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Editorial

Avian Flu A (H_7N_9) Infection: A New Largest Fifth Wave in China

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The initial wave of avian flu A H_7N_9 infection in China occurred from February to May 2013 after the human cases were reported to the World Health Organization (WHO) in late March and April 2013. It was likely related to at least in part, to implementation of control strategies including increased public awareness and closure of live-bird markets. Annual epidemics have occurred during influenza season since then, the majority of cases have occurred in China. In late 2016 and early 2017, the largest fifth wave of avian flu A H_7N_9 infection occurred. This new wave raised the number of cases with H_7N_9 avian influenza infection to 757 cases as of September 8, 2017 and at least 281 cases were fatal. One 67-year-old new male case with H_7N_9 avian influenza infection from Hunan province was reported as of September 8, 2017. China continues to report sporadic cases in summer months from a broad part of the country although cases have slowed since a sudden rise last fall that lasted into spring.

Five outbreak waves of avian influenza A (H_7N_9) infection have occurred since the low-pathogenic avian influenza A (H_7N_9) (LPAI H_7N_9) virus first emerged in spring 2013 in eastern China. Mutation of LPAI H_7N_9 by insertion of four amino acids (KRTA) in the hemagglutinin (HA) proteolytic cleavage site that contributes their pathotype switch from LPAI H7N9 to highly pathogenic avian influenza A (H_7N_9) (HPAI H_7N_9) virus. Both viruses contain an insertion of four amino acids (KRTA) in the HA proteolytic cleavage site. HPAI (H_7N_9) viruses have recently been isolated from humans and resulted in fatal outcome in Guangdong, China (A/Guangdong/17SF003/2016 (SF003) and A/Guangdong/17SF006/2017 (SF006)). Current fifth epidemic wave of emerging HPAI H_7N_9 virus infection is due to the insertion of four amino acids (KRTA) at the HA cleavage site that enabled trypsin-independent infectivity of this virus. A multidrug-resistant phenotype is conferred by the neuraminidase substitution R292K. furthermore, both viruses retain a series of genetic features leading to the ability to infect humans, for examples: 627K in the PB2 protein and 186V in the HA protein (H_3 numbering) that raise concerns regarding their pandemic potential. WHO advises that travelers to countries with known outbreaks of avian influenza should avoid entering areas where poultry may be slaughtered, or contact with any surfaces that appear to be contaminated with feces from poultry or other animals, poultry farms, and contact with animals in live-poultry markets. Travellers should follow good food safety and food hygiene practices and wash their hands often with soap and water.

A Taiwanese research group recently announced that a phase ½ trial of an inactivated cell-culture H_7N_9 vaccines was safe and immunogenic in adults ages 20 to 60 years old and published their findings in an early online edition of the Journal "Vaccine". They claimed that this is the first report of an H_7N_9 candidate vaccine evaluated in Asia where the virus emerged and is causing the highest disease burden although four other early-phase clinical trials of H_7N_9 vaccines recently have been published.

In conclusion, although HPAI H_7N_9 virus was thought to cause higher risk in poultry than the LPAI H_7N_9 virus, particularly regarding the receptor profile of HPAI H_7N_9 viruses, has implications on control strategies and surveillance both in public health and animal sectors. Critical role of antiretroviral surveillance and monitoring in the clinical management of influenza virus infection is an essential component of pandemic preparedness and emergency responses.

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