

Emergence and Threats of Influenza Viruses

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Description

The threat of influenza viruses to both veterinary and human public health has increased since the 1990s. The altering ecological factors and the increased global populations of poultry, pigs, and people occur at the same time. These factors include the redistribution of the human population to towns, rapid-fire mass transportation of people and contagious agents, increased global land use, climate change, and possible changes in viral ecology that immortalize largely pathogenic influenza viruses in the aquatic bird reservoir.

The increased genetic exchange among influenza viruses in wild aquatic birds, domestic poultry, and humans and the emergence of H5N1, H7N9, and H9N2 subtypes of influenza A virus cause a continuing trouble to humanity. At the human animal interfaces the basic and practical knowledge of influenza "A viruses" is considered to facilitate the development of new control strategies and modified agrarian practices that will reduce or prevent interspecies transmission. Influenza A viruses are of major concern to both veterinary and human public health because they continue to emerge and cause high mortality in domestic poultry and represent an on-going trouble to human health. There's acceptance of the "one world" concept of influenza with the recognition that aquatic birds are the major force of influenza viruses that sporadically transmit to domestic poultry, swine, and humans. When influenza A viruses spread from the submarine bird reservoir to domestic poultry, pigs, and people, they can evolve into viruses that cause mild or catastrophic diseases. For influenza viruses to spread from the submarine bird reservoir to humans, they must evolve from intestinal tropism in wild aquatic birds with a body temperature of 42°C to respiratory tract tropism in humans with a body temperature of 37°C. Also, the virus must change its receptor particularity on the hemagglutinin (HA) from a binding preference for sialic acid (SA)-alpha 2,3 in wild birds to SA-alpha 2,6 in humans. Thus, multiple inheritable changes are needed. The RNA genome of influenza has a high mutation rate, no evidence reading mechanism, and is segmented, which enables the virus to be highly variable, continually acquire mutations, and constantly reassort. Agrarian practices that inadvertently

facilitate the exchange of influenza A viruses at the wild bird domestic bird interface and at the domestic bird mammalian interface have been adopted to provide additional animal protein to an increasing human population. The fundamental knowledge of the properties of influenza A viruses are considered that permit them to be so variable and the molecular determinants of host range and pathogenicity involved in the birth of epidemic influenza viruses of domestic poultry, pigs, and humans.

Since the mid-1990s, the number of influenza threats to both veterinary and human public health has increased, including the genesis of triadic reassortant viruses that contain gene segments from wild submarine birds, swine, and humans. These include an epidemic H IN 1 influenza virus in 2009 that spread encyclopedically to humans and the H5N1 and H7N9 influenza viruses that continue to evolve and spread. Although neither the H5N I nor the H7N9 viruses have transmitted constantly among humans, the epidemic eventuality of these viruses cannot be overemphasized.

Influenza viruses are enveloped, negative sense, single stranded RNA viruses of the family Orthomyxoviridae, and they subsist as 3 different types A, B and C. Influenza A and B viruses are associated with seasonal pandemics in humans, and influenza C viruses generally cause sporadic infections. Only influenza viruses are found in a number of mammalian and bird species and they're further classified into subtypes based on the antigenic properties of their spike-like surface glycoproteins, HA and neuraminidase (NA). At present, 18 HA subtypes (HI-H18) and 11 NA subtypes (NI-NI I) have been recognized. Each virus contains 1 HA and 1 NA subtype, and most of the influenza A subtypes can be found in numerous possible combinations in aquatic bird populations, except H17, H18, N10, and NI1, which have been found only in bats. In particular, wild waterfowl are considered the main natural reservoir for influenza A viruses, therefore, they play a central role in influenza A virus ecology. Contrarily, only a limited influenza subtypes have come established in mammals and HI, H2, and H3 are the only ones that have caused epidemic and pandemic influenza in humans.