

## The Outbreak of Avian Influenza A (H7N9) in China: Current Status and Future Prospects

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In March 2013, an influenza outbreak caused by a novel influenza A (H7N9) virus occurred in China.<sup>[1-3]</sup> As of May 29, 2013, 132 confirmed cases, including 37 deaths (a case fatality rate of 28%), were reported to the World Health Organization. Since then, no new cases of A (H7N9) have been reported.<sup>[4]</sup> Can it be presumed that this A (H7N9) outbreak is over and, if so, will it re-emerge?

At this stage, no one can claim that the outbreak is completely over; however, in the absence of evidence to the contrary, it appears to have reached its peak. Nonetheless, public health authorities and researchers in China continue to maintain enhanced surveillance, and epidemiological investigation is ongoing, in order to more clearly define the origin of the virus, monitor its spread, and develop prevention and control measures.

Genomic signature analysis has confirmed the avian origin of A (H7N9), revealing 43 avian signatures to only 4 human signatures.<sup>[3]</sup> Phylogenetic analysis further indicates that its HA gene might have originated from H7N3 in ducks in Zhejiang Province, whereas its NA gene might have originated from migratory birds along the East Asian flyway. Its six internal genes may originate from H9N2 avian influenza viruses (AIVs) isolated from chickens and birds, such as bramblings in Beijing. Therefore, ducks and chickens in the Yangtze River Delta (YRD) region could have served as the intermediate hosts for this virulent A (H7N9) virus.<sup>[5]</sup> Based on this evidence, researchers are asking how migratory birds passed the virus to poultry. One theory proposed by Li *et al.*,<sup>[2]</sup> suggests that wild ducks first transmitted the virus to domesticated ducks, as both have similar patterns of behavior and habitats in the YRD, further passing it on to chickens. Chongming Island near Shanghai is the home of many wild birds. This may explain why Shanghai was the most affected area during the initial outbreak of A (H7N9).<sup>[6]</sup>

Unlike the highly pathogenic AIV, A (H5N1), which has killed millions of birds, A (H7N9) still has low patho-

genicity to birds and poultry, which thus act as hidden reservoirs for this zoonotic A (H7N9) virus. The live poultry markets in YZD have been confirmed to be the major risk factor for human infection of A (H7N9) virus since the virus was identified from the live poultry and the environment in these markets,<sup>[7]</sup> and closing the live poultry markets resulted in significant reduction of morbidity rate of A (H7N9).

Due to the lack of a vaccine against A (H7N9) virus, the prophylactic measures that should be taken may include: (1) staying away from live poultry markets and the surrounding environment; (2) avoiding touching live birds and their excretions or secretions; (3) performing hand hygiene; (4) maintaining respiratory hygiene; and (5) taking food safety measures.

A (H5N1) and other AIVs have shown a seasonal pattern whereby human cases in summer months are much lesser than those in winter months. We expect that A (H7N9) will follow the same seasonal pattern. However, since migratory birds were first implicated in H7N9 transmission, we cannot exclude the possibility that the virus may spread into other regions or countries with colder weather, given the widespread migratory patterns, thus causing a new outbreak there.

We now ask whether we should expect its re-emergence during the winter months and, if so, what precautionary steps should be taken. A global surveillance system should be established to monitor the spread of AIVs, particularly A (H7N9) and A (H5N1). Close collaboration between the epidemiologists responsible for monitoring AIVs in humans and those monitoring AIVs in migratory birds, poultry, and the environment is urgently needed. It is also important for researchers to identify the viral mutations or reassortments that may alter risks for animals or humans, in order to gain insight into critical viral characteristics, including antiviral resistance, transmissibility, and pathogenicity, followed by developing strategies to control the future spread of A (H7N9).

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