The EFSA Journal (2006) 357, 1-46, Opinion on "Migratory birds and their possible role in the spread of highly pathogenic Avian Influenza"

Scientific Opinion on

Migratory Birds and their Possible Role in the Spread of Highly Pathogenic Avian Influenza

Adopted by written procedure on 12th May 2006

EFSA-Q-2005-243

Summary

A qualitative risk assessment was conducted to determine 1) the likelihood of introduction of Asian lineage H5N1 highly pathogenic avian influenza virus by migratory birds into the EU, 2) the likelihood of it becoming endemic in wild birds in the EU and 3) the likelihood of transmission of infection to domestic poultry.

The conclusions reached included that the probability of the virus being released into the EU varied between low and high, depending on the species of migratory birds. A minority opinion was noted concluding that the risk was medium across species. In the light of this risk, it was recommended to educate poultry keepers in currently affected countries outside the EU in relation to minimum biosecurity standards. Surveillance should be enhanced in these countries in domestic poultry and wild birds, and vaccination programmes should be considered for controlling the infection. Trade with poultry and their products needs to be managed considering the risks of spreading virus between geographical areas. Research needs to be conducted to improve surveillance methods in poultry and widl birds. Wild bird migration data needs to be analysed to better understand the flyways used by the various species.

The risk of the virus becoming endemic in European wild bird populations was considered to vary between low and high depending on species. A minority opinion was received concluding that this risk was medium across species. This risk could be reduced by intensifying surveillance in wild birds within the EU, and use the data to inform biosecurity measures in domestic birds. The behaviour of wild birds within the EU needs to be better studied so that the dynamics of transmission within and between species are better understood.

The final step of the risk assessment indicates that there is a negligible risk of the virus infecting domestic poultry kept under a high biosecurity standard and not in high poultry density areas. The risk increases to very low if they are kept in high poultry density areas. For backyard and free-range poultry, and any poultry not kept under high biosecurity standards, it was concluded that the risk of introduction of Asian lineage H5N1 highly pathogenic avian influenza virus to the flock was low to medium. These risks emphasize the need to make better use of existing and new migratory bird behaviour data. Passive and active surveillance for AI in wild birds needs to be intensified. It should focus on the species identified in this risk assessment. Biosecurity measures for poultry holdings need to be reviewed, and research needs to be conducted to optimise their effectiveness. Poultry holdings should not be built in the vicinity of wetland areas. New vaccines and their use need to be researched.

Table of Contents

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, 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 (HPAIV) in order to produce an update of the recently published opinion as relevant new information and evidence becomes available.

1.3. 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 of the virus into the EU. Such pathways are considered explicitly in the EFSA scientific opinion "Animal health and welfare aspects of Avian Influenza" (EFSA 2005). EFSA is also working on a Scientific Opinion on

"Animal Health and Welfare risks associated with the import of wild birds other than poultry into the EU", where avian influenza is also considered.

An overall balanced assessment of the risk of entry of Asian lineage H5N1 HPAIV 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 (OIE 2004a).

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 very high (see Table 1.1). They are based on the data presented by the Working Group and evaluated in the scientific report (www.efsa.eu.int), 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 used in the table are to be interpreted within this range.

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. In the context of this risk assessment variation and uncertainty were both presented as uncertainty. 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.

In order to avoid duplication in the presentation of data in relation to avian influenza with the previous EFSA scientific opinion “Animal health and welfare aspects of avian influenza” (EFSA 2005), extensive reference will be made to that report.

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 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 in relation to their ability to reach the EU as indicated in Figure 2.1.

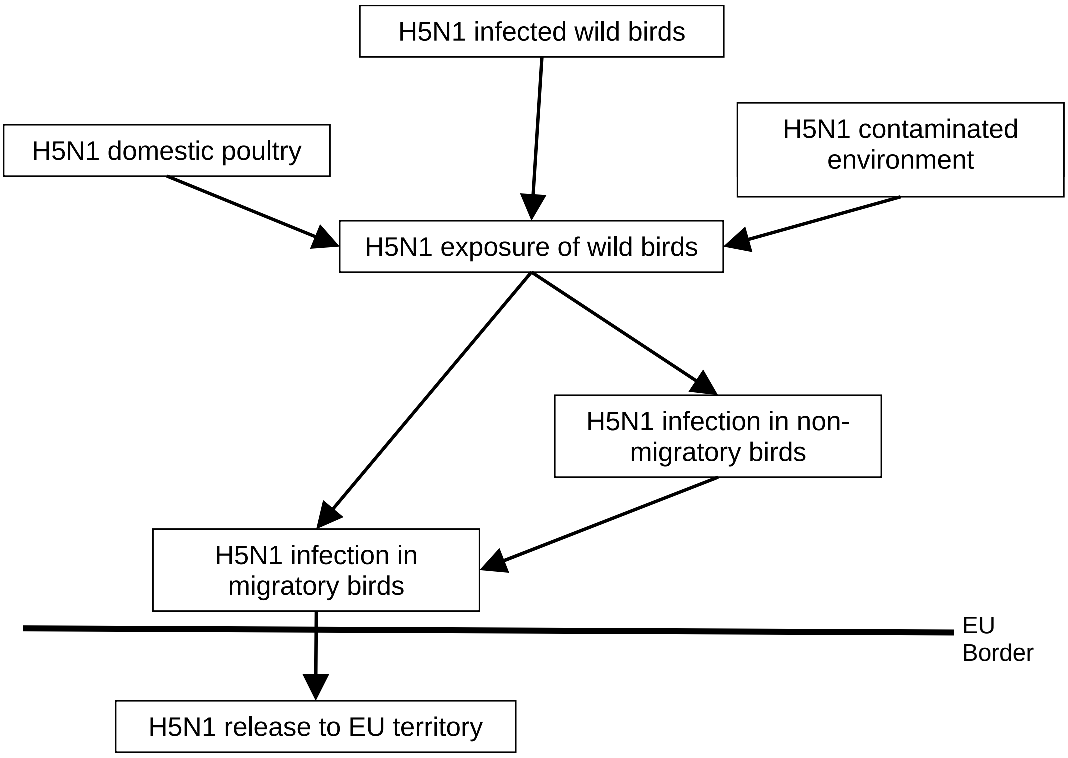

Figure 2.1. Release pathways of Asian lineage H5N1 HPAIV in territories outside the EU that may result in potential transmission of the virus leading to a release into EU territory (note that these pathways describe the potential mechanisms for release)

2.2. Risk Question 2 - Exposure and Consequence Assessment

What is the probability of Asian lineage H5N1 HPAIV Asian H5N1 virus transmission to:

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

Figure 2.2 describes the potential direct and indirect transmission 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 transmission from any species of wild bird to domestic bird populations (Risk question 2b).

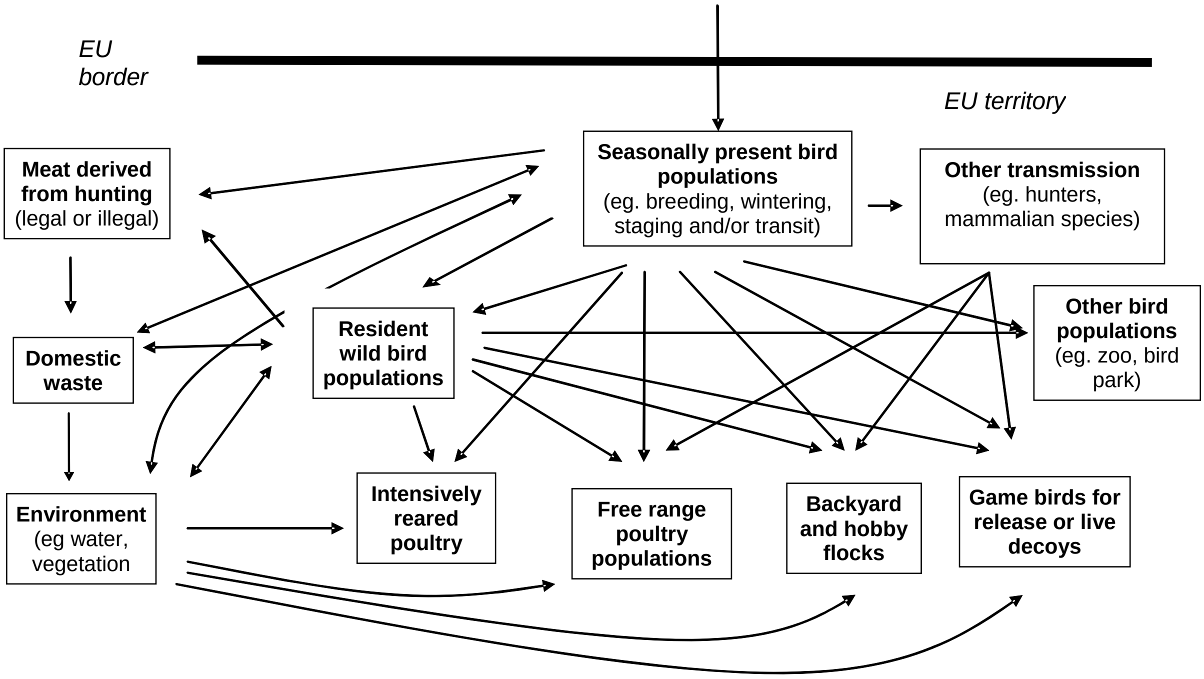

Figure 2.2. Exposure and consequence pathways for bird populations within the EU to Asian lineage H5N1 HPAIV after potential introduction of the virus by wild birds (note that these pathways include all potential direct and indirect exposure and transmission pathways)

3. Pathogenesis in Wild Birds

3.1. Pathotypes

Pathogenicity tests are used to differentiate between different virus types, but it needs to be recognised that the observed pathogenicity will be specific to the species in which they have been used.

3.2. Virulence Determinants

The overall constellation of the gene segments seems to govern the polygenic trait of influenza pathogenicity. No genetic markers have yet been identified which could be used for a predictive evaluation of pathogenicity in a species-dependent manner.

3.3. Pathogenicity

3.3.1. Natural infections

Existing reports of infections with Asian lineage H5N1 HPAIV in wild birds focus primarily on the *Anseriforme* and *Charadriiforme* Orders. These wild birds have typically been dead. It is not possible to draw general conclusions about the pathogenicity of the virus.

Pigeons can be susceptible to disease.

3.3.2. Experimental infections

Based on the limited number of transmission experiments reported in the peer-reviewed scientific literature, apart from Zebra finches, acute or peracute clinical disease generally 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 data suggests that infection may also result in mortality.

Mallards showed mild disease or neurological signs, and were subject to low to high mortality. Similar results were obtained for chestnut teals.

3.4. Minimal Infectious Dose

The minimal infectious dose in birds will depend on host species, route of infection and viral strain characteristics, and it can currently only be concluded that doses above 10^5 EID_{50} per bird have reliably lead to infection under experimental conditions.

The infective dose required to achieve infection under natural conditions may be different from what is needed experimentally.

3.5. Incubation Period

Incubation periods of Asian lineage H5N1 HPAIV in wild birds will vary according to host species, virus type and dose.

3.6. Excretion Route, Dose and Period

Excretion of virus in ducks occurs via the respiratory and the intestinal tract, and virus concentrations may be higher in the respiratory tract. The data from the quarantine facility in UK suggests that under similar circumstances aerosol transmission of infection may not be as effective, as exposure to contaminated material such as faeces or direct contact.

Excretion of Asian lineage H5N1 HPAIV as measured in experimentally inoculated mallards did not exceed $10^{6.0}$ EID_{50}.

The amount of virus excreted and the duration of excretion is 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 have been 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.

3.7. Survival and Morbility 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 H5N1 HPAIV 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).

3.8. Overall recommendations on Pathogenesis in wild birds

Studies are needed describing the pathogenesis following H5N1 infection in a range of wild bird species referred to in Table 13.1 since all studies to date have involved domestic birds, especially looking at viral shedding periods in situations where birds are not lethally affected.

4. Information about Countries and Ecological Zones Affected by Asian Lineage H5N1 HPAIV

4.1. Epidemiological Data on Asian Lineage H5N1 HPAIV Outbreaks in Poultry

4.1.1. Risk factors for infection in domestic poultry

4.1.1.1. Structure of production sectors and biosecurity

While in currently endemically infected regions large industrial type farms manage more birds, evidence suggests that in these same regions smallholder-based poultry farms (production sectors 3 and 4; FAO 2004) are more frequently affected by infection. This may be the consequence of differences in husbandry and trade practices affecting biosecurity.

4.1.1.2. Temporal changes in poultry population size

Census data suggest that in some countries during recent years small poultry holders have increased the size of their flocks. Biosecurity standards are assumed to have remained unaltered for those same farms. 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 HPAIV in Asia.

4.1.1.3. Role of waterbirds

Domestic and wild waterbirds are believed to have played a key role in the genesis of the 2003-2005 epidemics. The rice farming systems with their irrigated paddy fields provide an effective interface for transmission between domestic and wild waterbirds.

4.1.1.4. Role of mammal species

Carnivorous mammal species are susceptible to Asian lineage H5N1 HPAIV, and will become infected as the result of feeding on infected wild bird carcasses. They are not considered to be capable of transmitting infection to each other, and the likelihood of exposing other animal species is believed to be negligible.

4.1.1.5. Trade and live bird markets

There is strong evidence that virus dissemination is facilitated by mixing of different species of domestic poultry at live bird markets, as well as local trade.

4.1.1.6. Presence of infection in wild birds outside EU

Reports from affected areas indicate the isolation of Asian lineage H5N1 HPAI viruses from dead wild birds in countries outside the EU. And there is some evidence indicating the presence of these strains in live wild birds in affected areas.

4.1.1.7. 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 and surveillance systems and the effect of specific control measures introduced in infected places, including the use of vaccination.

4.1.2. Temporal and spatial pattern

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.

4.1.3. Molecular epidemiology of Asian lineage H5N1 HPAIV

Molecular epidemiological investigations on Asian lineage H5N1 HPAIV from different affected areas suggest that the perpetuation of infection in domestic poultry sectors in affected countries is more likely to be due to continuous regional movements of live poultry. Some wild bird species are very likely to be important for the introduction and long distance spread of the virus. Molecular studies also highlight the fact that the highest diversity of H5N1 HPAI viruses is seen in southern China which supports the “influenza epicentre” hypothesis.

4.2. Overall recommendations on epidemiological data on Asian lineage H5N1 HPAIV outbreaks in poultry

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.

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

5.1. Characteristics of Farming Systems and their Relationship with Poultry Husbandry outside the EU

5.1.1. Eastern Europe and Central Asia

Limited data is available regarding the major farming systems that support poultry production in Eastern European and Central Asian countries. It is therefore not possible to produce general conclusions, except that in Chechnya-Ingushetia and Turkey poultry are predominantly raised in backyard flocks. It appears plausible that this will also be the case in many of the other countries in this area. But variation will occur with respect to the importance of the different production sectors within and between countries.

5.1.2. South-east Asia and East Asia

The four most common systems in South-east Asia and East Asia, which include the major proportion of the rural poor, are the lowland rice, tree crop mixed, temperate mixed and upland intensive mixed farming systems. Lowland rice and the temperate mixed farming systems support the majority of poultry production.

5.1.3. African countries and Middle East

The farming systems in African countries and Middle East which support the majority of poultry production are part of the urban based farming systems.

5.2. Geographical Distribution of Poultry Population outside the EU

5.2.1. Eastern Europe and the Middle East

In Eastern Europe and the Middle East countries where information was available we conclude that high poultry densities are observed in areas around the Black sea, but a large variation within countries in terms of the number of farms and numbers of chickens is to be expected. The predominant poultry management system is smallholder-based and numerically backyard flocks are the most important poultry husbandry system.

5.2.2. Mekong region, Indonesia and China

The predominant structure of the poultry sector in South East Asian countries varies between countries from highly industrialised (Thailand) to backyard farming (Vietnam). Poultry farming plays a very important role for rural development in these countries and the majority of households raise poultry. Poultry farming is a growing sector with estimated annual growth rates around 5% per year.

5.2.3. African countries

There are several relatively small areas of moderately high poultry density, in particular in some West African countries and in South Africa.

5.3. Poultry Trade

In low income countries, the trade of poultry between small commercial family farms and markets is based on a complex set of intermediaries. Products can either be traded at long distances or at the village/city level.

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

Industrial poultry systems can be managed under biosecurity requirements that are assumed to reduce the likelihood of effective contact with infected wild birds. Therefore, trade of live poultry birds from these establishments is considered to be conducted in a way that helps to minimise the effective contact with infected wild birds.

5.4. Overall recommendations on characterization of regional poultry husbandry and production systems outside the EU

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.

Systems need to be developed that allow defining locations of poultry holdings and wetlands.

Recommendations for future research

Biosecurity measures need to be developed that are compatible with the livelihood needs of smallholder poultry producers.

6. Environmental Stability of Asian Lineage H5N1 HPAIV and Transmission

Conclusions

The environmental stability of influenza viruses has been addressed by only a small number of scientific studies. A number of reports have quasi-anecdotal character 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 considered here are difficult to compare since different strains and subtypes in different environmental conditions have been examined with various virus 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.

Virus survival in carcasses has been demonstrated to occur and may play a significant role in local spread of infection among wild birds, and for infection of scavenging species.

The role of aerosol for the transmission of Asian lineage H5N1 HPAIV is unclear, but it may be less important than faecal-oral transmission. This contrasts with human influenza viruses which are considered to be mainly transmitted via aerosol.

Recommendations

Surveillance activities should include systematic sampling of environmental surfaces and water of areas and premises with prior history of Asian lineage H5N1 HPAIV outbreaks.

Practical methods to ensure that water supplies to poultry premises are not contaminated with avian influenza viruses (or other pathogenic agents) have to be defined and made available to poultry producers.

Recommendations for future research

Experimental research should be conducted to assess the viability of H5N1 HPAIV 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. The consequences of virus survival in carcasses linked to predators and other wild fauna should be investigated and if possible monitored.

Research on the relative importance of different transmission mechanisms of Asian lineage H5N1 HPAIV, particularly via aerosol, is required.

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.

7. Diagnostic Methods for the Detection of Asian Lineage H5N1 HPAIV in Wild Bird Populations

Conclusions

Virus isolation in embryonated chicken eggs or cell cultures are sensitive methods that provide sufficient material for further virus characterisation by hemagglutination inhibition assays or nucleotide sequence analyses (OIE manual of diagnostic tests; EU Directive 1992/40). The disadvantages of virus isolation techniques are that they are time-consuming, and can only be performed safely under high biosecurity conditions if highly pathogenic avian influenza viruses are to be expected. It has been shown previously that virus genome detection by RT-PCR provides a rapid, sensitive and convenient alternative for virus isolation. These tests can be designed to detect all avian influenza A viruses, or specific influenza A virus subtypes, such as H5 or H7. Real-time RT-PCR assays generally employ single-tube format, are fast, and have the additional advantage that a specific probe facilitates detection of positive samples and increases assay specificity.

Serological sampling lacks the sensitivity to be of use for routine screening or confirmatory diagnosis of avian influenza, particularly as part of outbreak investigations. The currently available serological tests do not all distinguish between HP and LP strains. Furthermore, positive serological findings give no indication of current infection status. It may be of use for obtaining broard estimates of infection levels in wild bird populations.

Recommendations

Serological testing of wild birds for Asian lineage H5N1 HPAIV is not recommended as a routine screening or confirmatory diagnostic test. But it may be useful for studying prevalence in resident or migrating bird species H5N1 virus, if performed at accredited diagnostic laboratories.

Single-tube RT-PCR should be employed where possible to minimise the risk of cross contamination between different samples. Upon the identification of positive specimens, viral genetic material may be amplified by PCR and sequenced, and/or used for virus isolation and further characterisation by haemagglutination inhibition assays under appropriate conditions.

For H5-positive samples, the original specimens should subsequently be used for virus isolation in 10 to 12-day-old embryonated chicken eggs under BSL3+ conditions. If the initial virus isolation attempt is unsuccessful, a blind passage of the allantoic fluid of the inocculated eggs should be performed. Virus isolates are subsequently characterised using hemagglutination inhibition assays or neuraminidase inhibition assays with subtype-specific antisera. Alternatively, the H and N genes may be characterised by nucleotide sequencing. Nucleotide sequencing of the protease cleavage site in the H gene is an appropriate method to determine if the virus has a highly pathogenic genotype. The pathogenicity of influenza viruses may further be determined using the intravenous pathogenicity index (IVPI) in chickens (OIE manual of diagnostic tests; EU Directive 2005/94); Full genome sequencing of H5N1 HPAI viruses should be employed to determine the genetic relationship with other known strains. All virus isolates and positive specimens should be sent to CRL, Weybridge, UK.

Recommendations for future research

RNA isolation and conventional or real-time RT-PCR assays are based on the matrix gene of influenza A virus. Similar tests should be designed based on other parts of the viral genome, but it is important to ensure that the primer sequences are conserved in all avian influenza A viruses, including all described H5N1 HPAIV isolates. Influenza A virus positive specimens should subsequently be tested in RT-PCR assays specific for the H5 gene. Such assays should also be evaluated using recent H5N1 HPAIV isolates from around the world.

The relative specificity and sensitivity of the diagnostic methods utilised in surveillance programs needs to be determined.

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

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.

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]

8. Identification of Migratory Bird Species at Increased Exposure to Asian Lineage H5N1 HPAIV Infection

8.1. General Overview of Bird Migration Systems and Concepts

There are a wide variety of migration strategies between and 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.

It is important to emphasize that flyways maps are at best broad attempts to summarise the different migratory routes undertaken by individual species.

8.1.1. Site fidelity and predictability of occurrence

There is variation in site fidelity between migratory bird species and the likelihood of the same birds visiting the same sites between years.

Many waterbirds are highly site faithful and regular use of favoured habitats means that sites of importance can be identified with a high degree of

---

[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

confidence. Other species use wetlands more variably and are less predictable in their patterns of occurrence. Knowledge of species ecology allows evaluation of the extent to which any species is congregatory.

8.1.2. Factors which influence waterbird occurrence

Factors such as those outlined above result in varied potential for mixing of birds between and within species at different times of the year.

8.1.3. Data on wild bird migrations and its interpretation

Resightings of individually colour-marked birds, and recaptures of individually ringed birds, have shed light on networks of sites used in a single migration, for example refuelling stopovers and moulting sites. However, the means of deciphering actual routes taken by migrating birds require more sophisticated techniques, some of which are only just being implemented (e.g. satellite telemetry).

8.1.4. Quality of information on bird migration

Care should thus be taken about reliance on published sources of information. There is an urgent need to analyse and synthesise contemporary information from the considerable amount of archived ringing data that exists. This need was recognised by Africa-Eurasian Waterbird Agreement (AEWA) MoP3 in October 2005.

8.2. Identifying Areas of Concentration or Mixing

Conclusions

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.

Recommendations

There is an urgent need for systematic analysis of data on waterbird ringing recoveries so as to give a better assessment of 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 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 of waterbird populations.

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

Given that the distribution of most waterbirds occurring within the European Union, extend considerably beyond the EU25, studies such as those indicated above, need to be undertaken on a collaborative international basis. The Africa-Eurasian Waterbird Agreement (AEWA), to which the EU is a Contracting Party, provides such a mechanism for collaboration and joint working.

8.3. Phenology of Waterbird Migration

Conclusions

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 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.

8.4. Selecting Migratory Bird Species at Higher Risk of Becoming Exposed to Asian Lineage H5N1 HPAIV

8.4.1. Methodology

8.4.1.1. Initial list of species considered

Only birds from the orders *Anatidae* (ducks, geese and swans) and *Charadriiformes* (waders and gulls) are considered.

8.4.1.2. Factors associated with exposure to H5N1 HPAIV infection in migratory birds

Expert opinion and basic epidemiological principles suggest that species which are highly gregarious are more likely to become infected with Asian lineage H5N1 HPAIV since close contact between birds may result in the virus being more readily passed from bird to bird within flocks. Two components of gregariousness can be assessed, group size and group density.

The Greenland race of Greater White-fronted Goose *Anser albifrons flavirostris* was evaluated separately on the basis of significantly smaller group sizes and lower degree of mixing (below) compare to the nominate race *A. a. albifrons* which largely occurs on continental Europe.

8.4.1.2.1. Degree of mixing during migration/wintering periods

Species which readily mix with other species of waterbirds are thought to be more likely to become infected with Asian lineage H5N1 HPAIV since contact between species may result in the viral infection. Likewise, it is assumed that species which do not come into close contact with other species are at lower risk of infection.

As with gregariousness, there is currently no evidence to support this assumption.

8.4.1.2.2. Main habitat during migration/wintering

Habitat is assumed to be of importance with respect to the chances of a species becoming infected with AI viruses (outside the EU) as well as with chances that it may subsequently transmit it to other birds within the EU. As with gregariousness and mixing, there is currently no evidence to support this assumption, although it is reasonable to assume that a species occurring solely at sea poses considerably less risk of coming into contact with poultry than a species that uses agricultural habitats of a type also frequented by free-range poultry.

Where more than one habitat is used multiple coding has been applied. Note that the sequence of habitat code elements indicates relative use of the different habitats. Thus the code MF indicates that the species primarily occurs in marine areas but also can use freshwater habitats, whilst FM would indicate the converse.

8.4.2. Selecting migratory bird species more likely to be exposed to Asian lineage H5N1 HPAI

Conclusions

It needs to be noted that the selection of birds in this chapter was based on defining a set of rules taking into account bird behaviour as well as geographical areas likely to be endemically infected with H5N1 HPAIV, as an expert opinion judgement.

The resulting selection of species more likely to be exposed to Asian lineage H5N1 HPAIV on the basis of gregariousness or mixing is given in Table 11.2 of the Scientific Report (www.efsa.eu.int). The criterion “migration through infected area” was not applied due to the currently limited knowledge about the regions that are infected and the continuously changing data currently available. As a consequence of resource constraints, only migratory birds of the orders of *Anseriformes* and *Charadriiformes* were considered. Additional waterbird species might be epidemiologically relevant, but there is currently no evidence of the role of other birds (but see Section 13.4 of the Scientific Report, www.efsa.eu.int).

Note that a significant number of additional species not currently included in Table 11.2 of the Scientific Report (www.efsa.eu.int) are unlikely to be exposed to H5N1 HPAIV directly from poultry due to their use of habitats but remain likely to be exposed to infection from other wild birds at mixing and concentration areas and may therefore have a significant role in the epidemiology of Asian lineage H5N1 HPAIV in wild birds.

8.5. Implications of Spread of Asian Lineage H5N1 HPAIV for Vulnerable Waterbird Species

As well as impacts on poultry, and implications for human health, the spread of H5N1 HPAIV also has significant implications for the conservation of several species of globally threatened waterbirds in Europe.

8.6. Overall recommendations on identification of migratory bird species at increase exposure to Asian Lineage H5N1 HPAIV infection

All assessments of information presented here are adversely affected by the lack of the following key information identified by the Scientific Task Force on Avian Influenza convened in late August 2005 by the Convention on Migratory Species, and 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 3.18[2]; October 2005):

- "clarifying virus behaviour”:
    - i) in different waterbird populations (especially viral incubation periods, the infectious period in birds and the signs affecting individual wild birds), as well as determining their survival rates; and
    - ii) 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 HPAIV 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; and
- 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."

9. 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 sparse. Previously published studies show that species from several different families of waterbirds may carry influenza viruses. No H5N1 HPAIV has been reported yet from ongoing surveillance studies conducted by FAO as part of the afore-mentioned TCP project in Africa. No data are available from other surveillance studies outside the EU.

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.

---

[2] http://www.cms.int/avianflu/AEWA_Resolution_3_18.pdf

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.

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.

An efficient network of laboratory support for AI diagnosis in countries outside the EU needs to be developed.

Recommendations for future research

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).

10. Identification of Wild Bird Species currently more likely to be Infected with Asian Lineage H5N1 HPAIV and to Expose Domestic Poultry within the EU

10.1. Selection of Migratory Bird Species more likely to Expose Poultry to Asian Lineage H5N1 HPAIV in EU

10.1.1. Selecting migratory bird species more likely to expose poultry to Asian lineage H5N1 HPAIV in EU

Species were not selected if they were assessed as having zero or virtually zero probability of contact (both the risk of direct contact with poultry, as well as use of shared habitats or habitats recently vacated by domestic poultry). This filter only 'deselected' Lesser White-fronted Goose *Anser erythropus* and Marbled Teal *Marmaronetta angustirostris* (Table 13.1 of the Scientific Report, www.efsa.eu.int), both populations of which have small populations within the EU (see Section 11.4). All other species listed in Table 11.2 of the Scientific Report (www.efsa.eu.int) (a total of 25 species) were considered to have at least some probability of contact with domestic poultry within the EU.

10.2. Selection of Resident and other Wild Bird Species in the EU likely to come into Contact with Poultry

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 means of virus transmission to domestic poultry, although mortality has been recorded in some species of resident wild birds in association with several outbreaks of H5N1 HPAIV in domestic poultry (Kou et al. 2005; Perkins and Swayne 2003). 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.

Application of the decision criteria specified in Figure 13.2 of the Scientific Report (www.efsa.eu.int), results in the three groups of bird "bridge" species presented in Table 10.1.

Table 10.1. European bird species that live in proximity to domestic poultry and could therefore be considered bridge species (selected on the basis of decision tree presented in Figure 13.2 of the Scientific Report (www.efsa.eu.int)

Common name	*Scientific name*	*Probability of contact with poultry*
Group 1. Species intimately associated with poultry production in Europe		
Domestic Goose	*Anser anser domesticus*	High
Domestic Mallard	*Anas platyrhynchos*	High
Domestic Muscovy Duck	Cairina moschata	High
Feral Pigeon	*Columba livia*	High
House Sparrow	*Passer domesticus*	High
Group 2. Species which may share farmland also used by domesticated poultry in north Europe		
Eurasian Golden Plover	*Pluvialis apricaria*	Low
Northern Lapwing	*Vanellus vanellus*	Medium
Black-headed Gull	*Larus ridibundus*	High
Common Gull	*Larus canus*	High
Herring Gull	*Larus argentatus*	Low
Wood Pigeon	*Columba palumbus*	High
Eurasian Collared Dove	*Streptopelia decaocto*	High
Ring-necked Pheasant	*Phasianus colchicus*	High
Larks species	*Alauda & Galerida spp*	Low
Pipits		Low
Wagtails		Medium
Fieldfare	*Turdus pilaris*	Medium
Redwing	*Turdus iliacus*	Medium
Black-billed Magpie	*Pica pica*	High
Eurasian Jackdaw	*Corvus monedula*	High
Rook	*Corvus frugilegus*	Medium
Carrion Crow	*Corvus corone*	Medium
Raven	*Corvus corax*	Low
Starling	*Sturnus vulgaris*	High
Spotless Starling	*Sturnus unicolor*	High
House Sparrow	*Passer domesticus*	High
Eurasian Tree Sparrow	*Passer montanus*	High
Finches		Medium
Buntings	*Miliaria, Emberiza spp*	Medium
Group 3. Species which may share wetlands also used by domesticated waterbirds		
Egrets	*Egretta* spp.	Low
Herons	*Ardea* and other spp.	Medium
Cormorant	*Phalacrocrax carbo*	Medium
Storks	*Ciconia* spp.	Low
Mute Swan	*Cygnus olor*	Medium

Common name	*Scientific name*	*Probability of contact with poultry*
Greylag Goose	*Anser anser*	Medium
Canada Goose	*Branta canadensis*	Low
Ducks	*Anas* & *Aythya* spp. especially	Low
Mallard	*Anas platyrhynchos*	High
Common Coot	*Fulica atra*	Medium
Moorhen	*Gallinula chloropus*	Medium

10.3. Movements of Wild Bird Populations which may Affect Occurrence and Persistence of Asian Lineage H5N1 HPAIV within Europe

Given the number of important waterbird sites and the degree of complexity of European waterbird movements and migration systems, the exact spatial spread of the virus cannot be predicted but is likely to affect multiple regions.

10.4. Overall conclusions and recommendations on identification of wild bird species currently more likely to be infected with Asian Lineage H5N1 HPAIV and to expose domestic poultry within the EU

Conclusions

Using expert ornithological and epidemiological knowledge, groups of birds can be identified which have a higher probability of being relevant in both direct and indirect transmission of Asian lineage H5N1 HPAIV between wild birds and poultry.

Given the lack of systematic investigations into transmission dynamics in affected areas, the identification of bird species could not be based on published scientific data, but had to be based on expert opinion instead. The level of uncertainty is therefore high.

Given the number of important waterbird sites and the degree of complexity of European waterbird movements and migration systems, the exact spatial spread of the virus cannot be predicted but is likely to affect multiple regions.

Recommendations

Routine surveillance of wild birds is needed to establish whether wild birds are infected, and if so, the species concerned needs to be recorded. The need to identify cases of disease to species cannot be stressed enough. Wild birds represent a spectrum of behaviour and any risk assessment will be severely hampered without this fundamental piece of information for all surveillance programmes and cases of infection.

Surveillance activities should focus on the species identified in Table 13.1 of the Scientific Report (www.efsa.eu.int) and Table 10.1 of bird “bridge” species.

Recommendations for future research

There is a need to determine whether free-living wild birds, if infected with HPAI, can recover and/or carry the virus asymptomatically.

Field studies should be urgently undertaken on the behaviour of birds (*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 guidance on ways and means of reducing this risk.

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 determine what the duration of the excretion of the virus is.

The role of other, non-avian, bridge species, e.g. cat, fox, rat, dogs and mustelids, at least as mechanical vectors, merits investigation.

It is highly desirable that field studies be used to develop practical guidance on ways and means of reducing contact between wild waterbirds and domestic poultry - especially suitable for use in developing countries (village poultry situations).

Additional research on long distance migration of healthy birds is necessary to elucidate migratory flyways and staging areas for selected species. It is anticipated that the EURING/Wetlands International study (see Section 8.2) will make a substantial contribution to extending our knowledge of bird migration across Europe.

11. Surveillance of Wild Birds within EU regarding Infection with the Asian lineage H5N1 HPAIV

Conclusions

Passive surveillance in wild birds is valuable and can provide early warning of virus incursion as seen through recent mortality incidents in mute swans (*Cygnus olor*) and other species.

There is a continuing risk of introduction of AI from infected wild birds into poultry populations that may come into contact directly or indirectly with domestic poultry (EFSA, 2005). As a result surveillance systems have been enhanced in many areas especially Europe, both in wild birds and poultry, to better understand virus epidemiology and provide better early warning systems for detection of virus in poultry populations.

A prototype for a surveillance system has been developed by Swedish and Dutch researchers and been in operation in The Netherlands and Sweden since 2002.

System of sampling and specimen processing critically affect the outcome of laboratory tests. Methods should examine materials collected from both live and dead birds.

Screening by the use of RT-PCR targeting 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

Influenza virus surveillance studies in wild birds should be based on an effective sampling system that can be easily implemented at various sites and mirrors the relevant populations to be investigated. Ideally the catching and sampling systems should be harmonised between different sites across EU and beyond to allow meaningful interpretation of the prevalence and temporal patterns of the occurrence of different AI subtypes in specific bird populations.

The statistical properties of the sampling schemes need to be considered when interpreting the data. Biases affecting bird selection need to be recorded, and considered in data interpretation.

The potential host species of Asian H5N1 HPAI virus are largely unknown, and may be different from the natural hosts of LPAI viruses. Thus, monitoring a wider range of potential host species may be desirable. In addition, the existing surveillance networks should be adapted to include bird species that have the potential to migrate directly from areas where the Asian lineage H5N1 HPAIV has been detected in poultry and/or wild birds (see Chapter 10 of the Scientific Report, ww.efsa.eu.int).

Surveillance studies should include provision for timely examination of unusual wild bird mortality incidents involving one or more species in a single region or location. This is especially critical for evidence gathering in the context of Asian lineage H5N1 HPAIV presence in birds in areas that were previously considered to be free of the virus.

Appropriate health and safety precautions need to be defined for people collecting samples that may potentially contain zoonotic pathogens.

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

In addition, 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).

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

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, data should be collected and reported on the species of birds involved. To avoid ambiguity, reporting of such information should: i) involve the use of Latin species names; and ii) use a standardised taxonomic reference. In this respect the taxonomy of Sibley and Monroe (1990, with corrections of 1993) is recommended.

There is an urgent need to develop AI surveillance field skills in many countries – notably related to the techniques used for the trapping, live birds species identification, perhaps using centralised information sources (i.e. digital camera, e-mail), and sampling of waterbirds. These skills may be enhanced by the development of training courses and programmes, by existing centres of expertise, so as to encourage the international transfer of expertise.

Recommendations for future research

Further outbreaks of H5N1 HPAIV in poultry and domestic geese and ducks should routinely trigger surveillance in local populations of wild (water) birds. Information from such surveillance is essential to elucidate routes of infection.

Analyse cumulative bird ringing recovery data to estimate the importance of the connection between Asian, African and European bird populations.

Reservoir hosts for Asian lineage H5N1 HPAIV should be determined through surveillance programmes in a broader species range informed by migratory data linked to actual spread of the virus. There is a need to identify the duration of persistence of the AI virus in the wild fauna (and especially in species with the highest risk of transmission of the virus to domestic poultry in the EU infected areas).

12. Characterization of Regional Poultry Husbandry and Production Systems in the EU

Conclusions

The modelling procedure used to generate the poultry density distributions has not been validated against detailed national data. Based on these predictions, poultry population density is highly clustered within Europe, with particularly high densities occurring in Belgium and The Netherlands, the north-western region of France and Northern Ireland.

Based on currently available statistical data, farms with 1- 99 heads of broiler or layer chickens represent the majority of farms across EU member states. There is no data available at EU level regarding the spatial distribution of poultry holdings within countries, and their spatial distribution therefore currently has to estimated using statistical models. It is recognised that some EU countries have geo-referenced data on poultry farm locations, but this is usually restricted to farms belonging to poultry productions sectors 1 and 2 (FAO 2004).

Biosecurity measures at poultry farm level are incorporated in different pieces of EU legislation and include animal health and welfare measures, measures for control of environmental contamination, the reporting of suspected outbreaks of disease to the competent authority and for keeping of farm records. The actions of slaughterhouse operators are also the subject of statutory measures.

Biosecurity requirements for the marketing of live poultry are currently being regulated by Council Directive 90/539/EEC.

Currently, in case of suspicion and confirmation of Asian lineage H5N1 HPAIV outbreaks in poultry, the EU statutory legislation oversees the stamping-out of infected and suspected poultry, the identification of possible contacts via epidemiological inquiries, the restriction of movements for poultry commodities, waste, vehicles and persons, the set-up of zoning (protection and surveillance zones, the cleaning and disinfection of infected premises, vehicles and equipment and also the implementation of emergency vaccination of poultry flocks.

Following recent outbreaks of Asian lineage H5N1 HPAIV the following set of measures has been put in place by EU legislation:

- Establishment of safeguard measures by third countries and member states surveillance in poultry and wild birds
- Set-up of biosecurity and early detection systems
- Use of vaccination in zoos
- Approval of preventive vaccination in poultry.

A chronology of the latest EU legislation can be found on the DG Sanco Website: http://europa.eu.int/comm/food/animal/diseases/controlmeasures/avian/ai_addmeasures_en.htm.

Control strategies currently required by EU legislation after detection of H5N1 HPAIV in wild birds do not take the mobility of wild birds into account. Spatially limited risk management zones do not adequately consider the dynamic behaviour of bird populations.

According to the OIE Terrestrial Animal Health Code, no specific measures and including reporting are required after detection of HPAI in wild birds and no trade implications are expected (note: the relevant section in the OIE Animal Health Code is currently being updated).

Recommendations

The geographical distribution of all poultry production sector farms needs to be defined for all EU countries, and made available through EUROSTAT.

Alternative control strategies need to be developed to assure adequate risk mitigation and proportionate response after cases of H5N1 HPAIV in wild birds.

Appropriate biosecurity measures need to be developed that can also be applied by backyard chicken producers.

13. 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, survival, 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 of wild birds to the Asian lineage H5N1 HPAIV – directly or indirectly – outside the EU is considered.

13.1. Probability that Wild Birds are Exposed to Asian Lineage H5N1 HPAIV in Countries in which Virus is Present

13.1.1. Presence of susceptible wild birds

Based on current data and given the very wide distribution of birds, the probability of presence of susceptible wild birds in countries where Asian lineage H5N1 HPAIV occurs in domestic poultry is considered to be **very high** (low uncertainty).

13.1.2. Transmission pathways of the Asian lineage H5N1 HPAIV from domestic birds to wild birds

Surveillance results from countries where outbreaks of Asian lineage H5N1 HPAIV occur in domestic poultry, document the circulation of virus strains of very high similarity in both domestic and wild bird populations. Under husbandry conditions similar to the ones of East and South-East Asia, the probability of transmission of Asian lineage H5N1 HPAIV from domestic birds to wild birds is **high**, and **very high** (medium uncertainty) if free-grazing ducks are present. Specific investigations of transmission pathways have, however, not been conducted.

13.1.3. Probability of infection of wild birds with Asian lineage H5N1 HPAIV

In summary, the probability of infection of wild birds in a population after exposure to Asian lineage H5N1 HPAIV must be considered **very high** in *Anseriformes* and *Charadriiformes* and **high** in other wild birds (high uncertainty). Many *Anseriformes* and *Charadriiformes* are migratory, and therefore may be able to spread infection.

13.2. Probability that Asian Lineage H5N1 HPAIV Infected Wild Birds Reach Mixing or Concentration Areas

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**. The later 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.

Minority opinion by Dirk Pfeiffer and Mike Sharp:

Based on the data available for this analysis, the probability of migratory birds reaching mixing and concentration areas after infection with Asian lineage H5N1 HPAIV is medium (high uncertainty). 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.

In contrast to the Panel's majority opinion, it was felt that the available data does not provide justification to specify a low (=event is rare but does occur) or high (=event occurs very often) risk for any of the migratory species considered here. By adopting these, risk managers are provided with two conclusions that are more weighted towards the ends of the probability spectrum than can be supported by the data. The lack of understanding about the survival of infected migratory birds is captured in the high uncertainty attributed to the conclusion.

13.3. 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** (medium uncertainty) where there is a high density of birds.

13.4. Probability of Detection Given Infection

The probability of detection of Asian lineage H5N1 HPAI infection in wild birds at mixing and concentration areas is dependent on the extent of passive and active surveillance implemented, and currently is considered to be **low** (high uncertainty) outside the EU.

Under the assumption that Asian lineage H5N1 HPAIV may cause low or moderate mortality (although in some cases high mortality has resulted, e.g. Lake Qinghai), the probability of detection is **very low** (high uncertainty).

13.5. Probability of Infected Wild Birds Reaching Staging, Wintering, or Breeding Areas within EU

13.5.1. Selecting wild bird species more likely to be exposed to Asian lineage H5N1 HPAIV outside the EU and occurring in the EU

The degree of mixing (e.g. mixed foraging, mixed roosts, mixing at moulting areas) of infected birds with other bird species is considered to be another influential factor. Situations where there is a limited or no mixing would reduce the probability of exposure to a **negligible** level.

Gregariousness of a bird species is thought to be directly related to the probability of exposure to Asian lineage H5N1 HPAIV because the probability of cross infection increases with the number and density of birds in any areas. Birds living solitarily or in small groups (few tens of birds) resulting in low density of birds (>5 m between individuals) are thought to exhibit **negligible** probability of exposure.

The habitat used by a bird species (during migration and wintering or breeding) is anticipated to affect the probability of exposure to Asian lineage H5N1 HPAIV with birds preferring marine and/or littoral habitats experiencing **negligible** probability of exposure. Both water chemistry and temperature influence the survival of the virus.

Global infection status in relation to Asian lineage H5N1 HPAIV: the situation in winter and spring 2005/2006 is highly dynamic. The global distribution of Asian lineage H5N1 HPAIV alters the probability of virus circulation along flyways and at certain mixing and concentration areas. This in turn influences the European bird species at risk of exposure during migration. This assessment therefore needs to be continuously updated.

Although bird migration is a complex and highly variable process, movement patterns for individual bird species can be described. Such knowledge of timing and location ranges from reasonable precision of timing (e.g. some goose populations) and location to general patterns with significant uncertainty levels.

The probability of introduction of Asian lineage H5N1 HPAIV by a bird species is directly associated with the number of individual birds migrating into the EU. Species that are very common are presumed to have a higher risk (notably if they are susceptible) as a function of the greater numbers of individuals.

Using these criteria, a decision tree for identifying migratory bird species with an increased probability of carrying Asian lineage H5N1 HPAIV to the EU was developed based on data available in April 2006. Due to the dynamic situation at the time of writing, the factor "migration through infected area" was not applied. Factors "susceptibility", "gregariousness" and "mixing" were already considered. Applying this approach, a list of wild bird species of higher significance in terms of transmission of Asian lineage H5N1 HPAIV was obtained (Table 13.1, summary based on Table 11.2 of the Scientific Report, www.efsa.eu.int). This list needs to be updated when new data related to any of the factors listed above become available. The list is not a closed list and should be regularly updated. It can be used as a framework for targeting surveillance efforts in migratory birds. It is emphasised that population size is another influential parameter for species prioritisation, which must be applied according to the regional situation.

Table 13.1. European bird species with higher probability to contribute to transmission of Asian linage H5N1 HPAIV inside the European Union due to their susceptibility, habitat and behaviour (gregariousness and mixing). Data on breeding populations from BirdLife International (2004) and for biogeographical populations from Wetlands International (2002) (summary based on Table 11.2 of the Scientific Report)

Common name	*Scientific name*	*Population name*	*Population size EU25*	*Units*
Breeding populations				
Mute Swan	*Cygnus olor*	EU25 breeding population	68,000-92,000	Pairs
Lesser White-fronted Goose	*Anser erythropus*	EU25 breeding population	0-5	Pairs
Bean Goose	*Anser fabalis*	EU25 breeding population	2,300-3,200	Pairs
Greylag Goose	*Anser anser*	EU25 breeding population	65,000-87,000	Pairs
Canada Goose	*Branta canadensis*	EU25 breeding population	Unknown	Pairs
Barnacle Goose	*Branta leucopsis*	EU25 breeding population	5,900-7,600	Pairs
Eurasian Wigeon	*Anas penelope*	EU25 breeding population	70,000-120,000	Pairs
Common Teal	*Anas crecca*	EU25 breeding population	220,000-360,000	Pairs
Mallard	*Anas platyrhynchos*	EU25 breeding population	1,600,000-2,800,000	Pairs
Northern Pintail	*Anas acuta*	EU25 breeding population	16,000-27,000	Pairs
Garganey	*Anas querquedula*	EU25 breeding population	14,000-23,000	Pairs
Northern Shoveler	*Anas clypeata*	EU25 breeding population	30,000-38,000	Pairs
Marbled Teal	*Marmaronetta angustirostris*	EU25 breeding population	30-210	Pairs
Red-crested Pochard	*Netta rufina*	EU25 breeding population	4,200-12,000	Pairs
Common Pochard	*Aythya ferina*	EU25 breeding population	69,000-110,000	Pairs
Tufted Duck	*Aythya fuligula*	EU25 breeding population	180,000-290,000	Pairs
Coot	*Fulica atra*	EU25 breeding population	590,000-1,100,000	Pairs
Northern Lapwing	*Vanellus vanellus*	EU25 breeding population	830,000-1,300,000	Pairs
Ruff	*Philomachus pugnax*	EU25 breeding population	51,000-71,000	Pairs
Black-headed Gull	*Larus ridibundus*	EU25 breeding population	990,000-1,300,000	Pairs
Common Gull	*Larus canus*	EU25 breeding population	270,000-420,000	Pairs
Non-breeding populations				
Mute Swan	*Cygnus olor*	NW & C European population	250,000	Individuals
		Great Britain population	37,500	Individuals
		Ireland population	10,000	Individuals
Bewick's Swan	*Cygnus columbianus bewickii*	*Cygnus columbianus bewickii*	29,000	Individuals
Pink-footed Goose	*Anser brachyrhynchus*	Greenland/Iceland population	240,000	Individuals
		Svalbard population	37,000	Individuals
Greater White-fronted Goose (European race)	*Anser albifrons albifrons*	Baltic-North Sea population	1,000,000	Individuals

Common name	*Scientific name*	*Population name*	*Population size EU25*	*Units*
		Pannonic population	10,000-40,000	Individuals
Lesser White-fronted Goose	*Anser erythropus*	North European population	8,000-13,000	Individuals
Greylag Goose	*Anser anser anser*	Iceland population	89,100	Individuals
		NW Scotland population	9,000	Individuals
		NW Europea population	400,000	Individuals
		C Europe	25,000	Individuals
Canada Goose	*Branta canadensis*		Unknown	Individuals
Barnacle Goose	*Branta leucopsis*	Greenland population	54,100	Individuals
		Svalbard population	23,000	Individuals
Barnacle Goose	*Branta leucopsis*	Russian population	360,000	Individuals
Eurasian Wigeon	*Anas penelope*	NW Europe population	1,500,000	Individuals
		Black Sea/Mediterranean population	300,000	Individuals
Common Teal	*Anas crecca*	NW Europe population	400,000	Individuals
		Black Sea/Mediterranean population	750,000-1,375,000	Individuals
Mallard	*Anas platyrhynchos*	NW Europe	4,500,000	Individuals
		W Mediterranean population	1,000,000	Individuals
		E Mediterranean population	2,000,000	Individuals
Northern Pintail	*Anas acuta*	NW Europe population	60,000	Individuals
		Black Sea/Mediterranean population	1,000,000	Individuals
Garganey	*Anas querquedula*	W Africa population	>2,000,000-3,000,000	Individuals
Northern Shoveler	*Anas clypeata*	NW & C Europe	40,000	Individuals
		Black Sea, Mediterranean & W Africa population	450,000	Individuals
Marbled Teal	*Marmaronetta angustirostris*	W Mediterranean & W Africa population	3,000-5,000	Individuals
Red-crested Pochard	*Netta rufina*	C Europe & W Mediterranean population	50,000	Individuals
		Black Sea & E Mediterranean population	20,000-43,500	Individuals
Common Pochard	*Aythya ferina*	NE & NW Europe	350,000	Individuals
		Black Sea & E Mediterranean population	1,100,000	Individuals
Tufted Duck	*Aythya fuligula*	NW Europe	1,200,000	Individuals
		C Europe, Black Sea & Mediterranean population	700,000	Individuals
Coot	*Fulica atra*	NW Europe population	1,750,000	Individuals
		Black Sea/Mediterranean population	2,500,000	Individuals
Northern Lapwing	*Vanellus vanellus*	Europe population	2,800,000-4,000,000	Individuals
Ruff	*Philomachus pugnax*	W Africa population	>1,000,000	Individuals

Common name	*Scientific name*	*Population name*	*Population size EU25*	*Units*
Black-headed Gull	*Larus ridibundus*	N & C Europe population	5,600,000-7,300,000	Individuals
		Mediterranean population	1,300,000-1,700,000	Individuals
Common Gull	*Larus canus*	*Larus canus canus* (NW Europe)	1,300,000-2,100,000	Individuals
		Larus canus heinei (SE Europe, Black & Caspian Seas)	100,000-1,000,000	Individuals

13.5.2. Probability that wild birds infected with Asian lineage H5N1 HPAIV survive for extended periods and are able to travel long distances

Currently available data suggests that the likelihood is **medium** (high uncertainty) for the species identified in Section 13.5.1.

13.6. Conclusion on Probability of Release of Asian Lineage H5N1 HPAIV through Migratory Birds into EU

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 13.1 shows the preliminary list of bird species with higher probability to be exposed to Asian linage 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.

Minority opinion by Dirk Pfeiffer:

Release is defined as covering all biological pathways necessary to lead to the “importation” of the virus to the EU (OIE 2005). The release assessment includes the estimation of the probability for this entire process. It considers how it can be affected by various factors including risk management measures. The resulting conditional probability of release of Asian lineage H5N1 HPAIV into the EU through wild birds which became infected outside the EU is **medium** (high uncertainty) (Table 13.2). Using the interpretation given in Table 1.1, this means that Asian lineage H5N1 HPAIV can be expected to be released into the EU by migratory birds as a regular event (as distinct from rare or very often). It should be noted that this qualitative probability estimate is associated with a high level of uncertainty. It is particularly high as a result of the apparent variation of the pathogenicity of the virus in different species and their potential survival. There are a large number of species that are potentially affected but only one (Mallard *Anas platyrhynchos*) has been tested experimentally. This uncertainty affects both the migration to and from mixing and concentration areas. The probability of detection of infection in wild birds at mixing and concentration areas is extremely dependent on the level and type of surveillance, which is not standardised between countries.

In contrast to the Panel’s majority opinion, it was felt that the available data does not provide justification to specify a low or high risk for any of the migratory species considered here. By adopting these, risk managers are provided with two

conclusions that are more weighted towards the ends of the probability spectrum than can be supported by the data.

Table 13.2. Summary of qualitative assessment of the probability and uncertainty of elements of the release assessment pathways of Asian lineage H5N1 HPAIV introduction to the EU via migratory wild birds

Risk pathway	*Probability*	*Uncertainty*
Presence of susceptible wild birds in countries where Asian lineage H5N1 HPAIV occurs (see Section 13.1.1)	Very high	Low
Transmission of Asian lineage H5N1 HPAIV from domestic poultry to migratory or non-migratory wild birds under management conditions similar to East and South-east Asia via direct or indirect pathways (see Section 13.1.2)	High – very high *	Medium
Infection of wild birds after exposure to Asian lineage H5N1 HPAIV (see Section 13.1.3))	High - very high	High
Infected wild birds reach mixing or concentration areas (see Section 13.2)	Low to high (Minority opinion: Medium)	High
Transmission of Asian lineage H5N1 HPAIV between wild birds at mixing and concentration areas (see Section 13.3)	Very high	Medium
Detection of infection (see Section 13.4)	Very low – low **	High
Infected wild birds reach staging, wintering or breeding areas inside EU after infection outside EU (see Section 13.5.2)	Medium ***	High
Summary: Conditional probability of some Asian lineage H5N1 HPAIV being released into the EU by migratory birds (in species listed in Section 13.5.1; see Section 13.6)	High (Minority opinion: Medium***)	High
Summary: Conditional probability of some Asian lineage H5N1 HPAIV being released into the EU by migratory birds (in species not listed in Section 13.5.1; see Section 13.6)	Low (Minority opinion: Medium***)	High

* depending on whether free-grazing ducks are present
** depending on mortality caused
*** wild bird species identified in Section 13.5.1

13.7. Recommendations

It is to be noted that the different conclusion expressed in the minority opinion did not result in different recommendations, since the latter are relatively generic.

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.

14. Risk Assessment for Risk Question 2a: Exposure and Consequence Assessment for Wild Birds within the EU and subsequent Endemic Infection

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

14.1. Probability of Exposure of Non-Migratory Wild Birds to Asian Lineage H5N1 HPAIV in Wild Migratory Birds entering the EU

14.1.1. Presence of susceptible non-migratory wild birds in EU

Considering the conclusions drawn under 13.1.1 and the abundance and variety of wild birds in Europe, including species of documented susceptibility such as mallards (*Anas platyrhynchos*) and mute swans (*Cygnus olor*), the probability of susceptible non-migratory bird species being present is **very high** (medium uncertainty), at least in some regions. However, systematic data on susceptibility differences between species are not available. Investigations conducted in Europe (Fouchier et al. 2003) documented isolations predominantly of low pathogenic AI virus from ducks, geese and gulls. Regional differences in the abundance of susceptible species are expected as a consequence of their distribution and habitats. If common species such as sparrows are confirmed to be susceptible (Kou et al. 2005), the geographical differences may become less distinct.

In early 2006, Asian lineage H5N1 HPAIV was isolated repeatedly from wild birds in several European countries. Mute swans (*Cygnus olor*) were frequently over-represented in these outbreaks which may indicate an increased pathogenicity of Asian lineage H5N1 HPAIV in these birds, or sampling bias owing to their high visibility and frequent association with habitats close to human habitation.

14.1.2. Probability of direct exposure of non-migratory wild birds to Asian lineage H5N1 HPAIV

The probability of exposure of non-migratory birds will depend on whether the migratory bird species are carrying Asian lineage H5N1 HPAIV, the number of infected birds, the mechanism of shedding (faecal vs. tracheal), and the mortality. Based on available data, it is not possible to predict the most likely scenario. Considering the abundance and wide distribution of waterbirds and the inter-connection of wetlands, the probability of direct exposure of at least some non-migratory bird species to wild migratory birds is very high and so their potential exposure to Asian lineage H5N1 HPAIV carried by migratory birds is **high** (medium uncertainty), particularly if these non- migratory birds are waterbirds.

EU Member States are situated over a large geographical area with diverse climate and habitats. The presence of non-migratory species at a given point in time is therefore variable between and within countries. No general statement can be therefore made that is valid for all countries in terms of the probability of exposure of non-migratory birds to Asian lineage H5N1 HPAIV in migratory birds.

14.1.3. Probability of indirect exposure of non-migratory wild birds to Asian lineage H5N1 HPAIV

Transmission via the environment depends on the stability of the virus and on the overlap of bird habitats. Wetlands are expected to offer considerable potential for both direct and indirect exposure of non-migratory waterbirds. Considering climatic conditions in Europe, virus characteristics, the abundance of wetland habitats, the inter-connection of wetlands and the variety of wild birds in Europe, the probability of indirect exposure is **high** (medium uncertainty) for at least some regions and types of habitats in Europe. Regional differences are expected.

There is empirical evidence that birds scavenging on carcasses of other birds are at risk of becoming infected with Asian lineage H5N1 HPAIV. Based on current data, these birds are considered to be dead-end hosts, and therefore represent a **very low** (medium uncertainty) risk for spread. They were therefore not considered further in the risk assessment.

14.1.4. Probability of infection of wild birds following exposure to Asian lineage H5N1 HPAIV

There are very few data on inter-species transmission dynamics of Asian lineage H5N1 HPAIV. Experimental data document the influence of infection dose, host and virus factors. The probability of infection cannot be assessed by bird species at present. Based on empirical data collected in China and based on the number of wild bird species from which Asian lineage H5N1 HPAIV has been isolated in Europe it must be assumed that infection is possible, and can be categorized as **medium** (high uncertainty). For some species including mallards (*Anas platyrhynchos*) and mute swans (*Cygnus olor*), the probability of infection is **high** (high uncertainty).

14.1.5. Probability of detection of infection with Asian lineage H5N1 HPAIV in migratory and non-migratory wild birds

Surveillance for AI viruses in wild birds has been conducted in the EU since 1999. Surveillance activities are currently being expanded and are mandatory since 2005. Both passive and active surveillance programmes are in place in most MS.

The goal of surveillance activities is early detection of the introduction of Asian lineage H5N1 HPAIV. Samples positive for Asian lineage H5N1 HPAIV predominantly originated from dead birds. An increasing number of such positive samples were detected in early 2006. Whether this is due to an increased prevalence of virus or due to increased awareness and surveillance activities cannot be determined, although there has been an increase in surveillance activity by MS since the mandatory requirement was implemented. At present, the probability of detection of Asian lineage H5N1 HPAIV infection in wild birds is **medium to high** (high uncertainty) if the virus causes mortality (or sickness), if large and highly visible birds are affected and if the outbreak occurs in an area that is frequented by humans. In a scenario where the virus causes no clinical signs or if only birds in a remote area or small or less visible birds are affected, the probability of detection is **low** (low uncertainty). The detection probability depends on the overall size of the population, the proportion of infected birds within the population, and the proportion of the population that is sampled.

14.2. Probability of Persistence of Asian Lineage H5N1 HPAIV in Migratory and Non-Migratory Wild Birds within the EU

There are very few data on the dynamics of Asian lineage H5N1 HPAIV in wild birds and no data for Europe. Based on data published by Chen et al. (2006), there is some evidence that substrains of Asian lineage H5N1 HPAIV may be endemic in wild birds in southern China. The information about transmission between migratory bird species discussed under Risk Question 1 in Chapter 13 partly also applies here.

Based on knowledge of population dynamics of LPAI in waterbirds, it must be assumed that the probability of persistence in migratory and non-migratory wild birds in the EU is **medium** (high uncertainty). The most likely long-term scenario appears to be persistence of the Asian lineage H5N1 HPAIV in wild bird species with relatively large population size in which it causes no or low mortality.

14.3. Conclusion on Probability of Asian Lineage H5N1 HPAIV becoming Endemic in Migratory and Non-Migratory Birds in the EU

The conditional probability of Asian lineage H5N1 HPAIV being transmitted to non-migratory birds is highly dependent on the probability of release, the species introducing the virus, the number of birds affected and the pathogenicity of the virus strain. The probability of release through migratory birds at the time of writing is **low to high** (high uncertainty; see Section 13.6) and the subsequent probability of persistence of the virus in migratory and non-migratory wild bird species in the EU is **low to high** (high uncertainty; see Table 14.1). However, there is high uncertainty related to these conclusions 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 expected. Due to the dynamic nature of the global situation, the assessment may change quickly.

Minority opinion by Dirk Pfeiffer:

The conditional probability of Asian lineage H5N1 HPAIV being transmitted to non-migratory birds is highly dependent on the probability of release, the species introducing the virus, the number of birds affected and the pathogenicity of the virus strain. The probability of release through migratory birds at the time of writing is **medium** (high uncertainty; see Section 13.6) and the subsequent probability of persistence of the virus in migratory and non-migratory wild bird species in the EU is **medium** (high uncertainty; see Table 14.1). However, there is high uncertainty related to these conclusions 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 expected. Due to the dynamic nature of the global situation, the assessment may change quickly.

In contrast to the Panel's majority opinion, it was felt that the available data does not provide justification to specify a low or high risk for any of the migratory species considered here. By adopting these, risk managers are provided with two conclusions that are more weighted towards the ends of the probability spectrum than can be supported by the data.

Table 14.1. Summary of qualitative assessment of the probability and uncertainty of elements of exposure and consequence pathways of Asian lineage H5N1 HPAIV becoming endemic in migratory and non-migratory European wild birds

Risk pathway	*Probability*	*Uncertainty*
Input from release assessment: Conditional probability of migratory birds introducing Asian lineage H5N1 HPAIV into the EU (see Section 13.6)	Low to high (Minority opinion: Medium *)	High
Presence of susceptible non-migratory birds (see Section 14.1.1)	Very High	Medium
Direct exposure of non-migratory birds to migratory birds carrying Asian lineage H5N1 HPAIV (seee Section 14.1.2)	High	Medium
Indirect exposure of non-migratory birds to migratory birds carrying Asian lineage H5N1 HPAIV (see Section 14.1.3)	High	Medium
Infection of non-migratory wild birds after exposure to Asian lineage H5N1 HPAIV from migratory birds (see Section 14.1.4)	Medium – high *	High
Detection of infection in migratory and non-migratory wild birds (see Section 14.1.5)	Low or medium to high**	Low or High**
Persistence of infection in migratory and non-migratory bird populations (see Section 14.2)	Medium	High
Summary: Conditional probability of Asian lineage H5N1 HPAIV becoming endemic in non-migratory European wild birds depending of the susceptibity of the species	Low to high (Minority opinion: see below)	High
Summary: Conditional probability of Asian lineage H5N1 HPAIV becoming endemic in non-migratory European wild birds depending on temperature-dependent environmental conditions (water, etc)	Low to high (Minority opinion: see below)	High
Minority opinion: Summary: Conditional probability of Asian lineage H5N1 HPAIV becoming endemic in migratory and non-migratory European wild birds (see Section 14.3)	(Minority opinion: Medium)	High

* Depending on whether species is included in Section 13.5.1

**Depending on species, pathogenicity and level of surveillance

14.4. Recommendations

It is to be noted that the different conclusion expressed in the minority opinion did not result in different recommendations, since the latter are relatively generic.

Surveillance of species listed in Table 13.1 will provide an indication of the level of endemicity and help target biosecurity measures for domestic poultry.

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.

Recommendations for future research

The interactions between migratory and non-migratory wild birds and the dynamics of their movements within the EU need to be studied.

15. 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 transmission to domestic poultry within the EU as a consequence of infection in migratory birds (Question 1) or wild birds resident within the EU (Question 2a)?

15.1. Direct and Indirect Exposure of Poultry to Asian Lineage H5N1 HPAIV through Wild Birds

15.1.1. Factors influencing the probability of exposure relating to infected migratory birds

Influential factors with respect to the probability of exposure of domestic poultry are: Wild bird species carrying the virus, number of wild birds infected, time and location of introduction. A possible scenario will be that Asian lineage H5N1 HPAIV is introduced into Europe via migrating waterbirds. It might then be transmitted to non-migratory waterbirds and/or to domestic poultry.

The decision tree used to define the migratory wild bird species more likely to release Asian lineage H5N1 HPAIV produced a list species shown in (Table 13.1). This list was further refined using expert opinion to identify those migratory wild bird species which also are more likely to come into contact with domestic poultry (see Table 15.1, summary based on Table 13.1 of the Scientific Report, www.efsa.eu.int).

EU Member States are situated over a large geographical area with diverse climate and habitats. The presence of migratory bird species at a given point in time is therefore variable between and within countries. No general statement can be made that is valid for all countries in terms of the probability of direct exposure of poultry to Asian lineage H5N1 HPAIV from wild birds.

Table 15.1. Migratory waterbirds at increased probability of exposure to H5N1 HPAIV outside the EU, and migrating to EU countries where they are at increased probability of contact with EU poultry based on expert opinion (summary based on Table 13.1 of the Scientific Report, www.efsa.eu.int).

Common name	*Scientific name*	*Population name*	*Population size EU25*	*Units*
<u>Breeding populations</u>				
Mute Swan	*Cygnus olor*	EU25 breeding population	68,000-92,000	Pairs
Bean Goose	*Anser fabalis*	EU25 breeding population	2,300-3,200	Pairs

Common name	*Scientific name*	*Population name*	*Population size EU25*	*Units*
Greylag Goose	*Anser anser*	EU25 breeding population	65,000-87,000	Pairs
Canada Goose	*Branta canadensis*	EU25 breeding population	Unknown	Pairs
Barnacle Goose	*Branta leucopsis*	EU25 breeding population	5,900-7,600	Pairs
Eurasian Wigeon	*Anas penelope*	EU25 breeding population	70,000-120,000	Pairs
Common Teal	*Anas crecca*	EU25 breeding population	220,000-360,000	Pairs
Mallard	*Anas platyrhynchos*	EU25 breeding population	1,600,000-2,800,000	Pairs
Northern Pintail	*Anas acuta*	EU25 breeding population	16,000-27,000	Pairs
Garganey	*Anas querquedula*	EU25 breeding population	14,000-23,000	Pairs
Northern Shoveler	*Anas clypeata*	EU25 breeding population	30,000-38,000	Pairs
Marbled Teal	*Marmaronetta angustirostris*	EU25 breeding population	30-210	Pairs
Red-crested Pochard	*Netta rufina*	EU25 breeding population	4,200-12,000	Pairs
Common Pochard	*Aythya ferina*	EU25 breeding population	69,000-110,000	Pairs
Tufted Duck	*Aythya fuligula*	EU25 breeding population	180,000-290,000	Pairs
Coot	*Fulica atra*	EU25 breeding population	590,000-1,100,000	Pairs
Northern Lapwing	*Vanellus vanellus*	EU25 breeding population	830,000-1,300,000	Pairs
Ruff	*Philomachus pugnax*	EU25 breeding population	51,000-71,000	Pairs
Black-headed Gull	*Larus ridibundus*	EU25 breeding population	990,000-1,300,000	Pairs
Common Gull	*Larus canus*	EU25 breeding population	270,000-420,000	Pairs
Non-breeding populations				
Mute Swan	*Cygnus olor*	NW & C European population	250,000	Individuals
		Great Britain population	37,500	Individuals
		Ireland population	10,000	Individuals
Bewick's Swan	*Cygnus columbianus bewickii*	*Cygnus columbianus bewickii*	29,000	Individuals
Pink-footed Goose	*Anser brachyrhynchus*	Greenland/Iceland population	240,000	Individuals
		Svalbard population	37,000	Individuals
Greater White-fronted Goose (European race)	*Anser albifrons albifrons*	Baltic-North Sea population	1,000,000	Individuals
		Pannonic population	10,000-40,000	Individuals
Lesser White-fronted Goose	*Anser erythropus*	North European population	8,000-13,000	Individuals
Greylag Goose	*Anser anser anser*	Iceland population	89,100	Individuals
		NW Scotland population	9,000	Individuals
		NW Europea population	400,000	Individuals
		C Europe	25,000	Individuals
Canada Goose	*Branta canadensis*		Unknown	Individuals
Barnacle Goose	*Branta leucopsis*	Greenland population	54,100	Individuals
		Svalbard population	23,000	Individuals
Barnacle Goose	*Branta leucopsis*	Russian population	360,000	Individuals
Eurasian Wigeon	*Anas penelope*	NW Europe population	1,500,000	Individuals
		Black Sea/Mediterranean population	300,000	Individuals
Common Teal	*Anas crecca*	NW Europe population	400,000	Individuals
		Black Sea/Mediterranean population	750,000-1,375,000	Individuals
Mallard	*Anas platyrhynchos*	NW Europe	4,500,000	Individuals
		W Mediterranean population	1,000,000	Individuals
		E Mediterranean population	2,000,000	Individuals
Northern Pintail	*Anas acuta*	NW Europe population	60,000	Individuals
		Black Sea/Mediterranean population	1,000,000	Individuals

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

15.1.2. Factors influencing the probability of exposure relating to non-migratory birds

The probability of poultry exposure to non-migratory infected birds is influenced by the species of birds infected, the number of infected birds, the clinical signs in these birds and the contact between domestic and wild birds.

Additionally, non-migratory bird species were identified that could act as bridge species (Table 15.2, summary based on Table 10.1). Bridge species were defined as birds that live in close proximity to domestic poultry – perhaps sharing buildings or food sources. The list is not a closed list and should be regularly updated. It can be used as the basis for targeting surveillance efforts in wild birds.

EU Member States are situated over a large geographical area with diverse climate and habitats. The presence of wild bird species at a given point in time is therefore variable between and within countries. No general statement can be made that is valid for all countries in terms of the probability of exposure of poultry to Asian lineage H5N1 HPAIV from wild birds.

Table 15.2. Non-migratory European bird species that live in proximity to domestic poultry and which could expose domestic poultry to Asian lineage H5N1 HPAIV (summary based on Table 10.1)

Common name	*Scientific name*	*Probability of contact with poultry*
Group 1. Species intimately associated with poultry production in Europe		
Domestic Goose	*Anser anser domesticus*	High
Domestic Mallard	*Anas platyrhynchos*	High

Common name	*Scientific name*	*Probability of contact with poultry*
Domestic Muscovy Duck	Cairina moschata	High
Feral Pigeon	*Columba livia*	High
House Sparrow	*Passer domesticus*	High
Group 2. Species which may share farmland also used by domesticated poultry in north Europe		
Eurasian Golden Plover	*Pluvialis apricaria*	Low
Northern Lapwing	*Vanellus vanellus*	Medium
Black-headed Gull	*Larus ridibundus*	High
Common Gull	*Larus canus*	High
Herring Gull	*Larus argentatus*	Low
Wood Pigeon	*Columba palumbus*	High
Eurasian Collared Dove	*Streptopelia decaocto*	High
Ring-necked Pheasant	*Phasianus colchicus*	High
Larks species	*Alauda & Galerida spp*	Low
Pipits		Low
Wagtails		Medium
Fieldfare	*Turdus pilaris*	Medium
Redwing	*Turdus iliacus*	Medium
Black-billed Magpie	*Pica pica*	High
Eurasian Jackdaw	*Corvus monedula*	High
Rook	*Corvus frugilegus*	Medium
Carrion Crow	*Corvus corone*	Medium
Raven	*Corvus corax*	Low
Starling	*Sturnus vulgaris*	High
Spotless Starling	*Sturnus unicolor*	High
House Sparrow	*Passer domesticus*	High
Eurasian Tree Sparrow	*Passer montanus*	High
Finches		Medium
Buntings	*Miliaria, Emberiza spp*	Medium
Group 3. Species which may share wetlands also used by domesticated waterbirds		
Egrets	*Egretta* spp.	Low
Herons	*Ardea* and other spp.	Medium
Cormorant	*Phalacrocrax carbo*	Medium
Storks	*Ciconia* spp.	Low
Mute Swan	*Cygnus olor*	Medium
Greylag Goose	*Anser anser*	Medium
Canada Goose	*Branta canadensis*	Low
Ducks	*Anas* & *Aythya* spp. especially	Low
Mallard	Anas platyrhynchos	High
Common Coot	*Fulica atra*	Medium
Moorhen	*Gallinula chloropus*	Medium

15.1.3. Factors influencing the probability of indirect exposure of poultry

Indirect exposure of poultry is **higher than negligible** if surface water is used to which migratory or non-migratory infected birds have also access. The probability of indirect transmission of Asian lineage H5N1 HPAIV via contaminated forage or soil is unknown. In general, the probability of indirect exposure is most strongly influenced by the type of poultry production system (e.g. free-range production) and the related biosecurity measures (EFSA, 2005). Data from an outbreak in a UK quarantine facility suggests that aerosol transmission of infection from infected wild birds to chickens kept within the same airspace represents a very low risk.

Infected predator species could become infected by consumption of infected wild bird carcasses. If they have access to poultry populations kept under low biosecurity, they could expose poultry to infection.

15.1.4. Factors influencing the probability of exposure related to poultry management

Direct and indirect exposure of poultry can be prevented by biosecurity measures. Biosecurity is highest in intensively reared poultry and lower in free-range and backyard, village or hobby flocks, which also often are free-range. No data on the proportion of poultry kept under low biosecurity conditions are available for the EU. Such production systems are considered to be more prevalent in Eastern and Southern Europe. Additionally, the density of poultry is an influential factor on the probability of exposure. Regional differences with respect to poultry density exist and regional differences in the probability of exposure are therefore expected.

15.1.5. Conclusions on probability of exposure

In the context of Asian lineage H5N1 HPAIV, it is possible that infectious birds have in the recent past been present without there being transmission to poultry and also without significant mortality in wild bird populations.

The probability of exposure of free-range and backyard poultry is considered to be **high** (medium uncertainty), particularly if these are kept in the vicinity of wetland areas. Where high biosecurity standards are implemented on intensively reared poultry, the probability is **negligible** (low uncertainty). In densely populated poultry areas, even with high biosecurity measures, or if biosecurity is low in intensively reared poultry farms, the probability of exposure will be increased to **very low** (low uncertainty).

15.2. Probability of Domestic Poultry Becoming Infected Given Exposure to Asian lineage H5N1 HPAIV

Current data particularly from South-East Asian countries suggests that poultry are very susceptible to Asian lineage H5N1 HPAIV. It therefore has to be concluded that the probability of infection is **high** (low uncertainty).

15.3. Probability of Detection of Asian lineage H5N1 HPAIV in Infected Poultry

Infection with Asian lineage H5N1 HPAIV results in high mortality in domestic chicken species, and some mortality in domestic geese and ducks. The probability of detection of infection is therefore **very high** (low uncertainty).

15.4. Conclusion on Probability of Migratory or Non-Migratory Wild Birds Transmitting Asian Lineage H5N1 HPAIV to Domestic Poultry in the EU

As a result of the conditionality of the components of this risk assessment, the conclusions from the earlier components need to be considered. The relevant conclusions were that the probability of release of Asian lineage H5N1 HPAIV in migratory birds into the EU was **low to high** (high uncertainty) [Minority opinion: medium] and that the probability of it becoming endemic in non-migratory European wild birds was **low to high** (high uncertainty) [Minority opinion: medium].

In the light of these conclusions and the ones presented here for the current risk question, the probability of exposure of free-range and backyard poultry, and indoor poultry farms without high biosecurity standard is considered to vary between **low** to **medium** (high uncertainty), depending on the proximity of such poultry flocks to wild bird habitats such as wetland areas. For indoor poultry farms with high biosecurity standards, the probability is **negligible** (low uncertainty). If such farms are located in densely populated poultry areas, even with high biosecurity measures the probability will be increased to **very low** (low uncertainty).

Table 15.3. Summary of qualitative assessment of the probability and uncertainty of elements of exposure and consequence assessment for Asian lineage H5N1 HPAIV transmission from wild birds to poultry in the EU

Risk pathway	*Probability*	*Uncertainty*
Input from release assessment: Conditional probability of migratory birds infected with Asian lineage H5N1 HPAIV reaching EU (in species listed in Section 13.5.1; see Section 13.6)	Low to high (Minority opinion: medium)	High
Input from exposure assessment: Conditional probability of Asian lineage H5N1 HPAIV becoming endemic in migratory and non-migratory European wild birds (see Section 14.3)	Low to high (Minority opinion: Medium)	High
Exposure of free-range or backyard flocks (see Section 15.1.5)	High *	Medium
Exposure of intensively-reared or indoor flocks (see Section 15.1.5)	Negligible to very low **	Low
Transmission of Asian lineage H5N1 HPAIV to poultry (see Section 15.2)	High	Low
Detection of Asian lineage H5N1 HPAIV in poultry (see Section 15.3)	Very high	Low
Summary: Conditional probability of Asian lineage H5N1 HPAIV being transmitted from wild birds to poultry in free-range and backyard flocks in Europe or indoor flocks without high biosecurity standard (see Section 15.4)	Low – medium *	High
Summary: Conditional probability of Asian lineage H5N1 HPAIV being transmitted from wild birds to indoor poultry flocks kept under conditions of high biosecurity standard in a high poultry density population area (see Section 15.4)	Very low	Low
Summary: Conditional probability of Asian lineage H5N1 HPAIV being transmitted to poultry in Europe from wild birds to indoor poultry flocks kept under conditions of high biosecurity standard and in a low to moderately high poultry density population area (see Section 15.4)	Negligible **	Low

* Depending on proximity to wetlands

** Depending on density of farms and adherence to biosecurity measures

15.5. Recommendations

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 contaminanted 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, the general public should not conduct hunting or collect wild waterfowl themselves by some other method (note that they should still be encouraged to report finding dead birds), and the public should be encouraged to take basic hygiene precautions when visiting the vicinity of outbreak areas.
- Where vaccination is used, an appropriate number of unvaccinated sentinel birds should share the same environment as the vaccinated birds, ensuring that they are also exposed to faeces and beddings materials from the cages of the test birds.

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).

16. References

References used in this Scientific Opinion are available and are listed in the Scientific Report published at the EFSA web (www.efsa.eu.int).

17. 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, M. Sharp, K. Stärk, D. Stroud, B. Szewcyk, J. Veen, J. Waldenström, for the preparation of the Scientific Report, which has been used as the basis of this Scientific Opinion.

The scientific co-ordination for this Scientific Opinion has been undertaken by the EFSA AHAW Panel Scientific Officers, J. Serratosa and O. Ribó. Special acknowledgement is given to M. Pittman (AHAW scientific assistant) who moved to DG SANCO in February 2006.

Special acknowledgement is given to DG Environment, in particular Mr. Michael O'Briain. The following experts are also acknowledged for having contributed to the work of the working group: Ward Hagemeier (Wetlands International); François Moutou (AFSSA LERPAZ); Bjorn Olsen (Institute for Zoonotic Ecology and Epidemiology, Sweden); Mirzet Sabirovic (Department for Environment, Food and Rural Affairs, UK), Peter Cranswick and Rebecca Lee (Wildfowl & Wetlands Trust, UK), Andy Musgrove (BTO, UK), Ian Fisher (RSPB, UK), Ilya Maclean (British Trust for Ornithology), the British Trust for Ornithology, David Lacina, Philip Buckley and Andres Kuresoo (members of the Ornis Committee's Scientific Working Group).

18. AHAW Scientific Panel Members

The Scientific AHAW Panel adopted the current Scientific Opinion by written procedure on 12th May 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.