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International Disease Monitoring Unit

Qualitative Risk Assessments

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HPAI H5N1 SITUATION IN EUROPE AND POTENTIAL RISK FACTORS FOR THE INTRODUCTION OF THE VIRUS TO THE UNITED KINGDOM

Working document

Dr Mirzet Sabirovic
Simon Hall
Prof John Wilesmith
Dr Nick Coulson
Fred Landeg

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1 Summary

Highly pathogenic avian influenza (HPAI) H5N1 virus has been detected in many geographic locations in Asia, Europe, and some parts of Africa over the past two years. During the period from February to April 2006, the virus was detected in 13 EU Member States, mainly in dead wild waterbirds.

The recent experiences have demonstrated that the situation is evolving and that further developments are likely. While our epidemiological knowledge of the virus is improving, many elements of its transmission and dissemination remain largely uncertain.

It remains uncertain to what extent various pathways (see Fig.1 in the text) may play a role in the introduction and dissemination of the virus. For example, different local or other circumstances may result in various pathways playing a more significant role in the particular introduction and dissemination of the virus in the affected areas or to different parts of the world. Among other possible pathways, migratory birds have been shown to play a role in introducing the virus. Many uncertainties still remain regarding how widespread the virus may be worldwide, and regarding the epidemiology and ecology of the virus. Therefore, systematic and targeted studies at national and international level including various agencies and experts are required to understand the epidemiology and ecology of the virus and possible pathways for the introduction and dissemination of the virus.

Our understanding of the current epidemiological picture of H5N1 and our ability to predict future occurrence has limitations and any inferences made, therefore, have a great degree of uncertainty. This risk assessments builds upon our previous risk assessments (Defra, 2005 & 2006) and the recent developments and experiences in order to estimate, in a qualitative manner, the likelihood of the introduction of the virus to the UK by these pathways.

At this time, the risk assessment concludes that:

1.1 Legal trade

It is highly unlikely that legal trade in live poultry, gamebirds and their products would result in the introduction of HPAI H5N1 from affected Third Countries, or any area of the EU subject to restrictions because of the EU (and the UK) ban. The EU (and the UK) have also banned trade in pet and captive birds from all Third Countries regardless of their HPAI status while limited options for trade are being examined.

It is highly unlikely that legal trade in live poultry, gamebirds and their products would result in the introduction of HPAI H5N1 from EU approved and non-affected Third Countries, or any area of the EU not subject to restrictions. Therefore such trade may continue uninterrupted under the existing controls.

Despite the best efforts and compliance with EU rules, there is a limited possibility that birds may be traded before the disease is detected and officially notified. Thus, inspection and surveillance of the consignments of live poultry or game birds that have arrived in the UK from newly detected affected areas or areas close to these may be required to ensure that they are not incubating the disease.

1.2 Wild bird migration

It is probable that the likelihood of introduction of H5N1 to the UK by wild birds will be diminished during summer. This likelihood is expected to increase during the winter migration (from August to November) as birds migrate to the UK from or through areas that have had outbreaks of H5N1 during the last several months. It is currently difficult to estimate this likelihood because it remains uncertain to what extent, if any, the virus has been able to persist in bird populations in these areas.

It is likely that any outbreaks this autumn in countries located within wild bird flyways that overlap the UK, will represent an increase in the likelihood of the introduction of the virus to the UK. The likelihood may vary according to the species, location and time of occurrence, and will need to be assessed on a case-by-case basis. Outbreaks during winter in these countries are not likely to represent any significant increase of the likelihood of introduction of the virus to the UK than during autumn, though severe and prolonged cold weather could cause displacement of birds, with some of them arriving to the UK. Tools are currently being developed, based on known information of bird migration routes and abundance, to estimate this likelihood more accurately, and to assess changes in likelihood to the UK in the event of new outbreaks elsewhere. Nevertheless, a degree of uncertainty will remain.

It remains uncertain whether the virus has become established in local wild bird population in some EU Member States and to what extent this may have an impact on the potential introduction of the virus to domestic poultry. One indication of such development could be further sporadic detections from these Member States, particularly during the forthcoming moulting period when the resident wild waterfowl will congregate in large numbers. Therefore, it is essential to continue to maintain high biosecurity standards with regard to domestic poultry.

As it currently stands, continued monitoring of developments and targeted surveillance in the EU and the countries neighbouring the EU is vital in respect of wild birds, as is the analysis of the accumulated data to better understand the risks. Recent developments in the EU highlighted that surveillance, complemented with appropriate policy advice on biosecurity measures proportionate to the risks, were an effective way of detecting and preventing the introduction of the virus into commercial poultry operations.

Appropriate and practical epidemiological investigations and studies are required in the EU Member States in the areas where infection has been found in wild birds to identify the domestic poultry flocks that could be regarded as at risk. This would provide valuable epidemiological information to improve our understanding of potential risk factors and support the apparent effectiveness of the biosecurity measures. This is also important from an international trade perspective to ensure that safeguard measures are proportionate to the risks posed by the trade in commercial poultry, while protecting animal and public health.

1.3 Illegal imports

As with any disease outbreak in any country, there is an indeterminable likelihood of the introduction of H5N1 virus to the UK by illegal imports of live birds and their products. Nevertheless, this again emphasises the importance of implementing and maintaining appropriate enforcement control measures with regard to illegal imports to mitigate potential risks.

1.4 Mechanical transmission

As with any disease outbreak in any country, there is a low likelihood that the movement of people could transmit the pathogen by mechanical transfer after visiting areas where outbreaks have occurred. This emphasises the importance of maintaining and communicating appropriate advice on proportionate biosecurity measures to such categories of people to mitigate potential risks.

2 Introduction

This qualitative risk assessment considers the likelihood of the introduction of highly pathogenic avian influenza (HPAI) H5N1 virus to the UK. It builds on a number of previous qualitative risk assessments that have considered a range of possible pathways.

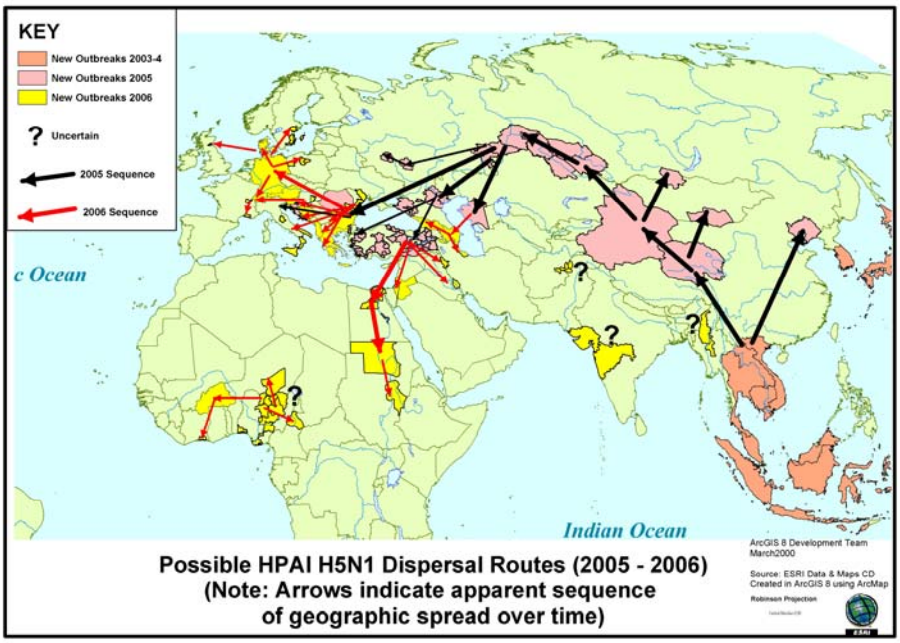
These risk assessments concluded that the overall likelihood of further spread over wide geographic areas was high. They also concluded that the likelihood of the introduction of the virus to the UK by various possible pathways (e.g. migrating birds, trade in poultry and poultry products, movement of people) varied from negligible to increased (but still low).

Our knowledge of the epidemiology and ecology of the virus and potential pathways for the introduction of the virus into unaffected areas has improved in recent months but still remains very limited. Our understanding of the current epidemiological picture and potential pathways for the spatial dissemination of the virus and ability to estimate the likelihood of introduction has limitations. Therefore, any inferences are associated with a great degree of uncertainty and are the subject of on-going reviews as new information becomes available.

Unless otherwise stated, this document uses official information received from the World Organisation for Animal Health, Paris, France (http://www.oie.int/eng/info/hebdo/A_INFO.HTM) and the European Commission, Brussels, Belgium (Animal Disease Notification System, Weekly Reports, CVO Emergency Notifications, SANCO Documents). It covers the period from October 2005 until early June 2006. Maps were produced using ESRI Data and maps CD - 2002.

3 Hazard identification

Between May 2005 and January 2006, outbreaks of HPAI H5N1 virus were reported in Asia and eastern Europe. At the beginning of 2006, the virus was reported in a



Possible HPAI H5N1 Dispersal Routes (2005 - 2006)
(Note: Arrows indicate apparent sequence of geographic spread over time)

number of the EU Member States and in some countries in sub-Saharan Africa. In summary, the map above outlines the spatial and temporal sequence of the virus spread during the years 2005 and 2006.

Recent developments and available epidemiological information are clearly of value in improving our ability to estimate the likelihood of introduction of the HPAI H5N1 virus to the UK via various pathways. These developments have been considered in the context of previously identified potential hazards for the introduction of HPAI H5N1 virus to the UK.

4 Risk assessment

4.1 Release Assessment

4.1.1 Terms and definitions

This release assessment considers the likelihood of HPAI virus introduction to the UK from the currently affected countries worldwide. For the purpose of the release assessment (Section 4.1) the following definitions will apply:

Term	Definition
HPAI	*"HPNAI viruses have an IVPI in 6-week-old chickens greater than 1.2 or, as an alternative, cause at least 75% mortality in 4-to 8-week-old chickens infected intravenously. H5 and H7 viruses which do not have an IVPI of greater than 1.2 or cause less than 75% mortality in an intravenous lethality test should be sequenced to determine whether multiple basic amino acids are present at the cleavage site of the haemagglutinin molecule (HA0); if the amino acid motif is similar to that observed for other HPNAI isolates, the isolate being tested should be considered as HPNAI"* (OIE, 2005)
Waterbirds	*"Means those species of birds that are ecologically dependant on wetlands for at least part of their annual cycle…"* (UNEP-CMS, 2005)

For the purpose of the release assessment (Section 4.1) the following terminology* will apply (OIE, 2004):

Term	Definition
Likelihood	Probability; the state or fact of being likely
Likely	Probable; such as well might happen or be true; to be reasonably expected
High	Extending above the normal or average level
Highly	In a higher degree
Low	Less than average; coming below the normal level
Negligible	Not worth considering; insignificant
Remote	Slight, faint
Would	To express probability; past of Will: expressing a wish, ability, capacity, probability or expectation

*This risk assessment uses the OIE recommended terminology. Defra consider that this is important to maintain consistency in expressing estimates. Defra is aware of some concerns that have been expressed about the appropriateness of this terminology for practical purposes (ie. clarity for the purpose of understanding by wider non-technical audience). Defra will consider this issue in the near future.

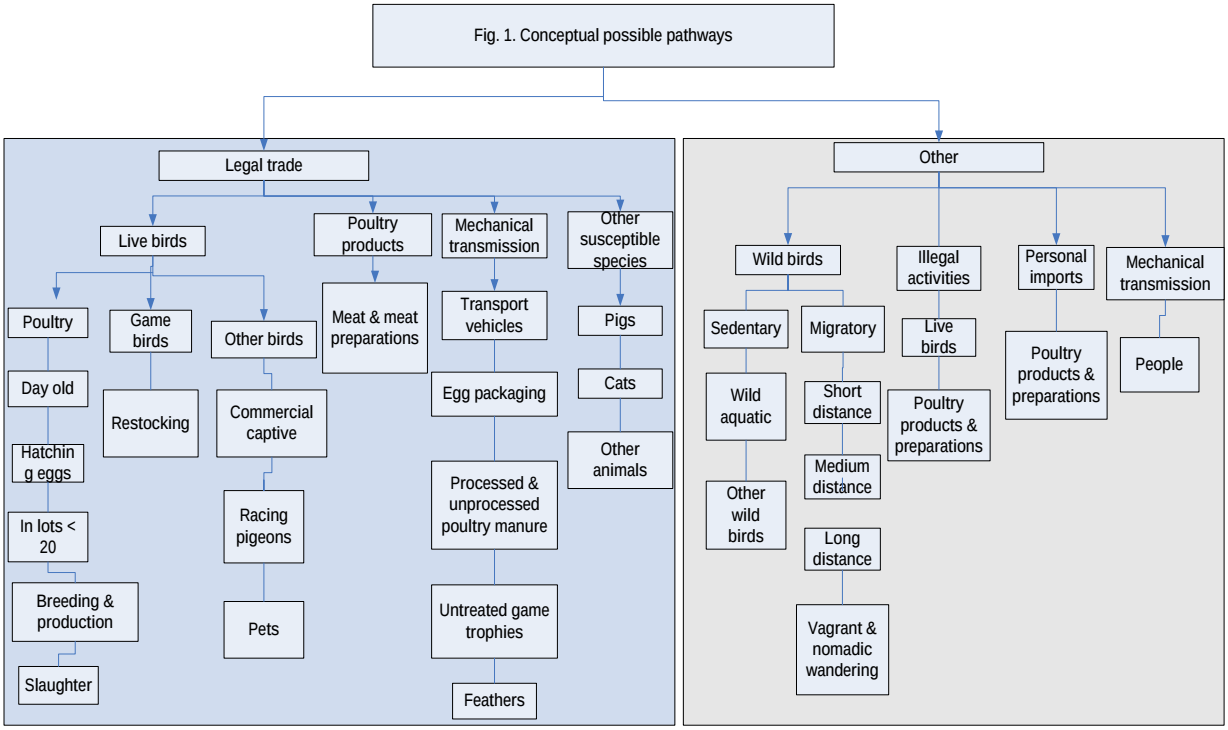
NOTE: Our qualitative risk assessments are undertaken to assist the process of identifying appropriate safeguard measures to prevent the introduction of HPAI H5N1 virus to the UK via legal trade, among other pathways specified. Any such measures must maintain appropriate level of protection without unduly restricting trade.

The UK appropriate level of protection is that legal importation of live animals or their products from EU Member States or Third Countries must present a negligible likelihood that the diseases of concern will be introduced.

With regard to other possible pathways, risk management measures proportionate to the likelihood identified may be selected to mitigate the risk.

4.1.2 Pathways

This risk assessment recognises that, conceptually, there are two broad groups of pathways (routes) by which the H5N1 virus can be introduced to the UK from currently affected regions in the world. These are summarised in Fig. 1.



4.1.2.1 Legal trade in live poultry and their products

4.1.2.1.1 Approved EU Third Countries

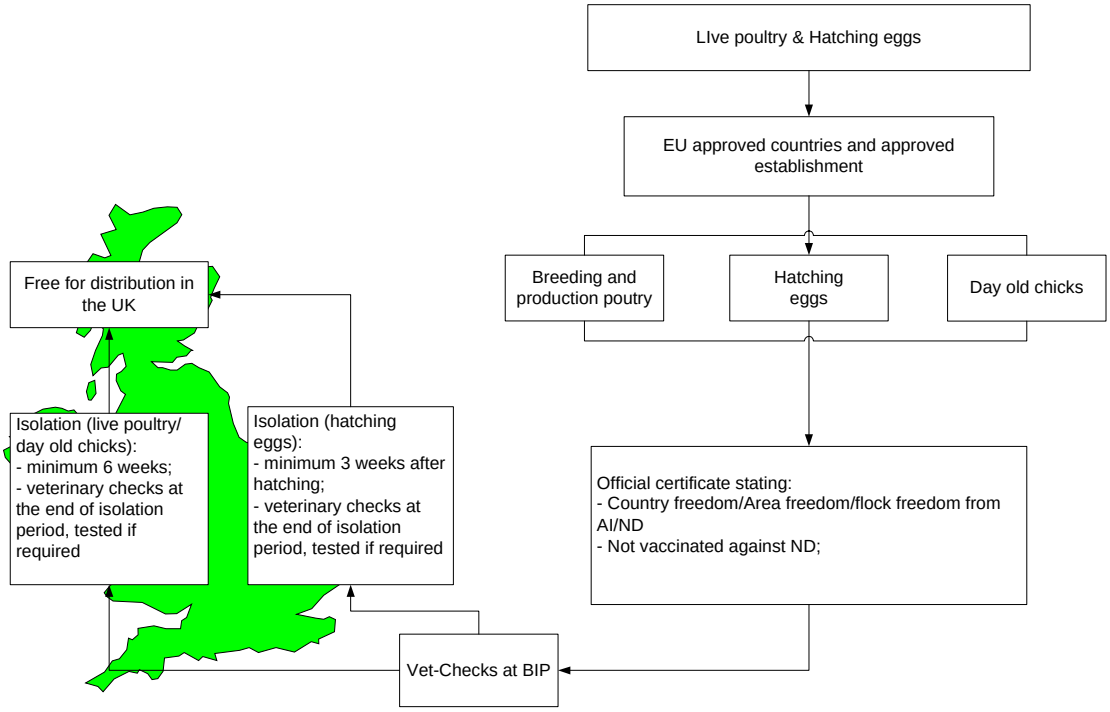
EU approves Third Countries to trade with the EU in live poultry and their products on the basis of the competence and integrity of national veterinary services and the animal health status of the country concerned. These countries must also implement legislation on disease notification, surveillance and disease controls to maximise disease detection and effective containment and eradication on their territories.

EU has banned imports of specified poultry commodities from approved Third Countries known to be affected with HPAI H5N1. Imports from these countries will not be admitted through any UK Border Inspection Posts (BIPs) and the same should apply at any EU border. Therefore, direct importation to the UK of live birds and their specified products from a Third Country known to be affected, or indirect importation

to the UK of live birds from a Third Country known to be affected through another Member State to the UK is highly unlikely to occur.

In accordance with international trade agreements, legal imports should continue undisrupted from approved Third Countries that have not reported an outbreak of H5N1. That means that the official veterinary services of EU approved Third Countries must certify that trade in live poultry, hatching eggs and day old chicks, including those of game birds, is carried out in accordance with EU rules (see Fig. 2). Most trade in these commodities is in high health status breeding birds or commercial poultry which should have been kept under conditions of high biosecurity.

Fig. 2. An overview of EU rules for importations of live poultry and hatching eggs from approved Third Countries



As indicated in Fig. 2, EU rules are risk based and specify multiple barriers designed to detect and prevent the spread of notifiable diseases including HPAI H5N1. In summary, traded commodities are subject to veterinary inspection, official certification and border inspections (BIPs) controls. The local Animal Health Divisional Office at the point of destination in the UK are notified of these consignments so that post-import checks may be carried out. This is done using the EU electronic notification system (TRACES - Trade Control and Expert System) for trade in live animals and their products. In Great Britain, the State Veterinary Service checks a specified proportion of consignments on the basis of identified risk.

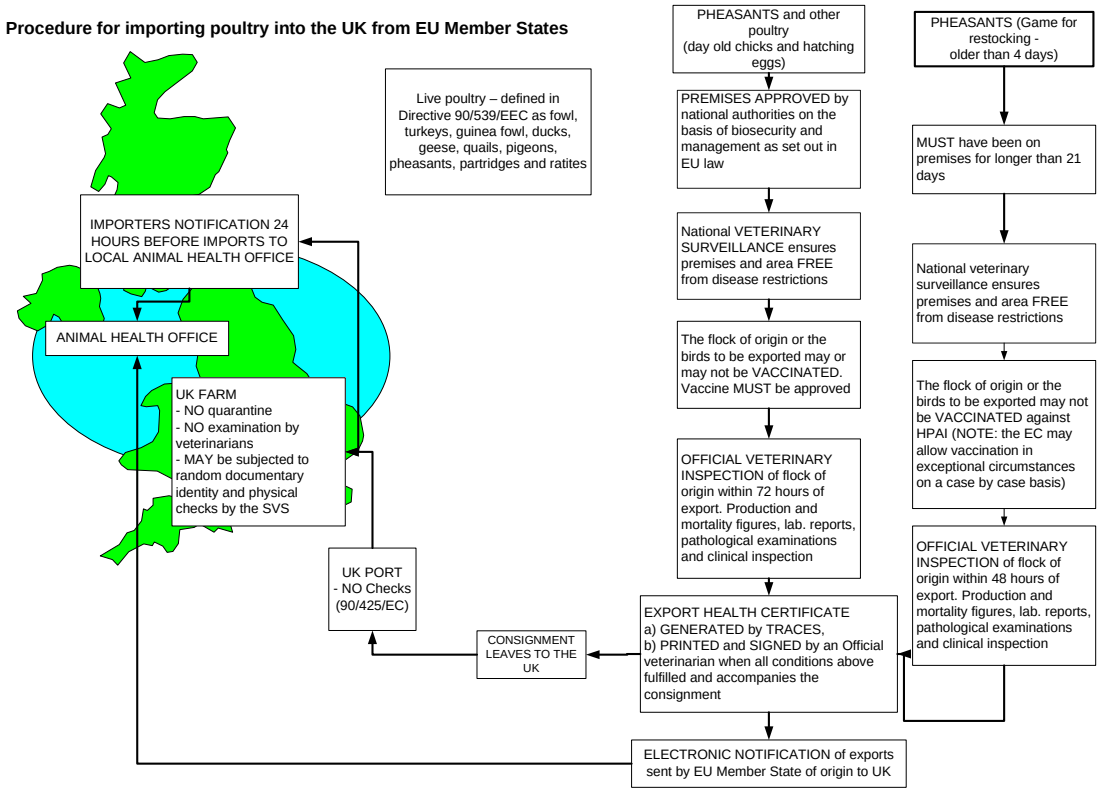
It is unlikely that the official veterinary authorities of any approved Third Country or any other Member State would permit infected live poultry to enter EU trade. The official veterinary services responsible for the holding of origin must certify that the poultry to be consigned are free from notifiable disease, including HPAI.

It is, however, possible that even when EU rules for trade in live poultry and game birds are fully complied with, there may be occasions when live birds may be consigned in good faith from a holding or region where disease may have been introduced but remains undetected, particularly if infected birds showed no clinical signs of the disease. For example, this could be because the species has low susceptibility, or during the incubation period when by definition there are no signs of disease. The Newcastle Disease outbreak in 2005 in pheasants legally imported to the UK from France highlighted the risk that disease may enter a holding and that birds may be traded before the disease is detected. This event emphasises the importance of inspection and surveillance of the consignments of live poultry or game birds that may have arrived to the UK from the affected areas or areas close to the affected areas.

4.1.2.1.2 EU Member States

EU approved Third Countries and EU Member States must implement legislation on intra-Community trade (see Fig. 3), disease notification, surveillance and disease controls. These measures are designed to maximise disease detection and effective containment and eradication. Movements of traded commodities are recorded on the TRACES. The EU rules prevent trade in these commodities from affected areas during an outbreak.

Fig.3. An overview of EU rules for intra-Community trade in live poultry



4.1.2.2 Mechanical transmission

Our previous risk assessments highlighted the importance of maintaining appropriate policy advice and communication on biosecurity measures to be observed at all times to ensure that potential mechanical transmission of the virus by the movement of fomites (e.g. poultry crates, egg packaging, feral birds) or transport vehicles is minimised.

Recent experience in France showed that the virus was detected in a commercial turkey flock in France in the Ain department in February 2006 soon after the virus was detected in wild birds in that area. It is believed that the virus was most likely introduced to this flock by visitors who breached biosecurity. No further disease incidents in commercial poultry have been reported from France since that outbreak.

4.1.2.2.1 Other susceptible species

Our previous risk assessment highlighted that close and direct exposure of various free-living avian species and free-living and domestic animals to HPAI H5N1 virus is likely to result in death. In epidemiological terms, this development is consistent with the concept of a self-limiting disease (a 'dead-end' host). The recent pattern of the virus detection in these species could indicate that these species may have become infected because of localised introduction and exposure to the virus from other species rather than horizontal transmission within the species concerned. However, there is no evidence to ascertain to what extent, if any, within group horizontal transmission may have played in their infection.

Recent reports on HPAI H5N1 virus in avian and mammalian species correlate with the known epidemiology of AI viruses and their ability to infect a variety of species following exposure. Therefore, these recent detections are not unexpected and need to be interpreted with care, particularly when referring to the virus's ability to infect 'new species'.

These conclusions will be reviewed when more detailed epidemiological information becomes available on differences in species susceptibility, the ecology of the virus and the pathways for introduction and subsequent spread.

4.1.2.3 Other pathways

4.1.2.3.1 Waterbird migration

The virus has been detected in 13 EU Member States, including the UK, since the beginning of February 2006. In all affected EU Member States, the virus was detected primarily in dead wild birds. Very limited emerging epidemiological evidence in Europe also suggests that the virus may be present in live, apparently healthy waterfowl (e.g. swans in Poland; gulls in Croatia).

Wild bird migration is a natural phenomenon which occurs annually in various parts of the world. These movements are mainly north to south and back, usually within established flyways. At the time of writing, our knowledge of the epidemiology of H5N1 in wild birds Europe is limited as it is only a few months since the infection was first detected. Our understanding of the current epidemiological picture and ability to

estimate any future occurrence has limitations, and therefore, any inferences are made with a great degree of uncertainty. Nevertheless, the available information is clearly of value in starting to improve our ability to estimate the risks in the context of the virus, susceptible hosts and their behaviour, and the environment.

4.1.2.3.1.1 Avian influenza virus

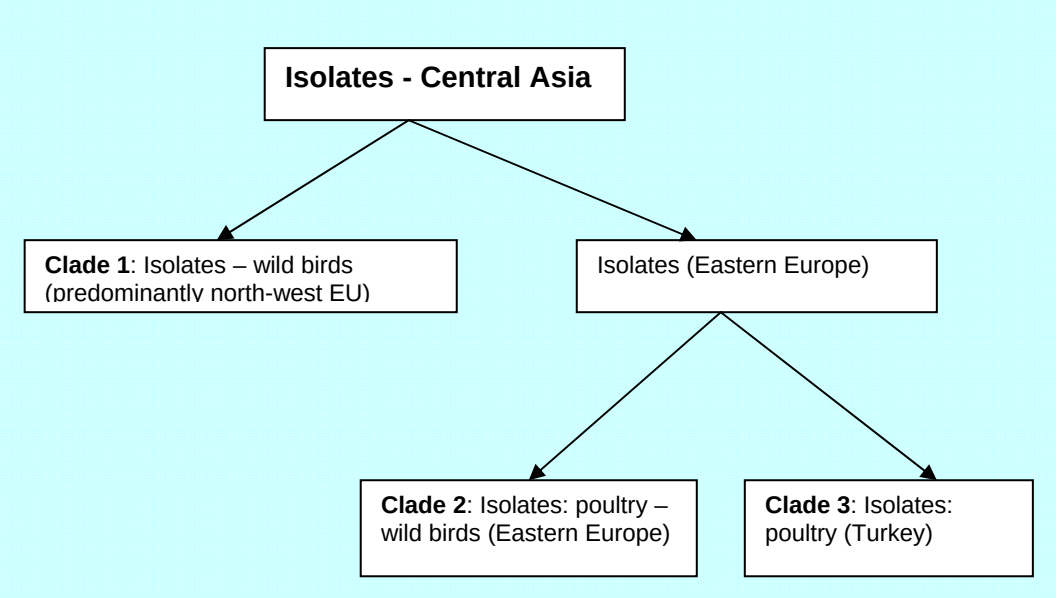
4.1.2.3.1.1.1 General

Sharp and others (1997) consider that different avian influenza (AI) virus subtypes are maintained by different bird species. While a particular subtype may infect more than one bird species, they appear to have different, species-specific levels of adaptation. Matroshovic and others (1999) consider that avian influenza viruses from aquatic birds undergo significant selective pressure in chickens, leading to definite changes in both the haemagglutinin (HA) and the neuraminidase (NA) during the adaptation process. A single substitution in the gene that codes for HA may result in additional glycolysation sites. This, in turn, may render the virus highly pathogenic in chickens by increasing the release of the virus from cells thereby facilitating its spread and replication in different tissues of chicken. These genetic features of the HA and NA clearly separate chicken viruses from the viruses of wild aquatic birds.

4.1.2.3.1.1.2 HPAI H5N1

It still remains uncertain to what extent the general knowledge on AI viruses applies to HPAI H5N1 virus. Genetic analysis of recent isolates shows that three separate clades of the Asian strain of the virus have been detected in the EU Member States and neighbouring countries. It also indicates a level of relationship between different outbreaks in Europe and varying host specificity. It should, however, be noted that only a limited number of isolates were available to the World Reference Laboratory for Avian Influenza, Weybridge, UK, which carried out the analysis (see Fig.4).

Fig.4. Virus isolates – genetic clades



One lineage comprises isolates that have been primarily isolated from wild birds with no associated outbreaks in poultry. This clade also contains virus isolates from China (Qinghai lake) in May 2005, southern Siberia (Novosibirsk) and in the EU (Germany – Rügen Island), Sweden and Denmark, thus suggesting direct evidence of linkage. The virus isolated from a single dead Whooper Swan (*Cygnus cygnus*) found washed up in a harbour in Scotland (UK) also belongs to this lineage. On the basis of genetic analysis, these isolates belong to a clade that is separate from apparently chicken-adapted strains.

The virus isolates from Turkey and Romania obtained in October 2005 are almost identical to the virus isolated in wild birds in China (Qinghai Lake) in May 2005, thus suggesting direct evidence of a linkage. However, genetic analysis of further isolates suggest that this virus may have subsequently evolved into two clades – one clade is indicative of the lineage of the virus that may be circulating between wild birds and domestic poultry (e.g. Romania). The other clade contains viruses that may be circulating between domestic poultry without involvement of wild birds (e.g. Turkey). Broadly, the results of genetic analysis seem to fit with the current knowledge of the spatial and temporal sequence of the virus spread during the years 2003 to 2006 (see map in section 3).

4.1.2.3.1.1.3 LPAI H5N1

In two instances, low pathogenic avian influenza (LPAI) of H5N1 type was reported from live waterbirds in the EU Member States. Italy has reported the detection of low pathogenic avian influenza (LPAI) virus of H5N1 type. The virus was isolated as a result of the ongoing surveillance programme for avian influenza. The source of the sample was an apparently healthy wild Mallard duck (*Anas platyrhynchos*) shot in the province of Modena (Emilia-Romagna region) during October 2005. Sequencing of the H gene of this virus shows a homology at the nucleotide level of 95% to previous H5 low pathogenic strains found in Europe while the homology to the recent 'Asian' H5N1 strain is 91%. These laboratory findings indicated that there is no link between this low pathogenic strain and the highly pathogenic 'Asian' H5N1 strain.

A LPAI H5N1 virus was isolated among several other AI isolates that have been obtained from samples collected from 30 targeted free-range flocks of hybrid Mallard/Muscovy ducks (*Anas platyrhynchos* x *Cairina moschata*) in France. The ducks were four to 12 weeks of age and showed no clinical signs of the disease. Further testing showed that the N1 gene of the virus was found to be closely related to an Italian LPAI H7N1 (Cherbonnel and others, 2006) but not to the N1 gene of the highly pathogenic 'Asian' H5N1 strain.

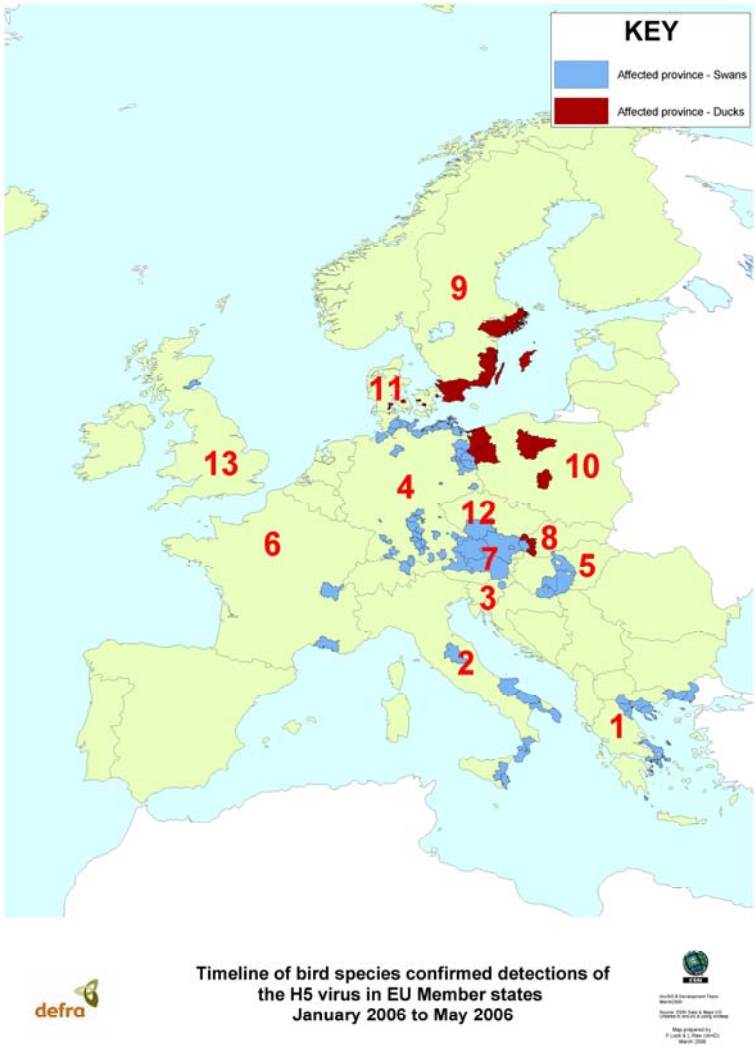
4.1.2.3.1.2 The host

It is notable that most detections of the virus in the affected EU Member States were made in dead wild waterbirds of the order *Anseriformes* (swans, ducks and geese). There is, however, emerging circumstantial evidence that live waterbirds (e.g. swans and gulls) may be infected with HPAI H5N1 virus without showing clinical signs.

4.1.2.3.1.2.1 Susceptibility

During the period from February to April 2006, HPAI H5N1 virus was detected in dead wild waterbirds collected at numerous locations in several affected EU Member States.

What appears to be a larger die-off in wild birds was noted in Germany, mainly around the Island of Rügen in the Baltic. However, in other affected parts of Germany, a relatively small number of dead wild birds were detected. Similarly, no large die-offs in wild birds have been reported from other affected EU Member States, where again, the virus was detected in only a relatively small number of dead wild birds.



The virus was detected in higher percentage in wild swans (Mute Swans – *Cygnus olor* and to a lesser extent in Whooper Swans – *Cygnus cygnus*) in eight affected EU Member States (Greece, Italy, Slovenia, Austria, France, Germany, Czech Republic, Hungary) compared to lower percentage of positive detections in different species of wild ducks (see adjacent map).

The virus appears to be primarily detected in higher percentage in different species of wild ducks in three affected EU Member States in the northern EU (Denmark, Sweden and Poland) in the Baltic Sea Region compared to lower percentage in wild swans (see map). In one Member State (Slovakia), the virus appears to be detected in equal percentage in wild swans and different species of wild ducks

In one EU Member State (UK-Scotland), the virus was only detected in one Whooper Swan washed up in a harbour. No further cases have been detected since, despite intensive surveillance in the affected area complemented by ongoing extensive surveillance in the UK.

Recent experiences in Europe suggested that the virus may be present in live and apparently healthy waterfowl. The Polish authorities reported that 113 live swans had been quarantined in one aviary in the Torunski region on 10 March 2006. At that time, samples were taken from 25 swans and 5 tested positive for H5 virus. One swan in the aviary died and was tested positive for H5N1. On 28 March, tracheal and

cloacal swabs and blood samples were taken from the remaining 112 live swans. Thirty-two swans tested positive for H5 virus. The virus was detected in:

a) Tracheal swab (1 swan)
b) Tracheal and cloacal swabs (5 swans)
c) Tracheal swabs and blood samples (4 swans)
d) Cloacal swabs (7 swans)
e) Cloacal swabs and blood samples (6 swans)
f) Tracheal and cloacal swabs and blood samples (9 swans)

This was the first time that the virus has been detected in live wild waterbirds in the EU that have not died as a consequence of infection. Nevertheless, any detailed extrapolation of data related to the virus spread within the flock should be carried out with care. This is because only 25 swans of the112 surviving (from the original 113) swans have been tested. These results can be compared to the 32 positive, in the remaining 112 swans sampled that tested positive 18 days afterwards. It is notable that at least 19 swans may have been at the viraemic stage at the time of second sampling after 18 days given that the virus was detected in their blood samples (see above). Detection of the virus in tracheal and cloacal swabs suggest that infected swans were shedding the virus by the respiratory and gastrointestinal routes at the time of sampling. It would be reasonable to assume that the swan density in the quarantine facility was unusually high. While this small study demonstrated the virus transmission between these housed swans, it is epidemiologically important to note that the infected swans did not show any clinical signs. All swans that tested positive were euthanized on 3 April 2006. The remaining 80 swans that tested negative were released from the quarantine aviary.

In March 2006, Croatia reported that HPAI H5N1 virus isolated from cloacal swabs collected from 30 live black-headed gulls (*Larus ridibundus*) as a part of routine surveillance of wild birds in the southern part of country on the Adriatic coast.

4.1.2.3.1.2.2 Age

It appears that all detections of the virus in the EU Member States would have been in fully-grown (ie. fledged) birds given the time of the year (winter) when the dead wild birds were submitted.

It has, however, been found that juvenile ducks are significantly more likely to be naturally infected with AI type A viruses than adults (Sharp and others, 1997). It is unknown whether this would also apply to natural infection with the HPAI H5N1 strain in particular and whether they would be likely to survive such infection and shed the virus for an extended period of time.

In experimental conditions HPAI H5N1 virus was shown to be lethal for seven out of eight 2-week old ducks. Two out of five week-old ducks inoculated with the virus died. These results show that some H5N1 isolates are capable of causing infection and death, however, lethality may be age dependant (Pantin-Jackwood and others, 2006). This could suggest a possibility that a proportion of ducks may be infected with the virus and could enter the moulting period when old feathers are shed and replaced by new feathers (in ducks and other waterbirds this lasts several weeks during which the birds are unable to fly) (Gains, 2006). Guberti and others (2006) undertook simulation studies with low pathogenic avian influenza (LPAI) virus which showed peaks of viral prevalence after nesting due to the population recruitment and

during moulting periods due to high host density. It is uncertain to what extent these simulation studies would apply to real infection with HPAI H5N1 virus.

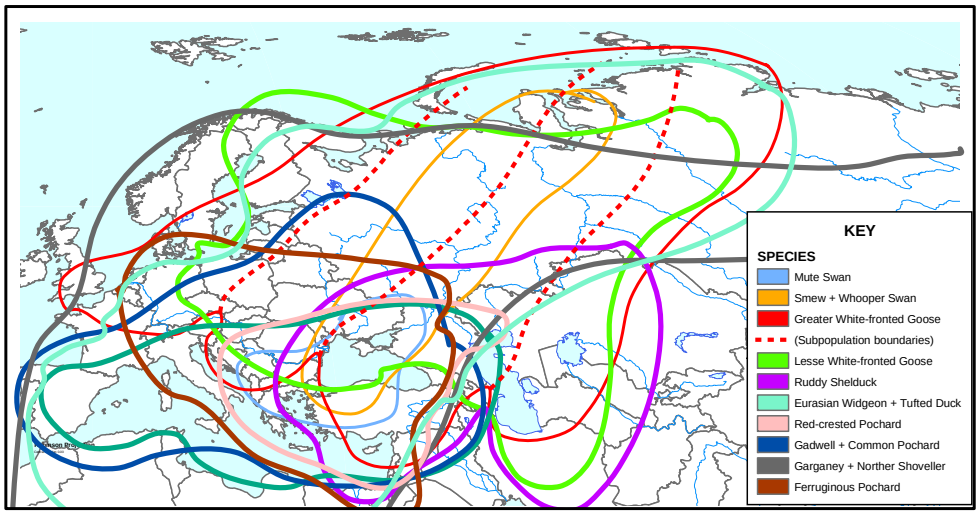
4.1.2.3.1.2.3 Other wild birds

HPAI H5N1 virus has also been detected in dead raptors and scavenging birds in some EU Member States. The virus has been reported to have been detected in live gulls in Croatia. At this time, the accumulated epidemiological evidence suggests that these bird species are unlikely to play a significant role in introductions of the virus over wide geographic areas, although the possibility that they may play a role in 'local' dissemination of the virus cannot be completely excluded. However, more studies at various levels (i.e. local, national, international) involving different agencies and interest groups would be required to ascertain their role as potential carriers of the virus without showing clinical signs of the disease.

4.1.2.3.1.2.4 Waterbirds migration and behaviour

At the time of writing, the spring migration of waterbirds and other wild birds has been completed. Broadly, the wild waterbirds and waders have departed from their wintering grounds in European wetlands to their breeding grounds. Their migration can be split into two main flyways - one north-east flyway to Scandinavia and Russia and one north-west flyway to Iceland, Greenland and Arctic Canada. Some areas in the northern part of the UK may receive breeding waterfowl from further south in Europe (e.g. France, Spain, north-west Africa).

There are several aspects of the epidemiology of infection in wild birds which are important in estimating the likelihood of the introduction of infection. Broadly, the extent to which migratory birds may contribute to future introductions will depend on their ability to become infected and pass infection to healthy individuals in their breeding grounds, and during the mingling that occurs in staging grounds including the ecology of the virus (i.e. its ability to survive in various environments)
The following map indicates the complexity of the situation and highlights difficulties in interpretation.



ArcGIS 8 Development Team
March2000

Source: ESRI Data & Maps CD
Created in ArcGIS 8 using ArcMap

Waterfowl Migration In Europe and western Asia

NOTE: The map above is based on information sourced from Wetlands International (Scott & Rose,1996). It does not necessarily reflect the true situation and should be regarded as an indicative rather than a definitive reflection of migratory flyways between Siberia and Europe. Also note that this map does not display major flyways between western Europe, Iceland, Greenland and Arctic Canada.

In our previous risk assessments we have emphasized that *Anatidae* (ducks, geese and swans) appear to have different migration systems (Scott and Rose 1996; Miyabayashi and Mundkur 1999). For ducks especially, flyways tend to be poorly defined. Migration occurs on a broad front, typically between a number of wetland staging areas [See also Stroud *et al.* 2005 for a recent review of migratory wader (shorebirds) biogeographic populations].

As mentioned, the virus has been detected in live and apparently healthy wild waterbirds (i.e. swans and gulls) in some EU Member States. Therefore, there is a possibility that the virus may be present in populations of wild birds, either in their breeding grounds or in local wild bird population in limited locations in the affected countries.

It is uncertain at present whether or not HPAI H5N1 virus infection will continue to establish or persist in wild bird populations throughout the year in Europe in the absence of further introductions. Similarly, if infection does persist, there is uncertainty as to whether infection will extend geographically and/or become established in a wider range of wild bird species.

As indicated on the map above, there is some potential limited mixing of the waterbird populations in Russia. However, it is uncertain at this stage whether there is any significant geographic and temporal overlap of waterbird populations and, hence, any mixing of waterbird populations that migrate from both European and Asian overwintering grounds to the breeding grounds in Russia. Some species of ducks appear to migrate from their breeding grounds in southern Siberia to the area around the Volga Basin and the Caspian Sea region.

While wetland habitats in Siberia support large numbers of breeding waterbirds, the Volga Basin and north Caspian regions are cross-roads for migratory waterbirds that use four major routes in Eurasia and East Europe. These two regions host the vast majority of migratory birds which nest in eastern Fennoscandia (Finland and the Scandinavian peninsula), northern-central territories of the Russian plain, Ural and parts of western Siberia on their way to overwintering grounds in east Africa. A small proportion of these birds overwinter in south-western Asia (Lvov and others 2001).

Ringing recoveries (Wernham and others, 2002) show that there is limited movement of birds between the UK and southern Russia. The extent and regularity of such movement are uncertain. Thus, these data should be treated as preliminary and with caution. Defra has consulted ornithological experts who consider that the normal flyway patterns for migrating birds would not usually include direct movement of waterbirds from eastern Europe to the UK. The majority of birds from Eastern Europe and the Danube Delta will either spend the winter there or disperse southwards. However, the potential for limited mixing at some contact points between the wild waterbird populations from Eastern Europe with the populations in the EU does exist.

With regard to these limited movements, there is no evidence that any of the extreme eastern recoveries of UK birds may have travelled that far in a single winter. It is

more likely that they may have paired with different mates in different breeding seasons and their migratory routes and thus wintering grounds may have changed from east to west over a period of several years. Although the UK hosts a very limited proportion of these species' populations during the winter, the majority of individuals breeding in southern Siberia are highly unlikely to reach Britain because they winter further east in Europe (for example in the Mediterranean) or in the Baltic for some species (Cranswick, 2005). Nevertheless, it needs to be emphasised that detailed, comprehensive information on tracking the birds is still not available.

Many species of waterbirds arrive in the UK from the arctic areas of Northern Canada, Greenland, Iceland, Fennoscandia and further east in the northern part of western Russia. Most of the waterbird species or populations wintering in the UK derive from northern (arctic or sub-arctic) areas. Further, several species of waterbirds have a marine distribution during winter, and, remain at sea.

It is indicative from the above maps that the virus was detected in greater percentages in dead wild ducks in northern EU Member States in the Baltic Sea region compared with a greater number of detections in swans in Germany (the Island of Rügen) and other affected central and south-eastern EU Member States. As mentioned above, it remains uncertain whether the virus may have been present in local populations in certain locations in northern EU Member States and if so, to what extent it may result in further spatial spread in the absence of further introductions.

It is less likely that wild waterbirds would migrate directly from their breeding grounds in the northern parts of western Russia to the UK without staging. It is likely that staging would delay migration such that it would be likely to be completed within a period of weeks rather than days although the speed of migration will depend on the species concerned. It is likely that congregation of these birds at their staging grounds would precipitate sporadic cases of disease in infected birds. On the other hand, a number of infected birds may not show clinical signs.

Direct migration is more likely in the case of waders or wild waterbirds that will arrive from Iceland, Canada and Greenland or western parts of the EU Member States in the North Sea region.

4.1.2.3.1.2.5 Domestic poultry

On a few occasions, there were reports of single affected domestic poultry flocks in a few EU Member States (see map below). In Austria, A sick swan was taken to an swan sanctuary in Graz in February 2006, subsequently resulting in infection of 3 ducks and 2 chickens kept in the same sanctuary.

In France, H5N1 was reported in turkeys at a commercial farm in Ain in February 2006.

In February, HPAI H5 virus was detected found in one mallard in a holding (fenced area) which included game birds (farmed mallards [*Anas platyrhynchos]*), pheasants, pigeons, backyard hens and peafowls) in Kalmar in Sweden.

In Germany, H5N1 was detected in turkeys at a farm in Sachsen in April 2006. The farm also housed geese and chickens but the outbreak only affected the turkeys.

In Denmark, H5N1 was found in backyard poultry within the county of Funen in May 2006. In Hungary, H5N1 was detected at a goose farm in Bács-Kiskun in June 2006.

All these outbreaks have been reported within one to several weeks after the detection of the virus in wild birds (see timeline for each country in Figure 5)

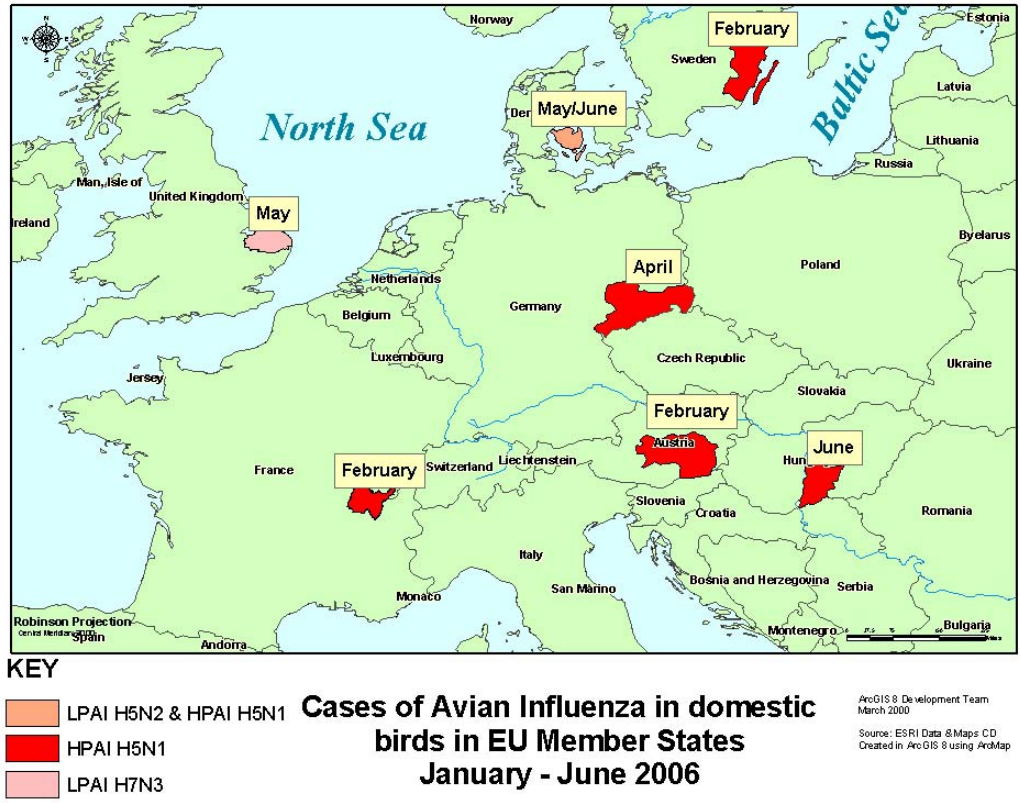
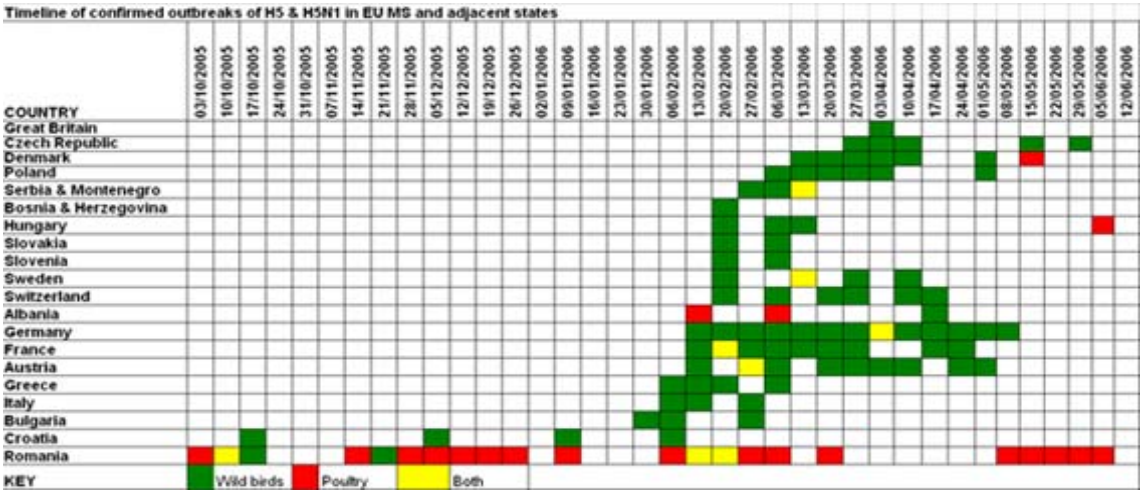


Fig. 5. Timeline of confirmed outbreaks of H5 and H5N1 in in free living and domestic birds EU MS and adjacent states January to June 2006



Romania is the only country in eastern Europe that continues to report cases of HPAI H5N1 in domestic poultry, mainly in backyard flocks. In the light of these developments it is likely that the virus may have become present in local backyard poultry or local wild bird population in discrete locations in Romania. This could increase the possibility that the virus may continue to be introduced in some parts of the EU and eventually arrive in the UK because of the potential for limited mixing at

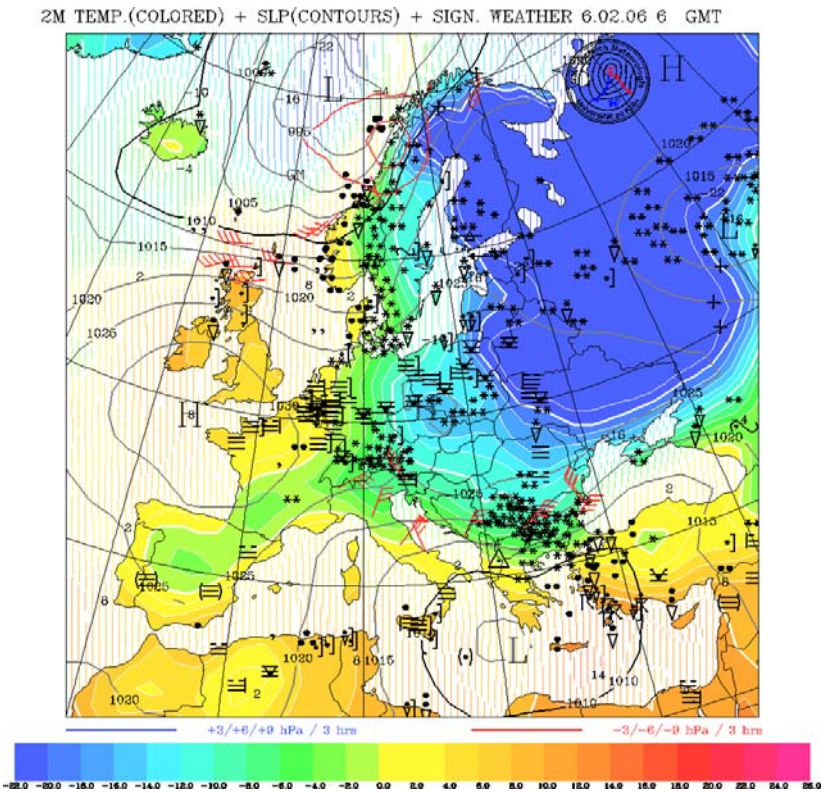
some contact points between the existing wild waterbird populations from Eastern Europe with the populations in the EU.

4.1.2.3.1.3 The environment

The evolving situation demonstrates that the virus has been detected over a broad geographic area within a relatively short period of time. This could demonstrate the existence of a potentially very mobile carrier of the virus. On the other hand, it remains uncertain whether the virus may have already been present in these and other areas at a very low level and escaped detection previously due to the absence of the sophisticated diagnostic tools that are now available.

4.1.2.3.1.3.1 Spatial and temporal spread

Between May 2005 and January 2006, outbreaks of HPAI H5N1 virus were reported in Asia and Eastern Europe. Since February 2006, the virus was reported in several EU Member States and in some countries in sub-saharan Africa. In summary, the following map outlines the spatial and temporal sequence of the virus spread during the years 2005 and 2006.



Cooler than average temperatures were observed in Eastern Europe and the Iberian Peninsula during January 2006 (NCDC, 2006).

By the beginning of February 2006, it was reported that the Black Sea was frozen within a radius of 300-400 meters from the shore due to worsening and harsh winter conditions.

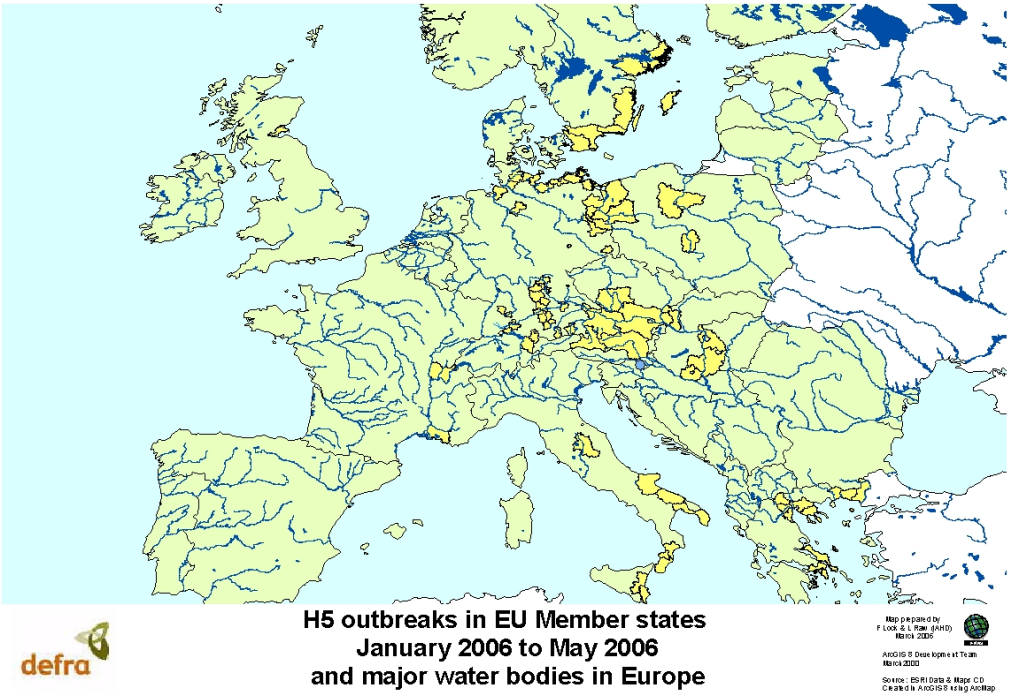
Similar cold weather conditions have been observed in the Baltic Sea around the coast of Germany in mid February 2006 (see map by Royal Meteorological Society, 2006).

Cold weather conditions may have resulted in the movement of many waterfowl (swans, ducks, geese) from frozen areas in eastern Europe. Such movements in periods of extreme cold weather are not unusual (Ridgin and Fox, 1990).

At the beginning of 2006, these conditions in the countries neighbouring the EU and in the EU may have caused temporary and erratic displacement of unknown numbers of birds from either northern parts of Europe or the Black Sea region, some of which may have been infected with the virus. The initial outbreaks of HPAI H5N1 in the EU

were sporadic and occurred at different and distant geographic locations within a relatively short period of time at the beginning of 2006 (see map below).

Subsequent outbreaks peaked in March 2006 and became clustered spatially and temporally in some EU Member States. The virus has also been detected in wild birds in the southern European countries neighbouring the EU (outbreaks not



included in the map but see timeline – Fig.5).

The majority of these outbreaks appear to have occurred in broader areas around major waterways (e.g. Danube River and tributaries). These may have coincided with the displacement of wild birds and their subsequent congregation in limited locations due to exceptional environmental (weather) conditions at the beginning of 2006. It remains to be seen whether similar weather conditions occur during the forthcoming winter (2006/2007).

4.1.2.3.2 Illegal imports

The H5N1 virus was isolated from live smuggled eagles in Belgium in 2004, raising the notion that smuggling could pose major threats for introducing and disseminating H5N1 virus worldwide (Van Borm and others, 2005). The EU has now banned trade in wild and captive birds from Third Countries while limited options for trade are examined. Some concerns have been expressed that this likelihood might be further increased because of the current ban on legal trade. However, there appears to be no direct evidence in the UK that illegal trade has increased since the ban.

We have previously emphasised that large-scale commercial illegal imports of poultry may be attempted from any country using false or forged documentation. However, thorough documentary checks and awareness at Border Inspection Posts (BIPs) are likely to mitigate this type of risk. The information on these intercepted consignments must also be entered into TRACES.

The scale of risk of illegal trade depends on the scale of the trade which, in turn, is difficult to quantify. On this basis, there is a need to improve our understanding of the nature and extent of illegal trade in live birds and enhance detection and prevention measures accordingly. This will also be in line with the current revision of the existing quarantine requirements to enable fully controlled legal trade to resume following a ban, so as to mitigate the risk from potentially increased illegal imports.

4.1.2.3.3 Personal imports

As with all disease agents, illegal imports from worldwide infected countries give rise to a constant background risk of infection. Personal imports of poultry meat and poultry products are currently not permitted from Third Countries and are subject to Customs inspection. Attempts to illegally import meat as personal imports have been recorded from many countries. Refrigeration of illegally imported meat is unlikely and makes detection by enforcement authorities more likely. The virus has been recovered from fresh duck meat (Tumpey and others, 2002), however, cooking temperatures for consumption purposes (usually above 70^0C) are considered sufficient to destroy the virus. The likelihood associated with the illegal personal import of poultry meat would appear to be negligible because it is likely that the meat will be cooked.

4.1.2.3.4 Mechanical transmission

Our previous risk assessment identified that in the case of H5N1 virus, the most likely categories of people which could present a risk for the virus introduction to the UK are:

- UK farm workers on holiday in countries where the H5N1 virus has been confirmed (high-risk countries),
- Migrant workers from high-risk countries working on UK livestock farms
- Military personnel,
- Tourists, particularly any staying in the countryside or visiting bird markets in high-risk countries,
- Hunters, birdwatchers or others who have physical contact with wildlife in high-risk countries and who then come into contact with birds in the UK.

Defra, the Department of Health and the Health Protection Agency are working together to ensure that the risk of human mechanical transmission from birds is addressed adequately through biosecurity on farms and other places where poultry are kept should they be visited by such categories of people.

5 Conclusions

Within the past two years HPAI H5N1 virus has been detected in many locations in Asia, Europe and parts of Africa. Many uncertainties still remain regarding how widespread the virus may be worldwide and regarding the epidemiology and ecology of the virus.

It is also uncertain to what extent different pathways (e.g. legal trade, illegal imports, mechanical transmission) may play a role in the introduction and dissemination of the

virus. Among possible pathways, migratory birds have been shown to play a role in introducing the virus.

On the basis of our previous risk assessments, available epidemiological information and recent experiences, this risk assessment concludes:

5.1 Legal trade

There is a negligible likelihood that legal trade in live poultry, gamebirds and their products would result in the introduction of HPAI H5N1 from affected Third Countries, or any area of the EU subject to restrictions because of the EU (and the UK) ban. The EU (and the UK) have also banned trade in pet and captive birds from all Third Countries regardless of their HPAI status while limited options for trade are being examined.

There is a negligible likelihood that legal trade in live poultry, gamebirds and their products would result in the introduction of HPAI H5N1 from EU approved and non-affected Third Countries, or any area of the EU not subject to restrictions. Therefore such trade should continue uninterrupted under existing rules.

Despite the best efforts and compliance with EU rules, there is a limited possibility that birds may be traded before the disease is detected and officially notified. Thus, inspection and surveillance of the consignments of live poultry or game birds that may have arrived to the UK from the newly detected affected areas or areas close to these may be required to ensure that they are not incubating the disease.

5.1.1 Wild bird migration

Wild bird migration is a natural phenomena and our knowledge of wild bird movements is constantly improving due to availability and application of modern technologies. Our knowledge of the epidemiology of H5N1 in wild birds in Europe is limited as it is only a few months since the infection was first detected. However, the available information is clearly of value in starting to improve our ability to assess the risks.

Spatial and temporal spread of the virus in some EU Member States may suggest that migratory wild waterfowl may have played a role in its introduction to certain locations in Europe. It appears that most detections of the virus in the affected EU Member States were made in dead wild waterbirds of the order *Anseriformes* (swans, ducks and geese). Therefore, there is an increased likelihood that these birds may play a greater role in the epidemiology of the virus. While some uncertainties remain with regard to potential species bias in carcass reporting, these detections would not be unexpected as ducks, geese, swans and related waterbirds are strongly suspected as the reservoir hosts for most influenza type A viruses.

There are a number of aspects of the epidemiology of infection in wild birds that are important in assessing the risks from the coming migration. These include the maintenance of infection in their northern breeding grounds in northern parts of Scandinavia, the Baltic states and western Russia, and if infection persists, whether infection will be more widespread in this area.

Recent epidemiological evidence in the EU suggests that the virus may be present in live wild waterfowl (i.e. swans in Poland). Therefore, there is a possibility that a certain number of infected but asymptomatic wild waterfowl from the affected northern EU Member States would carry the virus back to their breeding grounds in spring 2006. This possibility is difficult to estimate in the absence of targeted and practical surveillance studies. More systematic studies involving different agencies and interest groups are required to ascertain their role as potential carriers of the virus without showing clinical signs of the disease, including ecology of the virus.

Should the virus be present in the flyways of wild birds (e.g. in breeding grounds that stretch from the northern part of western Russia to the near Continent) this would increase the likelihood for introduction of the virus to other north-west European countries and the UK, particularly in areas known to host large concentrations of wild migratory waterbirds. However, migratory movements direct from breeding areas to the UK are less likely than migratory flights where birds stop at staging areas prior to arriving to the UK. Thus, any estimate of the likelihood of introduction of the virus to the UK should be reviewed in light of potential detection of the virus in wild birds in north-west European countries en-route to the UK.

Should the virus continue to be detected in Eastern Europe, this may increase the likelihood of the introduction of the virus to the UK from this area. However, direct movements to the UK are less likely from this region and the estimate of this likelihood should be reviewed in the light of potential detection of the virus in wild birds, mainly in north-east, central and southern Europe. These areas are well within the flyway that include the majority of waterbirds that migrate from southern Siberia southwards via the Volga Basin and the Caspian Sea region.

It is unknown at present whether H5N1 infection will persist in wild bird populations throughout the year in the EU or Europe in the absence of further introductions. Similarly, if infection does persist either within wild birds or their environment, there is uncertainty as to whether infection will remain confined to certain locations or extend geographically and/or become established in a wider range of wild bird species. One indication of such development could be further sporadic detections particularly during the forthcoming moulting period when the resident wild waterfowl will congregate in large numbers. The likelihood for further spread is difficult to estimate in the absence of targeted and practical surveillance studies. Nevertheless, this highlights importance to continue to maintain appropriate biosecurity standards with regard to preventing mixing of wild birds with domestic poultry.

Recent experiences suggested that other wild bird species (e.g. raptors, feral pigeons) can be affected with a fatal outcome. It still remains uncertain to what extent these species may play a role in the epidemiology of the virus and its potential spread over wider geographic areas. Thus, more systematic and targeted studies at various levels (i.e. local, national, international) are required to ascertain their role.

As it currently stands, continued monitoring of developments and targeted surveillance of wild birds in the EU and the countries neighbouring the EU are vital, as is the analysis of the accumulated data to better understand the risks. Recent developments in the EU highlighted that surveillance, complemented with appropriate policy advice on biosecurity measures proportionate to the risks were an effective way of detecting and preventing the introduction of the virus into commercial poultry operations.

Appropriate and practical epidemiological investigations and studies are required in the EU Member States in the areas where infection has been found in wild birds to identify the domestic poultry flocks that could be regarded as at risk. This would provide valuable epidemiological information to improve our understanding of potential risk factors and support the apparent effectiveness of the biosecurity measures. This is also important from an international trade perspective to ensure that safeguard measures are proportionate to the risks posed are taken regarding trade in commercial poultry while protecting animal and public health.

5.2 Illegal imports

As with any disease outbreak in any country, there is an indeterminable likelihood of the introduction of H5N1 virus to the UK by illegal imports of live birds and their products. Nevertheless, this again emphasises the importance of implementing and maintaining appropriate enforcement control measures with regard to illegal imports to mitigate potential risks.

5.3 Mechanical transmission

As with any disease outbreak in any country, there is a low likelihood that the movement of people could transmit the pathogen by mechanical transfer if visiting areas where outbreaks have occurred. This emphasises the importance of maintaining and communicating appropriate advice on proportionate biosecurity measures to such categories of people to mitigate potential risks.

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