

WHO RISK ASSESSMENT

Human infections with avian influenza A(H7N9) virus

10 May 2013

Summary

A total of 131 confirmed cases of human infection with avian influenza A(H7N9) virus have been reported to WHO by China National Health and Family Planning Commission and one case by the Taipei Centers for Disease Control (Taipei CDC). Although cases have been reported in both sexes and across a wide range of ages, most cases have occurred among middle-aged and older men. Thirty-two people have died, and most of the other cases are considered severe. In addition to the case reported by Taipei CDC (with a history of recent travel from Jiangsu), cases have been reported from Anhui, Fujian, Henan, Hunan, Jiangsu, Jiangxi, Shandong and Zhejiang, and the municipalities of Beijing and Shanghai.

Much remains unknown about this virus, including the animal reservoir(s) in which it is circulating, the main exposures and routes of transmission, and the scope of the spread of this virus among people and animals. Investigations are ongoing and evidence is inconclusive. Nevertheless, human infection appears to be related to exposure to live poultry or contaminated environments because:

- The virus in humans is genetically similar to that found in animals and the environment (live bird markets).
- Most human cases (approximately three out of four patients) report a history of exposure to animals, mostly chickens.
- The virus has been detected in poultry in live bird markets.
- The number of human cases appears to have decreased after closure of live animal markets.

Whether other potential reservoirs of this virus may exist, including in other domestic and wild bird species, and mammalian species, has not yet been determined. And although two family clusters have been reported, there is no evidence of sustained human-to-human transmission:

- Monitoring and testing of contacts (>2000 people) of confirmed cases has detected few infections.
- Testing of more than 20,000 people with influenza-like illness (ILI) in March and April has confirmed only six infections with H7N9. This finding suggests that milder cases of H7N9 infection are not occurring in large numbers.

This is the first time human infection with the avian influenza A(H7N9) subtype has been detected. Previously, sporadic cases of human infection with other influenza A(H7) viruses have been reported which were associated with outbreaks of infection in poultry. The few A(H7) human infections that have occurred generally resulted in mild illness and conjunctivitis, with the exception of one death.



Genetic and laboratory characterization of avian influenza A(H7N9) viruses isolated from humans indicates that:

- The virus contains a group of influenza virus genes from multiple origins.
- Some genetic changes, including amino acid substitutions associated with increased affinity to alpha 2-6 receptors, suggest that H7N9 may have greater ability to infect mammals, including humans, than other avian influenza viruses.
- Sequence variations among the genes of the isolates suggest that there has been more than one introduction of this virus from animal into humans.
- Genetically, these viruses are in general expected to be sensitive to the neuraminidase inhibitors oseltamivir and zanamivir, but resistant to the antiviral drugs amantadine and rimantadine.
- The isolates have a haemagglutinin structure that is associated with low pathogenicity in birds.

The virus has not been reported to cause severe disease in poultry. The absence of this signal limits the ability to easily detect the virus in birds, in contrast to avian influenza A(H5N1).

Risk assessment

This risk assessment supersedes the document posted on 13 April 2013. It has been prepared in accordance with WHO's published recommendations for rapid risk assessment of acute public health events and will be updated as more information becomes available. The risk has not changed since the previous assessment.

What is the risk that more human cases will occur in the affected areas?

The understanding of the epidemiology of this outbreak and virus remains limited, including the main reservoirs of infection and the extent of geographic spread among animals. However, it is likely that most human H7N9 infections have been associated with contacts with animals or live bird markets. Further human cases should be expected. Other avian influenza viruses such as H5N1 have demonstrated a seasonal pattern in which human cases have been less frequent in summer months and more frequent in winter months. It remains to be seen whether H7N9 infections will follow the same seasonal pattern. Most human cases have resulted in clinically severe illness.

What is the risk of human-to-human transmission?

There is no evidence of sustained human-to-human transmission. However, two family clusters suggest that limited human-to-human transmission may occur where there is close contact between cases and other people, as occurs in families and potentially in healthcare settings. Moreover, the genetic changes seen among these viruses that suggest adaptation to mammals is of concern, and further adaptation may occur. Should sustained human-to-human transmission occur with an increased number of clinically severe cases, health systems are likely to be strained.

What is the risk of international spread of H7N9 by travelers?

There is no indication that international spread has occurred. An infected person, whether symptomatic or not, who travels to another country, could spread the infection. However, as the virus does not



appear to cause sustained human-to-human transmission, extensive community spread is unlikely. If transmissibility were to increase, then the possibility of spread would likewise increase.

Does WHO recommend any travel precautions related to H7N9?

WHO does not advise special screening at points of entry with regard to this event, nor does it currently recommend any travel or trade restrictions.

Resources

Liu D, S. W. (2013). Origin and diversity of novel avian influenza A H7N9 viruses causing human infection: phylogenetic, structural, and coalescent analyses.

Lancet: [http://www.thelancet.com/journals/lancet/article/PIIS0140-6736\(13\)60938-1/fulltext](http://www.thelancet.com/journals/lancet/article/PIIS0140-6736(13)60938-1/fulltext)

Li Q, Z. L. (2013). Preliminary Report: Epidemiology of the Avian Influenza A (H7N9) Outbreak in China.

New England Journal of Medicine: <http://www.nejm.org/doi/full/10.1056/NEJMoa1304617#t=article>

Chen Y, L. W. (2013). Human infections with the emerging avian influenza A H7N9 virus from wet market poultry: clinical analysis and characterisation of viral genome.

Lancet: [http://www.thelancet.com/journals/lancet/article/PIIS0140-6736\(13\)60903-4/fulltext](http://www.thelancet.com/journals/lancet/article/PIIS0140-6736(13)60903-4/fulltext)

Cuiling Xu, Fiona Havers, Lijie Wang, Tao Chen, Jinghong Shi, Dayan Wang, Jing Yang, Lei Yang, Marc-Alain Widdowson, and Yuelong Shu. (2013). Monitoring Avian Influenza A(H7N9) Virus through National Influenza-like Illness Surveillance, China. *Emerging Infectious Diseases*:

http://wwwnc.cdc.gov/eid/article/19/8/13-0662_article.htm

Liu Q, L. L. (2013). Genomic signature and protein sequence analysis of a novel influenza A (H7N9) virus that causes an outbreak in humans in China. *Microbes and*

Infection: <http://www.ncbi.nlm.nih.gov/pubmed/23628410>

WHO. (2012). *Rapid Risk Assessment of Acute Public Health*

Events: http://www.who.int/csr/resources/publications/HSE_GAR_ARO_2012_1/en/

Additional Information

Most recent disease outbreak news can be found at: <http://www.who.int/csr/don/en/index.html>

Frequently Asked Questions and other information on human infections with avian influenza A(H7N9) are available at: http://www.who.int/influenza/human_animal_interface/influenza_h7n9/en/index.html



Public health relevant virological features of influenza A(H7N9) causing human infection in China: <http://www.euro.who.int/en/what-we-do/health-topics/communicable-diseases/influenza/publications/2013/public-health-relevant-virological-features-of-influenza-ah7n9-causing-human-infection-in-china>

