

**FAO EMPRES Wildlife Unit Fact Sheet:
Wildlife and H5N1 HPAI - Current Knowledge**

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INTRODUCTION

H5N1 highly pathogenic avian influenza (HPAI) virus that originated from domestic geese in 1996 in Guangdong Province in southern China (Xu, Subbarao, Cox et al. 1999) was first detected in humans and domestic chickens in Hong Kong in 1997 (Alexander 2007). Since 2003, H5N1 HPAI virus clade 2.2 has spread across Asia, Europe and Africa resulting in the loss of over 250 million domestic poultry including chickens, ducks, turkeys, quail and ostrich causing huge negative socioeconomic and livelihood impacts, as well as affecting food and protein resources, wildlife populations and public health (Alexander 2007). In 2005, the first large scale mortality in wild birds occurred in China and since then there has been increased interest and concern over the role of wild birds in the spread and maintenance of this virus. This Fact Sheet provides up to date information on aspects of the H5N1 virus in relation to wildlife, particularly wild birds. More information is also available on the Scientific Task Force on Avian Influenza and Wild Birds, jointly coordinated by the Convention on Migratory Species and FAO, www.aiweb.info.

VIRUS EVOLUTION

- Low pathogenic avian influenza (LPAI) viruses are found in a wide variety of wild bird species, but appear to be more commonly detected in waterfowl and gulls. These species of birds, in the *Anatidae* and *Charadriidae* families, form the host reservoir for a diverse avian influenza gene pool which causes no apparent morbidity or mortality in wild birds. The long distance migratory movement by many of these birds also allows for widespread global distribution of these LPAI viruses.
- HPAI viruses originate from LPAI viruses naturally circulating in wild birds. Once LPAI viruses pass from wild birds to poultry, mutation from low virulence to high virulence can occur and is most likely the origin of the current H5N1 HPAI virus strain. Spill back of a highly virulent strain into wild birds is rare, however this did occur in 2005 with H5N1 avian influenza virus (AIV) and has resulted in unusual and sporadic wild bird mortalities which are not typical of wild birds exposed to, or infected with LPAI viruses.
- In regions of Asia where H5N1 HPAI virus is endemic in poultry populations, the circulation of H5N1 AIV between co-habiting poultry and wild birds can occur and thus further evolutionary changes in H5N1 AIV viruses and clades are expected.

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- Studies show H5N1 HPAI viruses are becoming environmentally stable, making this an added risk factor for transmission of virus to poultry and people (Webster, Hulse-Post, Sturm-Ramirez et al. 2007).

TRANSMISSION

- H5N1 AIV replicates in the respiratory and intestinal tracts of ducks, geese and swans experimentally infected with this virus and shedding occurs longer and at higher concentrations from the respiratory than gastrointestinal systems (Alexander 2007; Brown, Stallknecht and Swayne 2008).
- The exact mechanism by which other birds become infected in the wild remains unknown (Alexander 2007). Data suggests viruses are exchanged among domestic poultry and wild birds in both directions with certain ecological systems, i.e. farmed wild ducks and markets, allowing for greater contact between species.
- Historically, H5N1 HPAI mortality events occurred when large numbers of birds congregated in one area due to moulting, breeding or severe climatic events that change congregation sites.
- While the domestic duck (*Anas platyrhynchos* var *domesticus*) appears to be the host species providing a source of virus maintenance once introduced into an area, the role of its wild ancestor, the mallard (*Anas platyrhynchos*) or any other wild species is not yet clear.
- The only cases of known wild bird to human transmission of H5N1 AIV infection occurred in Azerbaijan after exposure to the virus while plucking feathers from infected swans (WHO 2006).
- Hunting and farming of wild waterfowl, as well as cultural practices involving the release of wild birds at places of worship, can result in dispersal of infected birds within urban and rural human settlements (Karesh, Cook, Gilbert et al. 2007).

WILD BIRD SURVEILLANCE

- Since 2005, nearly all of the healthy wild birds sampled (~ 750,000) in Asia, Africa, Europe and Americas have been negative for the H5N1 AIV.
- Healthy wild birds positive for H5N1 AIV using reverse transcription polymerase chain reaction were detected in the following studies:
 - In 2004, four viruses were isolated from 38 free-living Eurasian tree sparrows (*Passer montanus*) in Pingyu county, China, also by virus isolation in embryonating chicken eggs (Kou, Lei, Yu et al. 2005).
 - Six migratory and resident ducks (species not recorded) out of over 13,000 wild birds sampled around Poyang Lake in China in 2005 (Chen, Smith, Li et al. 2006).
 - In Russia (Lake Chany), one great crested grebe (*Podiceps cristatus*), six mallards and 12 common pochards (*Aythya ferina*) during the summer of 2005 total number of wild birds tested is unknown (L'vov, Shchelkanov, Deriabin et al. 2006; Feare 2007).

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- In the fall of 2005, a pooled sample of black headed gulls in Croatia out of 6,142 wild birds tested (Savic, Labrovic, Zelenika et al. 2010).
 - One wild duck in Egypt in October 2005 out of 1,304 wild birds sampled (Saad, Ahmed, Gamal-Eldein et al. 2007).
 - A pooled sample from mute swans (*Cygnus olor*) in Poland during the spring of 2006 out over 100 swans tested (Minta, K., Domanska-Blicharz et al. 2006)
 - A pooled sample from herring gulls (*Larus argentatus*) in Denmark, 2006 out of 1,112 samples tested.
<http://www.foedevarestyrelsen.dk/fdir/Pub/2007005/rapport.htm>
 - In Switzerland 2008, one common pochard out of over 200 tested.
http://www.oie.int/wahis/public.php?page=single_report&pop=1&reportid=6917
 - In 2009, one hunter-killed duck in Bavaria out 38 shot at the same time (DEFRA 2009).
- To date, surveillance results demonstrate that a H5N1 AIV wild bird “reservoir” species (i.e. a healthy carrier capable of shedding virus for months to years) has not been found.
 - Reporting of surveillance results and data collection (e.g. age, species, time and location) in wild birds remains inadequate (Yasue 2006).
 - There is no serological test available for H5N1 HPAI. While seropositive H5N1 wild birds are reported from different countries, this indicates exposure to a H5 and a N1 virus of either high or low pathogenicity, and not specifically an H5N1 virus. This demonstrates the difficulty of interpreting serological tests.
 - Prior to 2007, only cloacal swabs were routinely collected during surveillance conducted on wild birds, thus H5N1 AIV may have gone undetected. To improve detection of the virus, current surveillance activities include both tracheal and oropharyngeal sampling.
 - Although over 750,000 wild birds have been sampled at a global level, this represents a small percentage of the total wild bird population or any single species population and given a low prevalence of H5N1AIV, sample sizes of species by geographic location may not have been large enough to detect H5N1 AIV.

WILD BIRD H5N1 AIV OUTBREAKS

- Over 100 species from 13 orders of free-ranging birds have been found to be positive for H5N1 AIV which is virulent in poultry but not necessarily wild birds. The vast majority of positive samples in wild birds have been from moribund or dead birds (USGS 2009).
- Wild birds that have died from H5N1 AIV infection fall into three general categories:
 - Waterbirds: migratory and non migratory waterfowl, shorebird and wader species;

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- Bridge species: both migratory and non-migratory species, that may transport the disease among poultry and wildlife;
- Scavengers: often predatory birds (migratory and non-migratory species) that acquire disease from infected dead or sick birds (Feare and Yasue 2006).
- Mute swans are a large, visible, mainly non-migratory species in Europe and East Asia and inhabit places often frequented by humans. Because of this and their high susceptibility to the virus, they were considered to be an excellent environmental sentinel of H5N1 HPAI (Hars, Ruetten, Benmergui et al. 2008). However, in January 2008, mute swans in England demonstrated viral resistance after a slow within flock transmission rate and asymptomatic birds were observed (DEFRA 2008)
- Several major wild bird mortality events have been reported since 2005
 - **Qinghai Lake, China** (May to June 2005) - Over 6,000 migratory wild birds were found dead including bar-headed geese (*Anser indicus*), great cormorants (*Phalacrocorax carbo*), great black-headed gulls (*Larus ridibundus*), brown-headed gulls (*Larus brunnicephalus*), ruddy shelducks (*Tardorna ferruginea*) and a few tufted ducks (*Aythya fuligula*) (Zhou, Shen Hui-Gang, Chen et al. 2006).
 - **Russia**
 - **Lake Chany** (July 2005) – Over 5,000 wild birds including pochards, mallards and teals (*Anas crecca*) died (L'vov, Shchelkanov, Deriabin et al. 2006).
 - **Chemburskie Plavni** (February 2006) – A mass mortality of over 2,000 wild waterbirds occurred. Individual wild bird mortality events were also reported in February from several locations in the north Caucasus (Gulenkin, Irza and Frolov 2009).
 - **Ubsu-Noor Lake** (May-June 2006) - In June, approximately 3,460 birds infected with H5N1 AIV died and included primarily great crested grebes and small numbers of red-crested pochards (*Aythya rufina*), mute swans, Eurasian coots (*Fulica atra*), great cormorants, and unidentified *Laridae* species (Savchenko 2006).
 - **Uvs Lake** (June 2010) – Approximately, 367 wild birds were found dead near the lake and consisted of great crested grebe, goosander (*Mergus merganser*), grey heron (*Ardea cinerea*), gadwall (*Anas strepera*), Eurasian spoonbill (*Platalea leucorodia*) (OIE 2010).
 - **Iran** (2005 to 2006) - Large scale mortalities in wild ducks (numbers and species unknown) occurred but H5N1 AIV was never confirmed apart from several mute swans on the Caspian coast.
<http://www.rian.ru/incidents/20051006/41622048.html>
 - **Azerbaijan** (2006) – Large scale mortalities of waterbirds were observed in the north of the country in February and March. The exact number of deaths is not known but estimates range from 15,000 to 25,000 birds. It is unknown whether H5N1 AIV infection accounted for all the mortalities;

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however, the few samples collected from dead wild birds were positive for the virus. Species composition was poorly documented but included: swans, coots (*Fulica atra*), cormorants, pelicans, gulls, magpies, ravens, pheasants and pigeons (Anonymous 2006). <http://kalmykia.kavkaz-uzel.ru/articles/93608/>; <http://www.day.az/print/news/society/41493.html> <http://www.rian.ru/incidents/20051006/41622048.html> <http://dagestan.kavkaz-uzel.ru/articles/89637/>

- Smaller numbers of wild birds have been found dead across Africa, Asia, and Europe:
 - **Europe** – Surveillance efforts conducted in 2005 to 2006 from the fall to winter found the virus in over 700 dead wild birds from 13 countries (including Bosnia-Herzegovina, Bulgaria, Croatia, Czech Republic, Georgia, Greece, Italy, Poland, Slovakia, Spain, Slovenia, Switzerland and United Kingdom); however, only four countries experienced concurrent outbreaks in domestic poultry. Overall, dead wild birds have been reported from 25 European countries.
 - **Asia** – In addition to the several large scale mortality events reported in the “major wild bird mortality events”, small numbers of dead wild birds (20-120) positive for H5N1 HPAI have been reported in 12 of 23 H5N1 HPAI infected countries with the largest numbers of deaths in China, Mongolia and Russia (Tyva Republic).
 - **Africa** – Small numbers of wild birds infected with H5N1 AIV have been reported in 4 of the 12 countries reporting H5N1 HPAI (Feare 2007).
- Most major wild bird die off events have took place in 2005 and 2006. Since then, there have been no large scale wild bird mortality events, suggesting wild birds have become less susceptible or developed some immune protection to H5N1 HPAI, circulating virus strains and clades have become less virulent, wild birds are being exposed to viruses less frequently, or transmission between poultry and wild birds or among wild birds is inefficient.
- Clade 2.3.2 was first detected in a black-crowned night heron (*Nycticorax nycticorax*) from Hong Kong in 2008. Since then, this clade has made significant movements west and has been detected in Mongolia in a bar-headed goose, ruddy shelduck and whooper swan (*Cygnus cygnus*) and in Russia, in a great-crested grebe, bean goose (*Anser fabilis*) and black-headed gull. Most recently, a H5N1 virus belonging to clade 2.3.2 was detected in a common buzzard (*Buteo buteo*) in Bulgaria.

WILD BIRD ECOLOGY DYNAMICS

- Since the large geographical expansion of H5N1 HPAI from eastern Asia in 2005 to Africa and Europe, millions of wild birds have made multiple inter-continental migrations through infected countries to breeding grounds, and back to non-breeding locations, moving through every country in the world. Yet, to date, H5N1 HPAI has only been detected in 63 of the over 200 countries or territories worldwide. This suggests that wild birds are not the primary spreader of H5N1 HPAI but that human movement of virus through trade, marketing, and fomites likely accounts for the significant spread of the virus.

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- Movement and trade of wild birds (legal and illegal) provide a mechanism for national, regional, international and inter-continental movement of H5N1 HPAI virus. The first documentations of the virus in Europe were due to such trade movements from Asia (Van Borm, Thomas, Hanquet et al. 2005; Chomel, Belotto and Meslin 2007). In a Chinese market, two apparently healthy domestic ducks were found positive for H5N1 HPAI and the virus was found to be highly pathogenic in experimentally infected chickens and ducks (Chen, Yang, Chen et al. 2009) further suggesting, trade at live markets may play a role in transferring diseases among the poultry and wildlife sectors.
- A primary risk factor for transmission of virus between wild and domestic ducks are domestic ducks raised in and near rice paddies (Gilbert, Xiao, Pfeiffer et al. 2008).
- Spatial-temporal analysis of satellite telemetry data and wild bird outbreaks in Asia strongly suggests the vectoring of H5N1 AIV by wild birds along the Central Asian flyway. In 2005, 1-2 months after the reported wildlife outbreaks at Qinghai Lake, wild bird mortalities were reported in Mongolia, a country that has minimal poultry production, importation and consumption. The outbreak sites were also remote wildlife habitats, far removed from any poultry production and urban centres.
- In 2009, following the northward (spring) departure of birds from H5N1 HPAI endemic areas in India and Bangladesh, large numbers of birds died after arriving to Qinghai Lake in China. Additional wild bird deaths were reported weeks later further along the flyway as birds arrived at the northern end of migratory routes into Mongolia and Russia at known summer breeding sites this strongly supports the spread of this virus from the arrival of infected wild birds.
- H5N1 AIV mortality events in wild birds and poultry do not consistently coincide with northern hemisphere fall and spring wild bird migrations which one would expect if wild birds were the primary mechanism for the spread of the disease.
- The potential for wild birds to shed virus during longer migrations remains unknown (Gaidet, Cattoli, Hammoumi et al. 2008). Research suggests birds infected with LPAI viruses have reduced and altered capacities to migrate (van Gils, Munster, Radersma et al. 2007); contrary to this, however, one intra-African migratory species flew hundreds of kilometres while shedding another highly pathogenic avian influenza virus of chickens, H5N2. In cases where wild birds are responsible for long distance disease transmission, leap-frog transmission (i.e. multiple wild bird transmissions linked together chronologically along a broad distance) is the most likely mode of virus transmission among wild birds.

WILD BIRD ISSUES STILL TO BE ADDRESSED

- Recognising the wide diversity of migration strategies for a given species, and the multitude of species that may play a role in H5N1 AIV transmission, a better understanding of wild bird population distribution, migration routes, habitat use, and daily movements is necessary. Only then can associations between mortality events and wild bird movements be examined temporally and spatially. Additionally, the role of seasonal events (e.g. food availability, weather, and temperature fluctuations) and crop or poultry production cycles in relation to bird movement and disease events needs to be assessed.

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- In order to identify the role of wild bird and avian influenza strain diversity in preventing infection of H5N1 HPAI or other HPAI strains, research is needed on cross protection, genetic resistance and other factors that affect host susceptibility and shedding in both poultry and wild birds.
- Wild bird avian influenza surveillance strategy needs to be targeted and account for the ecology of wild bird species and the epidemiology of the disease.
- Improved wild bird species identification and reporting to the OIE using binomial standard nomenclature, information on the precise location and timing of outbreak, as well as laboratory methods used to detect disease is required. Additionally, promotion of photographic documentation of affected species is needed.
- The exact reporting of detailed species information and outbreak locations should be strongly promoted when viruses are registered in genetic databases, rather than reporting the location of the reporting institute or laboratory that conducted analyses.
- Capacity building that facilitates migratory bird capture, standardised sampling and testing following OFFLU regulations and OIE codes, and appropriate wildlife surveillance strategies concurrently with poultry surveillance is needed, as well as long-term species and location-based targeted surveillance activities, particularly in endemic H5N1 HPAI regions.
- Improved sensitivity of field and laboratory diagnostic tools for testing of the various wild birds is required, as well as specificity to identify seropositive H5N1 AIV of low and high virulence.
- Better evaluation of the role of sentinel and priority wildlife species in avian influenza is needed to better focus surveillance activities.
- It is known that domestic ducks can serve as a reservoir for H5N1 HPAI and as certain free ranging duck species such as mallards are closely genetically related, it is possible they may also be a reservoir species. However, because other wild bird species can carry the H5N1 AIV without exhibiting symptoms, it is necessary to identify other temporary shedders of the virus, or true reservoir species.
- Strengthening of poultry outbreak investigations (backyard flocks, large farms, or markets) to include trained wildlife personnel can help improve collection of important epidemiological information or contribute in the following ways:
 - elucidating the role wild birds play in introducing H5N1 AIV to an area through an understanding of ecology and identification of species present;
 - capturing and sampling wild birds visiting the area where mortalities occur, conducting transects and surveys near the areas to identify possible high risk species and identifying simultaneous wild bird mortality events;
 - determining whether biosecurity and management practices at the site prevented virus spilling back into the environment;
 - evaluating the role of wildlife trade in disease introduction and dissemination;

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- evaluating the role of disease as an ecological driver of maintaining wild bird populations to sustainable levels as well as the effect of virulent H5N1 AIV on threatened or endangered populations and
- developing geospatial maps of interfaces where wild birds and poultry are most likely to interact and share pathogens;

SPECULATION ON DISEASE ECOLOGY (HOST, ENVIRONMENT AND VIRUS)

- Regular annual wild bird mortalities due to H5N1 HPAI, including the confirmed largest die off in 2005, have occurred at Qinghai Lake. Identifying the role salinity, pH, and temperature have on the stability of the virus and transmission among wild bird hosts needs to be assessed further.
- Epidemiological role of hunting and other means of harvesting waterfowl for consumption and trade, including the lack of biosecurity measures taken when cleaning hunted birds, have to be further evaluated as a mechanism facilitating disease introduction to agro-ecological environments.
- Free-living wild ducks are exposed to pressures that laboratory birds do not experience, such as periodic food shortages, temperature extremes, seasonal variations in population densities and metabolic stress from reproduction, moult, and seasonal migrations. All these factors may increase an individual's susceptibility to infection with H5N1 AIV. Research shows stress imposed from migration is significant and can lead to muscle damage and impairment in immunity, re-emergence of latent infections and affect other ecological aspects (Guglielmo, Piersma and Williams 2001; Landys, Piersma, Guglielmo et al. 2005). Experimental studies that more closely mimic the wild condition including effects of variable exposure doses, exposure routes, virus strains, and cross protection from exposure to different LPAI viruses is warranted.

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