Assessment of risk associated with influenza A(H5N8) virus

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Background

Avian influenza A(H5N8) viruses have been rapidly spreading, most likely via wild migratory birds in Asia and Europe in recent months and causing deaths in wild birds and outbreaks in domestic poultry.

Conclusion of current human risk of the avian influenza A(H5N8) virus

Human infection with the A(H5N8) virus cannot be excluded, although the likelihood is low, based on the limited information obtained to date. It should be noted that human infection with A(H5N6) of related clade 2.3.4.4 has already occurred. WHO will re-assess the risk associated with the virus when more information is available.

Understanding of the virus

Geographic distribution in animals:

During 2014, highly pathogenic avian influenza A(H5N8) viruses belonging to clade 2.3.4.4 of the A/goose/Guangdong/1/1996 lineage were detected in wild birds and poultry in China, Germany, Italy, Japan, Netherlands, Republic of Korea, Russian Federation, and the United Kingdom of Great Britain and Northern Ireland. The virus was then detected in North America in late 2014 and was detected sporadically in Canada and the United States of America (USA) in wild birds and poultry until mid-2015. A(H5N8) viruses were also detected in Taiwan, China and in Hungary and Sweden in 2015.

Since June 2016, countries in both Europe and Asia have detected infections in wild birds and/or domestic poultry with A(H5N8) including Austria, Croatia, Denmark, Germany, Hungary, India, Israel, Netherlands, Poland, Russian Federation and Switzerland. Many of these recent detections were associated with mortality in wild birds.

Further spread along the migratory route of wild birds is likely, and introduction into other countries could occur.¹

Virology:

Hemagglutinin (HA) and neuraminidase (NA) gene sequences obtained from viruses infecting wild birds in Germany indicate that the recent A(H5N8) viruses are distinguishable from those identified in Europe in 2014 and 2015 but can be grouped with other A(H5) viruses in clade 2.3.4.4, such as the A(H5N8) viruses detected in wild birds in the Tyva region of the Russian Federation during May-June of 2016. While some genetic changes were identified between the German viruses and previously recommended candidate vaccine viruses, more information including phenotypic data is needed to evaluate public health risk of these emerging clade 2.3.4.4 viruses.
**Antiviral susceptibility:**

NA inhibitor (NAI) susceptibility data from phenotypic assays are available for the A(H5N8) viruses recently detected in the Tyva region of the Russian Federation from May-June 2016. These viruses, which have closely related NA protein sequences to the recently reported A(H5N8) viruses, were shown to be sensitive to zanamivir and oseltamivir by the fluorometric neuraminidase inhibition assay. Available NA sequences from more recent A(H5N8) viruses do not contain any of the amino acid substitutions that are known to confer reduced inhibition in other NA subtypes. However, because the effect of NA amino acid substitutions on NAI susceptibility can differ between NA subtypes, specific studies of the N8 from the these viruses are necessary to determine whether novel substitutions may confer reduced NAI susceptibility. As no matrix gene segment sequence information is available so far from the recently reported A(H5N8) viruses, their susceptibility to adamantane drugs is yet to be assessed.

**Human infections:**

To date, no human cases of infection with influenza A(H5N8) have been detected. However, human cases of infection with related clade 2.3.4.4 A(H5N6) viruses have been detected and reported in China. Though human infections with A(H5) viruses are rare and generally occur in individuals exposed to sick or dead infected birds (or their environments), they can lead to severe illness or death in humans. Following outbreaks of influenza A(H5N8)/A(H5N2) in the USA, information on individuals with exposure to infected birds was collected, but no evidence of human infection with influenza A(H5) was detected among the persons involved in the study.

**Population immunity:**

Based on the available information of other A(H5) subtype viruses, human population immunity against the recently detected A(H5N8) viruses is expected to be minimal.

**Transmission in animal models:**

Studies of previously isolated influenza A(H5N8) viruses have indicated that the virus does not transmit efficiently in ferrets, which is a model for influenza infections in humans.

**Disease severity:**

Human infections have occurred with another A(H5) clade 2.3.4.4 virus, A(H5N6) since 2014; 6 out of 14 reported cases were fatal.

In summary, given the information at this time, the risk of human infection is low, but cannot be excluded. Of note, other neuraminidase subtypes with 2.3.4.4 clade HA genes are also detected in wild birds and poultry. Continued surveillance for all highly pathogenic avian influenza A(H5) viruses will be important to monitor their occurrence and evolution. Timely sharing of representative viruses and sequence information is critical for a complete assessment of the risk posed by these viruses.

**Public health advice**

- Avoid contact with any birds (poultry or wild birds) or other animals that are sick or are found dead and report them to the relevant authorities.
- Wash hands properly with soap or a suitable disinfectant.
- Follow good food safety and good food hygiene practices.
1. EMPRES Watch: H5N8 highly pathogenic avian influenza (HPAI) of clade 2.3.4.4 detected through surveillance of wild migratory birds in the Tyva Republic, the Russian Federation – potential for international spread.


