 protein, and animals vaccinated with commercial vaccines had low, but detectable, levels of NS1 antibodies. The use of a second ELISA with diluted sera identified a diagnostic test that results in seropositivity for antibodies to the NS1 protein only in infected birds. For the field application phase of this study, serum samples were collected from vaccinated and infected poultry, diluted, and screened for anti-NS1 antibodies. Field sera from poultry that received commercial AI vaccines were found to possess antibodies against AI virus, as measured by the standard agar gel precipitin (AGP) test, but they were negative by the NS1 ELISA. Conversely, diluted field sera from AI-infected poultry were positive for both AGP and NS1 antibodies. These results demonstrate the potential benefit of a simple, specific ELISA for anti-NS1 antibodies that may have diagnostic value for the poultry industries.

Descriptors: animals, viral blood antibodies, chickens, avian influenza A virus classification, avian influenza A virus immunology, avian influenza diagnosis, avian influenza immunology, avian influenza prevention and control, avian influenza virology, poultry, poultry diseases diagnosis, poultry diseases prevention and control, poultry diseases virology, non-U.S. Government research support, non-U.S. Government P.H.S. research support, turkeys, vaccination, viral nonstructural proteins chemical synthesis, viral nonstructural proteins immunology, viral vaccines administration and dosage, viral antibodies, influenza virus INS1 protein, viral nonstructural proteins, viral vaccines.

NAL Call Number: 41.8 Av5
Descriptors: avian influenza virus, inhibition assay, classification.

NAL Call Number: SF995.W4
Descriptors: avian influenza virus, ELISA, detection.

NAL Call Number: S13.S44
Abstract: The data on production of quadromas secreting bi-sitespecific monoclonal immunoglobulins to avian influenza A virus nucleoprotein and horseradsh peroxidase are presented. The monoclonal antibodies application in immunoassay was shown to be possible by development of test-system for avian influenza laboratory diagnostics.
Descriptors: immune system, immunoassay diagnostic method, laboratory diagnostics diagnostic method, nucleoprotein, ELISA, analytical method.

Descriptors: avian influenza virus, characterization, diagnosis, diagnostic techniques, DNA, genetic analysis, microarray, hybridization, subtyping, poultry, fowl.

NAL Call Number: SF604.C58
Descriptors: Newcastle disease, amino acid sequences, avian infectious bursitis, bronchitis, death,
diagnostic techniques, embryos, pathogenicity, polymerase chain reaction, reverse transcription, allantoic fluid, avian influenza virus, poultry, fowl.


NAL Call Number: 448.8 J826

Abstract: An economic method for quantitative assay of viruses is presented. In this "canule stick-plaque test" (German abbreviation SPT) samples of viruses, geometrically diluted and taken up by a canule, are inoculated by sticking into monolayer cell cultures overlayed with agar medium. A plaquelike CPE detectable by neutral red staining develops in the area of the inoculation. The frequency of this CPE formation depends on the concentration of viruses in the inoculated dilution. This dose-response allows calculation of the ID 50. In this way it is possible to carry out titration involving 6 dilutions and 10 inoculations per dilution using 3 common Petri dishes (6 cm in diameter), only. The sensitivity, accuracy, and reproductibility of this method are described and discussed.

Descriptors: plaque assay methods, viruses isolation and purification, chick embryo, cytopathogenic effect, viral, herpesvirus 1, suid isolation and purification, influenza A virus avian isolation and purification, sindbis virus isolation and purification, tissue culture.


Abstract: An optical immunoassay test, FLU OIA (BIOSTAR, USA), was evaluated for the diagnosis of influenza viral infection. The reactivity of the FLU OIA test was evaluated using 42 influenza strains (25 human influenza A, 12 human influenza B, 2 swine influenza A and 3 avian influenza A strains). The FLU OIA test showed positive results for all influenza strains. There was no evidence that cross-reactivity occurred with non-influenza viruses. The detection limit of the FLU OIA test was found to be 3.0-6.5 x 10(4) pfu/assay for human influenza A and B strains. The sensitivity and specificity of the FLU OIA test compared to isolation in cell culture was 89.7% and 76.0% for testing of 54 nasopharyngeal aspirate specimens. The FLU OIA test is rapid and easy for the detection of influenza A and B viral antigen and provide a valuable tool for the rapid diagnosis of influenza viral infection.

Descriptors: antigens, viral analysis, influenza A virus immunology, influenza B virus immunology, evaluation studies, immunoassay methods.


NAL Call Number: 41.8 Ex7

Abstract: Seven different hyperimmune serum samples from chickens or rabbits were conjugated with fluorescein isothiocyanate and reacted with reference influenza A strains. Conclusions are that direct immunofluorescence reliably detected avian influenza viruses and distinguished them from Newcastle disease virus. A diagnostic set of nine inactivated influenza A viruses is available, covering subtypes from H3 to H11.

Descriptors: fowl plague diagnosis, poultry diseases diagnosis, antibodies, viral analysis, influenza A virus avian immunology, poultry.


NAL Call Number: QR180.3.D4

Abstract: Single-radial-immunodiffusion (SRD) provides a sensitive and reproducible in vitro assay for haemagglutinin (HA) concentration in inactivated influenza vaccines. The use of SRD for human influenza vaccine standardization and application for equine and avian influenza vaccines is discussed. In clinical trials, vaccine HA concentration measured by SRD has been shown to be directly related to antibody
responses and to protection against challenge. The use of SRD may considerably reduce the usage of animals for potency testing of veterinary influenza vaccines.

**Descriptors:** influenza vaccine standards, vaccines, attenuated standards, antibodies, viral biosynthesis, chickens, horses, immunodiffusion standards, influenza prevention and control, influenza veterinary.


**NAL Call Number:** 41.8 Av5

**Descriptors:** avian influenza virus, diagnosis, embryos, ducks, pheasants, Psittaciformes, turkeys, Galliformes, California, Illinois, Montana, Washington, United States, OECD countries, reviews.


**NAL Call Number:** SF995.A1A9

**Abstract:** Rapid serum agglutination, haemagglutination inhibition and enzyme-linked immunosorbent assays were used to screen Swiss fancy breed chicken flocks for antibodies against 12 avian infectious agents. For this purpose, 1,002 blood samples from 40 flocks were collected and tested. Ten percent of the samples were positive for *Salmonella gallinarum-pullorum* and 62.5% of the flocks were affected. More than 75% of the flocks had antibodies against *Mycoplasma gallisepticum/Mycoplasma synoviae*, infectious bronchitis, infectious bursal disease, avian encephalomyelitis, infectious chicken anaemia and reoviral arthritis. Low prevalence of antibodies was recorded for *Salmonella enteritidis*, avian influenza, avian leukosis and Newcastle disease (2.0 to 4.0%).

**Descriptors:** monitoring, immunologic veterinary, *Mycoplasma* infections veterinary, poultry, poultry diseases epidemiology, *Salmonella* infections, animal epidemiology, serologic tests veterinary, antibodies, bacterial blood, antibodies, viral blood, monitoring, immunologic methods, *Mycoplasma* infections epidemiology, poultry diseases immunology, prevalence, serologic tests methods, Switzerland epidemiology.


**Descriptors:** diagnosis, prevention, treatment, avian influenza virus, fowl, Galliformes.


**NAL Call Number:** 41.9 T572

**Descriptors:** chickens, avian influenza virus, diagnosis, PCR, birds, domestic animals, Galliformes, influenza virus, livestock, orthomyxoviridae, poultry, useful animals, viruses.


**NAL Call Number:** 448.8 P942

**Descriptors:** hemagglutination inhibition tests, influenza immunology, antibodies, viral analysis, antibody formation, antigens, viral analysis, chick embryo, complement fixation tests, hemagglutination, viral, influenza A virus avian immunology, influenza A virus immunology, neutralization tests.


**Descriptors:** avian influenza virus, infectious bronchitis virus, Newcastle disease virus, polymerase chain reaction, China, Galliformes.


**NAL Call Number:** 41.8 Av5

**Abstract:** A competitive enzyme-linked immunosorbent assay (C-ELISA) employing a baculovirus-expressed recombinant nucleoprotein and a monoclonal antibody was developed for the detection of antibodies to type A influenza virus nucleoprotein. The performance of the C-ELISA was evaluated by testing 756 chickens, 1123 turkeys, 707 emus, and 1261 ostriches, for a total of 3847 serum samples. Relative to the agar gel immunodiffusion (AGID) test, the C-ELISA had a sensitivity of 100% for all four species. The C-ELISA's sensitivity relative to the hemagglutination-inhibition (HI) test results was 100% for chicken, turkey, and emu and 96.2% for the ostrich serum samples. More than 90% of the AGID-negative/C-ELISA-positive serum samples were found positive by HI for at least one influenza serotype. The specificity of C-ELISA relative to AGID ranged from 85.5% to 99.8% for sera collected from these species. These results indicated that the C-ELISA was more sensitive and more specific than the AGID test and as sensitive and as specific as the HI test. The C-ELISA has the potential to replace the AGID test for screening sera from avian species, including ratites, for detection of antibodies to type A influenza virus.

**Descriptors:** antibodies, viral immunology, enzyme linked immunosorbent assay, influenza A virus avian immunology, nucleoproteins immunology, chickens immunology, chickens virology, emus immunology, emus virology, fowl plague immunology, fowl plague virology, ostriches immunology, ostriches virology, turkeys immunology, turkeys virology.


**NAL Call Number:** SF604.C485

**Descriptors:** immunoprecipitation tests, serological surveys, avian influenza virus, diagnosis, management, outbreaks, pheasants, China.


**NAL Call Number:** QR46.J6

**Abstract:** A rapid culture assay which allows for the simultaneous typing and subtyping of currently circulating influenza A(H1N1), A(H3N2), and B viruses in clinical specimens was developed. Pools of monoclonal antibodies (MAbs) against influenza A and B viruses and MAbs HA1-71 and HA2-76, obtained by immunizing mice with the denatured hemagglutinin subfragments HA1 and HA2 of influenza virus A/Victoria/3/75, were used for immunoperoxidase staining of antigens in infected MDCK cells. MAb HA1-71 reacted exclusively with influenza A viruses of the H3 subtype, while MAb HA2-76 reacted with subtypes H1, H3, H4, H6, H8, H9, H10, H11, and H12, as determined with 78 human, 4 swine, and 10 avian influenza virus reference strains subtyped by the hemagglutination inhibition test. To determine if the technique can be used as a rapid diagnostic test, 263 known influenza virus-positive frozen nasal or throat swabs were inoculated into MDCK cells. After an overnight incubation, the cells were fixed and viral antigens were detected by immunoperoxidase staining. Influenza A viruses of the H1 and H3 subtypes were detected in 31 and 113 specimens, respectively. The subtypes of 10 influenza A virus-positive specimens could not be determined because they contained too little virus. Influenza B viruses were detected in 84 specimens, and 25 specimens were negative. We conclude that this assay is a rapid, convenient, non-labor-intensive, and relatively inexpensive test for detecting, typing, and subtyping influenza viruses in clinical specimens.

**Descriptors:** influenza virology, orthomyxoviridae classification, orthomyxoviridae isolation and purification, virus cultivation methods, antibodies, monoclonal, antibodies, viral, cell line, disease outbreaks, dogs, evaluation studies, false negative reactions, immunoenzyme techniques, influenza diagnosis, influenza epidemiology, influenza A virus avian classification, avian immunology, avian isolation and purification, human classification, human immunology, human isolation and purification, porcine classification, porcine immunology, porcine isolation and purification, influenza B virus classification, influenza B virus immunology, influenza B virus isolation and purification, mice, orthomyxoviridae immunology, serotyping, time factors.
Viral Typing and Characterization

NAL Call Number: 41.8 R312
Abstract: Seven influenza viruses isolated from turkeys in Great Britain since 1963 were typed by haemagglutination inhibition and neuraminidase inhibition tests as: A/turkey/England/63 (Hav 1 Nav 3), A/turkey/England/66 (Hav 6 N2), A/turkey/England/69 (Hav 7 N2), A/turkey/Scotland/70 (Hav ? Neq 1), A/turkey/England/N28/73 (Hav 5 N2), A/turkey/England/110/77 (Hav 6 N2), A/turkey/England/647/77 (Hav 1 Neq 1). A/turkey/Scotland/70 failed to show a haemagglutinin relationship with any of the representative strains and may possess a hitherto unreported haemagglutinin subtype. Intravenous pathogenicity tests in six-week-old birds showed only A/turkey/England/63 to have high virulence for turkeys and chickens. A/turkey/England/69 produced some signs of disease in chickens and, to a lesser extent, turkeys but all other isolates were avirulent.
Descriptors: influenza A virus avian immunology, antigens, viral analysis, chickens, fowl plague etiology, Great Britain, hemagglutination tests, turkeys microbiology.

Abstract: In the last two decades, various molecular biological methods were introduced in diagnostic virology. They are used for the rapid detection of viral nucleic acids, genetic characterization of the pathogens responsible for many viral infections and tracking of the origin and spread of viruses. In this review, the application of molecular biology methods, particularly the combined approach of amplifying defined fragments of viral genomes, using the polymerase chain reaction and subsequent nucleotide sequencing analysis, is described. Emphasis is placed on some of the few important viruses causing economically important diseases in poultry, like Newcastle disease virus, avian influenza virus, infectious bursal disease virus and chicken anaemia virus.
Descriptors: avian infectious bursitis, diagnosis, diagnostic techniques, DNA sequencing, fowl diseases, genomes, influenza, methodology, molecular biology, Newcastle disease, polymerase chain reaction, poultry, reviews, avian influenza virus, chicken anaemia virus, fowls, infectious bursal disease virus, Newcastle disease virus.

NAL Call Number: QR360.J6
Abstract: In April 1983, an influenza virus of low virulence appeared in chickens in Pennsylvania. Subsequently, in October 1983, the virus became virulent and caused high mortality in poultry. The causative agent has been identified as an influenza virus of the H5N2 serotype. The hemagglutinin is antigenically closely related to tern/South Africa/61 (H5N3) and the neuraminidase is similar to that from human H2N2 strains (e.g., A/Japan/305/57) and from some avian influenza virus strains (e.g., A/turkey/Mass/66 [H6N2]). Comparison of the genome RNAs of chicken/Penn with other influenza virus isolates by RNA-RNA hybridization indicated that all of the genes of this virus were closely related to those of various other influenza virus isolates from wild birds. Chickens infected with the virulent strain shed high concentrations of virus in their feces (10(7) 50% egg infective dose per g), and the virus was isolated from the albumin and yolk of eggs layed just before death. Virus was also isolated from house flies in chicken houses. Serological and virological studies showed that humans are not susceptible to infection with the virus, but can serve as short-term mechanical carriers. Analysis of the RNA of the viruses isolated in April and October by gel migration and RNA-RNA hybridization suggested that these strains were very closely related. Oligonucleotide mapping of the individual genes of virulent and avirulent strains showed a limited number of changes in the genome RNAs, but no consistent differences between the virulent and avirulent
strains that could be correlated with pathogenicity were found. Polyacrylamide gel analysis of the early (avirulent) isolates demonstrated the presence of low-molecular-weight RNA bands which is indicative of defective-interfering particles. These RNAs were not present in the virulent isolates. Experimental infection of chickens with mixtures of the avirulent and virulent strains demonstrated that the avirulent virus interferes with the pathogenicity of the virulent virus. The results suggest that the original avirulent virus was probably derived from influenza viruses from wild birds and that the virulent strain was derived from the avirulent strain by selective adaptation rather than by recombination or the introduction of a new virus into the population. This adaptation may have involved the loss of defective RNAs, as well as mutations, and thus provides a possible model for a role of defective-interfering particles in nature.

Descriptors: chickens microbiology, influenza A virus avian pathogenicity, RNA viral analysis, antigens, viral analysis, defective viruses genetics, Diptera microbiology, ducks microbiology, avian genetics, avian immunology, swine microbiology, viral interference, virus replication.


NAL Call Number: 448.8 V81

Descriptors: hemagglutinin glycoproteins, influenza virus genetics, influenza virology, influenza A virus human genetics, neuraminidase genetics, adolescent, adult, antigens, viral immunology, base sequence, child, preschool, DNA, viral, disease outbreaks, genes viral, Hong Kong epidemiology, infant, influenza epidemiology, human growth and development, human immunology, human isolation and purification, middle aged, molecular sequence data, phylogeny.


NAL Call Number: 442.8 R325

Abstract: A total of 145 influenza A viruses were isolated from ducks, geese and passerine birds in Ontario, Quebec and the Maritimes in July-August 1977. Antigenic characterization of these isolates included five hemagglutinin (Hsw1, Hav4, Hav5, Hav6, Hav7) and five neuraminidase subtypes (N1, N2, Neq1, Neq2, Nav1) in nine different combinations; one combination Hav7 Neq1 had not been previously reported. The majority of these viruses were Hsw1 N1, antigenically related to influenza viruses in pigs and humans. This large reservoir of influenza A viruses circulating in ducks may well be involved in the appearance of new viruses in other species, including humans.

Descriptors: animal population groups microbiology, animals, wild microbiology, birds microbiology, influenza A virus avian isolation and purification, Canada, disease reservoirs, ducks microbiology, hemagglutinins viral analysis, avian immunology, neuraminidase analysis, viral proteins analysis.


NAL Call Number: 41.8 Av5

Abstract: Low-pathogenicity avian influenza (LPAI) subtype H7N3 was diagnosed on a two-age broiler breeder farm in Abbotsford, British Columbia (BC), in early February 2004. The presenting complaint in the older index flock was feed refusal, with 0.5% mortality over 72 hr that resolved over the following week. Ten days after the initial complaint in the index flock, a younger flock in an adjacent barn experienced an abrupt spike in mortality (25% in 48 hr). The gross lesions of tracheal hyperemia and hilar pulmonary consolidation were subtle and nonspecific, and the diagnosis of avian influenza required laboratory confirmation. Two different viruses were isolated from the index farm: a LPAI (H7N3) was isolated from the older flock and a high-pathogenicity avian influenza (HPAI) (H7N3), which had an additional 21 base insertion at the hemagglutinin-cleavage site, was isolated from the younger flock. The presence of this insertion sequence and the similarity of adjacent sequences indicate that the LPAI had mutated into HPAI at some point
between the first and second barn. Despite enhanced on-farm biosecurity measures, the virus was not contained on the index farm and eventually spread to over 40 commercial poultry facilities before massive depopulation efforts enabled its eradication.

Descriptors: chickens virology, influenza A virus, avian pathogenicity, avian influenza pathology, virology, base sequence, British Columbia epidemiology, disease outbreaks veterinary, avian genetics, avian influenza epidemiology, lung pathology, molecular sequence data, pharynx pathology, phylogeny, RNA, viral, trachea pathology.


NAL Call Number: QR375.V6

Abstract: During the past years increasing incidences of influenza A zoonosis have made it of uppermost importance to possess methods for rapid and precise identification and characterisation of influenza A viruses. We present here a convenient one-step RT-PCR method that will amplify full-length haemagglutinin (HA) and neuraminidase (NA) directly from clinical samples and from all known subtypes of influenza A. We applied the method on samples collected in September 2003 from a Danish flock of mallards with general health problems and by this a previously undescribed influenza A subtype combination, H5N7, was identified. The HA gene showed great sequence similarity to the highly pathogenic avian influenza A virus (HPAIV) A/Chicken/Italy/312/97 (H5N2); however, the cleavage site sequence between HA1 and HA2 had a motif typical for low pathogenic avian influenza viruses (LPAIV). The full-length NA sequence was most closely related to the HPAIV A/Chicken/Netherlands/01/03 (H7N7) that infected chickens and humans in the Netherlands in 2003. Ten persons with direct or indirect contact with the Danish mallard ducks showed signs of influenza-like illness 2-3 days following the killing of the ducks, but no evidence of influence infections was detected. To our knowledge this is the first report of an H5N7 influenza A virus.

Descriptors: new avian influenza A virus, H5N7, mallard ducks, Danish, subtype, HA1, HA2, zoonosis, identification, gene.


NAL Call Number: 449.9 Un3r

Descriptors: influenza A virus avian immunology, hemagglutinin viral analysis, immune sera, neuraminidase immunology, virus cultivation.


NAL Call Number: SF995.W4

Descriptors: avian influenza virus, hens, layer, poultry, molecular characteristics.


NAL Call Number: SF995.A1A9

Abstract: Thirty-two Newcastle disease virus isolates from the 2000 Italian epidemic were characterized by monoclonal antibody binding pattern and nucleotide sequencing of approximately 400 base pairs of the fusion gene. In addition, the pathogenicity of six of these isolates was assessed by means of the intracerebral pathogenicity test (ICPI). The strains tested exhibited an ICPI ranging from 1.6 to 2.0. On the basis of the monoclonal antibody binding pattern, all isolates could be classified as belonging to group C1. Both monoclonal antibody and genomic analysis revealed a very high degree of homology, indicating a common source of infection. On the basis of the phylogenetic analysis, it appears that the Italian isolates are closely related to the recent isolates from the UK, Scandinavia and South East Europe, thus suggesting the circulation of this viral strain in Europe during the past 5 years.

Descriptors: epidemiology, infection, molecular genetics, veterinary medicine, Newcastle disease, viral
disease, intracerebral pathogenicity test analytical method, nucleotide sequencing molecular genetic method, phylogenetic analysis analytical method, homology.


**NAL Call Number:** 448.8 V81

**Abstract:** Influenza A viruses with subtype H13 hemagglutinin display an unusual host range. Although common in shorebirds, they are very rare or absent in wild ducks; additionally, H13 viruses have been isolated from a whale. To study the molecular basis for this host range, we have determined the complete nucleotide sequences of the hemagglutinin genes of three H13 influenza viruses from different species or geographical areas: A/gull/Maryland/77, A/gull/Astrachan (USSR)/84, and A/pilot whale/Maine/84. Based on the deduced amino acid sequences, H13 hemagglutinin shares the basic structure of other type A hemagglutinin subtypes such as H3, but has clearly diverged from other completely sequenced subtypes. Unique features of H13 hemagglutinin include the occurrence, near the receptor binding pocket, of residues Arg/Lys-227 and Trp-229 (H3 numbering); the significance of these are unknown. The sequence of the HA1-HA2 cleavage site resembles those of avirulent avian influenza viruses. The whale H13 hemagglutinin is similar to those from gulls, supporting the hypothesis that influenza viruses from avian sources can enter marine mammal populations but are probably not permanently maintained there. Antigenic analysis using a panel of monoclonal antibodies suggests that, like other subtypes, H13 viruses are heterogeneous, with different antigenic variants predominating in the eastern versus the western hemispheres.

**Descriptors:** hemagglutinins viral immunology, influenza A virus avian immunology, amino acid sequence, base sequence, genes viral, hemagglutinins viral classification, hemagglutinins viral genetics, avian classification, influenza A virus avian genetics, molecular sequence data, RNA viral genetics.


**NAL Call Number:** 500 N21P

**Abstract:** The pathogenicity of avian H5N1 influenza viruses to mammals has been evolving since the mid-1980s. Here, we demonstrate that H5N1 influenza viruses, isolated from apparently healthy domestic ducks in mainland China from 1999 through 2002, were becoming progressively more pathogenic for mammals, and we present a hypothesis explaining the mechanism of this evolutionary direction. Twenty-one viruses isolated from apparently healthy ducks in southern China from 1999 through 2002 were confirmed to be H5N1 subtype influenza A viruses. These isolates are antigenically similar to A/Goose/Guangdong/1/96 (H5N1) virus, which was the source of the 1997 Hong Kong "bird flu" hemagglutinin gene, and all are highly pathogenic in chickens. The viruses form four pathotypes on the basis of their replication and lethality in mice. There is a clear temporal pattern in the progressively increasing pathogenicity of these isolates in the mammalian model. Five of six H5N1 isolates tested replicated in inoculated ducks and were shed from trachea or cloaca, but none caused disease signs or death. Phylogenetic analysis of the full genome indicated that most of the viruses are reassortants containing the A/Goose/Guangdong/1/96-like hemagglutinin gene and the other genes from unknown Eurasian avian influenza viruses. This study is a characterization of the H5N1 avian influenza viruses recently circulating in ducks in mainland China. Our findings suggest that immediate action is needed to prevent the transmission of highly pathogenic avian influenza viruses from the apparently healthy ducks into chickens or mammalian hosts.

**Descriptors:** ducks virology, evolution, molecular, influenza A virus, avian genetics, avian pathogenicity, influenza, avian virology, chickens, China, genes, viral genetics, genotype, avian transmission, mice, molecular sequence data, phylogeny, virulence.


**Descriptors:** fowl plague microbiology, influenza A virus avian isolation and purification, birds, Brazil, feces
microbiology, fowl plague epidemiology, hemagglutination inhibition tests, serotyping.


**Descriptors:** birds microbiology, influenza A virus avian isolation and purification, antigens, viral analysis, culture media, feces microbiology, hemagglutination inhibition tests, hemagglutinins viral analysis, immune sera, avian immunology, virus cultivation.


**NAL Call Number:** 41.8 Av5

**Abstract:** The complete coding regions of the surface glycoproteins, nucleoprotein (NP), polymerase 2 (PB2), and matrix (M) of A/turkey/214845/02 and A/turkey/220158/99 (H7N3) low pathogenicity avian influenza (LPAI) viruses isolated in October 2002 in Italy were amplified and sequenced to determine the epidemiologic relationships with an A/turkey/Italy/4603/99 (H7N1/4603/99) LPAI virus isolated during the 1999-2001 epizootic in Italy. The hemagglutinin (HA) of H7N3 viruses showed 97.8% nucleotide similarity with A/turkey/Italy/4603/99 (H7N1), and NP, M, and PB2 gene similarities were 93.6%, 98.2%, and 96.2%, respectively. Phylogenetic analyses of HA, PB2, and M genes showed that H7N3 and H7N1 viruses were closely related. Sequence analysis revealed a 23 amino acid deletion in the stalk of the neuraminidase of H7N3 viruses and a unique deletion of amino acid glycine in position 17 in the NP gene of H7N1 virus.

**Descriptors:** disease outbreaks veterinary, genes, viral genetics, influenza A virus, avian genetics, avian isolation and purification, avian epidemiology, poultry diseases epidemiology, turkeys virology, hemagglutinin glycoproteins, influenza virus genetics, avian pathogenicity, avian virology, Italy epidemiology, membrane glycoproteins genetics, molecular biology, neuraminidase, nucleoproteins genetics, open reading frames, phylogeny, polymerase chain reaction, poultry diseases virology.


**NAL Call Number:** QR360.A1J6

**Abstract:** From October 1997 to January 1998, highly pathogenic H5N2 avian influenza viruses caused eight outbreaks of avian influenza in northern Italy. A nonpathogenic H5N9 influenza virus was also isolated during the outbreaks as a result of virological and epidemiological surveillance to control the spread of avian influenza to neighbouring regions. Antigenic analysis showed that the Italian H5N2 isolates were antigenically similar to, although distinguishable from, A/HK/156/97, a human influenza H5N1 virus isolated in Hong Kong in 1997. Phylogenetic analysis of the haemagglutinin (HA) genes showed that the highly pathogenic Italian viruses clustered with the Hong Kong strains, whereas the nonpathogenic H5N9 virus, despite its epidemiological association with the highly pathogenic Italian isolates, was most closely related to the highly pathogenic A/Turkey/England/91 (H5N1) strain. Like the HA phylogenetic tree, the nonstructural (NS) phylogenetic tree showed that the H5N2 Italian virus genes are clearly separate from those of the H5N9 strain. In contrast, results of the phylogenetic analysis of nucleoprotein (NP) genes indicated a closer genetic relationship between the two Italian virus groups, a finding suggesting a common progenitor. Comparison of the HA, NS and NP genes of the Italian H5 strains with those of the H5N1 viruses simultaneously circulating in Hong Kong revealed that the two groups of viruses do not share a recent common ancestor. No virological and serological evidence of bird-to-human transmission of the Italian H5N2 influenza viruses was found.

**Descriptors:** chickens virology, influenza A virus avian genetics, poultry diseases virology, base sequence, chick embryo, DNA, viral, fowl plague epidemiology, fowl plague transmission, fowl plague virology, genes viral, hemagglutinin glycoproteins, influenza virus classification, hemagglutinin glycoproteins, influenza virus genetics, avian classification, avian immunology, avian pathogenicity, Italy epidemiology, molecular sequence data, nucleoproteins classification, nucleoproteins genetics, phylogeny, poultry, poultry diseases epidemiology, poultry diseases transmission, sequence analysis, DNA methods, viral core proteins.
classification, viral core proteins genetics, viral nonstructural proteins classification, viral nonstructural proteins genetics.


**Abstract:** Background: In February 2003, highly pathogenic avian influenza A H5N1 viruses reemerged in humans. Despite repeated outbreaks in domestic poultry in Hong Kong since 1999, this was the first isolation of H5N1 from humans since the outbreak in Hong Kong in 1997, which resulted in 18 human cases and 6 deaths. Methods: To better understand the antigenic relationship between the 2003 H5N1 human virus A/Hong Kong/213/03 (HK/213) and other H5 viruses, post-infection ferret sera or post-infection human sera were tested for reactivity by hemagglutination-inhibition and microneutralization assays with H5N1 viruses circulating in Hong Kong or elsewhere in Asia since 1997. Results: The H5N1 virus isolated from a 9-year-old male in Hong Kong was antigenically distinguishable from recent H5N1 viruses isolated from wild birds in Hong Kong and from the human 1997 H5N1 viruses, using post-infection ferret sera. Likewise, sera from this case patient, collected 22 days post-symptom onset, reacted to high titers with the homologous HK/213 virus, but gave eightfold lower titers with A/Hong Kong/156/97, and other H5 viruses. Conclusion: These results suggest that this recent human H5N1 virus is antigenically distinguishable from current and previously circulating H5N1 viruses from Asia, including the viruses previously isolated from humans.

**Descriptors:** influenza H5N1, antigenicity, serology.


**NAL Call Number:** QR360.J6

**Abstract:** In wild aquatic birds and poultry around the world, influenza A viruses carrying 15 antigenic subtypes of hemagglutinin (HA) and 9 antigenic subtypes of neuraminidase (NA) have been described. Here we describe a previously unidentified antigenic subtype of HA (H16), detected in viruses circulating in black-headed gulls in Sweden. In agreement with established criteria for the definition of antigenic subtypes, hemagglutination inhibition assays and immunodiffusion assays failed to detect specific reactivity between H16 and the previously described subtypes H1 to H15. Genetically, H16 HA was found to be distantly related to H13 HA, a subtype also detected exclusively in shorebirds, and the amino acid composition of the putative receptor-binding site of H13 and H16 HAs was found to be distinct from that in HA subtypes circulating in ducks and geese. The H16 viruses contained NA genes that were similar to those of other Eurasian shorebirds but genetically distinct from N3 genes detected in other birds and geographical locations. The European gull viruses were further distinguishable from other influenza A viruses based on their PB2, NP, and NS genes. Gaining information on the full spectrum of avian influenza A viruses and creating reagents for their detection and identification will remain an important task for influenza surveillance, outbreak control, and animal and public health. We propose that sequence analyses of HA and NA genes of influenza A viruses be used for the rapid identification of existing and novel HA and NA subtypes.

**Descriptors:** wild aquatic birds, influenza A virus, black-headed gulls, *Larus ridibundus*, orthomyxoviridae, amino acids, genes, hemagglutinin, neuraminidase, immunodiffusion, immunologic techniques, laboratory techniques.


**NAL Call Number:** 448.8 V81

**Abstract:** To characterize differences in the receptor-binding specificity of H5N1 chicken viruses and viruses of aquatic birds, we used a panel of synthetic polyacrylamide (PAA)-based sialylglycopolymers that carried identical terminal Neu5Acalpha2-3Gal fragments but varied by the structure of the next saccharide residues. A majority of duck viruses irrespective of their HA subtype, bound with the highest affinity to trisaccharide Neu5Acalpha2-3Galbeta1-3GlcNAc, suggesting that these viruses preferentially recognize sialyloligosaccharide receptors with type 1 core (Galbeta1-3GlcNAc). Substitution of 6-hydroxyl group of...
GlcNAc residue of tested sialylglycopolymers by 6-sulfo group had little effect on receptor binding by duck viruses. By contrast, H5N1 chicken and human viruses isolated in 1997 in Hong Kong preferred receptors with type 2 core (Galbeta1-4GlcNAcbeta) and bound sulfated trisaccharide Neu5Acalpha2-3Galbeta1-4(6-HSO3)GlcNAcbeta (6-Su-3'SLN) with the extraordinary high affinity. Another chicken virus, A/FPV/Rostok/34 (H7N1), and several mammalian viruses also displayed an increased affinity for sulfated sialyloligosaccharide receptor. The binding of chicken and mammalian viruses to tracheal epithelial cells of green monkey decreased after treatment of cells with glucosamine-6-sulfatase suggesting the presence of 6-O-Su-3'SLN determinants in the airway epithelium. It remains to be seen whether existence of the 6-O-Su-3'SLN groups in the human airway epithelial cells might facilitate infection of humans with H5N1 chicken viruses.

Descriptors: influenza A virus, avian metabolism, lactose analogs and derivatives, lactose metabolism, receptors, virus metabolism, carbohydrate sequence, cell membrane metabolism, cells, cultured, cercopithecus aethiops, chickens virology, ducks virology, epithelial cells virology, gangliosides metabolism, influenza, avian transmission, influenza, avian virology, lactose chemistry, molecular sequence data, oligosaccharides chemistry, oligosaccharides metabolism, receptors, virus chemistry, trisaccharides metabolism, virus replication.


NAL Call Number: SF995.W4

Descriptors: avian influenza virus, pathogenicity, Mexico, America, biological properties, influenza virus, Latin America, microbial properties, North America, orthomyxoviridae, viruses.


NAL Call Number: SF604.V485

Abstract: El objeto del presente estudio fue determinar el comportamiento del VIA para conocer variaciones que pudiera indicar un cambio gradual de patogenicidad. Se realizo una encuesta con los laboratorios que hicieron aislamientos del virus, de enero a septiembre de 1994, y que fueron enviados a la Comision Mexico Americana para la Prevencion de Fiebre Aftosa y otras enfermedades exóticas, para realizar pruebas de patogenicidad. De un total de 64 aislamientos se obtuvo la informacion de 55 de ellos. La distribucion por estados fue que el 27 se aislaron en el Edo. de Mexico, el 25 en Jal., el 22 en Qro., el 7 en Gto., el S en Pue., en Mor. y Gro. El 4 y en Ags., Hgo. y Ver. El 2. Del total de los aislamientos el 49 se pudieron aislar al primer pase, el 31 al segundo pase, el 15 se aislaron al 3er pase y el 5 al 4o pase. Los aislamientos al 2o, 3o y 4o pase fueron mas frecuentes a partir de mayo. Las frecuencias de aislamiento a partir de traquea fueron de un 43, en pulmon de 38, de tonsilas cecales el 6, de bazo el 5, de encefalo el 4, de rinon y senos infraorbitarios el 2. La mortalidad embrionaria durante los aislamientos fue la siguiente: el 15 se presento entre 24 y 48 h, el 42 entre 48 y 72 h, de los cuales el mayor numero se presento en aislamientos al primer pase, y en 42 no se observo mortalidad. Las lesiones observadas fueron hemorragias en el embrion en un 24, de los cuales el mayor numero fue al primer pase, el 25 mostro congestion y en un 51 no se observaron lesiones. Por lo que se puede concluir que existen variaciones, en cuanto a su capacidad de producir lesiones y mortalidad, en los virus aislados durante este periodo, por lo que se requeriran otros estudios para identificar en que consisten esas variaciones.

Descriptors: chickens, avian influenza virus, diagnosis, pathogenicity, biological properties, birds, domestic animals, Galliformes, influenza virus, livestock, microbial properties, orthomyxoviridae, poultry, useful animals, viruses.


NAL Call Number: QR360.J6
Abstract: The kinetics of the appearance of influenza mRNA, the distribution of mRNA between free and membrane-associated polyribosomes, its poly(A) content, and the extent to which the genome was transcribed into mRNA early in infection were determined. Polyribosomes were prepared from influenza virus-infected cells labeled for 30-min periods at various times after infection with [3H]uridine. Most of the 3H-labeled RNA extracted from these polyribosomes sedimented as a heterogeneous 8S to 20S peak in sucrose gradients, and it was largely complementary to virion RNA. By the following criteria, the complementary RNA had properties normally ascribed to mRNA: (i) it labeled rapidly with [3H]uridine; (ii) after glutaraldehyde treatment, it banded with polyribosomes in CsCl density gradients; and (iii) it contained poly(A). In chick cells at 37 C, virus mRNA was first detectable at 45 min postinfection and reached its maximal rate of appearance at 2 to 2.5 h postinfection. The free and membrane-bound polyribosomes of infected cells were separated and were found to contain the same classes of mRNA. There was no absolute segregation of mRNA sequences into either polyribosome class although each probably contained distinct ratios of the different mRNA's. From 45 min postinfection onwards, both membrane-bound and free polysomal poly(A)-containing RNA contained sequences complementary to at least 80% of the genome RNA, whereas poly(A)-minus RNA contained sequences complementary to 90 to 100% of the genome. There was no evidence for the temporal control of transcription of influenza mRNA. At 31 C, when virus development was slowed relative to 37 C, complementary RNA first appeared at 1 h postinfection. At this time, total polysomal RNA contained sequences complementary to the whole genome.

Descriptors: influenza A virus avian metabolism, RNA messenger biosynthesis, RNA viral biosynthesis, base sequence, influenza A virus avian analysis, influenza A virus avian growth and development, poly A analysis, poliobyosomes analysis, polyribosomes metabolism, RNA messenger analysis, RNA viral analysis, temperature, time factors, tissue culture, transcription, genetic, virus replication.


NAL Call Number: 448.8 V81

Abstract: In March 1989 a severe outbreak of respiratory disease occurred in horses in the Jilin and Heilongjiang provinces of Northeast China that caused up to 20% mortality in some herds. An influenza virus of the H3N8 subtype was isolated from the infected animals and was antigenically and molecularly distinguishable from the equine 2 (H3N8) viruses currently circulating in the world. The reference strain A/Equine/Jilin/1/89 (H3N8) was most closely related to avian H3N8 influenza viruses. Sequence comparisons of the entire hemagglutinin (HA), nucleoprotein (NP), neuraminidase (NA), matrix (M), and NS genes along with partial sequences of the three polymerase (PB1, PB2, PA) genes suggest that six of the eight gene segments (PA, HA, NP, NA, M, NS) are closely related to avian influenza viruses. Since direct sequence analysis can only provide a crude measure of relationship, phylogenetic analysis was done on the sequence information. Phylogenetic analyses of the entire HA, NP, M, and NS genes and of partial sequences of PB1, PB2, and PA indicated that these genes are of recent avian origin. The NP gene segment is closely related to the gene segment found in the newly described H14 subtype isolated from ducks in the USSR. The A/Equine/Jilin/1/89 (H3N8) influenza virus failed to replicate in ducks, but did replicate and cause disease in mice on initial inoculation and on subsequent passaging caused 100% mortality. In ferrets, the virus caused severe influenza symptoms. A second outbreak of influenza in horses in Northeast China occurred in April 1990 in the Heilongjiang province with 48% morbidity and no mortality. The viruses isolated from this outbreak were antigenically indistinguishable from those in the 1989 outbreak and it is probable that the reduced mortality was due to the immune status of of the horses in the region. No influenza was detected in horses in Northern China in the spring, summer, or fall of 1991 and no influenza has been detected in horses in adjacent areas. Our analysis suggests that this new equine influenza virus in horses in Northeast China is the latest influenza virus in mammals to emerge from the avian gene pool in nature and that it may have spread to horses without reassortment. The appearance of this new equine virus in China emphasizes the potential for whole avian influenza viruses to successfully enter mammalian hosts and serves as a model and a warning for the appearance of new pandemic influenza viruses in humans. (ABSTRACT TRUNCATED AT 250 WORDS)

Descriptors: horse diseases microbiology, influenza A virus isolation and purification, orthomyxoviridae infections veterinary, antigens, viral genetics, antigens, viral immunology, base composition, chick embryo, China epidemiology, cloning, molecular, genes viral, horse diseases epidemiology, horses, influenza A virus

Abstract: BACKGROUND: To understand the characterization of genome of a strain of avian influenza A H9N2 virus repeatedly isolated from a child with influenza illness. Thereafter to reveal the origin of this H9N2 virus. METHODS: Viruses were passed in embryonated hen eggs and virion RNA was extracted from allantoic fluid and reverse transcribed to synthesize cDNA. cDNA was amplified by PCR and the PCR product was purified with a purification kit. Afterwards RNA sequence analysis was performed by dideoxynucleotide chain termination and a cloning method. Finally, phylogenetic analysis of the sequencing data was performed with MegAlign (Version 1.03) and Editseg (Version 3.69) softwares. RESULTS: Genome of A/Guangzhou/333/99 (H9N2) virus was closely related to avian influenza A H9N2 virus, but obvious difference from that of A/Duck/Hong Kong/Y439/97(H9N2) virus, as well as its genome did not include any RNA segment derived from human influenza A virus. However, the genes encoding the HA,NA,NP and NS proteins of A/Guangzhou/333/99 virus were derived from those of G9 lineage virus, the rest genes encoding the M and three polymerase (PB2, PB1 and PA) proteins were derived from G1 lineage strain. CONCLUSIONS: A/Guangzhou/333/99 virus was a reassortant derived from reassortment between G9 and G1 lineages of avian influenza A (H9N2) viruses. Therefore, the most possibility is that it is derived from avian influenza A virus directly. The results do not only demonstrate that avian influenza A (H9N2) virus could infect men, but also firstly prove that the genetic reassortment could be occurred between different genetic lineages of avian influenza A (H9N2) viruses in the nature.

Descriptors: genome, viral, influenza virology, influenza A virus avian genetics, base sequence, chick embryo, child, phylogeny.


Abstract: Genetic analysis of viral HA gene showed that there were 22 nucleotide differences in HA gene between goose and human H5N1 viruses. The sequence analysis of amino acid on viral protein molecules indicated that there were 7 and 9 position differences between goose and human, chicken H5N1 viruses, respectively. All the three viruses share multiple basic amino acids (R-E-R-R-R-K-K-R) at the cleavage site between HA1 and HA2 domain, that is associated with highly pathogenic H5 avian viruses. Except one more glycosylation site located at 156 position in the chicken strain, there were 7 glycosylation sites at same positions in three virus HA protein molecules. The analysis of NA protein molecule indicated that the stalk region which extends from the viral membrane up to amino acid 85, human and chicken viruses had a 19 amino-acid deletion as compared with that of goose virus, while the goose NA gene was closely related to A/Parrot/Ulster/73 (H7N1) virus. Therefore, goose H5N1 virus HA and NA genes were avian in origin and were different from those of human and chicken H5N1 viruses. In our knowledge, this is the first time that the avian H5N1 virus was found causing influenza outbreak in goose. Why was A/Goose/Guangdong/2/96(H5N1) virus virulent for geese? It might be related to the substitution of amino acid located at 138 position near by RBS on HA protein molecule and 19 amino acids insertion on NA protein molecule as compared with those of human and chicken H5N1 viruses.

Descriptors: influenza virology, influenza A virus avian genetics, influenza A virus human genetics, poultry diseases virology, amino acid sequence, chick embryo, geese virology, influenza veterinary, influenza A virus avian isolation and purification, influenza A virus human isolation and purification, molecular sequence data, sequence homology, amino acid.


NAL Call Number: 448.8 V81

Abstract: The reported transmission of avian H9N2 influenza viruses to humans and the isolation of these viruses from Hong Kong poultry markets lend urgency to studies of their ecology and pathogenicity. We found that H9N2 viruses from North America differ from those of Asia. The North American viruses, which infect primarily domestic turkeys, replicated poorly in inoculated chickens. Phylogenetic analysis of the hemagglutinin and nucleoprotein genes indicated that the Asian H9N2 influenza viruses could be divided into three sublineages. Initial biological characterization of at least one virus from each lineage was done in animals. Early isolates of one lineage (A/Chicken/Beijing/1/94, H9N2) caused as high as 80% mortality rates in inoculated chickens, whereas all other strains were nonpathogenic. Sequence analysis showed that some isolates, including the pathogenic isolate, had one additional basic amino acid (A-R/K-S-S-R-) at the hemagglutinin cleavage site. Later isolates of the same lineage (A/Chicken/Hong Kong/G9/97, H9N2) that contains the PB1 and PB2 genes similar to Hong Kong/97 H5N1 viruses replicated in chickens, ducks, mice, and pigs but were pathogenic only in mice. A/Quail/Hong Kong/G1/97 (H9N2), from a second lineage that possesses the replicative complex similar to Hong Kong/97 H5N1 virus, replicated in chickens and ducks without producing disease signs, was pathogenic in mice, and spread to the brain without adaptation. Examples of the third Asian H9N2 sublineage (A/Chicken/Korea/323/96, Duck/Hong Kong/Y439/97) replicated in chickens, ducks, and mice without producing disease signs. The available evidence supports the notion of differences in pathogenicity of H9N2 viruses in the different lineages and suggests that viruses possessing genome segments similar to 1997 H5N1-like viruses are potentially pathogenic in mammals. Copyright 2000 Academic Press.

Descriptors: influenza A virus avian genetics, influenza A virus avian pathogenicity, binding sites genetics, chickens virology, DNA complementary chemistry, DNA complementary genetics, glycosylation, hemagglutinins viral genetics, hemagglutinins viral metabolism, Hong Kong epidemiology, mice, mice inbred BALB c virology, molecular sequence data, phylogeny, poultry diseases epidemiology, RNA viral genetics, reverse transcriptase polymerase chain reaction, sequence analysis, DNA, virulence genetics, virus replication.


Abstract: OBJECTIVE: To understand the origin of HA and NA genes of swine influenza A (H9N2) viruses isolated from pigs in the mainland of China and on basis of these to reveal the pathogenecity of them in pigs.

METHODS: The target gene was amplified by PCR, the PCR product was ligated with PGEM-T Easy Vector (Promega company, USA) at 4 degrees, the recombined plasmid was transferred into DH-10-beta bacteria; positive colonies were selected and identified then digested with restriction enzyme. Afterwards, the nucleotide sequence was determined. Finally, phylogenetic analysis of the sequencing data was performed with MegAlign (Version 1.03) and Editseg (Version 3.69) softwares.

RESULTS: Two strains of swine influenza A(H9N2) virus isolated in the mainland had an amino acid residue, leucine (L) at position 226 (H3 numbering) on HA protein molecule found in H9N2 viruses isolated either in pigs or humans previously; the amino acid sequence at HA connecting peptide of isolates possessed R-L-S-R, whereas the other H9N2 viruses with virulence in poultry had R-S-S-R at HA connecting peptide. The two pig H9N2 isolates shared the same three-amino-acids deletion in the NA stalk at 62.64 position found in A/Shaoguan/408/98 and A/Swine/Hong Kong/9/98, as well as A/Duck/Hong Kong/Y280/97(H9N2) viruses. The analysis of the phylogenetic tree indicated that the HA and NA genes of new isolates were closely related to those of A/Chicken/Hong Kong/G23/97 and A/Chicken/Hong Kong/G9/97 and A/Shaoquan/408/98 viruses, respectively.

CONCLUSION: The HA and NA genes of swine influenza A(H9N2) viruses isolated in the mainland of China probably were derived from those of avian influenza A(H9N2) virus. The occurrence of substitution of amino acid sequence at HA connecting peptide, could result in the H9N2 virus from non pathogenic to pathogenic in pigs. However, avian influenza A(H9N2) virus had deletion in the stalk of the NA that resulted in host range transmission. Therefore they could infect pigs directly.

Descriptors: HA, NA, genes, swine influenza A, viruses, H9N2, pigs, China, pathogenecity, amino acids, deletion.

**NAL Call Number:** QR360.A1J6

**Abstract:** Polyadenylated transcripts synthesized in vitro by detergent-disrupted influenza virus resemble virus mRNAs in that they possess the complement of the 3’ terminus of the genome RNAs but lack sequences corresponding to the same 5’ terminal region, including the homologous sequence of nucleotides 1 to 22. Transcription is initiated at the 3’ terminus by both ApG and GpG as well as in the absence of added primer.

**Descriptors:** influenza A virus avian analysis, orthomyxoviridae analysis, RNA viral analysis, transcription, genetic, base sequence, cell free system, avian metabolism, nucleic acid hybridization, nucleotides analysis, poly A analysis, viral biosynthesis.


**NAL Call Number:** 448.8 V81

**Descriptors:** influenza A virus avian genetics, RNA viral analysis, adenosine metabolism, base sequence, chromatography, DEAE-cellulose, chromatography, thin layer, phosphorylation, ribonucleases pharmacology, ribonucleotides analysis, transcription, genetic.


**Descriptors:** avian influenza virus, identification, isolation, strains, hens, Jiangzi, China.


**NAL Call Number:** QR360.J6

**Abstract:** Influenza A viruses of the H13N2 and H13N9 subtypes were isolated from the lung and hilar node of a pilot whale. Serological, molecular, and biological analyses indicate that the whale isolates are closely related to the H13 influenza viruses from gulls.

**Descriptors:** cetacea microbiology, influenza A virus isolation and purification, whales microbiology, antigens, viral immunology, ferrets microbiology, hemagglutinins viral immunology, influenza A virus avian analysis, influenza A virus analysis, influenza A virus immunology, influenza A virus physiology, lung microbiology, lymph nodes microbiology, neuraminidase immunology, nucleic acid hybridization, RNA viral analysis, virus replication.


**NAL Call Number:** QR360.A1J6

**Abstract:** The haemagglutinin of A/Dk/alb/60/76, an influenza A virus isolated from feral ducks in Canada, possesses no antigenic relatedness to any of the 16 reference haemagglutinin subtypes. Results of serological tests (HI and double immunodiffusion) with monospecific antisera to the haemagglutinin of this virus indicate that it represents a new avian haemagglutinin subtype. We propose that this haemagglutinin be designated as Hav10 under the current system of nomenclature.

**Descriptors:** ducks microbiology, hemagglutinins viral immunology, influenza A virus avian immunology, chickens, cross reactions, hemagglutination inhibition tests, hemagglutinins viral classification, immunodiffusion, avian classification, avian pathogenicity.


**NAL Call Number:** 448.8 V81

**Descriptors:** influenza A virus avian pathogenicity, ovum virology, cell line, chick embryo, clone cells, dogs,

NAL Call Number: QR360.J6

Abstract: In 1997, an H5N1 influenza virus outbreak occurred in chickens in Hong Kong, and the virus was transmitted directly to humans. Because there is limited information about the avian influenza virus reservoir in that region, we genetically characterized virus strains isolated in Hong Kong during the 1997 outbreak. We sequenced the gene segments of a heterogeneous group of viruses of seven different serotypes (H3N8, H4N8, H6N1, H6N9, H11N1, H11N9, and H11N8) isolated from various bird species. The phylogenetic relationships divided these viruses into several subgroups. An H6N1 virus isolated from teal (A/teal/Hong Kong/W312/97 [H6N1]) showed very high (>98%) nucleotide homology to the human influenza virus A/Hong Kong/156/97 (H5N1) in the six internal genes. The N1 neuraminidase sequence showed 97% nucleotide homology to that of the human H5N1 virus, and the N1 protein of both viruses had the same 19-amino-acid deletion in the stalk region. The deduced hemagglutinin amino acid sequence of the H6N1 virus was most similar to that of A/shearwater/Australia/1/72 (H6N5). The H6N1 virus is the first known isolate with seven H5N1-like segments and may have been the donor of the neuraminidase and the internal genes of the H5N1 isolates. The high homology between the internal genes of H9N2, H6N1, and the H5N1 isolates indicates that these subtypes are able to exchange their internal genes and are therefore a potential source of new pathogenic influenza virus strains. Our analysis suggests that surveillance for influenza A viruses should be conducted for wild aquatic birds as well as for poultry, pigs, and humans and that H6 isolates should be further characterized.

Descriptors: genome, viral, influenza A virus avian genetics, birds, China, fowl plague, hemagglutinin glycoproteins, influenza virus genetics, avian classification, avian isolation and purification, avian pathogenicity, human classification, human genetics, human isolation and purification, human pathogenicity, mice, mice inbred BALB c, neuraminidase genetics, phylogeny, polymerase chain reaction, sequence analysis, DNA.


NAL Call Number: QR360.J6

Abstract: In October 1999, H4N6 influenza A viruses were isolated from pigs with pneumonia on a commercial swine farm in Canada. Phylogenetic analyses of the sequences of all eight viral RNA segments demonstrated that these are wholly avian influenza viruses of the North American lineage. To our knowledge, this is the first report of interspecies transmission of an avian H4 influenza virus to domestic pigs under natural conditions.

Descriptors: influenza A virus avian isolation and purification, pneumonia, viral virology, swine diseases virology, Canada epidemiology, influenza A virus avian genetics, molecular sequence data, phylogeny, pneumonia, viral epidemiology, swine, swine diseases epidemiology.


NAL Call Number: QR46.J6

Abstract: H3N3 and H1N1 influenza A viruses were isolated from Canadian pigs in 2001 and 2002. These viruses are phylogenetically related to waterfowl viruses and antigenically distinct from reference swine influenza viruses. The isolation of these viruses reemphasizes the potential for interspecies transmission of influenza viruses from waterfowl to pigs in North America.

Descriptors: influenza A virus, avian classification, swine virology, base sequence, birds, Canada, DNA primers, avian isolation and purification, molecular sequence data, phylogeny, reverse transcriptase polymerase chain reaction methods.

**NAL Call Number:** QR1.C8

**Descriptors:** carbohydrates analysis, hemagglutinins viral analysis, influenza A virus avian analysis, influenza A virus analysis, chemistry, glycopeptides analysis, avian immunology, human analysis, porcine analysis, influenza A virus classification, influenza A virus immunology, serotyping, species specificity.


**NAL Call Number:** QR355.P5

**Descriptors:** ELISA, isolation, identification, avian influenza virus, China.


**NAL Call Number:** 41.8 Av5

**Abstract:** The pathogenicity potential of two H13N2 influenza viruses, one isolated from turkeys and the other isolated from surface water, was evaluated in turkeys, chickens, and mallard ducks (*Anas platyrhynchos*) after intracranial and oculonasal inoculation. Both isolates replicated in turkey poults, causing depressed weight gain, morbidity and mortality; both also caused histopathological lesions, such as mild to severe pancreatitis, hepatitis, and nephritis in turkeys. These isolates replicated in mallard ducklings but not in chickens. There was depressed weight gain in ducklings given the H13N2 isolate from water. Neither isolate caused morbidity or mortality in ducklings or chicks after inoculation.

**Descriptors:** influenza A virus avian isolation and purification, turkeys microbiology, water microbiology, antibodies, monoclonal, chickens, cross reactions, ducks, fowl plague etiology, fowl plague pathology, avian immunology, avian pathogenicity, species specificity, virulence.


**NAL Call Number:** SF995.A1A9

**Abstract:** In the US, the isolation of H5 subtype avian influenza (AI) viruses has been uncommon in commercial chickens and turkeys, although sporadic isolations have been made from the live bird markets or its supply chain since 1986. In 2002, two different outbreaks of H5 AI occurred in commercial chicken or turkey operations. The first occurred in Texas and was identified as a H5N3 subtype AI virus. The second outbreak was caused by a H5N2 virus isolated from a turkey farm in California. In this study we analyzed recent H5 subtype AI viruses from different avian species and different sources in the US. Most recent H5 subtype isolates shared a high sequence identity and phylogenetically assorted into a separate clade from the Pennsylvania/83 lineage isolates. However, no established lineage was found within this clade and the recent H5 subtype isolates seemed to be the result of separate introductions from the wild bird reservoir. The Texas H5N3 isolate shared the lowest homology with the other recent isolates in the haemagglutinin gene and had a unique haemagglutinin cleavage site sequence of REKR/G (other recent isolates have the typical avirulent motif, RETR/G). Furthermore, this isolate had a 28 amino acid deletion in the stalk region of the neuraminidase protein, a common characteristic of chicken adapted influenza viruses, and may indicate that this virus had actually been circulating in poultry for an extended period of time before it was isolated. In agreement with genetic evidence, the Texas H5N3 isolate replicated better than other H5 isolates in experimentally infected chickens. The outbreak in Texas with a more chicken-adapted H5N3 virus underscores the importance of ongoing surveillance and control efforts regarding the H5 subtype AI virus in the US.

**Descriptors:** chickens virology, disease outbreaks veterinary, influenza A virus, avian genetics, avian epidemiology, poultry diseases epidemiology, turkeys virology, amino acid sequence, base sequence, geography, hemagglutinins genetics, avian pathogenicity, avian virology, molecular sequence data,
phylogeny, poultry diseases virology, reverse transcriptase polymerase chain reaction, sequence alignment, sequence analysis, DNA, sequence homology, species specificity, United States epidemiology.


NAL Call Number: QR360.J6

Abstract: An unprecedented outbreak of H5N1 highly pathogenic avian influenza (HPAI) has been reported for poultry in eight different Asian countries, including South Korea, since December 2003. A phylogenetic analysis of the eight viral genes showed that the H5N1 poultry isolates from South Korea were of avian origin and contained the hemagglutinin and neuraminidase genes of the A/goose/Guangdong/1/96 (Gs/Gd) lineage. The current H5N1 strains in Asia, including the Korean isolates, share a gene constellation similar to that of the Penfold Park, Hong Kong, isolates from late 2002 and contain some molecular markers that seem to have been fixed in the Gs/Gd lineage virus since 2001. However, despite genetic similarities among recent H5N1 isolates, the topology of the phylogenetic tree clearly differentiates the Korean isolates from the Vietnamese and Thai isolates which have been reported to infect humans. A representative Korean isolate was inoculated into mice, with no mortality and no virus being isolated from the brain, although high titers of virus were observed in the lungs. The same isolate, however, caused systemic infections in chickens and quail and killed all of the birds within 2 and 4 days of intranasal inoculation, respectively. This isolate also replicated in multiple organs and tissues of ducks and caused some mortality. However, lower virus titers were observed in all corresponding tissues of ducks than in chicken and quail tissues, and the histological lesions were restricted to the respiratory tract. This study characterizes the molecular and biological properties of the H5N1 HPAI viruses from South Korea and emphasizes the need for comparative analyses of the H5N1 isolates from different countries to help elucidate the risk of a human pandemic from the strains of H5N1 HPAI currently circulating in Asia.

Descriptors: avian influenza A virus genetics, avian influenza A virus pathogenicity, avian influenza A virus epidemiology, avian influenza A virus virology, adrenal glands pathology, adrenal glands virology, brain virology, chickens, complementary DNA, DNA viral chemistry, DNA viral isolation and purification, ducks, viral genes, hemagglutinin glycoproteins, influenza virus genetics, avian influenza A virus classification, Avian influenza A virus isolation and purification, avian influenza pathology, avian influenza transmission, Korea epidemiology, lung pathology, lung virology, mice, mice inbred BALB-C, molecular sequence data, neuraminidase genetics, pancreas pathology, pancreas virology, phylogeny, poultry, quail, RNA viral genetics, RNA viral isolation and purification, DNA sequence analysis, virulence, viral proteins genetics, virulence.


NAL Call Number: QR355.J6

Abstract: Avian influenza viruses have 15 different hemagglutinin (HA) subtypes (H1-H15). We report a procedure for the identification and HA-subtyping of avian influenza virus by reverse transcription-PCR (RT-PCR). The avian influenza virus is identified by RT-PCR using a set of primers specific to the nucleoprotein (NP) gene of avian influenza virus. The HA-subtypes of avian influenza virus were determined by running simultaneously 15 RT-PCR reactions, each using a set of primers specific to one HA-subtype. For a single virus strain or isolate, only one of the 15 RT-PCR reactions will give a product of expected size, and thus the HA-subtype of the virus is determined. The result of HA-subtyping was then confirmed by sequence analysis of the PCR product. A total of 80 strains or isolates of avian influenza viruses were subtyped by this RT-PCR procedure, and the result of RT-PCR gave an excellent (100%) correlation with the result of the conventional serological method. The RT-PCR procedure we developed is rapid and sensitive, and could be used for the identification and HA-subtyping of avian influenza virus in organ homogenates.

Descriptors: molecular genetics, infection, veterinary medicine, methods and techniques, influenza, avian, respiratory system disease, viral disease, ABI 377 automatic DNA sequencer PE applied biosystems, equipment, DNA sequencing recombinant DNA technology, analytical method, sequencing techniques,
reverse transcriptase polymerase chain reaction analytical method, applications, polymerase chain reaction, serology virological methodology.


Abstract: We analyzed the antigenic and genetic properties of 20 H9N2 viruses that have been isolated from domestic poultry in China during the last 10 years. Hemagglutination inhibition (HI) assays with the antisera of five selected viruses showed that 18 of the viruses could cross-react well with the antisera that were induced by A/chicken/Shijiazhuang/2/98, A/chicken/Guangxi/10/99 and A/chicken/Shanghai/10/01, though antigenic variation among these strains were observed. Two viruses, A/chicken/Shijiazhuang/2/98 and A/chicken/Heilongjiang/35/00, could react well with the homologous antisera but poorly with others. The antisera of A/chicken/Shandong/6/96, the current vaccine strain, and A/Chicken/Heilongjiang/35/00 could not cross-react efficiently with other viruses. Phylogenetic analysis showed that 19 of 20 viruses genetically were related to the Y-280 sub-lineage of Eurasia lineage, however, A/Chicken/Heilongjiang/35/00 was closely related to the early H9N2 isolate, A/Turkey/Wisconsin/66, and went into the North American lineage. These results are the first report about the antigenic and genetic diversity that existed among the H9N2 avian influenza viruses (AIV) isolated in Mainland China.

Descriptors: avian influenza virus, H9N2 subtype, antigenic analysis, genetic analysis, poultry, China, antisera.


Abstract: Pandemic influenza H2N2 viruses emerged in humans in 1957 and caused widespread morbidity and mortality in humans until 1968 when they were displaced by emerging H3N2 viruses. Although it is known that both the appearance and disappearance of H2N2 viruses involved reassortment between human and avian influenza viruses, genetic characterization of these viruses is limited. In this study, detailed genetic analysis of all eight gene segments of human H2N2 viruses isolated from 1957 until 1968 from geographically diverse regions was undertaken to establish a better understanding of the evolutionary nature of this virus. In addition, a number of human H3N2 viruses isolated from 1968 until 1972 were examined to investigate genetic events associated with the emergence of pandemic H3N2 viruses in humans. Phylogenetic analysis of all gene segments of human H2N2 viruses consistently demonstrated divergent evolution. Genes of late H2N2 isolates were located in either of two distinct clades (I and II). Analysis of H3N2 viruses of 1968 revealed that all gene segments that were retained from H2N2 viruses were most similar to H2N2 virus genes of clade I. However, genes of both lineages were found to cocirculate among H3N2 isolates of 1969-1971. Furthermore, each gene segment demonstrated unique phylogenic topologies, indicating multiple reassortment events between late H2N2 and/or H3N2 viruses. The H3N2 viruses of 1972 analyzed here appeared to possess the genome constellation that represents the ancestral virus of contemporary H3N2 viruses. This constellation was first observed among isolates of 1970 and was distinct from that found among the earliest human H3N2 viruses from 1968. This evidence demonstrates that establishment of H3N2 viruses in humans was associated with multiple-reassortment events that contributed to genetic diversity among viruses.

Descriptors: influenza, H2N2, H3N2, evolution, reassortment, hemagglutinin, neuraminidase, nucleoprotein, influenza virus genetics.


NAL Call Number: 41.8 Z52

Descriptors: birds microbiology, influenza A virus avian genetics, hemagglutinis viral genetics, porcine genetics, Israel, neuraminidase genetics, RNA viral genetics.


NAL Call Number: QR180.C62

Descriptors: birds microbiology, influenza A virus avian isolation and purification, turkeys microbiology, antigens, viral analysis, hemagglutinins viral analysis, avian classification, avian immunology, Israel, neuraminidase immunology, serotyping.


NAL Call Number: 41.8 V641

Descriptors: influenza A virus avian isolation and purification, turkeys microbiology, virus diseases veterinary, antibodies, viral analysis, bird diseases immunology, bird diseases microbiology, hemagglutination inhibition tests, avian immunology, Israel, turkeys immunology.


NAL Call Number: QH434.V57

Abstract: The hemagglutinin (HA) genes of 12 H9N2 influenza virus strains isolated from chickens in Mainland China during the period 1995-2002 were genetically analyzed. All the isolates possessed the same amino acid motif -R-S-S-R/G-L- at the cleavage site of HA. Except for the conserved amino acids, as is the case in the other avian influenza viruses, located in the receptor binding site, all of the 12 isolates possessed N at amino acid position 183; A, T, or V at position 190; K at position 137, whereas the representative strains of the other lineage (except Dk/HK/Y280/97-like lineage) virus of H9N2 viruses had H, E, and R at these positions respectively. These could be considered as the partial molecular markers of the H9 viruses isolated from chickens in Mainland China. Phylogenetic analyses showed HA genes of these isolates belonged to that of A/duck/Hong Kong/Y280/97-like virus lineage. No A/quail/Hong Kong/Gl/97-like virus was found in chicken, population since the outbreak of H9N2 influenza in Mainland China in 1992. The available evidence indicates that HA genes of H9 influenza virus circulating in Mainland China during the past years were well conserved.

Descriptors: chickens virology, hemagglutinin glycoproteins, influenza virus genetics, avian influenza A virus genetics, avian influenza virology, amino acid sequence, binding sites, China, molecular evolution, avian Influenza A virus isolation and purification, avian Influenza A virus classification, molecular sequence data, phylogeny, RNA, viral isolation and purification, viral metabolism, DNA sequence analysis, sequence homology, metabolism, virology, genetics.


NAL Call Number: 448.3 Ac83

Descriptors: molecular genetics, RT PCR, reverse transcriptase polymerase chain reaction, avian influenza virus.


NAL Call Number: 449.8 H343

Abstract: Two avian influenza viruses were employed; a virulent wild-type (WT) parent and the cold variant
(CV) which was an attenuated virus derived by genetic recombination at 25 C. The attenuated virus grows in embryonated eggs and chicken tracheal organ cultures. Infectious virus could be recovered from lung and turbinate. Infection with attenuated virus provided protection against infection with wild virus.

Descriptors: influenza A virus avian, chick embryo, hemagglutination inhibition tests, hemagglutination, viral, recombination, genetic, virulence.


NAL Call Number: SF604.P32

Descriptors: isolation, characterization, outbreaks, diagnosis, diseases, avian influenza virus, poultry, mortality, Pakistan.


NAL Call Number: SF604.P32

Descriptors: broilers, poultry farms, isolation, clinical aspects, mortality, outbreaks, avian influenza virus, characterization, Pakistan.


NAL Call Number: QR360.J6

Abstract: Since 1997, outbreaks of highly pathogenic (HP) H5N1 and circulation of H9N2 viruses among domestic poultry in Asia have posed a threat to public health. To better understand the extent of transmission of avian influenza viruses (AIV) to humans in Asia, we conducted a cross-sectional virologic study in live bird markets (LBM) in Hanoi, Vietnam, in October 2001. Specimens from 189 birds and 18 environmental samples were collected at 10 LBM. Four influenza A viruses of the H4N6 (n = 1), H5N2 (n = 1), and H9N3 (n = 2) subtypes were isolated from healthy ducks for an isolation frequency of over 30% from this species. Two H5N1 viruses were isolated from healthy geese. The hemagglutinin (HA) genes of these H5N1 viruses possessed multiple basic amino acid motifs at the cleavage site, were HP for experimentally infected chickens, and were thus characterized as HP AIV. These HA genes shared high amino acid identities with genes of other H5N1 viruses isolated in Asia during this period, but they were genetically distinct from those of H5N1 viruses isolated from poultry and humans in Vietnam during the early 2004 outbreaks. These viruses were not highly virulent for experimentally infected ducks, mice, or ferrets. These results establish that HP H5N1 viruses with properties similar to viruses isolated in Hong Kong and mainland China circulated in Vietnam as early as 2001, suggest a common source for H5N1 viruses circulating in these Asian countries, and provide a framework to better understand the recent widespread emergence of HP H5N1 viruses in Asia.

Descriptors: avian influenza A virus classification, avian influenza A virus isolation and purification, avian influenza virology, poultry virology, viral antigens, chickens virology, ducks virology, molecular epidemiology, ferrets, geese virology, avian influenza A virus genetics, avian influenza A viruspathogenicity, mice, molecular sequence data, neuraminidase genetics, phylogeny, sequence analysis, serotyping, Vietnam, virulence.


NAL Call Number: QR189.V32

Abstract: In 1997, 18 people were infected in Hong Kong with an avian influenza A(H5N1) virus from chicken. This type of interspecies transmission was never detected before and could have resulted in the development of a pandemic strain. The occurrence suggests that the pig is not needed for the emergence of
pandemic influenza virus strains. Characteristics of the strains involved are discussed in relation to the question why, on the one hand, these strains were able to infect humans but on the other hand were not able to start an epidemic.

Descriptors: epidemiology, infection, influenza, respiratory system disease, transmission, viral disease.

NAL Call Number: 41.8 Z52
Descriptors: wild birds, epidemiological surveys, avian influenza virus, avian paramyxovirus, poultry, Germany, Netherlands, Kenya.

Descriptors: recombinant veterinary vaccines, fowl pox virus, influenza virus, rabies virus, risk assessment, agricultural biotechnology, poultry.

NAL Call Number: 41.8 Av5
Abstract: The National Centre for Foreign Animal Disease (NCFAD) in Winnipeg, Manitoba, is the Canadian Food Inspection Agency’s (CFIA) newest high biocontainment laboratory. One of the functions of the NCFAD is to serve as a national reference laboratory for avian influenza. Between 1997 and 2001, 15 avian influenza virus isolates were characterized. These isolates originated from domestic poultry, imported caged birds held in quarantine, and wild birds. Diagnostic specimens were submitted to the NCFAD by CFIA field veterinarians, provincial veterinary diagnostic laboratories, and veterinary colleges. Characterization of isolates included the determination of H and N subtypes: H1, H6, H7, and H10 subtypes were isolated from domestic poultry; H3, H4, and three H13 viruses were isolated from water fowl, and six H3 viruses were isolated from caged birds being held in import quarantine. Selected isolates were characterized with respect to their pathogenic potential by intravenous inoculation of 4-to-6-wk-old chickens. A molecular-based protocol was used to assess the pathogenicity of one H7 isolate. During this period, work was also carried out toward validating our molecular pathotyping protocol for avian influenza viruses with H5 and H7 hemagglutinin subtypes.
Descriptors: infection, molecular genetics, veterinary medicine, virology, avian influenza, diagnosis, infectious disease, respiratory system disease, viral disease, molecular pathotyping clinical techniques, diagnostic techniques, genetic techniques, laboratory techniques, biocontainment laboratory veterinary diagnostic laboratories viral pathogenicity.

NAL Call Number: 41.8 Au72
Descriptors: Australia, avian paramyxoviruses, avian influenza viruses, isolation and characterization, Aves, wild birds, wild duck, pigeon, quail.

NAL Call Number: QR360.A1J6
Abstract: The complete genomes of three human H5N1 influenza isolates were characterized, together with the haemagglutinin (HA) and neuraminidase (NA) genes from two additional human isolates and one chicken isolate. These six influenza isolates were obtained from four different provinces of Thailand during the avian influenza outbreak in Asia from late 2003 to May 2004. All six Thailand isolates contained multiple
basic amino acids at the cleavage site in the HA gene. Amino acid residues at the receptor-binding site of the five human viruses were similar to those of the chicken virus and other H5N1 viruses from Hong Kong. The presence of amantadine resistance in the Thailand viruses isolated during this outbreak was suggested by a fixed mutation in M2 and confirmed by a phenotypic assay. All genomic segments of the Thailand viruses clustered with the recently described genotype Z. The Thailand viruses contained more avian-specific residues than the 1997 Hong Kong H5N1 viruses, suggesting that the virus may have adapted to allow a more efficient spread in avian species.

Descriptors: disease outbreaks, influenza epidemiology, influenza A virus, human genetics, RNA, viral genetics, amantadine pharmacology, antiviral agents pharmacology, chickens virology, drug resistance, viral, epidemiology, molecular, hemagglutinin glycoproteins, influenza virus genetics, influenza virology, avian genetics, human drug effects, human isolation and purification, avian influenza epidemiology, molecular sequence data, mutation, neuraminidase genetics, phylogeny, receptors, virus, sequence alignment, species specificity, Thailand epidemiology, viral matrix proteins genetics.


Abstract: Two H9N2 viruses were isolated, for the first time, from humans in Hong Kong in 1999. Isolation of influenza viruses with a novel subtype of the hemagglutinin (HA) drew attention of health care authorities worldwide from the view of pandemic preparedness. Sequence analysis of the HA genes reveals that HA of A/Hong Kong/1073/99 (H9N2) is most closely related to that of A/quail/HK/G1/97 (H9N2) that contains the internal genes similar to those of Hong Kong/97 (H5N1) viruses. Phylogenetic and antigenic analyses demonstrated the diversity among H9 HA. A/Hong Kong/1073/99 was shown to cause a respiratory infection in Syrian hamsters, suggesting that the virus can replicate efficiently in mammalian hosts. We developed a whole virion test vaccine with a formalin-inactivated egg-grown HK1073. Intraperitoneal administration of the vaccine twice to hamsters conferred a complete protection against challenge infection by the MDCK cell-grown homologous virus. Receptor specificity of HK1073 appeared different from that of other avian influenza viruses of H9 subtype which recognize preferentially alpha-2,3 linked sialic acid. Hemagglutination of HK1073 with guinea pig erythrocytes was inhibited by both alpha-2,3 and alpha-2,6 linked sialic acid containing polymers. These data suggested that HK1073 had acquired a broader host range, including humans. Together with data so far available, the present study suggested that isolation of the H9 influenza viruses from humans requires precaution against the emergence of a novel human influenza.

Descriptors: influenza virology, influenza A virus human isolation and purification, antigens, viral immunology, Asia, cattle, cultured cells, chick embryo, child, dogs, Europe, glycoconjugates pharmacology, guinea pigs, hamsters, hemagglutination tests, hemagglutination, viral, hemagglutinin glycoproteins, influenza virus genetics, hemagglutinin glycoproteins, influenza virus physiology, Hong Kong, horses, influenza prevention and control, influenza veterinary, avian classification, avian physiology, human classification, human genetics, human immunology, human physiology, porcine classification, porcine physiology, influenza vaccine immunology, lung virology, mesocricetus, N-acetylneuraminic acid metabolism, North America, phylogeny, poultry virology, poultry diseases virology, receptors, virus metabolism, sheep, species specificity, swine, swine diseases virology, vaccination, vaccines, inactivated, virion immunology, virus cultivation.


Abstract: For the prediction of future influenza pandemics, global surveillance of avian influenza has been continuing since 1991 and carried out in Russia, Mongolia, China and Japan from 2000 to 2003. Influenza virus isolates of 50 combinations of HA and NA subtypes have been identified and 3 strains selected from each of those are stocked. In addition, 47 other combinations have been generated by standard genetic reassortment procedure in the laboratory. Since we have already shown that influenza viruses have been fully adapted to ducks and cause no disease signs and are in evolutionary stasis in their natural reservoirs, virus isolates from ducks are ideal as vaccine strains. Thus, influenza viruses of 97 combinations of HA and NA subtypes are now available as vaccine strain candidates against emerging pandemic influenza in
humans, domestic animals and poultry.

Descriptors: global surveillance, vaccine, avian influenza virus, pandemic, prediction.


NAL Call Number: 448.8 V81

Descriptors: influenza A virus avian isolation and purification, avian metabolism, mutation, DNA directed RNA polymerases biosynthesis, DNA directed RNA polymerases metabolism, genes, genetic complementation test, hemagglutinins viral, neuraminidase biosynthesis, RNA viral biosynthesis, recombination, genetic, temperature, tissue culture, viral proteins biosynthesis.


NAL Call Number: 41.8 Au72

Descriptors: disease outbreaks veterinary, fowl plague diagnosis, fowl plague epidemiology, influenza A virus avian classification, poultry diseases diagnosis, poultry diseases epidemiology, amino acid sequence, antibodies, viral analysis, antibodies, viral immunology, base sequence, chickens, cloaca pathology, cloaca virology, DNA, viral analysis, DNA, viral chemistry, DNA, viral genetics, enzyme linked immunosorbent assay methods, enzyme linked immunosorbent assay veterinary, fowl plague pathology, hemagglutinins genetics, avian genetics, avian isolation and purification, poultry diseases pathology, specific pathogen free organisms, Victoria epidemiology.


NAL Call Number: 41.8 Au72

Descriptors: ducks virology, fowl plague virology, influenza A virus avian classification, poultry diseases virology, chick embryo, chickens, cloaca virology, fowl plague pathology, avian isolation and purification, avian pathogenicity, kidney pathology, poultry diseases pathology, specific pathogen free organisms, Victoria.


NAL Call Number: SF995.W4

Descriptors: chickens, avian influenza virus, Mexico, America, birds, domestic animals, domesticated birds, Galliformes, influenza virus, Latin America, livestock, North America, orthomyxoviridae, poultry, useful animals, viruses.


NAL Call Number: 41.8 R312

Abstract: Twenty-seven apparent paramyxoviruses, unrelated to known avian paramyxoviruses, were isolated at a Hong Kong dressing plant from the trachea or cloaca of birds originating from Hong Kong and the People's Republic of China. A total of 2443 apparently healthy ducks, geese and fowls was sampled and isolation frequencies were 1.3%, 1.0% and 0.5% respectively. Twenty of the isolates were from the cloaca; 11 were obtained in association with Newcastle disease virus and one with an avian influenza virus. The majority of the isolations were made in the winter months. All 27 isolates were serologically related although 11 representative isolates differed slightly in haemagglutinin properties. A representative isolate was not pathogenic for chickens. A serological survey of poultry indicated a relatively low incidence of infection.

Descriptors: paramyxoviridae isolation and purification, cloaca microbiology, Hong Kong, paramyxoviridae immunology, paramyxoviridae pathogenicity, poultry microbiology, trachea microbiology.

NAL Call Number: 448.8 V81
Descriptors: fowl plague transmission, fowl plague virology, influenza A virus avian classification, poultry diseases virology, zoonoses virology, antibodies, monoclonal, chick embryo, chickens virology, ducks virology, feces virology, geese virology, Hong Kong, avian isolation and purification, avian physiology, avian ultrastructure, mice, rats, turkeys virology, virus replication.


NAL Call Number: 448.3 AC85
Abstract: Current isolates of the subtypes H7N3 and H7N7 from 1979 to 1981 were examined and compared with the reference strains with regard to their antigenic variability and to their pathogenicity for birds and mammals in order to establish the potentiality of influenza A/H7 virus (Hav1) transmission from birds to mammals. The analysis of the electrophoretic mobility of virus-induced polypeptides and of the double-stranded RNA segments after hybridization revealed equal, similar and deviating patterns. A substantial drift was determined in the surface antigens, especially in the neuraminidase. The avian strains replicated also in mammalian cells and were pathogenic for mammals. All strains examined were reisolated from the infected mammals; they caused more pronounced inflammatory changes in the trachea and lungs of infected mammals than in those of birds.
Descriptors: influenza A virus avian isolation and purification, cell line, chick embryo, DNA replication, fowl plague microbiology, fowl plague transmission, hamsters, hemagglutination tests, avian classification, avian genetics, kidney, neuraminidase genetics, nucleic acid hybridization, RNA viral genetics, species specificity, viral proteins genetics, virus replication.

Descriptors: avian influenza virus, characteristics, subtypes.


NAL Call Number: 448.3 AC85
Abstract: We have used the mouse model to monitor the acquisition of virulence of a non-pathogenic influenza A virus upon adaptation to a new mammalian host. An avian strain, A/Mallard duck/Pennsylvania/10218/84 (H5N2) (Mld/PA/84) was adapted to mice by 23 serial lung-to-lung passages until a highly virulent mouse-adapted (MA) variant (Mld/PA/84-MA) emerged. This MA variant was characterized and compared to the parental strain as well as some of its intermediate passage variants. MA variant caused bronchopneumonia in mice with a high mortality rate (the virulence of Mld/PA/84-MA measured as log (EID50/LD50) was 1.75), while the parental, avirulent strain Mld/PA/84 did not cause illness and mortality in mice (log (EID50/LD50) was 7.25). Hemagglutination-inhibition (HAI) test with a set of hemagglutinin- (HA) specific monoclonal antibodies (MAbs) revealed antigenic differences between the parental strain and MA variant. Mld/PA/84-MA reacted with HA-specific MAbs in higher titers than the parental strain. The HA genes of the parental strain Mld/PA/84, the 1st, 3rd, 8th, and 15th intermediate passage variants, and Mld/PA/84-MA were sequenced. Three amino acid changes at positions 203, 273 and 320 were determined in the HA of MA variant. The first of them, Leu-->Pro (320), appeared in the HA stem region at the 8th passage. Two other in the HA1 globular region (Ser-->Phe (203) and Glu-->Gly (273)) appeared at the 15th passage. All of these substitutions were associated with the increase of viral infectivity for mouse lungs and changes in the HA antigenicity. The potential role of these changes in HA with respect to the process of viral interspecies transmission and acquisition of virulence for new host is discussed.
Descriptors: adaptation, physiological genetics, bronchopneumonia virology, influenza A virus avian


Abstract: Since the 1997 H5N1 influenza virus outbreak in humans and poultry in Hong Kong, the emergence of closely related viruses in poultry has raised concerns that additional zoonotic transmissions of influenza viruses from poultry to humans may occur. In May 2001, an avian H5N1 influenza A virus was isolated from duck meat that had been imported to South Korea from China. Phylogenetic analysis of the hemagglutinin (HA) gene of A/Duck/Anyang/AVL-1/01 showed that the virus clustered with the H5 Goose/Guandong/1/96 lineage and 1997 Hong Kong human isolates and possessed an HA cleavage site sequence identical to these isolates. Following intravenous or intranasal inoculation, this virus was highly pathogenic and replicated to high titers in chickens. The pathogenesis of DK/Anyang/AVL-1/01 virus in Pekin
ducks was further characterized and compared with a recent H5N1 isolate, A/Chicken/Hong Kong/317.5/01, and an H5N1 1997 chicken isolate, A/Chicken/Hong Kong/220/97. Although no clinical signs of disease were observed in H5N1 virus-inoculated ducks, infectious virus could be detected in lung tissue, cloacal, and oropharyngeal swabs. The DK/Anyang/AVL-1/01 virus was unique among the H5N1 isolates in that infectious virus and viral antigen could also be detected in muscle and brain tissue of ducks. The pathogenesis of DK/Anyang/AVL-1/01 virus was characterized in BALB/c mice and compared with the other H5N1 isolates. All viruses replicated in mice, but in contrast to the highly lethal CK/HK/220/97 virus, DK/Anyang/AVL-1/01 and CK/HK/317.5/01 viruses remained localized to the respiratory tract. DK/Anyang/AVL-1/01 virus caused weight loss and resulted in 22 to 33% mortality, whereas CK/HK/317.5/01-infected mice exhibited no morbidity or mortality. The isolation of a highly pathogenic H5N1 influenza virus from poultry indicates that such viruses are still circulating in China and may present a risk for transmission of the virus to humans.

Descriptors: foods, infection, molecular genetics, H5N1 avian influenza A virus infection, respiratory system disease, viral disease, molecular cloning molecular genetic method, pathogenetic analysis analytical method, duck meat, meat production.

NAL Call Number: 448.8 V81
Abstract: In this report, the genome of the Thai avian influenza virus A (H5N1); A/Chicken/Nakorn-Pathom/Thailand/CU-K2/04, isolated from the Thai avian influenza A (AI) epidemic during the early of 2004 was sequenced. Phylogenetic analyses were performed in comparison to AI viruses from Hong Kong 1997 outbreaks and other AI (H5N1) isolates reported during 2001-2004. Molecular characterization of the Thai AI (H5N1) HA gene revealed a common characteristic of a highly pathogenic AI (HPAI), a 20-codon deletion in the neuraminidase gene, a 5-codon deletion in the NS gene and polymorphisms of the M2 and PB2 genes. Moreover, the HA and NA genes of the Thai AI displayed high similarity to those of the AI viruses isolated from human cases during the same epidemic. Finally, our results demonstrated that the Thai AI emerged as a member of 2000's AI lineage with most of the genetic sequences closely related to the Influenza A/Duck/China/E319.2/03 (H5N1).
Descriptors: disease outbreaks veterinary, genome, viral, influenza A virus, avian genetics, avian influenza virology, amino acid sequence, codon, gene deletion, avian influenza A virus isolation and purification, avian influenza A virus pathogenicity, avian influenza epidemiology, molecular sequence data, phylogeny, polymorphism, genetic, poultry, sequence alignment, Thailand epidemiology, viral proteins genetics.

Descriptors: strains, pathogenicity, viral morphology, ducks, avian influenza virus, Galliformes.

NAL Call Number: 449.9 Un3r
Descriptors: virulence, epidemiology, avian influenza virus, molecular charcterization, strains.

NAL Call Number: 449.9 W892B
Descriptors: agglutinins, hemagglutinins, orthomyxoviridae immunology, birds microbiology, turkeys microbiology.

NAL Call Number: 448.8 V81

Descriptors: influenza A virus avian growth and development, intestines microbiology, virus replication, ducks, feces microbiology, hydrogen-ion concentration, avian ultrastructure, human growth and development, porcine growth and development, lung microbiology.


NAL Call Number: 41.8 Av5

Abstract: A hemagglutinating virus was isolated from a dead turkey in a small mixed free-range flock in Southern Germany. It was identified as influenza virus type A of subtype H7N7. The pathogenicity was low. An intravenous pathogenicity index of 0.03 was recorded, and the nucleotide sequencing revealed the amino acid sequence NVPEIPKGR*GLFG at the cleavage site of the hemagglutinin. Antibodies as well as virus were detected in the affected flock. Further virus spreading to other flocks was prevented by stamping out policy. Serological monitoring of contact flocks revealed one small backyard flock of 18 hens, which was positive. This flock was also destroyed. The origin of the virus could not be identified.

Descriptors: epidemiology, immune system, infection, avian influenza, infectious disease, respiratory system disease, viral disease, nucleotide sequencing genetic techniques, laboratory techniques, serology clinical techniques, diagnostic techniques, free range poultry flock, viral pathogenicity.


NAL Call Number: QR180.M53

Abstract: Ten influenza virus isolates were obtained from infected pigs from different places in Shandong province showing clinical symptoms from October 2002 to January 2003. All 10 isolates were identified in China's National Influenza Research Center as influenza A virus of H9N2 subtype. The complete genome of one isolate, designated A/Swine/Shandong/1/2003(H9N2), was sequenced and compared with sequences available in GenBank. The results of analyses indicated that the sequence of A/Swine/Shandong/1/2003(H9N2) was similar to those of several chicken influenza viruses and duck influenza viruses recently prevalent in South China. According to phylogenetic analysis of the complete gene sequences, A/Swine/Shandong/1/2003(H9N2) possibly originated from the reassortment of chicken influenza viruses and duck influenza viruses. It was found that the amino acid sequence at the HA cleavage site in Sw/SD/1/2003 is R-S-L-R-G, differing clearly from that of other H9N2 subtype isolates of swine influenza and avian influenza, which is R-S-S-R-G.

Descriptors: influenza veterinary, influenza A virus, porcine genetics, swine diseases virology, amino acid sequence, base sequence, chick embryo, guinea pigs, influenza virology, porcine chemistry, porcine isolation and purification, molecular sequence data, phylogeny, RNA, viral chemistry, viral genetics, rats, reverse transcriptase polymerase chain reaction veterinary, sequence analysis, DNA, sequence homology, nucleic acid, swine.


NAL Call Number: 448.8 V81

Abstract: Analysis of the sequences of all eight RNA segments of the influenza A/Goose/Guangdong/1/96 (H5N1) virus, isolated from a sick goose during an outbreak in Guangdong province, China, in 1996, revealed that the hemagglutinin (HA) gene of the virus was genetically similar to those of the H5N1 viruses isolated in Hong Kong in 1997. However, the remaining genes showed greater similarity to other avian influenza viruses. Notably, the neuraminidase gene did not have the 19-amino-acid deletion in the stalk region seen in the H5N1 Hong Kong viruses and the NS gene belonged to allele B, while that of the H5N1 Hong Kong viruses belonged to allele A. These data suggest that the H5N1 viruses isolated from the Hong Kong outbreaks derived their HA genes from a virus similar to the A/Goose/Guangdong/1/96 virus or shared

**Abstract:** Twenty-six influenza A viruses were isolated from cloacal and tracheal samples of 235 resident and 396 migratory ducks in Miyagi prefecture, Japan, in 1977-78. Of these, twelve were antigenically related to the avian-origin HSW1 virus, A/duck/Alberta/35/76 (HSW1N1), but their neuraminidase antigens were characterized as Nav2-3, Nav4 or N2. These antigenic configuration have not previously been reported. In addition, one strain in which the neuraminidase antigen was identified as Nav4, was demonstrated to be a mixture of two haemagglutinins, HSW1 and Hav7. Two distinct strains were separated from the mixture and characterized as HSW1Nav4 and Hav7Nav4. The antigenic identification of an additional 13 influenza A viruses revealed the presence of six haemagglutinin subtypes (Hav1, Hav3, Hav4, Hav6, Hav7, and Hav8) and five neuaraminidase subtypes (Nav1, Nav2-3, Nav4, Neq2, and N2) in various combinations. The results suggest that the avian influenza A viruses among feral ducks may be isolated in various combinations of haemagglutinins and neuraminidase subtypes in Japan, and that feral ducks may be the site of genetic recombination occurring as a result of dual infection with different subtypes of influenza A virus.

**Descriptors:** antigens, viral classification, ducks microbiology, influenza A virus immunology, influenza A virus isolation and purification, cloaca microbiology, hemagglutinins viral classification, Japan, neuraminidase immunology, trachea microbiology.


**NAL Call Number:** 41.8 Av5

**Abstract:** Between January 1997 and March 1998, 11 cases of H7N2 avian influenza (nonpathogenic) were diagnosed at the Laboratory of Avian Medicine and Pathology, Kenneth Square, PA. These cases involved either commercial leghorn laying hens or leghorn pullets raised in Pennsylvania. Grossly and histologically, the most striking lesion associated with disease was salpingitis, usually with edema and occasionally with oviduct necrosis. Fluid, fibrinous, and egg yolk material in the peritoneum (egg yolk peritonitis) as well as pulmonary congestion and pulmonary edema were also frequently seen. Oviduct lesions have rarely been described in association with avian influenza infections in previous outbreaks. Mortality in affected houses was mild to moderate (less than 4% total mortality during the outbreak), with concurrent mild to moderate egg production declines (2%-4% at the time of disease onset).

**Descriptors:** hens, pullets, avian influenza virus, infections, virulence, pathogenicity, diagnosis, histopathology, clinical aspects, symptoms, oviducts, necrosis, mortality, egg production, fecundity, case reports, Pennsylvania.
Zoonotic Implications


NAL Call Number: 472 N21

Descriptors: influenza prevention and control, influenza veterinary, poultry diseases epidemiology, zoonoses epidemiology, Asia epidemiology, influenza epidemiology, influenza transmission, influenza A virus, avian isolation and purification, poultry diseases prevention and control, poultry diseases transmission, poultry diseases virology, World Health Organization, zoonoses transmission, zoonoses virology.


NAL Call Number: 448.3 Ar23

Abstract: Antigenic reactivity of the three polymerase proteins PB1, PB2, and PA of type A influenza viruses of animal and human origin were analysed by radioimmunoprecipitation using monospecific antisera. Each of the polymerase monospecific antisera made against the polymerase proteins of the human A/WSN/33 (H1N1) influenza virus reacted efficiently with the homologous proteins of all the known thirteen HA subtype viruses of avian influenza virus, three subtypes of human influenza virus, swine and equine influenza viruses. This broad reactivity of each of the antisera indicated that the polymerase proteins are antigenically related among the type A influenza viruses and therefore can be considered as type specific antigens similar to the other viral internal proteins nucleoprotein (NP) and matrix protein (M). No electrophoretic migrational heterogeneity was found among the PB2 proteins of different subtype viruses, whereas PB1 protein exhibited minor variation. However, PA protein from among various viral subtypes showed considerable heterogeneity. Each of the polymerase antisera also immunoprecipitated additional antigenically related polypeptides with distinct electrophoretic mobilities from cells infected with each of the influenza viral subtypes.

Descriptors: DNA directed RNA polymerases immunology, influenza A virus human enzymology, influenza A virus enzymology, viral proteins immunology, antigens, viral immunology, human immunology, influenza A virus immunology, precipitin tests.


NAL Call Number: SF601.S8

Descriptors: avian influenza virus, viroses, mankind, zoonoses, pathogenicity, biological properties, infectious diseases, influenza virus, microbial properties, orthomyxoviridae, viruses, influenza.


NAL Call Number: SF481.M54

Descriptors: zoonoses, pathogenesis, avian influenza virus, poultry, humans, dangers.


NAL Call Number: 41.8 V641

Descriptors: birds microbiology, fowl plague epidemiology, influenza A virus avian isolation and purification, England, fowl plague microbiology, quarantine.


NAL Call Number: QR360.A1J6

Abstract: There is a significant difference in the ability of human influenza A virus H1N1 strains isolated up
to 1977 and those isolated later to rescue temperature-sensitive mutants of fowl plague virus with a defect in
the nucleoprotein (NP) gene. Therefore the NP genes of five human H1N1 and H3N2 influenza A virus
strains, isolated between 1950 and 1978, have been sequenced. By comparison with previous and more
recent isolates, an evolutionary pathway has been established. Three amino acid replacements were found
which might be responsible for the functional difference between the USSR (1977) and the Brazil (1978)
strains. The California (H1N1) strain isolated in 1978 had acquired by reassortment the NP gene of a human
H3N2 virus circulating at about 1977 as had been previously suggested by investigations involving RNase
fingerprint or hybridization techniques.

Descriptors: evolution, genes viral, influenza A virus human genetics, nucleoproteins genetics, viral core
proteins, viral proteins genetics, amino acid sequence, base sequence, chick embryo, chickens, influenza A
virus avian genetics, molecular sequence data, mutation, sequence homology, nucleic acid.

the nucleoprotein (NP) of recent swine, turkey, and human influenza A virus (H1N1) isolates. Virus
Research 22(1): 79-87. ISSN: 0168-1702.

NAL Call Number: QR375.V6

Abstract: The sequences of nucleoprotein (NP) genes of recent human and turkey isolates of influenza A
viruses, which serologically could be correlated to contemporary swine viruses, were determined. These
sequences were closely related to the NPs of these swine viruses and they formed a separate branch on the
phylogenetic tree. While the early swine virus from 1931 resembled the avian strains in consensus amino
acids of the NP and in its ability to rescue NP ts mutants of fowl plague virus in chicken embryo cells, the
later strains on that branch were different: at 15 positions they have their own amino acids and they rescued
the NP ts mutants only poorly. Of the NPs of the human New Jersey/76 isolates analysed, one clustered
with the recent H1N1 swine viruses of the U.S.A., the other one with contemporary human strains. Since the
NP is one of the main determinants of species specificity it is concluded that, although the H1N1 swine
isolates from the U.S.A. form their own branch in the phylogenetic tree, they can be transmitted to humans
and turkeys, but they do not spread further in these populations and so far have not contributed to human
pandemics. It is not very likely that they will do so in future, since its branch in the phylogenetic tree
develops further away from the human and avian branch.

Descriptors: influenza A virus avian genetics, human genetics, porcine genetics, nucleoproteins genetics,
fowl plague microbiology, influenza microbiology, phylogeny, sequence homology, nucleic acid, turkeys.

Anonymous (1999). Avian strain of influenza A virus isolated from humans in Hong Kong. Communicable

Descriptors: disease outbreaks, influenza epidemiology, influenza A virus avian, child, preschool, Hong
Kong epidemiology, infant.

A(H5N1) viruses from humans--Hong Kong, May-December 1997. JAMA the Journal of the American
Medical Association 279(4): 263-4. ISSN: 0098-7484.

NAL Call Number: 448.9 Am37

Descriptors: influenza epidemiology, influenza A virus avian isolation and purification, adolescent, adult,
child, child, preschool, Hong Kong epidemiology, influenza virology, middle aged.

influenza A(H5N1) viruses from humans--Hong Kong, 1997-1998. JAMA the Journal of the American
Medical Association 279(5): 347-8. ISSN: 0098-7484.

NAL Call Number: 448.9 Am37

Descriptors: influenza epidemiology, influenza A virus avian virology, influenza A virus avian isolation and purification,
Hong Kong epidemiology, seroepidemiologic studies.

Weekly 7(50): 441. ISSN: 1350-9357.

Descriptors: fowl plague transmission, influenza epidemiology, influenza A virus avian classification,
adolescent, bacterial typing techniques, chickens, child, preschool, fowl plague epidemiology, Hong Kong epidemiology, incidence, avian isolation and purification, middle aged, survival rate.


**NAL Call Number:** RA407.3.M56

**Descriptors:** avian influenza, human infection, transmission, Hong Kong.


**NAL Call Number:** RA407.3.M56

**Abstract:** A strain of influenza virus that previously was known to infect only birds has been associated with infection and illness in humans in Hong Kong. The first known human case of influenza type A(H5N1) occurred in a 3-year-old child who died from respiratory failure in May 1997. In Hong Kong, the virus initially was identified as influenza type A, but the subtype could not be determined using standard reagents. By August, CDC; the National Influenza Center, Rotterdam, the Netherlands; and the National Institute for Medical Research, London, United Kingdom, had independently identified the virus as influenza A(H5N1). An investigation conducted during August-September by the Hong Kong Department of Health and CDC excluded the possibility of laboratory contamination. Since this initial case was identified, six additional persons in Hong Kong have been confirmed to have influenza A(H5N1) infection, and two possible cases have been identified. This report summarizes the nine cases identified thus far and describes preliminary findings from the ongoing investigation, which indicate that multiple influenza A(H5N1) infections have occurred and that both the source and mode of transmission are uncertain at this time.

**Descriptors:** influenza epidemiology, influenza A virus avian isolation and purification, adolescent, adult, child, child, preschool, Hong Kong epidemiology, influenza virology, middle aged.


**NAL Call Number:** 41.8 In2

**Descriptors:** avian influenza virus infection, quarantine, clinical techniques, Food and Agriculture Organization, United Nations, World Health Organization, Office International des Epizooties, Asia.


**NAL Call Number:** RA407.3.M56

**Abstract:** As of January 6, 1998, a total of 16 confirmed and three suspected cases of human infection with avian influenza A(H5N1) viruses have been identified in Hong Kong. Confirmed cases are those from which an influenza A(H5N1) virus was isolated or in which a seroconversion to influenza A(H5N1) virus was detected by a neutralization assay. Suspected cases are those with influenza-like illness (ILI) and preliminary laboratory evidence of influenza A(H5N1) infection. This report summarizes interim findings from the ongoing epidemiologic and laboratory investigation of influenza A(H5N1) cases by health officials in Hong Kong and by CDC.

**Descriptors:** influenza epidemiology, influenza virology, influenza A virus avian isolation and purification, Hong Kong epidemiology, seroepidemiologic studies.


**NAL Call Number:** QR360.A1J6

**Abstract:** Monoclonal antibodies to the haemagglutinin (HA) of the avian H1 influenza virus A/duck/Alberta/35/76 were used to construct an operational antigenic map of the HA molecule and to study the interrelationships of H1 viruses from different hosts. Haemagglutination inhibition tests between the monoclonal antibodies and variants selected by them provided evidence of four antigenic regions which overlap to varying degrees. Avian H1 influenza viruses displayed a spectrum of reactivities to the
monoclonal antibody panel. Representatives of the epidemic strains of human H1 influenza viruses and early swine influenza viruses showed little or no reactivity with the monoclonal antibodies but swine influenza-like viruses isolated from pigs and humans in the last decade reacted with 11 of 17 antibodies. The antigenic similarity of these viruses to many avian isolates suggests that there has been a transfer of HA genetic information between mammalian and avian H1 influenza viruses.

Descriptors: hemagglutinins viral immunology, influenza A virus avian immunology, antibodies, monoclonal diagnostic use, epitopes, human immunology, porcine immunology, species specificity.


NAL Call Number: 449.9 W892B

Descriptors: antigens, viral analysis, influenza A virus avian immunology, porcine immunology, immunology, swine microbiology, turkeys microbiology, France, avian isolation and purification, porcine isolation and purification.


NAL Call Number: 41.8 M742

Descriptors: avian influenza virus, serum samples, turkeys, fowl, zoonoses, human strains, Hong Kong strain, Singapore strain, antibodies.


NAL Call Number: 448.8 V81

Abstract: Reassortants possessing the hemagglutinin (HA) gene from A/Equine/London/1416/73 (H7N7) [Eq/Lond] and five or more genes from A/Chicken/Pennsylvania/1370/83 (H5N2) [Ck/Penn] were lethal in chickens. This result demonstrates that horses can maintain influenza viruses whose HAs are capable of promoting virulence. Thus, reassortment of equine and avian influenza virus genes could generate viruses that might be lethal in domestic poultry.

Descriptors: fowls, horses, avian influenza virus, equine influenza virus, hemagglutininins, genes, amino acids, virulence, pathogenicity, mortality, molecular sequence data, EMBL m58657, GENBANK m58657.


NAL Call Number: 448.3 Ar23

Abstract: The partial sequencing of the internal and the neuraminidase genes of isolate 268/96 obtained from a woman with conjunctivitis showed all seven to have closest homology with avian influenza viruses. The entire nucleotide sequence of the haemagglutinin gene of 268/96 had close, 98.2%, homology with an H7N7 virus isolated from turkeys in Ireland in 1995. This appears to be the first reported case of isolation of an influenza A virus from a human being infected as a result of direct natural transmission of an avian influenza virus from birds.

Descriptors: influenza virology, influenza A virus avian genetics, adult, birds virology, genes viral, influenza epidemiology, influenza transmission, avian classification, influenza A virus avian isolation and purification, Ireland, molecular sequence data, phylogeny, turkeys virology.


Descriptors: disease outbreaks, fowl plague epidemiology, influenza epidemiology, Asia, Southeastern epidemiology, birds, chickens, influenza A virus avian, human.

**Descriptors:** human diseases, influenza virus A, epidemics, clinical aspects, diagnosis, reviews, Hong Kong.


NAL Call Number: 448.3 Ar23

**Abstract:** Volunteers inoculated with avian influenza viruses belonging to subtypes currently circulating in humans (H1N1 and H3N2) were largely refractory to infection. However 11 out of 40 volunteers inoculated with the avian subtypes, H4N8, H6N1, and H10N7, shed virus and had mild clinical symptoms: they did not produce a detectable antibody response. This was presumably because virus multiplication was limited and insufficient to stimulate a detectable primary immune response. Avian influenza viruses comprise hemagglutinin (HA) subtypes 1-14 and it is possible that HA genes not so far seen in humans could enter the human influenza virus gene pool through reassortment between avian and circulating human viruses.

**Descriptors:** influenza A virus avian pathogenicity, adult, antibodies, viral blood, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral immunology, avian isolation and purification, avian physiology, middle aged, species specificity, virus replication.


**Abstract:** The current outbreak of avian influenza in South East Asia has resulted in a small number of human deaths. Avian flu can pass from birds to humans, although the number of humans infected is low. The fear is that the avian flu virus could mutate in a human who was also infected with a common flu virus, creating a new strain that could pass from human to human. Nurses, especially those working in travel health, should keep themselves informed of the latest developments.

**Descriptors:** avian flu, outbreak, symptoms, South East Asia, human deaths, birds.


NAL Call Number: 448.8 L22

**Descriptors:** disease outbreaks, fowl plague transmission, influenza transmission, influenza virology, influenza A virus avian, zoonoses, Asia epidemiology, chickens virology, Hong Kong epidemiology, influenza epidemiology.


NAL Call Number: 448.8 V81

**Descriptors:** hemagglutinin glycoproteins, influenza virus genetics, influenza virology, influenza A virus human genetics, neuraminidase genetics, adolescent, adult, antigens, viral immunology, base sequence, child, preschool, DNA, viral, disease outbreaks, genes viral, Hong Kong epidemiology, infant, influenza epidemiology, human growth and development, human immunology, human isolation and purification, middle aged, molecular sequence data, phylogeny.


NAL Call Number: 448.3 Ar23

**Abstract:** Strains of an influenza H10N4 virus have been isolated during an outbreak of a respiratory disease in mink on the south-east coast of Sweden. This was the first example of a disease in mammals caused by the H10 subtype. We compared the A/mink/Sweden/84 strain with two recent avian H10N4 isolates, one from fowl and another from a mallard, both isolated in Great Britain in 1985 as well as the prototype A/chicken/Germany/N/49 (H10N7). The comparison was carried out by genomic analysis of the
strains by oligonucleotide fingerprinting and in bioassays on mink. The oligonucleotide fingerprint analysis revealed a high degree of genomic homology of around 98% between the viruses from mink, mallard and fowl. Only the recent avian isolates, that from the mallard and fowl could infect mink by contact, causing similar pathological and clinical signs and inducing seroconversion as did the mink virus. However, the susceptibility of mink to the fowl and mallard viruses by contact was less pronounced than that to the mink virus. Both the genomic homology and the similarities from the infectivity and pathogenicity studies between the mink virus and the recent avian isolates point to a direct invasion of the mink population by an avian H10N4 virus.

Descriptors: influenza A virus avian genetics, mink, orthomyxoviridae infections veterinary, chickens microbiology, disease outbreaks veterinary, ducks microbiology, fowl plague microbiology, fowl plague transmission, genes viral, avian isolation and purification, avian pathogenicity, nucleotide mapping, orthomyxoviridae infections microbiology, orthomyxoviridae infections transmission, RNA, viral, Sweden epidemiology.


Abstract: Two antigenically distinct H1N1 influenza A viruses were isolated during an outbreak of respiratory disease in Quebec swine in 1990/91. Analysis of haemagglutinin and partial nucleoprotein sequences indicated that one was a variant of the swine H1N1 influenza virus circulating in the American Midwest whereas the other was very similar to virus isolated from swine in 1930. The existence of this latter isolate supports the concept that influenza viruses can be maintained for long periods in swine, perhaps in geographically limited pockets. Serological evidence indicates that these distinct strains continued to circulate widely in south-central Quebec until at least 1993.

Descriptors: influenza A virus, porcine genetics, influenza A virus, porcine immunology, orthomyxoviridae infections veterinary, phylogeny, swine diseases virology, amino acid sequence, antigenic variation, antigens, viral analysis, base sequence, capsid genetics, disease outbreaks, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral analysis, hemagglutinins viral genetics, avian genetics, human genetics, molecular sequence data, orthomyxoviridae infections epidemiology, orthomyxoviridae infections virology, quebec epidemiology, sequence analysis, DNA, sequence homology, amino acid, swine, swine diseases epidemiology, viral core proteins genetics.


Abstract: The authors tried to decode the mechanism of influenza viruses species adaptation in the process of host changing. The functionally important replacement in the surface pocket domains were revealed, particularly in the conservative region 221-241, involving fibronectin-like part. Close replacements were revealed in the region 141-161. The method of construction of heteroduplexes between hemagglutinin RNA of duck, pig, and human viruses was used. The method showed that all heteroduplexes formed recombinogene structures. An unexpected effect of directional recombination was elicited for hemagglutinin RNA heteroduplexes in cases of duck-pig and human-pig viruses. During the directional recombination the following processes took place: the receptor-binding site of animal type was transmitted to the duck virus, while the human receptor-binding site was transmitted to the pig virus. According to the experimental data, a new hypothesis is formulated: the cascade mechanism of directional recombination for duck, animal and human viruses makes it possible for the recombinant viruses to overcome interspecies barriers.

Descriptors: adaptation, physiological genetics, genes viral genetics, hemagglutinins viral genetics, influenza A virus avian genetics, porcine genetics, recombination, genetic genetics, amino acid sequence, ducks microbiology, human genetics, molecular sequence data, nucleic acid heteroduplexes genetics, RNA viral genetics, swine microbiology, variation genetics genetics.

**NAL Call Number:** 448.3 Ar23

**Abstract:** Recombinants with known gene constellations between fowl plague virus (FPV) and various prototype influenza virus strains have been examined for neurovirulence in suckling mice. Strongly neurotropic recombinants were obtained from crosses between FPV and the strains virus N, Hong Kong, and PR8, but not between FPV and equi 2 or swine viruses. All highly neurotropic recombinants had RNA segment 4 (HA) derived from FPV and RNA segment 2 (Ptra gene) from the other prototype strain. The derivation of two other RNA segments of the polymerase complex, namely RNA segments 3 (Pol 2) and 5 (NP) and also segment 8 (NS) can modulate these properties. For example, if in recombinants between FPV and virus N in addition to RNA segment 2 also RNA segments 3 and/or 8 are derived from virus N, neurovirulence is further enhanced, while replacement of RNA segment 5 of FPV by the corresponding segment of virus N decreases or abolishes neurovirulence. The derivation of the other genes does not seem to be relevant for neurovirulence in the crosses mentioned above. Of the prototype strains tested, the turkey England (t. Engl.) strain is the only one which was highly neurotropic for sucking mice. Recombinants between FPV and t. Engl. which have kept the HA gene of t. Engl. were still neurotropic, while those with the HA gene of FPV were completely avirulent. The results obtained demonstrated that 1. the creation of influenza virus recombinants neurotropic for mice is not a rare event; 2. one of the parents should multiply well in mouse lungs; 3. the presence of a cleavable hemagglutinin is necessary, but not sufficient. In the pair FPV/turkey England the hemagglutinin of turkey England seems to determine neurovirulence.

**Descriptors:** influenza A virus, genetics, recombination, genetic, brain microbiology, cultured cells, embryo microbiology, fibroblasts, genes viral, avian genetics, pathogenicity, kidney, lung microbiology, mice, virulence.


**Descriptors:** ducks virology, avian influenza transmission, poultry diseases transmission, zoonoses, Asia epidemiology, food contamination, avian influenza epidemiology, poultry diseases epidemiology, public health.


**NAL Call Number:** 448.8 Sch9

**Abstract:** An avian influenza A virus which grows well in human leukemic myeloblasts was unable to replicate in normal human leukocytes. The virus adhered during the first hours of incubation to plastic surfaces and to leukocytes and was then released into the supernatant; care should be taken not to confuse this with viral growth.

**Descriptors:** influenza A virus, avian growth and development, leukocytes microbiology, adaptation, physiological, adsorption, adult, cell adhesion, granulocytes microbiology, leukemia, myelocytic, acute, lymphocytes microbiology, monocytos microbiology, plastics, tissue culture, virus replication.


**Descriptors:** disease outbreaks, influenza A virus, avian influenza, avian influenza epidemiology, avian influenza transmission, zoonoses, human, porcine, avian influenza prevention and control, poultry, risk factors, swine.


**NAL Call Number:** 448.8 J821

**Abstract:** In 1997, outbreaks of highly pathogenic influenza A (H5N1) among poultry coincided with 18 documented human cases of H5N1 illness. Although exposure to live poultry was associated with human illness, no cases were documented among poultry workers (PWs). To evaluate the potential for avian-to-
human transmission of H5N1, a cohort study was conducted among 293 Hong Kong government workers (GWs) who participated in a poultry culling operation and among 1525 PWs. Paired serum samples collected from GWs and single serum samples collected from PWs were considered to be anti-H5 antibody positive if they were positive by both microneutralization and Western blot testing. Among GWs, 3% were seropositive, and 1 seroconversion was documented. Among PWs, approximately 10% had anti-H5 antibody. More-intensive poultry exposure, such as butchering and exposure to ill poultry, was associated with having anti-H5 antibody. These findings suggest an increased risk for avian influenza infection from occupational exposure.

Descriptors: influenza etiology, influenza A virus, occupational diseases etiology, poultry virology, adolescent, adult, case control studies, Hong Kong epidemiology, influenza epidemiology, middle aged, occupational exposure, risk factors, seroepidemiologic studies, time factors.

NAL Call Number: 41.8 Av5
Abstract: Avian-like H5N1 influenza viruses isolated from humans in 1997 were shown to have two distinct pathogenic phenotypes in BALB/c mice, after intranasal inoculation and without prior adaptation to this host. To further understand the mechanisms of H5N1 pathogenicity, we investigated the consequences of the route of viral inoculation on morbidity and mortality, viral replication in pulmonary and systemic organs, and lymphocyte depletion. This study demonstrates the importance of extrapulmonary spread and replication, particularly in the brain, for the lethality of H5N1 viruses.
Descriptors: infection, avian influenza, infectious disease, respiratory system disease, viral disease, inoculation clinical techniques, therapeutic and prophylactic techniques, morbidity, mortality, pathogenic phenotypes, pathogenicity mechanisms, viral replication.

NAL Call Number: 448.8 L22
Descriptors: disease transmission, horizontal statistics and numerical data, fowl plague transmission, Asia epidemiology, fowl plague epidemiology, fowl plague prevention and control, influenza A virus avian, poultry, World Health Organization, zoonoses epidemiology, zoonoses transmission.

NAL Call Number: QR360.A1J6
Abstract: Novel H1N2 influenza A viruses which were first detected in pigs in Great Britain in 1994 were examined antigenically and genetically to determine their origins and establish the potential mechanisms for genetic reassortment. The haemagglutinin (HA) of all swine H 1 N2 viruses examined was most closely related to, but clearly distinguishable both antigenically and genetically from, the HA of human H1N1 viruses which circulated in the human population during the early 1 980s. Phylogenetic analysis of the HA gene revealed that the swine H 1 N2 viruses formed a distinct branch on the human lineage and were probably introduced to pigs shortly after 1980. Following apparent transfer to pigs the HA gene underwent genetic variation resulting in the establishment and cocirculation of genetically and antigenically heterogeneous virus populations. Genetic analyses of the other RNA segments of all swine H1N2 viruses indicated that the neuraminidase gene was most closely related to those of early 'human-like' swine H3N2 viruses, whilst the RNA segments encoding PB2, PB1, PA, NP, M and NS were related most closely to those of avian viruses, which have been circulating recently in pigs in Northern Europe. The potential mechanisms and probable progenitor strains for genetic reassortment are discussed, but we propose that the swine H1N2 viruses examined originated following multiple genetic reassortment, initially involving human H1N1 and 'human-like' swine H3N2 viruses, followed by reassortment with 'avian-like' swine H1N1 virus. These findings suggest multiple reassortment and replication of influenza viruses may occur in pigs many years before their detection as clinical entities.
Descriptors: influenza A virus avian genetics, human genetics, recombination, genetic, antigens, viral
immunology, base sequence, DNA, viral, Europe, genes viral, genotype, hemagglutination inhibition tests, hemagglutinin glycoproteins, influenza virus genetics, avian immunology, human immunology, molecular sequence data, phylogeny, sequence analysis, DNA, swine.


NAL Call Number: 501 L84Pb

Abstract: In 1982 we characterized the antigenic sites of the haemagglutinin of influenza A/PR/8/34, which is an influenza strain of the H1 subtype that was isolated from humans in 1934, by studying mutants which escaped neutralization by antibody. Four antigenic sites, namely Cb, Sa, Sb and Ca, were found to be located near the tip of the trimeric haemagglutinin spike. Based on the sequence of the haemagglutinin of the 1918 Spanish influenza, we can now specify the extent of divergence of antigenic sites of the haemagglutinin during the antigenic drift of the virus between 1918 and 1934. This divergence was much more extensive (40%) than the divergence (20%) in predicted antigenic sites between the 1918 Spanish influenza and an avian H1 subtype consensus sequence. These results support the hypothesis that the human 1918 pandemic originated from an avian virus of the H1 subtype that crossed the species barrier from birds to humans and adapted to humans, presumably by mutation and/or reassortment, shortly before 1918.

Descriptors: epidemiology, infection, molecular genetics, avian influenza, viral disease, pandemic influenza, epidemiology, respiratory system disease, viral disease, 1918 Spanish influenza pandemic, age related mortality, antigenic drift, antigenic site divergence, mortality rate, species barrier.


NAL Call Number: QR355.I5

Abstract: The hemagglutinin of an influenza virus isolated from a wild duck (Pintail, Anas acuta) in the USSR in 1976 had been found to be antigenically indistinguishable from the hemagglutinin of H2N2 viruses of human origin isolated in 1957. The hemagglutinins from viral preparations of the A/Anas acuta/Primorie/695/76 (H2Nav2) and A/Singapore/1/57 (H2N2) strains were purified by SDS gel chromatography as the subunits HA1 and HA2. Comparison of amino acid compositions and peptide maps of tryptic peptides containing [14C]-carboxymethylcysteine showed a striking degree of similarity between the H2 hemagglutinins.

Descriptors: hemagglutinins viral analysis, influenza A virus avian immunology, human immunology, amino acids analysis, ducks microbiology, peptides analysis.


NAL Call Number: 448.8 V81

Abstract: The nucleotide sequences of RNA segment 5 of an avian influenza A virus, A/Mallard/NY/6750/78 (H2N2), and a human influenza A virus, A/Udom/307/72 (H3N2), were determined and the deduced amino acid sequences of the nucleoprotein (NP) of these viruses were compared to two other avian and two other human influenza A NP sequences. The results indicated that there are separate classes of avian and human influenza A NP genes that can be distinguished on the basis of sites containing amino acids specific for avian and human influenza viruses and also by amino acid composition. The human influenza A virus NP genes appear to follow a linear pathway of evolution with the greatest homology (96.9%) between A/NT/60/68 (H3N2) and A/Udom/72, isolated only 4 years apart, and the least homology (91.1%) between A/PR/8/34 (H1N1) and A/Udom/72, isolated 38 years apart. Furthermore, 84% of the nucleotide substitutions between A/PR/8/34 and A/NT/60/68 are preserved in the NP gene of the A/Udom/72 strain. In contrast, a distinct linear pathway is not present in the avian influenza NP genes since the homology (90.3%) between the two avian influenza viruses A/Parrot/Ulster/73 (H7N1) and A/Mallard/78 isolated only 5 years apart is not significantly greater than the homology (90.1%) between strains A/FPV/Rostock/34 and A/Mallard/78 isolated 44 years apart and only 49% of the nucleotide substitutions between A/FPV/34 and
A/Parrot/73 are found in A/Mallard/78. A determination of the rate of evolution of the human influenza A virus NP genes suggested that there were a greater number of nucleotide substitutions per year during the first several years immediately following the emergence of a new subtype in 1968.

Descriptors: influenza A virus genetics, nucleoproteins genetics, viral proteins genetics, amino acid sequence, base sequence, evolution, genes viral, nucleoproteins classification, RNA viral genetics, sequence homology, nucleic acid, viral proteins classification.


NAL Call Number: QR360.J6

Abstract: The nucleotide sequence of the region of RNA segment 7 coding for the M1 and M2 proteins of avian influenza A/Mallard/New York/6750/78 was determined, and the deduced amino acid sequences were compared to other avian and human M protein sequences. The M2 proteins of the avian and human viruses have diverged much more than the M1 proteins, although amino acids specific for avian and human viruses were found in both M1 and M2 proteins.

Descriptors: genes viral, influenza A virus avian genetics, RNA viral genetics, viral proteins genetics, amino acid sequence, haplorhini microbiology, avian growth and development, messenger genetics.


NAL Call Number: 49.9 UN3R

Descriptors: disease surveys, avian influenza virus, humans, poultry, Hong Kong.


NAL Call Number: 448.8 J821

Abstract: The first outbreak of avian influenza A (H5N1) occurred among humans in Hong Kong in 1997. To estimate the risk of person-to-person transmission, a retrospective cohort study was conducted to compare the prevalence of H5N1 antibody among health care workers (HCWs) exposed to H5N1 case-patients with the prevalence among nonexposed HCWs. Information on H5N1 case-patient and poultry exposures and blood samples for H5N1-specific antibody testing were collected. Eight (3.7%) of 217 exposed and 2 (0.7%) of 309 nonexposed HCWs were H5N1 seropositive (P=.01). The difference remained significant after controlling for poultry exposure (P=.01). This study presents the first epidemiologic evidence that H5N1 viruses were transmitted from patients to HCWs. Human-to-human transmission of avian influenza may increase the chances for the emergence of a novel influenza virus with pandemic potential.

Descriptors: antibodies, viral blood, disease outbreaks, disease transmission, patient to professional, influenza transmission, influenza A virus avian immunology, adult, carrier state, cohort studies, avian classification, middle aged, retrospective studies, seroepidemiologic studies.


NAL Call Number: 448.8 V81

Descriptors: disease outbreaks veterinary, influenza veterinary, influenza A virus avian classification, human classification, poultry diseases virology, antigens, viral genetics, antigens, viral immunology, cloning, molecular, genome, viral, hemagglutination inhibition tests, hemagglutinins viral genetics, Hong Kong epidemiology, influenza epidemiology, avian genetics, avian immunology, human genetics, human immunology, molecular sequence data, Pakistan epidemiology, phylogeny, poultry diseases epidemiology,
sequence analysis, protein, viral proteins genetics, viral proteins immunology.


**NAL Call Number:** 448.8 J821

**Descriptors:** influenza A virus avian isolation and purification, antigens analysis, chick embryo, chickens, cross reactions, hemagglutination inhibition tests, immune sera analysis, avian classification, avian immunology, avian pathogenicity, microscopy, electron, neuraminidase analysis, neutralization tests, poultry diseases immunology, vaccination, viral vaccines administration and dosage.


**NAL Call Number:** QR360.A1J6

**Abstract:** In Italy, multiple H3N2 influenza viruses were isolated from chickens with mild respiratory disease and were shown to replicate in the respiratory tracts of experimentally infected chickens; this finding is the first to show that H3N2 influenza viruses can replicate and cause disease in chickens. H3N2 influenza viruses in pigs on nearby farms seemed a likely source of the virus; however, antigenic and molecular analyses revealed that the gene segments of the viruses in chickens were mainly of Eurasian avian origin and were distinguishable from those isolated from pigs and wild aquatic birds in Italy. Thus, several different H3 influenza viruses were circulating in Italy, but we failed to identify the source of the chicken H3N2 influenza viruses that have disappeared subsequently from Italian poultry. Until recently, the transmission of influenza viruses (other than the H5 and H7 subtypes) from their reservoir in aquatic birds to chickens was rarely detected and highly pathogenic and non-pathogenic viruses were considered to be restricted to poultry species. However, the recent reports of the transmission of H9N2 and H5N1 influenza viruses to chickens in Hong Kong and, subsequently, to humans and our findings of the transmission of H3N2 influenza viruses to domestic chickens in Italy suggest an increased role for chickens as an intermediate host in the ecology of influenza.

**Descriptors:** chickens, fowl plague virology, influenza veterinary, influenza A virus avian pathogenicity, poultry diseases virology, hemagglutination inhibition tests, hemagglutinin glycoproteins, influenza virus genetics, influenza virology, avian isolation and purification, avian physiology, porcine isolation and purification, porcine pathogenicity, Italy, molecular sequence data, sequence analysis, DNA, swine diseases virology, viral proteins genetics, virus replication.


**Abstract:** Among avian influenza viruses and avian paramyxoviruses are the aetiological agents of two of the most devastating diseases of the animal kingdom: (i). the highly pathogenic form of avian influenza, caused by some viruses of the H5 and H7 subtypes, and (ii). Newcastle disease, caused by virulent strains of APMV type 1. Mortality rates due to these agents can exceed 50% in naive bird populations, and, for some strains of AI, nearly 100%. These viruses may also be responsible for clinical conditions in humans. The virus responsible for Newcastle disease has been known to cause conjunctivitis in humans since the 1940s. The conjunctivitis is self-limiting and does not have any permanent consequences. Until 1997, reports of human infection with avian influenza viruses were sporadic and frequently associated with conjunctivitis. Recently, however, avian influenza virus infections have been associated with fatalities in human beings. These casualties have highlighted the potential risk that this type of infection poses to public health. In particular, the pathogenetic mechanisms of highly pathogenic avian influenza viruses in birds and the possibility of reassortment between avian and human viruses in the human host represent serious threats to human health. For this reason, any suspected case should be investigated thoroughly.

**Descriptors:** avulavirus isolation and purification, communicable disease control, disease outbreaks, fowl plague epidemiology, influenza A virus avian isolation and purification, Newcastle disease epidemiology, birds, fowl plague prevention and control, Italy epidemiology, Newcastle disease prevention and control, prognosis, risk assessment, survival analysis.
NAL Call Number: 475 AC8

Abstract: From the end of March to the beginning of December 1999, 199 outbreaks of low pathogenicity avian influenza (LPAI) were diagnosed in the Veneto and Lombardia regions, which are located in the northern part of Italy. The virus responsible for the epidemic was characterized as a type A influenza virus of the H7N1 subtype of low pathogenicity. On the 17th of December, highly pathogenic avian influenza (HPAI) was diagnosed in a meat turkey flock in which 100% mortality was observed in 72 h. The infection spread to the industrial poultry population of northern Italy including chickens, guinea-fowl, quail, pheasants, ducks and ostriches for a total of 413 outbreaks. Over 13 million birds were affected by the epidemic, which caused dramatic economic losses to the Italian poultry industry with severe social and economic implications. The possibility of H7 virus transmission to humans in close contact with the outbreaks was evaluated through a serological survey. Seven hundred and fifty nine sera were collected and tested for the detection of anti-H7 antibodies by means of the micro-neutralization (MN) and single radial haemolysis (SRH) tests. All samples resulted negative. A limited number of clinical samples were also collected for attempted virus isolation with negative results. Current European legislation considers LPAI and HPAI as two completely distinct diseases, not contemplating any compulsory eradication policy for LPAI and requiring eradication for HPAI. Evidence collected during the Italian 1999-2000 epidemic indicates that LPAI due to viruses of the H7 subtype may mutate to HPAI, and, therefore, LPAI caused by viruses of the H5 or H7 subtypes must be controlled to avoid the emergence of HPAI. A reconsideration of the current definition of avian influenza adopted by the EU, could possibly be an aid to avoiding devastating epidemics for the poultry industry in Member States.

Descriptors: disease outbreaks, leishmaniasis, visceral epidemiology, adolescent, adult, age distribution, antibodies, protozoan isolation and purification, Brazil epidemiology, child, child preschool, infant, leishmaniasis, visceral immunology, prevalence, seroepidemiologic studies, skin tests, urban population.


NAL Call Number: 475 AC8

Abstract: Natural infections with influenza A viruses have been reported in a variety of animal species including humans, pigs, horses, sea mammals, mustelids and birds. Occasionally devastating pandemics occur in humans. Although viruses of relatively few HA and NA subtype combinations have been isolated from mammalian species, all 15 HA subtypes and all 9 NA subtypes, in most combinations, have been isolated from birds. In the 20th century the sudden emergence of antigenically different strains transmissible in humans, termed antigenic shift, has occurred on four occasions, 1918 (H1N1), 1957 (H2N2), 1968 (H3N2) and 1977 (H1N1), each time resulting in a pandemic. Genetic analysis of the isolates demonstrated that 'new' strains most certainly emerged after reassortment of genes of viruses of avian and human origin in a permissive host. The leading theory is that the pig represents the 'mixing vessel' where this genetic reassortment may occur. In 1996, an H7N7 influenza virus of avian origin was isolated from a woman with a self-limiting conjunctivitis. During 1997 in Hong Kong, an H5N1 avian influenza virus was recognised as the cause of death of 6 of 18 infected patients. Genetic analysis revealed these human isolates of H5N1 subtype to be indistinguishable from a highly pathogenic avian influenza virus that was endemic in the local poultry population. More recently, in March 1999, two independent isolations of influenza virus subtype H9N2 were made from girls aged one to four who recovered from flu-like illnesses in Hong Kong. Subsequently, five isolations of H9N2 virus from humans on mainland China in August 1998 were reported. H9N2 viruses were known to be widespread in poultry in China and other Asian countries. In all these cases there was no evidence of human to human spread except with the H5N1 infections where there was evidence of very limited spread. This is in keeping with the finding that all these viruses possessed all eight genes of avian origin. It may well be that infection of humans with avian influenza viruses occurs much more frequently than originally assumed, but due to their limited effect go unrecognised. For the human population as a whole the main danger of direct infection with avian influenza viruses appears to be if people infected with an 'avian' virus are infected simultaneously with a 'human' influenza virus. In such circumstances reassortment could occur with the potential emergence of a virus fully capable of spread in the human population, but with
antigenic characteristics for which the human population was immunologically naive. Presumably this represents a very rare coincidence, but one which could result in a true influenza pandemic.

Descriptors: infection, avian influenza, respiratory system disease, viral disease, self limiting conjunctivitis, eye disease, genetic analysis genetic techniques, laboratory techniques.


NAL Call Number: QR360.J6

Abstract: Since the outbreak in humans of an H5N1 avian influenza virus in Hong Kong in 1997, poultry entering the live-bird markets of Hong Kong have been closely monitored for infection with avian influenza. In March 1999, this monitoring system detected geese that were serologically positive for H5N1 avian influenza virus, but the birds were marketed before they could be sampled for virus. However, viral isolates were obtained by swabbing the cages that housed the geese. These samples, known collectively as A/Environment/Hong Kong/437/99 (A/Env/HK/437/99), contained four viral isolates, which were compared to the 1997 H5N1 Hong Kong isolates. Analysis of A/Env/HK/437/99 viruses revealed that the four isolates are nearly identical genetically and are most closely related to A/Goose/Guangdong/1/96. These isolates and the 1997 H5N1 Hong Kong viruses encode common hemagglutinin (H5) genes that have identical hemagglutinin cleavage sites. Thus, the pathogenicity of the A/Env/HK/437/99 viruses was compared in chickens and in mice to evaluate the potential for disease outbreaks in poultry and humans. The A/Env/HK/437/99 isolates were highly pathogenic in chickens but caused a longer mean death time and had altered cell tropism compared to A/Hong Kong/156/97 (A/HK/156/97). Like A/HK/156/97, the A/Env/HK/437/99 viruses replicated in mice and remained localized to the respiratory tract. However, the A/Env/HK/437/99 isolates caused only mild pathological lesions in these tissues and no clinical signs of disease or death. As a measure of the immune response to these viruses, transforming growth factor beta levels were determined in the serum of infected mice and showed elevated levels for the A/Env/HK/437/99 viruses compared to the A/HK/156/97 viruses. This study is the first to characterize the A/Env/HK/437/99 viruses in both avian and mammalian species, evaluating the H5 gene from the 1997 Hong Kong H5N1 isolates in a different genetic background. Our findings reveal that at least one of the avian influenza virus genes encoded by the 1997 H5N1 Hong Kong viruses continues to circulate in mainland China and that this gene is important for pathogenesis in chickens but is not the sole determinant of pathogenicity in mice. There is evidence that H9N2 viruses, which have internal genes in common with the 1997 H5N1 Hong Kong isolates, are still circulating in Hong Kong and China as well, providing a heterogeneous gene pool for viral reassortment. The implications of these findings for the potential for human disease are discussed.

Descriptors: fowl plague virology, hemagglutinin glycoproteins, influenza virus genetics, influenza A virus avian genetics, poultry diseases virology, chickens, China epidemiology, disease outbreaks veterinary, fowl plague epidemiology, fowl plague pathology, Hong Kong epidemiology, immunohistochemistry, avian classification, avian pathogenicity, mice, mice inbred BALB c, molecular sequence data, phylogeny, poultry diseases epidemiology, poultry diseases pathology, sequence homology, nucleic acid, transforming growth factor beta blood.


NAL Call Number: RC111.R4

Abstract: The first outbreak of avian influenza A(H5N1) virus in humans occurred in Hong Kong in 1997. Infection was confirmed in 18 individuals, 6 of whom died. Infections were acquired by humans directly from chickens, without the involvement of an intermediate host. The outbreak was halted by a territory-wide slaughter of more than 1.5 million chickens at the end of December 1997. The clinical spectrum of H5N1 infection ranges from asymptomatic infection to fatal pneumonitis and multiple organ failure. Reactive hemophagocytic syndrome was the most characteristic pathologic finding and might have contributed to the lymphopenia, liver dysfunction, and abnormal clotting profiles that were observed among patients with severe infection. Rapid diagnosis with the use of reverse-transcription polymerase chain reaction and monoclonal antibody-based immunofluorescent assay were of great clinical value in the management of the outbreak. The experience of the H5N1 outbreak in Hong Kong underscores the importance of continuous
surveillance of influenza virus strains in humans and in other animal species.

**Descriptors**: infection, public health, avian influenza A virus infection, symptom, viral disease, liver dysfunction, digestive system disease, lymphopenia, blood and lymphatic disease, immune system disease, multiple organ failure, disease miscellaneous, pneumonitis, respiratory system disease, reactive hemophagocytic syndrome, blood and lymphatic disease, monoclonal antibody based immunofluorescent assay diagnostic method, reverse transcriptase polymerase chain reaction diagnostic method, polymerase chain reaction, abnormal clotting profiles disease outbreak mortality.


**NAL Call Number**: QR375.V6

**Abstract**: Twenty-four H1N2 influenza A viruses were newly isolated from pigs in the United States. These isolates originated from 19 farms in 9 different swine producing states between 1999 and 2001. All farms had clinical histories of respiratory problem and/or abortion. The viral isolates were characterized genetically to determine the origin of all eight gene segments. The results showed that all H1N2 isolates were reassortants of classical swine H1N1 and triple reassortant H3N2 viruses. The neuraminidase (NA) and PB1 genes of the H1N2 isolates were of human origin, while the hemagglutinin (HA), nucleoprotein (NP), matrix (M), non-structural (NS), PA and PB2 polymerase genes were of avian or swine origin. Fifteen of the 24 H1N2 isolates were shown to have a close phylogenetic relationship and high amino acid homology with the first US isolate of H1N2 (A/SW/IN/9K035/99). The remaining nine isolates had a close phylogenetic relationship with classical swine influenza H1N1 in the HA gene. All other genes including NA, M, NP, NS, PA, PB1 and PB2 showed a close phylogenetic relationship with the H1N2 (A/SW/IN/9K035/99) strain and triple reassortant H3N2 viruses. However, PB1 genes of two isolates (A/SW/KS/13481-S/00, A/SW/KS/13481-T/00) were originated from avian influenza A virus lineage. These results suggest that although there are some variations in the HA genes, the H1N2 viruses prevalent in the US swine population are of a similar genetic lineage.

**Descriptors**: influenza A virus, porcine genetics, antigens, viral, hemagglutinin glycoproteins, influenza virus genetics, porcine classification, porcine enzymology, porcine isolation and purification, molecular sequence data, neuraminidase genetics, phylogeny, swine, United States, variation genetics.


**NAL Call Number**: 448.8 L22

**Abstract**: BACKGROUND: In May, 1997, a 3-year-old boy in Hong Kong was admitted to the hospital and subsequently died from influenza pneumonia, acute respiratory distress syndrome, Reye's syndrome, multiorgan failure, and disseminated intravascular coagulation. An influenza A H5N1 virus was isolated from a tracheal aspirate of the boy. Preceding this incident, avian influenza outbreaks of high mortality were reported from three chicken farms in Hong Kong, and the virus involved was also found to be of the H5 subtype. METHODS: We carried out an antigenic and molecular comparison of the influenza A H5N1 virus isolated from the boy with one of the viruses isolated from outbreaks of avian influenza by haemagglutination-inhibition and neuraminidase-inhibition assays and nucleotide sequence analysis. FINDINGS: Differences were observed in the antigenic reactivities of the viruses by the haemagglutination-inhibition assay. However, nucleotide sequence analysis of all gene segments revealed that the human virus A/Hong Kong/156/97 was genetically closely related to the avian A/chicken/Hong Kong/258/97. INTERPRETATION: Although direct contact between the sick child and affected chickens has not been established, our results suggest transmission of the virus from infected chickens to the child without another intermediate mammalian host acting as a "mixing vessel". This event illustrates the importance of intensive global influenza surveillance.

**Descriptors**: fowl plague virology, influenza virology, influenza A virus avian genetics, human genetics, amino acid sequence, base sequence, chickens virology, child, preschool, disease outbreaks veterinary, fowl plague epidemiology, Hong Kong epidemiology, influenza epidemiology, avian isolation and purification, avian pathogenicity, human isolation and purification, molecular sequence data.

**NAL Call Number:** 448.8 V81

**Abstract:** Pigs have been proposed to act as the intermediate hosts in the generation of pandemic human influenza strains by reassortment of genes from avian and human influenza virus strains. The circulation of avian-like H1N1 influenza viruses in European pigs since 1979 and the detection of human-avian reassortants in pigs raises the question of whether these viruses actually have the potential to transmit and cause disease in humans. We now report the serologic and genetic characterization of two human influenza A viruses (A/Netherlands/5/93 [H3N2] and A/Netherlands/35/93 [H3N2]) that caused influenza in children in The Netherlands in 1993. The results show that these viruses are human-avian reassortants that were generated and currently still are circulating in European swine. This shows the pivotal role that pigs can play in the generation and transmission of avian influenza virus genes to humans and their potential to generate a new human pandemic strain.

**Descriptors:** swine, Netherlands, intermediate hosts, avian influenza virus, influenza virus, children, infection, disease transmission, genes, phylogeny, artiodactyla, biological competition, cell structure, chromosomes, disease transmission, domestic animals, Europe, evolution, hosts, influenza virus, livestock, mammals, nucleus, parasitism, pathogenesis, progeny, suidae, useful animals, viruses, Western Europe, human influenza virus, pandemics, genetic reassortment, nucleoprotein genes, structural genes.

Claas, E.C.J. (2000). *Pandemic influenza is a zoonosis, as it requires introduction of avian-like gene segments in the human population*. *Veterinary Microbiology* 74(1-2): 133-139. ISSN: 0378-1135.

**NAL Call Number:** SF601.V44

**Abstract:** Human influenza viruses manage to cause epidemics almost every year. The circulating viruses change their surface glycoproteins by accumulating mutations (antigenic drift) which results in variant viruses of the same subtype that are able to evade the immune pressure in the population. Every now and then, a completely new subtype of influenza A virus is introduced in the human population, which can result in an influenza pandemic. Pandemic human influenza viruses have been emerging for many centuries. Based on the genetic information of influenza viruses that have been isolated in this century, introduction of genes of the avian influenza virus reservoir obviously is required. Interspecies transmission, via another mammalian host and reassortment of avian and human influenza viruses are potential mechanisms for such an introduction. A summary of the cases in which influenza viruses containing avian-like gene segments were introduced into the human population is presented. In three cases, such infections resulted in conjunctivitis. Influenza-like illness and even pneumonia was reported in some other infections. Finally, a mortality rate of 33% was observed in the avian influenza A (H5N1) viruses that infected 18 people in Hong Kong in 1997. Although some of these viruses fulfilled some criteria of pandemic influenza viruses, they lacked the ability to rapidly spread through the human population.

**Descriptors:** molecular genetics, infection, epidemiology, conjunctivitis, eye disease, influenza virus infection, pandemic, viral disease, zoonosis, pneumonia, respiratory system disease, antigenic drift interspecies transmission mortality.


**NAL Call Number:** QR46.J6

**Abstract:** We compared the abilities of the six internal RNA segments of two avian influenza viruses, A/Mallard/Alberta/88/76 (H3N8) and A/Mallard/NY/6750/78 (H2N2), to confer attenuation on wild-type human influenza A/Bethesda/1/85 (H3N2) virus in seronegative adult volunteers. Live avian-human influenza A reassortant virus vaccines derived from either avian virus parent were comparable in the following properties: safety, infectivity, immunogenicity, and genetic stability. Since the avian influenza A/Mallard/Alberta/76 virus offered no clear advantage as a donor virus, we will conduct our future evaluations on live influenza A virus reassortants derived from the more extensively characterized avian influenza A/Mallard/NY/78 virus.

**Descriptors:** antibodies, viral biosynthesis, influenza prevention and control, influenza A virus avian
immunology, human immunology, influenza vaccine immunology, dose response relationship, immunologic, electrophoresis, polyacrylamide gel, enzyme linked immunosorbent assay, genes viral, hemagglutination inhibition tests, avian genetics, avian physiology, human genetics, human physiology, influenza vaccine adverse effects, vaccines, attenuated adverse effects, vaccines, attenuated immunology, vaccines, synthetic adverse effects, vaccines, synthetic immunology, virus replication.

NAL Call Number: QR46.J6
Abstract: A reassortant influenza A virus was produced by mating an avian influenza A/Pintail/Alberta/119/79 (H4N6) virus with wild-type human influenza A/Washington/897/80 (H3N2) virus. The avian-human influenza A reassortant virus contained the genes coding for the hemagglutinin and neuraminidase surface antigens of the human influenza wild-type virus and the six other RNA segments (internal genes) of the avian influenza A virus donor. In the lower respiratory tract of squirrel monkeys, this avian-human influenza reassortant virus, like its avian influenza A parent virus, was restricted approximately 100-fold in replication compared with the wild-type human influenza A virus. Despite this restriction of replication, infection of monkeys with the avian-human influenza A reassortant virus induced resistance to wild-type human influenza A virus challenge. In comparison with the wild-type human influenza A virus, the avian-human influenza A reassortant was also fully attenuated when 10(5.5) to 10(7.5) 50% tissue culture infective doses were administered to susceptible adult volunteers. Attenuation was indicated by a more than 300-fold reduction in virus shedding and lack of reactogenicity. The reassortant virus did not spread to susceptible contacts and could not be isolated from the blood or stools of infected adults. The 50% human infectious dose was 10(6.2) 50% tissue culture infective dose, indicating that this reassortant virus is only slightly less infectious for adults than a similarly derived avian-human influenza A/Washington/80 X A/Mallard/78 reassortant virus. These findings suggest that the avian influenza A/Pintail/79 virus may be a satisfactory donor of attenuating genes for production of live, attenuated avian-human influenza A reassortant virus vaccines.
Descriptors: influenza A virus human immunology, immunology, influenza vaccine immunology, adolescent, adult, genes viral, influenza immunology, influenza prevention and control, human genetics, genetics, influenza vaccine adverse effects, saimiri, vaccines, attenuated adverse effects, vaccines, attenuated immunology, virus replication.

NAL Call Number: QR46.J6
Abstract: The transfer of six internal RNA segments from the avian influenza A/Mallard/New York/6750/78 (H2N2) virus reproducibly attenuates human influenza A viruses for squirrel monkeys and adult humans. To identify the avian influenza A virus genes that specify the attenuation and host range restriction of avian-human (ah) influenza A reassortant viruses (referred to as ah reassortants), we isolated six single-gene reassortant viruses (SGRs), each having a single internal RNA segment of the influenza A/Mallard/New York/6750/78 virus and seven RNA segments from the human influenza A/Los Angeles/2/87 (H3N2) wild-type virus. To assess the level of attenuation, we compared each SGR with the A/Los Angeles/2/87 wild-type virus and a 6-2 gene ah reassortant (having six internal RNA segments from the avian influenza A virus parent and two genes encoding the hemagglutinin and neuraminidase glycoproteins from the wild-type human influenza A virus) for the ability to replicate in seronegative squirrel monkeys and adult human volunteers. In monkeys and humans, replication of the 6-2 gene ah reassortant was highly restricted. In humans, the NS, M, PB2, and PB1 SGRs each replicated significantly less efficiently (P less than 0.05) than the wild-type human influenza A virus parent, suggesting that each of these genes contributes to the attenuation phenotype. In monkeys, only the NP, PB2, and possibly the M genes contributed to the attenuation phenotype. These discordant observations, particularly with regard to the NP SGR, indicate that not all genetic determinants of attenuation of influenza A viruses for humans can be identified during studies
of SGRs conducted with monkeys. The PB2 and M SGRs that were attenuated in humans each exhibited a new phenotype that was not observed for either parental virus. Thus, it was not possible to determine whether avian influenza virus PB2 or M gene itself or a specific constellation of avian and human influenza A virus specified restriction of virus replication in humans.

Descriptors: influenza A virus avian genetics, human genetics, adult, base sequence, genes viral, human pathogenicity, human physiology, influenza vaccine isolation and purification, molecular sequence data, RNA viral genetics, saimiri, transfection, vaccines, attenuated isolation and purification, virulence genetics, virus replication genetics.


NAL Call Number: 448.8 V81

Abstract: The receptor specificity of 56 H2 and H3 influenza virus isolates from various animal species has been determined to test the relevance of receptor specificity to the ecology of influenza virus. The results show that the receptor specificity of both H2 and H3 isolates evaluated for sialic acid linkage specificity and inhibition of hemagglutination by horse serum correlates with the species of origin, as postulated earlier for H3 strains based on a limited survey of five human, three avian, and one equine strain. Elucidation of the amino acid sequence of several human H2 receptor variants and analysis of known sequences of H2 and H3 isolates revealed that receptor specificity varies in association with an amino acid change at residues 228 in addition to the change at residue 226 previously documented to affect receptor specificity of H3 but not H1 isolates. Residues 226 and 228 are leucine and serine in human isolates, which preferentially bind sialic acid alpha 2,6-galactose beta 1,4-N-acetyl glucosamine (SA alpha 2,6Gal), and glutamine and glycine in avian and equine isolates, which exhibit specificity for sialic acid alpha-2,3-galactose beta-1,3-N-acetyl galactosamine (SA alpha 2,3Gal). The results demonstrate that the correlation of receptor specificity and species of origin is maintained across both H2 and H3 influenza virus serotypes and provide compelling evidence that influenza virus hosts exert selective pressure to maintain the receptor specificity characteristics of strains isolated from that species.

Descriptors: influenza A virus avian metabolism, human metabolism, metabolism, receptors, virus metabolism, amino acid sequence, amino acids genetics, carbohydrate sequence, chick embryo, hemagglutinin glycoproteins, influenza virus, hemagglutinin viral genetics, molecular sequence data, species specificity, viral envelope proteins genetics.


NAL Call Number: 448.3 Ar23

Abstract: The M protein of avian, but not human, strains of influenza A viruses is synthesized in infected chicken erythrocytes. In dual infections an avian strain complemented the human virus and both the human and avian M proteins were expressed.

Descriptors: erythrocytes microbiology, influenza A virus avian metabolism, human metabolism, viral proteins biosynthesis, chick embryo, dactinomycin pharmacology, avian growth and development, human growth and development.


NAL Call Number: QR46.J6

Abstract: A simple molecular technique for rapid genotyping was developed to monitor the internal gene composition of currently circulating influenza A viruses. Sequence information from recent H1N1, H3N2, and H5N1 human virus isolates was used to identify conserved regions within each internal gene, and gene-specific PCR primers capable of amplifying all three virus subtypes were designed. Subtyping was based on subtype-specific restriction fragment length polymorphism (RFLP) patterns within the amplified regions. The strategy was tested in a blinded fashion using 10 control viruses of each subtype (total, 30) and was found to be very effective. Once standardized, the genotyping method was used to identify the origin of the internal
genes of 51 influenza A viruses isolated from humans in Hong Kong during and immediately following the 1997-1998 H5N1 outbreak. No avian-human or H1-H3 reassortants were detected. Less than 2% (6 of 486) of the RFLP analyses were inconclusive; all were due to point mutations within a restriction site. The technique was also used to characterize the internal genes of two avian H9N2 viruses isolated from children in Hong Kong during 1999.

Descriptors: genes viral, influenza virology, influenza A virus human classification, human genetics, polymorphism, restriction fragment length, disease outbreaks, Hong Kong, avian classification, avian genetics, avian isolation and purification, human isolation and purification, reverse transcriptase polymerase chain reaction.

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Canine Influenza Virus - Detection and Sampling.

Online: http://www.diaglab.vet.cornell.edu/issues/civ-dect.asp

Abstract: Canine influenza virus is a relatively new pathogen of dogs. It was first identified in racing greyhounds in 2004 and this virus appears to have been involved with significant respiratory problems on the dog tracks throughout the US for the last 2-3 years. The Virology Lab at Cornell isolated the first influenza virus from an animal that died during one of these clinical episodes. Evidence of infection of non-greyhounds by influenza virus has been found in Florida within the past year as part of the ongoing research efforts by Dr Cynda Crawford at the University of Florida on respiratory disease in dogs.

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Descriptors: birds microbiology, influenza A virus avian isolation and purification, antigens, viral analysis, culture media, feces microbiology, hemagglutination inhibition tests, hemagglutinins viral analysis, immune sera, avian immunology, virus cultivation.


NAL Call Number: 448.8 J8232

Descriptors: antibodies analysis, influenza immunology, influenza A virus avian immunology, adolescent, adult, aged, aging, child, child preschool, hemagglutination inhibition tests, infant, middle aged, statistics.


NAL Call Number: 448.3 Ar23

Abstract: A double antibody sandwich blocking ELISA, using a monoclonal antibody (MAb) against influenza A nucleoprotein (NP) was developed to detect antibodies against influenza. Collections of serum samples were obtained from human and various animal species. All influenza A subtypes induced antibodies against hemagglutinins and NP. A close correlation between titers of the hemagglutination inhibition (HI) test and the NP-ELISA was seen. Antibodies against influenza NP were demonstrated in serum samples from humans, ferrets, swine, horses, chickens, ducks, guinea pigs, mice, and seals. The serum samples were collected at intervals during prospective epidemiological studies, from experimental and natural infections, and vaccination studies. The decline of maternal antibodies was studied in swine and horses. The NP-ELISA enables rapid serological diagnosis and is suited for influenza A antibody screening, especially in species which harbor several influenza subtypes. The HI and neuraminidase inhibition tests, however, must still be used for subtyping.

Descriptors: antibodies, viral analysis, enzyme linked immunosorbent assay, influenza A virus immunology, nucleoproteins immunology, orthomyxoviridae infections immunology, viral core proteins immunology, ferrets, hemagglutination inhibition tests, horses, avian immunology, human immunology, porcine immunology, orthomyxoviridae infections veterinary, poultry, prospective studies, Rodentia, seals, species
de Jong, J.C., E.C. Claas, and A.D. Osterhaus (1998). Influenza A (H5N1) in Hong Kong: voorbode van een pandemie of alleen een wetenschappelijk interessant verschijnsel en een nuttige oefening in pandemiologie? [Influenza A (H5N1) in Hong Kong: forerunner of a pandemic or an only scientifically interesting phenomenon and a useful exercise in pandemiology?]. Tijdschrift Voor Diergeneeskunde 123(9): 278-82. ISSN: 0040-7453.

NAL Call Number: 41.8 T431

Abstract: From a three-year old boy in Hong Kong who died in May 1997 with an extensive influenza pneumonia an influenza A virus has been isolated which was, first at the National Influenza Centre of the Netherlands, identified as belonging to subtype H5N1. Presumably the patient had acquired the infection directly from an outbreak of fowl plague among chickens. As far as is known this is the first case of the isolation of an influenza virus belonging to one of the subtypes H4-H15 from a human influenza patient. At the end of 1997 seventeen more cases of human A (H5N1) influenza have been detected in Hong Kong, including five fatal cases. Genetic analyses of seven of these virus isolates did not reveal the occurrence of reassortment with a human or porcine influenza virus, which could have rendered the virus potentially pandemic. Man-to-man transmission of the virus has not been demonstrated but cannot be excluded either. This event has shown that the WHO surveillance of influenza viruses, although perhaps not perfect, has functioned well.

Descriptors: influenza virology, influenza A virus avian isolation and purification, chickens, child preschool, disease outbreaks veterinary, epidemiologic methods, fowl plague epidemiology, fowl plague virology, influenza epidemiology, influenza transmission, avian classification, avian genetics, poultry, poultry diseases epidemiology, poultry diseases virology, reassortant viruses genetics, zoonoses.


Abstract: Novel influenza viruses continuously emerge in the human population. Three times during the present century, an avian influenza virus subtype crossed the species barrier, starting a pandemic, and establishing itself for one to several decades in man. As the 1997 H5N1 event in Hong Kong indicated, the occurrence of another pandemic in the near future cannot be excluded. Sufficient vaccine may not be available to ameliorate the consequences of such an event, because of a shortage of time. During interpandemic periods, important antigenic drift variants sometimes arise at a point of time when, with the current state of the technique, production of a correspondingly adapted vaccine is also impossible. We may be able to solve these problems by increasing influenza surveillance and by adopting new ways of vaccine composition, production, formulation, presentation, and delivery. The recently developed anti-neuraminidase antivirals should only be considered as (valuable) adjuncts to vaccines.

Descriptors: antigenic variation, influenza epidemiology, orthomyxoviridae genetics, disease outbreaks, hn protein genetics, hemagglutinin glycoproteins, influenza virus genetics, influenza mortality, influenza prevention and control, influenza vaccine therapeutic use, orthomyxoviridae enzymology, orthomyxoviridae pathogenicity, reassortant viruses genetics, reassortant viruses pathogenicity, virulence.


NAL Call Number: 448.8 N442


NAL Call Number: 41.8 R3224
Descriptors: animals, domestic, orthomyxoviridae infections microbiology, orthomyxoviridae infections veterinary, antigens, viral analysis, chickens, epitopes, fowl plague microbiology, horse diseases microbiology, horses, influenza microbiology, influenza A virus avian immunology, human immunology, porcine immunology, mutation, recombination, genetic, swine, swine diseases microbiology.

NAL Call Number: 151.65 P96

Descriptors: influenza A virus avian immunology, orthomyxoviridae infections immunology, viruses immunology, chick embryo, haplorhini, hemagglutination inhibition tests, hemagglutination tests, neutralization tests, Newcastle disease immunology, Newcastle disease virus immunology, poultry, virus diseases immunology, virus diseases pathology.

NAL Call Number: 448.8 P942

Abstract: The method of specific adsorption followed by the use of antisera in HI test and competitive enzyme immunoassay was used to study the antigenic composition of hemagglutinins (HA) Hsw1 in influenza viruses isolated in 1982 from humans in Bulgaria and in 1976 in Canada from ducks as well as their antigenic relationships with HA of Hsw1 variant isolated from swine and man. Hemagglutinins of Hsw1 strains isolated from man in Bulgaria and Alma-Ata were found to be similar to HA of A/New Jersey/8/76 virus in two determinants and with hemagglutinin of the classic virus of swine in three determinants. The HA of A/duck/Alberta/35/76 virus was similar in three determinants to HA of A/New Jersey/8/76 virus and in two determinants with other Hsw1 variants. The similarities and differences in antigenic determinants of HA in Hsw1 viruses isolated from man and animals attest to their common origin and different modes of variability.
Descriptors: epitopes analysis, hemagglutinins viral immunology, influenza A virus avian immunology, human immunology, ducks, enzyme linked immunosorbent assay, immunosorbent techniques.


Abstract: Serological analysis of a group of 63 influenza H1N1 viruses isolated from pigs in Italy in the period 1976-1988 revealed the presence of two distinct antigenic subpopulations: some viruses possessed a haemagglutinin indistinguishable from that of viruses typically associated with pigs, i.e., A/New Jersey/8/76 (H1N1), whereas others showed a close antigenic relatedness with the haemagglutinin of avian-like H1 viruses. These findings represent further evidence that influenza A viruses from avian species may be transmitted to mammals. The surface and internal proteins of some of these viruses were also analyzed biochemically to evaluate the molecular relatedness among viruses circulating in non-human hosts.
Descriptors: hemagglutinins viral immunology, influenza A virus avian immunology, porcine immunology, orthomyxoviridae infections veterinary, swine microbiology, swine diseases microbiology, antibodies, monoclonal immunology, antigenic variation, electrophoresis, polyacrylamide gel, avian isolation and purification, porcine isolation and purification, Italy, orthomyxoviridae infections microbiology, orthomyxoviridae infections transmission, peptide mapping, species specificity.

NAL Call Number: QR360.J6

Abstract: In 1997, an outbreak of virulent H5N1 avian influenza virus occurred in poultry in Hong Kong (HK) and was linked to a direct transmission to humans. The factors associated with transmission of avian influenza virus to mammals are not fully understood, and the potential risk of other highly virulent avian influenza A viruses infecting and causing disease in mammals is not known. In this study, two avian and one
human HK-origin H5N1 virus along with four additional highly pathogenic H5 avian influenza viruses were analyzed for their pathogenicity in 6- to 8-week-old BALB/c mice. Both the avian and human HK H5 influenza virus isolates caused severe disease in mice, characterized by induced hypothermia, clinical signs, rapid weight loss, and 75 to 100% mortality by 6 to 8 days postinfection. Three of the non-HK-origin isolates caused no detectable clinical signs. One isolate, A/tk/England/91 (H5N1), induced measurable disease, and all but one of the animals recovered. Infections resulted in mild to severe lesions in both the upper and lower respiratory tracts. Most consistently, the viruses caused necrosis in respiratory epithelium of the nasal cavity, trachea, bronchi, and bronchioles with accompanying inflammation. The most severe and widespread lesions were observed in the lungs of HK avian influenza virus-infected mice, while no lesions or only mild lesions were evident with A/ck/Scotland/59 (H5N1) and A/ck/Queretaro/95 (H5N2). The A/ck/Italy/97 (H5N2) and the A/tk/England/91 (H5N1) viruses exhibited intermediate pathogenicity, producing mild to moderate respiratory tract lesions. In addition, infection by the different isolates could be further distinguished by the mouse immune response. The non-HK-origin isolates all induced production of increased levels of active transforming growth factor beta following infection, while the HK-origin isolates did not.

Descriptors: influenza virology, influenza A virus avian pathogenicity, human pathogenicity, hn protein, Hong Kong, immunohistochemistry, influenza pathology, avian isolation and purification, avian physiology, human isolation and purification, human physiology, mice, mice inbred BALB c, respiratory system pathology, respiratory system virology, transforming growth factor beta blood, virulence, virus replication.


NAL Call Number: QR360.A1J6

Descriptors: antigens analysis, neuraminidase analysis, orthomyxoviridae analysis, orthomyxoviridae immunology, recombination, genetic, electrophoresis, hemagglutination inhibition tests, hemagglutinins viral analysis, hybridization, genetic, immunodiffusion, influenza A virus avian.


Abstract: Background: In February 2003, highly pathogenic avian influenza A H5N1 viruses reemerged in humans. Despite repeated outbreaks in domestic poultry in Hong Kong since 1999, this was the first isolation of H5N1 from humans since the outbreak in Hong Kong in 1997, which resulted in 18 human cases and 6 deaths. Methods: To better understand the antigenic relationship between the 2003 H5N1 human virus A/Hong Kong/213/03 (HK/213) and other H5 viruses, post-infection ferret sera or post-infection human sera were tested for reactivity by hemagglutination-inhibition and microneutralization assays with H5N1 viruses circulating in Hong Kong or elsewhere in Asia since 1997. Results: The H5N1 virus isolated from a 9-year-old male in Hong Kong was antigenically distinguishable from recent H5N1 viruses isolated from wild birds in Hong Kong and from the human 1997 H5N1 viruses, using post-infection ferret sera. Likewise, sera from this case patient, collected 22 days post-symptom onset, reacted to high titers with the homologous HK/213 virus, but gave eightfold lower titers with A/Hong Kong/156/97, and other H5 viruses. Conclusion: These results suggest that this recent human H5N1 virus is antigenically distinguishable from current and previously circulating H5N1 viruses from Asia, including the viruses previously isolated from humans.

Descriptors: influenza H5N1, antigenicity, serology.


Abstract: Severe acute respiratory syndrome (SARS) is a new disease that caused large outbreaks in several countries in the first half of 2003, resulting in infection in more than 8,000 people and more than 900 deaths. The disease originated in southern China and a novel coronavirus (SARS CoV) has been implicated as the causative organism. We present an overview of the etiology, clinical presentation and diagnosis, based on the current state of knowledge derived from published studies and our experience in the National Microbiology Centre. Influenza is a zoonosis. This appreciation of influenza ecology facilitated recognition of
the H5N1 'bird flu' incident in Hong Kong in 1997 in what was considered to be an incipient pandemic situation, the chicken being the source of virus for humans and. The current outbreak of avian influenza in South East Asia has resulted in a small number of human deaths. These findings highlight the importance of systematic virus surveillance of domestic poultry in recognizing changes in virus occurrence, host range and pathogenicity as signals at the avian level that could presage a pandemic.


Descriptors: minks, viroses, avian influenza virus, pathogenesis, Carnivora, infectious diseases, influenza virus, mammals, Mustelidae, orthomyxoviridae, viruses.

NAL Call Number: SF601.V44
Abstract: An influenza A virus, A/mink/Sweden/84 (H10N4), was isolated from farmed mink during an outbreak of respiratory disease, histopathologically characterised by severe interstitial pneumonia. The virus was shown to be of recent avian origin and closely related to concomitantly circulating avian influenza virus. Serological investigations were used to link the isolated virus to the herds involved in the disease outbreak. Experimental infection of adult mink with the virus isolate from the disease outbreak reproduced the disease signs and pathological lesions observed in the field cases. The mink influenza virus also induced an antibody response and spread between mink by contact. The same pathogenesis in mink was observed for two avian influenza viruses of the H10N4 subtype, circulating in the avian population. When mink were infected with the prototype avian H10 influenza virus, A/chicken/Germany/N/49, H10N7, the animals responded with antibody production and mild pulmonary lesions but neither disease signs nor contact infections were observed. Detailed studies, including demonstration of viral antigen in situ by immunohistochemistry, of the sequential development of pathological lesions in the mink airways after aerosol exposure to H10N4 or H10N7 revealed that the infections progress very similarly during the first 24 h, but are distinctly different at later stages. The conclusion drawn is that A/mink/Sweden/84, but not A/chicken/Germany/N/49, produces a multiple-cycle replication in mink airways. Since the viral distribution and pathological lesions are very similar during the initial stages of infection we suggest that the two viruses differ in their abilities to replicate and spread within the mink tissues, but that their capacities for viral adherence and entry into mink epithelial cells are comparable.
Descriptors: animal husbandry, infection, respiratory system, influenza A virus infection, transmission, viral disease, pneumonia, interstitial, respiratory system disease, severe, respiratory disease, respiratory system disease, immunohistochemistry immunohistochemical, immunocytochemical techniques, analytical method, antibody response viral adherence.

NAL Call Number: 448.3 Ar23
Abstract: We compared two strains of avian influenza A viruses of subtype H10 by exposing mink to aerosols of A/mink/Sweden/3,900/84 (H10N4) naturally pathogenic for mink, or A/chicken/Germany/N/49, (H10N7). Lesions in the respiratory tract during the first week after infection were studied and described. Both virus strains caused inflammatory reactions in the lungs and antibody production in exposed mink but only mink/84 virus was reisolated. The lesions caused by mink/84 virus were more severe with higher area density of pneumonia, lower daily weight gain, and more virus in the tissues detected by immunohistochemistry. The results indicate that mink/84 (H10N4), but not chicken/49 virus (H10N7), established multiple cycle replication in infected cells in the mink.
Descriptors: influenza veterinary, influenza A virus avian pathogenicity, mink virology, antibodies, viral

**NAL Call Number:** 41.8 AC87

**Descriptors:** disease outbreaks veterinary, influenza A virus avian pathogenicity, mink microbiology, veterinary viral pneumonia viral pneumonia epidemiology, viral pneumonia microbiology, viral pneumonia pathology, Sweden.


**NAL Call Number:** 470 Sci2

**Descriptors:** disease outbreaks, influenza epidemiology, world health, cost of illness, influenza transmission, influenza virology, avian pathogenicity, influenza A virus, avian physiology, influenza vaccines administration and dosage, influenza vaccines supply and distribution, models, biological, orthomyxoviridae pathogenicity, orthomyxoviridae physiology, public health, reassortant viruses.


**NAL Call Number:** QH573.C42

**Descriptors:** genes viral, hemagglutinins viral genetics, influenza A virus avian genetics, influenza A virus human genetics, amino acid sequence, base sequence, cloning, molecular, ducks microbiology, epitopes, hemagglutinins viral immunology, influenza A virus avian immunology, influenza A virus human immunology, mutation.


**NAL Call Number:** QR360.J6

**Abstract:** Wild waterfowl captured between 1915 and 1919 were tested for influenza A virus RNA. One bird, captured in 1917, was infected with a virus of the same hemagglutinin (HA) subtype as that of the 1918 pandemic virus. The 1917 HA is more closely related to that of modern avian viruses than it is to that of the pandemic virus, suggesting (i) that there was little drift in avian sequences over the past 85 years and (ii) that the 1918 pandemic virus did not acquire its HA directly from a bird.

**Descriptors:** birds virology, evolution, molecular, hemagglutinin glycoproteins, influenza virus genetics, influenza history, influenza A virus avian genetics, influenza A virus human genetics, fowl plague virology, hemagglutinin glycoproteins, influenza virus history, history of medicine, 20th century, influenza epidemiology, influenza virology, molecular sequence data, phylogeny, RNA viral genetics, viral history, sequence analysis, DNA.


**NAL Call Number:** 448.8 V81

**Abstract:** The primary structure of the hemagglutinin of the apathogenic avian influenza virus A/chick/Germany/N/49 (H10N7) and of the serologically related strain A/mink/Sweden/84 (H10N4) pathogenic for mink has been elucidated by nucleotide sequence analysis, and the carbohydrates attached to the polypeptide have been determined. The H10 hemagglutinin has 65, 52, 46, 45, and 44% amino acid sequence homology with serotypes H7, H3, H1, H2, and H5, respectively. H10 and H7 hemagglutinins are also most closely related in their glycosylation patterns. There is a high sequence homology between both H10 strains supporting the concept that the mink virus has obtained its hemagglutinin from an avian strain. The sequence homology includes the cleavage site which consists of a single arginine as is the case with
most other hemagglutinins exhibiting low susceptibility to proteolytic activation. The similarity in hemagglutinin structure between both H10 strains is discussed in light of the distinct differences in the pathogenicity of both viruses.

**Descriptors:** hemagglutinins viral genetics, influenza A virus genetics, amino acid sequence, base sequence, carbohydrates analysis, chickens microbiology, glycosylation, hemagglutinins viral analysis, influenza A virus immunology, mink microbiology, molecular sequence data, sequence homology, nucleic acid.


**NAL Call Number:** QR355.A44

**Abstract:** The study of biological properties of influenza virus strains belonging to the same subtype A(H1N1) and closely antigenically related, but isolated from different animal species (man, pig and duck), demonstrated that avian strains were more resistant than those isolated from mammals to high temperature and low pH, as shown by titration of residual infectivity in cell cultures (MDCK) and by sialidase assay. The difference in behaviour could be correlated to biological adaptation of the virus to its host. Avian body temperature is 40 degrees C and influenza virus, in ducks, is enterotropic and therefore capable of passing through the low pH values in the upper digestive tract of the animal. These results do not contradict the hypothesis of a possible filiation between avian and mammalian orthomyxoviruses.

**Descriptors:** influenza A virus physiology, body temperature, cell line, ducks, hemagglutination tests, hydrogen-ion concentration, influenza A virus avian enzymology, avian growth and development, avian physiology, human enzymology, human growth and development, human physiology, porcine enzymology, porcine growth and development, porcine physiology, influenza A virus enzymology, influenza A virus growth and development, neuraminidase analysis, plaque assay, swine, temperature, virus replication.


**NAL Call Number:** 449.9 W892B

**Descriptors:** influenza epidemiology, influenza A virus, avian pathogenicity, zoonoses, Asia, birds.


**Descriptors:** disease outbreaks prevention and control, influenza epidemiology, influenza A virus classification, influenza A virus genetics, influenza A virus pathogenicity, zoonoses virology, birds, communicable disease control, influenza prevention and control, influenza transmission, avian influenza transmission, poultry, world health, zoonoses transmission.


**Abstract:** PURPOSE OF REVIEW: Recently, several previously unrecognized respiratory viral pathogens have been identified and several influenza A virus subtypes, previously known to infect poultry and wild birds, were transmitted to humans. Here we review the recent literature on these respiratory viruses. RECENT FINDINGS: Human metapneumovirus has now been detected worldwide, causing severe respiratory tract illnesses primarily in very young, elderly and immunocompromised individuals. Animal models and reverse genetic techniques were designed for human metapneumovirus, and the first vaccine candidates have been developed. Considerable genetic and antigenic diversity was observed for human metapneumovirus, but the implication of this diversity for vaccine development and virus epidemiology requires further study. Two previously unrecognized human coronaviruses were discovered in 2004 in The Netherlands and Hong Kong. Their clinical impact and epidemiology are largely unknown and warrant further investigation. Several influenza A virus subtypes were transmitted from birds to humans, and these viruses continue to constitute a pandemic threat. The clinical symptoms associated with these zoonotic transmissions range from mild respiratory illnesses and conjunctivitis to pneumonia and acute respiratory
distress syndrome, sometimes resulting in death. More basic research into virus ecology and evolution and
development of effective vaccines and antiviral strategies are required to limit the impact of influenza A virus
zoonoses and the threat of an influenza pandemic. SUMMARY: Previously unknown and emerging
respiratory viruses are an important threat to human health. Development of virus diagnostic tests, antiviral
strategies, and vaccines for each of these pathogens is crucial to limit their impact.

Descriptors: coronavirus infections epidemiology, influenza virology, avian influenza A virus,
metapneumovirus, paramyxoviridae infections epidemiology, respiratory tract infections virology, emerging
communicable diseases, disease outbreaks, influenza epidemiology, risk factors, paramyxoviridae infections
virology, coronavirus infections virology, influenza epidemiology.

Rimmelzwaan, M. Schutten, G.J. Van Doornum, G. Koch, A. Bosman, M. Koopmans, and A.D. Osterhaus
(2004). Avian influenza A virus (H7N7) associated with human conjunctivitis and a fatal case of acute
respiratory distress syndrome. Proceedings of the National Academy of Sciences of the United States of
America 101(5): 1356-61. ISSN: 0027-8424.

NAL Call Number: 500 N21P

Abstract: Highly pathogenic avian influenza A viruses of subtypes H5 and H7 are the causative agents of
fowl plague in poultry. Influenza A viruses of subtype H5N1 also caused severe respiratory disease in
humans in Hong Kong in 1997 and 2003, including at least seven fatal cases, posing a serious human
pandemic threat. Between the end of February and the end of May 2003, a fowl plague outbreak occurred in
The Netherlands. A highly pathogenic avian influenza A virus of subtype H7N7, closely related to low
pathogenic virus isolates obtained from wild ducks, was isolated from chickens. The same virus was
detected subsequently in 86 humans who handled affected poultry and in three of their family members. Of
these 89 patients, 78 presented with conjunctivitis, 5 presented with conjunctivitis and influenza-like illness,
2 presented with influenza-like illness, and 4 did not fit the case definitions. Influenza-like illnesses were
generally mild, but a fatal case of pneumonia in combination with acute respiratory distress syndrome
occurred also. Most virus isolates obtained from humans, including probable secondary cases, had not
accumulated significant mutations. However, the virus isolated from the fatal case displayed 14 amino acid
substitutions, some of which may be associated with enhanced disease in this case. Because H7N7 viruses
have caused disease in mammals, including horses, seals, and humans, on several occasions in the past,
they may be unusual in their zoonotic potential and, thus, form a pandemic threat to humans.

Descriptors: conjunctivitis etiology, fowl plague epidemiology, influenza A virus avian isolation and
purification, respiratory distress syndrome, adult etiology, amino acid sequence, birds, disease outbreaks,
fatal outcome, fowl plague virology, hemagglutinin glycoproteins, influenza virus chemistry, influenza A virus
avian classification, middle aged, molecular sequence data, Netherlands epidemiology, respiratory distress
syndrome, adult pathology.

orthomyxovirus in birds in South-East Asian area. Developments in Biological Standardization 39: 475-60.
ISSN: 0301-5149.

NAL Call Number: QR180.3.D4

Abstract: We have previously reported that some species of migrating ducks (pintail, mallard, widgeon and
falcated teal) possess in their sera antibodies against H antigens of human or avian influenza viruses. Such
findings have also been reported from other workers, and the appearance of new types of influenza viruses
accompanied by outbreaks of new influenza pandemics, or circulation of influenza virus antigens in animals,
birds and humans have been discussed on the basis of such findings. Recently a number of
orthomyxoviruses have been isolated from wild birds such as myna, banded parakeets, etc. imported from
India and some areas of South-East Asia. Some of them have H antigens not recognized previously, and
some are found to have more or less common reactions with human H3 antigen, and consequently antigens
Hav 7 and Heq 2, which are known to show cross-reaction with H3. The significance of such a fact in
connection with the appearance of a new influenza pandemic is discussed.

Descriptors: antibodies, viral, birds microbiology, influenza A virus avian immunology, Asia, Southeastern,
ducks, hemagglutinins viral, influenza A virus avian isolation and purification, Japan, neuraminidase
immunology.

**NAL Call Number:** 47.8 R523

**Descriptors:** avian influenza virus, disease control, epidemic, poultry, zoonoses, South East Asia.


**NAL Call Number:** QR360.J6

**Abstract:** An H5N1 avian influenza A virus was transmitted to humans in Hong Kong in 1997. Although the virus causes systemic infection and is highly lethal in chickens because of the susceptibility of the hemagglutinin to furin and PC6 proteases, it is not known whether it also causes systemic infection in humans. The clinical outcomes of infection in Hong Kong residents ranged widely, from mild respiratory disease to multiple organ failure leading to death. Therefore, to understand the pathogenesis of influenza due to these H5N1 isolates, we investigated their virulence in mice. The results identified two distinct groups of viruses: group 1, for which the dose lethal for 50% of mice (MLD50) was between 0.3 and 11 PFU, and group 2, for which the MLD50 was more than 10(3) PFU. One day after intranasal inoculation of mice with 100 PFU of group 1 viruses, the virus titer in lungs was 10(7) PFU/g or 3 log units higher than that for group 2 viruses. Both types of viruses had replicated to high titers (>10(6) PFU/g) in the lungs by day 3 and maintained these titers through day 6. More importantly, only the group 1 viruses caused systemic infection, replicating in nonrespiratory organs, including the brain. Immunohistochemical analysis demonstrated the replication of a group 1 virus in brain neurons and glial cells and in cardiac myofibers. Phylogenetic analysis of all viral genes showed that both groups of Hong Kong H5N1 viruses had formed a lineage distinct from those of other viruses and that genetic reassortment between H5N1 and H1 or H3 human viruses had not occurred. Since mice and humans harbor both the furin and the PC6 proteases, we suggest that the virulence mechanism responsible for the lethality of influenza viruses in birds also operates in mammalian hosts. The failure of some H5N1 viruses to produce systemic infection in our model indicates that multiple, still-to-be-identified, factors contribute to the severity of H5N1 infection in mammals. In addition, the ability of these viruses to produce systemic infection in mice and the clear differences in pathogenicity among the isolates studied here indicate that this system provides a useful model for studying the pathogenesis of avian influenza virus infection in mammals.

**Descriptors:** genes viral, influenza virology, influenza A virus physiology, variation genetics, Hong Kong epidemiology, immunohistochemistry, influenza epidemiology, mice, phylogeny, virus replication genetics.


**NAL Call Number:** 448.3 Ar23

**Abstract:** Electrophoretic mobility differences in polyacrylamide gels were detected between (35S)-methionine-labelled nucleoproteins (NPs) induced in monolayer cells by 15 human and 4 avian reference strains of influenza viruses. The (35S)-methionine-labelled tryptic peptides of nucleoproteins of these strains were also analyzed by peptide mapping technique. Based on several detectable hydrophilic peptides the NPs could be arranged in 7 clearly differentiable groups. After radioiodination of NPs from 4 human and 3 avian reference strains the tryptic peptide patterns showed one clear difference between human and avian strains.

**Descriptors:** influenza A virus analysis, nucleoproteins analysis, viral proteins analysis, electrophoresis, polyacrylamide gel, influenza A virus avian analysis, influenza A virus avian genetics, influenza A virus human analysis, influenza A virus human genetics, influenza A virus genetics, peptide fragments analysis, variation genetics.

NAL Call Number: 448.3 Ar23
Descriptors: influenza A virus avian growth and development, virus cultivation, virus replication, bone marrow microbiology, bone marrow cells, carcinoma, bronchogenic, cell line, chick embryo, clone cells, cytological techniques, cytopathogenic effect, viral, diploidy, epithelial cells, epithelium microbiology, fibroblasts microbiology, HeLa cells, hemagglutination inhibition tests, leukemia, myelocytic, acute, plaque assay.

NAL Call Number: 448.3 Ar23
Descriptors: bone marrow microbiology, bone marrow cells, influenza A virus avian growth and development, leukemia, myelocytic, acute microbiology, virus replication, adult, aged, cultured cells, hemadsorption, influenza A virus avian pathogenicity, middle aged, virulence, virus cultivation.

NAL Call Number: QR360.A1J6
Abstract: Recombinants of human influenza type A viruses, A/Krasnodar/101/1959 (H2N2) or A/Habarovsky/15/1976 (H3N2), and fowl plague virus (FPV), strain Weybridge (Hav1Neq1) were obtained. The genome of the recombinant obtained by recombination of influenza A/Habarovsky/15/1976 virus and FPV contained the genes 4 (HA) and 6 (NA) derived from the influenza A/Habarovsky virus and all the other genes [1, 2, 3, 5 (NP), 7 (M), 8 (NS)] from FPV. The genome of the recombinant of A/Krasnodar/101/1959 virus and FPV contained the genes 2, 4 (HA) and 6 (NA) derived from influenza A/Krasnodar virus and all the other genes [1, 3, 5, (NP), 7 (M), 8 (NS)] from FPV. The recombinants, like FPV, gave high virus yields in chick embryos and could multiply at high temperatures (40 and 42 degrees C), but, like human influenza viruses, were non-pathogenic for chickens and did not replicate in chick embryo fibroblast culture, but did replicate in a human conjunctiva cell line, clone 1-5C-4. The virion transcriptase of the recombinants, in a number of properties determined in vitro, was similar to FPV transcriptase but not to the human influenza virus enzyme.
Descriptors: influenza A virus avian genetics, influenza A virus human genetics, recombination, genetic, chick embryo, influenza A virus avian analysis, influenza A virus human analysis, peptides analysis, RNA viral analysis, viral proteins analysis, virus replication.

NAL Call Number: 448.3 Ar23
Abstract: Organ cultures of human nasal polyps were shown to support the replication of five out of seven human influenza A viruses and three out of six avian strains with varying degrees of efficiency. The ability to replicate was independent of the antigenic formula of the virus. The structure of nasal polyps closely resembled that of normal nasal mucosa and infection with influenza A virus resulted in histological changes analogous to those seen in natural infections. This system provides an in vitro method for more detailed studies of influenza A virus and possibly other respiratory virus infections of man.
Descriptors: influenza microbiology, influenza A virus physiology, nasal polyps microbiology, virus replication, influenza A virus avian physiology, influenza A virus human physiology, organ culture, species specificity.

**NAL Call Number:** 448.3 AC85

**Abstract:** Human influenza virus strains were easily grown and passaged in human nasal polyp organ cultures causing marked damage of the epithelium. Unlike to human strains, the animal influenza virus strain could be propagated for no longer than 2 or 3 passages and even the 1st passage failed to cause significant morphological changes of the epithelium cells.

**Descriptors:** influenza A virus avian growth and development, influenza A virus human growth and development, influenza A virus growth and development, nasal polyps microbiology, DNA replication, deer, influenza A virus genetics, nasal polyps pathology, organ culture, species specificity, virus replication.


**NAL Call Number:** 448.3 Ar23

**Abstract:** Samples collected in 1987 and 1988 in Brittany from influenza-infected swine made it possible to isolate and antigenically characterize two H1N2 recombinant viruses (Sw/France/5027/87 and Sw/France/5550/88). The former virus was cloned and reinoculated to swine to allow reproduction of the disease and reisolation of a strain similar to the original one. The serodiagnostic tests carried out on both the original sera and those from the experimentally infected animals confirmed that the virus was actually type Sw/H1N2.

**Descriptors:** influenza A virus, porcine isolation and purification, swine virology, antibodies, monoclonal, antibody formation, antigens, viral analysis, birds, cloning, molecular, France, influenza immunology, influenza A virus avian classification, influenza A virus avian isolation and purification, influenza A virus human classification, influenza A virus human isolation and purification, influenza A virus, porcine genetics, influenza A virus, porcine immunology, variation genetics.


**NAL Call Number:** 448.8 P942

**Abstract:** Mathematical methods were used to analyse the data on the antigenic specificity of H2 subtype hemagglutinin of human and avian influenza A viruses. This approach allowed the evaluation of possible evolitional relationships in this little-studied group of viruses. Influenza A (H2) viruses isolated from birds in the USA were found to represent a sufficiently isolated group, whereas European avian strains (A/duck/Germany/1215/73, A/pintail duck/Primor'e/695/76, A/duck/Marseilles/46/76) were close to "human" viruses. The A/Leningrad/1468/65, A/laughing gull/New Jersey/75/85, and A/pintail duck/Alberta/2728/77 strains represent marked antigenic variants apparently rather far gone as a result of hemagglutinin drift.

**Descriptors:** antigens, viral immunology, hemagglutinins viral immunology, influenza A virus avian immunology, influenza A virus human immunology, algorithms, antigenic variation immunology, antigens, viral classification, cluster analysis, ducks microbiology, evolution, hemagglutinins viral classification, influenza A virus avian classification, influenza A virus human classification.


**NAL Call Number:** 448.3 AC85

**Abstract:** Cross-protection of mice immunized with inactivated preparations of human and avian influenza A (H2) viruses was determined after lethal infection with mouse-adapted (MA) variants of human A/Jap x Bell/57 (H2N1) and avian A/NJers/78 (H2N3) viruses. The MA variants differed from the original strains by acquired virulence for mice and changes in the HA antigenicity. These studies indicated that mice vaccinated with human influenza A (H2) viruses were satisfactorily protected against challenge with A/Jap x Bell/57-MA variant; the survival rate was in the range of 61%-88.9%. Immunization of mice with the same
viral preparations provided lower levels of protection against challenge with A/NJers/78-MA variant. Vaccination of mice with the avian influenza A (H2) viruses induced better protection than with human strains against challenge with both MA variants. Challenge with A/NJers/78-MA variant revealed that 76.2%-95.2% of animals were protected when vaccinated with avian influenza virus strains isolated before 1980, and that the protection reached only 52.4%-60.0% in animals vaccinated with strains isolated in 1980-1985. The present study revealed that cross-protection experiments in a mouse model could provide necessary information for the development of appropriate influenza A (H2) virus vaccines with a potential for these viruses to reappear in a human population.


NAL Call Number: 500 N21P

Abstract: Although A/Hong Kong/156/97 (H5N1/97)-like viruses associated with the "bird flu" incident in Hong Kong SAR have not been detected since the slaughter of poultry in 1997, its putative precursors continue to persist in the region. One of these, Goose/Guangdong/1/96 (H5N1 Gs/Gd)-like viruses, reassorted with other avian viruses to generate multiple genotypes of H5N1 viruses that crossed to chickens and other terrestrial poultry from its reservoir in geese. Whereas none of these recent reassortants had acquired the gene constellation of H5N1/97, these events provide insight into how such a virus may have been generated. The recent H5N1 reassortants readily infect and kill chicken and quail after experimental infection, and some were associated with significant mortality of chickens within the poultry retail markets in Hong Kong. Some genotypes are lethal for mice after intra-nasal inoculation and spread to the brain. On this occasion, the early detection of H5N1 viruses in the retail, live poultry markets led to preemptive intervention before the occurrence of human disease, but these newly emerging, highly pathogenic H5N1 viruses provide cause for pandemic concern.

Descriptors: avian influenza virus, genotypes, genes, viral hemagglutinins, sialidase, nucleotide sequences, phylogenetics, strains, isolation, abattoirs, chickens, geese, ducks, pheasants, pathogenicity, experimental infections, mice, quails, hemagglutination inhibition test, amino acid sequences, Hong Kong, molecular sequence data, gene reassortants.


NAL Call Number: 41.8 Av5

Abstract: The H5N1 virus (H5N1/97) that caused the bird flu incident in Hong Kong in 1997 has not been isolated since the poultry slaughter in late 1997. But the donor of its H5 hemagglutinin gene, Goose/Guangdong/1/96-like (Gs/Gd/96-like) virus, established a distinct lineage and continued to circulate in geese in the area. In 2000, a virus from the Goose/Guangdong/1/96 lineage was isolated for the first time from domestic ducks. Subsequently, it has undergone reassortment, and these novel reassortants now appear to have replaced Gs/Gd/96-like viruses from its reservoir in geese and from ducks. The internal gene constellation is also different from H5N1/97, but these variants have the potential for further reassortment events that may allow the interspecies transmission of the virus.

Descriptors: epidemiology, infection, avian influenza, infectious disease, respiratory system disease, viral disease, interspecies viral transmission, viral lineage, viral reservoir.


NAL Call Number: 448.8 V81
Abstract: The H5N1 viruses (H5N1/97) associated with the "bird-flu" incident in the Hong Kong SAR have not been isolated since the slaughter of poultry in December 1997 brought that outbreak to an end. Recent evidence points to this virus as having arisen through a reassortment of a number of precursor avian viruses and a virus related to Goose/Guangdong/1/96 (H5N1) (Gs/Gd/96) was the likely donor of the H5 hemagglutinin. We characterize the Goose/Guangdong/1/96-like viruses isolated from geese and ducks imported into Hong Kong in the year 2000. Antigenically and genetically, these recent H5N1 viruses fall into two groups, one mainly associated with geese, and the other, recently transmitted to ducks. Further, viruses isolated from a goose and a duck in December 2000 have acquired NS, PA, M, and PB2 genes from the aquatic avian influenza gene pool through reassortment. For pandemic preparedness, it is important to monitor whether these reassortant viruses have the capacity for interspecies transmission to terrestrial poultry or mammals.

Descriptors: ducks virology, fowl plague transmission, geese virology, influenza A virus avian genetics, poultry diseases transmission, China, evolution, molecular, fowl plague virology, influenza A virus avian isolation and purification, molecular sequence data, phylogeny, poultry diseases virology, recombination, genetic, sequence analysis, DNA.


NAL Call Number: 500 N21P

Abstract: Infection with avian influenza A virus of the H5N1 subtype (isolates A/HK/212/03 and A/HK/213/03) was fatal to one of two members of a family in southern China in 2003. This incident was preceded by lethal outbreaks of H5N1 influenza in waterfowl, which are the natural hosts of these viruses and, therefore, normally have asymptomatic infection. The hemagglutinin genes of the A/HK/212/03-like viruses isolated from humans and waterfowl share the lineage of the H5N1 viruses that caused the first known cases of human disease in Hong Kong in 1997, but their internal protein genes originated elsewhere. The hemagglutinin of the recent human isolates has undergone significant antigenic drift. Like the 1997 human H5N1 isolates, the 2003 human H5N1 isolates induced the overproduction of proinflammatory cytokines by primary human macrophages in vitro, whereas the precursor H5N1 viruses and other H5N1 reassortants isolated in 2001 did not. The acquisition by the viruses of characteristics that enhance virulence in humans and waterfowl and their potential for wider distribution by infected migrating birds are causes for renewed pandemic concern.

Descriptors: influenza epidemiology, influenza virology, birds virology, cytokines biosynthesis, cytokines immunology, hemagglutination inhibition tests, Hong Kong, inflammation mediators immunology, influenza transmission, influenza veterinary, influenza A virus, avian genetics, avian immunology, avian pathogenicity, macrophages immunology, macrophages metabolism, mice, molecular sequence data, organ specificity, phylogeny, reassortant viruses immunology, reassortant viruses pathogenicity, time factors, virulence.


NAL Call Number: QR360.J6

Abstract: The transmission of H9N2 influenza viruses to humans and the realization that the A/Hong Kong/156/97-like (H5N1) (abbreviated HK/156/97) genome complex may be present in H9N2 viruses in southeastern China necessitated a study of the distribution and characterization of H9N2 viruses in poultry in the Hong Kong SAR in 1999. Serological studies indicated that H9N2 influenza viruses had infected a high proportion of chickens and other land-based birds (pigeon, pheasant, quail, guinea fowl, and chukka) from southeastern China. Two lineages of H9N2 influenza viruses present in the live-poultry markets were represented by A/Quail/Hong Kong/G1/97 (Qa/HK/G1/97)-like and A/Duck/Hong Kong/Y280/97 (Dk/HK/Y280/97)-like viruses. Up to 16% of cages of quail in the poultry markets contained Qa/HK/G1/97-like viruses, while about 5% of cages of other land-based birds were infected with Dk/HK/Y280/97-like viruses. No reassortant between the two H9N2 virus lineages was detected despite their cocirculation in the
poultry markets. Reassortant viruses represented by A/Chicken/Hong Kong/G9/97 (H9N2) were the major H9N2 influenza viruses circulating in the Hong Kong markets in 1997 but have not been detected since the chicken slaughter in 1997. The Qa/HK/G1/97-like viruses were frequently isolated from quail, while Dk/HK/Y280/97-like viruses were predominately associated with chickens. The Qa/HK/G1/97-like viruses were evolving relatively rapidly, especially in their PB2, HA, NP, and NA genes, suggesting that they are in the process of adapting to a new host. Experimental studies showed that both H9N2 lineages were primarily spread by the aerosol route and that neither quail nor chickens showed evidence of disease. The high prevalence of quail infected with Qa/HK/G1/97-like virus that contains six gene segments genetically highly related to HK/156/97 (H5N1) virus emphasizes the need for surveillance of mammals including humans.

Descriptors: genome, viral, influenza A virus avian isolation and purification, poultry virology, China, hemagglutination inhibition tests, influenza A virus avian genetics, phylogeny, temperature, virus replication.


Abstract: Avian influenza A viruses from Asia are recognized as the source of genes that reassorted with human viral genes to generate the Asian/57 (H2N2) and Hong Kong/68 (H3N2) pandemic strains earlier in this century. Here we report the genetic analysis of avian influenza A H1N1 viruses recently isolated from pigs in southern China, a host suspected to generate new pandemic strains through gene reassortment events. Each of the eight gene segments was of avian origin. Phylogenetic analysis indicates that these genes form an Asian sublineage of the Eurasian avian lineage, suggesting that these viruses are an independent introduction into pigs in Asia. The presence of avian influenza viruses in pigs in China places them in an optimal position for transmission to humans and may serve as an early warning of the emergence of the next human influenza virus pandemic.

Descriptors: Hunan, Jiangxi, Guizhou, Guangdong, swine, avian influenza virus, nucleotide sequence, genes, agglutinins, swine influenza virus, influenza virus, genotypes, mutation, animal viruses, proteins, nucleoproteins, Asia, cell structure, China, chromosomes, domestic animals, East Asia, genetics, genomes, influenza virus, livestock, nucleus, orthomyxoviridae, proteins, suidae, useful animals, viruses, nonstructural proteins, isolation, phylogenetics, structural genes, viral hemagglutinins, influenza virus A, matrix proteins.


Abstract: The origin of the H5N1 influenza viruses that killed six of eighteen infected humans in 1997 and were highly pathogenic in chickens has not been resolved. These H5N1 viruses transmitted directly to humans from infected poultry. In the poultry markets in Hong Kong, both H5N1 and H9N2 influenza viruses were cocirculating, raising the possibility of genetic reassortment. Here we analyze the antigenic and genetic features of H9N2 influenza viruses with different epidemiological backgrounds. The results suggest that the H9N2 influenza viruses of domestic ducks have become established in the domestic poultry of Asia. Phylogenetic and antigenic analyses of the H9N2 viruses isolated from Hong Kong markets suggest three distinct sublineages. Among the chicken H9N2 viruses, six of the gene segments were apparently derived from an earlier chicken H9N2 virus isolated in China, whereas the PB1 and PB2 genes are closely related to those of the H5N1 viruses and a quail H9N2 virus-A/quail/Hong Kong/G1/97 (Qa/HK/G1/97)-suggesting that many of the 1997 chicken H9 isolates in the markets were reassortants. The similarity of the internal genes of Qa/HK/G1/97 virus to those of the H5N1 influenza viruses suggests that the quail virus may have been the internal gene donor. Our findings indicate that the human and poultry H5N1 influenza viruses in Hong Kong in 1997 were reassortants that obtained internal gene segments from Qa/HK/G1/97. However, we cannot be certain whether the replicate complex of H5N1 originated from Qa/HK/G1/97 or whether the reverse transfer occurred; the available evidence supports the former proposal.

Descriptors: genes viral, influenza epidemiology, influenza veterinary, influenza A virus avian classification, influenza A virus avian genetics, influenza A virus human classification, influenza A virus human genetics, poultry diseases epidemiology, chick embryo, chickens, coturnix, ducks, feces virology, Hong Kong epidemiology, influenza virology, influenza A virus avian pathogenicity, molecular sequence data, phylogeny,

Abstract: OBJECTIVE: To understand whether the avian influenza A(H9N2) virus can infect men or not. METHODS: Seroepidemiological surveys for avian (H9N2) virus in human, chickens and pigs were conducted. The specimens for viral isolation were taken from throat of patients with influenza like disease, as well as from chickens, then the specimens were inoculated into embryonated chicken eggs. Afterward, the isolates were identified with HI and NI tests. Meanwhile, the patients who would be studied individually were found to carry H9N2 virus. RESULTS: Approximately 19% of human had antibody to H9N2 virus with HI titers >=20, 5 strains of influenza A (H9N2) virus were isolated from the patients. CONCLUSION: Avian influenza A(H9N2) virus can infect men.

Descriptors: antibodies, viral blood, influenza virology, influenza A virus avian pathogenicity, China epidemiology, influenza epidemiology, influenza A virus avian classification, influenza A virus avian isolation and purification, seroepidemiologic studies.


NAL Call Number: 448.8 V81

Abstract: In March 1989 a severe outbreak of respiratory disease occurred in horses in the Jilin and Heilongjiang provinces of Northeast China that caused up to 20% mortality in some herds. An influenza virus of the H3N8 subtype was isolated from the infected animals and was antigenically and molecularly distinguishable from the equine 2 (H3N8) viruses currently circulating in the world. The reference strain A/Equine/Jilin/1/89 (H3N8) was most closely related to avian H3N8 influenza viruses. Sequence comparisons of the entire hemagglutinin (HA), nucleoprotein (NP), neuraminidase (NA), matrix (M), and NS genes along with partial sequences of the three polymerase (PB1, PB2, PA) genes suggest that six of the eight gene segments (PA, HA, NP, NA, M, NS) are closely related to avian influenza viruses. Since direct sequence analysis can only provide a crude measure of relationship, phylogenetic analysis was done on the sequence information. Phylogenetic analyses of the entire HA, NP, M, and NS genes and of partial sequences of PB1, PB2, and PA indicated that these genes are of recent avian origin. The NP gene segment is closely related to the gene segment found in the newly described H14 subtype isolated from ducks in the USSR. The A/Equine/Jilin/1/89 (H3N8) influenza virus failed to replicate in ducks, but did replicate and cause disease in mice on initial inoculation and on subsequent passaging caused 100% mortality. In ferrets, the virus caused severe influenza symptoms. A second outbreak of influenza in horses in Northeast China occurred in April 1990 in the Heilongjiang province with 48% morbidity and no mortality. The viruses isolated from this outbreak were antigenically indistinguishable from those in the 1989 outbreak and it is probable that the reduced mortality was due to the immune status of of the horses in the region. No influenza was detected in horses in Northern China in the spring, summer, or fall of 1991 and no influenza has been detected in horses in adjacent areas. Our analysis suggests that this new equine influenza virus in horses in Northeast China is the latest influenza virus in mammals to emerge from the avian gene pool in nature and that it may have spread to horses without reassortment. The appearance of this new equine virus in China emphasizes the potential for whole avian influenza viruses to successfully enter mammalian hosts and serves as a model and a warning for the appearance of new pandemic influenza viruses in humans.

(ABSTRACT TRUNCATED AT 250 WORDS)

Descriptors: horse diseases microbiology, influenza A virus isolation and purification, orthomyxoviridae infections veterinary, antigens, viral genetics, antigens, viral immunology, base composition, chick embryo, China epidemiology, cloning, molecular, genes viral, horse diseases epidemiology, horses, influenza A virus avian immunology, influenza A virus genetics, influenza A virus immunology, influenza A virus pathogenicity, orthomyxoviridae infections epidemiology, orthomyxoviridae infections microbiology, phylogeny, species specificity, virus replication.


NAL Call Number: QR360.A1J6

Abstract: In May 1993, a severe epidemic of respiratory disease began in horses in Inner Mongolia and spread throughout horses in China. The disease affected mules and donkeys as well as horses but did not spread to other species, including humans. The severity of the disease raised the question of whether the outbreak might have been caused by the new avian-like influenza viruses detected in horses in China in 1989 or by current variants of A/equine/Miami/1/63 (H3N8) (equine-2) or by a reassortant between these viruses. Antigenic and sequence analysis established that all gene segments of the influenza virus causing the epidemic were of recent equine-2 origin and that the virus was not a reassortant. Serological analysis of post-infection horse sera provided evidence for the continued circulation of the A/Equine/Jilin/1/89 (Eq/Jilin) (H3N8) avian-like viruses in horses in Heilongjiang province with original antigenic sin-like responses. It is noteworthy that prior infection with the avian-like Eq/Jilin strain did not afford cross-protection against a current equine-2 strain. Serological evidence for the continued circulation of the avian-like H3N8 influenza virus in horses indicates that this virus has probably established itself in horses in Asia.

Descriptors: horse diseases epidemiology, influenza veterinary, influenza A virus genetics, antibodies, viral blood, antigens, viral immunology, base sequence, China epidemiology, disease outbreaks veterinary, genome, viral, horse diseases virology, horses, influenza epidemiology, influenza virology, influenza A virus classification, influenza A virus immunology, molecular sequence data, phylogeny, sequence analysis, DNA, sequence homology, nucleic acid, seroepidemiologic studies, serotyping.


NAL Call Number: 448.8 V81

Abstract: The reported transmission of avian H9N2 influenza viruses to humans and the isolation of these viruses from Hong Kong poultry markets lend urgency to studies of their ecology and pathogenicity. We found that H9N2 viruses from North America differ from those of Asia. The North American viruses, which infect primarily domestic turkeys, replicated poorly in inoculated chickens. Phylogenetic analysis of the hemagglutinin and nucleoprotein genes indicated that the Asian H9N2 influenza viruses could be divided into three sublineages. Initial biological characterization of at least one virus from each lineage was done in animals. Early isolates of one lineage (A/Chicken/Beijing/1/94, H9N2) caused as high as 80% mortality rates in inoculated chickens, whereas all other strains were nonpathogenic. Sequence analysis showed that some isolates, including the pathogenic isolate, had one additional basic amino acid (A-R/K-S-S-R-) at the hemagglutinin cleavage site. Later isolates of the same lineage (A/Chicken/Hong Kong/G9/97, H9N2) that contains the PB1 and PB2 genes similar to Hong Kong/97 H5N1 viruses replicated in chickens, ducks, mice, and pigs but were pathogenic only in mice. A/Quail/Hong Kong/G1/97 (H9N2), from a second lineage that possesses the replicative complex similar to Hong Kong/97 H5N1 virus, replicated in chickens and ducks without producing disease signs, was pathogenic in mice, and spread to the brain without adaptation. Examples of the third Asian H9N2 sublineage (A/Chicken/Korea/323/96, Duck/Hong Kong/Y439/97) replicated in chickens, ducks, and mice without producing disease signs. The available evidence supports the notion of differences in pathogenicity of H9N2 viruses in the different lineages and suggests that viruses possessing genome segments similar to 1997 H5N1-like viruses are potentially pathogenic in mammals. Copyright 2000 Academic Press.

Descriptors: influenza A virus avian genetics, influenza A virus avian pathogenicity, binding sites genetics, chickens virology, DNA complementary chemistry, DNA complementary genetics, glycosylation, hemagglutinins viral genetics, hemagglutinins viral metabolism, Hong Kong epidemiology, mice, mice inbred BALB c virology, molecular sequence data, phylogeny, poultry diseases epidemiology, RNA viral genetics, reverse transcriptase polymerase chain reaction, sequence analysis, DNA, virulence genetics, virus replication.


NAL Call Number: QH506.E46

Abstract: There are 15 subtypes of influenza A virus (H1-H15), all of which are found in avian species.
Three caused pandemics in the last century: H1 in 1918 (and 1977), H2 in 1957 and H3 in 1968. In 1997, an H5 avian virus and in 1999 an H9 virus caused outbreaks of respiratory disease in Hong Kong. We have determined the three-dimensional structures of the haemagglutinins (HAs) from H5 avian and H9 swine viruses closely related to the viruses isolated from humans in Hong Kong. We have compared them with known structures of the H3 HA from the virus that caused the 1968 H3 pandemic and of the HA--esterase--fusion (HEF) glycoprotein from an influenza C virus. Structure and sequence comparisons suggest that HA subtypes may have originated by diversification of properties that affected the metastability of HAs required for their membrane fusion activities in viral infection.

Descriptors: hemagglutinin glycoproteins, influenza virus chemistry, influenza A virus avian chemistry, porcine chemistry, orthomyxoviridae classification, amino acid motifs, amino acid sequence, amino acid substitution, crystallography, x-ray, evolution, molecular, hemagglutinin glycoproteins, influenza virus genetics, hemagglutinin glycoproteins, influenza virus physiology, hydrogen-ion concentration, avian classification, influenza A virus avian genetics, avian physiology, porcine classification, porcine genetics, porcine physiology, membrane fusion, models, molecular, molecular sequence data, protein conformation, protein structure, secondary, rotation, sequence alignment, sequence homology, amino acid, structure activity relationship.


Abstract: We have determined the structure of the HA of an avian influenza virus, A/duck/Ukraine/63, a member of the same antigenic subtype, H3, as the virus that caused the 1968 Hong Kong influenza pandemic, and a possible progenitor of the pandemic virus. We find that structurally significant differences between the avian and the human HAs are restricted to the receptor-binding site particularly the substitutions Q226L and G228S that cause the site to open and residues within it to rearrange, including the conserved residues, Y98, W153, and H183. We have also analyzed complexes formed by the HA with sialopentasaccharides in which the terminal sialic acid is in either alpha2,3- or alpha2,6-linkage to galactose. Comparing the structures of complexes in which an alpha2,3-linked receptor analog is bound to the H3 avian HA or to an H5 avian HA leads to the suggestion that all avian influenza HAs bind to their preferred alpha2,3-linked receptors similarly, with the analog in a trans conformation about the glycosidic linkage. We find that alpha2,6-linked analogs are bound by both human and avian HAs in a cis conformation, and that the incompatibility of an alpha2,6-linked receptor with the alpha2,3-linkage-specific H3 avian HA-binding site is partially resolved by a small change in the position and orientation of the sialic acid. We discuss our results in relation to the mechanism of transfer of influenza viruses between species.

Descriptors: biochemistry and molecular biophysics, virology, 1968 Hong Kong influenza pandemic.


Abstract: A hepatotropic variant of avian influenza virus A/Turkey/England 63 (Hav 1, Nav 3) was selected by serial passages in mouse liver. Adaptation to this organ was established after 13 in vivo passages and was found to improve during further passages as shown by increasing rates of replication in livers of ICR mice. The mutant virus finally selected was stable and differed from the original virus mainly in lethality upon intraperitoneal injection in mice, in its ability to grow to high titers in livers of susceptible animals and in plaque morphology in chick embryo fibroblasts. No differences were detected in hemagglutination inhibition and neutralization by standard mouse antisera. Pathogenicity for the liver was independent of the route of inoculation, included other laboratory animals sensitive to influenza virus and could be inhibited by amantadine. Fatal hepatitis in 50 per cent of susceptible mice by the intraperitoneal route required from 10 to 20 EID50-. Pathological changes consisted of severe necrosis of liver parenchyma accompanied by release of F antigen into the serum and were apparently due to virus replication in hepatic cells as evidenced by immunofluorescence. The main implications of this animal model for studies on experimental hepatitis and on myxovirus-host interactions in an organ not usually associated with influenza are discussed.

Descriptors: adaptation, physiological, hepatitis A microbiology, liver microbiology, mutation,
orthomyxoviridae growth and development, amantadine therapeutic use, antigens, viral, disease models, animal, guinea pigs, hamsters, hepatitis A pathology, hepatitis A prevention and control, liver immunology, liver pathology, mice, mice inbred strains, orthomyxoviridae immunology, orthomyxoviridae pathogenicity, rats, virus replication.

NAL Call Number: 448.8 Sch9
Descriptors: hepatitis, disease models, avian influenza virus, mice.

NAL Call Number: 448.8 D48
Descriptors: human medicine, infection, veterinary medicine, avian influenza, drug therapy, pathology, respiratory system disease, transmission, viral disease, coinfection, gene transfer, potential risk, prevention, recombination, zoonosis.

NAL Call Number: 470 Sci2
Abstract: In 1997, an H5N1 influenza A virus was transmitted from birds to humans in Hong Kong, killing 6 of the 18 people infected. When mice were infected with the human isolates, two virulence groups became apparent. Using reverse genetics, we showed that a mutation at position 627 in the PB2 protein influenced the outcome of infection in mice. Moreover, high cleavability of the hemagglutinin glycoprotein was an essential requirement for lethal infection.
Descriptors: influenza epidemiology, influenza virology, influenza A virus genetics, influenza A virus pathogenicity, amino acid sequence, birds virology, DNA, recombinant genetics, hemagglutinin glycoproteins, influenza virus chemistry, hemagglutinin glycoproteins, influenza virus genetics, hemagglutinin glycoproteins, influenza virus metabolism, Hong Kong epidemiology, influenza mortality, influenza transmission, influenza A virus avian genetics, avian pathogenicity, avian physiology, human genetics, human pathogenicity, human physiology, influenza A virus physiology, lung virology, mice, mutation, missense genetics, reassortant viruses genetics, reassortant viruses pathogenicity, reassortant viruses physiology, viral proteins chemistry, viral proteins genetics, viral proteins metabolism.

NAL Call Number: 448.8 V81
Descriptors: ducks virology, genes viral, influenza A virus human physiology, intestines virology, viral proteins genetics, virus replication, cell line, DNA, complementary, avian genetics, avian metabolism, human genetics, human pathogenicity, RNA viral metabolism, recombination, genetic, transcription, genetic, viral proteins metabolism.

NAL Call Number: QR1.T74
Abstract: In 1997, a highly pathogenic avian H5N1 influenza virus was transmitted directly from live commercial poultry to humans in Hong Kong. Of the 18 people infected, six died. The molecular basis for the high virulence of this virus in mice was found to involve an amino acid change in the PB2 protein. To eliminate the source of the pathogenic virus, all birds in the Hong Kong markets were slaughtered. In 1999, another avian influenza virus of H9N2 subtype was transmitted to two children in Hong Kong. In 2000-2002, H5N1 avian viruses reappeared in the poultry markets of Hong Kong, although they have not infected humans. Continued circulation of H5N1 and other avian viruses in Hong Kong raises the possibility of future human influenza outbreaks. Moreover, the acquisition of properties of human viruses by the avian viruses
currently circulating in southeast China might result in a pandemic.

Descriptors: communicable diseases, emerging virology, disease outbreaks, fowl plague virology, communicable diseases, emerging epidemiology, disease reservoirs, fowl plague epidemiology, Hong Kong epidemiology, influenza A virus avian genetics, avian pathogenicity, avian physiology, mice, virulence.

NAL Call Number: 449.9 W892B
Descriptors: antigens, viral analysis, influenza A virus, porcine immunology, influenza A virus immunology, antibodies, monoclonal immunology, hemagglutination inhibition tests, hemagglutination tests, immune sera, avian immunology, influenza A virus human immunology, porcine isolation and purification.

NAL Call Number: QR360.J6
Abstract: Influenza A viruses of the H13N2 and H13N9 subtypes were isolated from the lung and hilar node of a pilot whale. Serological, molecular, and biological analyses indicate that the whale isolates are closely related to the H13 influenza viruses from gulls.
Descriptors: cetacea microbiology, influenza A virus isolation and purification, whales microbiology, antigens, viral immunology, ferrets microbiology, hemagglutinins viral immunology, influenza A virus avian analysis, influenza A virus analysis, influenza A virus immunology, influenza A virus physiology, lung microbiology, lymph nodes microbiology, neuraminidase immunology, nucleic acid hybridization, RNA viral analysis, virus replication.

NAL Call Number: QR360.J6
Abstract: Influenza A virus isolates of the H4N5 subtype (which has previously been detected only in birds) were recovered from harbor seals dying of viral pneumonia on the New England coast from June 1982 through March 1983. When these isolates were compared with other mammalian and avian viruses in serological assays and RNA-RNA competitive hybridization, it was found that the seal viruses were most closely related antigenically and genetically to recent avian virus strains and were readily distinguishable from mammalian viruses, including H7N7 isolates recovered from seals in 1980. Unlike any previous isolates from mammals, these recent seal viruses replicate in the intestinal tracts of ducks, a characteristic of avian viruses. The association of avian viruses with influenza outbreaks in seals suggests that transmission of avian viruses to seals is occurring in nature. Potentially, this may be an example of the adaptation of avian viruses to mammals, which would represent an intermediate step in the evolution of new mammalian strains.
Descriptors: animal diseases microbiology, fowl plague veterinary, influenza A virus avian pathogenicity, pinnipedia microbiology, seals microbiology, animal diseases mortality, fowl plague microbiology, fowl plague mortality, avian isolation and purification.

NAL Call Number: QR1.I57
Abstract: The recent appearance of an avian influenza A virus in seals suggests that viruses are transmitted from birds to mammals in nature. To examine this possibility, avian viruses of different antigenic subtypes were evaluated for their ability to replicate in three mammals-pigs, ferrets, and cats. In each of these mammals, avian strains replicated to high titers in the respiratory tract (10(5) to 10(7) 50% egg infective doses per ml of nasal wash), with peak titers at 2 to 4 days post-inoculation, similar to the pattern of human and other mammalian viruses in these animals. Most avian strains were recovered for 5 to 9 days post-inoculation. One avian H1N1 virus initially replicated poorly in pigs, but was adapted to this host and...
even transmitted to other pigs. Replication of the avian viruses occurred in the respiratory tracts of mammals, whereas, in birds, they replicate in the intestinal tract as well. The infected mammals had no significant disease signs and produced low levels of humoral antibodies; however, challenge experiments in ferrets indicated that they were immune. These studies suggest that influenza A viruses currently circulating in avian species represent a source of viruses capable of infecting mammals, thereby contributing to the influenza A antigenic pool from which new pandemic strains may originate.

Descriptors: Carnivora microbiology, cats microbiology, ferrets microbiology, influenza A virus avian growth and development, swine microbiology, adaptation, physiological, antibodies, viral biosynthesis, antigens, viral analysis, avian immunology, human growth and development, porcine growth and development, respiratory system microbiology, virus replication.


NAL Call Number: 448.8 V81

Abstract: Avian influenza viruses replicate to high titers in the cells lining the intestinal tract of birds; however, human strains do not. A series of reassortant viruses with all six internal genes from an avian strain and one or both genes for the surface antigens from a human strain failed to transit and infect the intestinal tracts of ducks. However, these reassortants did replicate in the bursa of ducks after rectal inoculation. These studies provide the first evidence that the hemagglutinin and neuraminidase are critical for the enterotropism of avian viruses but are not essential for replication in other avian tissues.

Descriptors: hemagglutinins viral, influenza A virus avian physiology, human physiology, intestines microbiology, neuraminidase physiology, bursa of fabricius microbiology, ducks microbiology, genes viral, avian genetics, human genetics, recombination, genetic, virus replication.


NAL Call Number: 448.8 V81

Descriptors: influenza A virus avian pathogenicity, ovum virology, cell line, chick embryo, clone cells, dogs, fowl plague mortality, avian growth and development, avian isolation and purification, mice, organ specificity, sequence analysis, DNA, sequence analysis, protein, serial passage, tropism, virulence, virus replication.


NAL Call Number: 448.8 V81

Descriptors: genes viral, hemagglutinins viral genetics, influenza A virus human immunology, amino acid sequence, base sequence, DNA, viral, avian immunology, human classification, human genetics.


NAL Call Number: QR360.J6

Abstract: In 1997, an H5N1 influenza virus outbreak occurred in chickens in Hong Kong, and the virus was transmitted directly to humans. Because there is limited information about the avian influenza virus reservoir in that region, we genetically characterized virus strains isolated in Hong Kong during the 1997 outbreak. We sequenced the gene segments of a heterogeneous group of viruses of seven different serotypes (H3N8, H4N8, H6N1, H6N9, H11N1, H11N9, and H11N8) isolated from various bird species. The phylogenetic relationships divided these viruses into several subgroups. An H6N1 virus isolated from teal (A/teal/Hong Kong/W312/97 [H6N1]) showed very high (>98%) nucleotide homology to the human influenza virus A/Hong Kong/156/97 (H5N1) in the six internal genes. The N1 neuraminidase sequence showed 97% nucleotide homology to that of the human H5N1 virus, and the N1 protein of both viruses had the same 19-amino-acid deletion in the stalk region. The deduced hemagglutinin amino acid sequence of the H6N1 virus was most similar to that of A/shearwater/Australia/1/72 (H6N5). The H6N1 virus is the first known isolate with seven
H5N1-like segments and may have been the donor of the neuraminidase and the internal genes of the H5N1 viruses. The high homology between the internal genes of H9N2, H6N1, and the H5N1 isolates indicates that these subtypes are able to exchange their internal genes and are therefore a potential source of new pathogenic influenza virus strains. Our analysis suggests that surveillance for influenza A viruses should be conducted for wild aquatic birds as well as for poultry, pigs, and humans and that H6 isolates should be further characterized.

Descriptors: genome, viral, influenza A virus avian genetics, birds, China, fowl plague, hemagglutinin glycoproteins, influenza virus genetics, avian classification, avian isolation and purification, avian pathogenicity, human classification, human genetics, human isolation and purification, human pathogenicity, mice, mice inbred BALB c, neuraminidase genetics, phylogeny, polymerase chain reaction, sequence analysis, DNA.


NAL Call Number: QR67.C54

Abstract: Influenza pandemics, defined as global outbreaks of the disease due to viruses with new antigenic subtypes, have exacted high death tolls from human populations. The last two pandemics were caused by hybrid viruses, or reassortants, that harbored a combination of avian and human viral genes. Avian influenza viruses are therefore key contributors to the emergence of human influenza pandemics. In 1997, an H5N1 influenza virus was directly transmitted from birds in live poultry markets in Hong Kong to humans. Eighteen people were infected in this outbreak, six of whom died. This avian virus exhibited high virulence in both avian and mammalian species, causing systemic infection in both chickens and mice. Subsequently, another avian virus with the H9N2 subtype was directly transmitted from birds to humans in Hong Kong. Interestingly, the genes encoding the internal proteins of the H9N2 virus are genetically highly related to those of the H5N1 virus, suggesting a unique property of these gene products. The identification of avian viruses in humans underscores the potential of these and similar strains to produce devastating influenza outbreaks in major population centers. Although highly pathogenic avian influenza viruses had been identified before the 1997 outbreak in Hong Kong, their devastating effects had been confined to poultry. With the Hong Kong outbreak, it became clear that the virulence potential of these viruses extended to humans.

Descriptors: disease outbreaks prevention and control, disease outbreaks veterinary, fowl plague epidemiology, influenza epidemiology, influenza A virus avian pathogenicity, adaptation, physiological, disease vectors, fowl plague transmission, Hong Kong epidemiology, influenza virology, avian classification, Mexico epidemiology, Pennsylvania epidemiology, poultry, viral proteins, virulence.


NAL Call Number: QR360.J6

Abstract: We determined the deduced amino acid sequences of two H1 duck influenza A virus hemagglutinins (HAs) and found that the consensus sequence of the HA, determined directly from virus recovered from the intestinal tract, remains unchanged through many generations of growth in MDCK cells and chicken embryos. These two duck viruses differ from each other by 5 amino acids and from A/Dk/Alberta/35/1976 (F. J. Austin, Y. Kawaoka, and R. G. Webster, J. Gen. Virol. 71:2471-2474, 1990) by 9 and 12 amino acids, most of which are in the HA1 subunit. They are antigenically similar to each other but different from the Alberta virus. We compared these H1 duck HAs with the HAs of human isolates to identify structural properties of this viral glycoprotein that are associated with host range. By comparison to the human H1 HAs, the duck virus HA sequences are highly conserved as judged by the small fraction of nucleotide differences between strains which result in amino acid substitutions. However, the most striking difference between these duck and human HAs is in the number and distribution of glycosylation sites. Whereas duck and swine viruses have four and five conserved glycosylation sites per HA1 subunit, none of which are on the tip of the HA, all human viruses have at least four additional sites, two or more of which are on the tip of the HA. These findings stress the role of glycosylation in the control of host range and suggest that oligosaccharides on the tip of the HA are important to the survival of H1 viruses in humans but not in.
ducks or swine.

Descriptors: consensus sequence genetics, ducks microbiology, hemagglutiniins viral genetics, influenza A virus avian genetics, human genetics, amino acid sequence, antigens, viral genetics, antigens, viral immunology, cultured cells, consensus sequence immunology, feces microbiology, glycosylation, hemagglutinin glycoproteins, influenza virus, hemagglutiniins viral immunology, avian immunology, human immunology, models, molecular, molecular sequence data, protein processing, post translational, regulatory sequences, nucleic acid genetics, selection genetics, sequence homology, amino acid, variation genetics.


NAL Call Number: 448.8 P942

Abstract: Comparative studies of the antigenic properties of hemagglutinin (HA) of animal and human viruses revealed both similarities between them and complete differences in the composition of antigenic determinants. Avian influenza viruses A/chicken/Kamchatka/12/71, A/pintail/Primorie/730/76, and A/bat/Alma-Ata/73/77 were completely identical with human strains of influenza virus. Influenza A/horse/Miami/63 contains one antigenic determinant H3.1.HA of A/tern/Turkmenia/18/73 (Hav7) viruses has a peculiar set of antigens. Apart from two antigenic determinants H3.1 and H3.3 inherent in human virus strains, HA of A/tern/Turkmenia/18/73 virus contains an antigenic determinant the population of antibodies to which shows no relation to HA of subtypes Hav2-Hav9.

Descriptors: epitopes isolation and purification, influenza A virus human immunology, orthomyxoviridae immunology, complement fixation tests, epitopes analysis, hemagglutination inhibition tests, hemagglutinins viral analysis, hemagglutinins viral isolation and purification, immunoelectrophoresis, orthomyxoviridae isolation and purification.


NAL Call Number: QR360.A1J6

Abstract: A mammalian cell-adapted mutant of the Dobson strain of fowl plague virus (FPV-B) was characterized. Genetic analyses of recombinants between a ts mutant of this virus and either the non-adapted Dobson strain or the Rostock strain of FPV showed that the gene coding for the P3 protein of the adapted Dobson strain was sufficient to enable any recombinant to grow in L cells. The abortive cycle of wild-type Dobson strain (FPV+) was compared to the productive cycle of the mutant. By using 100 p.f.u./cell, no quantitative difference could be detected in infected L cells between polypeptides and cRNAs induced by FPV+ and FPV-B. However, the maturation of virions at the plasma membrane did not proceed correctly. At a lower m.o.i. the amounts of virus polypeptides decreased with the m.o.i. This decrease was not the same for all polypeptides and cRNA segments: HA, M and NA and their mRNAs decreased to a greater extent than the others. These results are discussed in relation to a possible biological activity of polypeptide P3.

Descriptors: genes viral, influenza A virus avian genetics, virus replication, avian growth and development, avian metabolism, L cells cell line, mice, mutation, RNA viral biosynthesis, recombination, genetic, viral proteins biosynthesis.


NAL Call Number: QD431.T3

Descriptors: influenza A virus, avian pathogenicity, SARS virus pathogenicity, severe acute respiratory syndrome virology, Asia epidemiology, disease outbreaks, avian influenza epidemiology, avian influenza transmission, avian influenza virology, poultry diseases epidemiology, poultry diseases transmission, poultry diseases virology, severe acute respiratory syndrome epidemiology, severe acute respiratory syndrome transmission, virulence, zoonoses epidemiology, zoonoses transmission.

Descriptors: chickens, avian influenza virus, Newcastle disease virus, host parasite relations, Hong Kong, Asia, birds, domestic animals, East Asia, Galliformes, influenza virus, livestock, orthomyxoviridae, paramyxoviridae, parasitism, poultry, useful animals, viruses.

NAL Call Number: QR360.J6

Abstract: Genetic and biologic observations suggest that pigs may serve as "mixing vessels" for the generation of human-avian influenza A virus reassortants, similar to those responsible for the 1957 and 1968 pandemics. Here we demonstrate a structural basis for this hypothesis. Cell surface receptors for both human and avian influenza viruses were identified in the pig trachea, providing a milieu conducive to viral replication and genetic reassortment. Surprisingly, with continued replication, some avian-like swine viruses acquired the ability to recognize human virus receptors, raising the possibility of their direct transmission to human populations. These findings help to explain the emergence of pandemic influenza viruses and support the need for continued surveillance of swine for viruses carrying avian virus genes.

Descriptors: hemagglutinin glycoproteins, influenza virus chemistry, influenza A virus avian metabolism, human metabolism, receptors, virus chemistry, adaptation, biological, amino acid sequence, amino acids, binding sites, ducks, hemagglutinin glycoproteins, influenza virus metabolism, avian classification, avian physiology, human classification, human physiology, molecular sequence data, phylogeny, receptors, virus metabolism, sequence homology, amino acid, swine, trachea virology.

NAL Call Number: 41.8 V6446

Abstract: An H5N1 avian influenza A virus was directly transmitted from birds to humans in 1997-1998 in Hong Kong, infecting 18 humans, 6 of whom died. Epidemiological studies indicate that there has been no human-to-human transmission of the virus, suggesting that human cases in Hong Kong originated from independent transmission of the virus from birds. The H5N1 viruses isolated from humans have still displayed avian virus-like receptor specificity. This property is consistent with the fact that the virus did not establish within human populations. Subsequently, in March of 1999, another avian virus with the H9N2 subtype was isolated from two persons in Hong Kong. This virus also did not have the capacity for human-to-human spread. However, this case suggests that all subtypes of avian viruses (except H1 and H3 viruses) could be novel human influenza viruses with pandemic potential. It also supports the contention that intensive monitoring of bird populations should be an integral part of control policies for new human pandemic of influenza.

Descriptors: epidemiology, infection, avian influenza, epidemiology, infectious disease, respiratory system disease, transmission, viral disease, viral transmission.

NAL Call Number: 448.8 J8232

Abstract: Recently, an avian influenza A virus (A/Hong Kong/156/97, H5N1) was isolated from a young child who had a fatal influenza illness. All eight RNA segments were of avian origin. The H5 hemagglutinin is not recognized by neutralizing Abs present in humans as a result of infection with the human H1, H2, or H3 subtypes of influenza A viruses. Subsequently, five other deaths and several more human infections in Hong Kong were associated with this avian-derived virus. We investigated whether influenza A-specific human CD8+ and CD4+ T lymphocytes would recognize epitopes on influenza A virus strains derived from swine or avian species, including the 1997 H5N1 Hong Kong virus strains. Our results demonstrate that adults living in an urban area of the U.S. possess influenza A cross-serotype reactive CD8+ and CD4+ CTL that recognize multiple epitopes on influenza A viruses of other species. Bulk culture cytotoxicity was demonstrated against avian and human influenza A viruses. Enzyme-linked immunospot assays detected precursor CTL specific for both human CTL epitopes and the corresponding A/HK/97 viral sequences. We hypothesize that these cross-reactive CTL might provide partial protection to humans against novel influenza
A virus strains introduced into humans from other species.

Descriptors: cd4 positive T lymphocytes immunology, CD4 positive T lymphocytes virology, CD8 positive T lymphocytes immunology, CD8 positive T lymphocytes virology, influenza A virus avian immunology, porcine immunology, cell line, chickens, cytotoxicity, immunologic genetics, ducks, enzyme linked immunosorbent assay, avian genetics, porcine genetics, leukocytes, mononuclear immunology, leukocytes, mononuclear virology, peptides genetics, peptides immunology, point mutation, stem cells immunology, stem cells virology, swine.


NAL Call Number: 41.8 Sch9

Abstract: The risk of zoonotic disease transmission when handling livestock or animal products is substantial. In industrialized countries, the classical zoonotic diseases such as tuberculosis or brucellosis are no longer in the foreground. Latent zoonoses such as salmonellosis and campylobacteriosis can cause serious disease in humans and have become a major public health problem during the past years. Since animals infected with these pathogens show only mild transient disease or no clinical signs at all, new concepts in the entire production line ("stable to table") are necessary in order to avoid human infection. Two emerging viruses with zoonotic potential--avian influenza virus and Nipah virus--have been found in Asia in 1997 and 1999. Both diseases had a major impact on disease control and public health in the countries of origin. In order to cope threats from infectious diseases, in particular those of public health relevance, a combined effort among all institutions involved will be necessary. The proposed "European Center for Infectious Diseases" and the "Swiss Center for Zoonotic Diseases" could be a potential approach in order to achieve this goal.

Descriptors: public health, infection, veterinary medicine, Campylobacteriosis, bacterial disease, Salmonellosis, animal product handling, livestock handling, meat inspection, foodborne zoonosis, food contamination prevention and control, food microbiology, meat microbiology, meat products microbiology, zoonoses transmission, animal husbandry, European Union, food handling, risk factors.


NAL Call Number: R99.N4

Descriptors: influenza, avian epidemiology, public health, communicable disease control methods, disease outbreaks statistics and numerical data, influenza A virus isolation and purification, avian influenza transmission, avian influenza virology, New Zealand epidemiology, poultry, risk factors, world health, zoonoses epidemiology, zoonoses transmission, zoonoses virology.


NAL Call Number: 41.8 V6439

Abstract: This review article deals with influenza as a zoonosis. The pathogenicity of viruses, clinical symptoms, diagnosis and methods of transmission of the disease between different animal species and man are presented.

Descriptors: avian influenza virus, swine influenza virus, zoonoses, viroses, disease transmission, diagnosis, symptoms, ELISA, Europe, Asia, North America, America, immunoenzyme techniques, immunological techniques, infectious diseases, pathogenesis.


Abstract: The paper explores the social representation of the 2001 Hong Kong avian bird flu epidemic from the perspective of local women. Fifty women were asked to describe their first thoughts about the flu, and these were subsequently explored. Thematic analysis of the semi-structured interviews revealed that the first thoughts were characterized by: (a) the origin of the epidemic, (b) anchors for it, (c) emotions about it, and (d) images of it. Aspersion concerning the lack of hygiene of Mainland Chinese chicken rearers and chicken
sellers in Hong Kong dominated the interviews. Other environmental factors were also stressed, as was regulation leniency and a drive to profit. Comparisons between old traditions and newer practices formed a central feature. The findings are discussed in terms of their continuity with western risk findings as well as their specific cultural nuances.

Descriptors: bird diseases epidemiology, food, social behavior, adult, bird diseases virology, culture, disease outbreaks, health behavior, Hong Kong epidemiology, hygiene, influenza A virus, avian isolation and purification, middle aged, questionnaires.


Descriptors: birds virology, disease outbreaks prevention and control, influenza A virus, avian genetics, avian influenza transmission, India, avian influenza pathogenicity, avian influenza diagnosis.


NAL Call Number: QH573.C42

Abstract: The complete sequence of a hemagglutinin (HA) gene of a recent human influenza A strain, A/Victoria/3/75, is 1768 nucleotides long and contains the information for 567 amino acids. It codes for a signal peptide of 16 amino acids, the HA1 chain of the mature hemagglutinin of 329 amino acids, a connecting region between HA1 and HA2 consisting of a single arginine residue and the HA2 portion of 221 amino acids. The sequence is compared with the hemagglutinin of two members of other subtypes, the human H2 strain A/Jap/305/57 and the avian Hav1 strain A/FPV/Rostock/34, and with one of the same H3 subtype, A/Memphis/3/72. To align the HA1 chain of different major subtypes several deletions/insertions of single amino acids must be invoked, but two more extensive differences are found at both ends, one leading to an extension of the amino terminal sequence of HA1 and the other (four residues) occurring in the region processed away between HA1 and HA2. Comparison of the HA1 of two H3 strains suggests that drift probably depends on single base mutations, some of which change antigenic determinants. The HA2 region, which apparently is not involved in the immune response, is highly conserved even between different subtypes, and single base substitutions account for all the observed diversity. A hydrophobic segment of 24 residues is present in the same position close to the carboxyl terminus of HA2 in both Victoria and FPV, and presumably functions in implantation into the lipid bilayer. The many conserved features not only in HA2 but also in HA1 suggest a rather rigid architecture for the whole hemagglutinin molecule.

Descriptors: genes viral, hemagglutinins viral genetics, influenza A virus human genetics, RNA viral genetics, amino acid sequence, base sequence, carbohydrates analysis, cloning, molecular, codon, DNA, viral genetics, epitopes, hemagglutinins viral analysis, avian genetics.


NAL Call Number: 470 Sci2

Descriptors: antiviral agents therapeutic use, disease outbreaks prevention and control, influenza prevention and control, influenza vaccines supply and distribution, world health, adjuvants, immunologic, antiviral agents supply and distribution, clinical trials, developed countries, developing countries, influenza epidemiology, influenza A virus, avian immunology, avian pathogenicity, orthomyxoviridae immunology, orthomyxoviridae pathogenicity, patents, United States, vaccines, synthetic.


NAL Call Number: 448.3 Ar23

Abstract: The nucleotide sequences of the HA1 domain of the H1 hemagglutinin genes of A/duck/Hong Kong/36/76, A/duck/Hong Kong/196/77, A/sw/North Ireland/38, A/sw/Cambridge/39 and A/Yamagata/120/86 viruses were determined, and their evolutionary relationships were compared with those of previously sequenced hemagglutinin (H1) genes from avian, swine and human influenza viruses. A pairwise
comparison of the nucleotide sequences revealed that the genes can be segregated into three groups, the avian, swine and human virus groups. With the exception of two swine strains isolated in the 1930s, a high degree of nucleotide sequence homology exists within the group. Two phylogenetic trees constructed from the substitutions at the synonymous site and the third codon position showed that the H1 hemagglutinin genes can be divided into three host-specific lineages. Examination of 21 hemagglutinin genes from the human and swine viruses revealed that two distinct lineages are present in the swine population. The swine strains, sw/North Ireland/38 and sw/Cambridge/39, are clearly on the human lineage, suggesting that they originate from a human A/WSN/33-like variant. However, the classic swine strain, sw/Iowa/15/30, and the contemporary human viruses are not direct descendants of the 1918 human pandemic strain, but did diverge from a common ancestral virus around 1905. Furthermore, previous to this the above mammalian viruses diverged from the lineage containing the avian viruses at about 1880.

Descriptors: evolution, hemagglutinins viral genetics, influenza A virus avian genetics, human genetics, porcine genetics, amino acid sequence, chick embryo, genes viral, hemagglutinin glycoproteins, influenza virus, avian classification, human classification, porcine classification, molecular sequence data, phylogeny, sequence homology, amino acid.


NAL Call Number: QR180.C62

Descriptors: disease reservoirs, influenza microbiology, influenza A virus genetics, orthomyxoviridae infections veterinary, genes viral, horses microbiology, influenza A virus avian, influenza A virus, porcine, orthomyxoviridae infections microbiology, orthomyxoviridae infections transmission, recombination, genetic.


NAL Call Number: QR360.J6

Abstract: In October 1999, H4N6 influenza A viruses were isolated from pigs with pneumonia on a commercial swine farm in Canada. Phylogenetic analyses of the sequences of all eight viral RNA segments demonstrated that these are wholly avian influenza viruses of the North American lineage. To our knowledge, this is the first report of interspecies transmission of an avian H4 influenza virus to domestic pigs under natural conditions.

Descriptors: influenza A virus avian isolation and purification, pneumonia, viral virology, swine diseases virology, Canada epidemiology, influenza A virus avian genetics, molecular sequence data, phylogeny, pneumonia, viral epidemiology, swine, swine diseases epidemiology.


NAL Call Number: 41.8 R3224

Descriptors: influenza A virus avian isolation and purification, swine diseases virology, antigens, viral analysis, enzyme linked immunosorbent assay veterinary, incidence, avian immunology, Ontario epidemiology, swine, swine diseases epidemiology, swine diseases immunology.


NAL Call Number: QR375.V6

Abstract: Since 1998, H3N2 viruses have caused epizootics of respiratory disease in pigs throughout the major swine production regions of the U.S. These outbreaks are remarkable because swine influenza in North America had previously been caused almost exclusively by H1N1 viruses. We sequenced the full-length protein coding regions of all eight RNA segments from four H3N2 viruses that we isolated from pigs in
the Midwestern U.S. between March 1998 and March 1999, as well as from H3N2 viruses recovered from a piglet in Canada in January 1997 and from a pig in Colorado in 1977. Phylogenetic analyses demonstrated that the 1977 Colorado and 1997 Ontario isolates are wholly human influenza viruses. However, the viruses isolated since 1998 from pigs in the Midwestern U.S. are reassortant viruses containing hemagglutinin, neuraminidase and PB1 polymerase genes from human influenza viruses, matrix, non-structural and nucleoprotein genes from classical swine viruses, and PA and PB2 polymerase genes from avian viruses. The HA proteins of the Midwestern reassortant swine viruses can be differentiated from those of the 1995 lineage of human H3 viruses by 12 amino acid mutations in HA1. In contrast, the Sw/ONT/97 virus, which did not spread from pig-to-pig, lacks 11 of these changes.

Descriptors: influenza A virus avian genetics, human genetics, porcine classification, porcine genetics, reassortant viruses genetics, genotype, influenza veterinary, influenza virology, molecular sequence data, North America, phylogeny, swine, swine diseases virology.


NAL Call Number: 41.8 Av5

Abstract: In the late 1990s, H5N1 and H9N2 avian influenza viruses caused respiratory infections in humans in Hong Kong. Exposure to domestic poultry in live-bird markets was significantly associated with human H5N1 disease. Seroepidemiologic studies conducted among contacts of H5N1-infected persons determined that human-to-human transmission of the avian H5N1 viruses occurred but was rare. The relatively high rates of H5 and H9 antibody seroprevalence among Hong Kong poultry workers in 1997 highlight the potential for avian viruses to transmit to humans, particularly those with occupational exposure. Such transmission increases the likelihood of reassortment between a currently circulating human virus and an avian virus and thus the creation of a strain with pandemic potential.

Descriptors: epidemiology, immune system, infection, respiratory infection, infectious disease, respiratory system disease, antibody seroprevalence, live bird markets, pandemic, potential public health, viral transmission.


NAL Call Number: 448.8 J821

Abstract: The first documented outbreak of human respiratory disease caused by avian influenza A (H5N1) viruses occurred in Hong Kong in 1997. The kinetics of the antibody response to the avian virus in H5N1-infected persons was similar to that of a primary response to human influenza A viruses; serum neutralizing antibody was detected, in general, >14 days after symptom onset. Cohort studies were conducted to assess the risk of human-to-human transmission of the virus. By use of a combination of serologic assays, 6 of 51 household contacts, 1 of 26 tour group members, and none of 47 coworkers exposed to H5N1-infected persons were positive for H5 antibody. One H5 antibody-positive household contact, with no history of poultry exposure, provided evidence that human-to-human transmission of the avian virus may have occurred through close physical contact with H5N1-infected patients. In contrast, social exposure to case patients was not associated with H5N1 infection.

Descriptors: antibodies, viral blood, hemagglutinin glycoproteins, influenza virus immunology, influenza immunology, influenza transmission, influenza A virus avian immunology, adolescent, adult, child, child, preschool, cohort studies, family health, infant, influenza virology, avian isolation and purification, interpersonal relations, middle aged, neutralization tests, poultry virology.


NAL Call Number: R41.B52

Abstract: In 1997 in Hong Kong, 18 human cases of respiratory illness were caused by an avian influenza A H5N1 virus. Although avian influenza viruses had not previously been known to cause respiratory illness in
humans, the H5N1 viruses caused severe illness and death, primarily in individuals aged > 12 years. The introduction of H5N1 viruses into humans raised concerns about the potential of these viruses to cause a pandemic. We have used the BALB/c mouse to better understand the pathogenesis of and immunity to the H5N1 viruses in a mammalian model. Previously, we demonstrated that H5N1 viruses isolated from humans replicated efficiently in the lungs of mice without prior adaptation to this host. Two general phenotypes of pathogenicity of H5N1 viruses, based on high and low lethality for mice, were observed. We now demonstrate that in addition to a lethal outcome, H5N1 viruses with a high pathogenicity phenotype exhibit additional features that include rapid and uncontrolled replication in the lungs of infected mice, dissemination and replication of the virus in other organs, and depletion of peripheral blood leukocytes. The BALB/c mouse model was also used to better understand the parameters of protective immunity to the H5N1 viruses. Prior infection with H5N1 viruses of low pathogenicity or an antigenically related non-pathogenic H5N3 virus protected mice from death by infection with a highly pathogenic HK/483 virus. Serum hemagglutination-inhibition antibody titers of 40 or greater were associated with protection of mice from death. Immunization of mice with baculovirus-expressed recombinant H5 hemagglutinin protein or a previously defined HS-specific synthetic peptide induced MHC class II restricted CTL activity. Mice that had CTL activity but no serum hemagglutination-inhibition antibody were not protected from a lethal challenge with H5N1 virus. These results suggest that antibody is required for protection of mice against lethal challenge with H5N1 viruses of the high pathogenicity phenotype.

Descriptors: influenza A virus avian immunology, avian pathogenicity, antibodies, viral blood, antigens, viral analysis, immunization, influenza virology, influenza vaccine immunology, mice, mice inbred BALB c, T lymphocytes, cytotoxic immunology, virus replication.

NAL Call Number: QR360.J6
Abstract: Highly pathogenic avian influenza A H5N1 viruses caused an outbreak of human respiratory illness in Hong Kong. Of 15 human H5N1 isolates characterized, nine displayed a high-, five a low-, and one an intermediate-pathogenicity phenotype in the BALB/c mouse model. Sequence analysis determined that five specific amino acids in four proteins correlated with pathogenicity in mice. Alone or in combination, these specific residues are the likely determinants of virulence of human H5N1 influenza viruses in this model.
Descriptors: influenza virology, influenza A virus avian genetics, avian pathogenicity, adolescent, adult, child, preschool, disease models, animal, infant, influenza physiopathology, avian classification, mice, mice inbred BALB c, middle aged, molecular sequence data, phenotype, sequence analysis, DNA, viral proteins genetics, virulence.

NAL Call Number: 448.3 Ar23
Abstract: Human-avian influenza reassortants possessing the HA gene of the avian parent virus were tested for their ability to replicate in MDCK cells at 37 degrees C and 31 degrees C. Both avian parent viruses, A/Duck/Ukraine/1/63 (H3N8) and A/Duck/Hoshimin/014/78 (H5N3) induced an efficient multi-cycle infection at 37 degrees C, but replicated poorly at 31 degrees C, whereas the human parent virus, MDCK-adapted variant of A/USSR/90/77 (H1N1) strain, replicated efficiently at both temperatures. The reassortant clone possessing the HA gene of A/Duck/Ukraine/1/63 virus and the other 7 genes of A/USSR/90/77 virus replicated at both temperatures almost as efficiently as the human parent virus. Among the reassortants between A/Duck/Hoshimin/014/78 and A/USSR/90/77, the clones possessing the HA and NA genes of the avian strain, or the HA, NA, NP, and NS genes of the avian strain, and the other genes of the human parent virus, replicated poorly at both temperatures, especially at 31 degrees C, whereas the reassortant possessing the HA, NA, and M genes of the avian virus replicated at both temperatures fairly efficiently. The results are discussed in connection with the limitations imposed by different genes upon avian influenza viruses' ability to replicate in mammalian cells.
Descriptors: genes viral, hemagglutinins viral physiology, influenza A virus avian pathogenicity, human

**Abstract:** In order to assess the degree of immune cross-protection among avian H2 influenza virus strains, mice were immunised with beta-propiolactone-inactivated virus preparations and infected intranasally with mouse-adapted variant of A/Black Duck/New Jersey/1580/78 (H2N3) strain. The experiments with 11 avian H2 strains revealed that both Eurasian and American H2 avian influenza viruses exhibit either high or moderate degree of cross-protection. The grouping of the strains in accordance with their cross-protection efficiency does not coincide with H2 phylogenetic branches. Several reassortant clones were obtained with the use of A/Pintail Duck/Primorie/695/76 (H2N3) strain and high-yield X-67 reassortant as parent viruses, among them a high-yield H2N3 reassortant. Taking into account the data on cross-protection among avian H2 strains, the high-yield H2N3 reassortant may be regarded as a prototype strain to be used for the preparation of killed vaccines in the case of a new appearance of avian H2 haemagglutinin in circulation in humans.

**Descriptors:** influenza prevention and control, influenza A virus avian genetics, avian immunology, influenza vaccine immunology, reassortant viruses immunology, chick embryo, cross reactions, immunization, influenza immunology, avian pathogenicity, mice, reassortant viruses genetics, vaccines, attenuated immunology.


**Abstract:** Molecular and genetic data are summarized on the origin of influenza A virus pandemic variants. Conceptual modifications of the reassortment theory of the origin of pandemic strains are discussed in connection with the appearance of new H5 and H9 avian influenza viruses, which caused the respiratory infection in man and which are presently in the focus of attention as possible agents of future pandemic.

**Descriptors:** epidemiology, infection, respiratory system, veterinary medicine, influenza A, respiratory system disease, viral disease, pandemic, strain origins, reassortment theory.


**Descriptors:** chickens microbiology, influenza A virus avian physiology, porcine physiology, influenza A virus physiology, mice microbiology, cloaca microbiology, avian pathogenicity, porcine pathogenicity, influenza A virus pathogenicity, orthomyxoviridae infections microbiology, orthomyxoviridae infections veterinary, poultry diseases microbiology, rodent diseases microbiology, trachea microbiology, virus replication.


**Abstract:** The sites of replication of influenza A viruses in ferrets and pigs were studied. The majority of the swine, equine, and avian influenza A viruses tested were recovered from the intestinal tract of ferrets as well as from the respiratory tract; most of the human influenza viruses studied were recovered only from the respiratory tract. In contrast with ferrets, only Hong Kong/1/68 (H3 N 2) influenza virus was recovered from the intestinal tract of pigs. Despite the large biological variability found in ferrets and in pigs, the results do establish that the majority of influenza viruses have the potential to replicate in the intestinal tissues of some mammals. Additionally, the study suggests that there are differences among the influenza A viruses in tissue
tropism in different mammals. Both viral and host genetic factors determine the tissue tropism of influenza viruses in mammals.

Descriptors: influenza A virus physiology, intestines microbiology, virus replication, ferrets, avian physiology, human physiology, porcine physiology, swine.


NAL Call Number: QR360.J6

Abstract: We determined the origin and evolutionary pathways of the PB1 genes of influenza A viruses responsible for the 1957 and 1968 human pandemics and obtained information on the variable or conserved region of the PB1 protein. The evolutionary tree constructed from nucleotide sequences suggested the following: (i) the PB1 gene of the 1957 human pandemic strain, A/Singapore/1/57 (H2N2), was probably introduced from avian species and was maintained in humans until 1968; (ii) in the 1968 pandemic strain, A/NT/60/68 (H3N2), the PB1 gene was not derived from the previously circulating virus in humans but probably from another avian virus; and (iii) a current human H3N2 virus inherited the PB1 gene from an A/NT/60/68-like virus. Nucleotide sequence analysis also showed that the avian PB1 gene was introduced into pigs. Hence, transmission of the PB1 gene from avian to mammalian species is a relatively frequent event. Comparative analysis of deduced amino acid sequences disclosed highly conserved regions in PB1 proteins, which may be key structures required for PB1 activities.

Descriptors: evolution, genes, structural, viral, influenza transmission, influenza A virus avian genetics, human genetics, viral proteins genetics, amino acid sequence, cloning, molecular, influenza epidemiology, porcine genetics, molecular sequence data, sequence homology, nucleic acid, species specificity, swine.


NAL Call Number: RC111.R4

Abstract: Widespread outbreaks of avian influenza in domestic fowl throughout eastern Asia have reawakened concern that avian influenza viruses may again cross species barriers to infect the human population and thereby initiate a new influenza pandemic. Simultaneous infection of humans (or swine) by avian influenza viruses in the presence of human influenza viruses could theoretically generate novel influenza viruses with pandemic potential as a result of reassortment of genome subunits between avian and mammalian influenza viruses. These hybrid viruses would have the potential to express surface antigens from avian viruses to which the human population has no preexisting immunity. This article reviews current knowledge of the routes of transmission of avian influenza A viruses to humans, places the risk of appearance of a new pandemic influenza virus in perspective, and describes the recently observed epidemiology and clinical syndromes of avian influenza in humans.

Descriptors: influenza A virus, viral diseases, zoonoses, birds, human, avian influenza virus.


NAL Call Number: RA648.5.E46

Abstract: Influenza virus is not known to affect wild felids. We demonstrate that avian influenza A (H5N1) virus caused severe pneumonia in tigers and leopards that fed on infected poultry carcasses. This finding extends the host range of influenza virus and has implications for influenza virus epidemiology and wildlife conservation.

Descriptors: zoo animals virology, influenza veterinary, influenza A virus, avian pathogenicity, Panthera virology, chickens virology, food microbiology, influenza virology, avian genetics, lung virology, meat virology, phylogeny, tigers virology, variation genetics.

Descriptors: cell nucleus microbiology, dactinomycin pharmacology, influenza A virus avian growth and development, ultraviolet rays, virus replication drug effects, virus replication radiation effects, antigens, viral analysis, autoradiography, cell fusion, cell line, cell nucleus immunology, cultured cells cytology, chick embryo, chickens, erythrocytes cytology, fluorescent antibody technique, hamsters, hemagglutinins viral, avian immunology, avian metabolism, kidney, l cells cell line, mice, neuraminidase biosynthesis, nucleoproteins biosynthesis, radiation effects, viral proteins biosynthesis.


Abstract: In February 2003, the highly pathogenic avian influenza-A virus, subtype H7N7, was the causative agent of a large outbreak of fowl plague in the Netherlands. Two days after visiting a poultry farm that was infected by fowl plague, a 57-year-old male veterinarian developed malaise, headache and fever. After 8 days he was admitted to hospital with signs of pneumonia. Five days later, his condition deteriorated alarmingly. Despite extensive pharmacotherapy he died 4 days later of acute pneumonia. Influenza-A virus, subtype H7N7, was identified by means of reverse transcriptase/PCR in broncho-alveolar washings that had been obtained earlier; routine virus culture yielded the isolate A/Nederland/219/03, which differs by 14 amino-acid substitutions from the first isolate in a chicken (A/kip/Nederland/1/03). Partly as a result of this case, the preventive measures were then adjusted; people who came into contact with infected poultry were given increased possibilities for vaccination and the administration of oseltamivir.


Abstract: Ecological studies on influenza viruses revealed that the hemagglutinin genes are introduced into new pandemic strains from viruses circulating in migratory ducks through domestic ducks and pigs in southern China. Experimental infection of pigs with 38 avian influenza virus strains with H1-H13 hemagglutinins showed that at least one strain of each HA subtype replicated in the upper respiratory tract of pigs. Co-infection of pigs with a swine virus and with an avian virus generated reassortant viruses. The results indicate that avian viruses of any subtype can contribute genes in the generation of reassortants. Virological surveillance revealed that influenza viruses in waterfowl reservoir are perpetuated year-by-year in the frozen lake water while ducks are absent.

Descriptors: influenza veterinary, bird diseases transmission, birds, horse diseases transmission, horses, influenza transmission, swine, swine diseases transmission, zoonoses.


ISSN: 0022-1317.

NAL Call Number: QR360.A1J6

Abstract: Pandemic strains of influenza A virus arise by genetic reassortment between avian and human viruses. Pigs have been suggested to generate such reassortants as intermediate hosts. In order for pigs to serve as 'mixing vessels' in genetic reassortment events, they must be susceptible to both human and avian influenza viruses. The ability of avian influenza viruses to replicate in pigs, however, has not been examined comprehensively. In this study, we assessed the growth potential of 42 strains of influenza virus in pigs. Of these, 38 were avian strains, including 27 with non-human-type haemagglutinins (HA; H4 to H13). At least one strain of each HA subtype replicated in the respiratory tract of pigs for 5 to 7 days to a level equivalent to that of swine and human viruses. These results indicate that avian influenza viruses with or without non-human-type HAs can be transmitted to pigs, thus raising the possibility of introduction of their genes into
humans. Sera from pigs infected with avian viruses showed high titres of antibodies in ELISA and neutralization tests, but did not inhibit haemagglutination of homologous viruses, cautioning against the use of haemagglutination-inhibition tests to identify pigs infected with avian influenza viruses. Co-infection of pigs with a swine virus and with an avian virus unable to replicate in this animal generated reassortant viruses, whose polymerase and HA genes were entirely of avian origin, that could be passaged in pigs. This finding indicates that even avian viruses that do not replicate in pigs can contribute genes in the generation of reassortants.

Descriptors: evolution and adaptation, genetics, immune system, infection, microbiology, vector biology, veterinary medicine, ELISA antibody hemagglutination inhibiting antibody mixing vessel neutralizing antibody pandemic strain origin reassortant virus generation swine virus avian virus co infection virus replication.

NAL Call Number: 448.3 AC85
Abstract: Recombinants between H3N2 human influenza viruses (A/Victoria/3/75 and A/Bangkok/1/79, low-yielding parents in chick embryos) and fowl plague virus (FPV, a high-yielding parent in chick embryos) have been obtained. The high reproductive capacity of recombinants in chick embryos has been shown to be due to the gene coding for M proteins.
Descriptors: genes viral, influenza A virus avian genetics, human genetics, recombination, genetic, viral proteins genetics, virus replication, chick embryo, avian physiology, human physiology, viral matrix proteins.

NAL Call Number: 448.3 Ar23
Abstract: During October of 1984 an influenza epidemic occurred on mink farms in the coastal region of South Sweden. Six strains of an influenza A virus were isolated. All six isolates were of the H 10 subtype in combination with N4. The H 10 subtype in combination with various N subtypes was hitherto only known to occur in avian strains, the prototype being the A/chicken/Germany/N/49 (H 10N7) virus.
Descriptors: disease outbreaks veterinary, influenza veterinary, influenza A virus avian pathogenicity, mink, influenza epidemiology.

NAL Call Number: QR360.J6
Abstract: In Hong Kong in 1997, a highly lethal H5N1 avian influenza virus was apparently transmitted directly from chickens to humans with no intermediate mammalian host and caused 18 confirmed infections and six deaths. Strategies must be developed to deal with this virus if it should reappear, and prospective vaccines must be developed to anticipate a future pandemic. We have determined that unadapted H5N1 viruses are pathogenic in mice, which provides a well-defined mammalian system for immunological studies of lethal avian influenza virus infection. We report that a DNA vaccine encoding hemagglutinin from the index human influenza isolate A/HK/156/97 provides immunity against H5N1 infection of mice. This immunity was induced against both the homologous A/HK/156/97 (H5N1) virus, which has no glycosylation site at residue 154, and chicken isolate A/Ck/HK/258/97 (H5N1), which does have a glycosylation site at residue 154. The mouse model system should allow rapid evaluation of the vaccine's protective efficacy in a mammalian host. In our previous study using an avian model, DNA encoding hemagglutinin conferred protection against challenge with antigenic variants that differed from the primary antigen by 11 to 13% in the HA1 region. However, in our current study we found that a DNA vaccine encoding the hemagglutinin from A/Ty/Ir/1/83 (H5N8), which differs from A/HK/156/97 (H5N1) by 12% in HA1, prevented death but not H5N1 infection in mice. Therefore, a DNA vaccine made with a heterologous H5 strain did not prevent infection by H5N1 avian influenza viruses in mice but was useful in preventing death.
Descriptors: hemagglutinin glycoproteins, influenza virus immunology, influenza prevention and control, influenza A virus avian immunology, influenza vaccine immunology, vaccines, DNA immunology, antibodies,

NAL Call Number: QR189.V32

Abstract: The cross-species transfer of a H5N1 influenza virus from birds to humans, and the systemic spread of this virus in mice, has accelerated the efforts to devise protective strategies against lethal influenza viruses. DNA vaccination with the highly conserved nucleoprotein gene appears to provide cross protection against influenza A viruses in murine models. Whether such vaccines would protect human hosts against different influenza A viruses, including strains with pandemic potential, is unclear. Our aim in this study is to evaluate the ability of a combination DNA vaccine consisting of two plasmids encoding the HA genes from two different subtypes and a DNA vaccine encoding the viral nucleoprotein gene from a H5 virus to induce protection against highly lethal infection caused by H5 and H7 influenza viruses in chickens. Chickens given a single dose of plasmids expressing H5 and H7 hemagglutinins protected the birds from infection by either subtype. However, birds immunized with nucleoprotein DNA and challenged with either A/Ck/Vic/1/85(H7N7) or A/Ty/Ir/1/83 (H5N8) showed definite signs of infection, suggesting inadequate immunity against viral infection. Fifty percent of the nucleoprotein DNA immunized birds survived infection by influenza A/Ty/Ir/1/83 (H5N8) virus (virus of same subtype) while 42% survived infection by influenza A/Ck/Vic/1/85/(H7N7) virus (virus of a different subtype). These studies demonstrate that immunization with DNA encoding a type-specific gene may not be effective against either homologous or heterologous strains of virus, particularly if the challenge virus causes a highly lethal infection. However, the combination of HA subtype vaccines are effective against lethal infection caused by viruses expressing any of the HA subtypes used in the combination preparation.

Descriptors: chickens immunology, hemagglutinin glycoproteins, influenza virus immunology, influenza veterinary, influenza A virus avian immunology, influenza vaccine immunology, nucleoproteins, poultry diseases prevention and control, vaccination veterinary, vaccines, DNA immunology, viral core proteins immunology, cos cells, Cerco pithecus aethiops, evaluation studies, hemagglutinin glycoproteins, influenza virus genetics, influenza immunology, influenza prevention and control, influenza transmission, avian genetics, mice, plasmids immunology, poultry diseases immunology, recombinant fusion proteins immunology, species specificity, transfection, viral core proteins genetics, zoonoses.


NAL Call Number: 448.8 L22

Abstract: BACKGROUND: An outbreak of highly pathogenic avian influenza A virus subtype H7N7 started at the end of February, 2003, in commercial poultry farms in the Netherlands. Although the risk of transmission of these viruses to humans was initially thought to be low, an outbreak investigation was launched to assess the extent of transmission of influenza A virus subtype H7N7 from chickens to humans. METHODS: All workers in poultry farms, poultry farmers, and their families were asked to report signs of conjunctivitis or influenza-like illness. People with complaints were tested for influenza virus type A subtype H7 (A/H7) infection and completed a health questionnaire about type of symptoms, duration of illness, and possible exposures to infected poultry. FINDINGS: 453 people had health complaints--349 reported conjunctivitis, 90 had influenza-like illness, and 67 had other complaints. We detected A/H7 in conjunctival samples from 78 (26.4%) people with conjunctivitis only, in five (9.4%) with influenza-like illness and conjunctivitis, in two (5.4%) with influenza-like illness only, and in four (6%) who reported other symptoms. Most positive samples had been collected within 5 days of symptom onset. A/H7 infection was confirmed in three contacts (of 83 tested), one of whom developed influenza-like illness. Six people had influenza A/H3N2 infection. After 19 people had been diagnosed with the infection, all workers received mandatory influenza virus vaccination and prophylactic treatment with oseltamivir. More than half (56%) of A/H7 infections reported here arose before the vaccination and treatment programme. INTERPRETATION: We noted an unexpectedly high number of transmissions of avian influenza A virus subtype H7N7 to people directly involved in handling infected poultry, and we noted evidence for person-to-person transmission. Our data
emphasise the importance of adequate surveillance, outbreak preparedness, and pandemic planning.

Descriptors: avian influenza A virus, transmission, humans, outbreak, poultry farms, sub type H7N7.


NAL Call Number: 448.8 P942

Abstract: Immunological analysis has shown hemagglutinins of avian viruses like hemagglutinins of human viruses to have a complex antigenic composition. Three antigenic determinants were discovered in hemagglutinin of A/Chicken/12/71 virus previously designated H3 and in hemagglutinin of A/Tern/18/73 virus previously designated Hav7. The H3 determinant and the second determinant are identical in avian and A/Hong Kong/1/68 human viruses. In addition, hemagglutinins of avian viruses have a determinant specific for each virus which is lacking in human influenza virus hemagglutinin.

Descriptors: antigens, viral isolation and purification, birds microbiology, hemagglutinins viral isolation and purification, influenza A virus avian immunology, human immunology, adsorption, chick embryo, complement fixation tests, epitopes, hemagglutination inhibition tests.


NAL Call Number: 448.8 P942

Abstract: Human and avian influenza A strains with a known amino acid sequence of NP protein were studied in radioimmunoprecipitation test with a panel of anti-NP monoclonal antibodies. Two of 7 MAbs (315 and IVE8) reacted with variable epitopes. One of the epitopes was present only in human strains, while the other in both human and avian strains, but absent in gull strains and in one human strain, A/Puerto Rico/8/34 (H1N1). The variations recognized by antibodies 315 and IVE8 correlated with amino acid substitutes in positions 16 and 353, respectively.

Descriptors: biochemistry and molecular biophysics, infection, amino acid substitution molecular variability.


Abstract: Throughout Eastern Asia, there is currently an epidemic of fowl plague or highly pathogenic avian influenza, on an unprecedented scale. The prospects for rapid containment are poor. The causative virus, influenza A of the H5N1 subtype, is of limited infectivity for humans. If infection occurs, however, then the consequences are serious and even fatal in a majority of cases. In view of the receptor specificity of avian influenza viruses, this may be related to individually increased susceptibility, which does not lead to further spread. However, it is known that influenza A viruses can readily adapt to replication in the human host by the acquisition of specific gene segments or even by mutations of the avian virus. The extreme scale of human contact with influenza virus of the H5N1 subtype at present engenders fear that there is a high risk of such adaptation and a subsequent pandemic spread. Adequate precautions are necessary, not only in terms of an acceleration of vaccine production but primarily in arranging for sufficient availability of the new antiviral drugs.

Descriptors: disease outbreaks, influenza A virus, avian pathogenicity, human pathogenicity, avian influenza transmission, zoonoses, chickens, avian genetics, human genetics.


Abstract: Avian influenza virus was not known to cause systemic infection in humans before. We report a 3-year-old boy with good past health who developed pneumonia caused by H5N1 avian influenza A virus (A/Hong Kong/156/97). The virus was isolated from a tracheal aspirate. There were complications of Reye's syndrome, adult respiratory distress syndrome, and multiple organ system failure. He had a history of receiving aspirin. His adult respiratory distress syndrome did not respond to endotracheal surfactant
replacement therapy. He died 6 days after admission. Clinicians should be alert to the importance of a new human influenza strain.

**Descriptors:** infection, pediatrics, pulmonary medicine, adult respiratory distress syndrome, respiratory system disease, pneumonia, respiratory system disease, H5N1 avian influenza infection, first case, respiratory system disease, viral disease, Reye's syndrome, digestive system disease, nervous system disease, endotracheal surfactant replacement therapy therapeutic method, case study.


**NAL Call Number:** 448.8 P942

**Abstract:** The results of the studies on fowl plague virus (FPV, Rostok strain) reproduction in Aedes aegypti mosquitoes are presented. The virus-containing allantoic fluid was inoculated intrathoracally in volumes of 0.1 and 0.2 microliter. The virus was isolated in chick embryos and could be detected at 5–14 days after inoculation. After inoculation of 0.1 microliter of virus it could be detected in doses of 0.5, 2.0, 1.75 Ig2 ID50, after inoculation of 0.2 microliter–in doses of 5, 1.5, and 0.5 Ig2 ID50.

**Descriptors:** Aedes microbiology, influenza A avian physiology, time factors, virus replication.


**NAL Call Number:** 448.8 L22

**Descriptors:** viroses, women, conjunctivitis, mankind, zoonoses, avian influenza virus, eye diseases, infectious diseases, influenza virus, mankind, organic diseases, orthomyxoviridae, viruses, influenza.


**NAL Call Number:** 448.8 P942

**Abstract:** Recombination of a human influenza virus with an avian influenza virus produced a H2Nav2 recombinant with the antigenic properties analogous to those of avian influenza virus (H2Nav2) isolated from wild ducks in the Far East, USSR. Recombination of two avian influenza viruses yielded a recombinant H2N2, an antigenic analogues of influenza A/Singapore/1/57 (H2N2) virus which had started an epidemic of influenza in 1957.

**Descriptors:** antigens, viral genetics, influenza A virus genetics, recombination, genetic, animals, wild, crosses, genetic, ducks microbiology, hemagglutination inhibition tests, influenza A virus human genetics, neuraminidase antagonists and inhibitors.


**NAL Call Number:** 448.8 P942

**Abstract:** Influenza virus A (H5N1) was isolated from the tracheal swab of a 3-year-old boy who died from influenza with the Raye syndrome in Hong Kong in May, 1997. Up to the present time, influenza viruses with hemagglutinin H5 were known to circulate only among birds. They caused a variety of diseases: from asymptomatic to epizootic with 100% mortality, particularly among chickens. The main difference between virulent and avirulent strains is as follows: virulent viruses are isolated from all tissues of an infected bird. A (H5) virus hemagglutinin, transformed into a virulent variant, becomes sensitive to cleavage by proteases of mammalian and avian cells. Intensive epidemiological surveillance of influenza in Hong Kong started by the WHO and Department of Public Health of Hong Kong in August-September, 1997, resulted in detection of 17 more cases with Influenza A (H5N1) in November-December 1997. all of the occurred before December 28, 1997 and were detected in hospitals and health centers of Hong Kong. Nine patients were children aged under 5 years. Six patients died as a result of complications (pneumonia) and exacerbations of concomitant chronic diseases. Virological and logical studies showed that the main route of infection transmission was
from birds to humans. Human to human transmission is probable. Study of 7 influenza A (H5N1) viruses isolated from patients showed that they contained all 8 RNA gene segments of avian virus. There are no reports about new cases of influenza A (H5N1) in humans in January 1998, and we can hope that the outbreak of Influenza A (H5N1) in Hong Kong caused by avian virus will not develop into a new influenza pandemic, although an unfavorable course of events is probable.

Descriptors: influenza virology, influenza A virus avian pathogenicity, chickens virology, Hong Kong epidemiology, influenza epidemiology, influenza physiopathology, avian genetics, RNA, viral, virulence.


NAL Call Number: 448.3 Ar23

Abstract: Influenza A virus of serotype Hav1 Neq1 (H7N7 by the 1980 revised influenza typing system proposed by WHO experts) was repeatedly isolated from lung and brain tissues taken from harbor seals (Phoca vitulina) found suffering from pneumonia on Cape Cod Peninsula (U.S.A.) in the winter of 1979-1980. The seal isolates, although of a serotype identical to some fowl plaque virus strains, were harmless to chickens and turkeys in transmission experiments. An earlier human infection by a Hav1 Neq1 influenza virus and the serologic relatedness of this avian serotype with the equine 1 serotype are cited in support of the view that influenza viruses with these antigenic characteristics seem to have a facility to pass from birds to mammals.

Descriptors: influenza microbiology, influenza A virus avian isolation and purification, Pinnipedia microbiology, pneumonia, viral microbiology, seals microbiology, antigens, viral immunology, brain microbiology, epitopes, avian immunology, lung microbiology.


NAL Call Number: SF997.5.E95E97

Abstract: Distemper and rabies vaccination are highly recommended because of the almost invariable fatal outcome of these conditions. Vaccination should constitute an important part of a ferret's preventative medicine program. With the current and anticipated development and licensing of new vaccines, practitioners are invited to gain awareness of the latest vaccine information. Establishment of a practice vaccination protocol with regards to the site of administration of rabies and distemper vaccines is paramount to document any future abnormal tissue reactions. Influenza is the most common zoonotic disease that is seen in ferrets. Although it generally is benign in most ferrets, veterinarians must take this condition seriously. The characteristic continuous antigenic variation of this virus may lead to more virulent strains; the recent emergence of avian influenza virus outbreaks; and the increased susceptibility of elderly, young, and immunosuppressed individuals.

Descriptors: ferrets virology, virus diseases veterinary, viruses isolation and purification, virus diseases diagnosis, virus diseases pathology, virus diseases prevention and control, viruses pathogenicity, diagnosis differential, virology.


Abstract: We live in an ever more connected global village linked through international travel, politics, economics, culture and human-human and human-animal interactions. The realization that the concept of globalization includes global exposure to disease-causing agents that were formerly confined to small, remote areas and that infectious disease outbreaks can have political, economic and social roots and effects is becoming more apparent. Novel infectious disease microbes continue to be discovered because they are new or newly recognized, have expanded their geographic range, have been shown to cause a new disease spectrum, have jumped the species barrier from animals to humans, have become resistant to antimicrobial agents, have increased in incidence or have become more virulent. These emerging infectious disease microbes may have the potential for use as agents of bioterrorism. Factors involved in the emergence of infectious diseases are complex and interrelated and involve all classifications of organisms transmitted in a variety of ways. In 2003, outbreaks of interest included severe acute respiratory syndrome, monkeypox and avian influenza. Information from the human genome project applied to microbial organisms and their hosts
will provide new opportunities for detection, diagnosis, treatment, prevention, control and prognosis. New technology related not only to genetics but also to satellite and monitoring systems will play a role in weather, climate and the approach to environmental manipulations that influence factors contributing to infectious disease emergence and control. Approaches to combating emerging infectious diseases include many disciplines, such as animal studies, epidemiology, immunology, ecology, environmental studies, microbiology, pharmacology, other sciences, health, medicine, public health, nursing, cultural, political and social studies, all of which must work together. Appropriate financial support of the public health infrastructure including surveillance, prevention, communication, adherence techniques and the like will be needed to support efforts to address emerging infectious disease threats.

Descriptors: communicable diseases, emerging economics, prevention and control, emerging transmission, climate, demography, disease susceptibility, disease transmission prevention and control, industry, politics, social conditions, economics, technology, travel, weather.


**NAL Call Number:** QR180.M53

**Abstract:** A "new" influenza virus will appear at some time in the future. This virus will arise by natural processes, which we do not fully understand, or it might be created by some bioterrorist. The world's population will have no immunity to the new virus, which will spread like wild-fire, causing much misery, economic disruption and many deaths. Vaccines will take time to develop and the only means of control, at least in the early stages of the epidemic, are anti-viral drugs, of which the neuraminidase inhibitors currently seem the most effective.

Descriptors: disease outbreaks prevention and control, influenza epidemiology, influenza prevention and control, antiviral agents therapeutic use, birds, chickens, China epidemiology, drug resistance, viral, influenza drug therapy, influenza virology, influenza A virus avian classification, avian physiology, models, molecular, neuraminidase physiology, orthomyxoviridae genetics, orthomyxoviridae immunology.


**NAL Call Number:** 470 Sci2

**Descriptors:** chickens virology, influenza epidemiology, influenza prevention and control, influenza A virus enzymology, influenza A virus pathogenicity, antiviral agents therapeutic use, drug industry methods, drug resistance, microbial, enzyme inhibitors therapeutic use, hn protein chemistry, hn protein genetics, hn protein metabolism, Hong Kong epidemiology, influenza diagnosis, influenza drug therapy, influenza A virus avian enzymology, avian genetics, avian immunology, avian pathogenicity, human enzymology, human genetics, human immunology, human pathogenicity, influenza A virus genetics, influenza A virus immunology, influenza vaccine biosynthesis, influenza vaccine economics, influenza vaccine immunology, models, molecular, mutation genetics, neuraminidase antagonists and inhibitors, neuraminidase chemistry, neuraminidase genetics, neuraminidase metabolism, protein conformation, RNA viral analysis, viral genetics, reassortant viruses enzymology, reassortant viruses genetics, reassortant viruses immunology, reassortant viruses pathogenicity, sialic acids therapeutic use.


**NAL Call Number:** 449.9 W892B

**Descriptors:** disease outbreaks prevention and control, influenza epidemiology, influenza A virus, avian pathogenicity, influenza prevention and control, influenza transmission, influenza virology, avian influenza epidemiology, avian influenza transmission, avian influenza virology, sentinel surveillance, world health, zoonoses virology.


**NAL Call Number:** RJ1.P35

**Abstract:** SARS and avian influenza have many common features. They both arose in Asia and originated
from animal viruses. They both have the potential to become pandemics because human beings lack antibodies to the animal-derived antigens present on the viral surface and rapid dissemination can occur from the relative ease and availability of high speed and far-reaching transportation methods. Pediatricians, in particular, should remain alert about the possibility of pandemic illnesses in their patients. Annual rates of influenza in children may be 1.5 to 3 times those in the adult population, and infection rates during a community epidemic may exceed 40% in preschool-aged children and 30% in school-aged children. Infected children also play a central role in disseminating influenza, as they are the major point of entry for the virus into the household, from which adults spread disease into the community. Of course, children younger than 24 months also are at high risk for complications from influenza. A 1999 Centers for Disease Control and Prevention projection of an influenza pandemic in the US paints a grim picture: 89,000 to 207,000 deaths, 314,000 to 734,000 hospitalizations, 18 million to 42 million outpatient visits, and 20 million to 47 million additional illnesses, at a cost to society of at least dollars 71.3 billion to dollars 166.5 billion. High-risk patients (15% of the population) would account for approximately 84% of all deaths. Although SARS has been kind to the pediatric population so far, there are no guarantees that future outbreaks would be as sparing. To aid readers in remaining up-to-date with SARS and avian influenza, some useful websites are listed in the Sidebar. Two masters of suspense, Alfred Hitchcock and Stephen King, may have been closer to the truth than they ever would have believed. Both birds and a super flu could bring about the end of civilization as we know it. But all is not lost—to paraphrase Thomas Jefferson, the price of health is eternal vigilance. Although we may not be able to prevent future pandemics, mankind has the ability to recognize new diseases and outbreaks as they occur, to study these infections and find ways to contain and treat them, and to implement the necessary measures to defeat them.

Descriptors: avian influenza prevention and control, severe acute respiratory syndrome prevention and control, adult, child, antiviral agents therapeutic use, disease outbreaks prevention and control, disease vectors, avian influenza diagnosis, avian influenza epidemiology, avian influenza transmission, pediatrics methods, population surveillance methods, severe acute respiratory syndrome diagnosis, severe acute respiratory syndrome epidemiology, severe acute respiratory syndrome transmission, world health, SARS.


NAL Call Number: RM265.A5132

Abstract: In 1997, an avian H5N1 influenza virus, A/Hong Kong/156/97 (A/HK/156/97), caused six deaths in Hong Kong, and in 1999, an avian H9N2 influenza virus infected two children in Hong Kong. These viruses and a third avian virus [A/Teal/HK/W312/97 (H6N1)] have six highly related genes encoding internal proteins. Additionally, A/Chicken/HK/G9/97 (H9N2) virus has PB1 and PB2 genes that are highly related to those of A/HK/156/97 (H5N1), A/Teal/HK/W312/97 (H6N1), and A/Quail/HK/G1/97 (H9N2) viruses. Because of their similarities with the H5N1 virus, these H6N1 and H9N2 viruses may have the potential for interspecies transmission. We demonstrate that these H6N1 and H9N2 viruses are pathogenic in mice but that their pathogenicities are less than that of A/HK/156/97 (H5N1). Unadapted virus replicated in lungs, but only A/HK/156/97 (H5N1) was found in the brain. After three passages (P3) in mouse lungs, the pathogenicity of the viruses increased, with both A/Teal/HK/W312/97 (H6N1) (P3) and A/Quail/HK/G1/97 (H9N2) (P3) viruses being found in the brain. The neuraminidase inhibitor Zanamivir inhibited viral replication in Madin-Darby canine kidney cells in virus yield assays (50% effective concentration, 8.5 to 14.0 microM) and inhibited viral neuraminidase activity (50% inhibitory concentration, 5 to 10 nM). Twice daily intranasal administration of Zanamivir (50 and 100 mg/kg of body weight) completely protected infected mice from death. At a dose of 10 mg/kg, Zanamivir completely protected mice from infection with H9N2 viruses and increased the mean survival day and the number of survivors infected with H6N1 and H5N1 viruses. Zanamivir, at all doses tested, significantly reduced the virus titers in the lungs and completely blocked the spread of virus to the brain. Thus, Zanamivir is efficacious in treating avian influenza viruses that can be transmitted to mammals.

Descriptors: antiviral agents therapeutic use, enzyme inhibitors therapeutic use, influenza drug therapy, influenza A virus avian drug effects, neuraminidase antagonists and inhibitors, sialic acids therapeutic use, administration, intranasal, antiviral agents administration and dosage, antiviral agents pharmacology, brain virology, cell line, dogs, enzyme inhibitors administration and dosage, enzyme inhibitors pharmacology,
genes viral, influenza virology, avian genetics, avian pathogenicity, kinetics, lung virology, mice, mice inbred BALB c, microbial sensitivity tests, sialic acids administration and dosage, sialic acids pharmacology, species specificity, virus replication drug effects.


NAL Call Number: QR355.A5

Abstract: In 1997, an H5N1 avian influenza A/Hong Kong/156/97 virus transmitted directly to humans and killed six of the 18 people infected. In 1999, another avian A/Hong Kong/1074/99 (H9N2) virus caused influenza in two children. In such cases in which vaccines are unavailable, antiviral drugs are crucial for prophylaxis and therapy. Here we demonstrate the efficacy of the neuraminidase inhibitor GS4104 (oseltamivir phosphate) against these H5N1 and H9N2 viruses. GS4071 (the active metabolite of oseltamivir) inhibited viral replication in MDCK cells (EC(50) values, 7.5-12 microM) and neuraminidase activity (IC(50) values, 7.0-15 nM). When orally administered at doses of 1 and 10 mg/kg per day, GS4104 prevented death of mice infected with A/Hong Kong/156/97 (H5N1), mouse-adapted A/Quail/Hong Kong/G1/97 (H9N2), or human A/Hong Kong/1074/99 (H9N2) viruses and reduced virus titers in the lungs and prevented the spread of virus to the brain of mice infected with A/Hong Kong/156/97 (H5N1) and mouse-adapted A/Quail/Hong Kong/G1/97 (H9N2) viruses. When therapy was delayed until 36 h after exposure to the H5N1 virus, GS4104 was still effective and significantly increased the number of survivors as compared with control. Oral administration of GS4104 (0.1 mg/kg per day) in combination with rimantadine (1 mg/kg per day) reduced the number of deaths of mice infected with 100 MLD(50) of H9N2 virus and prevented the deaths of mice infected with 5 MLD(50) of virus. Thus, GS4104 is efficacious in treating infections caused by H5N1 and H9N2 influenza viruses in mice.

Descriptors: acetamides pharmacology, antiviral agents pharmacology, influenza drug therapy, influenza A virus avian drug effects, human drug effects, neuraminidase antagonists and inhibitors, acetamides therapeutic use, antiviral agents therapeutic use, brain virology, cell line, dogs, enzyme inhibitors pharmacology, enzyme inhibitors therapeutic use, influenza virology, avian enzymology, avian pathogenicity, human enzymology, human pathogenicity, kidney, lung virology, mice, mice inbred BALB c, neuraminidase metabolism, rimantadine therapeutic use, virus replication drug effects.


Descriptors: disease control, mutations, virulence, avian influenza virus, ducks, Europe.


NAL Call Number: QR180.3.D4

Abstract: An influenza pandemic could arise unexpectedly with rapid spread across the world. The efficiency of production of a vaccine and the ability to administer it widely will be among the most important factors in the ability to protect public health. The current process for producing inactivated or live attenuated influenza vaccines requires six to nine months. That reduces considerably the likelihood that the vaccine will be available during the first wave of the pandemic. Therefore, a key element of preparedness is to optimize the production process and to reduce the vaccine development time. During the 1997 H5N1 outbreak in Hong Kong, seed viruses were prepared for production of inactivated and live-attenuated vaccines. We used the cold-adapted A/Ann Arbor/6/60 as the donor virus to generate live attenuated vaccines containing genetically modified HA and NA genes from H5N1 influenza viruses. These reassortants were shown to be safe and protective in animal models. This study indicates that production of live attenuated avian influenza
vaccines is feasible and that development of a library of reassortants containing different subtype HA and NA genes may reduce the vaccine preparation time for future influenza pandemics.

Descriptors: antigens, viral immunology, influenza prevention and control, influenza A virus avian immunology, influenza epidemiology, influenza vaccine administration and dosage.


NAL Call Number: QR360.J6

Abstract: Influenza virus A/seal/Mass/1/80 (H7N7) was adapted to grow in MDCK cells and chicken embryo cells (CEC) in the absence of exogenous protease. The biological properties of the virus variants obtained coincided with intracellular activation of the hemagglutinin (HA) by posttranslational proteolytic cleavage and depended on the cell type used for adaptation. MDCK cell-adapted variants contained point mutations in regions of the HA more distant from the cleavage site. It is proposed that these mutations are probably responsible, through an unknown mechanism, for enhanced cleavability of HA in MDCK cells. Such virus variants were apathogenic in chickens. CEC-adapted variants, on the other hand, contained an insertion of basic amino acids at the HA cleavage site, in addition to scattered point mutations. The insertions converted the cleavage sites in the variant virus HAs so that they came to resemble the cleavage site found in highly pathogenic avian influenza viruses. CEC variants with such cleavage site modifications were highly pathogenic for chickens. The lethal outcome of the infection in chickens demonstrated for the first time that an influenza virus derived from a mammalian species can be modified during adaptation to a new cell type to such an extent that the resulting virus variant becomes pathogenic for an avian species.

Descriptors: chickens microbiology, hemagglutinins viral metabolism, influenza A virus pathogenicity, pinnipedia microbiology, seals microbiology, amino acid sequence, base sequence, cell line, chick embryo, dogs, electrophoresis, gel, two dimensional, hemagglutinins viral genetics, influenza A virus genetics, molecular sequence data, mutation, peptide hydrolases metabolism, species specificity, virus replication.


NAL Call Number: RA648.5.E46

Abstract: To establish whether human-to-human transmission of influenza A H5N1 occurred in the healthcare setting in Vietnam, we conducted a cross-sectional seroprevalence survey among hospital employees exposed to 4 confirmed and 1 probable H5N1 case-patients or their clinical specimens. Eighty-three (95.4%) of 87 eligible employees completed a questionnaire and provided a serum sample, which was tested for antibodies to influenza A H5N1. Ninety-five percent reported exposure to >1 H5N1 case-patients; 59 (72.0%) reported symptoms, and 2 (2.4%) fulfilled the definition for a possible H5N1 secondary case-patient. No study participants had detectable antibodies to influenza A H5N1. The data suggest that the H5N1 viruses responsible for human cases in Vietnam in January 2004 are not readily transmitted from person to person. However, influenza viruses are genetically variable, and transmissibility is difficult to predict. Therefore, persons providing care for H5N1 patients should continue to take measures to protect themselves.

Descriptors: patient to professional disease transmission, health personnel, influenza transmission, avian influenza A virus growth and development, Western blotting, child, preschool child, adolescent, adult, viral blood antibodies, cross sectional studies, influenza immunology, influenza virology, avian influenza A virus immunology, middle-aged, neutralization tests, questionnaires, seroepidemiologic studies, Vietnam epidemiology.


NAL Call Number: 500 N21P

Abstract: In 1997, 18 cases of influenza in Hong Kong (bird flu) caused by a novel H5N1 (chicken) virus resulted in the deaths of six individuals and once again raised the specter of a potentially devastating
influenza pandemic. Slaughter of the poultry in the live bird markets removed the source of infection and no further human cases of H5N1 infection have occurred. In March 1999, however, a new pandemic threat appeared when influenza A H9N2 viruses infected two children in Hong Kong. These two virus isolates are similar to an H9N2 virus isolated from a quail in Hong Kong in late 1997. Although differing in their surface hemagglutinin and neuraminidase components, a notable feature of these H9N2 viruses is that the six genes encoding the internal components of the virus are similar to those of the 1997 H5N1 human and avian isolates. This common feature emphasizes the apparent propensity of avian viruses with this genetic complement to infect humans and highlights the potential for the emergence of a novel human pathogen.

Descriptors:  bird diseases transmission, influenza transmission, influenza A virus avian genetics, influenza A virus genetics, influenza A virus immunology, quail virology, antigens, viral chemistry, antigens, viral genetics, antigens, viral immunology, binding sites, bird diseases epidemiology, child, preschool, conserved sequence genetics, genes viral genetics, hemagglutinin viral chemistry, hemagglutinin viral genetics, hemagglutinin viral immunology, Hong Kong epidemiology, infant, influenza epidemiology, avian chemistry, avian classification, avian immunology, influenza A virus chemical, influenza A virus classification, molecular sequence data, neuraminidase chemistry, neuraminidase genetics, neuraminidase immunology, phylogeny, species specificity, variation genetics genetics.


NAL Call Number:  448.8 V81

Abstract: Although Southern China has been considered the epicenter of human influenza pandemics, little is known about the genetic composition of influenza viruses in lower mammals or birds in that region. To provide information on the molecular epidemiology of these viruses, we used dot blot hybridization and phylogenetic methods to study the internal genes (PB1, PB2, PA, NP, M, and NS) of 106 avian influenza A viruses isolated from a total of 11,798 domestic ducks, chickens, and geese raised in Southern China including Hong Kong. All 636 genes examined were characteristic of avian influenza viruses; no human or swine influenza genes were detected. Thus, influenza virus reassortants do not appear to be maintained in the domesticated birds of Southeast Asia, eliminating opportunities for further gene reassortment. Phylogenetic analysis showed that the internal genes of these viruses belong to the Eurasian avian lineage, supporting geographical separation of the major avian lineages. The PB1 genes were most similar to A/Singapore/57 (H2N2) and Hong Kong (H3N2) viral genes, supporting an avian origin for the recent human H2N2 and H3N2 pandemic strains. The majority of internal genes from avian influenza viruses in Southern China belong to the Eurasian lineage and are similar to viruses that have recently been transmitted to humans, swine, and horses. This study provides evidence that the transmission of avian influenza viruses and their genes to other species is unidirectional and that the transmission of mammalian influenza virus strains to domestic poultry is probably not a factor in the generation of new pandemic strains.

Descriptors: poultry, China, Hong Kong, avian influenza virus, genes, phylogeny, nucleotide sequence, mankind, epidemiology, Asia, cell structure, chromosomes, domestic animals, domesticated birds, East Asia, evolution, genomes, influenza virus, livestock, nucleus, useful animals, viruses, pandemics, sequence homology, gene flow, comparisons, man.


Descriptors: influenza, avian epidemiology, influenza, avian transmission.


Abstract: Pandemic influenza H2N2 viruses emerged in humans in 1957 and caused widespread morbidity and mortality in humans until 1968 when they were displaced by emerging H3N2 viruses. Although it is known that both the appearance and disappearance of H2N2 viruses involved reassortment between human and avian influenza viruses, genetic characterization of these viruses is limited. In this study, detailed genetic analysis of all eight gene segments of human H2N2 viruses isolated from 1957 until 1968 from
geographically diverse regions was undertaken to establish a better understanding of the evolutionary nature of this virus. In addition, a number of human H3N2 viruses isolated from 1968 until 1972 were examined to investigate genetic events associated with the emergence of pandemic H3N2 viruses in humans. Phylogenetic analysis of all gene segments of human H2N2 viruses consistently demonstrated divergent evolution. Genes of late H2N2 isolates were located in either of two distinct clades (I and II). Analysis of H3N2 viruses of 1968 revealed that all gene segments that were retained from H2N2 viruses were most similar to H2N2 virus genes of clade I. However, genes of both lineages were found to cocirculate among H3N2 isolates of 1969-1971. Furthermore, each gene segment demonstrated unique phylogenetic topologies, indicating multiple reassortment events between late H2N2 and/or H3N2 viruses. The H3N2 viruses of 1972 analyzed here appeared to possess the genome constellation that represents the ancestral virus of contemporary H3N2 viruses. This constellation was first observed among isolates of 1970 and was distinct from that found among the earliest human H3N2 viruses from 1968. This evidence demonstrates that establishment of H3N2 viruses in humans was associated with multiple-reassortment events that contributed to genetic diversity among viruses.

Descriptors: influenza, H2N2, H3N2, evolution, reassortment, hemagglutinin, neuraminidase, nucleoprotein, influenza virus genetics.

NAL Call Number: 448.8 P942

Abstract: Avian influenza A virus with H2 hemagglutinin has been adapted to mice for the first time. Alterations in the hemagglutinin of adapted variants of the virus as a result of adaptation to a new host are described. Hemagglutinin of a highly virulent adapted variant differed from the parental avirulent strain by antigenic structure, electrophoretic mobility, and receptor activity during interactions with murine red cells.
Descriptors: laboratory animals, avian influenza virus, pathotypes, host pathogen relations, adaptation, agglutinins, immunological factors, biological properties, chemophysical properties, experimental infection, in vivo experimentation, mice, biotypes, disease transmission, experimentation, infection, influenza virus, mammals, orthomyxoviridae, pathogenesis, pathology, proteins, Rodentia, useful animals, viruses.

NAL Call Number: 448.3 AC85

Abstract: The alterations of avian influenza A virus haemagglutinin (HA) H2 as a result of adaptation to mice were first investigated in this study. HA of mouse-adapted (MA) variant was somewhat different from that of the original strain in electrophoretical mobility, antigenic structure and in haemagglutination activity with mouse red blood cells.
Descriptors: hemagglutinins viral immunology, influenza A virus avian immunology, adaptation, physiological, cell line, chick embryo, dogs, electrophoresis, polyacrylamide gel, erythrocytes immunology, fowl plague immunology, fowl plague virology, hemagglutination tests, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral chemistry, mice.

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NAL Call Number: 448.3 AC85

Abstract: Human (H1) and avian (H2) influenza A viruses and their mouse-adapted (MA) variants were studied in radioimmunoprecipitation assay (RIPA) and infectivity neutralization test using a monoclonal antibody (MoAb) directed against a conserved antigenic epitope in the stem region of the haemagglutinin (HA) and reacting both with H1 and H2 subtypes of HA. Whereas the MA variant of avian influenza A virus

Descriptors: influenza, H2N2, H3N2, evolution, reassortment, hemagglutinin, neuraminidase, nucleoprotein, influenza virus genetics.
differed from the original strain in RIPA and neutralization tests, no differences were observed between the original human strain and its MA variant, as well as between the original H1 and H2 strains.

Descriptors: antibodies, viral immunology, antigens, viral immunology, epitopes, b lymphocyte immunology, hemagglutinin glycoproteins, influenza virus immunology, influenza A virus avian immunology, human immunology, adaptation, physiological, antibodies, monoclonal immunology, cell line, chick embryo, cross reactions, dogs, glycosylation, mice, neutralization tests, protein conformation, variation genetics.


NAL Call Number: 41.8 R25
Descriptors: DNA hybridization, influenza, paramyxoviruses, disease transmission, reviews, turkeys, wild birds, ducks, pigs, horses, review, Israel, ecological study.


NAL Call Number: R97.I87
Descriptors: avian influenza virus, transfer, turkeys, birds, ducks, Israel.


NAL Call Number: 448.3 AC85
Abstract: By recombination of ts mutants of fowl plague virus belonging to different complementation groups with two cold-adapted variants of human influenza virus, the number and gene localization of ts mutations occurring in these variants was determined. In the course of passaging of human influenza virus at lowered temperature, the number of genes with ts mutations increased.
Descriptors: genes viral, influenza A virus avian genetics, human genetics, cold, genetic complementation test, mutation, recombination, genetic.


NAL Call Number: QH434.V57
Abstract: H2 influenza virus caused a pandemic in 1957 and has the possibility to cause outbreaks in the future. To assess the evolutionary characteristics of H2 influenza viruses isolated from migratory ducks that congregate in Hokkaido, Japan, on their flyway of migration from Siberia in 2001, we investigated the phylogenetic relationships among these viruses and avian and human viruses described previously. Phylogenetic analysis showed that the PB2 gene of Dk/Hokkaido/107/01 (H2N3) and the PA gene of Dk/Hokkaido/95/01 (H2N2) belonged to the American lineage of avian virus and that the other genes of the isolates belonged to the Eurasian lineage. These results indicate that the internal protein genes might be transmitted from American to Eurasian avian host. Thus, it is further confirmed that interregional transmission of influenza viruses occurred between the North American and Eurasian birds. The fact that reassortants could be generated in the migratory ducks between North American and Eurasian avian virus lineage further stresses the importance of global surveillance among the migratory ducks.
Descriptors: ducks virology, emigration and immigration, influenza A virus, avian genetics, influenza, avian virology, viral proteins genetics, Asia, Europe, avian influenza A virus classification, molecular sequence data, North America, phylogeny, sequence analysis, DNA.


NAL Call Number: 41.8 Av5
Abstract: There is increasing evidence that stable lineages of influenza viruses are being established in chickens. H9N2 viruses are established in chickens in Eurasia, and there are increasing reports of H3N2,
H6N1, and H6N2 influenza viruses in chickens both in Asia and North America. Surveillance in a live poultry market in Nanchang, South Central China, reveals that influenza viruses were isolated from 1% of fecal samples taken from healthy poultry over the course of 16 months. The highest isolation rates were from chickens (1.3%) and ducks (1.2%), followed by quail (0.8%), then pigeon (0.5%). H3N6, H9N2, H2N9, and H4N6 viruses were isolated from multiple samples, while single isolates of H1N1, H3N2, and H3N3 viruses were made. Representatives of each virus subtype were experimentally inoculated into both quail and chickens. All the viruses replicated in the trachea of quail, but efficient replication in chickens was confined to 25% of the tested isolates. In quail, these viruses were shed primarily by the aerosol route, raising the possibility that quail may be the "route modulator" that changes the route of transmission of influenza viruses from fecal-oral to aerosol transmission. Thus, quail may play an important role in the natural history of influenza viruses. The pros and cons of the use of inactivated and recombinant fowl pox-influenza vaccines to control the spread of avian influenza are also evaluated.

Descriptors: epidemiology, infection, live poultry market, transmission route, aerosol, fecal, oral, viral, natural history.


Abstract: Avian influenza A viruses are the ancestral origin of all human influenza viruses. The outbreak of highly pathogenic (HP) avian H5N1 in Hong Kong in 1997 highlighted the potential of these viruses to infect and cause severe disease in humans. Since 1999, HP H5N1 viruses were isolated several times from domestic poultry in Asia. In 2001, a HP H5N1 virus, A/Duck/Anyang/AVL-1/2001 (Dk/Anyang), was isolated from imported frozen duck meat in Korea. Because of this novel source of HP H5N1 virus isolation, concerns were raised about the potential for human exposure and infection; we therefore compared the Dk/Anyang virus with HP H5N1 viruses isolated from humans in 1997 in terms of antigenicity and pathogenicity for mammals. At high doses, Dk/Anyang virus caused up to 50% mortality in BALB/c mice, was isolated from the brains and lymphoid organs of mice, and caused lymphopenia. Overall Dk/Anyang virus was substantially less pathogenic for mice than the H5N1 virus isolated from a fatal human case in 1997. Likewise, Dk/Anyang virus was apathogenic for ferrets. Dk/Anyang virus was antigenically distinguishable by hemagglutination-inhibition (HI) assay from human H5N1 viruses isolated in 1997 and avian H5N1 viruses isolated in 2001 in Hong Kong. Nevertheless, prior infection with Dk/Anyang virus protected mice from death after secondary infection with HP human H5N1 viruses. These results indicate that compared with HP human H5N1 viruses, Dk/Anyang virus is substantially less pathogenic for mammalian species. Nevertheless, the novel source of isolation of this avian H5N1 virus must be considered when evaluating the potential risk to public health.

Descriptors: infection, avian influenza, viral disease, duck meat, meat product.


NAL Call Number: QR360.J6

Abstract: During 1997 in Hong Kong, 18 human cases of respiratory illness, including 6 fatalities, were caused by highly pathogenic avian influenza A (H5N1) viruses. Since H5 viruses had previously been isolated only from avian species, the outbreak raised questions about the ability of these viruses to cause severe disease and death in humans. To better understand the pathogenesis and immunity to these viruses, we have used the BALB/c mouse model. Four H5N1 viruses replicated equally well in the lungs of mice without prior adaptation but differed in lethality for mice. H5N1 viruses that were highly lethal for mice were detected in multiple organs, including the brain. This is the first demonstration of an influenza A virus that replicates systemically in a mammalian species and is neurotropic without prior adaptation. The mouse model was also used to evaluate a strategy of vaccination against the highly pathogenic avian H5N1 viruses, using an inactivated vaccine prepared from nonpathogenic A/Duck/Singapore-Q/F119-3/97 (H5N3) virus that was antigenically related to the human H5N1 viruses. Mice administered vaccine intramuscularly, with or without alum, were completely protected from lethal challenge with H5N1 virus. Protection from infection was also observed in 70% of animals administered vaccine alone and 100% of mice administered vaccine with
The protective effect of vaccination correlated with the level of virus-specific serum antibody. These results suggest a strategy of vaccine preparedness for rapid intervention in future influenza pandemics that uses antigenically related nonpathogenic viruses as vaccine candidates.

Descriptors: influenza prevention and control, influenza virology, influenza A virus avian immunology, avian pathogenicity, human immunology, human pathogenicity, cell line, disease models, animal, disease outbreaks, dogs, influenza epidemiology, influenza immunology, avian growth and development, avian isolation and purification, influenza vaccine immunology, mice, inbred BALB c, vaccines, inactivated immunology.


NAL Call Number: 41.8 Av5

Abstract: The outbreak of avian influenza H5N1 in Hong Kong in 1997 raised concerns about the potential for the H5 subtype to cause a human pandemic. In 2001 a new H5N1 virus, A/Duck Meat/Anyang/AVL-1/2001 (A/Dkmt), was isolated from imported duck meat in Korea. The pathogenesis of this virus was investigated in mice. A/Dkmt virus had low infectivity but was lethal for mice at high doses, and at lethal doses, the virus replicated in the brains of infected mice. A/Dkmt virus cross-reacted poorly with ferret antisera raised against human H5N1 viruses, but prior infection with A/Dkmt virus protected mice from death after secondary infection with human H5N1 virus.

Descriptors: infection, avian influenza, infectious disease, respiratory system disease, viral disease, disease pathogenesis duck meat, contamination, poultry product, influenza pandemic, viral immunity.


NAL Call Number: 448.8 V81

Abstract: The most recent introduction of an avian influenza A virus without reassortment into mammals occurred in 1979 when H1N1 strains could be isolated from diseased pigs in northern Europe. This newly introduced avian virus formed a stable lineage in pigs and, in the meantime, spread all over Europe. In 1991 highly pathogenic H1N1 strains closely related to a contemporary swine virus were isolated from turkeys of a breeding farm near Bremen, Germany. Outbreaks in several farms in Germany, France, and the Netherlands indicate that the "avian-like" swine viruses can easily be reintroduced into an avian population causing severe economical losses.

Descriptors: swine, Germany, Netherlands, France, turkeys, swine influenza virus, avian influenza virus, animal viruses, proteins, genes, nucleotide sequence, artiodactyla, birds, cell structure, chromosomes, domestic animals, Europe, Galliformes, genomes, influenza virus, livestock, mammals, Mediterranean countries, nucleus, suidae, useful animals, viruses, western Europe, spread, amino acid sequences, comparisons.


NAL Call Number: 448.8 V81

Abstract: According to phylogenetic data, about 100 years ago an avian influenza virus passed the species barrier (possibly first) to pigs and (possibly from there) to humane. In 1979 an avian influenza A virus (as a whole, without reassortment) again entered the pig population in northern Europe, forming a stable lineage. Here it is shown that the early North European swine viruses exhibit higher than normal evolutionary rates and are highly variable with respect to plaque morphology and neutralizability by monoclonal antibodies. Our results are consistent with the idea that, in order to pass the species barrier, an influenza A virus needs a mutator mutation to provide an additional number of variants, from which the new host might select the best fitting ones. A mutator mutation could be of advantage under such stress conditions and might enable a virus to pass the species barrier as a whole even twice, as it seems to have happened about 100 years ago. This stressful situation should be over for the recent swine lineage, since the viruses seem to be adapted already to the new host in that the most recent isolates—at least in northern Germany—are genetically stable and seem to have lost the putative mutator mutation again.

NAL Call Number: QH431.A1G4
Abstract: Patterns of molecular evolution of the influenza virus proteins and genes are discussed. The subsets of all viral genes corresponding to statistically significant clusters on dendrogram were shown to fall into two distinct groups. The first group was characterized by the presence of an exact linear relationship between the year of the strain isolation and the evolutionary distance. The subsets of human influenza virus genes belong to this group. A method for eliminating the "frozen" strains from the subsets and for calculating the evolutionary rates without construction of phylogenetic trees has been elaborated. The substitution rates calculated according to this technique agreed with the data obtained previously. A linear relationship was not observed in the second group. This group was predominantly composed of avian influenza virus genes. The lack of linear correlation pointed to the cocirculation of a large amount of different influenza virus genomic segments in the avian population. An approach for an examination of the role of intragenic recombination in the development of the antigenic subtypes of hemagglutinin is suggested. Our results suggest that recombination did not play a considerable role in this process, and that all modern subtypes of this protein were probably formed before the introduction of the influenza viruses into the human population. These findings are consistent with the hypothesis that influenza viruses penetrated into human population from their pools in avian populations.
Descriptors: evolution and adaptation, genetics, influenza virus, human, avian.

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Descriptors: birds genetics, evolution, molecular, genes viral, influenza A virus avian genetics, human genetics, viral proteins genetics.

NAL Call Number: 448.8 V81
Abstract: Quail have emerged as a potential intermediate host in the spread of avian influenza A viruses in poultry in Hong Kong. To better understand this possible role, we tested the replication and transmission in quail of influenza A viruses of all 15 HA subtypes. Quail supported the replication of at least 14 subtypes.
Influenza A viruses replicated predominantly in the respiratory tract. Transmission experiments suggested that perpetuation of avian influenza viruses in quail requires adaptation. Swine influenza viruses were isolated from the respiratory tract of quail at low levels. There was no evidence of human influenza A or B virus replication. Interestingly, a human-avian recombinant containing the surface glycoprotein genes of a quail virus and the internal genes of a human virus replicated and transmitted readily in quail; therefore, quail could function as amplifiers of influenza virus reassortants that have the potential to infect humans and/or other mammalian species.

Descriptors: infection, molecular genetics, respiratory system, adaptation.


NAL Call Number: 41.8 C162

Descriptors: Carnivora, influenza veterinary, monkey diseases microbiology, nose microbiology, orthomyxoviridae pathogenicity, respiratory tract infections microbiology, antigen antibody reactions, birds, cross reactions, haplorhini, hemagglutination inhibition tests, horses, immune sera, influenza immunology, orthomyxoviridae isolation and purification, respiratory tract infections immunology, turkeys, virus replication.


NAL Call Number: QR360.J6

Abstract: In 1997 and 1998, H9N2 influenza A viruses were isolated from the respiratory organs of Indian ring-necked parakeets (Psittacula Krameri manillensis) that had been imported from Pakistan to Japan. The two isolates were closely related to each other (>99% as determined by nucleotide analysis of eight RNA segments), indicating that H9N2 viruses of the same lineage were maintained in these birds for at least 1 year. The hemagglutinins and neuraminidases of both isolates showed >97% nucleotide identity with those of H9N2 viruses isolated from humans in Hong Kong in 1999, while the six genes encoding internal proteins were >99% identical to the corresponding genes of H5N1 viruses recovered during the 1997 outbreak in Hong Kong. These results suggest that the H9N2 parakeet viruses originating in Pakistan share an immediate ancestor with the H9N2 human viruses. Thus, influenza A viruses with the potential to be transmitted directly to humans may be circulating in captive birds worldwide.

Descriptors: influenza transmission, influenza A virus avian classification, nucleoproteins, parakeets virology, amino acid sequence, Hong Kong, avian genetics, mice, inbred BALB c, molecular sequence data, phylogeny, RNA viral analysis, viral core proteins genetics.


NAL Call Number: QR360.J6

Abstract: Human influenza A viruses replicate in the upper respiratory tract at a temperature of about 33 degrees C, whereas avian viruses replicate in the intestinal tract at a temperature close to 41 degrees C. In the present study, we analyzed the influence of low temperature (33 degrees C) on RNA replication of avian and human viruses in cultured cells. The kinetics of replication of the NP segment were similar at 33 and 37 degrees C for the human A/Puerto-Rico/8/34 and A/Sydney/5/97 viruses, whereas replication was delayed at 33 degrees C compared to 37 degrees C for the avian A/FPV/Rostock/34 and A/Mallard/NY/6750/78 viruses. Making use of a genetic system for the in vivo reconstitution of functional ribonucleoproteins, we observed that the polymerase complexes derived from avian viruses but not human viruses exhibited cold sensitivity in mammalian cells, which was determined mostly by residue 627 of PB2. Our results suggest that a reduced ability of the polymerase complex of avian viruses to ensure replication of the viral genome at 33 degrees C could contribute to their inability to grow efficiently in humans.

Descriptors: influenza A virus avian metabolism, human metabolism, RNA viral metabolism, viral proteins metabolism, cell line, mutation, viral genetics, temperature, time factors, transcription, genetic, viral proteins genetics, virus replication.

NAL Call Number: QR360.J6

Abstract: Interspecies transmission of influenza A viruses circulating in wild aquatic birds occasionally results in influenza outbreaks in mammals, including humans. To identify early changes in the receptor binding properties of the avian virus hemagglutinin (HA) after interspecies transmission and to determine the amino acid substitutions responsible for these alterations, we studied the HAs of the initial isolates from the human pandemics of 1957 (H2N2) and 1968 (H3N2), the European swine epizootic of 1979 (H1N1), and the seal epizootic of 1992 (H3N3), all of which were caused by the introduction of avian virus HAs into these species. The viruses were assayed for their ability to bind the synthetic sialylglycopolymers 3'SL-PAA and 6'SLN-PAA, which contained, respectively, 3'-sialyllactose (the receptor determinant preferentially recognized by avian influenza viruses) and 6'-sialyl(N-acetyllactosamine) (the receptor determinant for human viruses). Avian and seal viruses bound 6'SLN-PAA very weakly, whereas the earliest available human and swine epidemic viruses bound this polymer with a higher affinity. For the H2 and H3 strains, a single mutation, 226Q-->L, increased binding to 6'SLN-PAA, while among H1 swine viruses, the 190E-->D and 225G-->E mutations in the HA appeared important for the increased affinity of the viruses for 6'SLN-PAA. Amino acid substitutions at positions 190 and 225 with respect to the avian virus consensus sequence are also present in H1 human viruses, including those that circulated in 1918, suggesting that substitutions at these positions are important for the generation of H1 human pandemic strains. These results show that the receptor-binding specificity of the HA is altered early after the transmission of an avian virus to humans and pigs and, therefore, may be a prerequisite for the highly effective replication and spread which characterize epidemic strains.

Descriptors: hemagglutinin glycoproteins, influenza virus metabolism, influenza A virus avian metabolism, receptors, virus metabolism, amino acid sequence, amino acid substitution, disease outbreaks, ducks virology, hemagglutinin glycoproteins, influenza virus chemistry, avian isolation and purification, models, molecular, molecular sequence data, mutation, missense, phylogeny, protein binding, sialos, sequence alignment, sialic acids metabolism, species specificity, swine virology.


NAL Call Number: QR360.J6

Abstract: In 1997, 18 confirmed cases of human influenza arising from multiple independent transmissions of H5N1 viruses from infected chickens were reported from Hong Kong. To identify possible phenotypic changes in the hemagglutinin (HA) and neuraminidase (NA) of the H5 viruses during interspecies transfer, we compared the receptor-binding properties and NA activities of the human and chicken H5N1 isolates from Hong Kong and of H5N3 and H5N1 viruses from wild aquatic birds. All H5N1 viruses, including the human isolate bound to Sia2-3Gal-containing receptors but not to Sia2-6Gal-containing receptors. This finding formally demonstrates for the first time that receptor specificity of avian influenza viruses may not restrict initial avian-to-human transmission. The H5N1 chicken viruses differed from H5 viruses of wild aquatic birds by a 19-amino-acid deletion in the stalk of the NA and the presence of a carbohydrate at the globular head of the HA. We found that a deletion in the NA decreased its ability to release the virus from cells, whereas carbohydrate at the HA head decreased the affinity of the virus for cell receptors. Comparison of amino acid sequences from GenBank of the HAs and NAs from different avian species revealed that additional glycosylation of the HA and a shortened NA stalk are characteristic features of the H5 and H7 chicken viruses. This finding indicates that changes in both HA and NA may be required for the adaptation of influenza viruses from wild aquatic birds to domestic chickens and raises the possibility that chickens may be a possible intermediate host in zoonotic transmission.

Descriptors: hemagglutinin glycoproteins, influenza virus metabolism, influenza A virus avian metabolism, human metabolism, alpha globulins metabolism, amino acid sequence, carbohydrates metabolism, chickens, fowl plague virology, Hong Kong, horseradish peroxidase metabolism, influenza veterinary, influenza virology, avian classification, avian isolation and purification, human classification, human isolation.
and purification, molecular sequence data, neuraminidase metabolism, ovomucin metabolism, phenotype, receptors, virus metabolism, sequence homology, amino acid.


NAL Call Number: 448.8 V81

Abstract: Avian influenza virus strains representing most hemagglutinin (HA) subtypes were compared with human influenza A (H1N1, H3N2) and B virus isolates, including those with no history of passaging in embryonated hen's eggs, for their ability to bind free N-acetylneuraminic acid (Neu5Ac) and sialyloligosaccharides in a competitive binding assay and to attach to gangliosides in a solid-phase adsorption assay. The avian viruses, irrespective of their HA subtype, showed a higher affinity for sialyl-3-lactose and the other Neu5Ac2-3Gal-terminated oligosaccharides and a lower affinity for sialyl-6-lactose than for free Neu5Ac, indicative of specific interactions between the HA and the 3-linked Gal and poor accommodation of 6-linked Gal in the avian receptor-binding site (RBS). Human H1 and H3 strains, by contrast, were unable to bind to 3-linked Gal, interacting instead with the asialic portion of sialyl-6-(N-acetyllactosamine). Different parts of this moiety were recognized by H3 and H1 subtype viruses (Gal and GlcNAc, respectively). Comparison of the HA amino acid sequences revealed that residues in positions 138, 190, 194, 225, 226, and 228 are conserved in the avian RBS, while the human HAs harbor substitutions at these positions. A characteristic feature of avian viruses was their binding to Neu5Ac2-3Gal-containing gangliosides. This property of avian precursor viruses was preserved in early human H3 isolates, but was gradually lost with further circulation of the H3 HA in humans. Consequently, later human H3 isolates, as well as H1 and type B human strains, were unable to bind to short Neu5Ac2-3Gal-terminated gangliosides, an incompatibility that correlated with higher glycosylation of the HA globular head of human viruses. Our results suggest that the RBS is highly conserved among HA subtypes of avian influenza virus, while that of human viruses displays distinctive genotypic and phenotypic variability.

Descriptors: biochemistry and molecular biophysics, evolution and adaptation, genetics, infection, microbiology, avian influenza A virus, biochemistry and biophysics, conservation, gangliosides, genotypic variability, hemagglutinin receptor binding site, hemagglutinin subtypes, human influenza A virus, human influenza B virus, H1N1 subtype, H3N2 subtype, infection phenotypic variability, sialyloligosaccharides.


NAL Call Number: 448.8 V81

Descriptors: influenza A virus avian metabolism, poultry virology, receptors, virus metabolism, amino acid substitution, Asia, binding sites, fowl plague transmission, fowl plague virology, hemagglutinin glycoproteins, influenza virus genetics, hemagglutinin glycoproteins, influenza virus metabolism, avian classification, avian genetics, human classification, human genetics, human metabolism, mutation, neuraminidase genetics, neuraminidase metabolism, phylogeny, viral envelope proteins genetics, viral envelope proteins metabolism.


NAL Call Number: 500 N21P

Abstract: The recent human infections caused by H5N1, H9N2, and H7N7 avian influenza viruses highlighted the continuous threat of new pathogenic influenza viruses emerging from a natural reservoir in birds. It is generally believed that replication of avian influenza viruses in humans is restricted by a poor fit of these viruses to cellular receptors and extracellular inhibitors in the human respiratory tract. However, detailed mechanisms of this restriction remain obscure. Here, using cultures of differentiated human airway epithelial cells, we demonstrated that influenza viruses enter the airway epithelium through specific target cells and that there were striking differences in this respect between human and avian viruses. During the course of a single-cycle infection, human viruses preferentially infected nonciliated cells, whereas avian viruses as well as the egg-adapted human virus variant with an avian virus-like receptor specificity mainly
infected ciliated cells. This pattern correlated with the predominant localization of receptors for human viruses (2-6-linked sialic acids) on nonciliated cells and of receptors for avian viruses (2-3-linked sialic acids) on ciliated cells. These findings suggest that although avian influenza viruses can infect human airway epithelium, their replication may be limited by a nonoptimal cellular tropism. Our data throw light on the mechanisms of generation of pandemic viruses from their avian progenitors and open avenues for cell level-oriented studies on the replication and pathogenicity of influenza virus in humans.

Descriptors: influenza A virus, avian pathogenicity, human pathogenicity, respiratory mucosa microbiology, bronchi, cell line, dogs, avian isolation and purification, avian physiology, human isolation and purification, human physiology, kidney, lectins, microscopy, confocal, nasal mucosa microbiology, sialic acids analysis, trachea.


NAL Call Number: QR360.J6

Abstract: Influenza virus neuraminidase (NA) plays an essential role in release and spread of progeny virions, following the intracellular viral replication cycle. To test whether NA could also facilitate virus entry into cell, we infected cultures of human airway epithelium with human and avian influenza viruses in the presence of the NA inhibitor oseltamivir carboxylate. Twenty- to 500-fold less cells became infected in drug-treated versus nontreated cultures (P < 0.0001) 7 h after virus application, indicating that the drug suppressed the initiation of infection. These data demonstrate that viral NA plays a role early in infection, and they provide further rationale for the prophylactic use of NA inhibitors.

Descriptors: bronchi virology, nasal mucosa virology, neuraminidase physiology, orthomyxoviridae physiology, trachea virology, acetamides pharmacology, orthomyxoviridae enzymology.


NAL Call Number: 41.8 Av5

Abstract: Two candidate formalin-inactivated vaccines, made from high-growth reassortant viruses with the HA and NA genes from avian viruses in a background of genes derived from A/Puerto Rico/8/34 (PR8), were prepared against H5N1 and H9N2 subtypes (designated as H5N1/PR8 and H9N2/PR8, respectively). These viruses bear the genotypes, antigenicity, and attenuation in mouse models that are desirable in candidate vaccines. The pathogenicity of the newly generated avian-human reassortant vaccine viruses was also evaluated in chickens. Neither H5N1/PR8 nor H9N2/PR8 were highly pathogenic for chickens. No clinical signs, gross lesions, or histological lesions were observed in chickens that were administered H5N1/PR8 either intranasally (i.n.) or intravenously (i.v.), and virus was not detected in oropharyngeal or cloacal swabs. When H9N2/PR8 was administered i.n., no clinical signs, gross lesions, or histological lesions were observed and no virus was detected in cloacal swabs. However, virus was isolated at low titer from oropharyngeal swabs of all eight chickens. Although no clinical signs were observed when H9N2/PR8 was administered i.v., mild tracheitis was seen in one of two chickens. Moderate amounts of antigen were observed in tracheal respiratory epithelium, and low titers of virus were recovered from oropharyngeal and cloacal swabs of some chickens. In summary, both reassortant vaccine viruses replicated poorly in chickens. These studies suggest that these candidate vaccine viruses carry a low risk of transmission to chickens.

Descriptors: epidemiology, infection, avian influenza, infectious disease, prevention and control, respiratory system disease, viral disease.


NAL Call Number: 448.3 Ar23

Abstract: Mink were found to be susceptible to the intranasal inoculation of human, swine, equine and avian influenza A viruses. The viruses were recovered until the 7th post inoculation (p.i.) day from the respiratory tract. The inoculated mink showed antibody response against these viruses. Contact infection in mink with A/Kumamoto/22/77 (H3N2) was possible.
Academic sources:


**Descriptors:** influenza A virus pathogenicity, orthomyxoviridae infections microbiology, antibodies, viral biosynthesis, disease models, animal, hemagglutination inhibition tests, influenza A virus immunology, influenza A virus isolation and purification, orthomyxoviridae infections immunology, orthomyxoviridae infections transmission, respiratory system microbiology.

**Descriptive:**

**Abstract:**

Many new, emerging and re-emerging diseases of humans are caused by pathogens which originate from animals or products of animal origin. A wide variety of animal species, both domestic and wild, act as reservoirs for these pathogens, which may be viruses, bacteria or parasites. Given the extensive distribution of the animal species affected, the effective surveillance, prevention and control of zoonotic diseases pose a significant challenge. The authors describe the direct and indirect implications for public health of emerging zoonoses. Direct implications are defined as the consequences for human health in terms of morbidity and mortality. Indirect implications are defined as the effect of influence of emerging zoonotic disease on two groups of people, namely: health professionals and the general public. Professional assessment of the importance of these diseases influences public health practices and structures, the identification of themes for research and allocation of resources at both national and international levels. The perception of the general public regarding the risks involved considerably influences policy-making in the health field. Extensive outbreaks of zoonotic disease are not uncommon, especially as the disease is often not recognised as zoonotic at the outset and may spread undetected for some time. However, in many instances, the direct impact on health of these new, emerging or re-emerging zoonoses has been small compared to that of other infectious diseases affecting humans. To illustrate the tremendous indirect impact of emerging zoonotic diseases on public health policy and structures and on public perception of health risks, the authors provide a number of examples, including that of the Ebola virus, avian influenza, monkeypox and bovine spongiform encephalopathy. Recent epidemics of these diseases have served as a reminder of the existence of infectious diseases and of the capacity of these diseases to occur unexpectedly in new locations and animal species. The need for greater international co-operation, better local, regional and global networks for communicable disease surveillance and pandemic planning is also illustrated by these examples. These diseases have contributed to the definition of new paradigms, especially relating to food safety policies and more generally to the protection of public health. Finally, the examples described emphasise the importance of intersectorial collaboration for disease containment, and of independence of sectorial interests and transparency when managing certain health risks.

**Descriptors:** communicable diseases, emerging epidemiology, disease outbreaks prevention and control, public health, zoonoses epidemiology, zoonoses etiology, communicable diseases, emerging prevention and control, communicable diseases, emerging transmission, international cooperation, morbidity, risk factors, world health.

**Abstract:**

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**Descriptors:** communicable diseases, emerging epidemiology, disease outbreaks prevention and control, public health, zoonoses epidemiology, zoonoses etiology, communicable diseases, emerging prevention and control, communicable diseases, emerging transmission, international cooperation, morbidity, risk factors, world health.


**NAL Call Number:** SF481.M54

**Descriptors:** disease control, disease prevention, disease surveys, disease transmission, epidemiology,
clinical aspects, diagnostic techniques, outbreaks, pathogenicity, poultry industry, public health, World Health Organization, zoonoses, human diseases, avian influenza virus.


**NAL Call Number:** 41.8 Av5
**Descriptors:** influenza veterinary, influenza A virus, porcine immunology, influenza A virus immunology, poultry diseases epidemiology, turkeys, antibodies, viral analysis, hemagglutination tests veterinary, immunodiffusion veterinary, influenza diagnosis, influenza epidemiology, avian immunology, poultry diseases diagnosis.


**NAL Call Number:** 448.8 P942
**Descriptors:** neuraminidase analysis, orthomyxoviridae enzymology, orthomyxoviridae physiology.


**NAL Call Number:** 448.8 N442
**Descriptors:** acetamides therapeutic use, antiviral agents therapeutic use, disease outbreaks prevention and control, influenza epidemiology, influenza transmission, influenza A virus, avian influenza classification, avian influenza genetics, avian influenza pathogenicity, birds, disease transmission prevention and control, genome, viral, influenza drug therapy, avian influenza transmission, avian influenza virology, neuraminidase antagonists and inhibitors, neuraminidase metabolism, virulence, zoonoses transmission, zoonoses virology.


**NAL Call Number:** RB37.A1C5
**Abstract:** Influenza is a virus that is capable of causing a pandemic of the human race. Influenza has the ability to infect humans by mutating and altering its pathogenic characteristics. Efforts must be made worldwide to educate people about the possibilities of a potential outbreak. Awareness of optimal conditions which could lead to viral mutation and human to human transmission of a neogenetic strain of influenza appears to be a key deterrent against future cases.

**Descriptors:** influenza genetics, influenza transmission, influenza A virus genetics, mutation, adolescent, adult, birds, child, preschool, disease outbreaks, Hong Kong epidemiology, infant, influenza physiopathology, influenza virology, influenza A virus avian genetics, middle aged, species specificity.


**NAL Call Number:** SF781.R4
**Abstract:** Emerging infectious diseases can be defined as infections that have newly appeared in a population or are rapidly increasing in incidence or geographic range. Many of these diseases are zoonoses, including such recent examples as avian influenza, severe acute respiratory syndrome, haemolytic uraemic syndrome (a food-borne infection caused by certain strains of *Escherichia coli*) and probably human immunodeficiency virus/acquired immune deficiency syndrome. Specific factors precipitating the emergence of a disease can often be identified. These include ecological, environmental or demographic factors that place people in increased contact with the natural host for a previously unfamiliar zoonotic agent or that promote the spread of the pathogen. These factors are becoming increasingly prevalent, suggesting that infections will continue to emerge and probably increase. Strategies for dealing with the problem include focusing special attention on situations that promote disease emergence, especially those in which animals...
and humans come into contact, and implementing effective disease surveillance and control. **Descriptors:** epidemiology, infection, public health, vector biology, veterinary medicine, SARS, severe acute respiratory syndrome, haemolytic uraemic syndrome, *Escherichia coli*, control, demographic factors, disease emergence, disease surveillance, ecological factors, environmental factors, geographic range, zoonosis.

**NAL Call Number:** 448.8 J821  
**Abstract:** In May 1997, a 3-year-old boy in Hong Kong died of a respiratory illness related to influenza A (H5N1) virus infection, the first known human case of disease from this virus. An additional 17 cases followed in November and December. A case-control study of 15 of these patients hospitalized for influenza A (H5N1) disease was conducted using controls matched by age, sex, and neighborhood to determine risk factors for disease. Exposure to live poultry (by visiting either a retail poultry stall or a market selling live poultry) in the week before illness began was significantly associated with H5N1 disease (64% of cases vs. 29% of controls, odds ratio, 4.5, P=.045). By contrast, travel, eating or preparing poultry products, recent exposure to persons with respiratory illness, including persons with known influenza A (H5N1) infection, were not associated with H5N1 disease.  
**Descriptors:** influenza etiology, influenza A virus avian isolation and purification, adolescent, adult, case control studies, child, preschool, Hong Kong, infant, influenza virology, matched pair analysis, middle aged, poultry, risk factors.

**NAL Call Number:** 448.3 Ar23  
**Abstract:** Growth characteristics of a wide range of influenza A viruses from different mammals and bird species were examined in an established line of canine kidney (MDCK) cells at an ordinary (37 degrees C) and a high temperature (42 degrees C). Although all viruses employed in the present study possessed a capability of replicating at 37 degrees C, virus growth at 42 degrees C showed considerable variation and reflected differences in the natural hosts of the isolates. All reference strains and isolates from bird species grew well in the MDCK cells maintained at 42 degrees C, but human viruses did not, showing an asymmetrical growth behavior. In contrast to this, growth of swine and equine viruses showed growth characteristics intermediate between human and avian viruses. Of the two swine viruses examined, replication of one strain occurred equally well at both temperatures and another failed to grow at 42 degrees C. Similarly, two of the three equine viruses tested belonging to H3N8 antigenic subtypes grew at 42 degrees C. However, the results obtained from comparison of plaque sizes and growth curves indicated that the replication of the above swine and equine viruses was restricted under a stringent temperature when compared to avian viruses. The detailed analysis of cloned viruses revealed that some of the swine and equine viruses contained two variants which are readily distinguished by growth behavior at 42 degrees C. Genome analysis of parental and virus clones by oligonucleotide mapping and migration profiles of RNA segments did not detect any differences among the above variants exhibiting the asymmetrical growth characteristics at 42 degrees C.  
**Descriptors:** influenza A virus avian growth and development, human growth and development, influenza A virus growth and development, cell line, genes viral, horses, avian genetics, human genetics, porcine genetics, porcine growth and development, influenza A virus genetics, plaque assay, RNA viral genetics, temperature.

**NAL Call Number:** 448.8 J821
Abstract: Reassortant influenza A viruses were produced by mating an avian virus (A/Mallard/NY/78, A/Mallard/Alberta/78, or A/Pintail/Alberta/79) with a wild-type human influenza A virus. From each mating a reassortant virus was obtained that contained the genes coding for the hemagglutinin and neuraminidase surface antigens of the human influenza A wild-type virus and the six other RNA segments (“internal genes”) of the avian influenza A virus parent. The avian-human reassortant influenza viruses produced resembled their avian virus parent in that they produced plaques on MDCK monolayers at 42°C, a temperature restrictive for the human influenza viruses. In the trachea of squirrel monkeys, each avian-human reassortant influenza virus was as restricted in its replication as was its avian influenza virus parent. Thus, one or more of the six internal genes of each avian parent virus was responsible for restriction of the reassortant virus in monkeys. The A/Washington/80 X A/Mallard/NY/78 reassortant virus retained its phenotype of restricted replication in monkeys after five serial passages in vivo. It also failed to transmit to cagemates or induce resistance to wild-type virus challenge, and it did not initiate a systemic or enteric infection. These findings form the basis for evaluation of these attenuated avian-human reassortant influenza A viruses as live attenuated vaccines for humans.

Descriptors: crosses, genetic, influenza A virus avian genetics, human genetics, neuraminidase genetics, chickens, child, ducks, hemagglutinins viral genetics, immunization, avian physiology, human physiology, saimiri, virus replication.


NAL Call Number: QR189.V32

Abstract: A reassortant virus possessing RNA segment 7, which codes for the M1 and M2 proteins, of the avian influenza A/Mallard/New York/6750/78 (H2N2) virus and the other seven RNA segments of the human influenza A/Udorn/307/72 (H3N2) virus had been shown previously to be markedly restricted in replication in the respiratory tract of squirrel monkeys. In contrast, a reassortant possessing segment 7 of another avian influenza virus, A/Pintail/Alberta/119/79 (H4N6), and the seven other RNA segments from the A/Udorn/72 virus was not restricted. The nucleotide and deduced amino acid sequence of the RNA segment 7 of each virus was determined to identify the structural basis for the attenuation phenotype specified by RNA segment 7 of the A/Mallard/78 virus. Analysis of the deduced amino acid sequences revealed only two amino acid differences in the M1 protein and one difference in the M2 protein, suggesting that the attenuation phenotype of a reassortant virus possessing segment 7 of the A/Mallard/78 virus may be specified by one to three amino acids. Reassortant viruses possessing RNA segment 6, which codes for the nucleoprotein, of either avian influenza virus and the other seven RNA segments of a human influenza virus were also restricted in replication in squirrel monkeys. A comparison of the deduced amino acid sequences of the two avian nucleoproteins demonstrated only three amino acid differences indicating that these two avian viruses possess NP genes that are highly related. The high degree of relatedness of both the NP and M proteins of these two avian viruses contrasts with their divergent surface antigens. (ABSTRACT TRUNCATED AT 250 WORDS)

Descriptors: genes viral, influenza A virus avian genetics, nucleoproteins genetics, viral core proteins, viral matrix proteins genetics, viral proteins genetics, amino acid sequence, base sequence, human genetics, RNA viral analysis, saimiri, virus replication.


NAL Call Number: 448.8 J821


Abstract: An influenza A reassortant virus that contained the hemagglutinin and neuraminidase genes of a virulent human virus, A/Udorn/72 (H3N2), and the six other influenza A virus genome segments from an avirulent avian virus, A/Mallard/New York/6750/78 (H2N2), was evaluated for its level of replication in squirrel monkeys and hamsters. In monkeys, the reassortant virus was as attenuated and as restricted in its level of replication in the upper and lower respiratory tract as its avian influenza virus parent. Nonetheless, infection with the reassortant induced significant resistant to challenge with virulent human influenza virus. In hamsters, the reassortant virus replicated to a level intermediate between that of its parents. These findings suggest that the nonsurface antigen genes of the avian parental virus are the primary determinants of restriction of replication of the reassortant virus in monkeys. Attenuation of the reassortant virus for primates is achieved by inefficient functioning of the avian influenza genes in primate cells, while antigenic specificity of the human influenza virus is provided by the neuraminidase and hemagglutinin genes derived from the human virus. This approach could lead to the development of a live influenza A virus vaccine that is attenuated for man if the avian influenza genes are similarly restricted in human cells.

Descriptors: influenza A virus avian genetics, human genetics, influenza vaccine immunology, antigens, surface genetics, epitopes genetics, epitopes immunology, hamsters, hemagglutinin genes, hemagglutinins immunology, neuraminidase genetics, neuraminidase immunology, saimiri, vaccines, attenuated immunology.


Abstract: Influenza A viruses have been isolated from a wide range of species. Aquatic birds, in which all 15 hemagglutinin subtypes have been found, are believed to be the reservoir of influenza A viruses from which new virus subtypes can episodically be transmitted to new hosts. Generally, avian influenza viruses replicate poorly in humans. However, adaptation of an avian virus to the human host may occur either through genetic reassortment or following direct transmission, and may result in influenza pandemics, as has been the case in 1918, 1957 and 1968. Several observations suggest that pigs, in which both avian and human influenza viruses replicate, are involved as a link and a mixing vessel in interspecies transmissions of influenza viruses. In addition, domestic poultry seem to serve as intermediate hosts for the acquisition of determinants that increase the potential of transmission of influenza viruses to mammals. The molecular bases for the host-specificity of human or avian influenza A viruses are not fully understood. The hemagglutinin and neuraminidase are considered as possible determinants of host-restriction because of different receptor specificities. In addition, genetic studies have indicated that gene segments encoding internal proteins, and especially the PB2 segment, harbor host-range determinants. This notion was strengthened by the fact that the six internal genes of avian H5N1 and H9N2 viruses that were responsible for respiratory disease in humans in Hong Kong in 1997 and 1999, respectively, were found to be very similar. However, the multiple genetic features of internal genes that contribute to host-specificity of influenza A viruses and to their potential for interspecies transmission, as well as the molecular mechanisms involved, are still to be understood.

Descriptors: biochemistry and molecular biophysics, infection, influenza, respiratory system disease, viral disease.

compatibility between polymerase proteins from human and avian strains of influenza A viruses. 

**NAL Call Number:** QR360.A1J6

**Abstract:** In order to determine how efficiently the polymerase proteins derived from human and avian influenza A viruses can interact with each other in the context of a mammalian cell, a genetic system that allows the in vivo reconstitution of active ribonucleoproteins was used. The ability to achieve replication of a viral-like reporter RNA in COS-1 cells was examined with heterospecific mixtures of the core proteins (PB1, PB2, PA and NP) from two strains of human viruses (A/Puerto Rico/8/34 and A/Victoria/3/75), two strains of avian viruses (A/Mallard/NY/6750/78 and A/FPV/-Rostock/34), and a strain of avian origin (A/Hong Kong/156/97) that was isolated from the first human case of H5N1 influenza in Hong Kong in 1997. In accordance with published observations on reassortant viruses, PB2 amino acid 627 was identified as a major determinant of the replication efficiency of heterospecific complexes in COS-1 cells. Moreover, the results showed that replication of the viral-like reporter RNA was more efficient when PB2 and NP were both derived from the same avian or human virus or when PB1 was derived from an avian virus, whatever the origin of the other proteins. Furthermore, the PB1 and PB2 proteins from the A/Hong Kong/156/97 virus exhibited intermediate properties with respect to the corresponding proteins from avian or human influenza viruses, suggesting that some molecular characteristics of PB1 and PB2 proteins might at least partially account for the ability of the A/Hong Kong/156/97 virus to replicate in humans.

**Descriptors:** influenza A virus avian genetics, influenza A virus human genetics, nucleoproteins, RNA replicase, viral core proteins genetics, viral core proteins metabolism, cos cells, chloramphenicol acetyltransferase, cloning, molecular, DNA, complementary, DNA directed RNA polymerases genetics, DNA directed RNA polymerases metabolism, influenza A virus avian metabolism, influenza A virus human metabolism, molecular sequence data, plasmids genetics, sequence analysis, DNA, transcription, genetic, transfection, viral proteins genetics, viral proteins metabolism, virus replication.


**Descriptors:** influenza A virus, avian pathogenicity, virulence, Asia epidemiology, disease outbreaks prevention and control, influenza epidemiology, influenza prevention and control, influenza transmission, influenza virology, avian influenza A virus classification, avian influenza A virus genetics, avian influenza A virus immunology, avian influenza epidemiology, avian influenza prevention and control, avian influenza transmission, avian influenza virology, poultry, receptors, virus physiology, viral vaccines, zoonoses epidemiology, zoonoses transmission, zoonoses virology.


**NAL Call Number:** 448.8 V81

**Abstract:** The nucleotide sequences of the M and NS1 genes of influenza virus A/Swine/Iowa/15/30 (A/SW/IW/30)(H1N1) were determined with cloned DNAs and compared with reported sequences of human and avian influenza viruses. A/SW/IW/30 virus was found to be closely similar to A/PR/8/34(H1N1) virus in the nucleotide sequences of the M and NS1 genes, the base differences between the two strains being 64 out of 1027 nucleotides in the M gene and 52 out of 740 in the NS1 gene. Based on the assumptions that these two viruses were derived from a common ancestor and that the rate of base changes per year was the same in man and in swine, it was estimated that the progenitor virus was in circulation during the period from 1915 to 1920. This estimation was compatible with the epidemiological findings suggesting that the progenitor of the swine influenza virus was the agent of the 1918 influenza pandemic. Furthermore, the M and NS1 gene sequences of A/FPV/Rostock/34(H7N6) virus were much closer to those of A/SW/IW/30 and A/PR/8/34 viruses than to A/duck/Alberta/60/76(H12N5) virus, but not as close as the A/SW/IW/30 virus was to A/PR/8/34 virus.

**Descriptors:** influenza A virus human genetics, influenza A virus, porcine genetics, influenza A virus genetics, base sequence, evolution, genes viral.

NAL Call Number: QR360.A1J6

Abstract: From immunological and phylogenetic analyses of H3 influenza viruses isolated from pigs and ducks in the People's Republic of China (China), Hong Kong, Taiwan and Japan, between 1968 and 1982, we arrived at the following conclusions. The H3 haemagglutinin and N2 neuraminidase genes from swine isolates can be segregated into four mammalian lineages, including: (i) the earliest human strains; (ii) early swine strains including Hong Kong isolates from 1976-1977; (iii) an intermediate strain between the early swine and recent human strains; and (iv) recent human strains. In this study we found an unusual swine strain (sw/Hong Kong/127/82) belonging to the third lineage which behaved like those of the early swine-like lineage in the haemagglutination inhibition test; but neuraminidase inhibition profiles with monoclonal antibodies indicated that this virus is related to late human strains. On the basis of pairwise comparisons of complete or partial nucleotide sequences the genes encoding the three polymerase proteins (PB2, PB1, PA), the nucleoprotein, the membrane protein and possibly the nonstructural proteins of sw/Hong Kong/127/82 are of the swine H1N1 lineage, whereas genes encoding the two surface glycoproteins belong to the human H3N2 lineage. In contrast, all RNA segments of one swine isolate (sw/Hong Kong/81/78) are similar to those of recent human H3N2 viruses. This study indicated that frequent interspecies infections between human and swine hosts appeared to occur during 1976-82. Although the evolutionary rates of human (0.0122/site/year), swine (0.0127/site/year) and avian (0.0193/site/year) virus genes are similar when based upon synonymous substitutions, nonsynonymous substitutions indicated that viral genes derived from human and swine viruses evolved about three times faster (0.0026-0.0027/site/year) than those of avian viruses (0.0008/site/year). Furthermore, the evolutionary mechanism by which human and swine H3 haemagglutinin genes evolve at a similar rate, based on nonsynonymous substitutions, appeared to be quite different from previous evidence which showed that human H1 haemagglutinin genes evolved about one fifth to one tenth that of human viruses, reflecting the conservative nature of the antigenic structure in the former.

Descriptors: evolution, genes viral genetics, hemagglutinins viral genetics, influenza A virus, porcine genetics, influenza A virus genetics, amino acid sequence, antibodies, monoclonal, antibodies, viral, antigenic variation genetics, China, hemagglutinins viral analysis, hemagglutinins viral immunology, Hong Kong, influenza A virus avian genetics, influenza A virus human immunology, influenza A virus human genetics, influenza A virus human immunology, influenza A virus, porcine immunology, influenza A virus immunology, molecular sequence data, neuraminidase analysis, neuraminidase genetics, RNA viral genetics, sequence analysis, DNA, sequence homology, amino acid, sequence homology, nucleic acid, swine.

NAL Call Number: 448.3 Ar23

Abstract: The characteristics of an avian influenza virus were compared in detail with those of human Asian (H2N2) influenza viruses. Antigenic analysis by different antisera against H2N2 viruses and monoclonal antibodies to both the hemagglutinin and neuraminidase antigens showed that an avian isolate, A/duck/Munchen/9/79 contained hemagglutinin and neuraminidase subunits closely related to those of the early human H2N2 viruses which had been prevalent in 1957. However, this avian virus gave low HI titers with absorbed and non-absorbed antisera to different human H2N2 viruses isolated in 1957. Like human Q phase variant, such as A/RI/5/-/57 (H2N2), hemagglutination of the above avian strain was not inhibited by the purified non-specific gamma-inhibitor from guinea pig serum. Growth behavior at restrictive temperature (42 degrees C) clearly differentiate the avian H2N2 virus from human influenza viruses, showing that the former virus grew well in MDCK cells at 42 degrees C but not the latters. Genomic analysis of these viruses revealed that the oligonucleotide map of H2N2 virus isolated from a duck was quite different from those of human H2N2 viruses from 1957 to 1967. The oligonucleotide mapping also indicated that different H2N2 influenza virus variants had co-circulated in humans in 1957.

Descriptors: influenza A virus avian immunology, influenza A virus human immunology, hemagglutinins
viral immunology, influenza A virus avian genetics, influenza A virus human genetics, influenza A virus growth and development, neuraminidase immunology, RNA viral genetics.

NAL Call Number: 448.8 V81

Abstract: In 1985 a fowl plague-like disease occurred in chickens in Lockwood, Victoria, Australia and caused high mortality. An H7N7 influenza virus was isolated from the chickens (A/Chicken/Victoria/1/85); additionally, an antigenically similar virus was isolated from starlings (A/Starling/Victoria/5156/85) and serological evidence of H7N7 virus infection was found in sparrows. Antigenic analysis with monoclonal antibodies to H7, oligonucleotide mapping of total vRNA, and sequence analysis of the HA genes established that the chicken and starling influenza viruses were closely related and probably came from the same source. There was high nucleotide sequence homology (95.3%) between the HA genes of A/Chick/Vic/85 and a fowl plague-like virus isolated from chickens in Victoria 9 years earlier [A/Fowl/Vic/76 (H7N7)]. The sequence homologies indicated that the A/Chick/Vic/85 and A/Fowl/Vic/76 were derived from a common recent ancestor, while another recent H7N7 virus, Seal/Mass/1/80 originated from a different evolutionary lineage. Experimental infection of chickens and starlings with A/Chick/Vic/1/85 (H7N7) was associated with high mortality (100%), transmission to contact birds of the same species, and virus in all organs. In sparrows one-third of the birds died after infection and virus was isolated from most organs; transmission to contact sparrows did not occur. In contrast, the H7N7 virus replicated in ducks and spread to contact ducks but caused no mortality. These studies establish that the host species plays a role in determining the virulence of avian influenza viruses, and provide the first evidence for transmission of virulent influenza viruses between domestic poultry and passerine birds. They support the hypothesis that potentially virulent H7N7 influenza viruses could be maintained in ducks where they cause no apparent disease and may sometimes spread to other wild birds and domestic poultry.

Descriptors: birds microbiology, hemagglutinins viral genetics, influenza A virus avian genetics, amino acid sequence, animals, wild microbiology, Australia, base sequence, chickens microbiology, disease reservoirs, genes viral, molecular sequence data, nucleotide mapping, RNA viral genetics, species specificity, virus replication.

NAL Call Number: 41.8 Av5

Abstract: Wildlife surveillance was conducted for influenza viruses in conjunction with the 1983-84 lethal H5N2 avian influenza epizootic in domestic poultry in Pennsylvania, New Jersey, Maryland, and Virginia. Virus-isolation attempts made on cloacal and tracheal swabs from 4,466 birds and small rodents within the quarantined areas and 1,511 waterfowl in nearby Maryland yielded only a single H5N2 isolate from a pen-raised chukar in Pennsylvania. Antibodies against hemagglutinin type 5 and/or neuraminidase type 2 were found in 33% of the aquatic birds tested; however, this finding could not be used to confirm previous H5N2 avian influenza virus activity because of the possibility of prior infections with multiple influenza subtypes. The low prevalence of lethal H5N2 avian influenza virus in wild birds and small rodents strongly indicated that these animals were not responsible for dissemination of the disease among poultry farms during the outbreak.

Descriptors: birds microbiology, disease outbreaks veterinary, fowl plague transmission, disease reservoirs microbiology, hemagglutinins viral analysis, neuraminidase analysis, orthomyxoviridae isolation and purification, paramyxoviridae isolation and purification, Pennsylvania.

NAL Call Number: QR360.J6
Abstract: Since 1997, outbreaks of highly pathogenic (HP) H5N1 and circulation of H9N2 viruses among domestic poultry in Asia have posed a threat to public health. To better understand the extent of transmission of avian influenza viruses (AIV) to humans in Asia, we conducted a cross-sectional virologic study in live bird markets (LBM) in Hanoi, Vietnam, in October 2001. Specimens from 189 birds and 18 environmental samples were collected at 10 LBM. Four influenza A viruses of the H4N6 (n = 1), H5N2 (n = 1), and H9N3 (n = 2) subtypes were isolated from healthy ducks for an isolation frequency of over 30% from this species. Two H5N1 viruses were isolated from healthy geese. The hemagglutinin (HA) genes of these H5N1 viruses possessed multiple basic amino acid motifs at the cleavage site, were HP for experimentally infected chickens, and were thus characterized as HP AIV. These HA genes shared high amino acid identities with genes of other H5N1 viruses isolated in Asia during this period, but they were genetically distinct from those of H5N1 viruses isolated from poultry and humans in Vietnam during the early 2004 outbreaks. These viruses were not highly virulent for experimentally infected ducks, mice, or ferrets. These results establish that HP H5N1 viruses with properties similar to viruses isolated in Hong Kong and mainland China circulated in Vietnam as early as 2001, suggest a common source for H5N1 viruses circulating in these Asian countries, and provide a framework to better understand the recent widespread emergence of HP H5N1 viruses in Asia.

Descriptors: avian influenza A virus classification, avian influenza A virus isolation and purification, avian influenza virology, poultry virology, viral antigens, chickens virology, ducks virology, molecular epidemiology, ferrets, geese virology, avian influenza A virus genetics, avian influenza A virus pathogenicity, mice, molecular sequence data, neuraminidase genetics, phylogeny, sequence analysis, serotyping, Vietnam, virulence.


NAL Call Number: 448.8 L22

Abstract: Background: In 1997, pathogenic avian influenza A/Hong Kong/97 (H5N1) viruses emerged as a pandemic threat to human beings. A non-pathogenic variant, influenza A/Duck/Singapore/97 (H5N3), was identified as a leading vaccine candidate. We did an observer-blind, phase I, randomised trial in healthy volunteers to assess safety, tolerability, and antigenicity of MF59-adjuvanted and non-adjuvanted vaccines. Methods: 32 participants were randomly assigned MF59, and 33 non-adjuvanted vaccine. Two doses were given 3 weeks apart, of 7.5, 15, or 30 mug haemagglutinin surface-antigen influenza A H5N3 vaccine. Antibody responses were measured by haemagglutination inhibition, microneutralisation, and single radial haemolysis (SRH). The primary outcome was geometric mean antibody titre 21 days after vaccination. Findings: The A/Duck/Singapore vaccines were safe and well tolerated. Antibody response to non-adjuvanted vaccine was poor, the best response occurring after two 30 mug doses: one, four, four, and one person of eleven seroconverted by haemagglutination inhibition, microneutralisation, and single radial haemolysis (SRH). The primary outcome was geometric mean antibody titre 21 days after vaccination. Antibody response to non-adjuvanted vaccine was poor, the best response occurring after two 30 mug doses: one, four, four, and one person of eleven seroconverted by haemagglutination inhibition, microneutralisation, and single radial haemolysis (SRH). Two 7.5 mug doses of MF59 adjuvanted vaccine gave the highest seroconversion rates: haemagglutination inhibition, six of ten; microneutralisation, eight of ten; H5N3 SRH, ten of ten; H5N1 SRH, nine of nine. The geometric mean titres of antibody, and seroconversion rates, were significantly higher after MF59 adjuvanted vaccine. Two 7.5 mug doses of MF59 adjuvanted vaccine gave the highest seroconversion rates: haemagglutination inhibition, six of ten; microneutralisation, eight of ten; H5N3 SRH, ten of ten; H5N1 SRH, nine of nine. The geometric mean titre of antibody to the pathogenic virus, A/Hong Kong/489/97 (H5N1), was about half that to A/Duck/Singapore virus. Interpretation: Non-adjuvanted A/Duck/Singapore/97 (H5N3) viruses are poorly immunogenic and doses of 7.5-30 mug haemagglutinin alone are unlikely to give protection from A/Hong Kong/97 (H5N1) virus. Addition of MF59 to A/Duck/Singapore/97 vaccines boost the antibody response to protection levels. Our findings have implications for development and assessment of vaccines for future pandemics.

Descriptors: infection, pharmacology, influenza, respiratory system disease, viral disease, antigenicity safety.


NAL Call Number: 448.8 L22

Descriptors: epidemiology, humans, infection, influenza, vaccination, clinical techniques, pandemic prevention.

**NAL Call Number:** 448.3 Ar22

**Descriptors:** influenza epidemiology, orthomyxoviridae immunology, birds, cross reactions, influenza A virus avian immunology, influenza A virus human immunology, influenza A virus, porcine immunology, Romania, swine.


**NAL Call Number:** SF601.V44

**Abstract:** Pig serum samples collected in southeastern China were examined for antibodies to influenza A viruses. Since the hemagglutination inhibition (HI) test does not accurately detect antibodies to the hemagglutinins (HAs) of "avian" influenza viruses, we utilized the neutralization (NT) test to detect subtype-specific antibodies to the HA of avian viruses in pig sera. Neutralizing antibodies to H1, H3, H4, and H5 influenza viruses were detected in the serum samples collected in 1977-1982 and 1998, suggesting that pigs in China have been sporadically infected with avian H4 and H5 viruses in addition to swine and human H1 and H3 viruses. Antibodies to H9 virus, on the other hand, were found only in the sera collected in 1998, not in those collected in 1977-1982, correlating with the recent spread in poultry and subsequent isolation of H9N2 viruses from pigs and humans in 1998. The present results indicate that avian influenza viruses have been transmitted to pig populations in southeastern China.

**Descriptors:** antibodies, viral blood, influenza veterinary, influenza A virus immunology, swine diseases epidemiology, China epidemiology, hemagglutination inhibition tests veterinary, hemagglutinins viral, influenza epidemiology, influenza transmission, influenza A virus avian immunology, influenza A virus human immunology, influenza A virus, porcine immunology, influenza A virus classification, neutralization tests veterinary, poultry, seroepidemiologic studies, specific pathogen free organisms, swine, swine diseases blood, swine diseases transmission, swine diseases virology.


**NAL Call Number:** 470 Sci2

**Descriptors:** influenza epidemiology, influenza virology, influenza A virus, avian, influenza, avian epidemiology, population surveillance, adult, southeastern Asia epidemiology, Cambodia epidemiology, disease outbreaks veterinary, influenza transmission, poultry.


**NAL Call Number:** 470 Sci2

**Descriptors:** disease outbreaks veterinary, influenza virology, influenza A virus, avian classification, avian influenza pathogenicity, avian influenza epidemiology, avian virology, birds, chickens, China epidemiology, disease reservoirs, influenza epidemiology, influenza prevention and control, influenza transmission, avian influenza prevention and control, avian influenza transmission, Japan epidemiology, Korea epidemiology, Vietnam epidemiology.


**NAL Call Number:** 470 Sci2

**Descriptors:** disease outbreaks veterinary, influenza epidemiology, influenza virology, influenza A virus, avian classification, avian influenza pathogenicity, avian influenza epidemiology, avian virology, birds, evolution, molecular, avian genetics, avian influenza virology, poultry, recombination, genetic.

Okazaki, K. (1983). *Studies on susceptibility of mink to influenza viruses--serological evidence of human influenza virus infection in mink, contact infection of mink with avian influenza viruses, and...*

Abstract: Influenza A viruses of different subtypes were isolated from fecal samples of ducks in their nesting areas in Siberia in summer from 1996 to 1998. Phylogenetic analysis of the NP genes of the isolates in Siberia and those in Hokkaido, Japan on their flyway of migration from Siberia to the south in autumn revealed that they belong to the Eurasian lineage of avian influenza viruses. It is noted that the genes of the isolates in Siberia are closely related to those of H5N1 influenza virus strains isolated from chickens and humans in Hong Kong in 1997 as well as to those of isolates from domestic birds in southern China. The results indicate that influenza viruses perpetuated in ducks nesting in Siberia should have contributed genes in the emergence of the H5N1 virus in Hong Kong. Vaccine prepared from avirulent A/duck/Hokkaido/4/96 (H5N3) influenza virus was potent enough to protect mice from challenge with lethal dose of the pathogenic H5N1 virus [19]. Intensive surveillance study of aquatic birds especially in Siberia is, therefore, stressed to provide information on the future pandemic influenza virus strains and for vaccine preparation.

Descriptors: ducks virology, genes viral, influenza A virus avian genetics, base sequence, DNA primers genetics, disease reservoirs, fowl plague immunology, fowl plague prevention and control, influenza A virus avian classification, influenza A virus avian pathogenicity, influenza vaccine pharmacology, Japan, mice, nucleoproteins genetics, phylogeny, poultry, Siberia, viral proteins genetics.


Descriptors: avian influenza virus, transmission, epidemiology, host range, mink.


Abstract: Given our recent discoveries that the ocular human pathogens adenovirus serotype 37 and enterovirus serotype 70 use sialic acid linked to galactose via alpha2,3 glycosidic bonds as a cellular receptor, we propose that the presence of this receptor in the eye also explains the ocular tropism exhibited by zoonotic avian influenza A viruses such as subtype H5N1 in Hong Kong in 1997, H7N7 in the Netherlands in 2003, H7N2 in the USA in 2003, and H7N3 in Canada in 2004. We also draw attention to the implications this hypothesis may have for epizootic and zoonotic influenza, and the initiation of future pandemics.

Descriptors: Adenoviridae classification, eye diseases virology, avian influenza pathology, cell surface physiology receptors, zoonoses virology, Adenoviridae pathology, birds, avian influenza epidemiology, avian influenza transmission, serotyping, zoonoses transmission, sialic acid.


Abstract: Since 1997, novel viruses of three different subtypes and five different genotypes have emerged as agents of influenza among pigs in North America. The appearance of these viruses is remarkable because there were no substantial changes in the overall epidemiology of swine influenza in the United States and Canada for over 60 years prior to this time. Viruses of the classical H1N1 lineage were virtually the exclusive cause of swine influenza from the time of their initial isolation in 1930 through 1998. Antigenic drift variants of these H1N1 viruses were isolated in 1991-1998, but a much more dramatic antigenic shift
occurred with the emergence of H3N2 viruses in 1997-1998. In particular, H3N2 viruses with genes derived from human, swine and avian viruses have become a major cause of swine influenza in North America. In addition, H1N2 viruses that resulted from reassortment between the triple reassortant H3N2 viruses and classical H1N1 swine viruses have been isolated subsequently from pigs in at least six states. Finally, avian H4N6 viruses crossed the species barrier to infect pigs in Canada in 1999. Fortunately, these H4N6 viruses have not been isolated beyond their initial farm of origin. If these viruses spread more widely, they will represent another antigenic shift for our swine population, and could pose a threat to the world's human population. Research on these novel viruses may offer important clues to the genetic basis for interspecies transmission of influenza viruses.

Descriptors: influenza virology, influenza A virus, porcine physiology, Canada epidemiology, fowl plague transmission, influenza A virus avian, influenza A virus, porcine classification, influenza A virus, porcine genetics, influenza A virus, porcine immunology, North America epidemiology, species specificity, swine, United States, variation genetics.


NAL Call Number: 448.3 Ar23

Abstract: Influenza virus infection in pigs is both an animal health problem and a public health concern. As such, surveillance and characterization of influenza viruses in swine is important to the veterinary community and should be a part of human pandemic preparedness planning. Studies in 1976/1977 and 1988/1989 demonstrated that pigs in the U.S. were commonly infected with classical swine H1N1 viruses, whereas human H3 and avian influenza virus infections were very rare. In contrast, human H3 and avian H1 viruses have been isolated frequently from pigs in Europe and Asia over the last two decades. From September 1997 through August 1998, we isolated 26 influenza viruses from pigs in the north central United States at the point of slaughter. All 26 isolates were H1N1 viruses, and phylogenetic analyses of the hemagglutinin and nucleoprotein genes from 11 representative viruses demonstrated that these were classical swine H1 viruses. However, monoclonal antibody analyses revealed antigenic heterogeneity among the HA proteins of the 26 viruses. Serologically, 27.7% of 2,375 pigs tested had hemagglutination-inhibiting antibodies against classical swine H1 influenza virus. Of particular significance, however, the rates of seropositivity to avian H1 (7.6%) and human H3 (8.0%) viruses were substantially higher than in previous studies.

Descriptors: influenza veterinary, influenza virology, influenza A virus avian isolation and purification, influenza A virus human isolation and purification, influenza A virus, porcine isolation and purification, swine diseases virology, amino acid sequence, influenza epidemiology, molecular sequence data, seroepidemiologic studies, swine, swine diseases epidemiology, United States epidemiology.


NAL Call Number: 501 L84Pb

Abstract: Proof that a newly identified coronavirus, severe acute respiratory syndrome coronavirus (SARS-CoV) is the primary cause of severe acute respiratory syndrome (SARS) came from a series of studies on experimentally infected cynomolgus macaques (Macaca fascicularis). SARS-CoV-infected macaques developed a disease comparable to SARS in humans; the virus was re-isolated from these animals and they developed SARS-CoV-specific antibodies. This completed the fulfilment of Koch's postulates, as modified by Rivers for viral diseases, for SARS-CoV as the aetiologic agent of SARS. Besides the macaque model, a ferret and a cat model for SARS-CoV were also developed. These animal models allow comparative pathogenesis studies for SARS-CoV infections and testing of different intervention strategies. The first of these studies has shown that pegylated interferon-alpha, a drug approved for human use, limits SARS-CoV replication and lung damage in experimentally infected macaques. Finally, we argue that, given the worldwide nature of the socio-economic changes that have predisposed for the emergence of SARS and avian influenza in Southeast Asia, such changes herald the beginning of a global trend for which we are ill prepared.

Descriptors: disease models, animal, ferrets, Macaca fascicularis, SARS virus, severe acute respiratory
syndrome etiology, zoonoses transmission, cats, severe acute respiratory syndrome physiopathology, severe acute respiratory syndrome transmission.


**NAL Call Number:** 41.8 J27  
**Descriptors:** birds microbiology, influenza A virus avian pathogenicity, mice microbiology, influenza A virus avian isolation and purification, Japan.

Oxford, J.S., R. Lambkin, A. Sefton, R. Daniels, A. Elliot, R. Brown, and D. Gill (2005). *A hypothesis: the conjunction of soldiers, gas, pigs, ducks, geese and horses in northern France during the Great War provided the conditions for the emergence of the "Spanish" influenza pandemic of 1918-1919.* Vaccine 23(7): 940-5. ISSN: 0264-410X.

**NAL Call Number:** QR189.V32  
**Abstract:** The Great Influenza Pandemic of 1918-1919 was a cataclysmic outbreak of infection wherein over 50 million people died worldwide within 18 months. The question of the origin is important because most influenza surveillance at present is focussed on S.E. Asia. Two later pandemic viruses in 1957 and 1968 arose in this region. However we present evidence that early outbreaks of a new disease with rapid onset and spreadability, high mortality in young soldiers in the British base camp at Etaples in Northern France in the winter of 1917 is, at least to date, the most likely focus of origin of the pandemic. Pathologists working at Etaples and Aldershot barracks later agreed that these early outbreaks in army camps were the same disease as the infection wave of influenza in 1918. The Etaples camp had the necessary mixture of factors for emergence of pandemic influenza including overcrowding (with 100,000 soldiers daily changing), live pigs, and nearby live geese, duck and chicken markets, horses and an additional factor 24 gases (some of them mutagenic) used in large 100 ton quantities to contaminate soldiers and the landscape. The final trigger for the ensuing pandemic was the return of millions of soldiers to their homelands around the entire world in the autumn of 1918.

**Descriptors:** communicable diseases, emerging history, disease outbreaks, influenza history, military personnel history, world war I, ducks, France, geese, history, 20th century, horses, influenza A virus, avian pathogenicity, swine.


**NAL Call Number:** QR360.J6  
**Abstract:** Influenza A viruses are the cause of annual epidemics of human disease with occasional outbreaks of pandemic proportions. The zoonotic nature of the disease and the vast viral reservoirs in the aquatic birds of the world mean that influenza will not easily be eradicated and that vaccines will continue to be needed. Recent technological advances in reverse genetics methods and limitations of the conventional production of vaccines by using eggs have led to a push to develop cell-based strategies to produce influenza vaccine. Although cell-based systems are being developed, barriers remain that need to be overcome if the potential of these systems is to be fully realized. These barriers include, but are not limited to, potentially poor reproducibility of viral rescue with reverse genetics systems and poor growth kinetics and yields. In this study we present a modified A/Puerto Rico/8/34 (PR8) influenza virus master strain that has improved viral rescue and growth properties in the African green monkey kidney cell line, Vero. The improved properties were mediated by the substitution of the PR8 NS gene for that of a Vero-adapted reassortant virus. The Vero growth kinetics of viruses with H1N1, H3N2, H6N1, and H9N2 hemagglutinin and neuraminidase combinations rescued on the new master strain were significantly enhanced in comparison to those of viruses with the same combinations rescued on the standard PR8 master strain. These improvements pave the way for the reproducible generation of high-yielding human and animal influenza vaccines by reverse genetics methods. Such a means of production has particular relevance to epidemic and pandemic use.

**Descriptors:** influenza A virus avian growth and development, influenza A virus human growth and
development, influenza vaccine, reassortant viruses growth and development, vero cells virology, Cercopithecus aethiops, influenza A virus avian genetics, influenza A virus human genetics, reassortant viruses genetics, viral nonstructural proteins genetics, virus cultivation, virus replication.


Descriptors: zoonoses, public health, humans, Newcastle disease virus, avian influenza virus.


NAL Call Number: SF601.V44
Abstract: One-hundred thirty-seven BALB/c mice were intranasally inoculated with neurotropic avian influenza A virus (H5N3). Thirty-nine of these mice died within 16 days post-inoculation (PID) and 98 of the mice recovered from the infection. To investigate whether viral antigens and genomes persist in the central nervous system (CNS) of recovered mice, immunohistochemistry and reverse transcription-polymerase chain reaction (RT-PCR) methods were performed. Histopathologically, mild interstitial pneumonia and non-suppurative encephalomyelitis restricted to the basal part of the frontal lobe of the cerebrum, brain stem and thoracic spinal cord were observed in BALB/c mice until 40 PID. Small amounts of viral antigens were detected in the brain and spinal cord and some viral RNA segments (NA, NP, M, PA, HA, NS, PB1) were intermittently detected in the CNS until 48 PID. Immunosuppression of these mice by dexamethazone (DEX) treatment did not increase the frequency of detection of the lesions, viral antigens or genomes. These findings suggest that viral genomes of neurovirulent influenza virus persist with restricted transcriptive activity in the CNS of the mice even after clinical recovery from the infection.

Descriptors: central nervous system virology, fowl plague virology, influenza A virus avian isolation and purification, RNA viral analysis, brain pathology, brain virology, central nervous system pathology, disease models, animal, fowl plague mortality, fowl plague pathology, immunohistochemistry veterinary, influenza A virus avian genetics, mice, mice inbred BALB c, random allocation, reverse transcriptase polymerase chain reaction veterinary, specific pathogen free organisms.


Descriptors: disease outbreaks, fowl plague virology, influenza mortality, Asia, southeastern epidemiology, birds, influenza A virus avian, influenza A virus human.


Descriptors: influenza, avian transmission, zoonoses transmission, influenza, avian epidemiology, poultry, Vietnam epidemiology.


Descriptors: influenza, avian epidemiology, birds, Carnivora, cat diseases epidemiology, cats, poultry, world health, World Health Organization.


NAL Call Number: QR360.A1J6
Abstract: In February 2004 a highly pathogenic avian influenza (HPAI) outbreak erupted in British Columbia. Investigations indicated that the responsible HPAI H7N3 virus emerged suddenly from a low
pathogenic precursor. Analysis of the haemagglutinin (HA) genes of the low and high pathogenic viruses isolated from the index farm revealed the only difference to be a 21 nt insert at the HA cleavage site of the highly pathogenic avian influenza virus. It was deduced that this insert most probably arose as a result of non-homologous recombination between the HA and matrix genes of the same virus. Over the course of the outbreak, a total of 37 isolates with, and 3 isolates without inserts were characterized. The events described here appear very similar to those which occurred in Chile in 2002 where the virulence shift of another H7N3 virus was attributed to non-homologous recombination between the HA and nucleoprotein genes.

Descriptors: veterinary disease outbreaks, hemagglutinins viral genetics, avian influenza A virus genetics, avian influenza epidemiology, genetic recombination, viral matrix proteins genetics, British Columbia.

NAL Call Number: QR360.J6

Abstract: Pigs are permissive to both human and avian influenza viruses and have been proposed to be an intermediate host for the genesis of pandemic influenza viruses through reassortment or adaptation of avian viruses. Prospective virological surveillance carried out between March 1998 and June 2000 in Hong Kong, Special Administrative Region, People's Republic of China, on pigs imported from southeastern China, provides the first evidence of interspecies transmission of avian H9N2 viruses to pigs and documents their cocirculation with contemporary human H3N2 (A/Sydney/5/97-like, Sydney97-like) viruses. All gene segments of the porcine H9N2 viruses were closely related to viruses similar to chicken/Beijing/1/94 (H9N2), duck/Hong Kong/Y280/97 (H9N2), and the descendants of the latter virus lineage. Phylogenetic analysis suggested that repeated interspecies transmission events had occurred from the avian host to pigs. The Sydney97-like (H3N2) viruses isolated from pigs were related closely to contemporary human H3N2 viruses in all gene segments and had not undergone genetic reassortment. Cocirculation of avian H9N2 and human H3N2 viruses in pigs provides an opportunity for genetic reassortment leading to the emergence of viruses with pandemic potential.

Descriptors: influenza A virus avian isolation and purification, influenza A virus human isolation and purification, swine virology, antibodies, viral blood, carrier state epidemiology, carrier state veterinary, cell line, China epidemiology, influenza epidemiology, influenza veterinary, influenza A virus avian classification, influenza A virus avian genetics, influenza A virus human classification, influenza A virus human genetics, molecular sequence data, phylogeny, sequence homology, nucleic acid, seroepidemiologic studies.

NAL Call Number: 41.8 Av5

Abstract: As of October 2001, the potential for use of infectious agents, such as anthrax, as weapons has been firmly established. It has been suggested that attacks on a nation's agriculture might be a preferred form of terrorism or economic disruption that would not have the attendant stigma of infecting and causing disease in humans. Highly pathogenic avian influenza virus is on every top ten list available for potential agricultural bioweapon agents, generally following foot and mouth disease virus and Newcastle disease virus at or near the top of the list. Rapid detection techniques for bioweapon agents are a critical need for the first-responder community, on a par with vaccine and antiviral development in preventing spread of disease. There are several current approaches for rapid, early responder detection of biological agents including influenza A viruses. There are also several proposed novel approaches in development. The most promising existing approach is real-time fluorescent PCR analysis in a portable format using exquisitely sensitive and specific primers and probes. The potential for reliable and rapid early-responder detection approaches are described, as well as the most promising platforms for using real-time PCR for avian influenza, as well as other potential bioweapon agents.

Descriptors: immune system, infection, molecular genetics, molecular diagnostics clinical techniques, diagnostic techniques, real time fluorescent polymerase chain reaction, real time fluorescent PCR, genetic techniques, laboratory techniques, agricultural bioweapon agents, bioterrorism, economic disruption, rapid disease detection.

NAL Call Number: 41.8 Av5

Abstract: Chickens, quail, and other land-based birds are extensively farmed around the world. They have been recently implicated in zoonotic outbreaks of avian influenza in Hong Kong. The possibility that land-based birds could act as mixing vessels or disseminators of avian/mammalian reassortant influenza A viruses with pandemic potential has not been evaluated. In this report, we investigated whether chickens and Japanese quail are susceptible to a mammalian influenza virus (A/swine/Texas/4199-2/98 (H3N2)). This virus did not grow in chickens and replicated to low levels in Japanese quail but did not transmit. Replacing the H3 gene of this virus for one of the avian H9 viruses resulted in transmission of the avian/swine reassortant virus among quail but not among chickens. Our findings demonstrated that Japanese quail could provide an environment in which viruses like the A/swine/Texas/4199-2/98 (H3N2) virus could further reassort and generate influenza viruses with pandemic potential.

Descriptors: epidemiology, infection, avian influenza, infectious disease, respiratory system disease, viral disease, pandemic potentials, zoonotic influenza outbreaks.


NAL Call Number: 41.8 Av5

Abstract: Seventeen avian species and two mammalian species were intranasally inoculated with the zoonotic A/chicken/Hong Kong/220/97 (chicken/HK) (H5N1) avian influenza (AI) virus in order to ascertain a relative range of susceptible hosts and the pathobiology of the resultant disease. A direct association was demonstrated between viral replication and the severity of disease, with four general gradations being observed among these species. These gradations included the following: 1) widespread dissemination with rapid and high mortality, 2) neurological disease relative to viral neurotropism, 3) asymptomatic infection or only mild transient depression associated with minor viral replication, and 4) absence of disease relative to minimal to no viral replication. This investigation not only demonstrates that the chicken/HK virus could infect multiple avian species, but also that the virulence of the chicken/HK virus varied significantly among avian species, including those species that are members of the same order.

Descriptors: epidemiology, infection, avian influenza, infectious disease, respiratory system disease, viral disease, inoculation, clinical techniques, therapeutic and prophylactic techniques, disease severity, disease susceptibility, host susceptibility, pathobiology, viral neurotropism, viral replication.


NAL Call Number: 41.8 Av5

Abstract: The H5N1 type A influenza viruses that emerged in Hong Kong in 1997 are a unique lineage of type A influenza viruses with the capacity to transmit directly from chickens to humans and produce significant disease and mortality in both of these hosts. The objective of this study was to ascertain the susceptibility of emus (Dramaius novaehollandiae), domestic geese (Anser anser domesticus), domestic ducks (Anas platyrhynchos), and pigeons (Columba livia) to intranasal (i.n.) inoculation with the A/chicken/Hong Kong/220/97 (H5N1) highly pathogenic avian influenza virus. No mortality occurred within 10 days postinoculation (DPI) in the four species investigated, and clinical disease, evident as neurologic dysfunction, was observed exclusively in emus and geese. Grossly, pancreatic mottling and splenomegaly were identified in these two species. In addition, the geese had cerebral malacia and thymic and bursal atrophy. Histologically, both the emus and geese developed pancreatitis, meningoencephalitis, and mild myocarditis. Influenza viral antigen was demonstrated in areas with histologic lesions up to 10 DPI in the geese. Virus was reisolated from oropharyngeal and cloacal swabs and from the lung, brain, and kidney of the emus and geese. Moderate splenomegaly was observed grossly in the ducks. Viral infection of the ducks was pneumotropic, as evidenced by mild inflammatory lesions in the respiratory tract and virus reisolation from oropharyngeal swabs and from a lung. Pigeons were resistant to HK/220 infection, lacking gross and histologic lesions, viral antigen, and reisolation of virus. These results imply that emus and geese are
susceptible to i.n. inoculation with the HK/220 virus, whereas ducks and pigeons are more resistant. These latter two species probably played a minimal epidemiologic role in the perpetuation of the H5N1 Hong Kong-origin influenza viruses.

Descriptors: infection, veterinary medicine, H5N1 avian influenza virus infection, etiology, mortality, viral disease, bursal atrophy, joint disease, cerebral malacia, nervous system disease, meningoencephalitis, nervous system disease, myocarditis, heart disease, neurologic dysfunction, nervous system disease, pancreatic mottling, digestive system disease, endocrine disease, pancreas, pancreatitis, digestive system disease, respiratory tract inflammation, respiratory system disease, splenomegaly, blood and lymphatic disease, thymic atrophy, endocrine disease, thymus.


NAL Call Number: 41.9 D23

Descriptors: avian influenza virus, pigs, poultry.


NAL Call Number: 41.9 D23

Descriptors: avian influenza virus, zoonoses, human death, Denmark, Holland.

Pilet, C. (1980). *Proceedings of an International Symposium, held on September 13 and 14, 1979 at the Ecole Nationale Veterinaire d'Alfort, France*. *Comparative Immunology, Microbiology and Infectious Diseases. Special Issue on Animal and Human Influenzas* 3(1/2): xvi + 246. ISSN: 0147-9571.

NAL Call Number: QR180.C62

Descriptors: influenza virus, humans, zoonoses, equine, porcine, avian, symposium.


Abstract: The last major human epidemics of infectious diseases have arisen from animals. Some of them are especially threatening. The authors call attention to the danger of spread of avian influenza, either directly or indirectly through genetic rearrangements. They underline the role of animals in the epidemiology of SARS, West Nile virus, hepatitis E, NIPA and Hendra virus, ehrlichiosis and Lyme disease. The authors recommend health surveillance not only in humans but also in animals; the teaching of zoonoses, and research on animal diseases transmissible to humans.

Descriptors: virus diseases transmission, zoonoses.


NAL Call Number: 448.8 P942

Abstract: Antigenic recombinants obtained by crossing of different human and animal influenza viruses were studied for some genetic markers and specific proteins in the resulting recombinants were analyses. In a number of cases the origin of inner virion proteins (NP and M) from one or the other parent and nonstructural NS proteins was established.

Descriptors: antigens, viral genetics, birds microbiology, influenza A virus avian genetics, influenza A virus human genetics, recombination, genetic, antigens, viral analysis, genetic markers, species specificity, viral proteins genetics.

Podchernyaeva, R.J., R.G. Webster, V.V. Skvorododka, A.I. Klimov, and V.M. Zhdanov (1989). *Molecular and biological properties of a variant of avian influenza A/Seal/Massachusetts/1/80 (H7N7) virus that is pathogenic for mice*. *Acta Virologica* 33(1): 38-42. ISSN: 0001-723X.

NAL Call Number: 448.3 AC85
Abstract: A/Seal/Mass/80 influenza virus has been shown to be closely related antigenically and genetically to avian influenza H7N7 viruses, however, the virus does not replicate efficiently in avian species but does replicate in most mammals, except mice (Hinshaw et al., Infect. Immun., 34, 351-361, 1981). In order to develop a model defining the molecular changes that occur during acquisition of virulence, the A/Seal/Mass/80 virus was adapted to growth in mouse lungs. The adaptation was accompanied by changes in a number of properties of the haemagglutinin as well as by changes in other genes of the virus as determined by RNA: RNA hybridization.

Descriptors: influenza A virus pathogenicity, genes viral, hemagglutinins viral, influenza A virus genetics, lethal dose 50, lung microbiology, mice, neutralization tests, nucleic acid hybridization, RNA viral analysis, serial passage, variation genetics, virulence.


NAL Call Number: 281.8 In32

Descriptors: avian influenza virus, disease prevention, disease transmission, hygiene, occupational transmission, poultry, poultry farming.


Descriptors: disease outbreaks, influenza transmission, influenza virology, influenza A virus human, poultry diseases transmission, poultry diseases virology, adolescent, adult, case control studies, chickens, child, child, preschool, ducks, Hong Kong epidemiology, infant, influenza epidemiology, influenza veterinary, middle aged, neutralization tests, population surveillance, poultry diseases epidemiology.


NAL Call Number: SF604.B7

Abstract: Epizootiological and virological surveys carried out between 1995 and mid-2000 corroborated the findings from the end of the 1970s that swine influenza did not cause any serious problems in pig herds in the Czech Republic. In the present study, no antibodies against either swine influenza virus, types A (H1N1) and A (H3N2), or avian influenza virus, A (H1N1), were demonstrated and no influenza virus was isolated. In contrast, antibodies against the human influenza virus isolated during the 1995 epidemic were found. The dynamics of antibody formation indicated that the human virus gradually disappeared from the pig population. It is possible that the human virus was introduced to the pig herds by infected animal attendants, in whom antibodies against this virus were also found. During the second human influenza epidemic in 1998/99, however, pigs remained free from antibody response to influenza virus.

Descriptors: swine, swine influenza virus, serotypes, antibodies, zoonoses, disease transmission, disease surveillance, Czech Republic, biological differences, domestic animals, Eastern Europe, epidemiology, Europe, immunological factors, influenza virus, livestock, orthomyxoviridae, pathogenesis, Suidae, useful animals, viruses.


NAL Call Number: RA648.5.E46

Descriptors: AIDS, acquired immunodeficiency syndrome, Ebola virus disease, SARS, severe acute respiratory syndrome, West Nile fever, avian influenza, bovine spongiform encephalopathy, prion disease, Edward Hicks artist, zoonosis, biography, history, epidemiology.


NAL Call Number: 448.3 Ar23

Abstract: Two hundred ninety-four subjects from Milan were tested for serum hemagglutination-inhibiting (HI) and neuraminidase-inhibiting (NI) antibodies to five avian influenza viruses. No HI antibodies were found
in all the serum samples. On the contrary, NI antibodies to each strain were detected depending on the year of birth of the subjects.

Descriptors: influenza immunology, influenza A virus avian immunology, hemagglutination inhibition tests, hemagglutinins viral immunology, influenza microbiology, influenza A virus avian pathogenicity, neuraminidase antagonists and inhibitors, neuraminidase immunology.


NAL Call Number: 448.8 P942

Abstract: A comparative analysis of involving the nucleocapsid protein (NP) into shaping-up of SDS-resistant oligomers was carried out presently in circulating epidemic strains of human influenza, viruses A and B. The study results of viral isolates obtained from clinical samples and recent standard strains revealed that the involvement of NP in the SDS-resistant oligomers, which are different in various subtypes of influenza A viruses. According to this sign, the human viruses A(9H3N2) are close to the avian ones, in which, as proved by us previously, virtually the entire NP transforms itself into the oligomers resistant to SDS. About 10-20% of NP are involved in shaping-up the virus influenza A(H1N1) of SDS-resistant oligomers. No SDS-resistant NP-oligomers were detected in influenza of type B. It is suggested that the prevalence of human viruses A(H3N2) in NP-oligomers are the peculiarities of NP structure and of the presence of the PB1 protein from avian influenza virus.

Descriptors: computer applications, infection, molecular genetics, SDS page, SDS polyacrylamide gel electrophoresis, electrophoretic techniques, laboratory techniques, comparative analysis laboratory techniques.


NAL Call Number: 448.3 AC85

Abstract: We have previously shown (Prokudina-Kantorovich EN and Semenova NP, Virology 223, 51-56, 1996) that the nucleoprotein (NP) of influenza A virus forms in infected cells oligomers which in the presence of SDS and 2-mercaptoethanol (ME) as reducing agent are stable at room temperature (RT) and dissociate at 100 degrees C. Here we report that the efficiency of intracellular NP oligomerization depends on the host origin of influenza A virus strain. Thus, in the cells infected with avian influenza A virus strains the viral NP was almost completely oligomerized and only traces of monomeric NP were detected by polyacrylamide gel electrophoresis (PAGE) in unboiled samples. However, in the cells infected with human influenza A virus strains, besides oligomeric NP also a significant amount of non-oligomerized monomeric NP was detected in unboiled samples. In purified virions of avian and human strains the same difference in NP monomers/oligomers ratio was detected as in the infected cells. A reassortant having all internal protein genes from a human strain and the glycoprotein genes from an avian strain revealed the same intracellular pattern of NP monomers/oligomers ratio as its parental human virus. These findings suggest that the type of NP oligomerization is controlled by the NP gene. The possible connection between the accumulation of protease-sensitive monomeric NP in cells infected with a human influenza strain and the parallel accumulation of cleaved NP in these cells is discussed.

Descriptors: influenza A virus metabolism, nucleoproteins metabolism, viral core proteins metabolism, biopolymers analysis, cell line, dogs, influenza A virus avian metabolism, influenza A virus human metabolism, influenza A virus genetics, nucleoproteins analysis, nucleoproteins genetics, reassortant viruses metabolism, species specificity, viral core proteins analysis, viral core proteins genetics.


NAL Call Number: 448.8 P942

Descriptors: bird diseases microbiology, orthomyxoviridae pathogenicity, bird diseases epidemiology,

**Descriptors:** influenza prevention and control, influenza A virus, avian immunology, influenza vaccines supply and distribution, drug industry, United States, vaccination.

**Descriptors:** disease outbreaks veterinary, food contamination, influenza, avian epidemiology, tigers, animal feed standards, animal feed virology, newborn animals, zoo animals, chickens, disease susceptibility veterinary, avian influenza mortality, avian influenza transmission, Thailand epidemiology.

**NAL Call Number:** 41.8 Ir4
**Descriptors:** avian influenza virus, diagnosis, disease control, disease prevention, disease transmission, fowl diseases, lesions, poultry, viral replication, zoonoses, fowl, reviews.

**Descriptors:** disease outbreaks prevention and control, influenza A virus, avian influenza, avian influenza prevention and control, avian influenza transmission, international cooperation, zoonoses transmission.

**Descriptors:** influenza prevention and control, influenza A virus, avian immunology, influenza vaccines, chickens, clinical trials, influenza virology.

**Abstract:** Annual outbreaks of influenza A infection are an ongoing public health threat and novel influenza strains can periodically emerge to which humans have little immunity, resulting in devastating pandemics. The 1918 pandemic killed at least 40 million people worldwide and pandemics in 1957 and 1968 caused hundreds of thousands of deaths. The influenza A virus is capable of enormous genetic variation, both by continuous, gradual mutation and by reassortment of genome segments between viruses. Both the 1957 and 1968 pandemic strains are thought to have originated as reassortants in which one or both human-adapted viral surface proteins were replaced by proteins from avian influenza strains. Analyses of the genes of the 1918 pandemic virus, however, indicate that this strain might have had a different origin. The haemagglutinin and nucleoprotein genome segments in particular are unlikely to have come directly from an avian source that is similar to those that are currently being sequenced. Determining whether a pandemic influenza virus can emerge by different mechanisms will affect the scope and focus of surveillance and prevention efforts.
**Descriptors:** influenza history, influenza virology, influenza A virus, human genetics, variation genetics, viral proteins genetics, disease outbreaks, hemagglutinin glycoproteins, influenza virus genetics, history, 20th century, influenza epidemiology, mutation, neuraminidase genetics, nucleoproteins genetics, reassortant viruses genetics, viral matrix proteins genetics, viral nonstructural proteins genetics.

Reina, J. (2002). Factores de virulencia y patogenicidad en las cepas gripales (virus influenza tipo A) aviares y humanas. [Factors affecting the virulence and pathogenicity of avian and human viral strains (influenza virus type A)]. *Enfermedades Infecciosas y Microbiologia Clinica* 20(7): 346-53. ISSN: 0213-005X.
**Abstract:** Most studies performed in avian viral strains seem to indicate that virulence is a polygenic phenomenon. However, hemagglutinin and neuraminidase and the genes codifying these substances
(genes 4 and 6) play an essential role in viral pathogenesis. Avian strains can be classified as avirulent or virulent according to the ability of hemagglutinin to be activated by endoproteases of the respiratory tract only or by proteases from other tissues. This ability is based on the progressive development of mutations that lead to the substitution of the normal amino acids at the point of hemagglutinin hydrolysis by the other basic amino acids that determine the amplification of the spectrum of hydrolysis and activation. Neuraminidase participates in the acquisition of virulence through its capacity to bind to plasminogen and by increasing the concentration of activating proteases. Adaptation to the host, through recognition of the cell receptor, is another factor determining the virulence and interspecies transmission of avian strains. From an epidemiological point of view, viral strains should be subtyped and the activating capacity of hemagglutinin should be determined to identify their degree of virulence.

**Descriptors:** influenza A virus avian pathogenicity, influenza A virus human pathogenicity, hemagglutinins, neuraminidase, peptide hydrolases, virulence.


**NAL Call Number:** R21.M43

**Descriptors:** avian influenza, humans, continual threat, birds, pigs.


**NAL Call Number:** 448.3 Ar23

**Abstract:** The base sequences of the coding region of the nucleoprotein (NP) genes of two H 10 influenza A viruses, one avian (virus N) and one mink virus, have been determined by primer extension. When the NP genes and the NP sequences derived from the only open reading frame of the two H 10 viruses were compared with those of other human and avian influenza A viruses, it turned out that the mink virus NP was highly related to that of other avian strains, but differed from that of the human strains. Comparison of the NP genes of the mink and avian strains of European origin suggests a direct lineage between them. Since the NP plays a major role in species specificity, it is assumed that an avian influenza virus has directly invaded the mink population.

**Descriptors:** base sequence, influenza A virus avian genetics, influenza A virus genetics, nucleoproteins genetics, RNA, viral, sequence homology, nucleic acid, viral proteins genetics, amino acid sequence, chickens microbiology, mink microbiology, molecular sequence data.


**NAL Call Number:** 410.9 P94

**Abstract:** Studies of the pathogenesis of influenza infection have involved the extensive use of animal models. The development of the current concepts of immunity to influenza and of the contribution the secretory immune system makes toward the protection of mucosal surfaces against influenza infection would have been impossible without this use of animals. The pathology and clinical signs of influenza infection in both natural and experimental hosts, the advantages and disadvantages of the most common experimental influenza infection models, and the contribution of animal models to the understanding of local and systemic immunity to influenza infection are discussed.

**Descriptors:** influenza immunology, influenza veterinary, antibody formation, disease models, animal, ferrets, fowl plague immunology, hamsters, haplorhini, horse diseases immunology, horses, influenza A virus avian, influenza A virus human, influenza A virus, porcine, influenza A virus, influenza vaccine administration and dosage, mice.


**Descriptors:** disease outbreaks, influenza epidemiology, influenza, avian transmission, zoonoses epidemiology, communicable diseases, emerging epidemiology, communicable diseases, emerging prevention and control, influenza prevention and control.

**NAL Call Number:** QR360.J6

**Abstract:** The question of how best to protect the human population against a potential influenza pandemic has been raised by the recent outbreak caused by an avian H5N1 virus in Hong Kong. The likely strategy would be to vaccinate with a less virulent, laboratory-adapted H5N1 strain isolated previously from birds. Little attention has been given, however, to dissecting the consequences of sequential exposure to serologically related influenza A viruses using contemporary immunology techniques. Such experiments with the H5N1 viruses are limited by the potential risk to humans. An extremely virulent H3N8 avian influenza A virus has been used to infect both immunoglobulin-expressing (Ig+/+) and Ig-/- mice primed previously with a laboratory-adapted H3N2 virus. The cross-reactive antibody response was very protective, while the recall of CD8(+) T-cell memory in the Ig-/- mice provided some small measure of resistance to a low-dose H3N8 challenge. The H3N8 virus also replicated in the respiratory tracts of the H3N2-primed Ig+/+ mice, generating secondary CD8(+) and CD4(+) T-cell responses that may contribute to recovery. The results indicate that the various components of immune memory operate together to provide optimal protection, and they support the idea that related viruses of nonhuman origin can be used as vaccines.

**Descriptors:** influenza prevention and control, influenza A virus avian immunology, influenza vaccine immunology, base sequence, birds, CD4 positive T lymphocytes immunology, CD8 positive T lymphocytes immunology, DNA, viral, disease models, animal, immunoglobulins immunology, influenza immunology, mice, mice inbred BALB c, mice, inbred c57bl, molecular sequence data.


**NAL Call Number:** QR189.V32

**Abstract:** Recently avian influenza A viruses of the H5N1 subtype were shown to infect humans in the Hong Kong area, resulting in the death of six people. Although these viruses did not efficiently spread amongst humans, these events illustrated that influenza viruses of subtypes not previously detected in humans could be at the basis of a new pandemic. In the light of this pandemic threat we evaluated and compared the efficacy of a classical non-adjuvanted subunit vaccine and a vaccine based on immune stimulating complexes (ISCOM) prepared with the membrane glycoproteins of the human influenza virus A/Hong Kong/156/97 (H5N1) to protect roosters against a lethal challenge with this virus. The ISCOM vaccine induced protective immunity against the challenge infection whereas the non-adjuvanted subunit vaccine proved to be poorly immunogenic and failed to induce protection in this model.

**Descriptors:** immune system, infection, pharmacology, lethal viral challenge, pandemic protective immunity, induction.


**NAL Call Number:** 448.8 V81

**Descriptors:** influenza A virus, porcine genetics, influenza A virus, porcine immunology, pneumonia, viral transmission, pneumonia, viral virology, swine virology, adult, cell line, child, preschool, ferrets, hemagglutination inhibition tests, immune sera immunology, influenza A virus, porcine isolation and purification, influenza A virus, porcine metabolism, likelihood functions, molecular sequence data, Netherlands, phylogeny, sequence homology, nucleic acid.


**NAL Call Number:** QR375.V6

**Descriptors:** avian influenza virus, RNA, nucleotide sequence, human strains.
NAL Call Number: 448.8 V81

Abstract: It has been previously reported that several human H1 influenza viruses isolated prior to 1956, in contrast to human H3 isolates which are quite specific for SA alpha 2,6Gal sequences, apparently recognize both SA alpha 2,3Gal and SA alpha 2,6Gal sequences (Rogers, G.N., and Paulson, J.C., Virology 127, 361-373, 1983). In this report human H1 isolates representative of two epidemic periods, from 1934 to 1957 and from 1977 to 1986, and H1 influenza isolated from pigs, ducks, and turkeys were compared for their ability to utilize sialyloligosaccharide structures containing terminal SA alpha 2,3Gal or SA alpha 2,6Gal sequences as receptor determinants. Five of the eight human isolates from the first epidemic period recognize both SA alpha 2,3Gal and SA alpha 2,6Gal linkages, in agreement with our previous results. Of the remaining three strains, all isolated towards the end of the first epidemic, two appear to prefer SA alpha 2,6Gal sequences while the third preferentially binds SA alpha 2,3Gal sequences. In contrast to the early isolates, 11 of 13 human strains isolated during the second epidemic period preferentially bind SA alpha 2,6Gal containing oligosaccharides. On the basis of changes in receptor binding associated with continued passage in the laboratory for some of these later strains, it seems likely that human H1 isolates preferentially bind SA alpha 2,6Gal sequences in nature, and that acquisition of SA alpha 2,3Gal-binding is associated with laboratory passage. Influenza H1 viruses isolated from pigs were predominantly SA alpha 2,6Gal-specific while those isolated from ducks were primarily SA alpha 2,3Gal-specific. Thus, as has been previously reported for H3 influenza isolates, receptor specificity for influenza H1 viruses appears to be influenced by the species from which they were isolated, human isolates binding preferentially to SA alpha 2,6Gal-containing oligosaccharides while those isolated from ducks prefer SA alpha 2,3Gal-containing oligosaccharides. However, unlike the SA alpha 2,6Gal-specific H3 isolates, binding to cell surface receptors by the H1 influenza viruses is not sensitive to inhibition by horse serum glycoproteins, regardless of their receptor specificity. These results suggest that, while the H1 and H3 hemagglutinins appear to be subject to similar host-derived selective pressures, there appear to be certain fundamental differences in the detailed molecular interaction of the two hemagglutinins with their sialyloligosaccharide receptor determinants.

Descriptors: influenza A virus avian metabolism, influenza A virus human metabolism, influenza A virus, porcine metabolism, influenza A virus metabolism, orthomyxoviridae metabolism, receptors, virus metabolism, ducks, hemagglutination inhibition tests, hemagglutination tests, species specificity, swine, turkeys.

NAL Call Number: 448.8 V81

Abstract: The binding of influenza virus to erythrocytes and host cells is mediated by the interaction of the viral hemagglutinin (H) with cell surface receptors containing sialic acid (SA). The specificity of this interaction for 19 human and animal influenza isolates was examined using human erythrocytes enzymatically modified to contain cell surface sialyloligosaccharides with the sequence SA alpha 2,6Gal beta 1,4GlcNAc; SA alpha 2,3Gal beta 1,4(3)GlcNAc; SA alpha 2,3Gal beta 1,3GalNAc; or SA alpha 2,6GalNAc. Although none of the viruses agglutinated cells containing the SA alpha 2,6GalNAc linkage, differential agglutination of cells containing the other three sequences revealed at least three distinct receptor binding types. Several virus isolates exhibited marked receptor specificity, binding only to cells containing the SA alpha 2,6Gal or the SA alpha 2,3Gal linkage, while others bound equally well to cells containing either linkage. Moreover, some viruses could distinguish between two oligosaccharide receptor determinants containing the terminal SA alpha 2,3Gal linkage when present in the SA alpha 2,3Gal beta 1,4(3)GlcNAc sequence or the SA alpha 2,3Gal beta 1,3GalNAc sequence binding cells containing only the former. The observed receptor specificities were not significantly influenced by the viral neuraminidases as shown by the use of the potent neuraminidase inhibitor 2-deoxy-2,3-dehydro-N-acetylneuraminic acid. Receptor specificity appeared, to some extent, to be dependent on the species from which the virus was isolated. In particular, human isolates of the H3 serotype all agglutinated cells containing the SA alpha 2,6Gal linkage, but not cells bearing the SA alpha 2,3Gal beta 1,3GalNAc sequence. In contrast, antigenically similar (H3) isolates from avian and equine species preferentially bound erythrocytes containing...
the SA alpha 2,3Gal linkage. This is of particular interest in view of the identification of the avian virus H3 hemagglutinin as the progenitor of the H3 hemagglutinin present on the current human Hong Kong viruses.


NAL Call Number: 448.8 V81

Abstract: Human and animal (avian and equine) influenza A virus isolates of the H3 serotype exhibit marked differences in their ability to bind specific sialyloligosaccharide sequences that serve as cell surface receptor determinants (G. Rogers and J. Paulson, 1983, Virology 127, 361-373). Whereas human isolates of this subtype strongly agglutinate enzymatically modified human erythrocytes containing the terminal SA alpha 2,6Gal sequence, avian and equine isolates preferentially agglutinate erythrocytes bearing the SA alpha 2,3Gal sequence. As shown in this report, a glycoprotein found in horse serum, alpha 2-macroglobulin, is a potent inhibitor of viral adsorption to the cell surface for human H3 isolates. In contrast, avian and equine isolates are poorly inhibited suggesting a correlation between receptor specificity and inhibitor sensitivity. Growth of a human H3 isolate (A/Memphis/102/72) on MDCK cells in the presence of horse serum resulted in an overall shift in the virus receptor specificity from preferential binding of the SA alpha 2,6Gal sequence to preferential binding of the SA alpha 2,3Gal sequence characteristic of avian and equine isolates. Clonally isolated variants of A/Memphis/102/72 grown in the presence or absence of horse serum exhibited binding properties that account for those observed in the field isolates. Clones which preferentially bound the SA alpha 2,6Gal linkage, like the parent human virus, were very sensitive to inhibition of hemagglutination by horse serum and equine alpha 2-macroglobulin. In contrast, receptor variants which preferentially bound the SA alpha 2,3Gal linkage, like the avian and equine isolate, were insensitive to such inhibitors. None of the variants was very sensitive to inhibition of hemagglutination by human alpha 2-macroglobulin. These results suggest that the presence, in vivo, of a glycoprotein inhibitor such as equine alpha 2-macroglobulin could suppress infection of influenza viruses bearing an H3 hemagglutinin with a SA alpha 2,6Gal specific, inhibitor sensitive phenotype, allowing growth to predominance of a virus which is SA alpha 2,3Gal specific and inhibitor insensitive as found in avian and equine isolates.

Descriptors: glycoproteins antagonists and inhibitors, influenza A virus avian drug effects, influenza A virus human drug effects, influenza A virus drug effects, receptors, virus drug effects, viral proteins antagonists and inhibitors, adsorption, chick embryo, ducks, erythrocytes immunology, erythrocytes microbiology, hemagglutination inhibition tests, hemagglutination tests, hemagglutinins viral analysis, horses, alpha macroglobulins pharmacology.


NAL Call Number: 448.8 V81

Abstract: Avian influenza A viruses of the H5 and H7 subtypes periodically cause severe outbreaks of disease in poultry. The question we wished to address in this study is whether these highly pathogenic strains constitute unique lineages or whether they and related nonpathogenic viruses are derived from common ancestors in the wild bird reservoir. We therefore compared the nucleotide and amino acid sequences of the hemagglutinin (HA) genes of 15 H5 and 26 H7 influenza A viruses isolated over 91 years from a variety of host species in Eurasia, Africa, Australia, and North America. Phylogenetic analysis indicated that the HA genes of H5 and H7 viruses that cause severe disease in domestic birds do not form unique lineages but share common ancestors with nonpathogenic H5 and H7 viruses. These findings predict that highly pathogenic avian H5 and H7 influenza A viruses will continue to emerge from wild bird reservoirs. Another important question is whether H7 influenza viruses found in mammalian species are derived from avian strains. We included eight equine influenza viruses and one seal isolate in the phylogenetic analysis of H7 HA genes. We could show that the HA genes of both, the equine and the seal viruses, shared ancestors.
with avian H7 HA genes. This indicates that currently circulating H7 viruses with an avian HA gene may have the potential to adapt to mammalian species and to cause an influenza outbreak in the new host.

**Descriptors:** avian influenza virus, agglutinins, genes, pathogenicity, phylogeny, nucleotide sequence, chemical composition, biological properties, cell structure, chromosomes, evolution, genomes, influenza virus, microbial properties, nucleus, orthomyxoviridae, proteins, viruses, viral hemagglutinins, structural genes, amino acid sequences.


**Descriptors:** Hong Kong influenza A, epidemiology, *Streptopelia decaocto*, zoo animals, birds, dogs, goats, human, fowl, Budapest.


**Descriptors:** avian influenza virus, orthomyxoviridae, Charadriiformes, terns, *Sterna hirunda*, mallard.


**NAL Call Number:** QR46.J6

**Descriptors:** zoonoses, influenza virus A and B, relationships, RNA, *Sus scrofa*, pigs, swine influenza virus, Wisconsin, United States.


**NAL Call Number:** 41.8 B45

**Abstract:** Findings based on molecular genetics and phylogeny indicate that avian species represent an important reservoir for influenza viruses and that virus strains of man and different mammals originated from avian influenza virus ancestors. In contrast to infectious agents causing classical zoonoses, influenza viruses have to alter their genetic make up in order to change their host range. The special, segmented structure of the viral RNA allows an exchange of gene(s) between two different influenza viruses (reassortment) resulting in viruses with different combinations of genome segments and thereby creating new biological properties. Under the selective pressure of the new host the most adapted virus variants will succeed which arose from a genetically heterogeneous virus population with additional mutations. In particular mutations of the genes encoding the polymerase complex (mutator mutations) would be advantageous for rapid adaptation in a hostile environment. The generation of influenza viruses capable of overcoming the species barrier is a rare event since only virus variants will succeed which are genetically stable and transmissible and which replicate efficiently in the new host. It is considered likely that pigs act as intermediate hosts for adaptation of avian viruses to man.

**Descriptors:** influenza transmission, influenza veterinary, orthomyxoviridae genetics, zoonoses, birds, mammals, mutation, orthomyxoviridae pathogenicity, species specificity, swine, variation genetics.


**Abstract:** Influenza virus Equine 1 (A/equine/Prague/56) has a hemagglutinin which is antigenically related to the hemagglutinin of fowl plague virus strain Rostock (FPV) and a neuraminidase which cross-reacts with the enzyme of virus N (A/chick/Germany/49). After a single injection of chickens with Equine 1 virus no hemagglutination inhibiting (HI) and neutralizing antibodies against FPV can be demonstrated, although the birds are fully protected against a lethal dose of FPV. HI and neutralizing antibodies against FPV appear after a second injection of Equine 1 virus several weeks after the first one. Liberation of newly synthesized FPV from the host cell is inhibited by antibodies cross-reacting with any antigen of virus surface.

**Descriptors:** antigens, viral administration and dosage, arteritis virus, equine immunology, influenza A
virus avian immunology, RNA viruses immunology, binding sites, antibody, epitopes, fluorescent antibody technique, hemadsorption, hemagglutination inhibition tests, hemagglutination tests, hemagglutinins viral isolation and purification, injections, intravenous, neuraminidase analysis, neutralization tests, plaque assay.

NAL Call Number: 448.8 P942
Abstract: A comparative immunological analysis of the composition of antigenic determinants (AGD) in hemagglutinins of human influenza A virus (HIAV) of the serosubtypes H1, H2, H3, and in hemagglutinins of animal influenza viruses (AIV) of the serosubtypes H1, H3-H6, H8-H11 with 25 polyclonal highly active sera was demonstrated. Using original monospecific mon AGD in HIAV and AIV hemagglutinins was demonstrated. Using original monospecific antibodies to individual AGD, those AGD contributing to similarity and differences between HIAV and AIV were determined. It was found that influenza A. virus strains isolated from man in the USSR in 1986 were identical in the antigenic structure of hemagglutinin with that isolated from a tern in 1973 (A/tern/Turkmenistan/18/73).
Descriptors: epitopes, genes viral, influenza A virus avian immunology, human immunology, antigens, viral immunology, cross reactions, hemagglutination tests, hemagglutinins viral genetics, hemagglutinins viral immunology, avian genetics, human genetics, neuraminidase genetics, neuraminidase immunology, species specificity.

NAL Call Number: QR46.J6
Abstract: From May to December 1997, 18 cases of mild to severe respiratory illness caused by avian influenza A (H5N1) viruses were identified in Hong Kong. The emergence of an avian virus in the human population prompted an epidemiological investigation to determine the extent of human-to-human transmission of the virus and risk factors associated with infection. The hemagglutination inhibition (HI) assay, the standard method for serologic detection of influenza virus infection in humans, has been shown to be less sensitive for the detection of antibodies induced by avian influenza viruses. Therefore, we developed a more sensitive microneutralization assay to detect antibodies to avian influenza in humans. Direct comparison of an HI assay and the microneutralization assay demonstrated that the latter was substantially more sensitive in detecting human antibodies to H5N1 virus in infected individuals. An H5-specific indirect enzyme-linked immunosorbent assay (ELISA) was also established to test children's sera. The sensitivity and specificity of the microneutralization assay were compared with those of an H5-specific indirect ELISA. When combined with a confirmatory H5-specific Western blot test, the specificities of both assays were improved. Maximum sensitivity (80%) and specificity (96%) for the detection of anti-H5 antibody in adults aged 18 to 59 years were achieved by using the microneutralization assay combined with Western blotting. Maximum sensitivity (100%) and specificity (100%) in detecting anti-H5 antibody in sera obtained from children less than 15 years of age were achieved by using ELISA combined with Western blotting. This new test algorithm is being used for the seroepidemiologic investigations of the avian H5N1 influenza outbreak.
Descriptors: antibodies, viral blood, influenza A virus avian immunology, serologic tests methods, adolescent, adult, blotting, western methods, blotting, western statistics and numerical data, child, preschool, cross reactions, enzyme linked immunosorbent assay methods, enzyme linked immunosorbent assay statistics and numerical data, hemagglutination inhibition tests methods, hemagglutination inhibition tests statistics and numerical data, Hong Kong epidemiology, influenza epidemiology, influenza immunology, influenza transmission, avian classification, avian pathogenicity, middle aged, neutralization tests methods, neutralization tests statistics and numerical data, sensitivity and specificity, seroepidemiologic studies, serologic tests statistics and numerical data.

NAL Call Number: 41.8 Av5
Abstract: The H5N1 viruses isolated from humans in Hong Kong directly infected both mice and ferrets without prior adaptation to either host. Two representative viruses, A/Hong Kong/483/97 (HK/483) and A/Hong Kong/486/97 (HK/486) were equally virulent in outbred ferrets but differed in their virulence in inbred mice. Both HK/483 and HK/486 replicated systemically in ferrets and showed neurologic manifestations. In contrast, intranasal infection of mice with HK/483, but not HK/486, resulted in viral spread to the brain, neurologic signs, and death. However, HK/486 was able to replicate in the brain and induce lethal disease following direct intracerebral inoculation.

Descriptors: infection, nervous system, avian influenza, infectious disease, respiratory system disease, viral disease, neurological infection manifestations.


NAL Call Number: 448.3 Ar23

Abstract: Human-avian and human-mammalian influenza A virus reassortant clones with the neuraminidase (NA) gene of the A/USSR/90/77 (H1N1) strain and hemagglutinin (HA) genes of H3, H4 and H13 subtypes had been shown in an earlier publication to produce low HA yields in the embryonated chicken eggs. The low HA titers had been shown to be due, at least in part, to the formation of virion clusters at 4 degrees C; the clustering was removed by the treatment with bacterial neuraminidase [Rudneva et al., Arch. Virol (1993) 133: 437-450]. By serial passages of the reassortants in chick embryos non-aggregating variants were selected: the variants produced HA titers of the same order as A/USSR/90/77 parent virus. The assessment of the virus yields by the analysis of the partially purified virus preparations from fixed volumes of the allantoic fluid revealed that actual virion yields of the initial reassortants were lower than the yields of their passaged variants or of the parent viruses. The passaged variant of a reassortant possessing the HA gene of A/Duck/Ukraine/1/63 (H3N2) virus differed from the original (non-passaged) reassortant and from the parent A/Duck/Ukraine/1/63 virus in the reaction with a panel of monoclonal antibodies against H3 hemagglutinin. The data suggest that some HA-NA combinations may lead to an incomplete functional match between HA and NA and to the formation of low-yield reassortants, thus representing a possible limiting factor in the emergence of new HA-NA combinations in natural conditions.

Descriptors: hemagglutinins viral biosynthesis, influenza A virus avian metabolism, human metabolism, neuraminidase biosynthesis, reassortant viruses metabolism, antibodies, monoclonal immunology, antibodies, viral immunology, antigens, viral immunology, cell line, chick embryo, dogs, epitopes, hemagglutinin glycoproteins, influenza virus, hemagglutinins viral genetics, avian genetics, human genetics, neuraminidase genetics, phenotype, reassortant viruses genetics, serial passage, variation genetics.


NAL Call Number: 448.8 J821

Abstract: Avian plague virus was used as antigen in a counterimmunoelectrophoresis technique. This virus was selected because it detects only type-specific influenza A antibodies in human sera, avoiding the possible interference of other antigens with anodic migration. The results with reference sera, as well as the correlation of positive sera found by counterimmunoelectrophoresis and complement fixation with the proposed antigen, in the absence of other types of antibodies to fowl plague virus antigen, support the conclusion that the counterimmunoelectrophoresis technique reveals type-specific antibodies. The test is more sensitive than immunodiffusion but less sensitive than complement fixation. Its sensitivity, simplicity, and rapidity make it suitable for serologic surveys of human influenza A.

Descriptors: antibodies, viral analysis, antigens, viral, immuno-electrophoresis, influenza immunology, influenza A virus avian immunology, antibody specificity, chick embryo, complement fixation tests, guinea pigs immunology, immune sera, immunodiffusion.

**Abstract:** Two H9N2 viruses were isolated, for the first time, from humans in Hong Kong in 1999. Isolation of influenza viruses with a novel subtype of the hemagglutinin (HA) drew attention of health care authorities worldwide from the view of pandemic preparedness. Sequence analysis of the HA genes reveals that HA of A/Hong Kong/1073/99 (H9N2) is most closely related to that of A/quail/HK/G1/97 (H9N2) that contains the internal genes similar to those of Hong Kong/97 (H5N1) viruses. Phylogenetic and antigenic analyses demonstrated the diversity among H9 HA. A/Hong Kong/1073/99 was shown to cause a respiratory infection in Syrian hamsters, suggesting that the virus can replicate efficiently in mammalian hosts. We developed a whole virion test vaccine with a formalin-inactivated egg-grown HK1073. Intraperitoneal administration of the vaccine twice to hamsters conferred a complete protection against challenge infection by the MDCK cell-grown homologous virus. Receptor specificity of HK1073 appeared different from that of other avian influenza viruses of H9 subtype which recognize preferentially alpha-2,3 linked sialic acid. Hemagglutination of HK1073 with guinea pig erythrocytes was inhibited by both alpha-2,3 and alpha-2,6 linked sialic acid containing polymers. These data suggested that HK1073 had acquired a broader host range, including humans. Together with data so far available, the present study suggested that isolation of the H9 influenza viruses from humans requires precaution against the emergence of a novel human influenza.

**Descriptors:** influenza virology, influenza A virus human isolation and purification, antigens, viral immunology, Asia, cattle, cultured cells, chick embryo, child, dogs, Europe, glycoconjugates pharmacology, guinea pigs, hamsters, hemagglutination tests, hemagglutination, viral, hemagglutinin glycoproteins, influenza virus genetics, hemagglutinin glycoproteins, influenza virus physiology, Hong Kong, horses, influenza prevention and control, influenza veterinary, avian classification, avian physiology, human classification, human genetics, human immunology, human physiology, porcine classification, porcine physiology, influenza vaccine immunology, lung virology, mesocricetus, N-acetylneuraminic acid metabolism, North America, phylogeny, poultry virology, poultry diseases virology, receptors, virus metabolism, sheep, species specificity, swine, swine diseases virology, vaccination, vaccines, inactivated, virion immunology, virus cultivation.
were compared antigenically with those of H2N2 human strains. The electrophoretic mobility of the viral proteins and of the S1-treated double-stranded RNAs from two human and six avian strains, as well as the results of EIA-tests using monoclonal antibodies to their matrix protein and nucleoproteins indicate an antigenic relationship between the avian isolates and human strains of H2N2 subtype. One of the avian strains had a reduced amount of matrix protein.

Descriptors: antigens, viral analysis, epitopes analysis, influenza A virus avian chemistry, human chemistry, RNA viral analysis, viral matrix proteins analysis, antibodies, monoclonal, ducks, enzyme linked immunosorbent assay, East Germany.


NAL Call Number: 448.8 V81

Abstract: H2N2 influenza A viruses caused the Asian pandemic of 1957 and then disappeared from the human population 10 years later. To assess the potential for similar outbreaks in the future, we determined the antigenicity of H2 hemagglutinins (HAs) from representative human and avian H2 viruses and then analyzed the nucleotide and amino acid sequences to determine their evolutionary characteristics in different hosts. The results of longitudinal virus surveillance studies were also examined to estimate the prevalence of avian H2 isolates among samples collected from wild ducks and domestic poultry. Reactivity patterns obtained with a large panel of monoclonal antibodies indicated antigenic drift in the HA of human H2 influenza viruses, beginning in 1962. Amino acid changes were clustered in two regions of HA1 that correspond to antigenic sites A and D of the H3 HA. By contrast, the antigenic profiles of the majority of avian H2 HAs were remarkably conserved through 1991, resembling the prototype Japan 57 (H2N2) strain. Amino acid changes were distributed throughout HA1, indicating that antibodies do not play a major role in the selection of avian H2 viruses. Phylogenetic analysis revealed two geographic site-specific lineages of avian H2 HAs: North American and Eurasian. Evidence is presented to support interregion transmission of gull H2 viruses. The human H2 HAs that circulated in 1957-1968 form a separate phylogenetic lineage, most closely related to the Eurasian avian H2 HAs. There was an increased prevalence of H2 influenza viruses among wild ducks in 1988 in North America, preceding the appearance of H2N2 viruses in domestic fowl. As the prevalence of avian H2N2 influenza viruses increased on turkey farms and in live bird markets in New York City and elsewhere, greater numbers of these viruses have come into direct contact with susceptible humans. We conclude that antigenically conserved counterparts of the human Asian pandemic strain of 1957 continue to circulate in the avian reservoir and are coming into closer proximity to susceptible human populations.

Descriptors: disease outbreaks, disease reservoirs, hemagglutinins viral genetics, influenza epidemiology, influenza A virus genetics, orthomyxoviridae infections epidemiology, Americas epidemiology, antibodies, monoclonal, antibodies, viral immunology, Asia epidemiology, birds microbiology, Europe epidemiology, evolution, fowl plaque epidemiology, fowl plaque genetics, genes viral genetics, hemagglutinin glycoproteins, influenza virus, influenza genetics, influenza A virus avian genetics, avian immunology, human genetics, human immunology, influenza A virus immunology, molecular sequence data, orthomyxoviridae infections genetics, phylogeny, population surveillance, time factors.


Descriptors: infection, occupational health, avian influenza A virus, viral pneumonia, veterinarian, human death, Netherlands.


NAL Call Number: RA648.5.E97

Abstract: There are three ways how influenza A viruses can escape the immune response in the human population: (1) By antigenic drift. This means by mutation and selection of variants under the selection
pressure of the immune system. These variants have amino acid replacements mainly in the epitopes of the hemagglutinin. (2) By antigenic shift. This means replacement of at least the hemagglutinin gene of the prevailing human strain by the allelic gene of an avian influenza virus by reassortment. (3) As a rare event, direct or indirect introduction of an avian influenza virus in toto into the human population. A prior introduction of an avian virus into pigs and an adaptation to the new host might be a presupposition for its final passage to humans. In this sense the nowadays situation is reminiscent to that of about 100 years ago, when an avian virus was presumably first introduced into pigs, and from there into humans. Immediately or some time thereafter the disastrous Spanish Flu in 1918/19 had killed at least 20,000,000 people in one winter. Pandemic strains can be created by all three means, however the most common way is by reassortment. In order to recognize a pandemic strain as soon as possible a worldwide surveillance system and collaborating laboratories equipped with corresponding modern technologies are required.

Descriptors: disease outbreaks, influenza epidemiology, influenza virology, orthomyxoviridae genetics, antigenic variation genetics, antigens, viral genetics, birds, genes viral genetics, influenza A virus avian genetics, avian immunology, porcine genetics, porcine immunology, orthomyxoviridae immunology, swine.


**NAL Call Number:** 448.8 V81

**Abstract:** The hemagglutinin (HA) gene of the influenza virus subtype H1N1 isolated from pigs and birds has been analyzed by the hybridization technique. According to the RNase protection data the HA genes of recent isolates from pigs in Northern Europe are genetically more closely related to those of isolates from birds in Europe and North America than to those of isolates from pigs in the United States, Taiwan, and Italy. Thus, two different H1N1 subtypes are circulating in the pig population. The results are consistent with the view that H1N1 viruses can be transmitted from birds to pigs and/or vice versa.

Descriptors: hemagglutinin viral genetics, influenza A virus avian genetics, porcine genetics, genetics, birds microbiology, genes viral, avian immunology, avian isolation and purification, porcine classification, porcine immunology, porcine isolation and purification, nucleic acid hybridization, swine microbiology.


**NAL Call Number:** QR360.J6

**Abstract:** To analyze the compatibility of avian influenza A virus hemagglutinins (HAs) and human influenza A virus matrix (M) proteins M1 and M2, we doubly infected Madin-Darby canine kidney cells with amantadine (1-aminoadamantane hydrochloride)-resistant human viruses and amantadine-sensitive avian strains. By using antisera against the human virus HAs and amantadine, we selected reassortants containing the human virus M gene and the avian virus HA gene. In our system, high virus yields and large, well-defined plaques indicated that the avian HAs and the human M gene products could cooperate effectively; low virus yields and small, turbid plaques indicated that cooperation was poor. The M gene products are among the primary components that determine the species specificities of influenza A viruses. Therefore, our system also indicated whether the avian HA genes effectively reassorted into the genome and replaced the HA gene of the prevailing human influenza A viruses. Most of the avian HAs that we tested efficiently cooperated with the M gene products of the early human A/PR/8/34 (H1N1) virus; however, the avian HAs did not effectively cooperate with the most recently isolated human virus that we tested, A/Nanchang/933/95 (H3N2).

Cooperation between the avian HAs and the M proteins of the human A/Singapore/57 (H2N2) virus was moderate. These results suggest that the currently prevailing human influenza A viruses might have lost their ability to undergo antigenic shift and therefore are unable to form new pandemic viruses that contain an avian HA, a finding that is of great interest for pandemic planning.

Descriptors: hemagglutinin glycoproteins, influenza virus metabolism, influenza A virus avian genetics, human genetics, reassortant viruses, viral matrix proteins metabolism, amantadine pharmacology, antiviral agents pharmacology, cell line, dogs, drug resistance, viral, fowl plague virology, hemagglutinin glycoproteins, influenza virus genetics, influenza virology, avian drug effects, avian growth and development, avian metabolism, human drug effects, human growth and development, human metabolism, kidney
cytology, kidney virology, plaque assay, poultry, viral matrix proteins genetics.


**NAL Call Number:** QH434.V57

**Abstract:** There are two different mechanisms by which influenza viruses might evolve: (1) Because the RNA genome of influenza viruses is segmented, new strains can suddenly be produced by reassortment, as happens, for example, during antigenic shift, creating new pandemic strains. (2) New viruses evolve relatively slowly by stepwise mutation and selection, for example, during antigenic or genetic drift. Influenza A viruses were found in various vertebrate species, where they form reservoirs that do not easily mix. While human influenza A viruses do not spread in birds and vice versa, the species barrier to pigs is relatively low, so that pigs might function as "mixing vessels" for the creation of new pandemic reassortants in Southeast Asia, where the probability is greatest for double infection of pigs by human and avian influenza viruses. Phylogenetic studies revealed that about 100 years ago, an avian influenza A virus had crossed the species barrier, presumably first to pigs, and from there to humans, forming the new stable human and classical swine lineages. In 1979, again, an avian virus showed up in the North European swine population, forming another stable swine lineage. The North European swine isolates from 1979 until about 1985 were genetically extremely unstable. A hypothesis is put forward stating that a mutator mutation is necessary to enable influenza virus to cross the species barrier by providing the new host with sufficient variants from which it can select the best fitting ones. As long as the mutator mutation is still present, such a virus should be able to cross the species barrier a second time, as happened about 100 years ago. Although the most recent swine isolates from northern Germany are again genetically stable, we nevertheless should be on the lookout to see if a North European swine virus shows up in the human population in the near future.

**Descriptors:** evolution and adaptation, immune system, infection, microbiology, veterinary medicine, antigenic drift evolution host infection molecular evolution pandemic reassortants phylogeny species barrier virology.


**NAL Call Number:** 448.8 V81

**Abstract:** There is evidence that the nucleoprotein (NP) gene of the classical swine virus (A/Swine/1976/31) clusters with the early human strains at the nucleotide sequence level, while at the level of the amino acid sequence, as defined by consensus amino acids and in functional tests, its NP is clearly "avian like." Therefore it was suggested that the Sw/31 NP had been recently under strong selection pressure, possibly caused by reassortment with other avian influenza genes, whose gene products have to cooperate intimately with NP (Gammelin et al., 1989. *Virology* 170, 71-80). This suggestion has been investigated by sequencing the genes of internal and nonstructural proteins of Sw/31. The data on these sequences and on the phylogenetic trees are not in accordance with that suggestion: all these genes cluster with the early human strains at the nucleotide level while, at the level of the amino acid sequence, most of them are more closely related to the avian strains, thus resembling NP in this respect. This indicates that these genes rather evolved concomitantly with the NP gene. Our data are in agreement with the suggestion that, at about the time of the Spanish Flu (1918/19), a human influenza A (H1N1) virus entered the pig population. Furthermore, it is known that the NP of the human influenza A viruses—in contrast to that of the avian and swine strains—has been under strong selection pressure to change (Gammelin et al., 1990. *Mol. Biol. Evol.* 7, 194-200. Gorman et al., 1990a. *J. Virol.* 64, 1487-1497). Thus, after transfer of a human strain into pigs, the selection pressure might be released, enabling the NP and the other genes of the swine virus to evolve back to the optimal avian sequences, especially at the functionally important consensus positions. The swine influenza viruses circulating since 1979 in Northern Europe—represented by A/Swine/Germany/2/81 (H1N1) -have all genes, so far examined, derived from an avian influenza virus pool and are different from the classical swine viruses.

**Descriptors:** influenza A virus, porcine genetics, phylogeny, RNA replicase, viral proteins genetics, chick embryo, consensus sequence, genes viral, nucleoproteins genetics, swine, viral core proteins genetics.


NAL Call Number: 448.8 J821

Abstract: The infectivity, immunogenicity, and efficacy of live, attenuated influenza A/Texas/1/85 (H1N1) and A/Bethesda/1/85 (H3N2) avian-human (ah) and cold-adapted (ca) reassortant vaccines were compared in 252 seronegative adult volunteers. The immunogenicity and efficacy of the H1N1 reassortant vaccine were also compared with those of the trivalent inactivated virus vaccine. Each reassortant vaccine was satisfactorily attenuated. The 50% human infectious dose was 10(4.9) for ca H1N1, 10(5.4) for ah H1N1, 10(6.4) for ca H3N2, and 10(6.5) TCID50 for ah H3N2 reassortant virus. Within a subtype, the immunogenicities of ah and ca vaccines were comparable. Five to seven weeks after vaccination, volunteers were challenged with homologous wild-type influenza A virus. The magnitude of shedding of virus after challenge was greater than 100-fold less in H1N1 vaccinees and greater than 10-fold less in H3N2 vaccinees compared with unimmunized controls. The vaccines were equally efficacious, as indicated by an 86%-100% reduction in illness. Thus, the ah A/Mallard/New York/6750/78 and the ca A/Ann Arbor/6/60 reassortant viruses are comparable.

Descriptors: influenza prevention and control, influenza A virus avian immunology, human immunology, influenza vaccine, adult, antibodies, viral biosynthesis, cold, double blind method, enzyme linked immunosorbent assay, hemagglutination inhibition tests, avian pathogenicity, avian physiology, human pathogenicity, human physiology, random allocation, vaccines, attenuated, vaccines, synthetic, virus replication.


Abstract: In order to identify molecular changes associated with the transmission of avian influenza A H5N1 and H9N2 viruses to humans, the internal genes from these viruses were compared to sequences from other avian and human influenza A isolates. Phylogenetically, each of the internal genes of all sixteen of the human H5N1 and both of the H9N2 isolates were closely related to one another and fell into a distinct clade separate from clades formed by the same genes of other avian and human viruses. All six internal genes were most closely related to those of avian isolates circulating in Asia, indicating that reassortment with human strains had not occurred for any of these 18 isolates. Amino acids previously identified as host-specific residues were predominantly avian in the human isolates although most of the proteins also contained residues observed previously only in sequences of human influenza viruses. For the majority of the nonglycoprotein genes, three distinct subgroups could be distinguished on bootstrap analyses of the nucleotide sequences, suggesting multiple introductions of avian virus strains capable of infecting humans. The shared nonglycoprotein gene constellations of the human H5N1 and H9N2 isolates and their detection in avian isolates only since 1997 when the first human infections were detected suggest that this particular gene combination may confer the ability to infect humans and cause disease. J. Med. Virol. 66:107-114, 2002. Published 2002 Wiley-Liss, Inc.

Descriptors: fowl plague transmission, influenza virology, influenza A virus avian genetics, human genetics, fowl plague virology, influenza transmission, avian classification, human classification, human isolation and purification, molecular sequence data, nasopharynx virology, phylogeny, viral proteins genetics.


NAL Call Number: aSF995.6.1615 1981a

Descriptors: avian influenza virus, techniques, vaccines, mammalian species, avian species.

Abstract: Five-week-old ddY mice were inoculated intranasally with a low virulent (4e) or highly virulent (24a5b) avian influenza virus strain originated from a water bird. None of mice in the 4e group showed clinical signs and brain lesions. Of the 24a5b group, two mice died and one mouse was killed at a moribund state at day 7 post-inoculation (PI). Four mice of the 24a5b group necropsied at day 5 or 7 PI had mild to severe encephalitis in the brain stem and the cerebellar white matter. Influenza virus antigen was detected in neurons, glial cells and vascular endothelium in the lesions. The distribution of the lesions seems to indicate the transneuronal invasion of the virus via cranial nerve fibers into the brain.

Descriptors: birds virology, brain pathology, encephalitis, viral pathology, influenza pathology, influenza A virus avian pathogenicity, antigens, viral analysis, brain virology, brain stem pathology, cerebellum pathology, encephalitis, viral virology, immunohistochemistry, avian isolation and purification, mice, necrosis, virulence.


Descriptors: influenza A virus avian isolation and purification, chickens, China, ducks, geese, hemagglutination inhibition tests, Hong Kong, neuraminidase analysis, poultry.


Abstract: In the last two decades, influenza A viruses have been found to occur throughout the animal kingdom, mainly in birds, notably aquatic ones, in which infection is largely intestinal, waterborne, and asymptomatic. The domestic duck of southern China, raised in countless numbers all year round mainly as an adjunct to rice farming, is the principal host of influenza A viruses. Studies based on Hong Kong H3N2 viruses from southern China suggest that pandemic strains originate from the domestic duck there and are transmitted to humans via the domestic pig, which acts as a "mixing vessel" for two-way transmission of viruses. This provides further support for the hypothesis that the region is a hypothetical influenza epicenter. Rural dwellers in the epicenter show serological evidence of contact with non-human influenza A viruses. Two hypotheses are advanced for the range of hemagglutinin (HA) subtypes of viruses that can cause pandemics (1) circle or cycle limited to H1, H2, and H3 subtypes, thereby implying that a virus of the H2 subtype will cause the next pandemic; and (2) spiral, by which any one of the 14 HA subtypes recorded to date may be involved. Consideration is given to the temporal and geographical factors and range of hosts, namely the duck, pig, and human, that need to be submitted to virus surveillance in China and beyond to attempt to anticipate a future pandemic. Evidence is presented that points strongly to pandemic influenza being a zoonosis.

Descriptors: ducks microbiology, influenza transmission, influenza A virus avian pathogenicity, human pathogenicity, porcine pathogenicity, swine microbiology, zoonoses transmission, China epidemiology, chronology, disease outbreaks prevention and control, feces microbiology, fresh water, influenza epidemiology, influenza microbiology, avian isolation and purification, human isolation and purification, porcine isolation and purification, reassortant viruses genetics.


Abstract: This account takes stock of events and involvements, particularly on the avian side of the influenza H5N1 'bird flu' incident in Hong Kong SAR in 1997. It highlights the role of the chicken in the many live poultry markets as the source of the virus for humans. The slaughter of chicken and other poultry across the SAR seemingly averted an influenza pandemic. This perspective from Hong Kong SAR marks the coming-of-age of acceptance of the role of avian hosts as a source of pandemic human influenza viruses and offers the prospect of providing a good baseline for influenza pandemic preparedness in the future. Improved surveillance is the key. This is illustrated through the H9N2 virus which appears to have provided
the 'replicating' genes for the H5N1 virus and which has since been isolated in the SAR from poultry, pigs and humans highlighting its propensity for interspecies transmission.

Descriptors: influenza transmission, influenza A virus avian pathogenicity, zoonoses transmission, chickens, disease outbreaks prevention and control, fowl plague transmission, Hong Kong epidemiology, influenza mortality, influenza virology, avian genetics.

NAL Call Number: 448.8 J821
Descriptors: antigens, viral immunology, influenza A virus, porcine immunology, influenza A virus immunology, swine microbiology, viral core proteins, antibodies, monoclonal immunology, antibodies, viral immunology, antigens, viral analysis, China, cross reactions, epitopes, hemagglutinins viral immunology, Hong Kong, avian immunology, human immunology, neuraminidase immunology, nucleoproteins immunology, Taiwan, viral proteins immunology.

NAL Call Number: QR1.S64
Abstract: Pandemic influenza is a zoonosis. Studies on influenza ecology conducted in Hong Kong since the 1970s in which Hong Kong essentially functioned as an influenza sentinel post indicated that it might be possible, for the first time, to have influenza preparedness at the baseline avian level. This appreciation of influenza ecology facilitated recognition of the H5N1 'bird flu' incident in Hong Kong in 1997 in what was considered to be an incipient pandemic situation, the chicken being the source of virus for humans and, if so, was the first instance where a pandemic may have been averted. The 2001 and 2002 H5N1 incidents demonstrated that it was possible to have an even higher order of baseline preparedness with the recognition in chicken of a range of genotypes of H5N1-like viruses before they had the opportunity to infect humans. Investigations of these incidents revealed a complex ecology involving variously precursor avian H5N1 virus in geese and ducks, and H9N2 and H6N1 viruses in quail, the quail possibly functioning as an avian 'mixing vessel' for key genetic reassortment events for onward transmission of H5N1 viruses highly pathogenic for chicken and humans. These findings highlight the importance of systematic virus surveillance of domestic poultry in recognizing changes in virus occurrence, host range and pathogenicity as signals at the avian level that could presage a pandemic. For example, there is now an increasing prevalence of avian influenza viruses in terrestrial (in contrast to aquatic) poultry. Prior to 1997, no particular virus subtype other than H4N6 would have been considered a candidate for pandemicity and this was based, in the absence of any other data, on its high frequency of occurrence in ducks in southern China. Now, with the isolation of H5N1 and H9N2 viruses from humans supported by genetic, molecular and biological studies on these and other avian isolates, there is credible evidence for the candidacy, in order, of H5N1, H9N2 and H6N1 viruses. These viruses have been made available for the production of diagnostic reagents and exploratory vaccines. The 1997 incident upheld the hypothesis that southern China is an epicentre for the emergence of pandemic influenza viruses. However, the intensification of the poultry (chicken) industry worldwide coupled with the spread of viruses such as the Eurasian lineage of H9N2 suggest that the genesis of a pandemic could take place elsewhere in the world. This re-emphasizes the importance of systematic virus surveillance of poultry globally for international public health and for economic and food concerns. Faced with an incipient pandemic in 1997, Hong Kong brought in international experts to join the investigative effort. Good teamwork at all levels is essential in dealing with the many facets. The threat of a pandemic should not be minimized, nor should governments be lulled into a sense of false security. The media is a powerful channel and has the responsibility and the avenues to convey and influence public perception of events. Close liaison between the media and those on the operational side ensures effective, accurate and timely dissemination of information. This will enhance public confidence in the investigative process and in steps taken for its safety and health.

Descriptors: epidemiology, infection, public health, respiratory system, influenza, respiratory system disease, viral disease, epidemics, pandemics, viral occurrence.


Abstract: This study examined the evolution and variation of the human influenza virus nucleoprotein gene from the earliest isolates to the present. Phylogenetic reconstruction of the most parsimonious evolutionary path connecting 49 nucleoprotein sequences yielded a single lineage. The average calculated rate of mutation was 3.6 nucleotide substitutions per year \((2.3 \times 10^{-3}\) substitutions per site per year). Thirty-two percent of these mutations resulted in amino acid substitutions, and the remainder were silent mutations. Analysis of virus isolates from China and elsewhere showed no significant differences in their rate of evolution, genetic diversity, or mean survival time. The nearly constant rate of change was maintained through the two antigenic shifts, and there were no obvious changes in the number or types of mutations associated with the changes in the surface proteins. A detailed comparison of the changes that have occurred on the main evolutionary path with those that have occurred on the side branches of the phylogenetic tree was made. This showed that while 35% of the mutations on the side branches resulted in amino acid changes, only 21% of those on the main path affected the protein sequence. These results suggest that although the rate of change of the human influenza virus nucleoprotein is much higher than that previously described for avian influenza viruses, there are measurable constraints on the evolution of the surviving virus lineage. Comparison of the nucleoproteins of virus isolates adapted to chicken embryos with the nucleoproteins of those grown only in MDCK cells revealed no consistent differences between the virus pairs. Thus, although the nucleoprotein is known to be critical for host specificity, its adaptation to growth in eggs apparently involves no immediate selective pressures, such as are found with hemagglutinin.

Descriptors: evolution, genes viral genetics, influenza A virus human genetics, nucleoproteins, viral core proteins genetics, amino acid sequence, cultured cells, chick embryo, cloning, molecular, molecular sequence data, mutagenesis, polymerase chain reaction, sequence analysis, DNA, sequence homology, amino acid, time factors, variation genetics.


Abstract: The Asian/57, Hong Kong/68, and Russian/77 pandemics of this century appeared or reappeared in China. Interspecies transmission and genetic reassortment of influenza viruses have been implicated in the origin of these human pandemic influenzas viruses. Pigs have been suspected to be the "mixing vessel" where reassortment occurs. To investigate this possibility, 104 porcine influenza viruses collected at random from Southern China from 1976 to 1982, including 32 H3N2 isolates and 72 H1N1 isolates, were studied using dot blot hybridization, partial sequencing, and phylogenetic analysis. There were 29 of 32 H3N2 isolates characteristic of viruses originally derived from humans; the other 3 isolates were reassortants containing genes from porcine and human influenza viruses. Phylogenetic analyses of the polymerase B1 (PB1) genes showed that interspecies transmission from humans to pigs has happened multiple times in pigs in Southern China. All 72 H1N1 isolates were of porcine origin characteristic of classical porcine H1N1 influenza virus. Analysis of 624 genes of porcine influenza viruses from Southern China failed to detect any evidence for avian influenza virus genes. This contrasts to what is currently found in Europe, where the majority of porcine influenza virus isolates are of avian origin.

Descriptors: swine, Guangdong, Hong Kong, Taiwan, mankind, influenza virus, swine influenza virus, disease transmission, hosts, provenance, phylogeny, genes, artiodactyla, Asia, biological competition, cell structure, China, chromosomes, domestic animals, East Asia, evolution, influenza virus, livestock, mammals, nucleus, parasitism, pathogenesis, suidae, useful animals, viruses, pandemics, genetic reassortment, virus mixing vessels, man.


Abstract: The human influenza pandemics of 1957 and 1968 were caused by reassortant viruses that possessed internal gene segments from avian and human strains. Whether genetic reassortment of human
and avian influenza viruses occurs during interpandemic periods and how often humans are infected with such reassortants is not known. To provide this information, we used dot-blot hybridization, partial nucleotide sequencing and subsequent phylogenetic analysis to examine the 6 internal genes of 122 viruses isolated in humans between 1933 and 1992 primarily from Asia, Europe, and the Americas. The internal genes of A/New Jersey/11/76 isolated from a human fatality at Fort Dix, New Jersey in 1976 were found to be of porcine origin. Although none of the geographically and temporally diverse collection of 122 viruses was an avian-human or other reassortant, cognizance was made of the fact that there were two isolates from children from amongst 546 influenza A isolates obtained from The Netherlands from 1989-1994 which were influenza A reassortants containing genes of avian origin, viruses which have infected European pigs since 1983-1985. Thus, genetic reassortment between avian and human influenza strains does occur in the emergence of pandemic and interpandemic influenza A viruses. However, in the interpandemic periods the reassortants have no survival advantage, and the circulating interpandemic influenza viruses in humans do not appear to accumulate avian influenza virus genes.

**Descriptors:** epidemiology, genetics, infection, microbiology, public health, genetic reassortment genetics infection internal genes interpandemic influenza virus interspecies transmission pandemic influenza virus pathogen virology zoonotic infections.


**NAL Call Number:** SF602.M8

**Descriptors:** avian influenza virus, human, zoonoses, diagnosis, disease distribution, disease prevalence, disease transmission, epidemiology, poultry, zoonoses.


**NAL Call Number:** SF601.V484

**Abstract:** This review aims to illustrate the extent to which wildlife act as reservoirs of infectious agents that cause disease in domestic stock, pet and captive animals and humans. More than 40 agents are described. In the case of some of these, e.g. *Cryptosporidium* spp., *Escherichia coli* O157 and malignant catarrhal fever, the current evidence is that wildlife either does not act as a reservoir or is of limited importance. However, in the case of many important diseases, including bovine tuberculosis, Weil's disease, Lyme disease, avian influenza, duck virus enteritis and looping ill, wild animals are considered to be the principal source of infection. Wildlife may be involved in the epidemiology of other major diseases, such as neosporosis, Johne's disease, mucosal disease and foot and mouth disease, but further studies are needed. The UK would benefit from a more positive approach to the study of wildlife and the infections they harbour.

**Descriptors:** epidemiology, infection, vector biology, veterinary medicine, *Cryptosporidium* infection, parasitic disease, transmission, *Escherichia coli* infection, bacterial disease, transmission, Johne's disease, infectious disease, Lyme disease, bacterial disease, Weil's disease, bacterial disease, avian influenza, viral disease, bovine tuberculosis, bacterial disease, duck virus enteritis, digestive system disease, viral disease, foot and mouth disease, viral disease, malignant catarrhal fever, bacterial disease, neoplastic disease, mucosal disease, infectious disease, neosporosis, infectious disease.


**NAL Call Number:** SF481.M54

**Descriptors:** avian influenza virus, poultry, zoonoses, disease transmission, human, Hong Kong.


**NAL Call Number:** SF781.R4

**Abstract:** Although of zoonotic origin, pathogens or infections posing a global threat to human health such as human immunodeficiency virus, severe acute respiratory syndrome or emerging influenza type A viruses may actually have little in common with known, established zoonotic agents, as these new agents merely underwent a transient zoonotic stage before adapting to humans. Evolution towards person-to-person
transmission depends on the biological features of the pathogen, but may well be triggered or facilitated by external factors such as changes in human exposure. Disease emergence may thus be depicted as an evolutionary response to changes in the environment, including anthropogenic factors such as new agricultural practices, urbanisation, or globalisation, as well as climate change. Here the authors argue that in the case of zoonotic diseases emerging in livestock, change in agricultural practices has become the dominant factor determining the conditions in which zoonotic pathogens evolve, spread, and eventually enter the human population. Livestock pathogens are subjected to pressures resulting from the production, processing and retail environment which together alter host contact rate, population size and/or microbial traffic flows in the food chain. This process is illustrated by two study cases: a) livestock development in the 'Eurasian ruminant street' (the area extending from central Asia to the eastern Mediterranean basin) and the adjacent Arabian peninsula b) poultry production in Southeast Asia. In both scenarios, environmental factors relating to demography, land pressure and imbalances in production intensification have led to an unstable epidemiological situation, as evidenced by the highly pathogenic avian influenza upsurge early in 2004, when the main outbreaks were located in areas which had both large scale, peri-urban commercial holdings and a high density of smallholder poultry units.

Descriptors: physiological adaptation, agriculture methods, animal diseases epidemiology, animal diseases transmission, animal husbandry methods, animals, environment, molecular evolution, humans, population density, population dynamics, world health, zoonoses.


NAL Call Number: 448.3 Ar23
Abstract: The effects of monoclonal antibody (MAb) C179 recognizing a conformational epitope in the middle of the hemagglutinin (HA) stem region were examined in a mouse model in the experiments of prevention and treatment of lethal bronchopneumonia caused by influenza A virus of H5 subtype. To model the lethal infection, avian non-pathogenic strain A/mallard duck/Pennsylvania/10218/84 (H5N2) was adapted to mice. This resulted in highly pathogenic pneumovirulent mouse-adapted (MA) variant, which was characterized. Three amino acid changes were found in the HA1 subunit of HA of MA virus. One of these was located inside the region of the conformational epitope recognized by MAb C179. However, this substitution was not significant for the recognition of HA and virus neutralization by MAb C179 in vitro and in vivo. Intraperitoneal administration of two different concentrations of MAb C179 one day before or two days after the virus challenge significantly decreased mortality rate. These results suggest that MAb C179 is efficient not only in the prevention and treatment of H1 and H2 influenza virus bronchopneumonia, as was reported previously, but also of H5-induced bronchopneumonia as well, and demonstrate in vivo the existence of a common neutralizing epitope in the HAs of these three subtypes.

Descriptors: antibodies, monoclonal therapeutic use, antibodies, viral therapeutic use, bronchopneumonia therapy, hemagglutinin glycoproteins, influenza virus immunology, influenza A virus avian genetics, pneumonia, viral therapy, antibodies, monoclonal pharmacology, antibodies, viral pharmacology, bronchopneumonia prevention and control, bronchopneumonia virology, cell line, disease models, animal, dose response relationship, drug, epitopes genetics, epitopes immunology, hemagglutinin glycoproteins, influenza virus genetics, avian drug effects, avian immunology, mice, molecular sequence data, neutralization tests, pneumonia, viral prevention and control, pneumonia, viral virology, sensitivity and specificity.


ISSN: 0001-723X.
NAL Call Number: 448.3 AC85
Abstract: We have used the mouse model to monitor the acquisition of virulence of a non-pathogenic influenza A virus upon adaptation to a new mammalian host. An avian strain, A/Mallard duck/Pennsylvania/10218/84 (H5N2) (Md/PA/84) was adapted to mice by 23 serial lung-to-lung passages until a highly virulent mouse-adapted (MA) variant (Md/PA/84-MA) emerged. This MA variant was...
characterized and compared to the parental strain as well as some of its intermediate passage variants. MA variant caused bronchopneumonia in mice with a high mortality rate (the virulence of Mld/PA/84-MA measured as log (EID50/LD50) was 1.75), while the parental, avirulent strain Mld/PA/84 did not cause illness and mortality in mice (log (EID50/LD50) was 7.25). Hemagglutination-inhibition (HAI) test with a set of hemagglutinin- (HA) specific monoclonal antibodies (MAbs) revealed antigenic differences between the parental strain and MA variant. Mld/PA/84-MA reacted with HA-specific MAbs in higher titers than the parental strain. The HA genes of the parental strain Mld/PA/84, the 1st, 3rd, 8th, and 15th intermediate passage variants, and Mld/PA/84-MA were sequenced. Three amino acid changes at positions 203, 273 and 320 were determined in the HA of MA variant. The first of them, Leu-->Pro (320), appeared in the HA stem region at the 8th passage. Two other in the HA1 globular region (Ser-->Phe (203) and Glu-->Gly (273)) appeared at the 15th passage. All of these substitutions were associated with the increase of viral infectivity for mouse lungs and changes in the HA antigenicity. The potential role of these changes in HA with respect to the process of viral interspecies transmission and acquisition of virulence for new host is discussed.

Descriptors: adaptation, physiological genetics, bronchopneumonia virology, influenza A virus avian pathogenicity, amino acid substitution, antigenic variation, chick embryo, genes viral, hemagglutination tests, hemagglutinins viral genetics, hemagglutinins viral immunology, hydrogen-ion concentration, avian genetics, avian immunology, lung immunology, lung microbiology, mice, molecular sequence data, virulence.


NAL Call Number: QR360.J6

Abstract: Reassortant viruses which possessed the hemagglutinin and neuraminidase genes of wild-type human influenza A viruses and the remaining six RNA segments (internal genes) of the avian A/Pintail/Alberta/119/79 (H4N6) virus were previously found to be attenuated in humans. To study the genetic basis of this attenuation, we isolated influenza A/Pintail/79 X A/Washington/897/80 reassortant viruses which contained human influenza virus H3N2 surface glycoprotein genes and various combinations of avian or human influenza virus internal genes. Twenty-four reassortant viruses were isolated and first evaluated for infectivity in avian (primary chick kidney [PCK]) and mammalian (Madin-Darby canine kidney [MDCK]) tissue culture lines. Reassortant viruses with two specific constellations of viral polymerase genes exhibited a significant host range restriction of replication in mammalian (MDCK) tissue culture compared with that in avian (PCK) tissue culture. The viral polymerase genotype PB2-avian (A) virus, PB1-A virus, and PA-human (H) virus was associated with a 900-fold restriction, while the viral polymerase genotype PB2-H, PB1-A, and PA-H was associated with an 80,000-fold restriction of replication in MDCK compared with that in PCK. Fifteen reassortant viruses were subsequently evaluated for their level of replication in the respiratory tract of squirrel monkeys, and two genetic determinants of attenuation were identified. First, reassortant viruses which possessed the avian influenza virus nucleoprotein gene were as restricted in replication as a virus which possessed all six internal genes of the avian influenza A virus parent, indicating that the nucleoprotein gene is the major determinant of attenuation of avian-human A/Pintail/79 reassortant viruses for monkeys. Second, reassortant viruses which possessed the viral polymerase gene constellation of PB2-H, PB1-A, and PA-H, which was associated with the greater degree of host range restriction in vitro, were highly restricted in replication in monkeys. Since the avian-human influenza reassortant viruses which expressed either mode of attenuation in monkeys replicated to high titer in eggs and in PCK tissue culture, their failure to replicate efficiently in the respiratory epithelium of primates must be due to the failure of viral factors to interact with primate host cell factors. The implications of these findings for the development of live-virus vaccines and for the evolution of influenza A viruses in nature are discussed.

Descriptors: genes viral, influenza A virus genetics, nucleoproteins genetics, RNA directed DNA polymerase genetics, viral core proteins, viral proteins genetics, genotype, influenza A virus pathogenicity, phenotype, saimiri, temperature, virulence, virus replication.

Abstract: An avian-human reassortant influenza A virus deriving its genes coding for the hemagglutinin and neuraminidase from the human influenza A/Washington/897/80 (H3N2) virus and its six "internal" genes from the avian influenza A/Mallard/NY/6750/78 (H2N2) virus (i.e., a six-gene reassortant) was previously shown to be safe, infectious, nontransmissible, and immunogenic as a live virus vaccine in adult humans. Two additional six-gene avian-human reassortant influenza viruses derived from the mating of wild-type human influenza A/California/10/78 (H1N1) and A/Korea/1/82 (H3N2) viruses with the avian influenza A/Mallard/NY/78 virus were evaluated in seronegative (hemagglutination inhibition titer, less than or equal to 1:8) adult volunteers for safety, infectivity, and immunogenicity to determine whether human influenza A viruses can be reproducibly attenuated by the transfer of the six internal genes of the avian influenza A/Mallard/NY/78 virus. The 50% human infectious dose was 10(4.9) 50% tissue culture infectious doses for the H1N1 reassortant virus and 10(5.4) 50% tissue culture infectious doses for the H3N2 reassortant virus. Both reassortants were satisfactorily attenuated with only 5% (H1N1) and 2% (H3N2) of infected vaccines receiving less than 400 50% human infectious doses developing illness. Consistent with this level of attenuation, the magnitude of viral shedding after inoculation was reduced 100-fold (H1N1) to 10,000-fold (H3N2) compared with that produced by wild-type virus. The duration of virus shedding by vaccines was one-third that of controls receiving wild-type virus. At 40 to 100 50% human infectious doses, virus-specific immune responses were seen in 77 to 93% of volunteers. When vaccinees who has received 10(7.5) 50% tissue culture infectious doses of the H3N2 vaccine were experimentally challenged with a homologous wild-type human virus only 2 of 19 (11%) vaccinees became ill compared with 7 of 14 (50%) unvaccinated seronegative controls (P < 0.025; protective efficacy, 79%). Thus, three different virulent human influenza A viruses have been satisfactorily attenuated by the acquisition of the six internal genes of the avian influenza A/Mallard/NY/78 virus. The observation that this donor virus can reproducibly attenuate human influenza A viruses indicates that avian-human influenza A reassortants should be further studied as potential live influenza A virus vaccines.

Descriptors: hemagglutinins viral immunology, influenza A virus avian immunology, human immunology, neuraminidase immunology, viral vaccines immunology, adult, antibodies, viral biosynthesis, avian growth and development, human growth and development, virus replication.


Abstract: We evaluated the abilities of three different avian influenza A viruses to attenuate the wild-type human influenza A/Korea/1/82 (H3N2) virus in squirrel monkeys, chimpanzees, and adult seronegative human volunteers. Two of these, avian influenza A/Mallard/NY/78 and A/Mallard/Alberta/76 viruses, appeared to be satisfactory donors of attenuating genes for the production of live influenza A reassortant virus vaccines for human use because the reassortants exhibited an acceptable balance between attenuation and immunogenicity.

Descriptors: influenza A virus avian immunology, human immunology, influenza vaccine immunology, antibodies, viral biosynthesis, avian genetics, avian physiology, human genetics, human physiology, Pan troglodytes, recombination, genetic, saimiri, vaccines, attenuated, virus replication.


Abstract: We evaluated the abilities of three different avian influenza A viruses to attenuate the wild-type human influenza A/Korea/1/82 (H3N2) virus in squirrel monkeys, chimpanzees, and adult seronegative human volunteers. Two of these, avian influenza A/Mallard/NY/78 and A/Mallard/Alberta/76 viruses, appeared to be satisfactory donors of attenuating genes for the production of live influenza A reassortant virus vaccines for human use because the reassortants exhibited an acceptable balance between attenuation and immunogenicity.

Descriptors: influenza A virus avian immunology, human immunology, influenza vaccine immunology, antibodies, viral biosynthesis, avian genetics, avian physiology, human genetics, human physiology, Pan troglodytes, recombination, genetic, saimiri, vaccines, attenuated, virus replication.

Sokolova, N.L. (1974). Dynamics of the formation of antihaemagglutinins to various types of avian influenza


NAL Call Number: QR360.J6

Abstract: In 1979, an H1N1 avian influenza virus crossed the species barrier, establishing a new lineage in European swine. Because there is no direct or serologic evidence of previous H1N1 strains in these pigs, these isolates provide a model for studying early evolution of influenza viruses. The evolutionary rates of both the coding and noncoding changes of the H1N1 swine strains are higher than those of human and classic swine influenza A viruses. In addition, early H1N1 swine isolates show a marked plaque heterogeneity that consistently persist after a few passages. The presence of a mutator mutation was postulated (C. Scholtissek, S. Ludwig, and W. M. Fitch, Arch. Virol. 131:237-250, 1993) to account for these observations and the successful establishment of an avian H1N1 strain in swine. To address this question, we calculated the mutation rates of A/Mallard/New York/6750/78 (H2N2) and A/Swine/Germany/2/81 (H1N1) by using the frequency of amantadine-resistant mutants. To account for the inherent variability of estimated mutation rates, we used a probabilistic model for the statistical analysis. The resulting estimated mutation rates of the two strains were not significantly different. Therefore, an increased mutation rate due to the presence of a mutator mutation is unlikely to have led to the successful introduction of avian H1N1 viruses in European swine.

Descriptors: evolution and adaptation, infection, molecular genetics, evolutionary rates, independence mutational rates, independence viral transmission.


NAL Call Number: 448.8 J821

Abstract: Characteristics of avian-human (ah) and cold-adapted (ca) influenza A/Kawasaki/9/86 (H1N1) reassortant vaccine viruses were compared in 37 seronegative adults and 122 seronegative infants and children. The 50% human infectious dose (HID50) in infants and children was 10(2.9) and 10(2.6) TCID50 for the ah and ca vaccine, respectively. The ah influenza A/Kawasaki/9/86 reassortant was reactogenic: 24% of infants and children infected with greater than or equal to 100 HID50 had fever greater than or equal to 39.4 degrees C. Since H3N2 ah vaccines were previously shown to be adequately attenuated, it is reasonable to suggest that the genes that code for hemagglutinin and neuraminidase of the H1N1 virus apparently influence the reactogenicity of reassortant viruses derived from the avian influenza A/Mallard/New York/6750/78 donor virus. Because this avian virus does not reproducibly confer a satisfactory level of attenuation to each subtype of influenza A virus, it is not a suitable donor virus for attenuation of wild-type influenza viruses. In contrast, the ca A/Ann Arbor/6/60 donor virus reliably confers attenuation characteristics to a variety of H1N1 and H3N2 influenza A viruses.

Descriptors: influenza prevention and control, influenza A virus avian immunology, human immunology, influenza vaccine adverse effects, adult, child, preschool, infant, influenza etiology, avian pathogenicity, human pathogenicity, vaccines, attenuated adverse effects, vaccines, synthetic adverse effects, virulence.


NAL Call Number: 448.8 J821

Abstract: Randomized, placebo-controlled studies with 10(3)-10(7) 50% tissue-culture infectious dose (TCID50) of avian-human (ah) and cold-adapted (ca) influenza A/Bethesda/85 (H3N2) reassortant viruses
were completed in 106 seronegative young children 6-48 months of age. Although the reassortants differed in six of eight RNA segments, they exhibited similar properties in level of attenuation, infectivity, immunogenicity, and efficacy. The 50% human infectious dose was 10(4.6) TCID50 for ah and 10(4.4) for ca vaccines. Both reassortants were satisfactorily attenuated with restricted replication and were no more reactogenic than placebo. The mean peak titer of virus shed was 10(1.5) (ah) to 10(2.0) (ca) TCID50/ml, and each of 37 isolates tested retained their characteristic vaccine phenotypes. Infection with ah or ca virus conferred immunity to experimental challenge with homologous virus. These findings indicate that both ah and ca influenza A/Bethesda/85 (H3N2) reassortants should be suitable vaccine candidates for use in healthy infants and young children.

Descriptors: influenza prevention and control, influenza A virus avian immunology, human immunology, influenza vaccine immunology, antibodies, viral biosynthesis, child, preschool, cold, dose response relationship, immunologic, double blind method, enzyme linked immunosorbent assay, immunoglobulin G biosynthesis, infant, avian isolation and purification, human isolation and purification, randomized controlled trials, vaccines, attenuated immunology, vaccines, synthetic immunology.


Abstract: Sporadic human infection with avian influenza viruses has raised concern that reassortment between human and avian subtypes could generate viruses of pandemic potential. Vaccination is the principal means to combat the impact of influenza. During an influenza pandemic the immune status of the population would differ from that which exists during interpandemic periods. An emerging pandemic virus will create a surge in worldwide vaccine demand and new approaches in immunisation strategies may be needed to ensure optimum protection of unprimed individuals when vaccine antigen may be limited. The manufacture of vaccines from pathogenic avian influenza viruses by traditional methods is not feasible for safety reasons as well as technical issues. Strategies adopted to overcome these issues include the use of reverse genetic systems to generate reassortant strains, the use of baculovirus-expressed haemagglutinin or related non-pathogenic avian influenza strains, and the use of adjuvants to enhance immunogenicity. In clinical trials, conventional surface-antigen influenza virus vaccines produced from avian viruses have proved poorly immunogenic in immunologically naive populations. Adjuvanted or whole-virus preparations may improve immunogenicity and allow sparing of antigen.


NAL Call Number: 448.8 L22

Descriptors: clinical immunology, humans, infection, vaccination, clinical techniques, immune response.


NAL Call Number: 448.8 N442

Descriptors: disease outbreaks prevention and control, influenza transmission, influenza A virus, avian influenza classification, avian genetics, biomedical research, birds, disease transmission prevention and control, influenza epidemiology, influenza virology, avian influenza transmission, swine, zoonoses transmission.


**Abstract:** Genes of an influenza A (H5N1) virus from a human in Hong Kong isolated in May 1997 were sequenced and found to be all avian-like (K. Subbarao et al., Science 279:393-395, 1998). Gene sequences of this human isolate were compared to those of a highly pathogenic chicken H5N1 influenza virus isolated from Hong Kong in April 1997. Sequence comparisons of all eight RNA segments from the two viruses show greater than 99% sequence identity between them. However, neither isolate's gene sequence was closely (>95% sequence identity) related to any other gene sequences found in the GenBank database. Phylogenetic analysis demonstrated that the nucleotide sequences of at least four of the eight RNA segments clustered with Eurasian origin avian influenza viruses. The hemagglutinin gene phylogenetic analysis also included the sequences from an additional three human and two chicken H5N1 virus isolates from Hong Kong, and the isolates separated into two closely related groups. However, no single amino acid change separated the chicken origin and human origin isolates, but they all contained multiple basic amino acids at the hemagglutinin cleavage site, which is associated with a highly pathogenic phenotype in poultry. In experimental intravenous inoculation studies with chickens, all seven viruses were highly pathogenic, killing most birds within 24 h. All infected chickens had virtually identical pathologic lesions, including moderate to severe diffuse edema and interstitial pneumonitis. Viral nucleoprotein was most frequently demonstrated in vascular endothelium, macrophages, heterophils, and cardiac myocytes. Asphyxiation from pulmonary edema and generalized cardiovascular collapse were the most likely pathogenic mechanisms responsible for illness and death. In summary, a small number of changes in hemagglutinin gene sequences defined two closely related subgroups, with both subgroups having human and chicken members, among the seven viruses examined from Hong Kong, and all seven viruses were highly pathogenic in chickens and caused similar lesions in experimental inoculations.


**Abstract:** Type A influenza viruses can infect a wide range of birds and mammals, but influenza in a particular species is usually considered to be species specific. However, infection of turkeys with swine H1N1 viruses has been documented on several occasions. This report documents the isolation of an H1N2 influenza virus from a turkey breeder flock with a sudden drop in egg production. Sequence analysis of the virus showed that it was a complex reassortant virus with a mix of swine-, human-, and avian-origin influenza genes. A swine influenza virus with a similar gene complement was recently reported from pigs in Indiana. Isolation and identification of the virus required the use of nonconventional diagnostic procedures. The virus was isolated in embryonated chicken eggs by the yolk sac route of inoculation rather than by the typical chorioallantoic sac route. Interpretation of hemagglutination-inhibition test results required the use of turkey rather than chicken red blood cells, and identification of the neuraminidase subtype required the use of alternative reference sera in the neuraminidase-inhibition test. This report provides additional evidence that influenza viruses can cross species and cause a disease outbreak, and diagnosticians must be aware that the variability of influenza viruses can complicate the isolation and characterization of new isolates.
Abstract: Avian species, particularly waterfowl, are the natural hosts of influenza A viruses. Influenza viruses bearing each of the 15 hemagglutinin and nine neuraminidase subtypes infect birds and serve as a reservoir from which influenza viruses or genes are introduced into the human population. Viruses with novel hemagglutinin genes derived from avian influenza viruses, with or without other accompanying avian influenza virus genes, have the potential for pandemic spread when the human population lacks protective immunity against the new hemagglutinin. Avian influenza viruses were thought to be limited in their ability to directly infect humans until 1997, when 18 human infections with avian influenza H5N1 viruses occurred in Hong Kong. In 1999, two human infections with avian influenza H9N2 viruses were also identified in Hong Kong. These events established that avian viruses could infect humans without acquiring human influenza genes by reassortment in an intermediate host and highlighted challenges associated with the detection of human immune responses to avian influenza viruses and the development of appropriate vaccines.

Descriptors: influenza virology, influenza A virus avian pathogenicity, antibodies, viral biosynthesis, birds, disease models, animal, disease outbreaks, fowl plague epidemiology, Hong Kong epidemiology, immunity, cellular, influenza epidemiology, influenza immunology, avian genetics, avian immunology, influenza vaccine isolation and purification, mammals, models, biological, phylogeny, species specificity, virulence.

Abstract: An avian H5N1 influenza A virus (A/Hong Kong/156/97) was isolated from a tracheal aspirate obtained from a 3-year-old child in Hong Kong with a fatal illness consistent with influenza. Serologic analysis indicated the presence of an H5 hemagglutinin. All eight RNA segments were derived from an avian influenza A virus. The hemagglutinin contained multiple basic amino acids adjacent to the cleavage site, a feature characteristic of highly pathogenic avian influenza A viruses. The virus caused 87.5 to 100 percent mortality in experimentally inoculated White Plymouth Rock and White Leghorn chickens. These results may have implications for global influenza surveillance and planning for pandemic influenza.

Descriptors: hemagglutinin glycoproteins, influenza virus genetics, influenza virology, influenza A virus avian genetics, avian pathogenicity, amino acid sequence, cell line, chickens, child, preschool, disease outbreaks, fatal outcome, fowl plague virology, genes viral, hemagglutinin glycoproteins, influenza virus chemistry, Hong Kong epidemiology, influenza epidemiology, avian isolation and purification, molecular sequence data, neuraminidase genetics, phylogeny, virulence, virus replication.

Abstract: The characterization of an avian influenza A (H5N1) virus isolated from a child with a fatal respiratory illness. The virus caused 87.5 to 100 percent mortality in experimentally inoculated White Plymouth Rock and White Leghorn chickens. These results may have implications for global influenza surveillance and planning for pandemic influenza.

Descriptors: hemagglutinin glycoproteins, influenza virus genetics, influenza virology, influenza A virus avian genetics, avian pathogenicity, amino acid sequence, cell line, chickens, child, preschool, disease outbreaks, fatal outcome, fowl plague virology, genes viral, hemagglutinin glycoproteins, influenza virus chemistry, Hong Kong epidemiology, influenza epidemiology, avian isolation and purification, molecular sequence data, neuraminidase genetics, phylogeny, virulence, virus replication.


Descriptors: fowl plague transmission, influenza virology, influenza A virus avian genetics, avian isolation and purification, birds, fowl plague virology, genes viral, influenza diagnosis, avian classification, avian pathogenicity.
The present study evaluated gull influenza A viruses as donors of attenuating genes for the production of live, attenuated influenza A H1N1 and H3N2 avian-human (ah) reassortant viruses for use as vaccines to prevent disease due to influenza A viruses in humans. The previously evaluated duck influenza A viruses were abandoned as donors of attenuating avian influenza virus genes because clinical evaluation of H1N1 and H3N2 ah reassortant virus vaccines derived from duck viruses documented residual virulence of H1N1 reassortants for seronegative infants and young children. Gull influenza A viruses occupy an independent ecologic niche and are rarely isolated from species other than gulls. The possibility of using gull influenza A viruses as donors of internal gene segments in ah reassortant viruses was evaluated in the present study using three different gull viruses and three human influenza A viruses. Gull-human H3N2 reassortant influenza A viruses with the desired 6-2 genotype (six internal avian influenza virus genes and the two human influenza virus surface glycoprotein genes) were readily generated and were found to be attenuated for squirrel monkeys and chimpanzees. However, ah reassortant viruses with gull and human influenza A H1N1 genes were difficult to generate, and reassortants that had the desired genotype of six gull virus genes with human influenza A H1 and N1 genes were not isolated despite repeated attempts. The gull PB2, NP and NS genes were not present in any of the gull-human H1N1 reassortants generated. The underrepresentation of these three gene segments suggests that reassortants bearing one or more of these three gene segments might have reduced viability indicative of a functional incompatibility in their gene products. The difficulties encountered in the generation of a 6-2 gull-human H1N1 reassortant virus are sufficient to conclude that the gull influenza A viruses tested would not be useful as donors of sets of six internal genes to attenuate human influenza A viruses. This study also identifies influenza virus gene segments that appear to be incompatible for generation of reassortants. Elucidation of the molecular basis of this restriction may provide information on intergenic interactions involved in virion assembly or packaging.

Descriptors: influenza A virus avian genetics, human genetics, reassortant viruses genetics, cell line, chick embryo, chickens, dogs, genotype, Pan troglodytes, reassortant viruses isolation and purification, reassortant viruses physiology, reproducibility of results, saimiri, tissue culture, vaccines, attenuated genetics, vaccines, attenuated isolation and purification, viral vaccines genetics, viral vaccines isolation and purification, virus replication.


NAL Call Number: SF781.E53 2000
Descriptors: Aves, virus transmission, avian influenza viruses, ecology, epidemiology, zoonotic potential implications.

NAL Call Number: 41.8 V6426
Descriptors: avian influenza virus, poultry.

In the influenza H5N1 virus incident in Hong Kong in 1997, viruses that are closely related to H5N1 viruses initially isolated in a severe outbreak of avian influenza in chickens were isolated from humans, signaling the possibility of an incipient pandemic. However, it was not possible to prepare a vaccine against the virus in the conventional embryonated egg system because of the lethality of the virus for chicken embryos and the high level of biosafety therefore required for vaccine production. Alternative approaches, including an avirulent H5N4 virus isolated from a migratory duck as a surrogate virus, H5N1 virus as a reassortant with avian virus H3N1 and an avirulent recombinant H5N1 virus generated by reverse genetics, have been explored. All vaccines were formalin inactivated. Intraperitoneal immunization of mice with each of vaccines elicited the production of hemagglutination-inhibiting and virus-neutralizing antibodies, while intranasal vaccination without adjuvant induced both mucosal and systemic antibody responses that protected the mice from lethal H5N1 virus challenge. Surveillance of birds and animals, particularly aquatic birds, for viruses to provide vaccine strains, especially surrogate viruses, for a future pandemic is stressed.

Descriptors: influenza immunology, influenza A virus avian immunology, influenza vaccine immunology, communicable disease control, disease outbreaks, influenza prevention and control, influenza vaccine administration and dosage, mice, vaccination.


Abstract: The majority of influenza A viruses isolated from wild birds, but not humans, can replicate in the duck intestinal tract. Here we demonstrate that all duck isolates tested universally retain sialidase activities under low pH conditions independent of their neuraminidase (NA) subtypes. In contrast, the sialidase activities of most isolates from humans and pigs practically disappear below pH 4.5, with the exception of four human pandemic viruses isolated in 1957 and 1968. Sequence comparisons among duck, human, and swine N2 NA subtypes indicate that amino acids at positions 153, 253, 307, 329, 344, 347, 356, 368, 390, and 431 may be associated with the low pH stability of duck and human pandemic N2 NAs. This finding suggests that the low pH stability of duck influenza A virus NA may be a critical factor for replication in the intestinal tract through the digestive tract of ducks, and that the properties of NAs are important for understanding the epidemiology of the influenza virus.

Descriptors: influenza virology, influenza A virus avian enzymology, human enzymology, neuraminidase metabolism, ducks, enzyme stability, hydrogen-ion concentration, influenza transmission, avian physiology, human physiology, porcine enzymology, phylogeny, sequence analysis, swine.


Abstract: The "Spanish" influenza pandemic killed at least 20 million people in 1918-1919, making it the worst infectious pandemic in history. Understanding the origins of the 1918 virus and the basis for its exceptional virulence may aid in the prediction of future influenza pandemics. RNA from a victim of the 1918 pandemic was isolated from a formalin-fixed, paraffin-embedded, lung tissue sample. Nine fragments of viral RNA were sequenced from the coding regions of hemagglutinin, neuraminidase, nucleoprotein, matrix protein 1, and matrix protein 2. The sequences are consistent with a novel H1N1 influenza A virus that belongs to the subgroup of strains that infect humans and swine, not the avian subgroup.

Descriptors: genes viral, influenza virology, influenza A virus human genetics, porcine genetics, RNA viral genetics, algorithms, base sequence, hemagglutinin glycoproteins, influenza virus genetics, history of
medicine, 20th century, influenza history, avian genetics, human classification, human pathogenicity, porcine classification, porcine pathogenicity, lung virology, molecular sequence data, neuraminidase genetics, nucleoproteins genetics, phylogeny, polymerase chain reaction, viral core proteins genetics, viral matrix proteins genetics, virulence.


**NAL Call Number:** 41.8 Av5
**Descriptors:** epidemiology, infection, Spanish influenza, epidemiology, infectious disease, respiratory system disease, viral disease, avian influenza, epidemiology, infectious disease, respiratory system disease, viral disease, 1918 Spanish influenza pandemic virulence.


**Abstract:** A case of human fowl plague keratoconjunctivitis occurred after accidental laboratory exposure. The conjunctivitis was characterised by follicle formation and a mucopurulent discharge, and ran a self-limiting course over two weeks. The keratitis was of an unusual type and consisted of small intraepithelial opacities, which appeared after one week and resolved completely over the next three weeks. The infection, confirmed by viral culture, was produced by Dutch strain (Hav 1 Neq 1) of fowl plague virus.

**Descriptors:** influenza A virus avian isolation and purification, keratoconjunctivitis etiology, laboratory infection etiology, adult, keratoconjunctivitis microbiology.


**NAL Call Number:** 41.8 Au72
**Descriptors:** chickens, avian influenza, epidemiology, prevention and control, Asia epidemiology, Australia.


**NAL Call Number:** QR360.J6

**Abstract:** An avian influenza A virus, A/Mallard/NY/6750/78(H2N2), was restricted in replication in the respiratory tract of squirrel monkeys. Avian-human influenza A reassortant viruses possessing the six RNA segments coding for nonsurface proteins (i.e., internal genes) of this avian virus were as restricted in replication in squirrel monkeys as their avian influenza parent. These findings indicated that restriction of replication of the avian influenza virus is a function of one or more of its internal genes. For an investigation of which of the avian influenza genes was responsible for restricted replication in the respiratory tract of primates, reassortant viruses were produced that contained human influenza virus surface antigens from the A/Udorn/72(H3N2) virus and one or more of the internal genes derived from the avian influenza virus parent. Avian-human reassortant influenza A viruses containing only the nucleoprotein or matrix protein RNA segment from the avian influenza virus parent were as restricted in their growth as an avian-human influenza reassortant virus containing each of the six avian influenza internal genes. In addition, an avian-human influenza reassortant virus possessing only the avian RNA 1 and nonstructural genes (which by themselves do not specify restricted replication) manifested a significant reduction of virus replication in squirrel monkey tracheas. Thus, the avian nucleoprotein and matrix genes appear to play a major role in the host range restriction exhibited by the A/Mallard/78 virus and its reassortants, but the combination of RNA 1 and nonstructural genes also contributes to restriction of replication.

**Descriptors:** genes viral, influenza A virus genetics, nucleoproteins genetics, viral proteins genetics, virus replication, birds microbiology, heat, influenza A virus physiology, RNA viral analysis, saimiri microbiology, trachea microbiology, viral matrix proteins.


Descriptors: genes viral, influenza A virus avian genetics, recombination, genetic, virus replication, avian physiology, membrane proteins genetics, nucleoproteins genetics, respiratory system microbiology, saimiri.


Abstract: Eighteen cases of human influenza A H5N1 infection were identified in Hong Kong from May to December 1997. Two of the six fatal cases had undergone a full post-mortem which showed reactive hemophagocytic syndrome as the most prominent feature. Other findings included organizing diffuse alveolar damage with interstitial fibrosis, extensive hepatic central lobular necrosis, acute renal tubular necrosis and lymphoid depletion. Elevation of soluble interleukin-2 receptor, interleukin-6 and interferon-gamma was demonstrated in both patients, whereas secondary bacterial pneumonia was not observed. Virus detection using isolation, reverse transcription-polymerase chain reaction and immunostaining were all negative. It is postulated that in fatal human infections with this avian subtype, initial virus replication in the respiratory tract triggers hypercytokinemia complicated by the reactive hemophagocytic syndrome. These findings suggest that the pathogenesis of influenza A H5N1 infection might be different from that of the usual human subtypes H1-H3.

Descriptors: influenza pathology, influenza virology, influenza A virus avian isolation and purification, adolescent, adult, bone marrow pathology, cytokines blood, disease outbreaks, fatal outcome, Hong Kong epidemiology, influenza epidemiology, lung pathology, lymphoid tissue pathology, postmortem changes.


Descriptors: ecology, wild birds, vector biology, avian influenza, transmission, Australia.


NAL Call Number: 448.8 M45

Abstract: In December 2003, the largest outbreak of highly pathogenic avian influenza H5N1 occurred among poultry in 8 Asian countries. A limited number of human H5N1 infections have been reported from Vietnam and Thailand, with a mortality rate approaching 70%. Deaths have occurred in otherwise healthy young individuals, which is reminiscent of the 1918 Spanish influenza pandemic. The main presenting features were fever, pneumonitis, lymphopenia, and diarrhea. Notably, sore throat, conjunctivitis, and coryza were absent. The H5N1 strains are resistant to amantadine and rimantadine but are susceptible to neuraminidase inhibitors, which can be used for treatment and prophylaxis. The widespread epidemic of avian influenza in domestic birds increases the likelihood for mutational events and genetic reassortment. The threat of a future pandemic from avian influenza is real. Adequate surveillance, development of vaccines, outbreak preparedness, and pandemic influenza planning are important. This article summarizes the current knowledge on avian influenza, including the virology, epidemiology, diagnosis, and management of this emerging disease.

Descriptors: communicable diseases, emerging epidemiology, disease outbreaks statistics and numerical data, influenza A virus, avian genetics, avian influenza pathogenicity, avian influenza epidemiology, poultry diseases epidemiology, world health, amantadine therapeutic use, antiviral agents therapeutic use, Asia epidemiology, communicable diseases, emerging diagnosis, emerging prevention and control, emerging virology, disease outbreaks prevention and control, drug resistance, multiple, viral, family characteristics, forecasting, avian influenza diagnosis, avian influenza prevention and control, avian influenza virology, mutation genetics, neuraminidase antagonists and inhibitors, patient isolation, population surveillance, poultry, poultry diseases diagnosis, poultry diseases prevention and control, poultry diseases virology, recombination, genetics, rimantadine therapeutic use, vaccination, zoonoses epidemiology, zoonoses virology.

Descriptors: fowl plague transmission, influenza virology, influenza A virus avian genetics, avian isolation and purification, adolescent, adult, anti bacterial agents therapeutic use, antiviral agents therapeutic use, chickens virology, child, preschool, ducks virology, influenza epidemiology, influenza radiography, influenza therapy, lung radiography, RNA viral analysis, reverse transcriptase polymerase chain reaction, treatment outcome, Vietnam epidemiology.


Abstract: This paper is concerned with a stochastic model, describing outbreaks of infectious diseases that have potentially great animal or human health consequences, and which can result in such severe economic losses that immediate sets of measures need to be taken to curb the spread. During an outbreak of such a disease, the environment that the infectious agent experiences is therefore changing due to the subsequent control measures taken. In our model, we introduce a general branching process in a changing (but not random) environment. With this branching process, we estimate the probability of extinction and the expected number of infected individuals for different control measures. We also use this branching process to calculate the generating function of the number of infected individuals at any given moment. The model and methods are designed using important infections of farmed animals, such as classical swine fever, foot-and-mouth disease and avian influenza as motivating examples, but have a wider application, for example to emerging human infections that lead to strict quarantine of cases and suspected cases (e.g. SARS) and contact and movement restrictions.

Descriptors: classical swine fever epidemiology, classical swine fever virus growth and development, veterinary disease outbreaks, biological models, classical swine fever prevention and control, classical swine fever transmission, epidemiologic methods, Netherlands epidemiology, stochastic processes, swine.


Abstract: The nonstructural (NS) genes of avian influenza A viruses have been divided into two groups on the basis of nucleotide sequence homology, which we have referred to here as alleles A and B. We sequenced the NS genes of eight additional avian influenza A viruses in order to define the differences between these two alleles more thoroughly. Four of the viruses had NS gene sequences which resembled that of A/FPV/Rostock/34 and belonged to allele A while the other four viruses had NS gene sequences more similar to that of A/Duck/Alberta/76 and belonged to allele B. There was approximately 90% sequence homology within alleles and 72% homology between alleles. As previously reported the NS genes of human influenza A viruses belong to allele A. We constructed single gene avian-human reassortant influenza A viruses containing an allele A or B NS gene segment from an avian influenza A virus and all other genes from a human influenza A virus and tested these reassortants for their ability to grow in the respiratory tract of a nonhuman primate. Reassortants containing an avian NS gene segment of allele B were significantly restricted in growth in the respiratory tract of squirrel monkeys while reassortants with an allele A NS gene segment were not. The divergent evolution of the B NS allele in birds may have resulted in gene products which do not function optimally in cooperation with genes from a human virus in viral replication in primate respiratory epithelium.

Descriptors: capsid genetics, influenza A virus avian genetics, human growth and development, viral core proteins genetics, alleles, amino acid sequence, base sequence, genes viral, human genetics, molecular sequence data, nasopharynx microbiology, saimiri microbiology, sequence homology, nucleic acid, trachea microbiology, viral nonstructural proteins, virus replication.

**NAL Call Number:** QR189.V32

**Abstract:** A unique requirement for live attenuated reassortant influenza vaccines is the need to generate new reassortant vaccine viruses with the appearance of each new antigenic variant. Thus, the attenuation phenotype conferred by the attenuated donor influenza virus must remain genetically stable during the generation of each new reassortant vaccine virus. In this study we used nucleotide sequence analysis to evaluate the genetic stability of the attenuating M and NP genes of the avian influenza A/Mallard/NY/6750/78 attenuated donor virus during the in vitro generation and subsequent in vivo replication of avian-human (AH) influenza A reassortant vaccine viruses in monkeys and humans. Nucleotide sequence changes in the M and NP genes occurred at a rate of approximately 0.61 substitutions/1000 nt/reassortant during in vitro generation of four AH reassortant viruses. Only two nucleotide sequence changes occurred in the M and NP gene segments of four isolates of H1N1 or H3N2 AH vaccine viruses following 6-8 days of replication in seronegative children, and neither change affected amino acids previously identified as playing a potential role in attenuation. In addition, there were no changes in the nucleotide sequence of the M and NP genes of single gene AH reassortant viruses following five serial passages in squirrel monkeys. Finally, there was no change in the level or duration of replication of the single gene reassortant viruses in the upper or lower respiratory tract of monkeys following serial passage. (ABSTRACT TRUNCATED AT 250 WORDS)

**Descriptors:** influenza A virus avian genetics, influenza vaccine genetics, nucleoproteins, viral core proteins genetics, viral matrix proteins genetics, base sequence, cloning, molecular, avian pathogenicity, avian physiology, human genetics, human pathogenicity, human physiology, molecular sequence data, mutation genetics, polymerase chain reaction, recombination, genetic physiology, saimiri, vaccines, attenuated genetics, vaccines, synthetic genetics, virus replication genetics.


**NAL Call Number:** QR189.V32

**Abstract:** Recent outbreaks of avian influenza in humans have demonstrated the need for vaccines for influenza viruses with pandemic potential. Recombinant hemagglutinins are an attractive option for such vaccines because they do not require handling potentially highly pathogenic influenza viruses for vaccine production. In order to evaluate the immunogenicity, optimum dosing and timing of administration of a recombinant baculovirus-expressed H5 HA (rH5) in humans, 147 healthy adults were assigned randomly to receive intramuscular rH5 as two doses of 25, 45 or 90 microg each, one dose of 90 microg followed by a dose of 10 microg, or two doses of placebo, at intervals between doses of 21, 28 or 42 days. All doses of rH5 were well tolerated. The rH5 vaccine was modestly immunogenic at high dose. Neutralizing antibody responses to a titer of 1:80 or greater were seen in 23% (14/60) of individuals after a single dose of 90 microg, and in 52% (15/29) after two doses of 90 microg. Varying intervals between doses from 21 to 42 days had no significant effect on antibody responses to vaccination. These results suggest that baculovirus-expressed H5 HA can induce functional antibody in individuals who have not had prior exposure to H5 viruses, but that further studies to improve the immunogenicity of the vaccine are needed.

**Descriptors:** hemagglutinin glycoproteins, influenza virus immunology, influenza A virus human immunology, influenza vaccine adverse effects, influenza vaccine immunology, vaccines, synthetic adverse effects, vaccines, synthetic immunology, adult, antibodies, viral immunology, dose response relationship, immunologic, enzyme linked immunosorbent assay, hemagglutinin glycoproteins, influenza virus genetics, immunization schedule, kinetics, neutralization tests, vaccination.


**NAL Call Number:** 448.8 V81

**Descriptors:** orthomyxoviridae, ultraviolet rays, antigens, birds, complement fixation tests, genetics, hemagglutination inhibition tests, horses, influenza, influenza A virus avian, radiation effects, swine.


**NAL Call Number:** 448.8 J826

**Descriptors:** antibodies analysis, antigens analysis, orthomyxoviridae immunology, adult, age factors, aged, antigen antibody reactions, depression, chemical, ducks, hemagglutination inhibition tests, influenza A virus avian immunology, middle aged, neutralization tests, periodic acid pharmacology, potassium pharmacology, turkeys.


**NAL Call Number:** 41.8 Au72

**Descriptors:** epidemiological surveys, mutations, outbreaks, pathogenicity, serological surveys, disease distribution, disease prevalence, disease surveys, disease transmission, disease vectors, waterfowl, wild birds, Anseriformes, avian influenza virus, Charadriiformes, ducks, fowl.


**NAL Call Number:** 448.8 N442

**Descriptors:** disease transmission, vertical, influenza transmission, influenza A virus, avian genetics, adult, child, fatal outcome, influenza virology, avian influenza isolation and purification, avian influenza transmission, lung radiography, phylogeny, poultry, reverse transcriptase polymerase chain reaction, zoonoses transmission.


**NAL Call Number:** RA648.5.E46

**Abstract:** In April 1999, isolation of avian influenza A (H9N2) viruses from humans was confirmed for the first time. H9N2 viruses were isolated from nasopharyngeal aspirate specimens collected from two children who were hospitalized with uncomplicated, febrile, upper respiratory tract illnesses in Hong Kong during March 1999. Novel influenza viruses have the potential to initiate global pandemics if they are sufficiently transmissible among humans. We conducted four retrospective cohort studies of persons exposed to these two H9N2 patients to assess whether human-to-human transmission of avian H9N2 viruses had occurred. No serologic evidence of H9N2 infection was found in family members or health-care workers who had close contact with the H9N2-infected children, suggesting that these H9N2 viruses were not easily transmitted from person to person.

**Descriptors:** disease transmission, horizontal statistics and numerical data, disease transmission, patient to professional statistics and numerical data, fowl plague transmission, influenza A virus avian isolation and purification, avian pathogenicity, antibodies, viral blood, birds, child, preschool, cohort studies, fowl plague immunology, Hong Kong epidemiology, infant, avian immunology, retrospective studies.

**Abstract:** Pigs can be infected with both human and avian influenza A virus (IAV) strains and are therefore considered to be important intermediates in the emergence of new IAV strains due to mixing of viral genes derived from human, avian, or porcine influenza viruses. These reassortant strains may have potential to cause pandemic influenza outbreaks in humans. The innate immune response against IAV plays a significant role in containment of IAV in the airways. We studied the interactions of IAV with porcine surfactant protein D (pSP-D), an important component of this first line defense system. Hemagglutination inhibition analysis shows that the distinct interactions of pSP-D with IAV mediated by the N-linked carbohydrate moiety in the carbohydrate recognition domain of pSP-D depend on the terminal sialic acids (SAs) present on this carbohydrate. Analysis by both lectin staining and by cleavage with linkage-specific sialidases shows that the carbohydrate of pSP-D is exclusively sialylated with alpha(2,6)-linked SAs, in contrast to surfactant protein A, which contains both alpha(2,3)- and alpha(2,6)-linked SAs on its N-linked carbohydrate. Enzymatic modification of the SA-linkages present on pSP-D demonstrates that the type of SA-linkage is important for its hemagglutination-inhibitory activity, and correlates with receptor-binding specificity of the IAV strains. The SAs present on pSP-D appear especially important for interactions with poorly glycosylated IAV strains. It remains to be elucidated to what extent the unique sialylation profile of pSP-D is involved in host range control of IAV in pigs, and whether it facilitates adaptation of avian or human IAV strains that can contribute to the production of reassortant strains in pigs.

**Descriptors:** influenza A virus metabolism, pulmonary surfactant associated protein D chemistry, sialic acids metabolism, swine, carbohydrate conformation, carbohydrate sequence, chickens, hemagglutination inhibition tests, molecular sequence data, molecular structure, neuraminidase metabolism, pulmonary surfactant associated protein A chemistry, pulmonary surfactant associated protein A metabolism, pulmonary surfactant associated protein D metabolism, pulmonary surfactants chemistry, receptors, cell surface, sialic acids chemistry.


NAL Call Number: 41.8 T431

Descriptors: animal husbandry methods, avian influenza prevention and control, poultry diseases prevention and control, animal husbandry standards, hygiene, avian influenza transmission, poultry, poultry diseases transmission, zoonoses.


NAL Call Number: 41.8 T431

Descriptors: disease outbreaks veterinary, avian influenza, prevention and control, avian influenza transmission, public health, zoonoses, birds, disease outbreaks prevention and control, feces virology, avian mortality, risk factors, vaccination veterinary.


NAL Call Number: 470 Sci2

Descriptors: hemagglutinin glycoproteins, influenza virus genetics, influenza virology, influenza A virus avian genetics, avian pathogenicity, chickens, child, preschool, disease outbreaks, fowl plague virology, genes viral, hemagglutinin glycoproteins, influenza virus chemistry, Hong Kong epidemiology, influenza epidemiology, influenza transmission, avian physiology, sequence analysis, DNA, virus replication.


NAL Call Number: 448.3 Ar23


**NAL Call Number:** 44.8 In282

**Descriptors:** bovine spongiform encephalopathy, avian influenza virus, Coronavirus, disease control, disease distribution, disease prevalence, disease prevention, epidemiology, livestock, zoonoses, human, prions.


**NAL Call Number:** RM260.J6

**Abstract:** Recent cross species transmission of avian influenza has highlighted the threat of pandemic influenza. Oseltamivir (Tamiflu(R)) has been shown to be effective in the treatment and prevention of epidemic influenza infection in adults, adolescents and children (>1 year). Although oseltamivir has not been approved for prophylactic use in children, it has been shown to be effective. Oseltamivir is also active against avian influenza virus strains. Evidence suggests that lower doses or shorter durations of treatment/chemoprophylaxis other than those approved may not be effective and may contribute to emergence of viral resistance. Safety data from dose ranging studies show that 5 day courses of 150 mg twice daily for treatment and 6 week courses of 75 mg twice daily for prophylaxis were as well tolerated as the approved dose regimens. The use of oseltamivir in a pandemic is influenced by the goals of the pandemic plan developed by the responsible Government and Health Authority. To optimize use of antiviral medications, processes will be needed to collect, collate and report outcome data from treated patients and/or from use for chemoprophylaxis of pandemic influenza during the first-wave outbreaks. If oseltamivir is included in a national or regional pandemic plan, stockpiling of the material, either in the form of capsules or the bulk active pharmaceutical ingredient will be necessary. In the absence of a stockpile, there is no guarantee that an adequate supply of oseltamivir will be available.

**Descriptors:** pharmacology, infection, pulmonary medicine, human medicine, oseltamivir, Tamiflu, adults, adolescents, children, pandemic influenza.

Watts, J. (2004). Asian nations step up action to curb spread of avian influenza. Outbreak is spreading at an unprecedented speed, WHO says, and nowhere can be considered safe. *Lancet* 363(9406): 373. ISSN: 1474-547X.

**NAL Call Number:** 448.8 L22

**Descriptors:** chickens, disease outbreaks veterinary, influenza epidemiology, influenza A virus, avian influenza, avian epidemiology, southeastern Asia epidemiology, child, influenza prevention and control, influenza virology, avian influenza prevention and control, avian influenza transmission, world health organization.


**NAL Call Number:** 448.8 L22

**Abstract:** BACKGROUND: In response to the emergence of severe infection capable of rapid global spread, WHO will issue a pandemic alert. Such alerts are rare; however, on Feb 19, 2003, a pandemic alert was issued in response to human infections caused by an avian H5N1 influenza virus, A/Hong Kong/213/03. H5N1 had been noted once before in human beings in 1997 and killed a third (6/18) of infected people. The 2003 variant seemed to have been transmitted directly from birds to human beings and caused fatal pneumonia in one of two infected individuals. Candidate vaccines were sought, but no avirulent viruses antigenically similar to the pathogen were available, and the isolate killed embryonated chicken eggs. Since traditional strategies of vaccine production were not viable, we sought to produce a candidate reference virus using reverse genetics. METHODS: We removed the polybasic aminoacids that are associated with high virulence from the haemagglutinin cleavage site of A/Hong Kong/213/03 using influenza reverse genetics techniques. A reference vaccine virus was then produced on an A/Puerto Rico/8/34 (PR8) backbone on WHO-approved Vero cells. We assessed this reference virus for pathogenicity in in-vivo and
in-vitro assays. FINDINGS: A reference vaccine virus was produced in Good Manufacturing Practice (GMP)-grade facilities in less than 4 weeks from the time of virus isolation. This virus proved to be non-pathogenic in chickens and ferrets and was shown to be stable after multiple passages in embryonated chicken eggs. INTERPRETATION: The ability to produce a candidate reference virus in such a short period of time sets a new standard for rapid response to emerging infectious disease threats and clearly shows the usefulness of reverse genetics for influenza vaccine development. The same technologies and procedures are currently being used to create reference vaccine viruses against the 2004 H5N1 viruses circulating in Asia.

Descriptors: disease outbreaks prevention and control, influenza vaccines immunology, orthomyxoviridae immunology, orthomyxoviridae infections prevention and control, antibodies, viral immunology, Asia epidemiology, birds, communicable disease control methods, drug design, genetic engineering, Hong Kong epidemiology, influenza A virus, avian immunology, human immunology, avian influenza prevention and control, avian influenza virology, orthomyxoviridae chemistry, orthomyxoviridae growth and development, orthomyxoviridae infections immunology, orthomyxoviridae infections virology, plasmids immunology, poultry diseases immunology, poultry diseases prevention and control, poultry diseases virology, reassortant viruses chemistry, reassortant viruses growth and development, reassortant viruses immunology, transformation, genetic immunology, virulence factors isolation and purification.


NAL Call Number: QR360.J6

Abstract: During 1998, severe outbreaks of influenza were observed in four swine herds in the United States. This event was unique because the causative agents, H3N2 influenza viruses, are infrequently isolated from swine in North America. Two antigenically distinct reassortant viruses (H3N2) were isolated from infected animals: a double-reassortant virus containing genes similar to those of human and swine viruses, and a triple-reassortant virus containing genes similar to those of human, swine, and avian influenza viruses (N. N. Zhou, D. A. Senne, J. S. Landgraf, S. L. Swenson, G. Erickson, K. Rossow, L. Liu, K.-J. Yoon, S. Krauss, and R. G. Webster, J. Virol. 73:8851-8856, 1999). Because the U.S. pig population was essentially naive in regard to H3N2 viruses, it was important to determine the extent of viral spread. Hemagglutination inhibition (HI) assays of 4, 382 serum samples from swine in 23 states indicated that 28.3% of these animals had been exposed to classical swine-like H1N1 viruses and 20.5% had been exposed to the triple-reassortant-like H3N2 viruses. The HI data suggested that viruses antigenically related to the double-reassortant H3N2 virus have not become widespread in the U.S. swine population. The seroreactivity levels in swine serum samples and the nucleotide sequences of six additional 1999 isolates, all of which were of the triple-reassortant genotype, suggested that H3N2 viruses containing avian PA and PB2 genes had spread throughout much of the country. These avian-like genes cluster with genes from North American avian viruses. The worldwide predominance of swine viruses containing an avian-like internal gene component suggests that these genes may confer a selective advantage in pigs. Analysis of the 1999 swine H3N2 isolates showed that the internal gene complex of the triple-reassortant viruses was associated with three recent phylogenetically distinct human-like hemagglutinin (HA) molecules. Acquisition of HA genes from the human virus reservoir will significantly affect the efficacy of the current swine H3N2 vaccines. This finding supports continued surveillance of U.S. swine populations for influenza virus activity.

Descriptors: influenza veterinary, influenza A virus, porcine genetics, swine diseases virology, antigenic variation, cross reactions, hemagglutination, viral, hemagglutinin glycoproteins, influenza virus genetics, influenza epidemiology, influenza virology, avian genetics, human genetics, porcine isolation and purification, phylogeny, reverse transcriptase polymerase chain reaction, sequence homology, nucleic acid, seroepidemiologic studies, swine, swine diseases epidemiology, United States epidemiology.


NAL Call Number: 501 L84Pb

Abstract: Pandemic influenza in humans is a zoonotic disease caused by the transfer of influenza A viruses or virus gene segments from animal reservoirs. Influenza A viruses have been isolated from avian and mammalian hosts, although the primary reservoirs are the aquatic bird populations of the world. In the aquatic birds, influenza is asymptomatic, and the viruses are in evolutionary stasis. The aquatic bird viruses
do not replicate well in humans, and these viruses need to reassort or adapt in an intermediate host before they emerge in human populations. Pigs can serve as a host for avian and human viruses and are logical candidates for the role of intermediate host. The transmission of avian H5N1 and H9N2 viruses directly to humans during the late 1990s showed that land-based poultry also can serve between aquatic birds and humans as intermediate hosts of influenza viruses. That these transmission events took place in Hong Kong and China adds further support to the hypothesis that Asia is an epicentre for influenza and stresses the importance of surveillance of pigs and live-bird markets in this area.

Descriptors: epidemiology, evolution and adaptation, infection, vector biology, avian influenza, viral disease, pandemic influenza, epidemiology, respiratory system disease, viral disease, evolutionary stasis, viral transmission.

NAL Call Number: 470 Sci2

NAL Call Number: QR355.A72 no.13
Abstract: Although influenza viruses are not spread from human to human through the conventional food chain, this is not necessarily the case for the transmission of the precursors of the human pandemic influenza viruses. Aquatic birds of the world are the reservoirs for all influenza A viruses; the virus is spread by fecal-oral transmission in untreated water. Influenza A viruses are frequently transmitted to domestic poultry and two of the 15 subtypes H5 and H7 can become highly pathogenic and have the capacity to decimate commercial poultry flocks. Less frequently, avian influenza viruses are transmitted between species-to pigs, horses and sea mammals. This transmission involves mutational, reassortant or recombinational events and can occur through fecal contamination of unprocessed avian protein or through the water. The transmission of avian influenza viruses or virus genes to humans is postulated to occur through pigs that act as the intermediate host. This involves either multiple mutational or reassortant events and is believed to occur by airborne transmission. Once avian influenza viruses are established in mammals, they are transmitted from animal to animal by the respiratory airborne route. The transmission of avian influenza virus from their reservoir in wild aquatic birds to domestic poultry and to mammalian species including humans can be prevented by treatment of the water supply and of avian protein sources with disinfectants or by heating. Agricultural authorities have recommended the separation of wild aquatic and domestic poultry and of pig and poultry farming. It is theoretically possible to reduce the possibility of the next pandemic of influenza in humans by changes in agricultural practices so that ducks are separated from pigs and people.
Descriptors: birds virology, influenza epidemiology, influenza transmission, influenza A virus avian, zoonoses virology, disease reservoirs, fowl plague transmission, fowl plague virology, influenza prevention and control, influenza veterinary.

NAL Call Number: 448.8 L22
Abstract: CONTEXT: Live-animal markets (wet markets) provide a source of vertebrate and invertebrate animals for customers in tropical and subtropical regions of the world. Wet markets sell live poultry, fish, reptiles, and mammals of every kind. Live-poultry markets (mostly chicken, pigeon, quail, ducks, geese, and a wide range of exotic wild-caught and farm-raised fowl) are usually separated from markets selling fish or red-meat animals, but the stalls can be near each other with no physical separation. Despite the widespread availability of affordable refrigeration, many Asian people prefer live animals for fresh produce. Wet markets are widespread in Asian countries and in countries where Asian people have migrated. Live-poultry markets were the source of the H5N1 bird-influenza virus that transmitted to and killed six of 18 people in Hong
Kong. STARTING POINT: Yi Guan and colleagues (Science 2003; 302: 276-78) recently reported the isolation of severe acute respiratory syndrome (SARS) coronavirus (CoV) from Himalayan palm civets (*Paguna larvata*) in wet markets in Shenzen, southern China. These researchers also found serological evidence of infection in raccoon dogs (*Nyctereutes procyonoides*). Serological evidence for SARS CoV in human beings working in these markets, taken together with the earliest cases of SARS in restaurant workers, supports the contention of a potential zoonotic origin for SARS. WHERE NEXT? Will SARS reappear? This question confronts public-health officials worldwide, particularly infectious disease personnel in those regions of the world most affected by the disease and the economic burden of SARS, including China, Taiwan, and Canada. Will the virus re-emerge from wet markets or from laboratories working with SARS CoV, or are asymptomatic infections ongoing in human beings? Similar questions can be asked about a pandemic of influenza that is probably imminent. Knowledge of the ecology of influenza in wet markets can be used as an early-warning system to detect the reappearance of SARS or pandemic influenza.

**Descriptors:** food industry methods, influenza epidemiology, severe acute respiratory syndrome epidemiology, zoonoses transmission, communicable diseases, emerging epidemiology, communicable diseases, emerging transmission, communicable diseases, emerging veterinary, disease outbreaks statistics and numerical data, disease reservoirs veterinary, disease vectors, Hong Kong epidemiology, influenza transmission, influenza veterinary, influenza A virus avian isolation and purification, poultry diseases epidemiology, poultry diseases transmission, severe acute respiratory syndrome transmission, severe acute respiratory syndrome veterinary, zoonoses epidemiology, zoonoses virology.


**NAL Call Number:** 448.8 V81

**Descriptors:** orthomyxoviridae isolation and purification, recombination, genetic, antigens, heterophile, chickens, epitopes, genetics, microbial, hemagglutination inhibition tests, hemagglutinins viral analysis, hybridization, genetic, immunization, influenza A virus avian enzymology, avian immunology, lung, neuraminidase, neutralization tests, orthomyxoviridae enzymology, orthomyxoviridae immunology, tissue extracts, turkeys, viral vaccines.


**NAL Call Number:** 448.8 V81

**Descriptors:** orthomyxoviridae enzymology, orthomyxoviridae growth and development, orthomyxoviridae immunology, orthomyxoviridae isolation and purification, orthomyxoviridae pathogenicity, recombination, genetic, antigens analysis, centrifugation, density gradient, chick embryo, fetal membranes, fibroblasts, hemagglutination inhibition tests, hemagglutination tests, hemagglutinins viral analysis, hybridization, genetic, immune sera, influenza microbiology, influenza A virus avian enzymology, avian growth and development, avian immunology, avian pathogenicity, lung microbiology, neuraminidase analysis, rabbits, sucrose, swine, tissue culture, turkeys, virulence, virus replication.


**NAL Call Number:** 501 L84Pb

**Abstract:** The only direct evidence for transmission of influenza viruses between species comes from studies on swine influenza viruses. Antigenically and genetically identical Hsw1N1 influenza viruses were isolated from pigs and man on the same farm in Wisconsin, U.S.A. The isolation of H3N2 influenza viruses from a wide range of lower animals and birds suggests that influenza viruses of man can spread to the lower orders. Under some conditions the H3N2 viruses can persist for a number of years in some species. The isolation, from aquatic birds, of a large number of influenza A viruses that possess surface proteins antigenically similar to the viruses isolated from man, pigs and horses provides indirect evidence for interspecies transmission. There is now a considerable body of evidence which suggests that influenza viruses of lower animals and birds may play a role in the origin of some of the pandemic strains of influenza A viruses.
There is no direct evidence that the influenza viruses in aquatic birds are transmitted to man, but they may serve as a genetic pool from which some genes may be introduced into humans by recombination. Preliminary evidence suggests that the molecular basis of host range and virulence may be related to the RNA segments coding for one of the polymerase proteins (P3) and for the nucleoprotein (NP).

Descriptors: influenza transmission, influenza A virus genetics, orthomyxoviridae infections veterinary, birds microbiology, ducks microbiology, fowl plague transmission, genes viral, influenza A virus avian genetics, mammals microbiology, RNA viral genetics, recombination, genetic, species specificity.

NAL Call Number: 448.8 V81
Descriptors: influenza A virus physiology, orthomyxoviridae infections veterinary, pinnipedia microbiology, seals microbiology, antigens, viral analysis, birds microbiology, conjunctivitis etiology, genes viral, influenza A virus avian immunology, influenza A virus isolation and purification, mammals microbiology, orthomyxoviridae infections microbiology, RNA viral genetics, virus replication.

NAL Call Number: QR180.3.D4
Abstract: Studies on influenza viruses from feral ducks trapped in Canada in August 1976, gave a 26% isolation rate from cloacal samples of juvenile birds. Several different influenza A viruses were isolated, some of which possessed novel hemagglutinin and/or neuraminidase antigens. Influenza A viruses isolated from the rectum of feral ducks replicate in the upper respiratory tract and also in the intestinal tract of feral and domestic ducks. Representative human influenza viruses of the H0N1, H3N2 and Hsw1 N1 subtypes replicate in the upper respiratory tract of ducks but not in the intestinal tract. The A/Hong Kong/68 [H3N2] influenza virus that has not been isolated from man for several years was recently isolated from pigs originating from The People's Republic of China. A/Victoria/3/75-like influenza viruses that are currently circulating in man were also isolated from pigs. Both the A/Hong Kong/68 and the A/Victoria/75-like viruses transmitted readily from pig to pig in experimental studies. The susceptibility of ducks and pigs to infection with human influenza viruses suggests that these animals may play an important role in the ecology of influenza A viruses.
Descriptors: influenza etiology, influenza A virus avian immunology, avian isolation and purification, porcine immunology, porcine isolation and purification, influenza A virus isolation and purification, antibodies, viral, cloaca microbiology, disease outbreaks, ducks microbiology, hemagglutinins viral isolation and purification, swine microbiology, virus replication.

NAL Call Number: SF781.R4
Abstract: The evolution of influenza is a continuing process involving viral and host factors. The increasing frequency of emergence of the highly pathogenic H5N1, H7N3 and H7N7 influenza viruses and the panzootic spread of H9N2 influenza virus, all of which can be potentially transmitted to humans, are of great concern to both veterinary and human public health officials. The question is how soon the next pandemic will emerge. A convergence of factors, including the population densities of poultry, pigs and humans, are likely factors affecting the evolution of the virus. Highly concentrated poultry and pig farming, in conjunction with traditional live animal or 'wet' markets, provide optimal conditions for increased mutation, reassortment and recombination of influenza viruses. Strategies to reduce the evolution of influenza and the emergence of pandemics include the separation of species, increased biosecurity, the development of new vaccine strategies and better basic knowledge of the virus. More effective co-operation between scientists and veterinary and public health officials is required to achieve these goals.
Descriptors: epidemiology, evolution and adaptation, infection, public health, poultry, host disease vector, avian influenza virus, drug therapy, etiology, immunology, prevention and control, transmission, influenza, human, veterinary medicine, medical sciences.

NAL Call Number: 448.8 V81

Abstract: A large pool of avirulent influenza viruses are maintained in the wild ducks and shorebirds of the world, but we know little about their potential to become virulent. It is well established that the hemagglutinin (HA) is pivotal in determining virulence and that a constellation of other genes is also necessary (R. Rott, M. Orlich, and C. Scholtsissek, 1976, J. Virol. 19, 54-60). The question we are asking here is the ability of avirulent influenza viruses to provide the gene constellation that will complement the HA from a highly virulent virus and for the reassortant to be virulent. Reassortant influenza viruses were prepared between ultraviolet treated A/Chicken/Pennsylvania/1370/83 (H5N2) [Ck/Penn] and influenza viruses from natural reservoirs. These viruses included examples of the predominant subtypes in wild ducks, shorebirds, and domestic poultry. Attention was given to the influenza viruses from live poultry markets, for it is possible that these establishments may be important in mixing of influenza genes from different species and the possible transmission to domestic and mammalian species. The reassortants were genotyped by partial sequencing of each gene and were tested for virulence in chickens. Each of the reassortants contained the hemagglutinin and matrix (M) genes from Ck/Penn and a majority of genes from the viruses from natural reservoirs indicating a preferential association between the HA and M genes. The reassortants containing multiple genes from wild ducks and a cleavable HA were avirulent indicating that the gene pool in ducks may not have a high potential to provide genes that are potentially virulent. In contrast, a disproportionate number of viruses from shorebirds and all avirulent H5N2 influenza viruses from city markets provided a gene constellation that in association with cleavable H5 HA were highly virulent in chickens. An evolutionary tree based on oligonucleotide mapping established that the H5N2 influenza viruses from birds in city markets are closely related.

Descriptors: hemagglutinins viral genetics, influenza A virus avian pathogenicity, poultry diseases microbiology, animals, wild microbiology, antibodies, monoclonal, birds microbiology, disease reservoirs, genes viral, hn protein, hemagglutinins viral immunology, avian genetics, oligonucleotides analysis, poultry microbiology, viral envelope proteins genetics, viral envelope proteins immunology, viral matrix proteins genetics, virus replication.


NAL Call Number: 470 Sci2

Descriptors: molecular genetics, infection, epidemiology, Spanish flu, viral disease, influenza, respiratory system disease, viral disease, influenza virulence virology world population growth.


Abstract: In this report we examine the hypothesis that aquatic birds are the primordial source of all influenza viruses in other species. Two partly overlapping reservoirs of influenza A viruses exist in migrating waterfowl and shorebirds throughout the world. These species harbor influenza viruses of all the known hemagglutinin and neuraminidase subtypes. In contrast to the rapid, progressive changes in both the nucleotide and amino acid sequences of mammalian virus gene lineages, avian virus genes show far less variation and, in most cases, appear to be in evolutionary stasis. There are periodic exchanges of influenza virus genes or whole viruses between species, giving rise to pandemics of disease in humans, lower animals, and birds. The periodic exchange of influenza viruses between species has been illustrated by the appearance of new pandemic influenza viruses in humans, including the Spanish influenza of 1918, the Asian influenza of 1957, and the Hong Kong influenza of 1968. Transmission of avian influenza viruses to swine in Europe in 1979 has resulted in the appearance of human-avian reassortant influenza viruses in pigs in Italy and in children in the Netherlands. These studies provide evidence supporting the possibility that pigs serve as a mixing vessel for reassortment between influenza viruses in mammalian and avian hosts and raise the question of whether the avian influenza viruses now circulating in European swine are the precursors of the next human pandemic virus.

Descriptors: epidemiology, genetics, infection, microbiology, vector biology, veterinary medicine,
epidemiology genetics vectors.


Abstract: Fifty years ago, the age-old scourge of infectious disease was receding in the developed world in response to improved public health measures, while the advent of antibiotics, better vaccines, insecticides and improved surveillance held the promise of eradicating residual problems. By the late twentieth century, however, an increase in the emergence and re-emergence of infectious diseases was evident in many parts of the world. This upturn looms as the fourth major transition in human-microbe relationships since the advent of agriculture around 10,000 years ago. About 30 new diseases have been identified, including Legionnaires’ disease, human immunodeficiency virus (HIV)/acquired immune deficiency syndrome (AIDS), hepatitis C, bovine spongiform encephalopathy (BSE)/variant Creutzfeldt-Jakob disease (vCJD), Nipah virus, several viral hemorrhagic fevers and, most recently, severe acute respiratory syndrome (SARS) and avian influenza. The emergence of these diseases, and resurgence of old ones like tuberculosis and cholera, reflects various changes in human ecology: rural-to-urban migration resulting in high-density peri-urban slums; increasing long-distance mobility and trade; the social disruption of war and conflict; changes in personal behavior; and, increasingly, human-induced global changes, including widespread forest clearance and climate change. Political ignorance, denial and obduracy (as with HIV/AIDS) further compound the risks. The use and misuse of medical technology also pose risks, such as drug-resistant microbes and contaminated equipment or biological medicines. A better understanding of the evolving social dynamics of emerging infectious diseases ought to help us to anticipate and hopefully ameliorate current and future risks. Descriptors: communicable diseases diagnosis, communicable diseases etiology, cardiovascular diseases diagnosis, cardiovascular diseases etiology, communicable disease control, communicable diseases, emerging, demography, disease outbreaks, health, international cooperation, neoplasms diagnosis, neoplasms etiology, public health, risk, risk factors, time factors, world health.

Abstract: Since time immemorial animals have been a major source of human infectious disease. Certain infections like rabies are recognized as zoonoses caused in each case by direct animal-to-human transmission. Others like measles became independently sustained with the human population so that the causative virus has diverged from its animal progenitor. Recent examples of direct zoonoses are variant Creutzfeldt-Jakob disease arising from bovine spongiform encephalopathy, and the H5N1 avian influenza outbreak in Hong Kong. Epidemics of recent animal origin are the 1918-1919 influenza pandemic, and acquired immune deficiency syndrome caused by human immunodeficiency virus (HIV). Some retroviruses jump into and out of the chromosomal DNA of the host germline, so that they oscillate between being inherited Mendelian traits or infectious agents in different species. Will new procedures like animal-to-human transplants unleash further infections? Do microbes become more virulent upon cross-species transfer? Are animal microbes a threat as biological weapons? Will the vast reservoir of immunodeficient hosts due to the HIV pandemic provide conditions permissive for sporadic zoonoses to take off as human-to-human transmissible diseases? Do human infections now pose a threat to endangered primates? These questions are addressed in this lecture. Descriptors: infection, Creutzfeldt Jakob disease, behavioral and mental disorders, nervous system disease, prion disease, acquired immunodeficiency syndrome (AIDS), immune system disease, viral disease, bovine spongiform encephalopathy, nervous system disease, prion disease, influenza, respiratory system disease, viral disease, measles, viral disease, plague, bacterial disease, smallpox, viral disease, typhus, bacterial disease, yellow fever, viral disease, animal to human transmission, zoonosis.
NAL Call Number: QR360.J6

Abstract: Wild aquatic birds are the primary reservoir of influenza A viruses, but little is known about the viruses' gene pool in wild birds. Therefore, we investigated the ecology and emergence of influenza viruses by conducting phylogenetic analysis of 70 matrix (M) genes of influenza viruses isolated from shorebirds and gulls in the Delaware Bay region and from ducks in Alberta, Canada, during >18 years of surveillance. In our analysis, we included 61 published M genes of isolates from various hosts. We showed that M genes of Canadian duck viruses and those of shorebird and gull viruses in the Delaware Bay shared ancestors with the M genes of North American poultry viruses. We found that North American and Eurasian avian-like lineages are divided into sublineages, indicating that multiple branches of virus evolution may be maintained in wild aquatic birds. The presence of non-H13 gull viruses in the gull-like lineage and of H13 gull viruses in other avian lineages suggested that gulls' M genes do not preferentially associate with the H13 subtype or segregate into a distinct lineage. Some North American avian influenza viruses contained M genes closely related to those of Eurasian avian viruses. Therefore, there may be interregional mixing of the two clades. Reassortment of shorebird M and HA genes was evident, but there was no correlation among the HA or NA subtype, M gene sequence, and isolation time. Overall, these results support the hypothesis that influenza viruses in wild waterfowl contain distinguishable lineages of M genes.

Descriptors: animals, wild virology, birds virology, ecology, evolution, molecular, influenza A virus, avian genetics, viral matrix proteins genetics, ducks virology, avian classification, avian isolation and purification, molecular sequence data, phylogeny, sequence analysis, DNA.


Descriptors: animal diseases, disease control, disease transmission, decision making, economic analysis, losses, epidemiology, foot and mouth disease, Aphthovirus, avian influenza virus, swine fever virus.

NAL Call Number: RC114.5.A7

Descriptors: epidemiology, disease vectors, avian influenza virus, insects, Coleoptera, Diptera, Musca domestica, Hydrotae aenesens, Coproica hirtula, Alphitobius diaperinus, Dermentes maculatus.


Descriptors: avian influenza, epidemiology, outbreaks prevention, control, mortality, transmission, Laos, poultry, rural health, veterinarians, zoonoses, emerging infectious diseases.


NAL Call Number: RB145.A21B57

Abstract: Lymphadenopathy may appear as a common symptom of infectious or malignant diseases. We report a 20 year old male patient, worker in an avian slaughter house, who presented with axillary, infracavicular, and inguinal lymphadenopathy, splenomegaly, granulocytopenia (0.9 Gpt/l), and monocytosis (17% out of 2.9 Gpt/l leukocytes). Thrombocytopenia (39 Gpt/l) was found to be caused by HLA-antibodies and antiplatelet autoantibodies. There were no clinical signs of infection, pneumonia nor B symptoms. Lymphadenectomy 27 months ago had revealed chronic non-granulomatous lymphadenitis and follicular hyperplasia, no malignancy. Previous histologic findings had been confirmed by second biopsy of recurrent axillary lymphomas. No infectious agent had been identified so far, broad serologic and immunological
testings had been negative. Bone marrow biopsy revealed normal hematopoiesis. The patient was admitted to neurologic department due to seizures 27 months after onset of lymphadenopathy. Cerebrospinal fluid revealed lymphocytic pleocytosis, no malignant cells, microbiological and serological testings were negative. MRI of the cerebrum was without any pathologic finding. Due to a 4 months prednisolone therapy, lymphadenopathy resolved and platelet count normalized, but seizures reappeared after stop of steroid therapy. Broad infectiologic screening was negative including human influenza virus antibodies, but hemagglutination inhibition test (HI-test) revealed low concentrations of anti avian influenza virus A/Duck/Ukraine/1/63 (H3N8) antibodies. HI-test was strongly reactive (1:128) to avian A/duck/Czech/56 (H4N6) with slight titer reduction after a 2 months interval. Human infections may be caused by the H1, H2, or H3 influenza subtype in combination with various neuraminidases. Therefore, HI-titer to avian influenza H3N8 could indicate cross-reactivity to human viruses. Singular reports of infection in humans with H5, H7, as well as H9 subtype reflect typical symptoms of influenza or pneumonia. However, there are no reports so far concerning detection of avian H4 antibodies in humans. Furthermore, during the year 2000 there was not even a single proof of anti avian H4 antibodies out of almost 180 000 birds screened in Germany. We conclude that chronic lymphadenopathy, non-specific symptoms and cerebral infection in our patient might be related to atypical avian influenza. To our knowledge this should be a rare, if not the first report on detection of anti avian influenza H4 antibodies in humans.

Descriptors: clinical immunology, infection, neurology, cerebral infection, infectious disease, nervous system disease, granulocytopenia, blood and lymphatic disease, immune system disease, lymphadenopathy, blood and lymphatic disease, immune system disease, monocytosis, blood and lymphatic disease, seizures, nervous system disease, splenomegaly, blood and lymphatic disease, thrombocytopenia, blood and lymphatic disease, meeting abstract, meeting poster.


NAL Call Number: SF995.A1A9

Abstract: The nucleotide sequence encoding the HA1 portion of the haemagglutinin gene of the influenza virus A/turkey/Germany/2482/90, isolated from birds kept in an area of many pig farms, was determined and compared with those of recent avian and swine influenza isolates. It was found to be closest to the 'avian-like' swine H1N1 influenza viruses that have been reported in Europe since the early 1980s and may represent good evidence for transmission of these viruses back to birds after they have become established in pigs.

Descriptors: animal husbandry, genetics, infection, methods and techniques, microbiology, veterinary medicine, avian influenza virus Ha1, nucleotide sequence, hemagglutinin gene H1 isolate, infection, molecular genetics, pathogen, swine farm proximity, viral transmission.


Abstract: During normal interpandemic influenza seasons, immune responses to vaccines are quite predictable and meet the licensing criteria of the European Union (EU) Committee for Proprietary Medicinal Products (CPMP). In a pandemic situation, large sections, if not all of the community will be immunologically naive and therefore new immunisation strategies will be needed. In 1976 and 1977 H1N1 vaccines were prepared and tested clinically. To stimulate 'protective' antibody responses, two doses of vaccine were needed in people below the age of 24 years (no previous experience of H1N1 virus), whereas one conventional dose was adequate in older people. In 1997, the highly pathogenic avian influenza H5N1 virus caused widespread concern when it infected man, with lethal effects. Due to safety concerns it was necessary to adopt new strategies for vaccine development and one such strategy was to produce vaccine from an avirulent H5N3 virus, A/Duck/Singapore-Q/F119-2/97. Clinical trials of a subunit vaccine prepared from A/Duck/Sing/97 virus revealed that even two doses of twice the normal vaccine concentration (i.e. 30 mug haemagglutinin) were poorly immunogenic, whereas an H5N3 vaccine adjuvanted with microfluidised emulsion (MF) 59 stimulated antibody levels that complied with CPMP criteria after two half strength doses
NAL Call Number: 501 L84Pb

Abstract: Pandemic influenza presents special problems for vaccine development. There must be a balance between rapid availability of vaccine and the safeguards to ensure safety, quality and efficacy of vaccine. Vaccine was developed for the pandemics of 1957, 1968, 1977 and for the pandemic alert of 1976. This experience is compared with that gained in developing vaccines for a possible H5N1 pandemic in 1997-1998. Our ability to mass produce influenza vaccines against a pandemic threat was well illustrated by the production of over 150 million doses of ‘swine flu’ vaccine in the USA within a 3 month period in 1976. However, there is cause for concern that the lead time to begin vaccine production is likely to be about 7-8 months. Attempts to reduce this time should receive urgent attention. Immunogenicity of vaccines in pandemic situations is compared over the period 1968-1998. A consistent feature of the vaccine trials is the demonstration that one conventional 15 mug haemagglutinin dose of vaccine is not sufficiently immunogenic in naive individuals. Much larger doses or two lower doses are needed to induce satisfactory immunity. There is some evidence that whole-virus vaccines are more immunogenic than split or subunit vaccines, but this needs substantiating by further studies. H5 vaccines appeared to be particularly poor immunogens and there is evidence that an adjuvant may be needed. Prospects for improving the development of pandemic vaccines are discussed.


NAL Call Number: 41.8 Av5

Abstract: Avian influenza virus was isolated from the conjunctiva of a male emu chick. Clinical observations included ocular discharge, dyspnea, and mild respiratory signs. Lesions included conjunctivitis, tracheitis, bronchopneumonia, and airsaccultis. Escherichia coli was isolated from the conjunctiva and the sinus, and Staphylococcus sp. was isolated from the conjunctiva. Influenza A viral nucleoprotein was detected immunohistochemically in epithelial cells of the bronchi, lung parenchyma and tracheal mucosa, and mononuclear inflammatory cells within the exudate of the bronchial lumen; conjunctiva, air sacs, kidney, intestine, and liver were negative for the viral nucleoprotein. The isolated influenza virus was typed as H10N7 and was determined to be nonpathogenic for chickens.

Descriptors: veterinary medicine, respiratory system, sense organs, virology, airsaccultis, respiratory system disease, bronchopneumonia, respiratory system disease, conjunctivitis, eye disease, dyspnea, respiratory system disease, ocular discharge, eye disease, respiratory disease, respiratory system disease, tracheitis, respiratory system disease, case study.

Descriptors: avian influenza, humans, poultry, WHO, weekly record.

Descriptors: influenza prevention and control, influenza A virus avian immunology, influenza vaccine, birds virology, influenza epidemiology, avian genetics, sentinel surveillance, vaccination, Vietnam.

**NAL Call Number:** 449.8 Am3

**Abstract:** Genetic reassortment between influenza A viruses in humans and in animals and birds has been implicated in the appearance of new pandemics of human influenza. To determine whether such reassortment has occurred in the United States, the authors compared the genetic origins of gene segments of 73 swine influenza virus isolates (1976-1990), representing 11 states, and 11 turkey virus isolates (1980-1989), representing eight states. The host origin of gene segments encoding the internal proteins of H1N1 swine and turkey influenza viruses was identified by developing a dot-blot assay. All gene segments of swine influenza viruses were characteristic of influenza virus genes from that species, indicating that pigs may not be frequent participants in interspecies genetic exchange and reassortment of influenza viruses in the United States. In contrast, 73% of the turkey influenza virus isolates contained genes of swine origin. One turkey isolate was a reassortant having three genes characteristic of avian influenza virus and three of swine origin. These findings document a high degree of genetic exchange and reassortment of influenza A viruses in domestic turkeys in the United States. The molecular biologic techniques used by the authors should aid future epidemiologic studies of influenza pandemics.

**Descriptors:** disease vectors, influenza transmission, influenza A virus, porcine genetics, reassortant viruses genetics, swine microbiology, turkeys microbiology, immunoblotting, influenza microbiology, human genetics, polymerase chain reaction, United States.


**NAL Call Number:** 448.8 V81

**Abstract:** Analysis of the sequences of all eight RNA segments of the influenza A/Goose/Guangdong/1/96 (H5N1) virus, isolated from a sick goose during an outbreak in Guangdong province, China, in 1996, revealed that the hemagglutinin (HA) gene of the virus was genetically similar to those of the H5N1 viruses isolated in Hong Kong in 1997. However, the remaining genes showed greater similarity to other avian influenza viruses. Notably, the neuraminidase gene did no have the 19-amino-acid deletion in the stalk region seen in the H5N1 Hong Kong viruses and the NS gene belonged to allele B, while that of the H5N1 Hong Kong viruses belonged to allele A. These data suggest that the H5N1 viruses isolated from the Hong Kong outbreaks derived their HA genes from a virus similar to the A/Goose/Guangdong/1/96 virus or shared a progenitor with this goose pathogen.

**Descriptors:** geese virology, hemagglutinin glycoproteins, influenza virus genetics, influenza virology, influenza A virus avian genetics, human genetics, chickens virology, DNA, viral chemistry, DNA, viral genetics, disease outbreaks, fowl plague epidemiology, fowl plague virology, genes viral, Hong Kong epidemiology, influenza epidemiology, avian classification, avian isolation and purification, human classification, molecular sequence data, neuraminidase genetics, phylogeny, sequence analysis, DNA, viral nonstructural proteins genetics.


**NAL Call Number:** 448.3 Ar23

**Descriptors:** fowl plague transmission, mink microbiology, orthomyxoviridae infections transmission, influenza A virus avian growth and development, human growth and development, porcine growth and development, influenza A virus growth and development, species specificity.


**NAL Call Number:** QR189.V32

**Abstract:** Antigenic analysis of human and avian H2 influenza virus was carried out with monoclonal antibodies to the HA molecules of H2 influenza viruses isolated in the early stage of an H2 pandemic. The study revealed antigenic differences between inhibitor sensitive (Japan+/57, RI+57) and inhibitor resistant
strains (Japan-/57, Ri-/57). This indicates that the receptor-binding specificity of the haemagglutinin can markedly influence the antigenic analysis obtained with monoclonal antibodies in HI test. Minor antigenic differences (microheterogeneity) could be detected between different H2 influenza viruses isolated in 1957. Minor antigenic variation continued in the H2 viruses until 1961, but significant antigenic drift occurred in 1962 so that viruses isolated after that date reacted with few monoclonal antibodies. Analysis of avian H2 influenza viruses suggested antigenic differences between the different avian H2 haemagglutinin, but no correlation between the year of isolation and the progressive antigenic drift similar to that seen in the human strains was found.

Descriptors: antigens, viral immunology, hemagglutinins viral immunology, influenza A virus avian immunology, human immunology, antibodies, monoclonal immunology, antigens, viral genetics, genes viral, hemagglutinins viral genetics, avian genetics, human genetics, variation genetics.


Descriptors: influenza prevention and control, avian influenza A virus classification, avian influenza prevention and control, birds, China, Hong Kong, influenza etiology, avian influenza A virus pathogenicity, avian influenza virus complications, prognosis, World Health Organization.


NAL Call Number: QR360.J6

Abstract: Reverse genetics was used to analyze the host range of two avian influenza viruses which differ in their ability to replicate in mouse and human cells in culture. Engineered viruses carrying sequences encoding amino acids 362 to 581 of PB2 from a host range variant productively infect mouse and human cells.

Descriptors: influenza A virus avian genetics, viral proteins genetics, cell line, genes viral, avian chemistry, avian pathogenicity, mice, sequence analysis, protein, species specificity, transfection.


NAL Call Number: QR360.A1J6

Abstract: The haemagglutinins (HAs) of five H3 influenza A viruses isolated from domestic ducks and one from a goose in southern China were analysed antigenically and genetically. The patterns of reactivity of two of the duck viruses and the goose virus with a panel of monoclonal antibodies to 10 different epitopes on the H3 HA were similar to those of influenza viruses isolated from wild ducks and pigs, as well as those of the earliest human H3 viruses. The other three isolates from domestic ducks were different from each other and from these viruses antigenically. Sequence analysis revealed that the HA genes of the two duck viruses and the goose virus were closely related to those of isolates from wild ducks and pigs; the identities between the deduced amino acid sequence of the HA of one of the isolates from domestic ducks and those of isolates from a wild duck and a pig were 98.7% and 99.5%, respectively. The antigenic and genetic similarity between these H3 HAs suggests that in southern China, the hypothetical influenza epicentre, domestic ducks may have played a role in the introduction of avian influenza viruses to pigs from feral ducks. The findings also support the hypothesis that the pig was a 'mixing vessel', producing a new human pandemic strain, A/Hong Kong/68 (H3N2), by genetic reassortment.

Descriptors: ducks microbiology, influenza microbiology, influenza A virus avian immunology, human immunology, amino acid sequence, antibodies, monoclonal immunology, base sequence, China, DNA, viral, geese microbiology, hemagglutinins viral genetics, hemagglutinins viral immunology, influenza transmission, avian genetics, human genetics, molecular sequence data, sequence alignment, swine microbiology.

Abstract: BACKGROUND: Human infection with an avian influenza A virus (subtype H5N1) was reported recently in Hong Kong. We describe the clinical presentation of the first 12 patients and options for rapid viral diagnosis. METHODS: Case notes of 12 patients with virus-culture-confirmed influenza A H5N1 infection were analysed. The clinical presentation and risk factors associated with severe disease were defined and the results of methods for rapid virus diagnosis were compared. FINDINGS: Patients ranged from 1 to 60 years of age. Clinical presentation was that of an influenza-like illness with evidence of pneumonia in seven patients. All seven patients older than 13 years had severe disease (four deaths), whereas children 5 years or younger had mild symptoms with the exception of one who died with Reye's syndrome associated with intake of aspirin. Gastrointestinal manifestations, raised liver enzymes, renal failure unrelated to rhabdomyolysis, and pancytopenia were unusually prominent. Factors associated with severe disease included older age, delay in hospitalisation, lower-respiratory-tract involvement, and a low total peripheral white blood cell count or lymphopenia at admission. An H5-specific reverse-transcription PCR assay (RT-PCR) was useful for rapid detection of virus directly in respiratory specimens. A commercially available enzyme immunoassay was more sensitive than direct immunofluorescence for rapid viral diagnosis. Direct immunofluorescence with an H5-specific monoclonal antibody pool was useful for rapid exclusion of H5-subtype infection. INTERPRETATION: Avian Influenza A H5N1 virus causes human influenza-like illness with a high rate of complications in adults admitted to hospital. Rapid H5-subtype-specific laboratory diagnosis can be made by RT-PCR applied directly to clinical specimens.

Descriptors: disease outbreaks, influenza diagnosis, influenza virology, influenza A virus avian isolation and purification, adult, child, preschool, fluorescent antibody technique, direct, fowl plague transmission, Hong Kong epidemiology, immunoenzyme techniques, infant, influenza epidemiology, influenza transmission, middle aged, polymerase chain reaction methods, risk factors, time factors.


Abstract: Antigenic relationships between human influenza A viruses containing hemagglutinins of HO and H1 subtypes and animal and avian influenza viruses Hsw1 and Hav5 were studied by immunoadsorption using inorganic base of the sorbent. Direct and indirect relations due to the presence in hemagglutinin of common antigenic determinants and hapten groups were revealed. The strains representing drift variations within one subtype differed by the spectrum of hapten determinants typical of other subtypes. No common determinant typical for all members of this group was isolated.

Descriptors: antigens, viral analysis, hemagglutinins viral analysis, influenza A virus avian immunology, human immunology, porcine immunology, influenza A virus immunology, epitopes analysis, hemagglutination inhibition tests, immunosorbent techniques.


Descriptors: avian influenza A virus, strain variations, human, protein components.


Abstract: avian influenza A virus, strain variations, human, protein components.

ISSN: 1052-9276.

Descriptors: antigenic variation physiology, influenza virology, orthomyxoviridae pathogenicity, orthomyxoviridae physiology, antigenic variation genetics, birds virology, disease reservoirs, evolution, molecular, hemagglutinin glycoproteins, influenza virus chemistry, hemagglutinin glycoproteins, influenza virus genetics, hemagglutinin glycoproteins, influenza virus metabolism, influenza epidemiology, influenza transmission, neuraminidase genetics, neuraminidase metabolism, orthomyxoviridae enzymology, orthomyxoviridae genetics.


NAL Call Number: QR360.A1J6

Abstract: We previously reported that nucleoproteins (NPs) of human influenza viruses are cleaved in infected cells, and, as a result, two forms of NP, uncleaved (mol. wt. 56000) and cleaved (mol. wt. 53000) were accumulated late in infection. Here, we report that NPs of animal influenza viruses of non-human origin (isolated from pigs, equids, seals, whales, birds) exhibited proteolytic resistance in infected cells and did not undergo a change in mol. wt. in the course of infection. The resistance of the animal virus NPs to proteolytic cleavage was shown to be a virus-specific property and not the consequence of a low level of proteolysis in infected cells. Influenza A/H3N2 viruses isolated from pigs in Hong Kong in 1976 were found to have a cleavable NP like that of 'human' viruses, supporting the hypothesis concerning the 'human' origin of these strains. The NP of human influenza virus (A/Aichi/2/68) adapted to an animal host (mouse) retained susceptibility to limited intracellular proteolysis. Thus, NP resistance to cleavage seems to be a stable viral characteristic enabling the NP56 ---- NP53 modification to be used as an indication of the origin of influenza viruses.

Descriptors: influenza microbiology, influenza A virus human metabolism, nucleoproteins metabolism, orthomyxoviridae metabolism, viral proteins metabolism, chick embryo, influenza metabolism, avian metabolism, porcine metabolism, peptide hydrolases metabolism, peptides analysis, peptides metabolism, virus cultivation.


Descriptors: influenza prevention and control, avian influenza A virus isolation and purification, avian influenza transmission, zoonoses transmission, influenza transmission, influenza veterinary, avian influenza A virus pathogenicity, poultry.


NAL Call Number: 448.3 Ar23

Abstract: The three last pandemic strains of influenza A virus -Asian/57, Hong Kong/68 and Russian/77 - are believed to have originated in China. The strains responsible for the 1957 and 1968 human pandemics were reassortants incorporating both human and avian influenza viruses, which may have arisen in pigs. We therefore undertook a population-based study in the Nanchang region of Central China to establish the prevalence, types and seasonal pattern of human influenza infection and to screen serum samples from animals and humans for evidence of interspecies transmission of influenza viruses. Two definite influenza seasons were demonstrated, one extending from November to March and the other July to September. The profile of antibodies to commonly circulating human influenza viruses was no different in Nanchang and neighboring rural communities than in Memphis, Tennessee, USA. In particular, Chinese women who raised
pigs in their homes were no more likely to have been exposed to influenza virus than were subjects who seldom or never had contact with pigs. However, we did obtain evidence using isolated H7 protein in an enzyme-linked immunoabsorbent assay for infection of pig farmers by an avian H7 influenza virus suggesting that influenza A viruses may have been transmitted directly from ducks to humans. The results of the serological survey also indicated that pigs in or near Nanchang were infected by human H1N1 and H3N2 influenza viruses, but not with typical swine viruses. We found no serological evidence for H2 influenza viruses in humans after 1968.

Descriptors: animal husbandry, climatology, epidemiology, infection, public health, vector biology, veterinary medicine, disease transmission epidemiology interspecies transmission seasonal infection.


NAL Call Number: QR360.J6

Abstract: In late summer through early winter of 1998, there were several outbreaks of respiratory disease in the swine herds of North Carolina, Texas, Minnesota, and Iowa. Four viral isolates from outbreaks in different states were analyzed genetically. Genotyping and phylogenetic analyses demonstrated that the four swine viruses had emerged through two different pathways. The North Carolina isolate is the product of genetic reassortment between H3N2 human and classic swine H1N1 influenza viruses, while the others arose from reassortment of human H3N2, classic swine H1N1, and avian viral genes. The hemagglutinin genes of the four isolates were all derived from the human H3N2 virus circulating in 1995. It remains to be determined if either of these recently emerged viruses will become established in the pigs in North America and whether they will become an economic burden.

Descriptors: genome, viral, influenza A virus avian genetics, human genetics, porcine genetics, reassortant viruses, amino acid sequence, birds virology, molecular sequence data, swine virology.


NAL Call Number: QR360.J6

Abstract: The H5N1 avian influenza virus that killed 6 of 18 persons infected in Hong Kong in 1997 was transmitted directly from poultry to humans. Viral isolates from this outbreak may provide molecular clues to zoonotic transfer. Here we demonstrate that the H5N1 viruses circulating in poultry comprised two distinguishable phylogenetic lineages in all genes that were in very rapid evolution. When introduced into new hosts, influenza viruses usually undergo rapid alteration of their surface glycoproteins, especially in the hemagglutinin (HA). Surprisingly, these H5N1 isolates had a large proportion of amino acid changes in all gene products except in the HA. These viruses maybe reassortants each of whose HA gene is well adapted to domestic poultry while the rest of the genome arises from a different source. The consensus amino acid sequences of "internal" virion proteins reveal amino acids previously found in human strains. These human-specific amino acids may be important factors in zoonotic transmission.

Descriptors: fowl plague virology, genes viral, genome, viral, influenza A virus avian genetics, amino acid sequence, chickens, evolution, molecular, fowl plague epidemiology, fowl plague transmission, hemagglutinins genetics, Hong Kong epidemiology, molecular sequence data, sequence alignment.


NAL Call Number: 448.3 C33 (1)

Abstract: 400 human sera were tested both in hemagglutination inhibition (HI) and neuraminidase inhibition (NI) tests for antibodies to avian and animal influenza virus subtypes. In the H1 test we only found antibodies to the avian subtype Hav 7 and the animal subtypes Hsw 1 and Heq 2 whereby the latter was mainly demonstrated in elderly persons 60 to 100 years old. The findings of Hav 7 are due to H 3 antibodies and reflect the relationship between both antigens. In the NI test we obtained positive results in 21.8% of the
human sera with the neuraminidase subtype N 3 (Nav 2/3) with a peak in persons who were 60 to 70 years old. 11.0% of the sera contained antibodies to the neuraminidase subtype N 8 (Neq 2) and were found exclusively in people 60 to 100 years old, and 9.3% of sera showed positive reactions with the subtype N5 (Nav 5). Until now an immunological relationship between the neuraminidase subtypes N 1, N 2, and N 3 is not known, and could'nt be found in our own studies. Contaminations of antigens can also be excluded. The possible origin of these antibodies to avian neuraminidase subtypes is discussed.

Descriptors: antibodies, viral analysis, influenza A virus avian immunology, neuraminidase immunology, adolescent, adult, aged, child, preschool, Germany, East, hemagglutination inhibition tests, infant, porcine immunology, middle aged, serologic tests methods.

NAL Call Number: QR360.J6
Abstract: Highly pathogenic avian influenza A H5N1 viruses caused outbreaks of disease in domestic poultry and humans in Hong Kong in 1997. Direct transmission of the H5N1 viruses from birds to humans resulted in 18 documented cases of respiratory illness, including six deaths. Here we evaluated two of the avian H5N1 viruses isolated from humans for their ability to replicate and cause disease in outbred ferrets. A/Hong Kong/483/97 virus was isolated from a fatal case and was highly pathogenic in the BALB/c mouse model, whereas A/Hong Kong/486/97 virus was isolated from a case with mild illness and exhibited a low-pathogenicity phenotype in mice. Ferrets infected intranasally with 10(7) 50% egg infectious doses (EID(50)) of either H5N1 virus exhibited severe lethargy, fever, weight loss, transient lymphopenia, and replication in the upper and lower respiratory tract, as well as multiple systemic organs, including the brain. Gastrointestinal symptoms were seen in some animals. In contrast, weight loss and severe lethargy were not noted in ferrets infected with 10(7) EID(50) of two recent human H3N2 viruses, although these viruses were also isolated from the brains, but not other extrapulmonary organs, of infected animals. The results demonstrate that both H5N1 viruses were highly virulent in the outbred ferret model, unlike the differential pathogenicity documented in inbred BALB/c mice. We propose the ferret as an alternative model system for the study of these highly pathogenic avian viruses.
Descriptors: disease models, animal, ferrets, influenza physiopathology, influenza A virus avian pathogenicity, adolescent, child, preschool, influenza pathology, influenza virology, lung pathology, lung virology, virulence, virus replication.

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