The importance of surveillance of avian and swine influenza

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Recent outbreaks of highly pathogenic avian influenza (HPAI) have spread from Southeast Asia to the north-west involving Qinghai Lake, Xinjiang Province in China, Mongolia, Russia, Kazakhstan, Turkey, Croatia, Ukraine, Nigeria, Egypt, and European countries. H5N1 viruses isolated from dead water birds in Erhel Lake in Mongolia in July 2005 are genetically closely related to those isolated from birds in Qinghai Lake, Croatia, and Nigeria and phylogenetically different from isolates from birds in Vietnam, Thailand, Japan, and Korea. It is of concern that these H5N1 HPAI viruses may perpetuate in the lakes where migratory ducks nest in summer. In the surveillance of avian influenza carried out in Mongolia in September 2005, no H5N1 virus was isolated from migratory ducks that flew from Siberia, indicating that HPAI H5N1 virus has not yet perpetuated in their nesting lakes in Siberia. It is important to continue intensive surveillance of avian influenza in migratory water birds.

These H5N1 HPAI viruses caused severe disease with high mortality in humans in Viet Nam, Thailand, Cambodia, Indonesia, Egypt, China, Turkey Azerbaijan, and Iraq. The second concern is that only the H5N1 virus is assumed to cause next pandemic influenza in humans. Each of the known subtypes of influenza viruses perpetuates among migratory ducks and their nesting lake water in nature. Since avian viruses of any subtype can contribute genes in the generation of reassortants in pig, none of the 16 HA and 9 NA subtypes can be ruled out as potential candidates for future pandemic strains. Surveillance of swine influenza presently became more important as well as that of avian influenza.

Avian influenza virus isolates have been characterized and stored for vaccine strain candidates and diagnostic use. Influenza virus isolates of 49 combinations of HA and NA subtypes have been isolated from fecal samples of ducks in Alaska, Siberia, Mongolia, Taiwan, China, and Japan. So far, 78 other combinations have been generated by the genetic reassortment procedure in chicken embryos. Thus, avian influenza viruses of 127 combinations of HA and NA subtypes have been stocked. Their pathogenicity, antigenicity, genetic information and yield in chicken embryo have been analyzed and registered in the database.

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