



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

Contributors: Les Sims, Sergei Khomenko, Akiko Kamata, Guillaume Belot, Jonathan Bastard, Elisa Palamara, Mirko Bruni, Sophie von Dobschuetz, Gwenaelle Dauphin, Eran Raizman, Juan Lubroth

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Summary

A Goose/Guangdong/96 lineage H5N8 highly pathogenic avian influenza (HPAI) virus of clade 2.3.4.4 was detected in migratory birds at Lake Ubsu-Nur in the Tyva Republic of the Russian Federation, located on the Central Asian Flyway, in early June 2016 (World Organisation for Animal Health (OIE), 2016; Department for Environment, Food and Rural Affairs, 2016). In past seasons, detection of HPAI virus in this region of the Russian Federation was followed by detection of similar viruses in other

locations, especially to the west and south of the Tyva Republic. All countries along this flyway and those to the west in the former Soviet Republics, the Middle East, Eastern Europe and even Africa (especially West Africa) should be on the alert for incursions of this virus. Movement of virus within 18 months of first detection in southern Russia to the Korean Peninsula and Japan has also occurred on two occasions (2006 and 2010). Proactive surveillance and early reporting of these results by Russian scientists is an excellent demonstration of how surveillance is used as a tool for early warning. Note that as the virus may not necessarily be fatal for wild birds, the first evidence of infection may only be when spillover occurs into domestic poultry populations, especially galliformes, which are more likely to show signs of disease when infected.

Background

The event

Testing of samples collected in late May and early June 2016 during a targeted survey for avian influenza and Newcastle disease viruses at Ubsu-Nur (Anonymous, 2016), on the border between western Mongolia and the Tyva Republic in the Russian Federation, resulted in detection of H5N8 HPAI virus belonging to clade¹ 2.3.4.4 (see Map 1). The virus was confirmed in samples from several species of waterbirds, including six black-headed gulls (*Larus ridibundus*), four grey herons (*Ardea cinerea*), four great cormorants (*Phalacrocorax carbo*), one

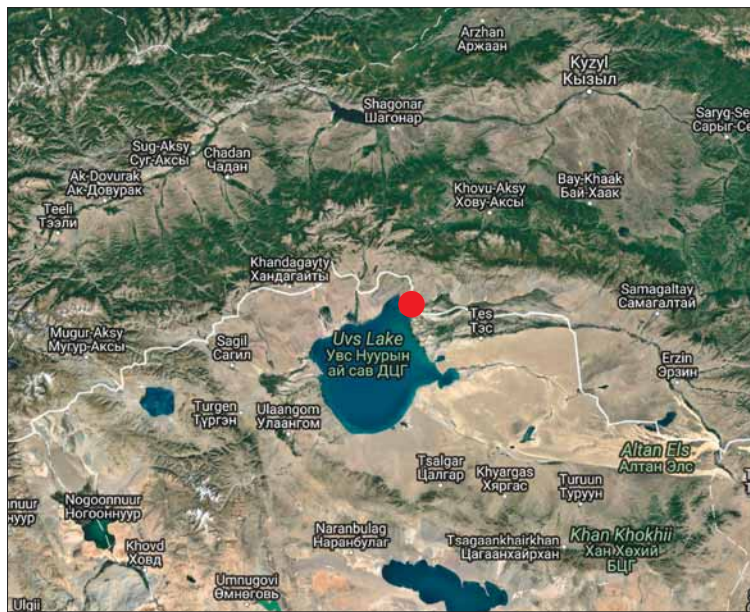
great-crested grebe (*Podiceps cristatus*), one common tern (*Sterna hirundo*) and one duck (family Anatidae; species unidentified) (OIE, 2016). The variety of species in which H5N8 HPAI virus was detected represents a typical waterbird community that can roost at the same sites, though would occur in different habitat types and use different feeding methods. Although some carcasses of birds were found, there were no large-scale mortalities due to avian influenza of the magnitude observed in 2006 (Savchenko *et al.*, 2012), at least in the Russian sector of the lake (OIE, 2016).

This is the fifth known occasion that Goose/Guangdong/96 lineage H5 HPAI virus has been detected in wild migratory birds at this particular location. The absence of keeping of domestic poultry in the vicinity of Lake Ubsu-Nur strongly suggests that the virus was introduced to this location by wild waterbirds. With currently ongoing moulting and post-breeding movements of waterbirds, there is a possibility that the pathogen could be introduced into the Siberian lowland, thus opening a way for the virus to invade stopover sites along the West Eurasian and Afro-Eurasian waterbird migration systems. Prior to 2016, waterbird mortalities at Ubsu-Nur due to Goose/Guangdong-lineage H5N1 HPAI virus were observed in 2006 (clade 2.2), 2009, 2010 (both clade 2.3.2.1c) and 2015 (clade 2.3.2.1c).

In May–June 2006, about 4 000 waterbirds (mainly breeding and particularly juvenile great-crested grebes) died at the site due to H5N1 virus infection. A further 400 dead birds were found during the summer die-offs in 2009 and 2010, including great crested grebe, bean goose (*Anser fabalis*), Pallas's gull (*Ichthyaetus ichthyaeus*), Eurasian

¹ A formal system of clade nomenclature has been established for haemagglutinin sequences of highly pathogenic H5 viruses belonging to the Goose/Guangdong/96 lineage (see Smith *et al.*, 2015; available at <http://www.ncbi.nlm.nih.gov/pubmed/25966311>).

Map 1. Location of the site of wild bird sampling at Lake Ubsu-Nur, on the border between western Mongolia and the Tyva Republic, the Russian Federation.



Map data ©2016 Google, Imagery ©2016 TerraMetrics



surveillance location at Ubsu-Nur Lake

Source: FAO

spoonbill (*Platalea leucorodia*), great cormorant, unidentified *Anatidae*, egrets and other species. In May–June 2015, eight carcasses were found: from *Sterna* sp. (2), common coot (1) (*Fulica atra*) and great-crested grebe (5). An additional 100 samples were collected from shot waterbirds belonging to the orders Podicipediformes, Pelecaniformes, Anseriformes, Charadriiformes and Gruiformes. A number of samples were found positive, either serologically (*Ph. carbo*, red-crested pochard *Netta rufina*) or virologically (*Sterna* sp. (2), *P. cristatus* (2)). Unfortunately, it was unclear from the information provided whether positive samples came from dead or live birds (Anonymous, 2015). Notably, all Ubsu-Nur die-offs (2006–2016) took place in the period May–June, which corresponds with the breeding season for most of the species found to be infected. This suggests that early

summer movements of *Anatidae* resulting in introduction of H5 HPAI to Ubsu-Nur (and elsewhere) lead to infection of a diversity of breeding waterbirds and their subsequent involvement in the transmission cycle.

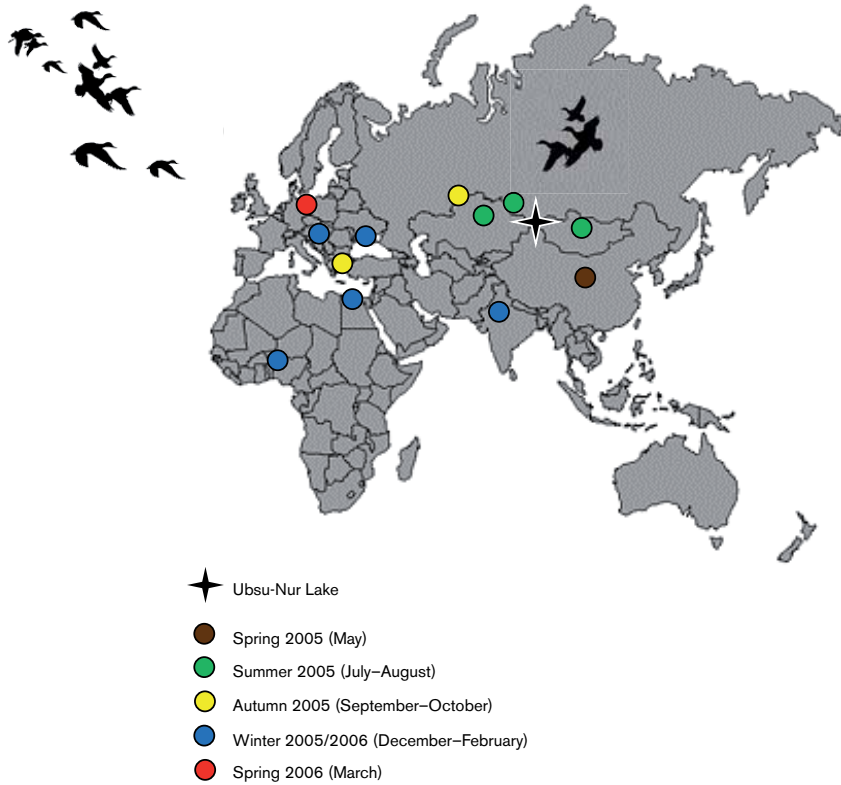
On all but one occasion, when Goose/Guangdong/96 lineage H5 HPAI virus was detected in migratory birds in Ubsu-Nur it was followed by detection of similar viruses along the Central Asian Flyway to South Asia (Bangladesh in 2007; Nepal in 2010) or to the west (Bulgaria and Romania in 2010). In 2005, the detection of this lineage elsewhere in the Central Asian Flyway in the southern part of the Russian Federation heralded the first spillover of Asian-origin H5N1 HPAI into Europe, the Middle East and Africa. An H5N1 virus found in the same location in 2014 was followed by detection of similar viruses in West Africa and Eastern Europe.

The location

Lake Ubsu-Nur (Ubsu-Nur, Uvs-Nuur – latitude 50.3 N, longitude 92.7 E) is a 70 km by 80 km shallow brine lake (average salinity 18.5–19.7 g per litre, locally varying), located mainly within Mongolia with a small part crossing into the Tyva Republic, the Russian Federation (Commission of the Russian Federation of the United Nations Educational, Scientific and Cultural Organization (UNESCO), 2016). It is the largest of the lakes in Uvs Hollow, located on a biogeographical divide between Siberia and Central Asia, where the world's most northern desert meets the most southern tundra of the Northern Hemisphere. Ubsu-Nur is a huge wetland area that congregates a great abundance and diversity of aquatic birds that stop over or come for breeding. It is an important stopover site for migratory birds using the Central Asian Flyway, which covers a large continental area of Eurasia between the Arctic Ocean and the Indian Ocean (Convention on the Conservation of Migratory Species of Wild Animals (CMS), 2016). However, some breeding species of Uvs Nur such as Swan Goose (*Anser cygnoides*) (Murygina, 2014) overwinter exclusively in central and southeast China (Yellow River and the coast of the East China Sea), thus providing a possible direct link from the epicentre of HPAI evolution to the Central Asian Flyway system.

Summertime densities of 2 000 individual waterbirds per 10 km of the shoreline are reported (Ozerskaya, 2008). The lake received relatively little attention from ornithologists and it is only now that both its Russian and Mongolian parts are being more comprehensively investigated. During a 2014 survey, Archimaeva (Murygina, 2014), whose expedition surveyed the whole perimeter of the lake, found many colonies of waterbirds, which were exceptionally abundant at the mouth of Tesin-Gol river just south of the Russian sector of the lake. Gulls, terns, great cormorants, grey herons, various species of ducks, whooper swans (*Cygnus cygnus*) and large concentrations of Eurasian spoonbills (*Platalea leucorodia*), as well as multiple species of waders were reported to be present at this site. Greylag goose (*Anser anser*) and Swan goose (*Anser cygnoides*) broods were also recorded, the latter implying a possible direct connection to China. It is also noted that Ubsu-Nur is an important summer staging area for non-breeding individuals and a moulting site for waterfowl changing their primaries, including ducks, swans and geese, who arrive from other destinations due to particularly favourable conditions and virtual lack of disturbance from humans.

Map 2. Transcontinental west-southwest spread of H5N1 HPAI clade 2.2 virus from Asia to Europe and Africa between May 2005 and April 2006.



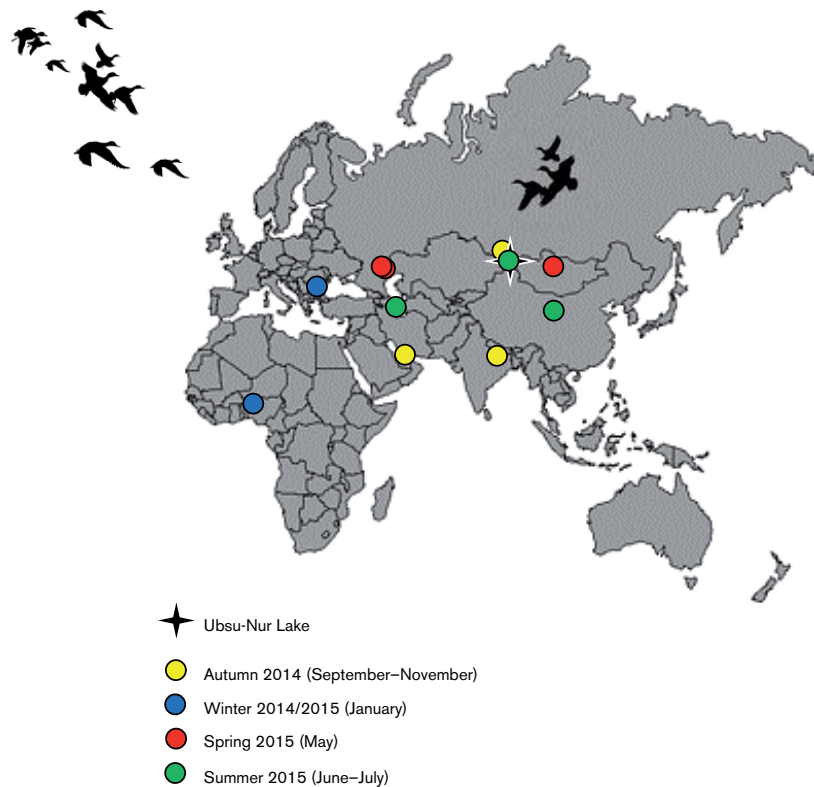
Source: FAO

Map 3. Transcontinental west-southwest spread of H5N1 HPAI clade 2.3.2.1c from Central Asia to Europe and Southern Asia between May 2009 and April 2010.



Source: FAO

Map 4. Transcontinental spread of H5N1 HPAI new clade 2.3.2.1c virus from Central Asia to Europe, Southern Asia between September 2014 and July 2015.



Source: FAO

The concern

The detection of clade 2.3.4.4 virus in the south of the Russian Federation represents an early warning for countries to the west of this location that this H5N8 virus can, once again, emerge in the Afro-Eurasian flyway systems as waterbird breeding and moulting seasons progress and are followed by the fall migration to the overwintering areas. The findings at Lake Ubsu-Nur correspond broadly with the breeding season of resident species and onset of moulting and postbreeding aggregation of waterfowl.

This repeated pattern whereby Goose/Guangdong/96-lineage H5 is detected in wild birds in the southern Russian Federation (Ubsu-Nur or other Siberian wetlands to the west of Ubsu-Nur) can trigger HPAI occurring in other wild birds and poultry populations later in the season (from September to December onwards). Countries bordering the Caspian and Black seas (Azerbaijan, Bulgaria, Romania, the Russian Federation, Turkey, Ukraine) and possibly also Western Europe, should be on high alert given virus spread to these places in the winter of 2005/06 (Ottaviani *et al.*, 2010) and subsequent years (Sharshov *et al.*, 2012).

Learning from the past

In some regions, trade-related activities constitute the most important risk factor for local and cross-border spread of HPAI virus. However, it is clear that wild birds have played a major role in introducing the virus into new areas over long distances and probably at times played a role in sustaining the transmission cycle of at least several Goose/Guangdong-lineage H5 viruses between the years (Sims and Brown, 2016). Long distance transmission associated with wild birds has been observed periodically since 2003 and occurred in several major waves; for example, from mainland Asia to Japan, and from Asia to Europe, North America and, apparently, to Africa. Although wild birds were implicated in the long distance intercontinental spread of clade 2.3.4.4 virus from Asia to northern Europe and North America in 2014–2015, this virus was not detected in the southern part of the Russian Federation prior to intercontinental spread (a similar virus was only detected from a Eurasian Wigeon (*Anas penelope*) in the Sakha Republic in the northeastern part of the Russian Federation in September 2014 (OIE, 2014). Therefore, these cases are not considered further in this report.

In the following sections, we outline three occasions in which positive findings in wild

birds in the south-central part of Siberia in the Russian Federation (in 2005/06, 2009 and 2014) were followed by detection of the same virus in wild birds or poultry further west and south, suggesting that such a scenario of spread may repeat itself in 2016/17. In two of these cases (2005 and 2009), a similar virus was also detected in the Republic of Korea and Japan (winter of 2006/07 and 2010/11), some 18 months after the first detection in southern Siberia.

H5N1 HPAI clade 2.2, 2005/06

In May 2005, a major die-off of birds in Qinghai Lake, China was caused by clade 2.2 H5N1 HPAI (Chen *et al.*, 2006). Clade 2.2 H5N1 HPAI virus was then detected in southern Russia in July 2005 (in Novosibirskaya Oblast) and gradually spread west (Adlhoj, 2005). Westward spread resulted in two massive waves of outbreaks in poultry: in July–August 2005 in the south of the Siberian lowland, and during the winter of 2005/06 in the areas just north of the Caucasus. Although no reports on surveillance findings or wild bird die-offs from Ubsu-Nur were received in 2005, Mongolia reported cases of H5N1 HPAI clade 2.2 in late July/early August 2005 further south, in

Khunt Nuur (300 km from Lake Ubsu-Nur) and Erhel Nuur (OIE, 2005).

As shown in Map 2, clade 2.2 H5N1 HPAI virus was detected in Kazakhstan in August, and in Croatia, Romania and Turkey in October 2005. This was followed by the detection of the virus in Ukraine in December 2005. The virus was next detected in West Africa and Egypt. It further spread across central and northern Europe, starting in February 2006 following a spell of very cold weather. Disease, mainly in poultry, associated with this clade 2.2 virus was also reported in Afghanistan, India, Iran (Islamic Republic of), Iraq, Israel, Jordan, Pakistan and Palestine in the first quarter of 2006 (Sharshov, 2012). Virus was subsequently detected at Lake Ubsu-Nur in the Tyva Republic in June 2006 and highly similar viruses were reported from the Republic of Korea and Japan in the winter of 2006/07.

H5N1 HPAI clade 2.3.2.1c, 2009/10

Another wild bird die-off occurred in Qinghai Province in northwestern China (Genggahu Lake, saline) in May 2009 from which a H5N1 clade 2.3.2.1c HPAI virus was isolated. This was followed in June 2009 by a report of 58 wild birds from Lake Ubsu-Nur testing positive for a closely related virus. A similar virus was also detected in wild birds in Mongolia in Erhel Nuur (OIE, 2009a) and Doitiin Tsagaan Nuur (OIE, 2009b), 800 km from Ubsu-Nur. By October, a single case was reported in Western Russia in Moskovskaya Oblast (OIE, 2009c). This was followed by incursions of a closely related virus as far as Romania and Bulgaria (i.e. common buzzards, *Buteo buteo*) in 2010 with a similar virus also being detected in Nepal (OIE, 2010) and Iran (Kord *et al.*, 2011). Clade 2.3.2.1c virus was again detected in birds at Lake Ubsu-Nur in 2010 and was followed by outbreaks associated with very similar virus to that found in the Tyva Republic and Mongolia in the Republic of Korea and Japan the following winter, thereby repeating a pattern seen in 2006.

H5N1 HPAI clade 2.3.2.1c, winter 2014/15

A clade 2.3.2.1c virus that was clearly differentiated from the one detected in 2009/10 was found in poultry in September 2014 in Altayskiy Kray, the Russian Federation. Similar viruses were subsequently detected in India (Tosh *et al.*, 2016), in the Middle East (Naguib *et al.*, 2015) and in Eastern Europe and West Africa, initially in Nigeria (Monne *et al.*, 2015). Outbreaks in falcons (*Falco* spp.) in

Dubai were likely the result of hunting trips to Central Asia resulting in contact between falcons and wild birds, or importation of birds of prey from those areas (Naguib *et al.*, 2015; Kord *et al.*, 2011) (Map 4).

The virus in West Africa subsequently caused a significant number of outbreaks in domestic poultry in Nigeria (468 outbreaks, as of 25 July 2016) as well as in Burkina Faso (39), Cameroon (17), Côte d'Ivoire (33), Ghana (47) and the Niger (2) (Emergency Prevention System for Transboundary Animal and Plant Pests and Diseases (EMPRES), 2016) and remains endemic. This introduction followed a similar pattern to outbreaks in 2006 that were preceded by detection of virus in the southern part of the Russian Federation. It is not known whether these viruses arrived in West Africa by wild birds or other routes, but phylogenetic evidence suggests that the former is possible (Kord *et al.*, 2011; Monne *et al.*, 2016).

Clade 2.3.2.1c virus was subsequently detected in western Kazakhstan in May (including dead *Ph. Carbo*), in the Volga Delta (Dalmatian pelicans, *Pelecanus crispus* and rooks), and Novosibirsk (mainly rooks; *Corvus frugilegus*) in the Russian Federation, in Iran (Islamic Republic of) in June 2015 and in the Tyva Republic at Ubsu-Nur Lake in June 2015 in two Great Crested Grebe (*Podiceps cristatus*) and two Common Terns (*Sterna hirundo*) (OIE, 2015). A similar virus was also detected in Inner Mongolia in May 2015 and Qinghai in July 2015 (Bi *et al.*, 2016).

Conclusions

The surveillance conducted at Lake Ubsu-Nur and the prompt reporting by the Russian Federation, providing information on the subtype and clade of the virus, are highly valuable for early warning and outbreak preparedness purposes. Countries and places in Central Asia, the Caucasus, the Middle East, Europe and West Africa – especially those that have experienced outbreaks in 2005/06, 2009/10 and/or 2014/15 (as shown in Maps 2, 3 and 4) – should be on alert over the next 6 to 12 months, as westward and southern spread of the H5N8 virus is likely. If the virus enters Egypt or West Africa, where H5N1 HPAI viruses are already present or even entrenched in poultry populations it would further complicate disease control. South Asia may also be at risk of incursion of this H5N8 HPAI clade 2.3.4.4 virus, potentially arriving there with fall migration in 2016. Based on past experience, this virus could also arrive in the Republic of Korea and Japan within the next 18 months. Clade 2.3.4.4 virus is already circulating widely in China.

Though considered a zoonotic virus, clade 2.3.4.4 viruses have so far shown limited propensity for causing disease in humans (less than 20 human cases of Influenza A(H5N6) and none to date for influenza A(H5N8). Molecular evidence from sequence information is awaited to assess whether the virus identified at Lake Ubsu-Nur has features typical of viruses that can cause disease in mammals.

Retrospective outlook at H5N1 HPAI virus dynamics in the last 11 years strongly suggests that waterbirds of Central Asia can propagate newly emergent avian influenza viruses to their breeding or moulting quarters during spring migration. Once delivered to stopover or moulting locations these viruses have the potential to spread in colonially breeding non-Anatidae species (gulls, terns, cormorants, spoonbills etc.) and result in more or less detectable mortalities (depending on their respective properties). This may facilitate further spread from wetland to wetland. Additional monitoring and systematic seasonal surveillance at selected wetland sites in Central Asia could prove to be a very useful means of forecasting avian influenza epidemics in Eurasia, the Middle East or Africa.

Recommendations

Countries located to the west and south of Tyva Republic; in particular, those that have been affected by clade 2.2 H5N1 HPAI in 2005–2006, and clade 2.3.2.1c virus in 2009–2010 and 2014–2015 should be on high alert for incursions of the virus. Likewise, passive surveillance should be intensified in these places through raising of local awareness about the importance of reporting sick or dead birds, both poultry and wild birds. These should be tested for avian influenza viruses. National authorities need to ensure the means for laboratory testing are in place to detect clade 2.3.4.4 viruses. The OIE/FAO Network of Expertise on Animal Influenza (OFFLU) can advise on appropriate tests and protocols (see www.offlu.net).

It is recommended that farmers and poultry producers enhance their biosecurity measures in order to prevent potential virus introduction from wild birds or their faeces.

General recommendations include:

- Keep poultry and other animals wherever possible away from wild birds: screens, fencing or nets can be used to avoid possible contacts between species and help prevent transmission.
- Report sick or dead animals: It is important that all signs of illness or sudden and unexplained deaths in

- poultry, farmed birds, wild birds or other animals are reported to local authorities (veterinary services, public health officials, community leaders etc.) so that they can deal with them safely and help stop diseases from spreading.
- Hunting associations and wildlife authorities should be notified of the possibility of the H5N8 and other viruses presence in waterfowl hunted at the end of summer and during fall migration 2016. Hunters may provide very efficient means of introducing avian influenza viruses to poultry through fomites and by feeding scraps to poultry and, therefore, have to be warned of the risk and informed about mitigation measures.
 - Wash your hands often. You should always do so after handling birds or other animals, when cooking or preparing animal products, and before eating.
 - Eat well-cooked meat products.
 - Do not prepare sick or dead animals for food and do not give or sell them to others. Such animals should also not be fed to other animals.
 - Seek immediate advice from your physician if you show signs of fever after being in contact with poultry, farmed birds, wild birds or other animals.

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CONTACT :))

The Emergency Prevention System (EMPRES) is an FAO programme, founded in 1994, with the goal of enhancing world food security, fighting transboundary animal and plant pests and diseases and reducing the adverse impact of food safety threats. EMPRES-Animal Health is the component dealing with the prevention and control of transboundary animal diseases (TADs).

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