

## Bird flu in live poultry markets are the source of viruses causing human infections

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On 31 March 2013, the Chinese National Health and Family Planning Commission announced human cases of novel H7N9 influenza virus infections. A group of scientists, led by Professor Chen Hualan of the Harbin Veterinary Research Institute at the Chinese Academy of Agricultural Sciences, has investigated the origins of this novel H7N9 influenza virus and published their results in Springer's open access journal *Chinese Science Bulletin*.

Following analysis of H7N9 influenza viruses collected from live poultry markets, it was found that these viruses circulating among birds were responsible for <u>human infections</u>. These results provide a basis for the



government to take actions for controlling this <u>public health threat</u>. The novel H7N9 influenza virus was identified in China as the agent, that causes a flu-like disease in humans, resulting in some deaths.

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, <u>contaminated soil</u>, 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 <u>GISAID database</u>. Genetic analysis of these isolates revealed high homology across all eight <u>gene segments</u>. The analysis of these novel H7N9 <u>influenza virus</u> isolates showed that that the six internal genes were derived from avian H9N2 viruses, but the ancestor of their hemagglutinin (HA) and neuraminidase (NA) genes is unknown.

HA receptor-binding specificity is a major molecular determinant for the host range of influenza viruses. Within the HA protein of novel H7N9 viruses, there was a leucine residue at position 226, which is characteristic of the HA gene in human influenza viruses. This finding implies that H7N9 viruses have partially acquired human receptorbinding specificity.

The authors conclude: "We suggest that strong measures, such as continued surveillance of avian and human hosts, control of animal movement, shutdown of live poultry markets, and culling of poultry in affected areas, should be taken during this initial stage of virus prevalence to prevent a possible pandemic. Additionally, it is also



imperative to evaluate the pathogenicity and transmissibility of these H7N9 viruses, and to develop effective vaccines and antiviral drugs so as to reduce their adverse effects upon human health."

**More information:** Shi J Z, Deng G H, Liu P H, et al (2013). Isolation and characterization of H7N9 viruses from live poultry markets—Implication of the source of current H7N9 infection in humans. *Chinese Science Bulletin*. DOI: 10.1007/s11434-013-5873-4

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