Influenza A virus subtype H1N1

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This flu subtype is related to a current event: 2009 swine flu outbreak**. Information may change rapidly as the event progresses.**

Influenza A virus subtype H1N1, also know as **A(H1N1)** or simply **H1N1**, is a subtype of influenzavirus A and the most common cause of influenza in humans. Some strains of H1N1 are endemic in humans, including the strain(s) responsible for the 1918 flu pandemic and the many strains that cause influenza worldwide each year. Other strains of H1N1 are endemic in pigs and in birds. The 1918 flu pandemic killed 50–100 million people worldwide from 1918 to 1919.[1]

Low pathogenic H1N1 strains still exist in the wild today, causing roughly half of all flu infections in 2006.[2]

In March and April 2009, an outbreak of influenza in Mexico has confirmed 192 cases, and 26 fatalities with the new strain of H1N1 were detected.[3] As of April 28, the new strain was suspected to have infected more than 2,500 individuals worldwide, with 152 attributed deaths (see 2009 swine flu outbreak). The U.S. Centers for Disease Control warned that it was possible the outbreak could develop into a pandemic.[4]

On April 27, 2009, the World Health Organization raised alertness from level 3 to level 4 (max 6) worldwide[5], since (sustained) human-to-human transfer of the virus was confirmed.

Etymology

In the name H1N1 the "H" refers to the hemagglutinin protein, and the "N" refers to the neuraminidase protein.

Spanish flu

The Spanish flu, also known as *La Gripe Española*, or *La Pesadilla*, was an unusually severe and deadly strain of avian influenza, a viral infectious disease, that killed some 50 million to 100 million people worldwide over about a year in 1918 and 1919. It is thought to be one of the most deadly pandemics in human history. It was caused by the H1N1 type of influenza virus[6], which is similar to bird flu of today, mainly H5N1 and H5N2. [*citation needed*]

The Spanish flu caused an unusual number of deaths because it, like H5N1, caused a cytokine storm in the body. The virus infected lung cells, leading to overstimulation of the immune system via release of cytokine bursts into the lung tissue. This leads to

extensive leukocyte migration towards the lungs, causing destruction of lung tissue and secretion of liquid into the organ, making it difficult for the patient to breathe. People with strong immune systems (such as young adults) were more susceptible to the disease than young children and the elderly.

Russian flu

The more recent Russian flu was a 1977–1978 flu epidemic caused by strain *Influenza A/USSR/90/77 (H1N1)*. It infected mostly children and young adults under 23 because a similar strain was prevalent in 1947–57, causing most adults to have substantial immunity. Some have called it a flu pandemic but because it only affected the young it is not considered a true pandemic. The virus was included in the 1978–1979 influenza vaccine.[7][8][9][10]

Mexican influenza / Antigenic shift

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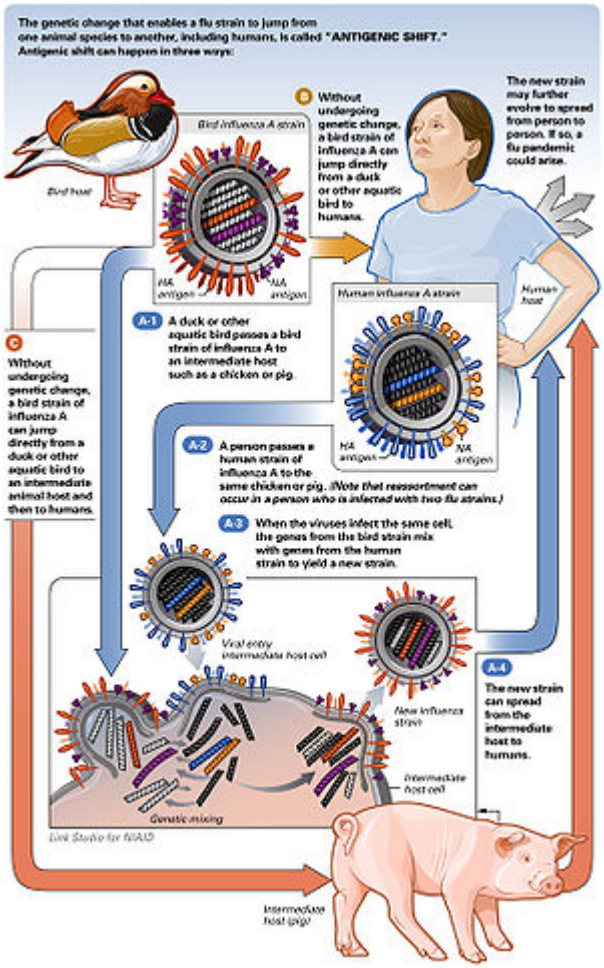

Antigenic shift is the process by which *at least* two different strains of a virus, (or different viruses), especially influenza, combine to form a new subtype having a mixture of the surface antigens of the two original strains. The term *antigenic shift* is more often applied specifically, (but is not limited) to the influenza literature, as it is the best known example (e.g. visna virus in sheep[1]). Antigenetic shift is a specific case of reassortment or viral shift that confers a phenotypic change.

In terms of virology, the marine ecosystem has been largely unstudied, but due to its extraordinary volume, high viral density (100 million viruses per mL in coastal waters, 3 million per mL in the deep sea[2]) and high cell lysing rate (as high as 20% on average[*citation needed*]); marine viruses' antigenic shift and genetic recombination rates must be quite high.[3] This is most striking when one considers that the coevolution of prokaryotes and viruses in the aquatic environment has been going on since before eukaryotes appeared on earth.

Antigenic shift is contrasted with antigenic drift, which is the natural mutation over time of known strains of influenza (or other things, in a more general sense) which may lead to a loss of immunity, or in vaccine mismatch.[*citation needed*] Antigenic drift occurs in all types of influenza including influenzavirus A, influenza B and influenza C. Antigenic shift, however, occurs only in influenzavirus A because it infects more than just humans.[4] Affected species include other mammals and birds, giving influenza A the opportunity for a major reorganization of surface antigens. Influenza B and C principally infect humans, minimizing the chance that a reassortment will change its phenotype drastically.[5]

Antigenic shift is important as it is a pathway that viruses may follow to enter a new niche, and so should not be overlooked in the emergence of new viral pathogens.[*citation needed*] It could occur with primate viruses and may be a factor to consider for the appearance of new viruses in the human species such as HIV.[*citation needed*] Due to the structure of its genome HIV does not undergo reassortment, but it does recombine freely and via superinfection HIV can produce recombinant HIV strains that differ significantly from their ancestors.

Flu strains are named after their types of hemagglutinin and neuraminidase surface proteins, so they will be called, for example, H3N2 for type-3 hemagglutinin and type-2 neuraminidase. When two different strains of influenza infect the same cell simultaneously, their protein capsids and lipid envelopes are removed, exposing their RNA, which is then transcribed to mRNA. The host cell then forms new viruses that combine their antigens; for example, H3N2 and H5N1 can form H5N2 this way. Because the human immune system has difficulty recognizing the new influenza strain, it may be highly dangerous. Influenza viruses which have undergone antigenic shift have caused the Asian Flu pandemic of 1957, the Hong Kong Flu pandemic of 1968, and the Swine Flu scare of 1976. Until recently, such combinations were believed to have caused the infamous Spanish Flu outbreak of 1918 which killed 40~100 million people worldwide[*citation needed*]; however more recent research suggests the 1918 pandemic was caused by the antigenic drift of a fully avian virus to a form that could infect humans

efficiently.[6][7] One increasingly worrying situation is the possible antigenic shift between avian influenza and human influenza. This antigenic shift could cause the formation of a highly virulent virus.

The Mexican influenza virus isolated from patients in the United States was found to be made up of genetic elements from four different flu viruses – North American Mexican influenza, North American avian influenza, human influenza, and swine influenza virus typically found in Asia and Europe – "an unusually mongrelised mix of genetic sequences."[11] This new strain appears to be a result of reassortment of human influenza and swine influenza viruses, in all four different strains of subtype H1N1. However, as the virus has not yet been isolated in animals to date and also for historical naming reasons, the World Organisation for Animal Health (OIE) suggests it be called "Mexican influenza".[12]

Several complete genome sequences for U.S. flu cases were rapidly made available through the Global Initiative on Sharing Avian Influenza Data (GISAID).[13][14] Preliminary genetic characterization found that the hemagglutinin (HA) gene was similar to that of swine flu viruses present in U.S. pigs since 1999, but the neuraminidase (NA) and matrix protein (M) genes resembled versions present in European swine flu isolates. The six genes from American swine flu are themselves mixtures of swine flu, bird flu, and human flu viruses.[15][16] While viruses with this genetic makeup had not previously been found to be circulating in humans or pigs, there is no formal national surveillance system to determine what viruses are circulating in pigs in the U.S.[17]

Role in transmission of influenza viruses from animals to people

Influenza A viruses are found in many different animals, including ducks, chickens, pigs, whales, horses, and seals.[5] Influenza B viruses circulate widely principally among humans, though it has recently been found in seals.[8]

There are 16 different hemagglutinin subtypes and 9 different neuraminidase subtypes[*citation needed*], all of which have been found among influenza A viruses in wild birds.[*citation needed*] Wild birds are the primary natural reservoir for all subtypes of influenza A viruses and are thought to be the source of influenza A viruses in all other animals.[4] Most influenza viruses cause asymptomatic or mild infection in birds; however, the range of symptoms in birds varies greatly depending on the strain of virus. Infection with certain avian influenza A viruses (for example, some strains of H5 and H7 viruses) can cause widespread disease and death among some species of wild and especially domestic birds such as chickens and turkeys.

Pigs can be infected with both human and avian influenza viruses in addition to swine influenza viruses. Infected pigs get symptoms similar to humans, such as cough, fever,

and runny nose. Because pigs are susceptible to avian, human and swine influenza viruses, they potentially may be infected with influenza viruses from different species (e.g., ducks and humans) at the same time.[*citation needed*] If this happens, it is possible for the genes of these viruses to mix and create a new virus.

For example, if a pig were infected with a human influenza virus and an avian influenza virus at the same time, an antigenic shift could occur, producing a new virus that had most of the genes from the human virus, but a hemagglutinin or neuraminidase from the avian virus. The resulting new virus would likely be able to infect humans and spread from person to person, but it would have surface proteins (hemagglutinin and/or neuraminidase) not previously seen in influenza viruses that infect humans, and therefore to which most people have little or no immune protection. If this new virus causes illness in people and can be transmitted easily from person to person, an influenza pandemic can occur.[5]