influenza virus lethal assortants

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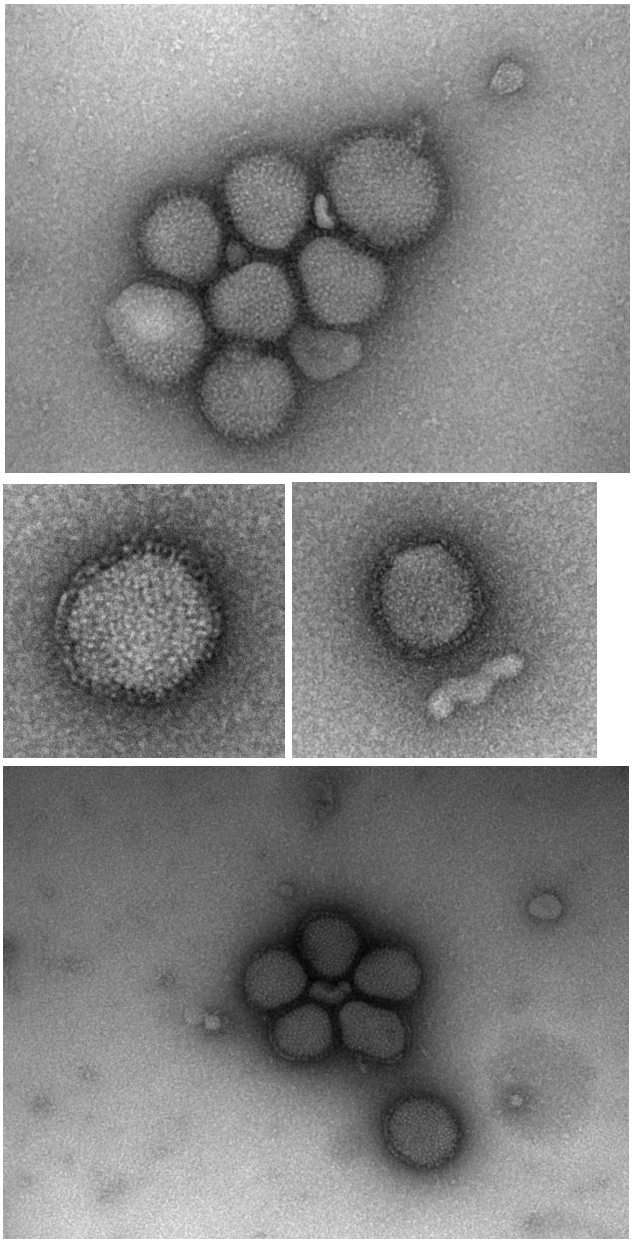
Influenza A viruses are divided into subtypes based on antigenic differences between their surface glycoproteins, haemagglutinin (HA) and neuraminidase (NA), both of which are important determinants for neutralizing antibodies. To date, 18 HA subtypes and 11 NA subtypes have been identified. A “H5N1 virus” refers to an influenza virus subtype that has HA 5 and NA 1 proteins. Theoretically, 198 (18 x 11) different subtypes of type A influenza are possible. Among them, highly pathogenic avian influenza (HPAI) viruses are normally associated with H5, H7, and H9 subtypes (Alexander, 2000).

In April 2009, a new strain of H1N1 influenza virus appeared from a unique mixture of assorted genes closely related to swine-origin H1N1 influenza viruses. Although World Health Organization (WHO) has declared the end of this “swine flu” pandemic, the virus continues to circulate with other seasonal viruses in many countries. In a recent event, a novel low pathogenic avian influenza virus (LPAI) H7N9 was reported in China on April 1, 2013 by WHO (CDC, 2013). This new endemic had caused fatal infections to human although the virus is low pathogenic in poultry, thus has led to a greater concern of another pandemic after the HPAI H5N1 “bird flu” occurrence. There is no concrete evidence of human-to-human transmission for H7N9 virus. Early this year, another novel LPAI subtype H18N10 that is able to cause fatality in human, was reported in China. Study indicated that both of the novel LPAI carry internal genes from an LPAI H9N2 (Garcia-Sastre and Schmolke, 2014), indicating that the on-going H9N2 virus circulation may play a critical role in the emergence of the next influenza virus catastrophic wave.



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