

WHO RISK ASSESSMENT

Human infections with influenza A(H7N9) virus

13 April 2013

Summary of available information

As of 13 April 2013, a total of 49 confirmed cases of human infection with avian influenza A(H7N9) virus have been reported to WHO by the China National Health and Family Planning Commission. Among these cases, the ages range from 4 to 87; 15 are female. Eleven persons have died, and the majority of the additional cases are considered severe. Of the 49 cases, 6 have been reported today and further investigations are taking place. The cases have been reported from three provinces: Anhui, Jiangsu and Zhejiang, and two municipalities, Beijing and Shanghai. All locations are in Eastern and Northern China.

Two confirmed cases have been associated with possible family clusters, in which one and two additional family members, respectively, developed severe pneumonia. Close contacts of confirmed cases and health care workers caring for cases have been monitored for infection. So far, among the contacts who have been tested by polymerase chain reaction, none has been shown to have infection.

This is the first time human infection with this influenza subtype, avian influenza A(H7N9) virus, has been detected. Previously, sporadic cases of human infection with other influenza A(H7) viruses have been reported. Those cases were associated with outbreaks of infection in poultry in other countries. These earlier influenza A(H7) human infections generally resulted in mild influenza illness with some conjunctivitis.

Genetic and laboratory characterization of the first three of these H7N9 viruses isolated from humans indicates that:

- the virus contains a group of avian influenza virus genes from three different avian influenza viruses;
- to date, genetic analyses of the isolates have shown certain changes, including amino acid substitutions associated with increased affinity to alpha 2-6 receptors, which suggests that the H7N9 virus may have greater ability to infect mammalian species, including humans, than most other avian influenza viruses;
- there are sequence variations among the genes of three isolates that suggest there has been more than one introduction of this virus from animal into humans;
- these viruses are expected to be sensitive to the neuraminidase inhibitor drugs 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.

There are several gaps in critical information at this time, including the animal reservoir(s) in which this virus is circulating, the main exposures and routes of transmission for how human infections have been acquired, and the current scope of the spread of this virus among animal and human populations. Avian influenza A(H7N9) viruses have now been isolated from poultry (including duck) and pigeon in the live bird markets in some areas of China, but whether other potential reservoirs of



this virus may exist, including in other domestic and wild bird species, and mammalian species such as pigs, has not yet been determined clearly.

So far, this virus has not been associated with reports of severe disease in poultry.

Risk assessment

This initial risk assessment, which has been prepared in accordance with WHO's published recommendations for rapid risk assessment of acute public health events¹ will be updated as further information becomes available.

What is the risk of the occurrence of further cases in the affected areas of China and other areas?

The epidemiology of this virus among animals, including the main reservoirs of infection among animals and the extent of geographic spread, is not yet established. However, it is likely that most human H7N9 infections so far are associated with infection among as-of-yet undetermined animals and that further human cases of infection should be expected.

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

There is no evidence of sustained human-to-human transmission. However the two possible family clusters suggest that limited human-to-human transmission may occur where there is close contact between cases and other individuals, as occurs in families and, potentially, healthcare settings. Moreover, the genetic changes seen among these viruses suggesting adaptation to mammals is of concern, and further adaptation may occur.

What is the risk of international spread?

At this time, there is no information to indicate international spread of this virus. However, it is possible that an infected person, who may or may not have symptoms, could travel to another country. However, if the virus cannot sustain human-to-human transmission, as appears to be the current situation, then extensive community spread is unlikely.

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

References

Most recent disease outbreak news can be found at:

<http://www.who.int/csr/don/en/index.html>

Background and summary of human infection with influenza A(H7N9) virus (as of 5 April 2013):

http://www.who.int/influenza/human_animal_interface/update_20130405/en/index.html

Frequently Asked Questions on human infection with influenza A(H7N9) virus, China:

http://www.who.int/influenza/human_animal_interface/faq_H7N9/en/index.html

¹ Available from http://www.who.int/csr/resources/publications/HSE_GAR_ARO_2012_1/en/ accessed 10 April 2013



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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>

