Evolution of Highly Pathogenic Avian Influenza type H5N1 in Europe: review of disease ecology, trends and prospects of spread in autumn-winter 2006

1. Introduction

Following the introduction of H5N1 HPAI into Turkey in October 2005, the disease has been reported (as of August 2006) in poultry or wild birds in 26 European countries. From October 2005 onwards, outbreaks of HPAI in domestic poultry have been reported in Albania, Austria, Azerbaijan, Denmark, France, Germany, Hungary, Romania, Russian Federation, Serbia, Turkey and Ukraine, with over 230 recorded outbreaks in Romania alone. With the exception of Albania, all countries also detected HPAI in wild birds. Thirteen countries reported HPAI in wild birds only (Bosnia-Herzegovina, Bulgaria, Croatia, Czech Republic, Georgia, Greece, Italy, Poland, Slovakia, Spain, Slovenia, Switzerland, United Kingdom). HPAI was also reported in mammals (cats, dogs, and stone marten) and captive wild birds (game and zoo birds).

Recurrence of the disease was observed in Croatia, Hungary, Romania, the Russian Federation, Turkey and Ukraine. No positive cases of HPAI were reported from Armenia, Macedonia or Moldova, although they share borders with known infected countries. In addition, 20 human cases were observed in the European region (WHO classification), with nine deaths. Azerbaijan reported eight human cases in March 2006, of which five were fatal, and Turkey reported another eight human cases in January 2006, of which another five were fatal.[1]

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Based on the migratory flyways of *Anatidae* from the West Siberian Lowlands and Scandinavia, the period for migration (which usually precedes the first frost), and the timing and location of HPAI H5N1 outbreaks observed in 2005 in Eastern Europe, it is possible that wild birds played a role in disease introduction and movement during last year’s epidemic. Due to the seasonal occurrence of the disease, and particularly with reports of new outbreaks in the same ecosystems of China and Russia in spring 2006, it is possible that a similar situation could occur in the approaching weeks with the migratory movement of wild birds from their northern breeding grounds.

The Eastern Europe and Caucasus region is at particularly high risk of HPAI introduction and spread due to a large rural poultry sector with predominantly backyard poultry[2] often roaming freely, and a general lack of hygiene and biosecurity associated with poultry-rearing even in commercial farms. Although a few countries (Turkey and Ukraine) have substantial, vertically-integrated commercial poultry industries, most others are characterised by backyard poultry. Veterinary and human health services infrastructures vary greatly and most need restructuring (including policy and legislation) and standards need to be improved. Many economies of the region are in transition and large socio-economic gaps exist among countries. Domestic poultry trade, often informal and unmonitored, within and among countries is an important factor contributing

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[1] World Health Organization, 2006

[2] In Romania, backyard poultry accounts for 70% of the country's poultry population. (World Bank, Romania)

to the spread of HPAI. Furthermore, limited resources make it difficult for the smaller countries to cope with disease control. Insufficient transparency or weak surveillance activities can also complicate early warning and response activities in the region.

Data collected during the 2005 and 2006 (January-September) H5N1 epidemic were analysed for possible trends in disease occurrence or spread. The results are summarized in this report which provides an outlook on the possible recurrence of H5N1 in Europe in the coming months.

2. Methods

Epidemiological data and information collected by FAO and used for analytical purposes were derived from a number of sources including the OIE, published scientific papers, official government disease reports, and reports from FAO (including EMPRES-i) collaborators and consultants. Use of information from local media or newspapers served as an alert to FAO to obtain factual data using its own verification and validation procedures. At times, the quality of the data is less than optimal for the purpose of disease and epidemiological intelligence and FAO recognises that what has been reported may not always reflect what actually occurred. More often than not, the number of outbreaks reported (and character of the outbreaks, species, numbers affected or at risk, etc) by a given country is underestimated or underreported, especially where the disease might be endemic.

When possible, spatial/temporal analysis was used to explore the role of identified risk factors in the occurrence of avian influenza and estimate the likelihood of observing another wave of outbreaks in Europe in 2006. HPAI outbreak data in a Geographical Information Systems (GIS) environment was analysed using geo-processing tools and some partial exploratory spatial data techniques. Critical information for spatial analyses and mapping on date of occurrence, species infected and type of virus was collected to study possible trends and forecast potential future outbreaks of H5N1 in 2006 and 2007

H5N1 HPAI occurrence in the Russian Federation was used as a model for further evaluation because, since the disease was reported in 2005 and in 2006 (January-September), it was possible to make a partial comparison of disease level and pattern of spread. In addition, since the occurrence of HPAI in Russia in 2005 preceded the spread of the disease west and south into Europe and Africa, it was considered that the understanding of HPAI epidemiological features in Russia could represent a valid indicator for forecasting disease recurrence in Europe if migratory birds play a major role in dissemination of disease along some migratory routes.

3. Results and Discussion

Figure 1 summarises histograms of occurrence of reported cases of HPAI in Asia, Europe and Africa from late 2003 to date. The information presented in Figure 1 combines outbreaks of H5N1 in poultry (not number of cases) and occurrence in wildlife. Even though reported cases in wildlife are overshadowed by those in poultry, one of the more striking events in 2005 was a major outbreak in wild birds in Qinghai Lake of China followed by the spread of the disease in Mongolia, Russia, Kazakhstan, and subsequently by waves of outbreaks in Europe and Africa. The events of Qinghai Lake were remarkable for two reasons: the number of wild birds that died from the disease in comparison to wild bird mortalities elsewhere and the distance from where known occurrence had been reported in wild birds or poultry.

In autumn 2005, the disease spread westwards and was reported for the first time in Europe where wild bird events were initially observed in the Russian Federation, followed by Turkey and Romania. During the 2005-2006 winter, the disease was detected in wild birds in Western Europe. In early 2006, the disease was reported almost simultaneously in Egypt and Nigeria. Overall, more than 700 cases in Europe but only three wild birds cases in Africa have been notified since 2005[3].

In Russia, the disease occurred in both 2005 and 2006, making it possible to compare disease intensity and geographical distribution

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[3] Cameroon (wild duck, species unknown, family Anantidae), Côte d'Ivoire (Sparrow Hawk Accipiter nisus), and Nigeria (wild vulture, species unknown, family Accipitridae).

over a two-year period. Map 1 shows outbreaks that occurred between 2005 and 2006. The disease reached Russia in July 2005 and 52 HPAI events were recorded both in domestic and wild birds. Three main peaks were observed (Figure 2). During the first two peaks, more than three cases a week were reported in the period July-November 2005 before the disease spread to the rest of Europe. The third peak occurred in May-July 2006. A few outbreaks were also reported in February 2006, suggesting that the virus might have persisted in the environment between 2005 and 2006 without having been reintroduced from Southeast Asia as likely happened in 2005. However, data not available for analysis from East or Southeast Asia could contradict this working hypothesis.

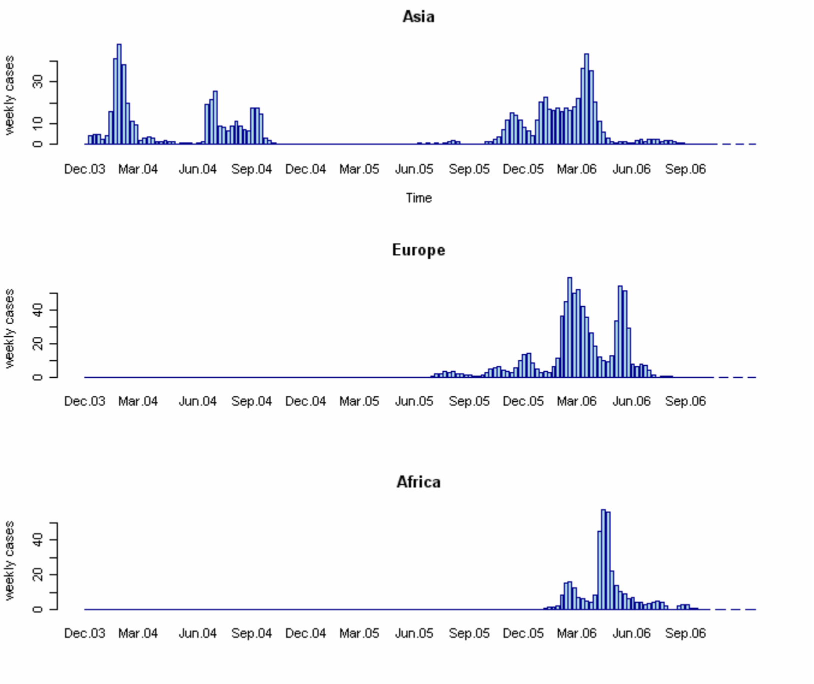


Figure 1: Worldwide HPAI temporal spread since December 2003

3-week moving average of confirmed HPAI events for both domestic and wild birds.

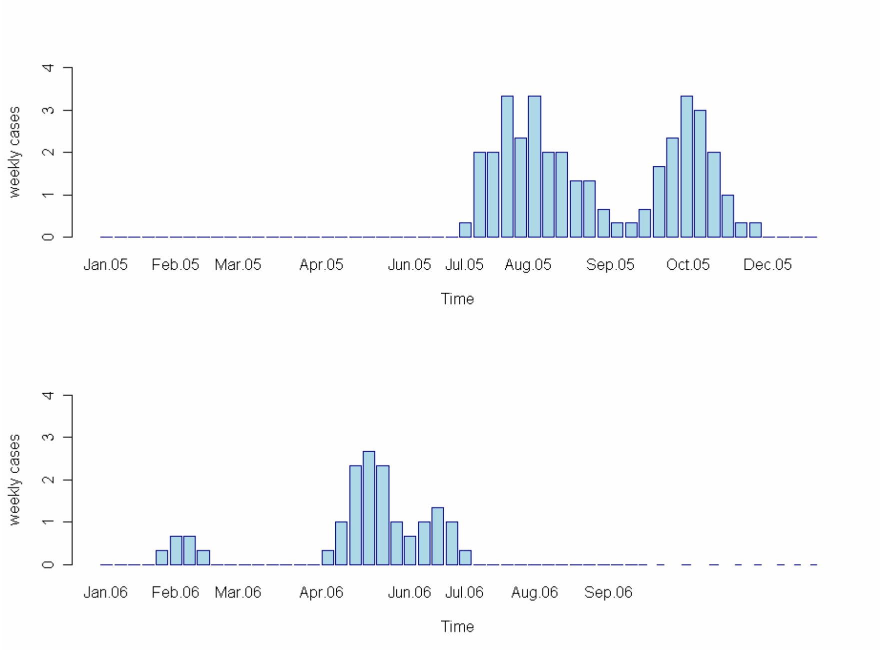
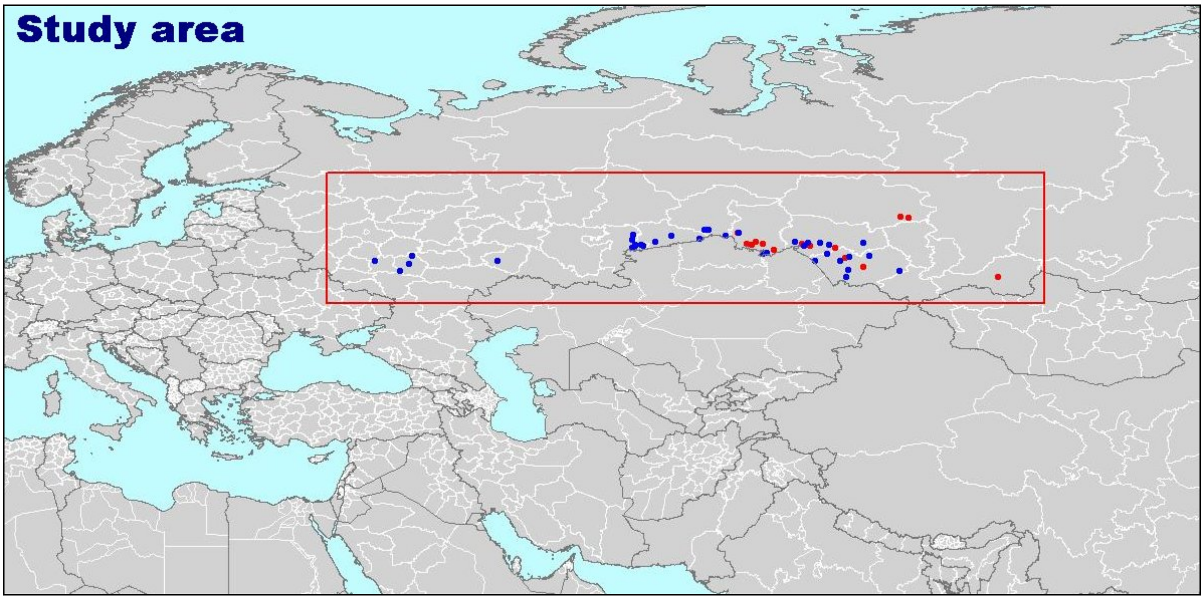


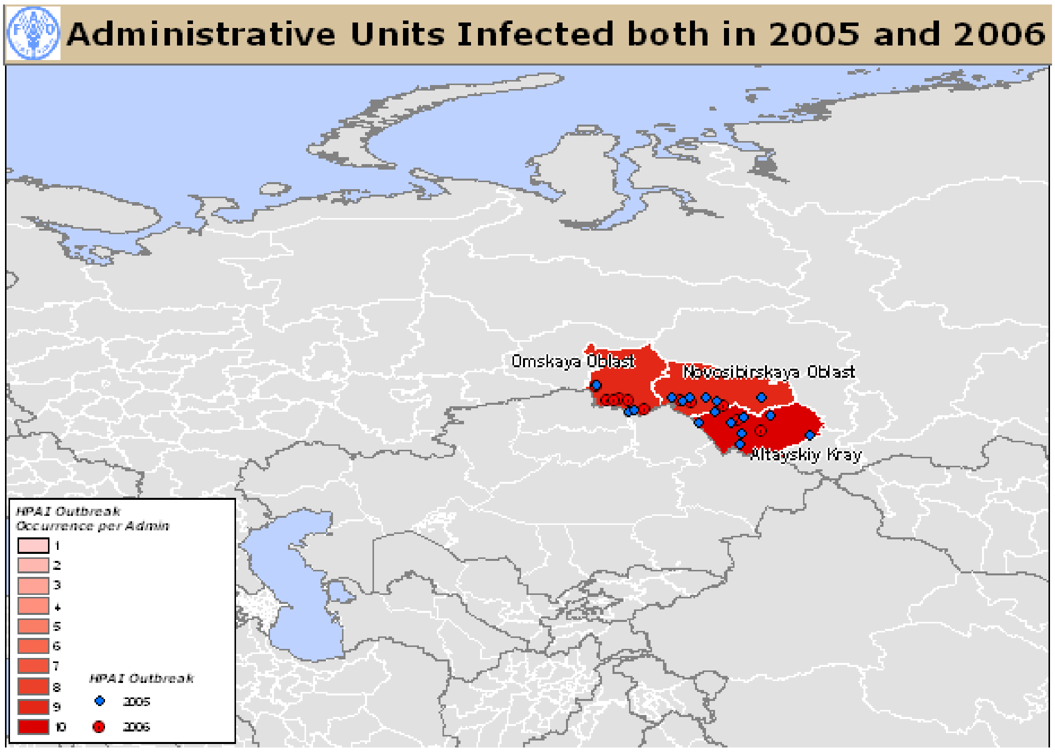
Figure 2: Comparative HPAI temporal spread in the Russian Federation in 2005 and 2006 (January-September)

3-week moving average of confirmed HPAI events for both domestic and wild birds.



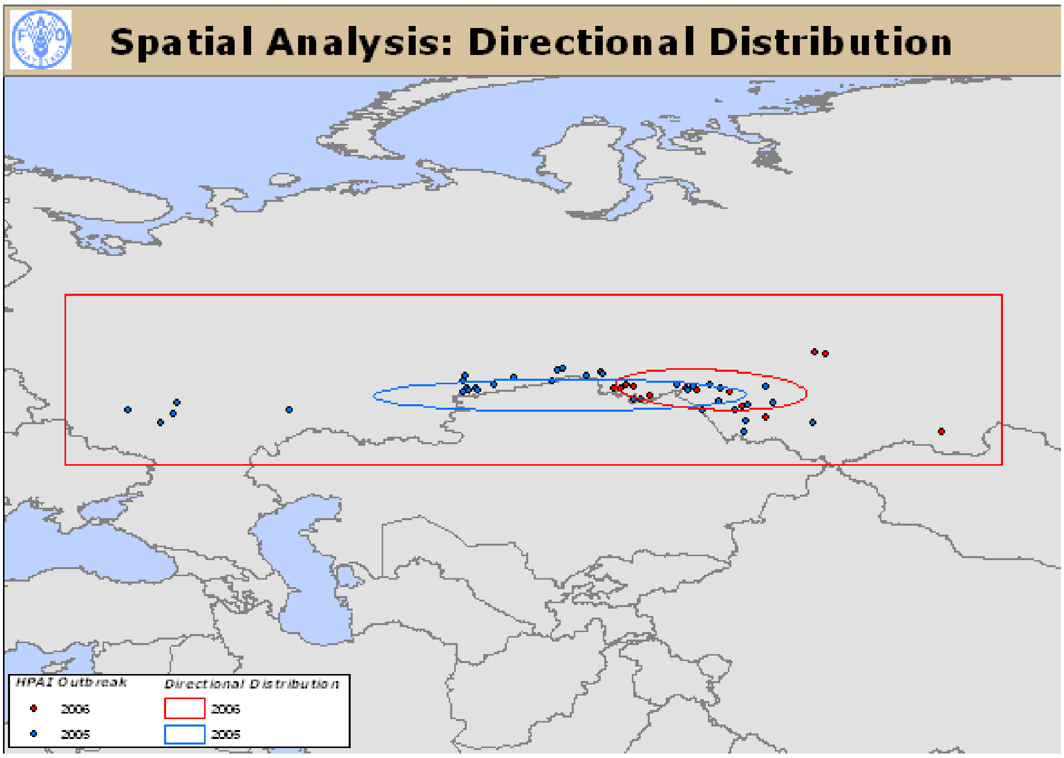
Map 1: HPAI outbreaks in 2005 (blue) and 2006 (red and partial data).

The histograms in Figure 2 show the number of recorded outbreaks in 2005 against those in 2006. Nine administrative units were affected in 2005, experiencing from 1-8 outbreaks each during a five-month episode (15 July–11 November 2005), whereas only five administrative units were infected in 2006. In 2006 the disease appeared more clustered in space and time (5 May–2 July) compared to 2005. Administrative units affected both in 2005 and in 2006 (partial data) are represented in Map 2 which indicates locations in which the disease may have persisted over the two years in three administrative regions.



Map 2: Administrative units infected in both 2005 and 2006 (partial data)

Interestingly, these administrative units (provinces) match those that have recorded the highest number of outbreaks respectively in 2005 and in 2006, suggesting a parallel between level and persistence of the disease in these areas and a possible "epicentre" for virus or disease maintenance in Russia. This hypothesis is also supported by measures of geographic distribution of data which allow calculation of values of the distribution, such as the centre, its compactness and orientation and show that the centre of disease occurrence in such a great land mass has a similar occurrence in space or in time. In 2006, the epicentre of disease occurrence is shifted slightly to the east compared to 2005.



Map 3: Standard deviational ellipses

Other environmental and human variables such as poultry density (Map 4) and wetland density (Map 5) were analysed and overlaid with maps of H5N1 HPAI outbreaks to define and quantify the potential correlation between such variables and the occurrence of HPAI outbreaks in a spatial context.

The analysis of outbreak density (data not shown) depicts the existence of two different outbreak patterns: the 2006 (partial data) outbreak data is more clustered and uniform, the 2005 pattern is more heterogeneous and dispersed.

A cumulative density surface for 2005-2006 outbreaks was first created in GIS and overlaid with poultry and wetland densities for visual inspection. Map 6 depicts the overlay showing how areas of higher outbreak density intersect with areas of higher wetland density. However the type of HPAI cases (wild birds or poultry outbreaks) would be important to differentiate[4] an overall positive correlation between wetland and poultry density, especially in central and eastern areas.

One important element is the temporal dimension of disease occurrence and spread which shows clearly that disease had its peak earlier in 2006 than in 2005, and was controlled faster (16 documented HPAI events in 2006 versus 36 events in 2005; Figure 2). Whereas in 2005 the virus was first observed in July 2005 before spilling over into Central and Western Europe in October 2005, no HPAI outbreaks have been reported since mid-July 2006 in the Russian Federation.

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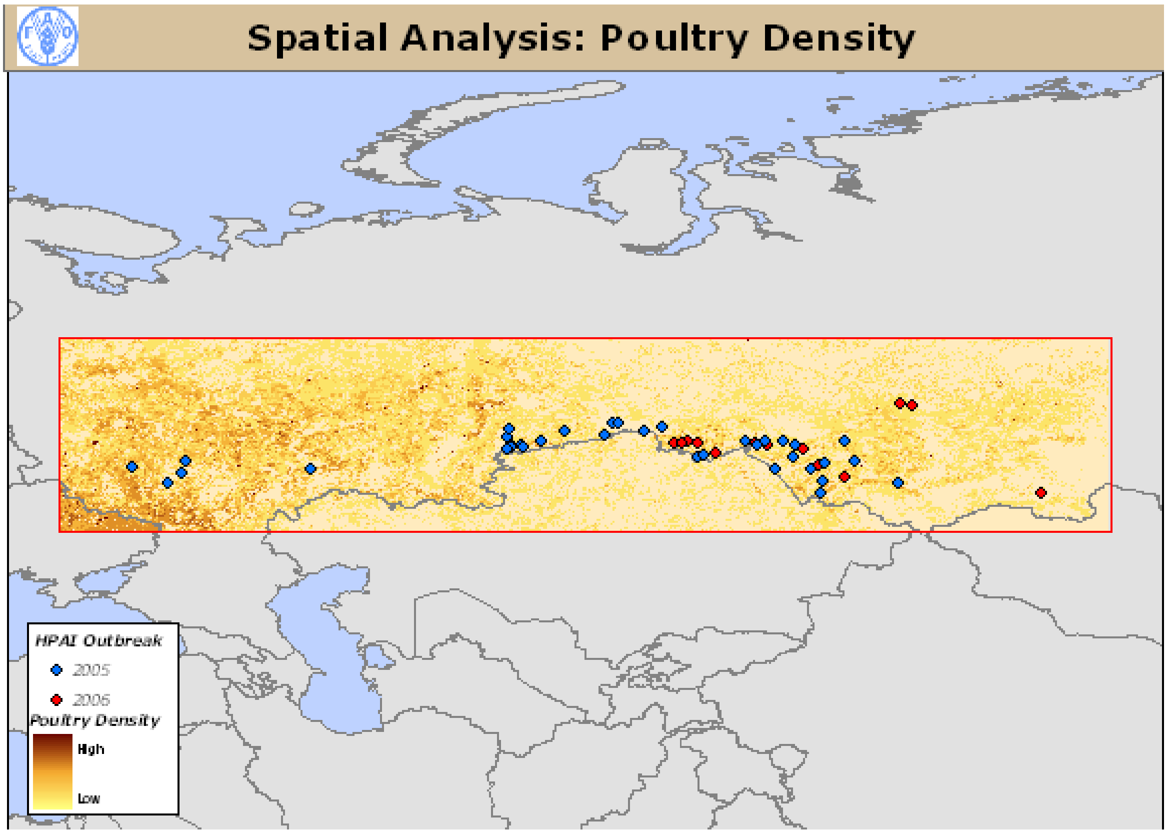
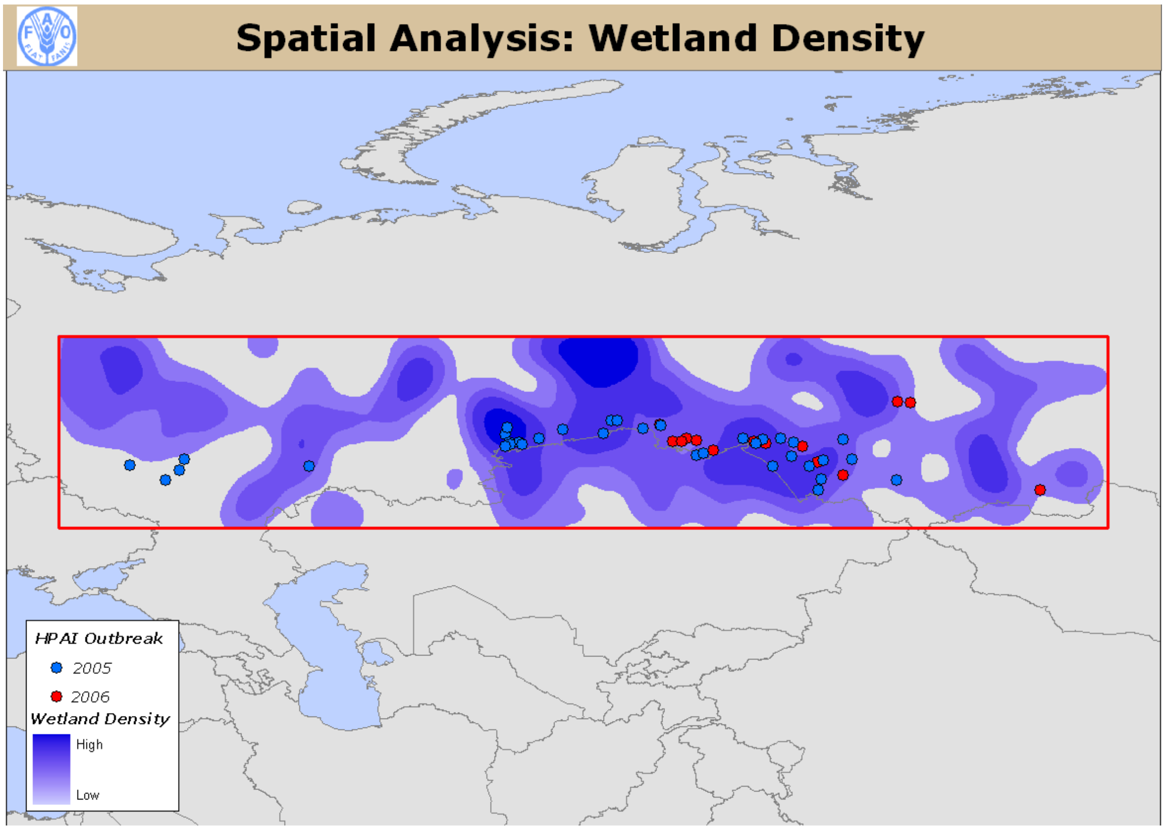
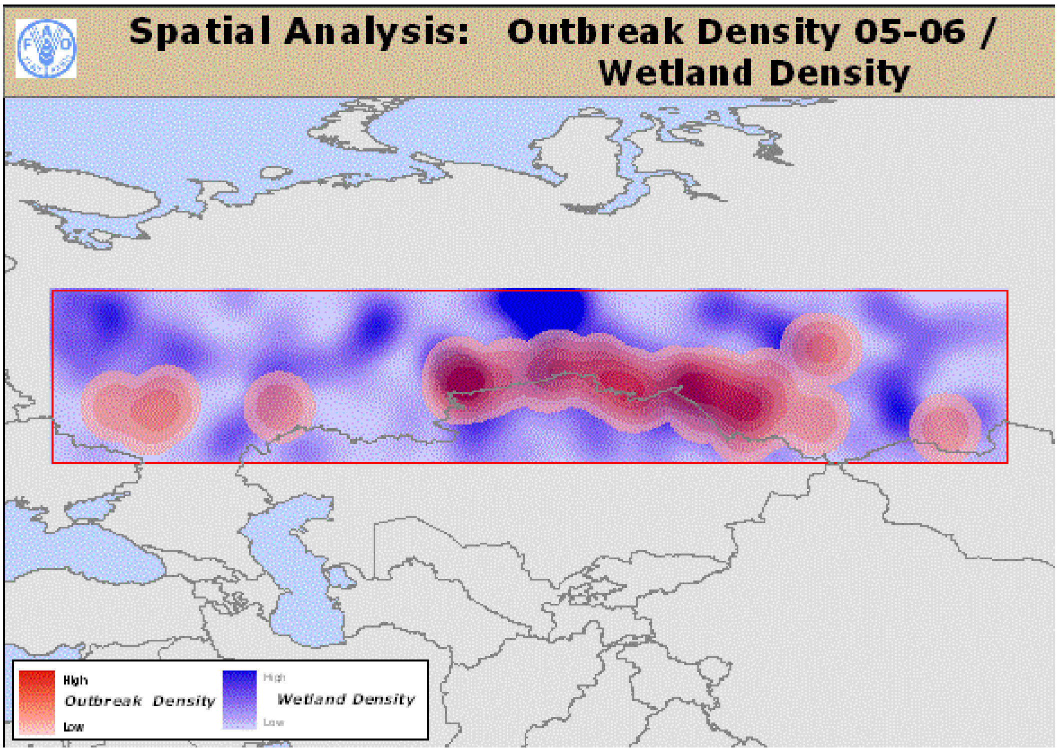
[4] Ongoing work across Eurasia by EMPRES.



Map 4: Poultry density and HPAI outbreaks in 2005



Map 5: Wetland density and HPAI outbreaks in 2005 and 2006



Map 6: Outbreak density for 2005 and 2006 (partial data) overlaid on wetland density and HPAI outbreaks in 2005 and 2006

HPAI virus ecology and wild bird migration dynamics

Large populations of species undertake seasonal migration from their northern summer breeding areas to southern wintering areas. One of the main evolutionary advantages of spring migration back to the Palaearctic and Neartic habitats of the north is that *Anatidae* exploit food resources available during the short massive burst of hatching insects and plant growth in the spring and early summer in the Arctic.

The breeding season is short in the Arctic and some species of birds prior to migration to wintering grounds move smaller distances to locations that are safe from predators; this allows time for moulting and a period in which the birds are unable to fly. Pre-migration concentrations of ducks in moulting areas may be a critical stage in AI virus transmission among species, especially since immunologically naive juvenile birds could be at increased risk of becoming infected from exposure to H5N1 HPAI leading to potential shedding of virus into lakes that support thousands of birds. Once moult is complete, the large diversity of species could then potentially migrate to many different stop-over sites on their way to wintering grounds, potentially introducing the virus during autumn migrations, on condition that the birds had become infected, were healthy enough to migrate, and were shedding virus as they moved. These are all important aspects of H5N1 HPAI disease ecology that require further study in a controlled environment and in the field.

The Central and Eastern areas of Europe are criss-crossed by overlapping migration flyways and hosts numerous wetlands, rivers and shorelines providing sanctuary for many wild (both migratory and non-migratory) birds which can come into direct contact with open-housed backyard poultry in the vicinity of surface waters. With reports of avian influenza H5N1 virus isolations from migratory waterfowl in many countries in Asia and Europe, it is considered that these birds could play a role in virus introduction, although other factors such as legal or illegal trade of birds and poultry greatly contribute to disease spread within and across regions.

Based on the migratory flyways of some *Anatidae* from West Siberian Lowlands and Scandinavia, the timing of migration (which may precede the timing of the first frost), and the timing and location of HPAI H5N1 cases in Eastern Europe (Romania, Turkey, Ukraine), it is possible that wild birds may have played a role in disease introduction and long distance movement into Europe. One of the key missing field findings is the identification of a reservoir species that harbours the virus, is clinically healthy to fly and sheds H5N1 HPAI virus. Conversely, some of the species that were identified in Central and Western Europe as infected (and clinically affected or dead) may have picked up the virus at a recent stopover point prior to their flight to Europe[5]. In the event that field studies identify a case regarding a migratory bird that is healthy, is infected with the H5N1 virus, and sheds the virus, how does that translate to the population of its species as a whole?

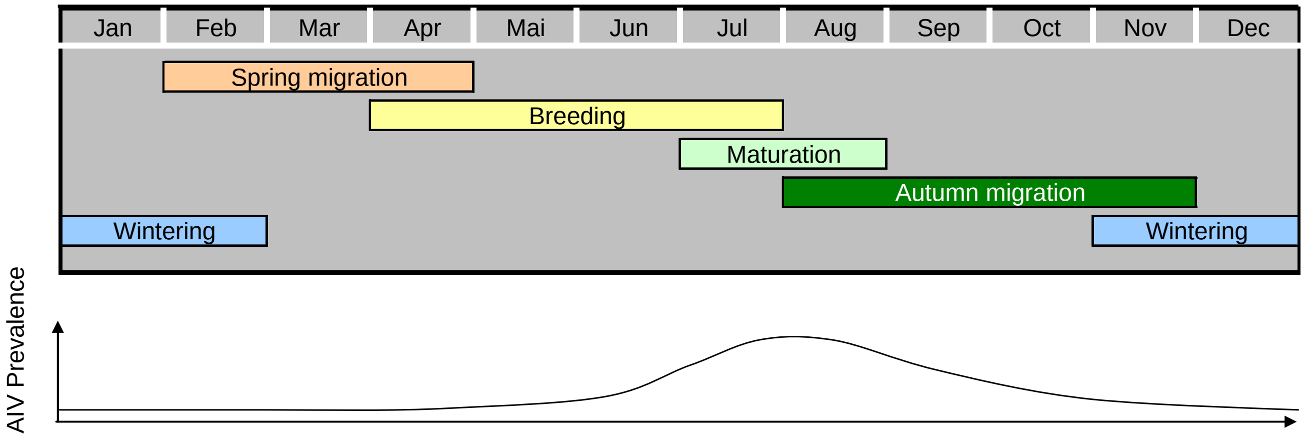


Figure 4. HPAI spread from the West Siberian Lowland to the eastern Mediterranean and beyond, from M. Gilbert et al. FAO Report, February 2006

A synergic mechanism between wild birds and poultry – disease dynamics at the interface

The range of wild bird reservoirs for non-pathogenic AI viruses includes more than 12 orders of birds, but historically the majority of isolations have been in *Anseriformes*, in particular *Anatidae* (ducks, swans and geese) and *Charadriiformes* (shorebirds). *Anatidae* harbour the highest diversity and prevalence of AI viruses and past outbreaks of HPAI in poultry have been traced back to strains originating in ducks. Based on this information, and the high number of ducks, geese and swans that have died from H5N1 HPAI over the past year, *Anatidae* may be more likely to transmit an avian influenza virus to domestic poultry, especially with a known maintenance host in Southeast Asia, the mallard duck (*Anas platyrhynchos*) for H5N1. Furthermore, domestic ducks (also of the *Anas platyrhynchos* species) have been shown to be able to excrete large amount of H5N1 virus while the majority of the population remain healthy.

Between 2005 and 2006, over 200,000 *healthy* wild birds were tested for H5N1 HPAI and, to date, only six birds have tested positive. In addition, it is known that numerous *sick* wild birds have tested positive for H5N1 HPAI and that certain wild bird species are highly susceptible to the virus, with moderate to high mortalities recorded.

The FAO/OIE International Scientific Conference on Avian Influenza and Wild Birds, held in Rome in May 2006, concluded that both wild and domestic birds appear to be involved in the spread and persistence of H5N1, although it has been acknowledged that control of the disease should be effected at the level of poultry.

Current information suggests that poultry are primarily responsible for the development of massive virus loads associated with outbreaks and high mortality at farms, but that wild birds may serve as the vector to transport H5N1 HPAI away from the farm thus introducing the virus to new geographic locations.

It is believed that amplification of disease in domestic birds and movements of wild birds may form one synergic mechanism responsible for the intercontinental spread of H5N1, along with both legal and illegal trade.

If true, the current hypothesis, that a spillover of H5N1 virus from poultry to wild birds and back to poultry is a powerful mechanism for virus maintenance, rapid,

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[5] Lack of prior tracking of bird movements makes it difficult to establish where and when the virus might have been picked up; even although the incubation period for HPAI H5N1 is relatively short, any given bird could have made one or more stopovers prior to or during its flight to Europe.

major, geographical expansion of H5N1 can have a positive aspect in a control or management programme: remove one link in the chain and the entire system collapses (poultry, people's livelihoods, and healthy trade are protected and progress can be made on conservation efforts). The outbreaks that took place in spring 2006 near Qinghai Lake in China show similarities with the start of the 2005 panzootic; so does the initial outbreak pattern in the summer of 2006 involving the Novosibirsk-Omsk area in Russia.

However, certainly due to improved control measures and husbandry applied to outbreaks in poultry farms and the establishment of efficient early warning, awareness and disease surveillance for HPAI by the Russian authorities, the chain of poultry infections noticed from late summer 2005 did not repeat itself in the period August-September 2006. With the information available to date, this suggests that wild and domestic bird synergy in virus propagation may not repeat itself in autumn 2006. Extrapolation of the events of 2005 and those of 2006 could suggest that repetition of the scenario experienced in 2005 in central and western Europe may be unlikely. Should there be outbreaks in Central and Eastern Europe, these are likely to occur later in the year than they did in 2005.

4. Conclusion

HPAI has now become endemic in many parts of the world and could eventually continue for years with intermittent cycles of outbreaks. Experience in several countries (Romania, Turkey) has shown how quickly the H5N1 virus can spread and become established in poultry. Informal domestic poultry trade within and among countries in the region may also contribute to the dispersal of HPAI. The role of wild life, their migratory behaviour and movement patterns, and identification of the viruses they carry remain key in developing sound programmes for risk mitigation (both from a safe poultry production and conservationist view). Another aspect which requires study concerns the possible "bridge species" that share common ecosystems between natural habitats such as wetland areas and poultry production farms or households (i.e., *Corvus spp*.).

There is need to develop and maintain a high level of preparedness both at country and regional level with careful monitoring and surveillance of the disease, and with effective disease control and prevention measures that would reduce the risks of (re)introduction and re-emergence of outbreaks.

Unless the technical and institutional gaps are specifically addressed to effectively control and eradicate HPAI, the livelihoods of local communities in many countries where village households maintain free range flocks of poultry as a source of income and food will be in serious jeopardy. The presence of the virus will pose a constant threat to human beings and cause serious economic losses to the poultry sector (due to deaths, culling, export and marketing bans) and to avian wildlife-generated tourism. Therefore there is an urgent need to invest resources to strengthen disease surveillance systems through improved laboratory diagnostic capacity and veterinary services, training of farmers and community health workers in disease diagnosis, early reporting and emergency response. Veterinarians and their services would also benefit from close interaction with wildlife biologists during disease investigations and surveillance sampling. Support must also be provided to improve communication and awareness of the disease and importance of disease control programmes at the national and regional levels to progressively eradicate the disease.

In this review, we suggest that the spillover of HPAI from poultry to wild birds and back to poultry providing a powerful mechanism for rapid, major, geographical expansion of H5N1. The issue which is now receiving priority attention from FAO is whether the containment of H5N1 in poultry may also lead to a disruption of virus circulation in wild birds. One place where potential transmission from wild to domestic birds can occur is in the vicinity of wetlands, river systems and flood plain agriculture. Waterfowl come to irrigated crop areas for feed and can possibly interact with domestic ducks and geese. There could also be direct contact with terrestrial poultry kept in the open or interaction with "bridge species". Ducks, geese, turkeys and chicken have all been incriminated as "index cases" in local virus propagation. The virus transmission from poultry back to wild birds probably involves identical scenarios in viral spillback to wild birds from open poultry systems affected by HPAI and the presence of water bodies. To gain a better understanding of the complexities involved between wild birds and poultry, FAO and its partners are embarking on several field studies to look more closely at wild bird behaviour in response to changing weather conditions. Satellite imagery, for example, provides real time information on the occurrence of sudden cold weather spells that may trigger significant short-term migration, or more general temperature and frost patterns that may initiate earlier migration.

Given the nature of HPAI, which is highly infectious, transboundary, important to livestock trade, and presents a serious global threat to human health, the control of HPAI at country level must form part of a larger, regionally coordinated initiative to control the disease. National and regional efforts need to be coordinated at international level and FAO can play a determinant role in close collaboration with international organisations such as OIE and WHO, advanced research institutions, OIE/FAO reference centres, the OFFLU network, regional organisations (EC, ECO, GCC, ADAD, UMA, ASEAN, SAARC, etc.), wildlife groups and the private sector. This will support development of a long-term global vision, inter-regional cooperation and coordination. From a technical point of view, international coordination will generate global disease information and promote development of appropriate tools and methodologies for HPAI control and surveillance in domestic and wild birds. All European countries will benefit greatly from regional and international linkages by being able to utilise and adopt harmonised standards in disease control methodologies, diagnostics, impact assessment and regulatory issues.

Through ECTAD and the FAO/OIE Crisis Management Centre (CMC) in Rome, FAO will also be able to streamline and respond to requests from countries in the region for support, including the deployment of rapid assessment teams, the provision of essential supplies and equipment, and the organisation of training and capacity-building activities.

It remains possible that H5N1 occurrence in Europe will recur – in, for example, the winter of 2006-2007. Should this occur, it is also possible that it will be with less intensity because occurrences of outbreaks to the east have also been less intense. Nevertheless, livestock veterinary and wildlife services must maintain their surveillance operations on maximum alert. Other countries around the world should improve their systems for transboundary animal disease surveillance, contingency planning, and response capabilities for any emergency event as Europe showed in 2006.

No doubt there is today a better understanding of HPAI and much investment has gone into national infrastructures and capacity to respond to animal health emergencies around the world, but there is no room for complacency at the national, regional or international levels when it comes to promoting animal health – whether it be at the livestock, wildlife or environmental levels.

Understanding wild bird movement

In mid-2006, funding provided by the Swiss and US governments enabled FAO to collaborate with the Mongolian Academy of Sciences and Mongolian Wildlife Science Conservation Centre, US Geological Survey and the Wildlife Conservation Society on a project in northeastern Mongolia where telemetry units were placed on whooper swans (*Cygnus cygnus*), a species severely affected by H5N1 HPAI and potentially playing a role in disease spread.

With additional investments, FAO and its partners are eager to integrate the ecology of more wild bird species to improve understanding of the behaviour and potential risks of the transmission of global pathogens from wildlife to livestock or from livestock to wildlife.

To view the whooper swan locations please access the following USGS project website. http://www.werc.usgs.gov/sattrack/whooperswan/index.html

FAO is grateful to the USGS for data collation and mapping and to the veterinary authorities of the Russian Federation for the shared data.

5. References

EMPRES Watch: Updated situation of Highly Pathogenic Avian Influenza (H5N1) in Asia. August 2006. http://www.fao.org/docs/eims/upload//211696/EW_asia_aug06.pdf

EMPRES Watch: Avian influenza spread into Europe. Situation Update (July-October 2005).November 2005.

http://www.fao.org/docs/eims/upload/195004/EW_HPAI_Europe.pdf

FAO/OIE International Scientific Conference on Avian Influenza and Wild Birds. Roma, May 30-31 2006. http://www.fao.org/ag/againfo/subjects/en/health/diseases-cards/conference/index_en.html

Gilbert *et al*. Anatidae Migration in the Western Palaearctic and Spread of Highly Pathogenic Avian Influenza Virus. Emerging Infectious Disease. Volume 12, Number 11–November 2006 (cited October 2006).