



European Food Safety Authority- EFSA-Q-2005-243

Scientific Statement on

Migratory birds and their possible role in the spread of highly pathogenic avian influenza

Adopted by written procedure on the 4th of April 2006

EFSA-Q-2005-243

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1. Terms of Reference

1.1. Background

The recent spread of Highly Pathogenic Avian Influenza (HPAI) H5N1 virus from Southeast Asia to central and western China, Russia (Siberia), Kazakhstan, Mongolia, Croatia, Ukraine, Romania, Turkey, Nigeria, etc. has raised serious concerns that wild birds, including migratory birds might be one of the more important causes of this geographical spread of the disease.

1.2. Mandate

In the light of the recent developments described above, and the recently adopted opinion on “Animal health and welfare aspects of avian influenza”, the Commission asks the European Food Safety Authority to issue a further scientific opinion on AI, taking into account the most recent scientific evidence and epidemiological information, which should address in particular the following:

1. the risk posed by wild birds and particularly migratory birds in the spread of the Asian lineage H5N1 HPAI virus strain;
2. the risk that populations of wild birds will become a reservoir of the Asian lineage H5N1 HPAI virus;
3. taking into account the response to points 1 and 2, the risk that the virus may pose for entry, exposure, contamination, transmission and spread to birds and poultry on the EU territory due to migratory birds flying along the different migratory pathways crossing the territory.

In addition, the Commission assumes that EFSA will continue to closely monitor any further scientific developments in this field and specially those related to the risk posed by wild birds and particularly migratory birds in the spread of the Asian lineage H5N1 HPAI virus in order to produce an update of the recently published opinion as relevant new information and evidence becomes available.

1.3. Introduction to this Scientific Statement

This statement is based on a draft report received from the Working Group of experts on migratory birds. This scientific statement is in fact, the first part of a more comprehensive scientific opinion expected to be adopted at next plenary meeting on 26-27 April.

Given the recent epidemiological developments within the EU in relation to avian influenza occurrence (recent outbreaks in wild birds and domestic poultry, and new scientific data on occurrence of the disease in cat, dogs and mustelids), the Scientific Panel for AHAW, considered it necessary to follow this approach rather than waiting for the full scientific opinion. Due to the urgent management needs, it adopted this Statement to support the Commission with the timely development of control and surveillance measures.

1.4. Approach

In consultation with the Commission it was further specified that, in the initial phase of this risk assessment, the mandate would place primary focus on:

1. The probability of introduction of the Asian lineage H5N1 HPAIV by wild birds into Member States and the subsequent risk of a) the development of an endemic situation in wild birds in Member States and b) the transmission of the virus to domestic poultry and,
2. The identification of risk factors to be considered by Member States in order to classify regions or establishments as being at increased risk of exposure from the Asian lineage H5N1 HPAIV carried by wild birds.

Based on this specification, it needs to be emphasized that pathways other than those of wild birds that are known or hypothesised to exist and are relevant to the introduction of the Asian lineage H5N1 HPAIV to the EU were deliberately excluded from this assessment. This means that the conclusions from the current risk assessment do not have a comparative element with other possible paths of introduction. Such pathways are considered explicitly in the EFSA scientific opinion “Animal health and welfare aspects of Avian Influenza”. An overall balanced assessment of the risk of entry of Asian lineage H5N1 HPAI to the EU must, however, take into consideration all the possible routes of transmission, including factors assessed in both reports. This risk assessment (RA) - addressing the risk questions specified by the Commission- follows the methodology for RA (which can be summarised as: assessing risk release, exposure, consequences and overall risk estimation), as defined by the World Organisation for Animal Health.

This risk assessment was conducted as a qualitative assessment, since a quantitative approach would have required detailed epidemiological information which currently is not available for this disease.

Within the qualitative risk assessment, probabilities are assessed and described textually on a scale from negligible (meaning that they cannot be differentiated from zero, and in practical terms can be ignored), through to extremely high (see Table 1-1). They are based on the opinion of the risk assessors and experts included in the Working Group, taking into account all the data presented in the risk assessment document, and are internally consistent across the different risk questions included in the risk assessment. As no quantitative assessment has been undertaken, they cannot be placed on a precise numerical scale. However probability, mathematically, has a range from 0 to 1 and the textual descriptions employed are presented as within this range.

In order to avoid duplication, extensive reference will be made to data presented in the EFSA scientific opinion “Animal health and welfare aspects of avian influenza” (www.efsa.eu.int).

Table 1-1: Interpretation of probability categories used in this risk assessment (adapted from OIE, 2004a)

Probability category	Interpretation
Negligible	Event is so rare that it does not merit to be considered.
Very low	Event is very rare but cannot be excluded.
Low	Event is rare but does occur.
Medium	Event occurs regularly.
High	Event occurs very often.
Very high	Event occurs almost certainly.

In addition to the risk estimate, the level of uncertainty is indicated in the results of this risk assessment. The terms and criteria for usage are listed in Table 1-2.

Table 1-2: Qualitative categories for expressing uncertainty in relation to qualitative risk estimates

Uncertainty category	Interpretation
Low	There are solid and complete data available; strong evidence is provided in multiple references; authors report similar conclusions.
Medium	There are some but no complete data available; evidence is provided in small number of references; authors report conclusions that vary from one another.
High	There are scarce or no data available; evidence is not provided in references but rather in unpublished reports or based on observations, or personal communication; authors report conclusions that vary considerably between them.

2. Risk Pathways

Risk pathways describe the series of events required to occur so that the hazard under consideration results in the unwanted outcome specified. In this risk assessment, the hazard is defined as the pathogenic organism Asian lineage H5N1 HPAIV. The unwanted outcomes are defined in the risk questions. To assess the risk, the probability that each stage in the risk pathway will occur needs to be separately considered. The following provides an overview of the risk pathways, and information required to assess the risks.

2.1. Risk Question 1 - Release Assessment

What is the probability of introduction of HPAI virus (specifically the Asian lineage H5N1 HPAIV) to the territory of the European Union by migratory wild birds?

Risk question 1 includes issues related to pathogenesis, resistance, epidemiology and dynamics of Asian lineage H5N1 HPAIV in wild birds outside the EU that would lead to the potential presence of the Asian lineage H5N1 HPAIV in wild birds outside the EU. The exposure of wild birds to the Asian lineage H5N1 HPAIV – directly or indirectly – outside the EU is considered. Exposure is affected by:

- the occurrence of Asian lineage H5N1 HPAIV in domestic poultry,
- the transmission of the Asian lineage H5N1 HPAIV from domestic poultry to wild birds,
- the transmission of the Asian lineage H5N1 HPAIV among wild birds,

- the survival of the Asian lineage H5N1 HPAIV in the environment
- the survival of infected wild birds.
- the ability of infected wild birds to migrate and
- the re-transmission of HPAIV from migratory wild birds to poultry (or from migratory wild birds to sedentary/resident wild birds and then to poultry)

The release assessment further considers the location, population structures, behaviour and flyways of wild birds as indicated in Figure 2-1, which would enable “release”, i.e. entry of the virus into the EU.

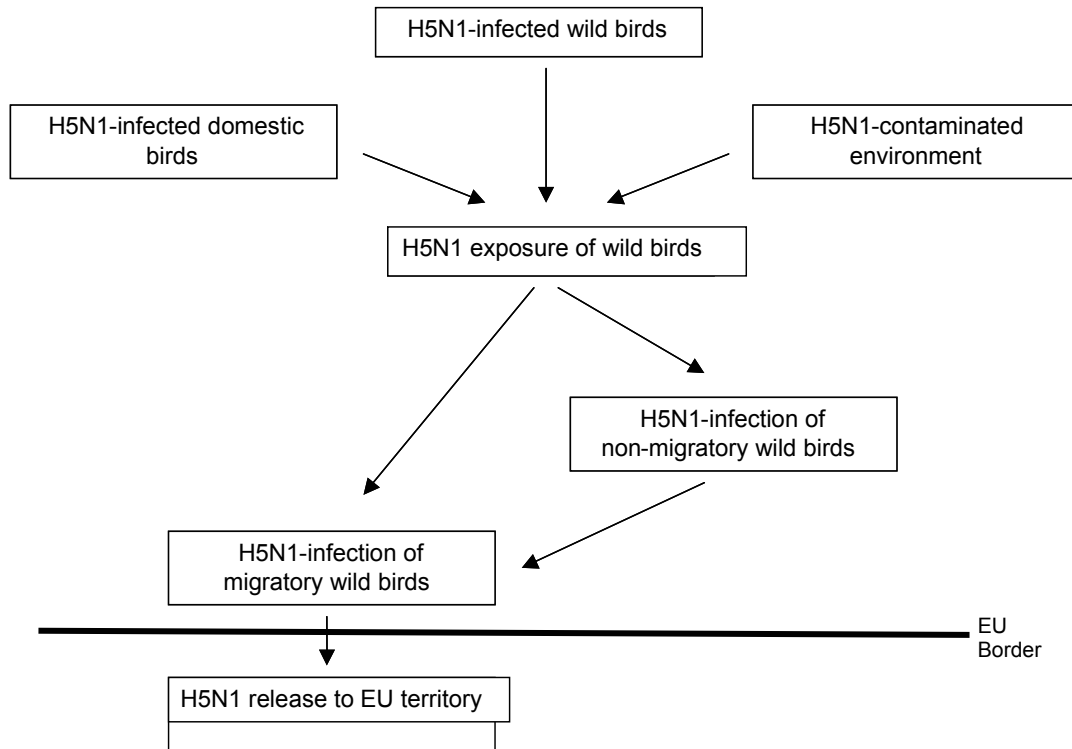


Figure 2-1: Release pathways of Asian lineage H5N1 HPAIV in territories outside the EU that may result in potential transmission of the virus leading to a release into EU territory (note that these pathways describe the potential mechanisms for release)

2.2. Risk Question 2 - Exposure and Consequence Assessment

Given release (i.e. entry to the EU) of Asian lineage H5N1 HPAIV Asian H5N1 virus, what is the probability of exposure and infection for:

- wild birds within the EU and the infection subsequently becoming endemic in wild bird populations?
- domestic poultry within the EU as a consequence of infection in migratory birds (Question 1) or wild birds resident within the EU (Question 2a)?

Exposure pathways within the EU

Figure 2-2 describes the potential direct and indirect exposure pathways of the Asian lineage H5N1 HPAIV virus assuming release of the virus by wild birds into the EU territory. The pathways cover both the exposure after establishment of the Asian lineage H5N1 HPAIV virus within the residential wild bird population (Risk question 2a) as well as the exposure pathways from any species of wild bird to domestic bird populations (Risk question 2b).

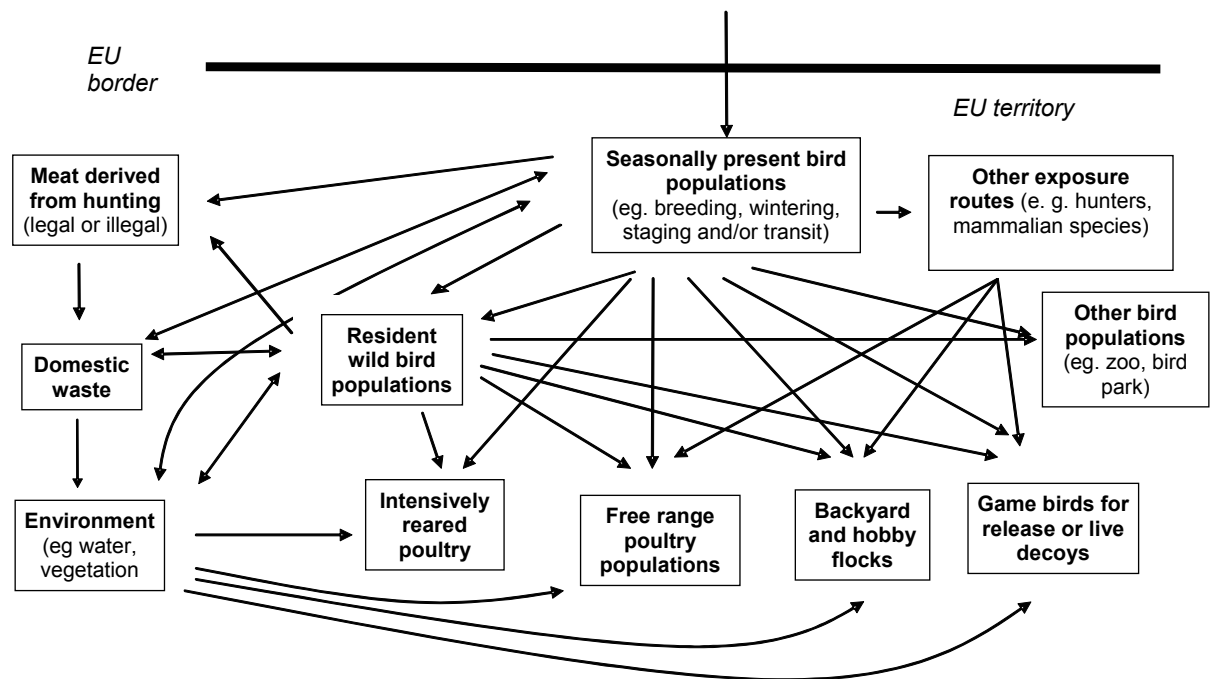


Figure 2-2: Exposure and consequence pathways for bird populations within the EU to Asian lineage H5N1 HPAIV after potential introduction of the virus by wild birds (note that these pathways include all potential direct and indirect exposure and transmission pathways)

As can be seen from Figure 2-2 the exposure routes are numerous and complex.

Infection and the potential for endemicity within the EU

Given exposure, infection and the potential for endemicity will depend upon a number of factors in particular species and host susceptibility and dose to which a bird is exposed.

3. Pathogenesis in Wild Birds

3.1. Pathogenicity, Epidemiology and natural history of Asian lineage H5N1 HPAIV

Based on the limited number of transmission experiments reported in the peer-review scientific literature, apart from zebra finches, acute or peracute clinical disease does not seem to occur amongst the bird species assessed. Pigeons and gulls were found to show no or only very limited disease, although recent newly reported cases in pigeons suggest they are not fully resistant to disease. Mallards showed mild disease or neurological symptoms, and were subject to low to high mortality.

3.2. Excretion Route, Dose and Period in wild birds

Excretion of virus in ducks occurs via the respiratory and the intestinal tract, but virus concentrations may be higher in the respiratory tract.

Excretion of Asian lineage H5N1 HPAIV as measured in experimentally inoculated mallards did not exceed $10^{6.0}$ EID₅₀.

The amount of virus excreted and the duration of excretion are reduced for strains which exhibit low pathogenicity in ducks. Little information is available for other species but some species have been shown to excrete virus at much lower levels than those recorded for ducks.

Duration and magnitude of excretion varied according to the viral pathotype. Viruses expressing high pathogenicity in mallards were excreted for up to 17 days, whereas those of low pathogenicity ceased to be excreted between days 7 to 10 after infection.

3.3. Survival and mobility of wild birds following Infection

The epidemiological data from the EU over the last 3 months indicates the presence of virus in some wild bird species without occurrence of infection in local poultry populations. There is an increasing body of evidence showing that HP H5N1 virus can be carried without clinical signs by several species of wild birds (ducks, sparrows, swans, etc). Consequently, it is likely that the virus could be carried over long distances by wild birds (especially migratory birds).

3.4. Pathogenesis of Asian Lineage H5N1 HPAIV in EU-resident Wild Birds

Conclusions

The pathogenesis and the resulting clinical signs of an H5N1 HPAIV of Asian lineage are heavily influenced by viral strain characteristics and host species conditions. Thus, no uniform pathogenesis pattern can be specified. Taking into consideration that H5N1 HPAI viruses of Asian lineage have been shown to constantly evolve in terms of antigenic properties and pathogenicity, the properties of descendants of such viruses may be encountered within the range defined by both extremes, ie. peracute death and/or neurological signs and asymptomatic infections.

Recommendation

Field and experimental studies are needed to describe the pathogenesis following H5N1 infection in a range of wild bird species referred to in Table 12.1 since all studies to date have involved domestic birds. These studies should particularly investigate viral shedding periods in situations where birds are not lethally infected.

3.5. Epidemiological Data on Asian Lineage H5N1 HPAI Outbreaks in Poultry

3.5.1. Risk factors for infection of poultry

Domestic waterfowl, specific farming practices and agro-ecological environments as well as trade practices have been identified to play a key role in the occurrence, maintenance and spread of Asian lineage H5N1 HPAI.

Several reports in relation to HPAI infected South-East Asian countries have indicated that husbandry and marketing related risk factors are implicated in the initiation of transmission and circulation of infection in domestic poultry farms in the region. These risk factors are outlined and summarized in Table 3-1. The movement of birds between holdings is a risk factor associated with trade that is commonly ranked high for all sectors of poultry farms whereas the importance of husbandry risk factors varies between farm sector types.

Table 3-1 Trade and husbandry-related risk factors associated with the occurrence of HPAI H5N1 outbreaks in Vietnam and Thailand

Trade related

Sale of poultry at live bird markets
Major cultural festivals with peak sale / consumption
Pre-marketing health checks
Movement of poultry between holdings
Movement of poultry across administrative borders
The return to the holding of origin of birds that were brought to the markets for sale

Husbandry related

Farming of multiple species within one farm unit
Movement of fomites into the poultry holdings, allowing poultry access to ponds, lakes and rice fields.
Keeping poultry over or near ponds and rice fields
Birds entering homes where other birds are housed as pets
Use of untreated chicken faeces as fertilizers or livestock feed
Lack of adoption of an "all in – all out" husbandry system
Use of untreated water for human and animal consumption
Disposal of dying and dead birds

Sources: (Rushton, Viscarra et al. 2004; Veterinaires Sans Frontieres 2004; Martin, Sims et al. 2006).

3.5.2. Poultry production sectors and biosecurity

Experience from production systems particularly in South-East and East Asia indicates that small commercial farms and flocks belonging to smallholders are more likely to be exposed to infection than large commercial farms. Quantitatively, more outbreaks occur in smaller holdings although, for a number of the infected countries, more poultry are raised in large farms. In Thailand, for example, a study of confirmed cases of infection in July to September 2004 demonstrated that 64% of infected farms/premises or holdings contained 1000 or less poultry.

Within infected countries, the disease appears to have spared many areas of high poultry population density.

3.5.3. Increases in poultry populations

FAO livestock statistics demonstrate the marked increase in the number of poultry being raised in Asia over the past 7 years. In some countries, smallholders have markedly increased the size of their flocks in response to market demand but have not concurrently increased biosecurity levels to match this investment. In addition there has been little or no government intervention to ensure that biosecurity was implemented. This factor probably played a role in the emergence of H5N1 HPAI in Asia.

3.5.4. The role of waterfowl

Domestic waterfowl are believed to have played a key role in the genesis of the 2003-2005 epidemics.

However, the response of domestic ducks to infection with H5N1 viruses is variable. Some viruses cause serious disease, with ducks displaying neurological signs while others remain clinically silent despite dissemination to muscle tissue and the central nervous system. Reasons for this variation are the subject of on-going research.

3.5.5. Exposure and infection at live bird markets

"AI virus transmission was possible and occurred through movements of live and dead birds, contaminated equipment and vehicles, contaminated eggs, feed, water, insect vectors, and human vectors. In fact, any fomite that had contact with contaminated manure was capable of transmitting the virus. It was remarkably easy to isolate AI virus anywhere or from any inanimate object associated with an infected poultry flock".

3.5.6. Host susceptibility: Wild bird species

The main hosts of avian influenza viruses that have been demonstrated to date are *Anseriformes* (ducks, geese) but other orders have also been found to be infected including *Charadriiformes* (shorebirds such as plovers, turnstones, sandpipers and gulls),

3.5.7. The effect of surveillance and control measures

Other factors affecting the detection of disease and therefore the perception of disease patterns in the region include the quality of disease reporting surveillance systems and the effect of specific control measures introduced in infected places, including the use of vaccination.

3.5.8. Patterns of spread recorded up to date under molecular epidemiology of H5N1 infections

Since 2001, H5N1 viruses have continued to circulate in mainland China. H5N1 viruses were isolated exclusively from aquatic poultry during 2000 but from 2001 onwards they were isolated from both domestic waterfowl and other poultry species, with the highest rate of isolation from ducks. Seasonal patterns were observed, peaking from October to March, when the mean temperature is below 20°C and the relative humidity is high. This is in agreement with the fact that the survival and viability of influenza A virus increases at lower environmental temperatures.

The reported patterns of disease spread have differed significantly among infected countries in Asia. These variations are likely to reflect differences in the poultry production sectors in each country, the extent of infection at the time when disease was first reported and the density of poultry in infected areas. One common feature observed has been the rapid spread and geographical extension of outbreaks that have now left their original epicentre of infection in South-East and East Asia, to spread across Asia to Europe and Africa.

In the newly infected countries, the disease usually was initially detected in domestic poultry flocks, mainly small scale farming units, but was also reported in wild birds in several countries.

3.5.9. Molecular epidemiology of H5N1 in Asia

Genetic analysis of isolates from Mongolia (July, 2005) show a close genetic relationship with wild bird isolates from Qinghai Lake outbreak (April/May, 2005). Genetic sequences from virus isolates obtained from 2005 wild bird outbreaks in Kazakhstan, Russia, Turkey, Romania and several Western Europe countries have also established a relationship with the virus strain isolated in China around the Qinghai Lake.

Genetic characterisation of isolates from southeast China, Vietnam, Thailand and Indonesia has shown that H5N1 viruses have been introduced to different South-East Asian regions from southern China between 2001 and 2005. This

study also highlights the fact that the highest diversity of HPAI H5N1 viruses is seen in southern China which supports the “influenza epicentre” hypothesis. In addition to that Chen et al (2006) have shown that there has been an establishment of regional virus sub-lineages. This suggests that the epidemiological perpetuation of infection in domestic poultry sectors is more likely to be due to continuous regional movements of live poultry.

3.5.10. Evidence of transmission from poultry to wild birds and from wild birds to poultry

The events observed recently in many Western Europe countries indicate that H5N1 virus was introduced through wild birds to previously non-infected countries or areas. In two cases, poultry flock in Turkey and ducks and pheasants in Sweden, the occurrence of infection were in wild birds followed by infection of domestic poultry flocks.

Without taking into consideration other factors such as trade of live birds of the cases that occurred in the world (and particularly from the EU) over the last months can be assumed to be the result of primary introduction of the virus by wild birds. And if the infection was not detected early and if the domestic flocks were not well protected by appropriate biosecurity measures, the virus could spill over to domestic flocks; and then further transmission is likely to occur to other domestic flocks and local or migratory wild birds.

Across many parts of Asia and Europe there is significant opportunity for wild birds to share environments with domestic waterfowl, especially where the latter are allowed to graze or are raised on ponds. Evidence from South-East Asia suggests that at this interface it is possible for H5N1 HPAI viruses to cycles back and forth between wild birds and domestic waterfowl, without clinical disease necessarily being detectable.

3.6. Geographic Distribution of HPAI H5N1 Infection in Wild Bird Populations

Conclusions

Over the previous months (2005 - March 2006), several countries in the EU identified presence of AI virus in dead wild birds without infection having been found in domestic poultry. In two countries, infection in wild birds (predominately in wild ducks, geese, swans and prey birds) was followed by infection by the same Asian Lineage HPAI H5N1 in domestic poultry. The succession of the two events suggests a likely causal effect.

There are non-EU countries in Europe that apply the same or equivalent rules for which information is available and to a lesser extent from those countries that are at least influenced by EU strategies. In case of outbreaks in poultry flocks occurring in these regions, epidemiological data is often insufficient to allow inferences about the likely causes of these outbreaks.

Recommendations

There is a need for enhanced active and passive AI surveillance for wild birds particularly in regions of high risk for EU considering the flyways of migratory birds, such as Africa. Outbreaks in wild bird populations need to be accompanied by epidemiological investigations that will lead to a better understanding of the factors allowing the persistence of the virus in the wild fauna. Whenever possible

outbreaks in domestic flocks should be followed up by epidemiological investigations aimed at identifying the causes.

4. Characterization of Regional Poultry Husbandry and Production Systems outside the EU

4.1. Trade of poultry in small-scale poultry production systems

Conclusions

Information about the structure of poultry farming systems outside the EU is often insufficient to allow conclusions about the relationship with infection dynamics.

Recommendation

The poultry husbandry and production systems need to be described in geographical regions around the world which have the potential to become a source of AI infection for the EU.

Establish a wild bird and a farmed poultry census based on GIS (Geographical Information System) to quickly identify the locations of poultry holdings and typical waterfowl refuges (wetlands).

5. Environmental Stability of Asian Lineage H5N1 HPAI Virus

Conclusions

The environmental stability of influenza viruses has been investigated in only a few scientific studies. A number of reports have quasi-anecdotal characteristics and are difficult to verify. Particular interest has focussed on the retention of infectivity in surface waters and poultry products. The results of the small number of studies are difficult to compare since different strains and subtypes in different environmental conditions have been examined with various detection methods.

Virus survival is greatest in moist faeces, significant in water especially if it is cold and little survival occurs in dry and sunny conditions.

It is not clear whether aerosol transmission of influenza viruses represents an important transmission mode in poultry and in wild birds. However, given that the physical and chemical composition of avian and human influenza virus particles is comparable, aerosol transmission between birds should be considered a possibility. Since Asian lineage H5N1 HPAI viruses have been reported to replicate to higher titres in trachea than in the intestinal tract of experimentally infected birds and their contacts, aerosol transmission may be particularly relevant for this virus lineage.

Recommendations

Surveillance studies should include systematic sampling of environmental surfaces and water in areas and premises with a prior history of Asian lineage HNP AI H5N1 outbreaks.

Recommendations for future research

Experimental research should be promoted in order to assess the viability of AIV in tropical and in salt-water environments. The latter is important given the number of waterbirds that occur in salt or brackish waters

Research is required on virus survival in carcasses.

More data are required in relation to the survival of Asian lineage HNPAAI H5N1 viruses under environmental conditions and compare these data with other related influenza viruses.

Experimentally validated diagnostic tools need to be developed for detecting the virus in water in order to obtain indicators of the presence of the virus in naturally infected areas.

Experimental studies are needed to determine the distance necessary for airborne transmission of the virus between individual birds and between poultry farms.

Virus survival in carcasses has been demonstrated, but the consequences of such persistence of virus linked to predators and other wild fauna should be investigated and if possible monitored.

6. Diagnostic Methods for the Detection of Asian H5N1 HPAI Virus in Wild Bird Populations

Recommendations

Because serological methods cannot distinguish between HP and LP strains and antibody findings do not allow inferences in relation to the likely location where wild birds might have become infected, serological surveillance of wild birds for H5N1 HPAI cannot be recommended.

It is recommended to set up a global laboratory network to complement the diagnostic support currently provided by internationally recognized laboratories such as Weybridge (EU) and Padova (OIE).

Proper precautions should be taken for people collecting samples that may potentially contain zoonotic pathogens.

6.1. Harmonised Testing Strategy for EU

Conclusions

Although many wild bird species may harbour influenza viruses, birds of wetlands and aquatic environments such as *Anseriformes* (particularly ducks, geese, and swans) and *Charadriiformes* (particularly gulls, terns, and waders) constitute the major natural virus reservoir.

Systems of sampling and specimen processing critically affect the outcome of laboratory tests.

Screening by the use of RT-PCR that targets the matrix gene is an effective methodology that is highly sensitive and should be supported by attempted isolation of virus from PCR positive specimens to provide virus for further characterisation where possible.

Not all molecular diagnostics methodologies are fully harmonized but are the subject of current evaluation.

Recommendations

Harmonised sampling and testing protocols for an EU wide programme would be beneficial.

Diagnostic methods should examine materials collected from both live and dead birds.

The relative specificity and sensitivity of the diagnostic methods should be determined.

Development of rapid and sensitive screening assays that minimise the need for a cold-chain will be advantageous.

Serological surveillance of wild birds for H5N1 HPAI is not recommended.

Outbreaks of HPAI H5N1 in poultry and domestic waterfowl should routinely trigger surveillance in local populations of wild (water) birds. Information from such surveillance is essential for defining routes of infection.

Long-term surveillance for AIVs should especially include strategically important mixing areas (e.g. International Waddensea, Gulf of Sivash, etc.)

There is an urgent need to develop AI surveillance field skills in many countries – particularly in relation to the techniques used for the trapping and sampling of waterbirds. These skills may be enhanced by the development of specific training courses and programmes by existing centres of expertise,.

Any bioassay for pathogenicity involving live birds should minimise suffering by killing birds at the earliest time after the scientific objective has been achieved, e.g. clinical signs of severe disease, rather than allowing the birds to die naturally (OECD 2000).¹

Where available, historic material should be tested to investigate possible previous introduction of HPAI viruses.

Studies should be undertaken to establish the validity of the molecular signature that discriminates HP/LP AIV with a view to using this to replace the current bioassay.

7. Migratory Birds: Evaluating and Assessing Species at Higher Risk of H5N1 Infection

7.1. General Overview of Bird Migration Systems and Concepts

Conclusions

There are many different types of bird movement and evaluation of risk needs to differentiate between these. The main types of movement are summarised in Table 7-1.

¹ OECD (2000) Guidance document on the recognition assessment of use of clinical signs as humane endpoints for experimental animals used in Safety evaluation. Monograph 19. <http://www.oecd.org/ehs/test/mono19.pdf>

Table 7–1: Definition of different types of bird migration

Type of migration	Explanation
Seasonal migration	For northern hemisphere birds, this is (generally) migration from breeding areas to more southerly non-breeding (wintering) areas. Timing of migration varies between seasons but commences at the end of the breeding period in late summer or autumn. Return, northwards, migration to breeding areas occurs in the spring.
Post-breeding dispersal	Typically non-directional movement away from breeding areas by young birds born that year.
Irruption	Major population movements, typically of species breeding in north temperate areas.
Reverse migration	Situations where birds 'back-track' along migration routes as a consequence of unexpectedly severe climatic conditions.
Cold weather movements	Movements, often of significant numbers of birds away from areas experiencing extreme, severe winter weather in search of milder conditions (e.g. Ridgill & Fox 1990).
'Rains' migration	Movements of tropical birds in arid or semi-arid zones in response to the onset of wide-scale rains and thus the creation of suitable temporary wetland habitats.
Moult migration	The movement of birds prior to moult to secure locations, often at high latitudes or altitudes, where the birds are less at risk from predators when they are flightless (Salomonsen 1968).
Abmigration	The transfer of a bird from one flyway to another, typically as a result of males pairing, on shared wintering grounds, with a philopatric female from another flyway system.
Loop-migration	Where some species use different routes on during spring and autumn seasonal migrations. Typically such different routes are determined by seasonal availability of habitats on certain areas.

Migration strategies of longer distance migrant bird species vary according to the frequency and duration of stop-overs at staging areas.

In summary, there are a wide variety of migration strategies between and even within different bird species. Migration routes can thus vary:

- by species (and by population within species) and the extent of migratory path can vary, both by:
 - total length of flight-path
 - number and duration of stops along flight-path ('hop, skip and jump' strategies)
- by age of individual;
- by sex of individual;
- by individual;
- by season; and
- with weather.

7.1.1. Factors which influence waterbird migration and numbers

Conclusions

Periods of prolonged cold weather can significantly alter numbers of waterbirds in their wintering area. The onset of frozen conditions can trigger significant population movements by some species as they disperse in search of milder, more favourable conditions. Such events (particularly to the cold winter in 2005-2006) were very likely at the origin of the introduction of HP H5N1 virus to some EU countries by wild birds moving from the eastern parts of Europe.

Periods of extreme dry weather can also cause significant movements of waterbirds and thus changes in numbers at key sites.

Considerable information exists on waterbird populations, but the amount of available data is poorly organised to carry out an adequate risk assessment and possible analysis by risk managers and others.

As well as seasonal migration, waterbirds can exhibit movements at other times of the year in response to extreme weather conditions, notably periods of prolonged cold weather in mid-winter. In these conditions, waterbirds may move considerable distances to seek milder weather conditions.

Recommendations

There is an urgent need for systematic analysis of data on waterbird ringing recoveries so as to allow a better assessment of the contemporary distributional limits of biogeographical populations and their migratory movements. This work should be encouraged on a co-operative, international basis, and integrated with reviews of waterbird survey and census information. The development of further flyway atlases should be a priority, and consideration should be given as to how new web-based technologies can be used to integrate and disseminate information, both about population movements as well as on the locations and importance of key sites. More interactive, GIS-based systems, internationally accessible through the internet might prove to be easier and more cost-effective to keep up-to-date in the light of developing knowledge about waterbird populations.

Synthesised maps for shorebird flyways exist, although these are widely misinterpreted as applying to other waterbird taxa. There is an urgent need for maps with synthesised information on the migration systems of other waterbird groups.

There is a need to improve the methods to investigate and assess movement patterns of wild birds.

There is a need for international synthesis of information concerning migration phenology, for example identifying which species arrive in which country in which month. Although much (scattered) national information exists, this is hardly collated internationally other than for a few species. Such information has considerable policy relevance in terms of identifying high risk periods.

7.2. Evaluating Species more likely to be infected with HPAI H5N1 - Potential Exposure Paths

Conclusions

In the draft report species more likely to be infected were evaluated and with special attention on European *Anseriformes* and *Charadriiformes*, a selection was made of those that are migratory (see Table 9.1).

Recommendation

Other bird species which may not currently be exposed or become infected (e.g. insectivores and no contact with faeces of other birds, sea birds and others birds) but are particularly relevant because of their significant impact in relation to migration from Africa (e.g. swallows) will have to be considered.

Recommendations for further research

All the assessments presented here, are tempered by the following key information needs, identified by the Scientific Task Force on Avian Influenza convened in late August 2005 by the Convention on Migratory Species. They

were subsequently highlighted again as central information needs by the third Meeting of Parties of the African-Eurasian Agreement on the conservation of migratory waterbirds (Resolution 3.18²; October 2005):

- "clarifying virus behaviour:
 - in different waterbird populations (especially viral incubation periods, the infectious period in birds and the symptoms affecting individual wild birds), as well as determining their survival rates; and
 - in the aquatic habitats which are waterbird breeding, staging and non-breeding (wintering) areas;
- establishing informed assessment of the possibility of transmission from wild populations to domestic flocks, including by non-waterbird species found near poultry-keeping areas;
- clarifying prevalence of HPAI in wild bird populations;
- identifying the nature of migration routes and timings for key migratory waterbirds so as to expand and/or refine existing ecological monitoring of these populations;
- developing a combined risk assessment based on the known behaviour of the virus, risks of transmission, routes and timing of migratory species, as well as known poultry husbandry techniques;
- Assessments of risk depend to a large extent on expert judgement; with much critical data and information on the processes of transmission of HPAI H5N1 by wild birds being either weak or entirely lacking.

8. Surveillance of Wild Birds outside EU regarding Infection with the Asian Lineage H5N1 HPAIV

Conclusions

Long-term influenza virus surveillance studies outside the EU territory are still sparse. Information based on the small number of reported studies indicates that different families of wetland birds may carry influenza viruses.

Recommendations

Considering the scarce information currently available from surveillance schemes in wild bird populations outside the EU territory the following recommendations may apply:

- There is a need for rapid publication and exchange of information derived from surveillance systems that are currently in place. A web-based clearing house on information derived from surveillance programmes should be set up.
- Waders in the *Charadriidae* and *Scolopacidae* families should be included in influenza virus surveillance studies.
- The HPAI field surveillance in infected areas (such as Africa) has to be strengthened.
- To build and maintain an efficient network of laboratory support for AI diagnosis in countries outside the EU.

² web-link

9. Identification of Species currently more likely to be infected by HPAI H5N1

The biological role of pigs and carnivores such as dogs and cats in the epidemiology of Asian lineage H5N1 is not currently understood.

A preliminary list of European bird species that live in proximity to domestic poultry and which are more likely to expose domestic poultry to HPAI H5N1 if asymptotically infected wild birds are present is presented in Table 9.1 below:

Table 9-1. Preliminary list of European bird species that live in proximity to domestic poultry

Common name	Scientific name	Risk of contact with poultry	EU or international population size
1. Species intimately associated with poultry production in Europe			
Domestic Goose	<i>Anser anser domesticus</i>	High	
Domestic Mallard	<i>Anas platyrhynchos</i>	High	
Domestic Muscovy Duck	<i>Cairina moschata</i>	High	
Feral Pigeon	<i>Columba livia</i>	High	
House Sparrow	<i>Passer domesticus</i>	High	
2. Species which may share farmland also used by domesticated poultry in north Europe			
Eurasian Golden Plover	<i>Pluvialis apricaria</i>	Low	
Northern Lapwing	<i>Vanellus vanellus</i>	Medium	
Black-headed Gull	<i>Larus ridibundus</i>	High	
Common Gull	<i>Larus canus</i>	High	
Herring Gull	<i>Larus argentatus</i>	Low	
Wood Pigeon	<i>Columba palumbus</i>	High	
Eurasian Collared Dove	<i>Streptopelia decaocto</i>	High	
Ring-necked Pheasant	<i>Phasianus colchicus</i>	High	
Larks	<i>Alaura</i> <i>Galerida</i>	Medium	
Pipits		Medium	
Wagtails		Medium	
Fieldfare	<i>Turdus pilaris</i>	High	
Redwing	<i>Turdus iliacus</i>	High	
Song Thrush	<i>Turdus philomilos</i>	Medium	
Black-billed Magpie	<i>Pica pica</i>	High	
Eurasian Jackdaw	<i>Corvus monedula</i>	High	
Rook	<i>Corvus frugilegus</i>	Medium	
Carrion Crow	<i>Corvus corone</i>	Medium	
Raven	<i>Corvus corax</i>	Low	
Starling	<i>Sturnus vulgaris</i>	High	
Spotlees starling	<i>Sturnus unicolor</i>	High	
House Sparrow	<i>Passer domesticus</i>	High	
Eurasian Tree Sparrow	<i>Passer montanus</i>	High	
Finches	<i>Fringilla</i> <i>Carduelis</i>	Medium	
Buntings	<i>Miliaria</i> <i>Emberiza</i>	Medium	

Common name	Scientific name	Risk of contact with poultry	EU or international population size
3. Some wild waterbirds which may share wetlands also used by domesticated waterbirds			
Egrets	<i>Egretta spp.</i>	Low	
Hérons	<i>Ardea and other spp.</i>	Medium	
Storks	<i>Ciconia spp.</i>	Low	
Mute Swan	<i>Cygnus olor</i>	Medium	
Greylag Goose	<i>Anser anser</i>	Medium	
Ducks	<i>Anas & Aythya spp. especially</i>	Low	
Common Coot	<i>Fulica atra</i>	Medium	
Moorhen	<i>Gallinula chloropus</i>	Medium	

Wild birds that utilise habitats shared with domestic poultry have the potential to act as bridge species for the transmission of virus between migratory wild birds and domestic poultry, by virtue of their close contact with domestic poultry or indirectly via shared water and soil. At present, it is not clear whether bridge species have been the mechanism of virus transmission to domestic poultry, although mortality has been recorded in some species of resident wild birds in association with several outbreaks of HPAI H5N1 in domestic poultry. Neither is it clear whether, if it occurs, such transmission of virus would be via shedding of the virus from infected birds or by mechanical means.

Non-avian bridge species e.g. cat, fox, rat, dogs and mustelids may act at least as mechanical vectors, but it is no known whether they can also transmit by other mechanisms. There is evidence that some mammal species may show a positive response to H5N1 serological testing. However, those were not considered in the draft report.

9.1. Factors influencing the Spread and Maintenance of HPAI H5N1 in Europe

Conclusions

The recent cases observed in wild birds in most of the countries in the EU show that some species of wild birds (mainly waterfowl such as ducks, swans) are definitely carrying HP H5N1. These wild birds are considered to be responsible for the introduction of the virus in the EU. Infected wild bird populations are present in some geographical areas in several EU countries, but it is not understood which factors contribute to the maintenance or disappearance of infection in wetlands. The possibility that HPAIV had been introduced during previous years cannot be excluded.

Recommendations

Targeted surveillance of wild birds in the vicinity of outbreaks of avian influenza should be used to establish the infection status of wild birds, as well as the species concerned.

If outbreaks are occurring outside the EU it is essential to carry out epidemiological investigations to identify the origin of infection, such that the relative importance of wild birds in the spread of the infection can be determined in comparison with other factors such as movement of live domesticated birds, fomites etc.

It is highly desirable that field studies are conducted to develop practical interventions which will lead to reduced risk of contact between wild waterbirds and domestic poultry. It is important to also consider methods which are suitable for use in developing countries (village poultry situations).

Field studies should be urgently undertaken on the behaviour of resident bird species (e.g. crows, pigeons, etc.) that associate with man and may act as a bridge between waterbirds and poultry - with the aim of developing practical interventions that lead to reduced risk of contact and transmission.

Studies should be urgently undertaken, in particular on some of the species of asymptomatic wild birds that currently seem to be the most important in this regard, so that experimental data can confirm or rule out the role of each individual species as virus carriers over long distances, and what the duration of the excretion of the virus is.

10. Surveillance of Wild Birds within EU regarding Infection with the Asian Lineage H5N1 HPAIV

Conclusions

Current attempts at risk assessment suffer from a lack of quantitative information on bird migration and on the interaction amongst wild birds either infected or non-infected with Asian lineage HPAI H5N1.

The following can currently be concluded about the role of wild birds in the introduction of Asian lineage HPAI H5N1 from South East Asia, into Central Asia and Europe:

- Through passive surveillance the Asian lineage HPAI H5N1 virus has been found in wild bird populations in regions where poultry populations are free from infections.
- Up until now, active surveillance in wild birds in the EU Member States has not resulted in the detection of Asian lineage HPAI H5N1 virus. Nevertheless, very recent preliminary data from Poland show that in a flock of swans (*Cygnus olor*) in which HPAI H5N1 virus infected dead swans had been detected a few days earlier, the virus was then also isolated from healthy swans (personal communication Commission/chief veterinary officer Poland).
- Recent passive surveillance undertaken in the EU has led to the discovery of infected dead birds over recent months in several geographical areas in EU countries.
- To date, infection with Asian lineage HPAI H5N1 virus in cats and dogs and mustelids (stone marten and mink) has only been detected in areas where the presence of the virus has been demonstrated in wild birds.

Recommendations

A formal European network for wild bird surveillance should be established to facilitate data collection across member states, enhancement of data analysis for mapping migratory pathways and to provide a structured uniform programme of targeted surveillance of wild bird populations. Such a programme should also create a web-based system to act as a means of rapid dissemination of surveillance results.

A standardised pro-forma for the reporting of surveillance data, which provides information also on type of surveillance, species identification and sampling strategy should be developed as a matter of urgency.

Reservoir hosts for Asian lineage H5N1 HPAI should be determined through surveillance programmes to be conducted in a broad species range informed by migratory data linked to information on current spread of the virus. There is a need to identify the duration of persistence of the AI virus in the wild fauna, and particularly in species with the highest risk of transmission of the virus to domestic poultry in the EU infected areas.

To assess the risk posed by migratory birds in transporting HPAI, it is necessary to assess and monitor occurrence of AI in key species at strategic migratory sites and at different times during the migration and breeding cycles of the respective species. In this context, a strategic approach to surveillance that targets key wetlands where migratory flyways intersect, as well as major spring and autumn staging areas, is essential.

Cumulative bird ringing recovery data need to be analysed to estimate the importance of the connection between Asian, African and European bird populations and improve methods to determine wild birds movements.

A significant proportion of the results of AIV surveillance, both in the EU and elsewhere do not identify the bird species involved (e.g. “ducks”, “pigeons”, “sparrows”, etc.). To maximize the value of AIV surveillance, it is essential that data always be collected and reported on the species of birds involved. To avoid ambiguity, reporting of such information should always: i) involve the use of Latin species names; and ii) use a standardised taxonomic reference. In this respect the use of the taxonomy of Sibley and Monroe (1990, with corrections of 1993) is recommended.

Accumulation and evaluation of data from across Europe and the world are necessary to develop a better understanding of the factors associated with the persistence of the virus in wild birds, environment and wild fauna in the present infected areas in EU.

The development of national capacity to develop and implement field programmes for AIV surveillance should be assisted through the development of national and international training courses and programmes.

11. Risk Assessment for Risk Question 1: Release Assessment

What is the probability of introduction of HPAI virus (specifically the Asian lineage H5N1 HPAIV) to the territory of the European Union by migratory wild birds?

Risk Question 1 includes issues related to pathogenesis, resistance, epidemiology and dynamics of Asian lineage H5N1 HPAIV in wild birds outside the EU that would lead to potential presence of the Asian lineage H5N1 HPAIV in wild birds entering the EU. The exposure and infection of wild birds to the Asian lineage H5N1 HPAIV – directly or indirectly – outside the EU is considered.

11.1. Probability that uninfected wild birds in a region in which Asian lineage H5N1 HPAIV is present are exposed to, and infected by that virus

11.1.1. Given the presence of avian lineage H5N1 HPAIV in a region, the probability that infection is already present in wild birds within that region

The probability of infection of at least some wild birds in specific populations following exposure to Asian lineage H5N1 HPAIV must be considered **high** in other wild birds and **very high** in *Anseriformes* and *Charadriiformes*. Many *Anseriformes* and *Charadriiformes* are migratory.

11.2. Probability that wild birds infected with the Asian lineage H5N1 HPAIV reach mixing or concentration areas outside the EU

Based on the data available for this analysis, the probability of birds with asymptomatic infection reaching mixing and concentration areas after infection with Asian lineage H5N1 HPAIV will depend on the species and range from **low to high**. This assumption is most likely to be true for birds of the orders *Anseriformes* and *Charadriiformes*, and particularly if the distances to be covered are short.

11.3. Probability of transmission at mixing or concentration areas

Under the assumption that birds carrying the Asian lineage H5N1 HPAIV arrive at a mixing or concentration area, the probability of transmission to other wild birds is assessed to be **very high** where there is high density of birds.

11.4. Probability of detection in wild birds outside the EU given infection

The probability of detection of Asian lineage H5N1 HPAIV in wild birds at mixing and concentration areas is dependent on the extent of passive and active surveillance implemented and currently is considered **low** outside of the EU.

11.5. Total probability of entry to the EU of wild migratory birds with Asian lineage H5N1 HPAIV

Conclusions

The probability of migratory birds becoming infected with Asian lineage H5N1 HPAIV and releasing the virus can vary from **low to high** depending on the species which are infected. Table 11.1 shows the preliminary list of bird species with higher probability to be exposed to Asian lineage H5N1 HPAIV during migration outside the European Union. However, the uncertainty associated with these risks can differ greatly due to the lack of data about species carrying the virus, whether asymptomatic or not, the prevalence of the infection in the wild birds, the effectiveness of the passive and active surveillance systems in countries outside Europe.

Table 11.1. Preliminary list of bird species with higher probability to be exposed to Asian lineage H5N1 HPAIV during migration outside the European Union due to their susceptibility and behaviour (gregariousness and mixing) and habitat use

Common name	Scientific name
Swans	

Common name	Scientific name
Bewick's Swan	<i>Cygnus columbianus</i>
Mute Swan	<i>Cygnus olor</i>
Geese	
Pink-footed Goose	<i>Anser brachyrhynchus</i>
Bean Goose	<i>Anser fabalis</i>
Greater White-fronted Goose (European race)	<i>Anser albifrons albifrons</i>
Lesser White-fronted Goose	<i>Anser erythropus</i>
Greylag Goose	<i>Anser anser</i>
Barnacle Goose	<i>Branta leucopsis</i>
Brent Goose	<i>Branta bernicla</i>
Red-breasted Goose	<i>Branta ruficollis</i>
Canada Goose	<i>Branta canadensis</i>
Ducks	
Eurasian Wigeon	<i>Anas penelope</i>
Common Teal	<i>Anas crecca</i>
Mallard	<i>Anas platyrhynchos</i>
Northern Pintail	<i>Anas acuta</i>
Garganey	<i>Anas querquedula</i>
Northern Shoveler	<i>Anas clypeata</i>
Marbled Teal	<i>Marmaronetta angustirostris</i>
Red-crested Pochard	<i>Netta rufina</i>
Common Pochard	<i>Aythya ferina</i>
Tufted Duck	<i>Aythya fuligula</i>
Waders	
Northern Lapwing	<i>Vanellus vanellus</i>
Eurasian Golden Plover	<i>Pluvialis apricaria</i>
Black-tailed Godwit	<i>Limosa limosa</i>
Ruff	<i>Philomachus pugnax</i>
Gulls	
Black-headed Gull	<i>Larus ridibundus</i>
Common Gull	<i>Larus canus</i>

Recommendations to reduce the probability of viable Asian lineage H5N1 HPAIV entering the EU

In countries outside the EU where the infection may originate from the following measures are recommended:

- Local poultry keepers need to be educated in relation to the need of establishing a minimum set of biosecurity measures to minimise the risk of introduction and spread of infection. These will involve reduced opportunity for contact between poultry and wild birds.
- It is essential to enhance surveillance of poultry and wild birds, and develop contingency plans for AI outbreaks as well as strengthen biosecurity.
- Vaccination should be considered as a tool to supplement biosecurity measures (see previous AI EFSA Scientific Opinion, www.efsa.eu.int).
- The trade of poultry and poultry products needs to be controlled more strictly, notably in relation to movements where the outbreaks may occur.

Recommendations for future research

In order to improve the effectiveness of surveillance of poultry and wild birds, geographical and temporal sampling adequate to detect virus at a given

incidence need to be developed. Surveillance methods to be investigated should include sampling of live (capture/release and hunted sample) and dead birds. Practical methods for monitoring population sizes need to be developed so that more reliable prevalence estimates can be obtained.

Virological studies need to be conducted to determine the amount or level of virus in sampled material.

Existing ringing and count data for wild birds needs to be analysed to elucidate migration routes and networks of sites used by birds migrating to or through Europe and or outbreak areas outside the EU.

Existing surveillance data should be examined to identify gaps in information which then should be addressed by specific research activities. Poultry husbandry needs to be described in geographical areas where such information currently is deficient.

The risk and the specific mechanisms of indirect or direct transmission of virus between wild birds and domestic poultry need to be investigated.

Vaccines preventing the carrier state need to be improved and eventually be used in wild fauna.

12. Risk Assessment for Risk Question 2a: Exposure and consequence assessment of wild birds within the EU and subsequent endemic infection

What is the probability of Asian lineage H5N1 HPAIV Asian H5N1 virus transmission to wild birds within the EU and subsequent endemic infection of wild bird populations?

12.1. Factors influencing probability of exposure of EU birds to Asian lineage H5N1 HPAIV via seasonal migration of wild birds

The probability of introduction of Asian lineage H5N1 HPAIV by a bird species is correlated with the number of individual birds migrating into the EU. Species that are very common represent a higher risk (notably if they are susceptible) as a result of the greater number of individuals (see Table 12.1).

Table 12.1. Preliminary list of bird species with higher probability to transmit Asian lineage H5N1 HPAIV inside the European Union due to their susceptibility, habitat and behaviour (gregariousness and mixing).

Common name	Scientific name	Population name	Population size EU25	Units
Breeding populations				
Mute Swan	<i>Cygnus olor</i>	EU25 breeding	68,000-92,000	Pairs
Lesser White-fronted Goose	<i>Anser erythropus</i>	EU25 breeding	0-5	Pairs
Bean Goose	<i>Anser fabalis</i>	EU25 breeding	2,300-3,200	Pairs
Greylag Goose	<i>Anser anser</i>	EU25 breeding	65,000-87,000	Pairs
Canada Goose	<i>Branta canadensis</i>	EU25 breeding	Unknown	Pairs
Barnacle Goose	<i>Branta leucopsis</i>	EU25 breeding	5,900-7,600	Pairs
Eurasian Wigeon	<i>Anas penelope</i>	EU25 breeding	70,000-120,000	Pairs
Common Teal	<i>Anas crecca</i>	EU25 breeding	220,000-360,000	Pairs
Mallard	<i>Anas platyrhynchos</i>	EU25 breeding	1,600,000-2,800,000	Pairs
Northern Pintail	<i>Anas acuta</i>	EU25 breeding	16,000-27,000	Pairs

Common name	Scientific name	Population name	Population size EU25	Units
Garganey	<i>Anas querquedula</i>	EU25 breeding	14,000-23,000	Pairs
Northern Shoveler	<i>Anas clypeata</i>	EU25 breeding	30,000-38,000	Pairs
Marbled Teal	<i>Marmaronetta angustirostris</i>	EU25 breeding	30-210	Pairs
Red-crested Pochard	<i>Netta rufina</i>	EU25 breeding	4,200-12,000	Pairs
Common Pochard	<i>Aythya ferina</i>	EU25 breeding	69,000-110,000	Pairs
Tufted Duck	<i>Aythya fuligula</i>	EU25 breeding	180,000-290,000	Pairs
Coot	<i>Fulica atra</i>	EU25 breeding	590,000-1,100,000	Pairs
Northern Lapwing	<i>Vanellus vanellus</i>	EU25 breeding	830,000-1,300,000	Pairs
Ruff	<i>Philomachus pugnax</i>	EU25 breeding	51,000-71,000	Pairs
Black-headed Gull	<i>Larus ridibundus</i>	EU25 breeding	990,000-1,300,000	Pairs
Common Gull	<i>Larus canus</i>	EU25 breeding	270,000-420,000	Pairs
Non-breeding populations				
Mute Swan	<i>Cygnus olor</i>	NW & C European	250,000	Individuals
		Great Britain	37,500	Individuals
		Ireland	10,000	Individuals
Bewick's Swan	<i>Cygnus columbianus bewickii</i>	<i>Cygnus columbianus bewickii</i>	29,000	Individuals
Pink-footed Goose	<i>Anser brachyrhynchus</i>	Greenland/Iceland	240,000	Individuals
		Svalbard	37,000	Individuals
Greater White-fronted Goose (European race)	<i>Anser albifrons albifrons</i>	Baltic-North Sea	1,000,000	Individuals
		Pannonic	10,000-40,000	Individuals
Lesser White-fronted Goose	<i>Anser erythropus</i>	North European	8,000-13,000	Individuals
Greylag Goose	<i>Anser anser anser</i>	Iceland	89,100	Individuals
		NW Scotland	9,000	Individuals
		NW Europea	400,000	Individuals
		C Europe	25,000	Individuals
Canada Goose	<i>Branta canadensis</i>		Unknown	Individuals
Barnacle Goose	<i>Branta leucopsis</i>	Greenland	54,100	Individuals
		Svalbard	23,000	Individuals
Barnacle Goose	<i>Branta leucopsis</i>	Russian	360,000	Individuals
Eurasian Wigeon	<i>Anas penelope</i>	NW Europe	1,500,000	Individuals
		Black Sea/Mediterranean	300,000	Individuals
Common Teal	<i>Anas crecca</i>	NW Europe	400,000	Individuals
		Black Sea/Mediterranean	750,000-1,375,000	Individuals
Mallard	<i>Anas platyrhynchos</i>	NW Europe	4,500,000	Individuals
		W Mediterranean	1,000,000	Individuals
		E Mediterranean	2,000,000	Individuals
Northern Pintail	<i>Anas acuta</i>	NW Europe	60,000	Individuals
		Black Sea/Mediterranean	1,000,000	Individuals
Garganey	<i>Anas querquedula</i>	W Africa	>2,000,000-3,000,000	Individuals

Common name	Scientific name	Population name	Population size EU25	Units
Northern Shoveler	<i>Anas clypeata</i>	NW & C Europe	40,000	Individuals
		Black Sea, Mediterranean & W Africa	450,000	Individuals
Marbled Teal	<i>Marmaronetta angustirostris</i>	W Mediterranean & W Africa	3,000-5,000	Individuals
Red-crested Pochard	<i>Netta rufina</i>	C Europe & W Mediterranean	50,000	Individuals
		Black Sea & E Mediterranean	20,000-43,500	Individuals
Common Pochard	<i>Aythya ferina</i>	NE & NW Europe	350,000	Individuals
		Black Sea & E Mediterranean	1,100,000	Individuals
Tufted Duck	<i>Aythya fuligula</i>	NW Europe	1,200,000	Individuals
		C Europe, Black Sea & Mediterranean	700,000	Individuals
Coot	<i>Fulica atra</i>	NW Europe	1,750,000	Individuals
		Black Sea/Mediterranean	2,500,000	Individuals
Northern Lapwing	<i>Vanellus vanellus</i>	Europe	2,800,000-4,000,000	Individuals
Ruff	<i>Philomachus pugnax</i>	W Africa	>1,000,000	Individuals
Black-headed Gull	<i>Larus ridibundus</i>	N & C Europe	5,600,000-7,300,000	Individuals
		Mediterranean	1,300,000-1,700,000	Individuals
Common Gull	<i>Larus canus</i>	<i>Larus canus canus</i> (NW Europe)	1,300,000-2,100,000	Individuals
		<i>Larus canus heinei</i> (SE Europe, Black & Caspian Seas)	100,000-1,000,000	Individuals

12.2. Probability of infection of EU birds, given exposure

The probability will depend upon host susceptibility, pathogenicity of strain, etc.

12.3. Overall conclusion on probability of infection of EU wild birds

The conditional probability of Asian lineage H5N1 HPAIV being transmitted to resident birds is highly dependent on the wild bird species introducing the virus, the number of infected birds and the pathogenicity of the virus strain. There is high uncertainty due to the lack of data on inter-species transmission dynamics of Asian lineage H5N1 HPAIV as well as on the consequences of infection of European wild birds. Very high regional differences are assumed. Due to the dynamic nature of the global situation, the assessment may change rapidly.

The conditional probability of Asian lineage H5N1 HP AIV becoming endemic in non-migratory European wild birds will depend on the species present in a specific area and also on the climate, mainly temperature conditions according to the physico-chemical resistance properties of the virus as described in this report.

Recommendations

Risk assessments in the EU have to be conducted taking into consideration the regional climatic conditions, density of poultry flocks, migratory pathways, presence of wetlands, nature of population and species of wild birds.

Such an approach requires identifying the regions and not necessarily the countries with a similar level of risk, in order to carry out an analysis based of complementary data collected in the different countries. For this purpose, a strong collaboration between member states is absolutely necessary in order to be able to perform regional risk assessment rather than separate national risk assessments.

13. Risk Assessment for Risk Question 2b:

Exposure and consequence assessment for domestic poultry as a consequence of wild bird infection

What is the probability of Asian lineage H5N1 HPAIV Asian H5N1 virus exposure and infection of domestic poultry within the EU as a consequence of infection in migratory birds (Question 1) or wild birds resident within the EU (Question 2a)?

13.1. Overall conclusion

The conditional probability of Asian lineage H5N1 HPAIV being transmitted from wild birds to poultry kept in free-range and backyard holdings in Europe or those not having high biosecurity measures is **high**. For indoor poultry holdings, the probability is generally **low** providing that strict biosecurity measures are in place. However, the probability increases particularly for indoor holdings localized in the proximity of wetlands and with increasing prevalence of infection in the wild birds present in these wetlands.

However, the AHAW Panel will, in accordance with the mandate of the Commission produce a new risk assessment which will more comprehensively assess the risk of AI infection for poultry populations in the EU. This will take account of the current report, the previous risk assessment in September 2005, new scientific data including recent epidemiological findings.

13.2. Recommendations to reduce the probability of transmission of Asian lineage H5N1 HPAIV from wild birds to poultry in the EU

There is a need of setting up of a European database with relevant data on migratory wild birds. Such a database should include information on the number and the location of infected birds.

Passive and active surveillance amongst wild bird populations within the EU should be intensified.

Biosecurity measures for all types of poultry holding need to be reviewed, according to EFSA previous opinion (www.efsa.eu.int). In particular

- Staff hygiene should be assessed where there is a risk of staff contact with waterfowl or other infected animals.
- Building access for wild birds or other infected animals needs to be prevented.

- Use of water and feed that may be contaminated by infected birds needs to be prevented.
- Since the risk of infection in the vicinity of migratory waterfowl refuges may be higher than in other locations, it would be better to avoid locating poultry units to be set up newly near to such refuges. For existing production units located in such areas, biosecurity measures need to be strengthened and compliance may need to be audited.
- In geographical areas where HPAI infection is likely to pose a risk to domestic poultry, these birds should not be kept outside.
- If there is an outbreak of HPAI in wild birds, game birds and ducks should not be released to the wild during the risk periods, particularly if this is done in large numbers and the birds are attracted to return by being fed subsequently.
- If there is an outbreak of HPAI in wild birds, then hunting or collecting wild waterfowl by some other method should not occur and the public should be encouraged to take basic hygiene precautions.

13.3. Recommendations for future research

At a national level, those species of wild birds should be identified that are most closely associated with poultry holdings, of all management types, and this information should be used to review and, if necessary, revise biosecurity measures.

Research on vaccination stated in the previous EFSA scientific opinion on AI, should be already taken into consideration (www.efsa.eu.int).

14. References

References used in this statement are available and are listed in the current Draft Scientific Report. After the possible adoption at the next AHAW Panel Plenary Meeting on 26-27 April the Scientific Report will be published at the EFSA web.

15. Working Group Members and Acknowledgements

The AHAW Panel wishes to thank the members of the working group chaired by panel member D.U. Pfeiffer: I. Brown, R. Fouchier, N. Gaidet, V. Guberti, T. Harder, R. Langston, V. Martin, R.S. Magalhaes, K. Stärk, D. Stroud, B. Szewczyk, J. Veen, J. Waldenström, for the preparation of the Draft Scientific Report, which has been used as the basis of this Scientific Statement. The final Scientific Opinion will be submitted for possible adoption at the Plenary Meeting on 26-27 April.

The scientific co-ordination for this Statement has been undertaken by the EFSA AHAW Panel Scientific Officers, J. Serratos and O. Ribo.

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16. AHAW Scientific Panel Members

The Scientific AHAW Panel adopted the current Statement by written procedure on the 5th of April 2006. Members of the AHAW Panel are :

Bo Algers, Harry J. Blokhuis, Donald Maurice Broom, Ilaria Capua, Stefano Cinotti, Michael Gunn, Jörg Hartung, Per Have, Xavier Manteca Vilanova, David B. Morton, Michel Pépin, Dirk Udo Pfeiffer, Ronald John Roberts, José Manuel Sánchez Vizcaino, Alejandro Schudel, James Michael Sharp, Georgios Theodoropoulos, Philippe Vannier, Marina Verga, Martin Wierup, Marion Wooldridge.