

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

In the past few weeks, WHO has received from China reports of human infection with influenza A(H7N9) virus. The influenza A(H7N9) virus is one subgroup among the larger group of H7 viruses, which normally circulate among birds.

Human infections with other subgroups of H7 influenza viruses (H7N2, H7N3, and H7N7) have previously been reported in the Netherlands, Italy, Canada, United States of America, Mexico and the United Kingdom. Most of these infections occurred in association with poultry outbreaks. The infections mainly resulted in conjunctivitis and mild upper respiratory symptoms, with the exception of one death, which occurred in the Netherlands.

These recent reports from China are the first cases of human infection with H7N9 viruses.

Epidemiology

The reported laboratory-confirmed cases have come from several different provinces in eastern China and are not known to be linked. All patients so far have been severely ill, and some have died. For the latest information on cases and outcomes, see:

- [Disease Outbreak News \(DONs\)](#)

Two family clusters have been reported. Beyond these two clusters, no cases have been reported among contacts or in health care workers associated with confirmed cases.

The source of infection and the mode of transmission are currently unknown. No association with outbreaks of disease among animals or clear exposure to animals has been established. Some of the confirmed cases had contact with animals or with environments in which animals were located. The virus has been found in a pigeon in a market in Shanghai. The possibility of animal-to-human transmission is being investigated, as is the possibility of human-to-human transmission. The family cluster raises the possibility of human-to-human transmission, but two of the cases in that cluster have not been laboratory confirmed and there is no other evidence pointing toward sustained transmission among people.

Clinical presentation

The main clinical feature among most patients is respiratory diseases resulting in severe pneumonia. Symptoms include fever, cough and shortness of breath. Patients have required intensive care and mechanical ventilation. Information is, however, still limited about the full spectrum of disease that this infection might cause.

Virology

The HA gene is genetically distinct from the HA gene of other H7 viruses. The six internal genes are derived from influenza A(H9N2) viruses circulating in birds in eastern Asia. The NA gene is similar to the NA genes from influenza A(H1N9) viruses detected in birds in previous years.

We do not know why cases of influenza A(H7N9) virus infection are being detected now, as we do not know how these persons were infected. Sequence analyses have shown that the genes of the influenza A(H7N9) viruses from the first human cases in China are of avian (bird) origin. However, these genes also show signs of adaptation to growth in mammalian species. These adaptations include an ability to bind to mammalian cell receptors, and to grow at temperatures close to the normal body temperature of mammals (which is lower than that of birds).

Treatment

Laboratory testing conducted in China has shown that the influenza A(H7N9) viruses are sensitive to the anti-influenza drugs known as neuraminidase inhibitors (oseltamivir and zanamivir). When these drugs are given early in the course of illness, they have been found to be effective against seasonal influenza virus and influenza A(H5N1) virus infection. There is no experience yet with the use of these drugs for the treatment of H7N9 infection.

Prevention

No vaccine for the prevention of influenza A(H7N9) infections is currently available, although viruses have already been isolated and characterized from the initial cases. The first step in development of a vaccine is the selection of candidate viruses that could go into a vaccine. WHO, in collaboration with partners, will continue to characterize available influenza A(H7N9) viruses to identify the best candidate viruses. These candidate vaccine viruses can then be used for the manufacture of vaccine should this become necessary. While the source of infection and the mode of transmission have not yet been determined, it is prudent to follow good hygiene practices to prevent infection. For advice on infection prevention, contact with animals and food preparation, see:

- [Frequently Asked Questions on human infection caused by the avian influenza A\(H7N9\) virus](#)

Guidance for infection prevention and control in health care settings is available at:

- [Infection prevention and control of epidemic- and pandemic-prone acute respiratory diseases in health care](#)

Current activities

WHO has closely monitored the situation since detection of the first case and has been working with partners to ensure a high degree of preparedness should the new virus be found to be sufficiently transmissible to cause community outbreaks. We have also been working with animal health partners to investigate possible circulation in animals. Some viruses are able to cause limited human-to-human transmission under condition of close contact, as occurs in families, but are not transmissible enough to cause larger community outbreaks.

Actions taken by WHO in coordination with national authorities and technical partners include the following:

- Information is being provided to countries under the International Health Regulations (IHR).
- Enhanced surveillance for pneumonia cases of unknown origin to ensure early detection and laboratory confirmation of new cases.
- Epidemiological investigation, including assessment of suspected cases and contacts of known cases.
- Close collaboration with animal health partners, specifically the World Organization for Animal Health (OIE), the Food and Agriculture Office of the United Nations (FAO) and the OIE/FAO Network of Expertise on Animal Influenza (OFFLU), to investigate possible circulation of this virus in animals and to ensure that materials and information, including laboratory test reagents, are shared between animal health and public health laboratories.
- Continuous risk assessment of the situation in collaboration with the WHO Global Influenza Surveillance and Response System (GISRS), which is comprised of WHO Collaborating Centres for Reference and Research on Influenza, National Influenza Centres and Essential Regulatory Laboratories (see http://www.who.int/influenza/gisrs_laboratory/en/); in animal health laboratories, coordinated by the WHO-OFFLU collaboration; and with other technical partners.

WHO recommendations

Based on the current situation and available information, WHO advises the following:

- When laboratories testing for influenza viruses detect an influenza A virus by RT-PCR assays using primers for the conserved M genes and then find that tests using currently available H1, H3 and H5 primers are negative, such unsubtypeable influenza A viruses should be sent urgently to a WHO Collaborating Centre for further analysis:
 - [WHO Collaborating Centres and Essential Regulatory Laboratories](#)
- When a laboratory or Member State finds such an unsubtypeable influenza A virus, the finding should be reported to WHO through the International Health Regulations national focal point as is required under the IHR.
- The same surveillance strategy applies as for human infections with highly pathogenic avian influenza A (H5N1) virus.
- Clinicians and laboratory specialists should consider the possibility of human infection with influenza in any person presenting with severe acute respiratory disease.
- Clinicians are reminded of standard guidance for infection control and contact tracing around such cases.
- Standard guidance should also be applied for vigorously investigating clusters of severe respiratory infections and such infections in health care workers who have been caring for patients with severe acute respiratory disease.
- 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.

Summary

Any animal influenza virus that develops the ability to infect people can theoretically cause a pandemic. However, whether the influenza A(H7N9) virus could actually cause a pandemic is unknown. Experience has shown that some animal influenza viruses that have been found to occasionally infect people have not gone on to cause a pandemic while others have done so. Surveillance and the investigations now underway will provide some of the information needed to make this determination.

WHO continues to work closely with national authorities and technical partners to gain a better understanding of this disease in humans and will continue to provide updated information. WHO will continue to reassess the situation as it evolves. As more information becomes available WHO will revise its guidance and actions accordingly.