



HPAI in Europe 2007: Concurrent Outbreaks in Poultry and Wild Birds

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1. Introduction

With the renewed emergence of H5N1 highly pathogenic avian influenza (HPAI) virus causing mortality in poultry and wild birds in Europe, questions continue to arise from both the poultry production sector and wildlife sectors about the mode of introduction of this disease into Europe, and the role that wild birds play in the maintenance and spread of HPAI.

Although there is some debate on whether wild birds or domesticated birds (poultry and ducks) are the original source of this H5N1 HPAI strain, many virologists believe that the virus evolved through intensive bird rearing and production activities and then spilled over into wild bird populations. The virus may be undergoing small changes while circulating in wild birds, but the reality of this disease is that it is likely circulating back and forth amongst the poultry and wildlife sectors. This is likely the reality we are challenged with managing over the next 10-20 years.

As of July 13, 2007, the ongoing outbreaks in Europe reveal that deaths occurred in: 1) 1800 domestic turkeys in the Czech Republic starting on 21 June; 2) 8 mute swans (*Cygnus olor*) and a Canada goose (*Branta canadensis*) on 25 June in Germany; 3) 153 black-necked grebes (*Podiceps nigricollis*) in Germany and 3 mute swans in France on 4 July; 4) a domestic goose in Germany on 8 July, and 5) a mute swan in the Czech Republic on 10 July.

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As both wild birds and the poultry sector are involved in this outbreak, it is necessary to carefully examine all of the facts, identify the unknowns, and develop the best hypothesis for how this HPAI re-emergence occurred in Europe, how disease spread after emergence, and what might be expected to be seen over the next few months based on the natural history of the wildlife species involved, environmental conditions, genetic make up of the virus currently circulating, and other aspects of trade or agricultural production that can help explain the current series of events.

2. The initial outbreak in the Czech Republic

The original outbreak was identified in a turkey farm in the Czech Republic. The news (Czech News Agency, 22/06/07) said that the source of infection was speculated to be the hay used in the farm: "Veterinarians believe that the turkeys bred at the farm got infected through hay litter. The hay came from near a pond and could be contaminated by droppings of birds living in the wild", but this has never been officially confirmed. This explanation is possible but it needs a series of events to take place: 1) wild birds used the pond where the hay was from and they were shedding virus at the time,

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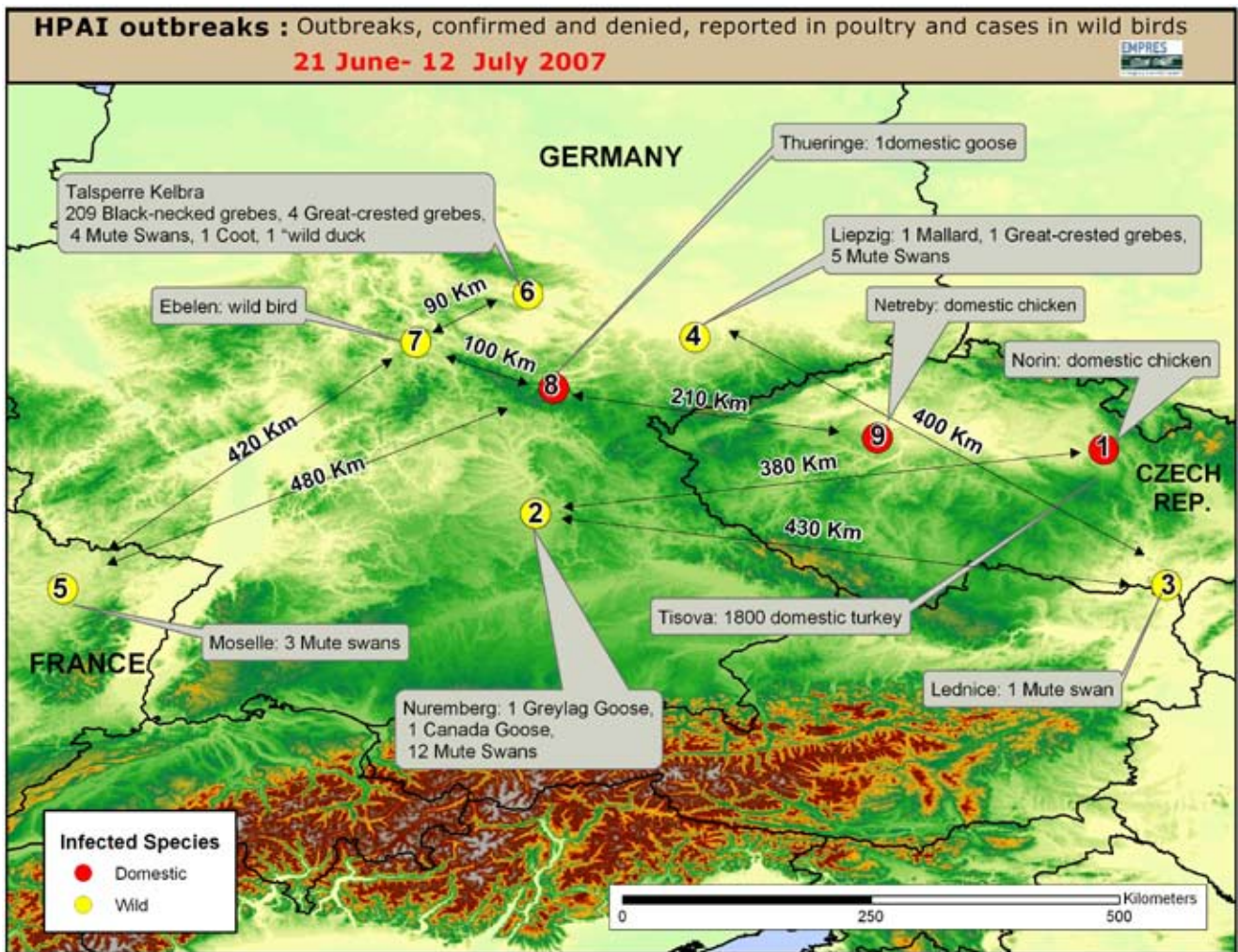


Figure 1. Outbreak locations, number and species involved as well as distances between outbreak locations from 21 June to 12 July, 2007

2) faeces contaminated hay to be used in the farm, 3) virus survive in >25-30°C temperatures in the hay, and 4) turkeys ingested infective doses of virus. Other possible modes of entry of the virus onto the affected turkey farm based on epidemiological investigations have not been provided by official sources.

While introduction of H5N1 HPAI from wild birds can not be ruled out, as we have seen from many past H5N1 HPAI outbreaks that initially occurred in poultry facilities, a much more classical explanation for the initial outbreak is importation of contaminated egg shells or their crates, poultry, or unintentional spread of disease by workers, equipment, or other fomites. Thus far, no information exists to support these introduction mechanisms either, further emphasizing the need for thorough epidemiological investigations that take into consideration a full evaluation of biosecurity as well as production, trade, and wildlife mechanisms of disease introduction.

3. The role of wild birds and surveillance

The events that have unfolded over the past month indicate that wild birds have died in Germany, France, and the Czech Republic from H5N1 HPAI. In carefully examining the role that these birds may have played in introduction, maintenance, or spread of disease, it is essential to link the natural history of the species involved, with the chronology of the outbreaks. The mortalities being observed in wild birds are in non-migratory, resident species (mute swan, Canada goose, coot, mallard), or in species that would have migrated into Europe at least 2 months ago (black-necked and great-crested grebes). Therefore, if wild birds were the source of introduction for all of these events that started in late June, they would have likely brought the disease into the region sometime in March or April and the virus would have needed to persist for several months either in the environment, or in an avian (wildlife or agricultural sector) or mammalian host.

To date from surveys and surveillance in wild birds, with the analysis of over 300,000 free-ranging healthy bird samples in over 40 countries, only a very few rare samples from healthy wild birds have been shown to be positive for H5N1 HPAI virus. Therefore, we could say that a wildlife reservoir for this disease has not yet been clearly identified. In fact, to answer this question whether wild birds are reservoirs or not, additional surveillance is necessary, and a more focused approach is warranted with emphasis on determining whether healthy wild birds are found to be positive for H5N1 HPAI near, adjacent to, or on infected poultry farms, demonstrating movement of virus either from poultry to wild birds, or *visa versa*.

Regarding the current situation in Europe, additional surveillance on species (avian and mammalian) visiting the index farms(s) in the Czech Republic, and sampling of other healthy wild birds including some from the species that have died as well as other species that have not died but share natural habitats where dead wild birds have been found, would greatly improve our understanding of the role that wild birds (and other species) may play in the epidemiology of this disease. Most of the time, migratory birds do not land where domestic birds are reared, but other "bridge species" may play a role in moving disease between natural and agricultural habitats. This is another area that is relatively unexplored from a wildlife surveillance standpoint.

4. Viral persistence in the environment

Although it has been shown experimentally that persistence of several Asian strains of H5N1 HPAI virus in water is dependent on pH, salinity and temperature and ranges from 3-4 days at warm temperatures (28°C), environmental sampling at the sites where wild birds have died would also benefit our understanding of possible routes of disease transmission. It is unlikely that the current strain of H5N1 HPAI arrived with migrating wild birds and persisted for up to 6 weeks in water. However, there is insufficient knowledge of the stability or maintenance of H5N1 virus in sediments, invertebrates, and on vegetation which again emphasizes the need to conduct additional research to learn about this agent. To date, many wild bird species that have died from H5N1 HPAI are birds that either dive (as is the case with grebes), or dabble in the mud/sediment (dabbling ducks), or stir up sediment through their foraging behaviour (swans/geese). This may be a series of coincidences or may be a clue as

to what makes certain wild bird species more susceptible to infection. Focused surveillance on these species would provide insight into whether this is a coincidence or of relevance to H5N1 HPAI disease ecology.

5. A possible explanation for the spread of H5N1 HPAI virus after introduction to the Czech Republic

A more likely explanation of the events observed since 21 June is that the disease has spilled over from the turkey farms in the Czech Republic resulting in wild bird infections. Although no recognized migrations are occurring at this time of year in Europe (or the rest of the world for that matter as in this time frame all long distance migration has ceased and birds are in their breeding or moulting habitats), it is certainly conceivable that swans could have become infected in the Czech Republic and flown relatively short distances from the Czech Republic to Germany where they died. Another scenario might be that bridge species (sparrows, jays, etc.) may have carried the disease from the index farm out into more natural habitats where swans became infected.

The distance from the index farm to the location of where the first wild birds died from disease is approximately 380 km. The distances to all sequential outbreak locations in either wild birds or poultry range from approximately 90-480 km. The distances between these outbreak locations can be explained by 1) short or medium length movements of swan, goose, grebe, coot or mallard that eventually died and were recovered, or 2) shorter movements of multiple birds that transmitted the virus along the distance between 2 outbreak locations, and eventually the indicator species (swan, goose, or grebe) was recovered dead.

Recently, research has demonstrated that susceptibility differs among domestic duck species and that mute swans are a species that pose the greatest susceptibility to lethal infection. This suggests mute swans are good ecological sentinels in that infection tends to kill them and they are large enough birds that their carcasses are easily found. Further research has shown that some waterfowl species can shed virus for up to 4 days before becoming ill suggesting they can potentially spread H5N1 HPAI virus between limited geographic regions, and according to the researchers, these species are not likely long-term reservoirs for this virus.

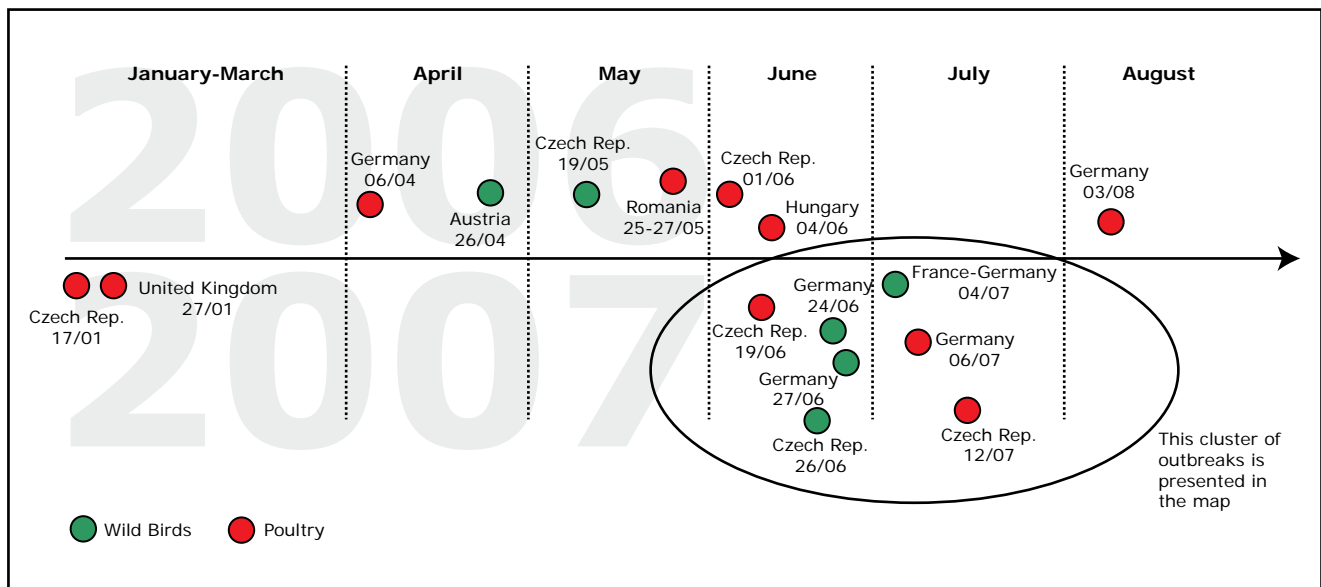


Figure 2: Time line of poultry outbreaks and wild bird cases in 2006 and 2007 in Europe

6. What does the genetic typing of the virus suggest?

Preliminary analysis indicates that the two viruses isolated from separate poultry infections in the Czech Republic share 100% identity and 99.6% identity with the mute swan isolate from the Czech Republic. The isolate from a mute swan in Bavaria (Germany) is 99.2% homologous to the Czech isolate from turkeys and other isolates obtained from wild birds in Germany and France also group closely with the virus from the Czech Republic. This suggests local dispersal of the same virus after introduction.

According to the Friedrich Loeffler Institute, phylogenetic analysis of the Czech isolate for HA1 reveals closest genetic similarity (99.5% at the nucleotide level) to recent viruses isolated from poultry and 'captive hunting' falcons in Kuwait in March 2007. These isolates group more widely with contemporary and 2006 strains from Bangladesh, Pakistan, and Azerbaijan, but they appear to be less related to viruses isolated from both wild birds and poultry during the outbreaks in EU Member States in 2006 and different from the viruses obtained during outbreaks in Hungary and the UK at the beginning of 2007. Therefore, the current outbreak in Europe represents a new introduction of virus into Europe, however the source remains unknown.

7. Looking ahead - what to expect over the next 2-4 months

The re-emergence of H5N1 HPAI in Europe is not an unexpected event, and in many ways, was just a matter of time. It is known that H5N1 HPAI is endemic in a variety of countries in Asia, it is re-emerging in multiple countries in Africa and the Black-Sea Basin, and low pathogenic avian influenzas are endemic in a variety of migratory bird populations. This historical information suggests that new infections in the EU region, potentially linked with agricultural production systems and trade, or possibly through wild bird movements, were likely to occur. In the case of recent introduction of H5N1 HPAI virus in Europe in the Czech Republic; 1) the source of virus introduction remains undetermined, 2) no wild bird reservoirs of the virus have been identified, but 3) it is possible that once introduced, wild birds may have moved the disease short distances.

As we are at the end of breeding season in Europe for wild birds (June/July), many species will start to make local movements to moulting sites where thousands of birds often congregate. During this time, birds are sedentary and flightless while they replace their flight feathers prior to making long distance migrations to over-wintering sites. The moult period is also a time of high metabolic demand, and follows on breeding season which is also physiologically demanding. Therefore, if some individual wild birds or species are healthy mid to long term carriers of the virus, and they move to high density moulting sites while shedding virus,

one would expect to observe many wild bird mortalities in susceptible birds, including immunologically naive juvenile birds. As well, if shedding occurring at high density moult sites, large numbers of wild birds would be expected to be exposed and then make their fall migration, resulting in large scale dispersal of disease as birds leave Europe and head to warmer climates throughout the Mediterranean Basin, sub-Saharan Africa, or the Middle East. This has not been the scenario of events over the last 2 years despite there being H5N1 HPAI circulating in poultry and causing wild bird mortalities during breeding season just prior to moult. We see nothing different in this year's situation, therefore, we do not expect to see large scale wild bird mortalities or large scale dispersal of disease emanating from the current outbreaks in Europe.

As has been previously emphasized by FAO, H5N1 HPAI is primarily a poultry disease, and while wild birds undoubtedly play a role in the epidemiology of the disease, control and management efforts should be focused in the agricultural sector and its trade practices. Based on data collected by FAO through July 15, 2007, the number of poultry outbreaks of H5N1 HPAI in Europe is lower in 2007 than in 2006. Since we believe that normally, H5N1 HPAI viral loads get amplified in the poultry sector and then spill over into wildlife resulting in wild bird mortalities and local dispersal of disease, lower numbers of poultry events in Europe should result in fewer wild bird infections, an overall lower viral load circulating in this region, fewer spill over events into wild birds, and ultimately, fewer outbreaks in wildlife and poultry. This rationale proved successful in predicting fewer outbreaks in the winter of 2006-2007 (see EMPRES Watch, October 2006 available at http://www.fao.org/docs/eims/upload//214878/EW_europe_oct06_hpai.pdf) and we believe that the disease cycle in Europe will again be halted by a combination of management steps including keeping agricultural flocks separated from wild birds, ensuring that biosecurity measures are strictly adhered to, properly disposing of poultry manure, used feed, dead poultry, contaminated eggs or other materials including water that passes through infected premises. Further efforts to understand illegal trade movements of poultry and wildlife would also help prevent further emergence of disease in Europe and other parts of the world.

8. Acknowledgements

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