Influenza A Features: Pandemic in the Horizon

Author: Patricia Bolivar PhD Epidemiology Candidate at Walden University
Date: March 25, 2013

In the 15th century the name “influenza” was given to an epidemic attributed to the “influence of the stars” described by an abrupt onset of fever and respiratory symptoms; sore throat, cough, headache, myalgia and in some persons gastrointestinal involvement including abdominal pain, vomiting, and diarrhea (Nelson & Williams, 2007). Influenza pandemics have been described and documented as devastating as the bubonic plague of the 14th century causing millions of deaths worldwide (Nelson & Williams, 2007). In the 19th century four influenza pandemics were described associated with animals especially horses. In the 20th century three pandemics associated with swine and birds (wild bird, shorebirds, and water fowl) as a reservoir occurred initiated at a specific geographic location and spread globally rapidly due to increase in population and transportation systems (Cox & Subbarao, 2000).

Influenza virus is an RNA, single stranded, and helical shaped virus belonging to the Orthomyxovirus family which has been studied since the 1930s. Influenza viruses have been classified as A, B, or C based on antigenic nuclear material (CDC, 2011). Only types A and B have epidemiological association with human seasonal morbidity and mortality (Cox & Subbarao, 2000). Influenza A, responsible for human epidemics and pandemics, has subtypes determined by surface glycoproteins antigens: hemagglutinin (H) which role is to facilitate virus attachment to cells and neuraminidase (N) which role is to allow virus penetration into epithelial cells of the respiratory system. Influenza viruses antigens affecting humans also found in a variety of animals are H1, H2, and H3 and N1 and N2 (CDC, 2011). Antigenic variations occur in influenza virus types A and B due to H and N genes point mutations, known as antigenic drift,
include deletions, substitutions, and insertions producing minor changes, same subtype, which result in annual epidemics (CDC, 2011 and Nelson & Williams, 2007). Major influenza antigenic changes caused by exchange of gene segments with another subtype of influenza A virus in humans and birds, known as antigenic shift, create a new subtype which may result in a pandemic (CDC, 2011). Swine being in contact with birds and humans is believed to provide the “mixing vessel” host for pandemic variants responsible for pandemics (Nelson & Williams, 2007 and CDC, 2011). The changing nature of the virus renders humans susceptible unless adequate influenza A type and subtypes are included in trivalent vaccines to stimulate the antibody response needed to combat the infection (Monto, 2008).

Transmission of influenza virus occurs between adult and children by either direct contact with influenza virus laden droplets expelled from infected persons in 5 to 10 days from the day of symptoms onset through cough or sneeze or indirect contact with fomites and surfaces contaminated with the virus through the mouth, nose or eyes (CDC, 2011). Infection of influenza A subtypes (H3N2) and (H1N1) and B types are related to age with children having higher attack rates than adults, H3N2 associated with more severity, and H1N1 as a milder infection (Monto, 2008). Avian influenza H5N1 known as “bird flu” is enzootic in many bird populations in Southeast Asia. H5N1 is an influenza A virus variant strain mutated by influenza shifts highly virulent and pathogenic to both animals and humans with an overall mortality rate of 57% not yet transmitted efficiently from human to human (Nelson & Williams, 2007). Outbreaks and disease cases in birds and humans have been reported since 2003 in China, Indonesia, Vietnam, Pakistan, Egypt, Iran, Iraq, and Turkey arising serious concerns on the possibility of a pandemic. H5N1 may efficiently cause human to human transmission as the virus adapts to humans by acquiring specific gene segments to adapt to the human host without an intermediate host genetic
reassortment (Cox & Subbarao, 2000). H5N1 pose a world’s pandemic threat of a tremendous impact. Trillions of dollars are currently being raised and invested to improve global surveillance, communication at the local and national level with the World Health Organization, development of an effective vaccine available in billion doses after the initial virus emergence human to human transmission, antiviral drugs stockpiles and distribution sites, and development of public health strategies on epidemic and transmission control.

References


