Medical Xpress

Source identification of H7N9 influenza virus causing human infections

April 25 2013

In March 2013, a novel H7N9 influenza virus was identified in China as the etiological agent of a flu-like disease in humans, resulting in some deaths. A group of scientists, led by Professor Chen Hualan (National Avian Influenza Reference Laboratory, State Key Laboratory of Veterinary Biotechnology, Harbin Veterinary Research Institute, Chinese Academy of Agricultural Sciences) have investigated the origins of this novel H7N9 influenza virus (Shi et al., 2013). Following analysis of H7N9 influenza viruses collected from live poultry markets, it was found that these viruses circulating among birds were responsible for human infections. These novel H7N9 viruses are reassortants in which the six internal genes were derived from avian H9N2 viruses; however the origins of their hemagglutinin (HA) and neuraminidase (NA) genes were unclear.

A total of 970 samples were collected from live poultry markets and poultry farms located in Shanghai and Anhui Province. Samples analyzed included drinking water, feces, contaminated soil, and cloacal and tracheal swabs. Of these samples, 20 were positive for the presence of H7N9 influenza viruses. All of the positive samples originated from live poultry markets in Shanghai. Of these 20 positive samples, 10 were isolated from chickens, 3 from pigeons, and 7 were from environmental samples.

The complete genome of three H7N9 isolates, from a chicken, pigeon, and environmental sample, was sequenced and deposited into the GISAID database. Genetic analysis of these isolates revealed high

homology across all eight gene segments. Phylogenetic analysis of these novel H7N9 influenza virus isolates showed that that the six internal genes were derived from avian H9N2 viruses, but the ancestor of their HA and NA genes is unknown. According to the GenBank database, the HA genes of the novel isolated viruses were most similar to those from duck H7N3 influenza viruses, sharing 95.2

More information: Shi J Z, Deng G H, Liu P H, et al. Isolation and characterization of H7N9 viruses from live poultry markets—Implication of the source of current H7N9 infection in humans. Chin Sci Bull, 2013, 58, doi:10.1007/s11434-013-5873-4. link.springer.com/article/10.1 … 07/s11434-013-5873-4

Provided by Science China Press

Citation: Source identification of H7N9 influenza virus causing human infections (2013, April 25) retrieved 2 May 2024 from https://medicalxpress.com/news/2013-04-source-identification-h7n9-influenza-virus.html

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