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.

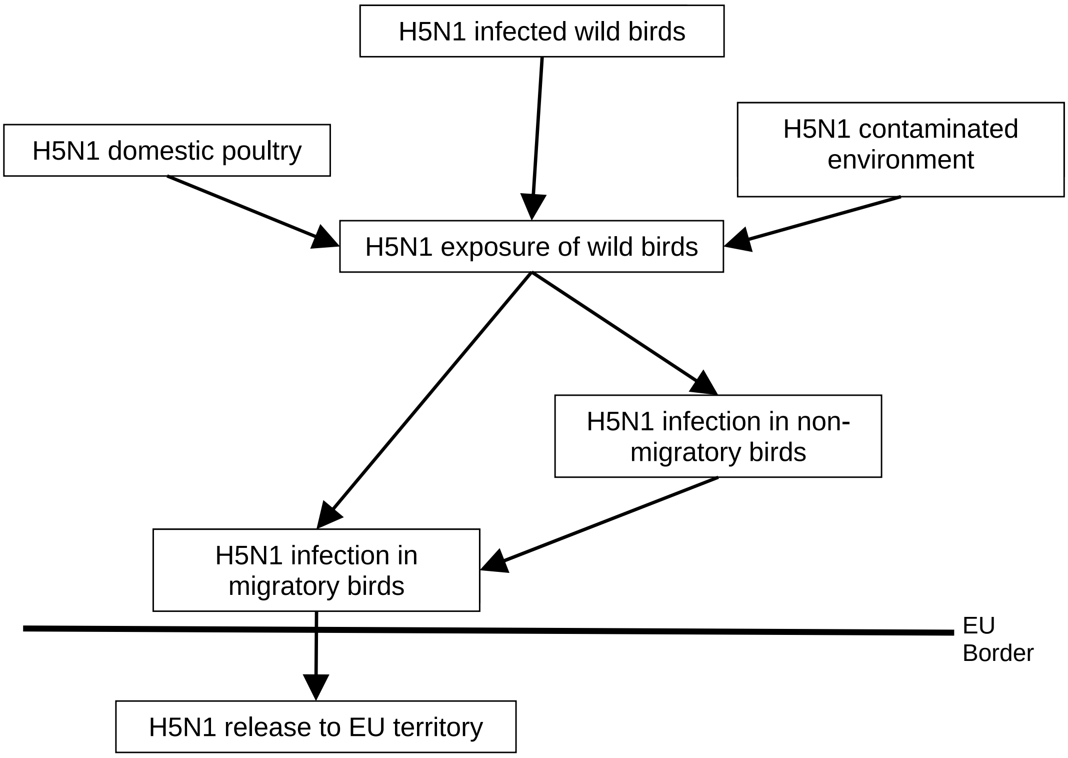


Figure 2.1. Release pathways of Asian lineage H5N1 HPAIV in territories outside the EU that may result in potential transmission of the virus leading to a release into EU territory (note that these pathways describe the potential mechanisms for release)

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).

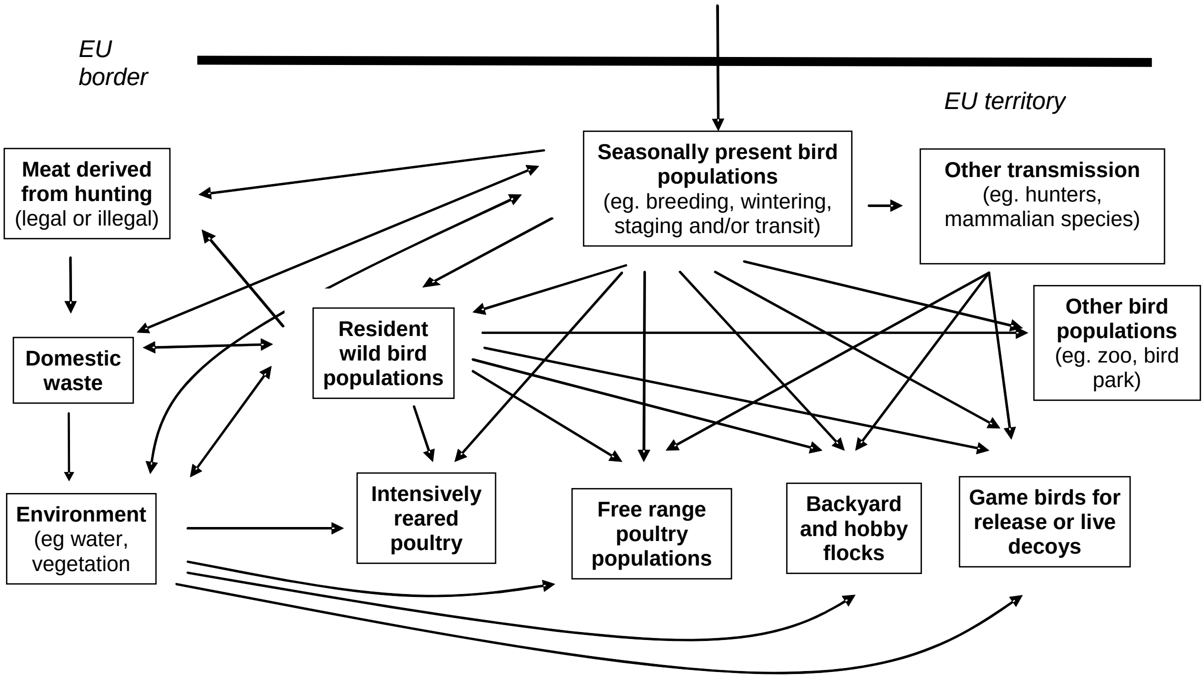


Figure 2.2. Exposure and consequence pathways for bird populations within the EU to Asian lineage H5N1 HPAIV after potential introduction of the virus by wild birds (note that these pathways include all potential direct and indirect exposure and transmission pathways)

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
<u>Non-breeding populations</u>				
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*
<u>Group 1. Species intimately associated with poultry production in Europe</u>		
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.

Annex to *The EFSA Journal* (2006) 357, 1-46, “Migratory birds and their possible role in the spread of highly pathogenic Avian Influenza”

Scientific Report 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

Table of Contents

1. Abbreviations

AEWA	African Eurasian Agreement on the conservation of migratory waterbirds
AI	Avian Influenza
Asian lineage H5N1 HPAIV	Eurasian strains of highly pathogenic avian influenza virus of subtype H5N1
BSL3+	Biosafety Level number 3+
CIRAD	Agricultural Research Centre for International Development
D.I.P.	Days post infectionem = days after infection
EFSA	European Food Safety Authority
EID_{50}	Egg-infective dose
ESRI	GIS provider
EU	European Union comprising 25 Member States (MS): Austria, Belgium, Cyprus, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Italy, Ireland, Latvia, Lithuania, Luxembourg, Malta, Netherlands, Poland, Portugal, Slovak Republic, Slovenia, Spain, Sweden, United Kingdom.
EURING	European Organisation for co-ordinated bird ringing
FAO	Food and Agriculture Organisation of the United Nations (UN)
GDR	Former German Democratic Republic
IBA	Important bird area
IVPI	Intravenous Pathogenicity Index
IWC	International Waterbird Census
H	Haemagglutinin
HPAI	highly pathogenic avian influenza
HP	highly pathogenic
HRS	High risk species (revise)
LPAI	low pathogenic avian influenza
LP	low pathogenicity
MS	Member States
N	Neuraminidase
NOAA-CIRES	National Oceanic&Atmospheric Administration/Cooperative Institute for Research in Environment & Sciences
NP	Nucleoprotein
NRCS	United States of America Natural Resources Convention Service
NS	Non structural protein
NWHC	United States of America National Wildlife Health Centre
OIE	Office International des Epizooties – World Organisation for Animal Health
PB2	Polymerase protein (complex) B2
PCR	Polymerase Chain Reaction
pH –value	pH (abbr. power of hydrogen) = measure of the activity of hydrogen ions (H+) in a solution and, therefore, its acidity or alkalinity.
p.i.	post inoculation
RNA	Ribonucleic acid
SPA	Special Protection Areas classified under the Directive on the conservation of wild birds (EC/79/409)
SPF	Specified pathogen free eggs
RA	Risk assessment

$TCID_{50}$	**Tissue culture infective doses**
UNESCO	**United Nations Educational, Scientific and Cultural Organisation**
USDA	**United States of America Department of Agriculture**
USGS	**United States of America Geological Service**
WBDB	**World Birds Data Base**

2. Glossary and Definitions

Biogeographical population

A population of a species or a sub-species that is either geographically detached from other populations at all times of the year, or at some times of the year only, or is a specified part of a continuous distribution so defined for the purposes of conservation management.

Bird population movements

The movement of populations of birds between two locations. This may involve a number of different biological processes, including seasonal migration, post-breeding dispersion and cold weather movements. It generally excludes more local and short-term movements shown by some birds between feeding and roost areas. See Alerstam (1993) and Bairlein *et al.* (2002) for more information.

Concentration area

Essentially similar to mixing areas - an area where many individuals of a bird species typically congregate. Usually such areas are located in regions used in the non-breeding season, notably migration staging areas or moulting areas. Whilst mixing areas are defined by multi-species use, concentration areas may also relate to sites where there is a high density of a single species (such as some traditional goose roosts).

Decoy birds

Captive birds which are used for the purposes of attracting wild birds to an area such that they may be either captured or killed.

Exposure

The condition of being subjected to a source of risk.

Flyway

Biogeographical systems of migration routes, used by birds, that directly link sites and ecosystems in different countries and continents.

Fomite

A fomite is any inanimate object or substance capable of absorbing, retaining, and transporting contagious or infectious organisms (from germs to parasites) from one individual to another.

Migration/migratory birds

The Convention on Migratory Species defines migratory species as being "…the entire population or any geographically separate part of the population of any species or lower taxon of wild animal, a significant proportion of whose members cyclically and predictable cross one or more national jurisdictional boundaries". However this is a definition derived in the context of an international treaty rather than being a biological treaty. Species can show either long- or short distance migration according to their ecological or other migratory strategies, generally between breeding and wintering areas. See Alerstam 1993 and Bairlein et al. 2002 for more information.

Mixing area

Areas where there is the potential for many (waterbird) species to come into contact with each other (which in the context of this risk assessment results in risk of between-species transmission of AIVs). Many wetlands support multiple species of waterbirds -

the more important of these (as defined by the Ramsar Convention) are those holding >20,000 waterbirds.

Partial migrants

Species of birds in any one locality, where either only a proportion of the population is migratory, or where resident individuals of one population are joined in another season by a different migratory population of the same species.

Peracute

Very acute clinical disease

Poultry

EU definition according Council Directive 90/539/EEC (EC,1990) ‘poultry’ shall mean fowl, turkeys, guinea fowl, ducks, geese, quails, pigeons, pheasants, partridges and ratites (Ratitae) reared or kept in captivity for breeding, the production of meat or eggs for consumption, or for restocking supplies of game.

According to OIE and in line with the revised legislation for the control of AI (EC, 2005c) ‘poultry’ is defined as ‘all birds reared or kept in captivity for the production of meat or eggs for consumption, for the production of other commercial products, for restocking supplies of game, or for breeding these categories of birds’.

Game birds for release are legally considered as ‘poultry’

Production sectors (poultry) (FAO, 2004)

Poultry production sectors can be described according to production and marketing systems:

- Industrial integrated system with high level biosecurity and birds/products marketed commercially (Sector 1)
- Commercial non-integrated poultry production system; moderate to high biosecurity; birds and products marketed commercially (Sector 2)
- Commercial poultry production system; minimum biosecurity; birds/products in live bird markets (Sector 3)
- Village or back yard production — no biosecurity, informal marketing system (Sector 4)

Ramsar convention

The convention on wetlands signed in Ramsar (Iran) in 1971 is an intergovernmental treaty which provides the framework for national action and international cooperation for the conservation and wise use of wetlands and their resources.

Release assessment

Release assessment consists of describing the biological pathway(s) necessary for an activity to 'release' (that is, introduce) pathogenic agents into a particular environment, and estimating the probability of that complete process occurring. The release assessment describes the probability of the 'release' of each of the potential hazards (the pathogenic agents) under each specified set of conditions with respect to amounts and timing, and how these might change as a result of various actions, events or measures (OIE 2004).

Resident birds

Birds at any particular locality that are not migratory, that is, all or the majority of the population remain in the same locality year-round. Note that some species may be migratory in one part of their range, but resident in another. Typically a number of species occurring in northern Europe (Scandinavia) are migratory there although resident species further south in Europe.

Resistance (virus)

Is the ability of the virus to withstand any agent or environmental effect.

Staging areas

Those areas used by migratory birds to refuel and recover body condition during either autumn (post-breeding) or spring (pre-nuptial) migration periods.

Waterbirds

Bird species otherwise also called waterfowl.

Wild birds

EU legislation on the conservation of wild birds (Council Directive 79/409/EEC (EC,1979) defines wild birds as 'all species of naturally occurring birds in the wild state'. However, this definition excludes some non-native wild birds which can occur in considerable numbers in some Member States.

Wintering areas

Those regions used by migratory birds during the non-breeding period (for Europe, typically the autumn and winter). These areas are at one set of termini of migration systems or flyways (breeding areas are at the opposite termini).

3. Terms of Reference

3.1. 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.

3.2. 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.

3.3. 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 3.1). They are based on the data presented by the Working Group in this scientific report 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 3.1. 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 3.2.

Table 3.2. 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.

The AHAW Panel following the mandate received from the Commission entrusted the WG experts to provide all available data, presented in this Scientific Report. The AHAW Panel drafted the scientific conclusions and recommendations based on the data presented in the scientific report, adopting the Scientific Opinion following the written procedure on 12th May 2006, including a Minority Opinion from 2 Panel Members. However, in order to maintain the consistency, Conclusions and Recommendations have been kept in both Scientific Opinion and Scientific Report.

4. Risk Question(s) Used as the Basis for this Risk Assessment

The risk questions were formulated on the basis of the mandate for this risk assessment. The risk question should be as specific as possible in order to focus the efforts of the Working Group.

The following risk questions were defined:

Release assessment (Risk question 1)

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

Exposure and consequence assessment (Risk question 2)

- What is the probability of transmission of the Asian lineage H5N1 HPAI virus
    a) to wild birds (residential and seasonally present) within the EU and the subsequent establishment of an endemic infection of wild bird populations and
    b) to domestic poultry within the EU as a consequence of infection in migratory birds (Question 1) or residential birds (Question 2a)?

5. 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 (see Chapter 4). 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.

5.1. 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 5.1.

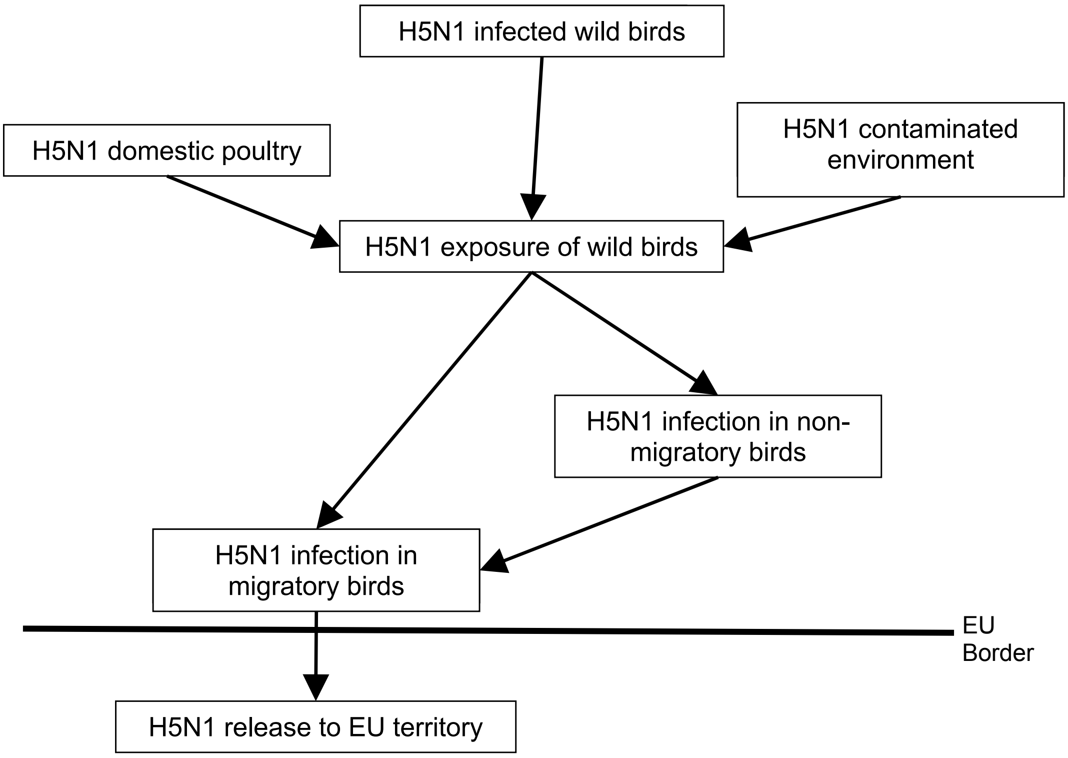


Figure 5.1. Release pathways of Asian lineage H5N1 HPAIV in territories outside the EU that may result in potential transmission of the virus leading to a release into EU territory (note that these pathways describe the potential mechanisms for release)

5.2. 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 5.2 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).

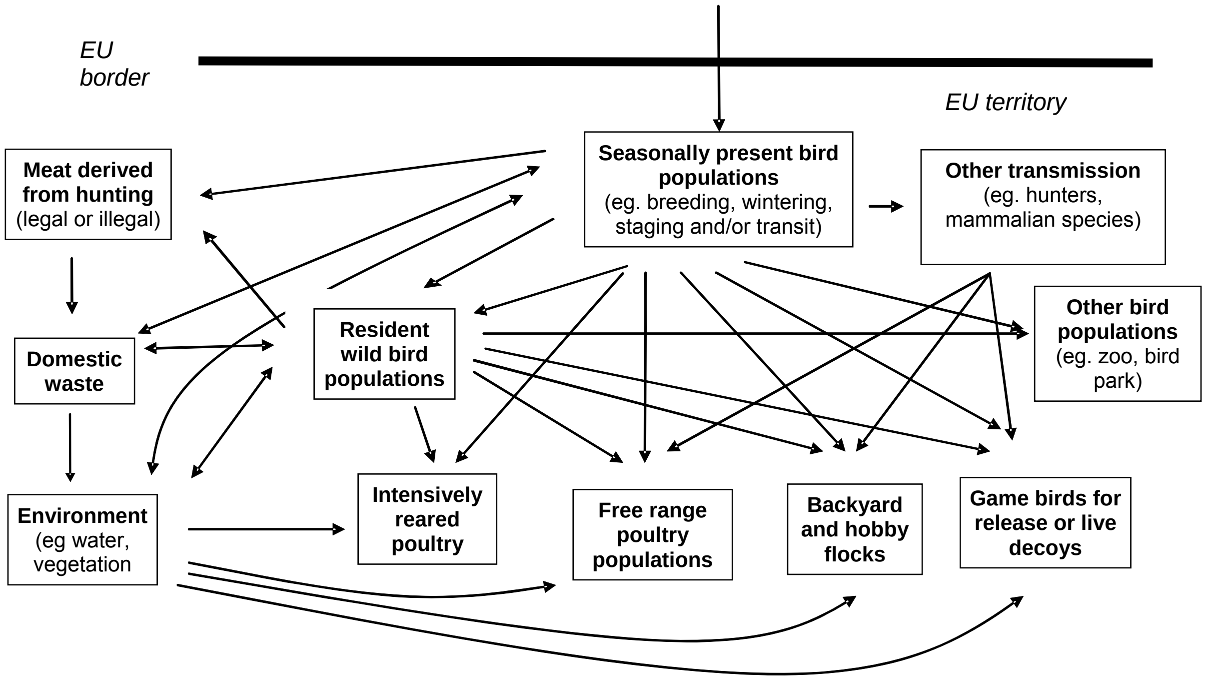


Figure 5.2. Exposure and consequence pathways for bird populations within the EU to Asian lineage H5N1 HPAIV after potential introduction of the virus by wild birds (note that these pathways include all potential direct and indirect exposure and transmission pathways)

6. Pathogenesis in Wild Birds

Basic characteristics of avian influenza viruses are discussed in detail in the earlier Scientific Opinion (EFSA 2005) and are only briefly mentioned in this report with specific focus on the Asian lineage H5N1 HPAIV in migratory birds and the related risk of transmission to domestic birds. This section focuses on wild birds, while information on pathogenesis in domestic birds can be obtained from the earlier Scientific Opinion (EFSA 2005).

The host range of avian influenza viruses (AIV) comprises large numbers of bird species across many orders. These viruses have a worldwide distribution. Morbidity and mortality vary with respect to the species infected and the properties of the viral strain, and presence of other infections or adverse environmental conditions (EFSA 2005).

6.1. Pathotypes

Data

Principally, two pathotypes of avian influenza viruses can be distinguished based on their low pathogenic (LP) or high pathogenic (HP) potentials. The intravenous pathogenicity index (IVPI) is used to distinguish between LP and HP pathotypes (Allan et al. 1977). It is based on intravenous inoculation of 10 six-week old chickens with a standardized dose of the virus isolate to be tested. The chickens are observed over a period of ten days for clinical signs. Results of clinical investigations are integrated into an index which indicates a HPAI virus when values greater 1.2 are obtained. Alternatively, a HPAIV isolate is encountered when at least seven out of ten (70 %) inoculated chicken die within the observation period. The pathogenicity classification is specific to chickens, but similar results have been obtained for related birds in the Galliformes (Alexander et al. 1978; Perkins and Swayne 2001). But it has also been reported that HP viruses have been LP for ducks (Alexander et al. 1978; Sturm-Ramirez et al. 2005).

Conclusions

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.

6.2. Virulence Determinants

Data

Although differences between HPAI and LPAI isolates associated with their relative pathogenicity have been described, molecular determinants distinguishing between LPAI and HPAI isolates that are associated with their pathogenicitiy profiles in birds. It is, however, clear that neither genotype patterns nor antigenicity characteristics are capable of grouping these isolates with respect to their virulence. While a number of point mutations in the PB2, NP and NS genes have been tentatively associated with increased virulence in mammals (Hatta et al. 2001; Gabriel et al. 2005; Seo et al. 2005), the overall constellation of the gene segments seems to play a major role in the polygenic trait of influenza pathogenicity.

The Asian lineage H5N1 HPAIV has not remained genetically static since its emergence in 1997 in Hong Kong. In contrast, this virus has developed most vividly with respect to its genetic composition (genotypes A, B, C, D, E, V, W, X, Y, Z, and Z+: Guan et al. 2002,2002a; Li et al. 2004), its antigenic make-up (Guan et al. 2004; Sturm-Ramirez et al. 2005; Webster et al. 2006) and its pathogenicity for birds and mammals (Hulse-Post et al. 2004; Sturm-Ramirez et al. 2005).

Traceable to the precursor virus A/goose/Guandong/96, a series of antigenically similar viruses with distinct genotypes evolved in the late 1990's through reassortment with several other influenza viruses of unknown provenances. Finally, the so-called genotype Z became dominant. These viruses revealed high pathogenicity in chicken but induced only moderate, mainly neurologic, disease in geese and were asymptomatic in ducks (Shortridge et al. 1998; Perkins and Swayne 2002; Webster et al. 2002). Since 2002, viruses of the Z genotype were isolated which displayed increasing virulence to ducks and, as can be deduced from the outbreaks at two waterbird parks in Hong Kong, also for other waterbirds (Ellis et al. 2004).

Conclusions

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.

6.3. Pathogenicity

6.3.1. Natural infections

Data

Also see Section 7.1.1.7.

Most wild bird species are considered to be susceptible to infection with avian influenza viruses (Stallknecht 1998), and currently > 60 species are reported to have been affected by H5N1 HPAIV induced mortality (review by Olsen et al. 2006).

Wild birds of the *Anseriforme* and *Charadriiforme* Orders are a major reservoir of LPAI viruses (Webster et al. 1992; Kaleta et al. 2005).

Globig et al. (2006) sampled 3,183 wild birds between March 2003 and January 2005 from 80 different locations around Germany, and they examined them for infection with AIV. These were from 79 wild bird species from eleven Orders, particularly *Anseriformes* and *Charadriiformes.* They included locally resident as well as migrating wild bird species. Prevalence of AIV was 3.5% and 1.3% amongst pooled (n=1151) and individual (n=3183) samples, respectively. They detected 92.5% of all positive samples (n=40) in wild duck species. Infection prevalence was highest in ducks during autumn/early winter in the northern coastal parts of Germany with 9.8% of 194 pools on the island Föhr and 17.7% of 102 pools from the Baltic coast in Western Pomerania. The authors indicate that many of the infected species were migrating ducks which have their breeding grounds in Northern Europe and Asia. The same study also examined samples from 387 waders, none of which was positive for AIV.

In a 2005 outbreak in Qinghaihu Lake, China, several wild bird species were affected, including the bar-headed goose (*Anser indicus*), great black-headed gull (*Larus ichthyaetus*), and brown-headed gull (*Larus brunnicephalus*) (Liu et al 2005). The mortality figures have not been published.

Small numbers of deaths in wild pigeons (*Columba livia*) have been reported from Turkey, Iraq and Romania in the context of larger scale outbreaks in domestic poultry (OIE 2006).

Conclusions

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.

6.3.2. Experimental infections

Data

A list of experimental infections using Asian lineage H5N1 HPAIV in non-poultry species is presented in Table 6.1. The clinical signs of infection are coded according to Perkins and Swayne (2003) as follows:

a) Clinical signs in peracute and acute courses are indistinct and often only severe depression, laboured breathing and, rarely, neurological dysfunction are seen. Mortality rates usually exceed 75% within a week. The viruses replicate to high titers in all tissues.
b) Neurologic signs prevail. Mortality rates are reduced but may still be substantial. Highest viral titers are consistently found in the brain.
c) Mild clinical signs, at best, can be detected. There is no mortality and virus can only be found occasionally in internal organs.
d) In some asymptomatic courses hardly any sign of viral replication can be detected. Re-isolation of virus is only exceptionally possible.

Swayne (pers. comm.) reports that experimental studies have been conducted in pigeons (*Columba livia*) using viruses isolated from dead pigeons in Thailand. Even direct inoculation of these viruses into nasal cavity of pigeons caused limited infections with between 60-80% of the pigeons not becoming infected.

Table 6.1. Results of Asian lineage H5N1 HPAIV inoculation experiments in wild bird species

Species	*Virus, Dose*	*Route of infection*	*Incubation period*	*Morbidity*	*Mortality*	*Clinical signs* [c]	*Excretion dose*	*Excretion period*	*Reference*
Laughing gull (*Larus atricilla*, n=8)	A/ck/HK/220/97, $10^{6.0}$ EID_{50}	oculo-naso-oral	n.r.	0/8[a]	0/8[b]	C	< $10^{1.7}$ EID_{50}	< 7 days	Perkins and Swayne 2002
Emu (*Dramaius novahollandiae*, n=2)	A/ck/HK/220/97, $10^{6.0}$ EID_{50}	oculo-naso-oral	n.r.	1/2	0/2	B	n.r.	n.r.	Perkins and Swayne 2002a
Pigeon (*Columba livia*, n=10)	A/ck/HK/220/97, $10^{6.0}$ EID_{50}	oculo-naso-oral	n.r.	0/10	0/10	D	n.r.	n.r.	Perkins and Swayne 2002a
Zebra finches (*Taeniopygia guttata*, n=9)	A/ck/HK/220/97, $10^{6.0}$ EID_{50}	oculo-naso-oral	n.r.	7/7	7/7	A	n.r.	n.r.	Perkins and Swayne 2003
Budgerigar (*Melapsittacus undulatus*, n=10)	A/ck/HK/220/97, $10^{6.0}$ EID_{50}	oculo-naso-oral	n.r.	7/8	6/8	B	n.r.	n.r.	Perkins and Swayne 2003
House finch (*Carpadacus mexicanus*, n=11)	A/ck/HK/220/97, $10^{6.0}$ EID_{50}	oculo-naso-oral	n.r.	7/9	4/7	B	n.r.	n.r.	Perkins and Swayne 2003
House sparrow (*Passer domesticus*, n=7)	A/ck/HK/220/97, $10^{6.0}$ EID_{50}	oculo-naso-oral	n.r.	3/7	0/7	C	n.r.	n.r.	Perkins and Swayne 2003
European starling (*Sturnus vulgaris*, n=4)	A/ck/HK/220/97, $10^{6.0}$ EID_{50}	oculo-naso-oral	n.r.	0/4	0/4	D	n.r.	n.r.	Perkins and Swayne 2003
Mallard (*Anas platyrhynchos*, n=2-3 per virus)	17 different strains, isolated in HK between 1997-2003; $10^{5.7}$ – $10^{8.5}$ EID_{50}	oculo-naso-oral, cloacal, tracheal	3 days	viruses isolated until 2002: None; virus isolated ≥ 2002: high	viruses isolated until 2002: None; virus isolated ≥ 2002: moderate	viruses isolated until 2002: C virus isolated ≥ 2002: B	viruses isolated until 2002: ≤ $10^{4.5}EID_{50}$/ml; virus isolated ≥ 2002: ≤ $10^{5.7}EID_{50}$/ml	at least 5-6 days; tracheal excretion more consistent and higher titers than cloacal excretion	Sturm-Ramirez et al. 2004

Species	*Virus, Dose*	*Route of infection*	*Incubation period*	*Morbidity*	*Mortality*	*Clinical signs* [c]	*Excretion dose*	*Excretion period*	*Reference*
Mallard (*Anas platyrhynchos*, n=2 per virus)	13 different strains, isolated in SE Asia between 1997-2004; $10^{6.0}$ EID_{50}	oculo-naso-oral, cloacal, tracheal	3 days	viruses isolated until 2002: low; viruses isolated 2002-03: mainly high; viruses isolated 2004: mainly low	viruses isolated until 2002: low; viruses isolated 2002-03: mainly high; viruses isolated 2004: mainly low	viruses isolated until 2002 and in 2004: C virus isolated 2002-03: B	n.r.	at least 7 days, some until 17 days; tracheal excretion more consistent and higher titers than cloacal excretion	Hulse-Post et al. 2005
Mallard (*Anas platyrhynchos*, n=2 per virus)	23 different strains, isolated in SE Asia in 2003, 2004; $10^{6.0}$-$10^{7.0}$ EID_{50}	oculo-naso-oral, cloacal, tracheal	3 days	8 viruses: low; 15 viruses: high	8 viruses: low; 15 viruses: moderate - high	8 viruses: C; 15 viruses: B	8 viruses: median titer $10^{3.5}$ (day 3, trachea); 15 viruses: median titer 10^4 (day 3, trachea); cloacal excretion grossly reduced: median titer $10^{0.5}$	at least 5 days	Sturm-Ramirez et al. 2005
Chestnut teal (*Anas castanea*; n=16 incl 4 contact birds)	A/Muscovy duck/Vietnam/453/2004; 2 different doses, but dose n.r.	n.r.	>3 days		Dose 1: 1/6 plus 2/2 contacts; Dose 2: ?/6 plus 0.2 contacts	n.r.	n.r.	n.r	Gleeson et al. 2006 [abstract]

[a] Diseased/total number of inoculated birds
[b] Dead/total number of inoculated birds
[c] See 6.3.2 for grading scheme
n.r. for not reported

Conclusions

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.

6.4. Minimal Infectious Dose

Data

In vivo titrations of Asian lineage H5N1 HPAI viruses have not been published to date. In inoculation experiments doses exceeding 10^5 EID_{50} per bird have reliably lead to infection (see Table 6.1).

Conclusions

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.

6.5. Incubation Period

Data

In mallards and chestnut teals infected with isolates which are highly pathogenic for ducks, signs have been reported to develop within 3 – 5 days p.i. (Sturm-Ramirez et al. 2004; Sturm-Ramirez et al. 2005; Hulse-Post et al. 2005; Gleeson et al. 2006; see Table 6.1).

Conclusions

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

6.6. Excretion Route, Dose and Period

Data

Both, inoculated and contact-infected mallard ducks showed higher virus titers in tracheal compared with cloacal swabs by 3 days p.i. (Sturm-Ramirez et al. 2004). Following experimental infection of mallard ducks, Hulse-Post et al. (2005) reported higher virus titers in the trachea than the cloaca amongst inoculated ducks, but the reverse for contact-infected ducks. Exposure of mallard ducks to 2002 HPAI isolates resulted in higher titres in drinking water than for a selection of viruses from 1961-2001 (Sturm-Ramirez et al. 2004).

Peak excretion titres of up to $10^{8.7}$ egg-infective dose 50% (EID_{50}) per gram feces have been measured for highly adapted AIV of low pathogenicity (Webster et al. 1978). Data from published studies are presented in Table 6.1. Hulse-Post et al. (2005) reported longer excretion periods for the newer 2003-4 H5N1 viruses (11-17 days) than for the ones from 1997/2001 (2-5 days).

Species found in experimental infections to be partially resistant to H5N1-induced disease (starlings, pigeons) at best excreted low doses of infectious virus (Perkins and Swayne 2003; Werner, personal comm.).

The epidemiological investigation associated with the detection of Asian lineage H5N1 AIV in quarantine facilities in South England revealed that infection was brought in by infected birds of the mesia (*Leiothrix argentauris*) species. While infection appears to have spread amongst these either prior or while in the quarantine facilities, none of the other bird species kept in the same epidemiological unit including 4 sentinel chickens did get infected during the exposure period from 28 Sept to 20 Oct 2005 (Defra 2005).

Conclusions

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.

6.7. Survival and Morbility following Infection

Data

Data from published studies on survival of infected wild bird species under experimental conditions are presented in Table 6.1.

In wild ducks, up to 10% of birds in surveillance studies have been shown to be infected by H5, and up to 20% by N1 subtype viruses (Fouchier et al. 2003; Munster et al. 2005). Partial humoral immunity in addition to cellular immunity targeting the internal genes could lead to significantly attenuated courses of infections with H5N1 HPAIV. On the one hand this may increase mobility but on the other hand reduced viral replication and excretion may ensue.

Sturm-Ramirez et al. (2004) found that mallard ducks experimentally infected with strains of the H5N1 HPAIV from before early 2002 did not show signs and continued to gain weight. In the same study, infection with late 2002 isolates was reported to have caused significant morbidity and mortality such that clinical disease was observed by day 3 p.i., and 3 of 6 ducks were dead by day 4 p.i., and the surviving birds suffered from severe CBS dysfunction.

No experimental data are available about the mobility of wild birds infected by Asian lineage H5N1 HPAIV. Recent H5N1 AIV field isolates represent a heterogenous mixture of different pathotypes (Chen et al. 2006). Upon passaging such mixtures through duck variants exhibiting a low pathogenicity profile may be preferentially selected (Hulse-Post et al. 2005). However, these viruses retain their highly pathogenic potential for gallinaceous birds, so the possibility that apparently healthy mallards may subclinically excrete and spread Asian lineage H5N1 virus highly pathogenic for *Galliformes* must be considered.

Chen et al. (2005) present evidence that wild birds can carry H5N1 HPAIV and although the virus was found in apparently healthy migratory ducks, there is no evidence as to whether they were healthy enough to migrate long distances and so whether the virus could be transmitted over such long distances via this mechanism at this stage. Neither does the paper specify which species of migratory ducks carried H5N1 HPAIV so there remains the possibility that they were not migratory individuals.

In addition, it should be noted that numerous wild bird species have had previous exposure to LPAIV, which could result in partial (homosubtypic) immunity and subclinical infections even more than reported in experimental infections.

Reports from various countries in Europe indicate that wild birds can be infected without showing clinical disease. These include reports in relation to sero-positivity in apparently healthy mute swans (*Cygnus olor*) in Croatia and Italy. More detailed investigations are under way in Poland, where sampling of a flock of mute swans indicated the presence of infected birds not showing clinical disease, diagnosed on the basis of virus detection (Polish CVO – Report on Actvities - File GIWz 400-258/06 of May 6 2006).

Conclusions

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).

6.8. Overall recommendations on Pathogenesis in wild birds

Studies are needed describing he pathogenesis following H5N1 infection in a range of wild bird species referred to in Table 16.2 since all studies to date have involved domestic birds, especially looking at viral shedding periods in situations where birds are not lethally affected.

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

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

The H5N1 HPAIV which has caused the Asian epidemic had emerged by at least 1996, when it caused an outbreak of influenza with high death rates in domestic geese in Guangdong in China (Xu et al. 1999). It caused an outbreak of severe disease in poultry in Hong Kong SAR, when also 18 people were clinically affected resulting in six deaths (Chan 2002; Sims et al. 2003).

7.1.1. Risk factors for infection in domestic poultry

7.1.1.1. Specific trade- and husbandry related risk factors

Various non- peer reviewed reports have been included in the published reviews by Sims et al. (2005), Morris et al. (2005) and Martin et al. (2006) who describe the specific characteristics of the infected production systems in South-East and East Asia. These authors have identified significant risk factors based on a combination of data and expert opinion. The most important risk factors for infection of domestic poultry are presented in Table 7.1. The movement of birds between holdings is a trade-related risk factor that is considered to be important across all poultry production sectors, whereas risk factors associated with poultry husbandry vary in their relative importance between these sectors.

Table 7.1. Trade- and husbandry-related risk factors associated with the occurrence of H5N1 HPAIV outbreaks in South-East and East Asia (note that references include reviews and expert opinon)

Risk factors	*Source*
Trade-related	
Sale of poultry at live bird markets	Sims et al. 2003; Morris et al. 2005
Major cultural festivals with peak sale / consumption	Gilbert et al. 2004; Pfeiffer 2005
Lack of pre-marketing health checks	Morris et al. 2005
Movement of poultry between holdings	Rushton et al. 2004; Morris et al. 2005
Movement of poultry across administrative borders	Rushton et al. 2004; Morris et al. 2005
Return to the holding of origin for birds that were for sale in markets	Veterinaires Sans Frontieres 2004
Husbandry-related	
Farming of multiple species within one farm unit	Veterinaires Sans Frontieres 2004; Morris et al. 2005
Movement of fomites into the poultry holdings	Morris et al. 2005
Keeping poultry over or near ponds and rice fields	Gilbert et al. 2004
Grazing of ducks on paddy fields	Gilbert et al. 2004; Pfeiffer 2005
Birds entering homes where other birds are housed as pets	Morris et al. 2005
Use of untreated chicken faeces as fertilizers or livestock feed	Morris et al. 2005
Lack of adoption of “all in – all out” husbandry system	Veterinaires Sans Frontieres 2004
Inadequate disposal of dying and dead birds	Morris et al. 2005

7.1.1.2. Structure of production sectors and biosecurity

Data

Small commercial farms and flocks of smallholders/villagers (Poultry production sectors 3 and 4) appear to be more likely to experience outbreaks than larger commercial farms (Poultry production sectors 1 and 2; Gilbert et al. 2006; Karesh et al. 2005). Numerically, more outbreaks occur in these smaller holdings even though, for a number of the infected countries, more poultry are raised in large farms.

In Thailand, a study of confirmed cases of infection between July and September 2004 showed that 64% of infected farms contained 1000 or less poultry (Gilbert et al. 2006). Similarly, Tiensin et al. (2005) reported that a total of 83% of infected flocks confirmed by laboratories were backyard chickens (56%) or ducks (27%).

In Thailand, some areas of high poultry population density were less likely to be affected by H5N1 HPAIV than those with lower density, possibly reflecting the improved biosecurity and management practices of large industrial farms (production sector 1 and 2) located in these areas (Gilbert et al. 2006).

Conclusions

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.

7.1.1.3. Temporal changes in poultry population size

Data

FAO livestock statistics demonstrate the marked increase in the number of poultry being raised in Asia over the past 7 years. In some countries, smallholders have markedly increased the size of their flocks in response to market demand (Martin et al. 2006).

Conclusions

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.

7.1.1.4. Role of waterbirds

Data

Domestic ducks in China were known to have become infected with Asian lineage H5N1 HPAIV before 1999 (Sims et al. 2003a). Based on available published data, since 1999 domestic geese and ducks are believed to have had a key role in the genesis of the 2003-04 epidemics given their ability to asymptomatically carry HPAI viruses and for high levels of excretion once infected (Sturm-Ramirez et al. 2005; Hulse-Post et al. 2005; Gilbert et al. 2006).

In Thailand, Gilbert et al. (2006) described a strong association between occurrence of H5N1 outbreaks and abundance of free-grazing ducks and, to a lesser extent, native chickens, fighting cocks, wetlands, and humans. Free-grazing ducks are common in rice paddy farming systems.

Conclusions

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.

7.1.1.5. Role of mammal species

Data

Ferrets have been experimentally infected and differences in virulence were observed between Asian lineage H5N1 AIV strains, ranging from lethal infections to mild disease (Govorkova et al. 2005). There is evidence of infection with H5N1 HPAIV in a domestic cat (*Felis catus*) that had eaten an infected dead pigeon (*Columba levia*) during the H5N1 HPAIV outbreak in Thailand in 2004 (Songserm et al. 2006). Cats were shown to be susceptible to experimental infection to which they responded with systemic lethal disease (Kuiken et al. 2004; Rimmelzwaan et al. 2006). More recently, natural infections in cats have been reported during the outbreak of H5N1 HPAIV of a Qinghai-like virus lineage in wild birds in the northeast of Germany (Wolf et al. 2006). Three cats and one stone marten succumbed to a systemic infection. At least one of these cats had been observed to have developed neurological signs. The exact sources of the infections were not identified, but the cats had been allowed to freely roam in an area where contact with carcasses of infected wild birds had been possible. In addition, there are also suggestions of dogs being susceptible to natural challenge with H5N1 in Thailand (Butler 2006). Since this finding is based on serological data, a non-lethal course of the infection must be assumed for those particular dogs.

Conclusions

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.

7.1.1.6. Trade and live bird markets

Data

In the north American state of Pennsylvania/Virginia it was suggested that the H5N2 HPAIV was spread by movements of live and dead birds, contaminated equipment and vehicles, contaminated eggs, feed, water, insect vectors, and human vectors during outbreaks in the 1980s (Fichtner 1987).

There is evidence of outbreaks of Asian lineage H5N1 HPAIV in live bird markets (Ellis et al. 2004).

Conclusions

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.

7.1.1.7. Presence of infection in wild birds outside EU

Data

Surveys of wild birds (mostly found dead) around the globe have demonstrated the presence of avian influenza viruses of all known H and N subtypes in various normal free-ranging avian species, including species that follow patterns of seasonal migration. The main hosts of avian influenza viruses are *Anseriformes* (ducks, geese) but other orders have also been found to be infected including *Charadriiformes* (shorebirds such as plovers, turnstones, sandpipers and gulls). (Alexander 2000).

In the course of the on-going outbreak of Asian lineage H5N1 HPAI, infections in wild birds were reported from:

- Japan [crows *(Corvus)*; Mase et al. 2005],
- South Korea [magpies *(Pica pica)*; Kwon et al. 2005], and
- Hong Kong [tree sparrow *(Passer montanus)*, feral pigeon *(Columba spp.)* peregrine falcon *(Falco peregrinus);* Li et al. 2004].

In Hong Kong, outbreaks involving large numbers of birds were reported in late 2002 (Ellis et al. 2004). These outbreaks affected aquatic birds which were kept in two parks. Individuals of several species of ducks, geese and swans as well as herons, egrets, and flamingos were affected. Domestic birds of gallinaceous species, kept in cages close to open ponds of these parks were not affected and proved to be free of virus. At the same time isolated cases of H5N1 HPAIV infections were noted in two grey herons *(Ardea cinerea)* and a black-headed gull *(Larus ridibundus)* at different locations in Hong Kong (Ellis et al. 2004). From a UK quarantine station, infection with Asian lineage H5N1 HPAIV was reported for captive cage birds (Defra 2005).

A large scale outbreak of Asian lineage H5N1 HPAIV, which started in April and lasted until June 2005 at a nature reserve at Lake Qinghai in the Northwest of China (Chen et al. 2006; Liu et al. 2005). Up to 6,000 wild birds died, among them highly migratory species such as the bar-headed goose *(Anser indicus)* of which thousands were affected, in addition to cormorants and gulls that died of the infection.

Recently, healthy tree sparrows (*Passer montanus*) in a province in central China were found to harbour and excrete H5N1 HPAIV of different genotypes (Kou et al. 2005). These viruses were highly pathogenic for chickens but not for domestic ducks and mice.

In addition, crows in Japan, magpies in Korea (Kwon et al. 2005), a peregrine falcon in Hong Kong (Li et al. 2004) and several passerine and psittacine species in Thailand, and – in a large ornithological collection – in Cambodia have been reported infected with Asian lineage H5N1 HPAI viruses.

Mongolia reported the death of about 90 wild birds out of an otherwise healthy population of roughly 6,000, in lakes in the north of the country. H5N1 HPAIV was isolated from a dead whooper swan but not from healthy animals (OIE 2006).

The data presented in Table 7.2 summarises reported isolation of H5N1 HPAIV in wild birds.

Table 7.2. Reported cases of Asian Lineage H5N1 HPAIV in wild birds found dead outside the EU in 2004/2005 (OIE 2004, 2005, 2006)

Country	*Species*	*AI Pathotype*	*Month/Year*
China (Hong Kong SAR)	Peregrine falcon, grey heron, black headed gull, little egret, captive greater flamingo	H5N1	Jan 2004
Cambodia	Wild birds in a zoo collection	H5N1	Feb 2004
Japan	Crows	H5N1	Mar 2004
Republic of Korea	Magpies	H5N1	Mar 2004
Thailand	Pigeons, open-bill storks, little cormorant, red-collar dove, scaly breasted Munia, black drongo	H5N1	Dec 2004
China (Hong Kong SAR)	Grey heron	H5N1	Dec 2004
China	Bar-headed geese, great black-headed gulls, brown-headed gulls. ruddy shelducks and great cormorants	H5N1	Apr 2005
Mongolia	Bar-headed geese and whooper swan	Influenza A subtype H5	Aug 2005
Russia (Siberia)	Wild birds	H5N1	Aug 2005
Kazakhstan	Wild birds	H5N1	Aug 2005
Romania	Swan	H5N1	Oct 2005

Conclusions

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.

7.1.1.8. 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.

7.1.2. Temporal and spatial pattern

Data

South East Asia

Asian lineage H5N1 HPAI viruses were isolated exclusively from waterbirds during 2000, but from 2001 onwards they were isolated from both waterbirds and chickens, with the highest rate of isolation from ducks. Since 2001, H5N1 HPAI viruses have continued to circulate in mainland China. Seasonal outbreak patterns were observed, peaking from October to March, when the mean temperature is below 20°C (Li et al. 2004).

In Vietnam, analysis of the temporal pattern of Asian lineage H5N1 HPAIV outbreaks between 2003 and 2005 show a marked seasonal pattern (Pfeiffer 2005). During that period, major outbreaks in poultry have occurred around the annual Tet holiday festivities from late December to March.

The major areas affected in Vietnam have been concentrated around the Red River and Mekong River deltas in the North and South of the country, respectively (Pfeiffer 2005).

In Thailand, outbreaks were concentrated in the Central, the Southern part of the Northern, and eastern regions of Thailand which constitute wetland water reservoirs and dense poultry areas (Gilbert et al. 2006).

Eastern Europe and other parts of Europe

In July and August 2005, avian influenza outbreaks have progressively spread in a north-westerly and followed by a westerly direction, affecting Mongolia, Russia and Kazakhstan. The disease that was initially detected in domestic poultry flocks, mainly small scale farming units, was also reported in wild birds in the three countries. The disease further spread to Europe where in some countries the infection in birds is still active. Human deaths have been reported in Turkey (OIE, 2006).

Africa

From February to April 2006 several African countries have reported outbreaks of Asian lineage H5N1 HPAIV infection in domestic poultry farms (OIE 2006). These include Niger, Nigeria, Cameroon, Burkina Faso and Egypt.

Conclusions

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.

7.1.3. Molecular epidemiology of Asian lineage H5N1 HPAIV

Data

In 2001, the first reported cases of infection and disease in domestic poultry with H5N1 HPAI viruses since 1997 occurred (Sims et al. 2003a; Sims et al 2003). Multiple H5N1 HPAI viruses were detected in domestic poultry through surveillance of live bird markets in Hong Kong and southern China. In total, seven different genotypes were detected, including one goose/GD/96-like virus and six other genotypes that contained genes from other Type A influenza viruses, presumed to be from waterbirds. Of these genotypes at least three were very similar to viruses isolated previously from ducks and/or geese from southern China (Li et al. 2004; Sims et al. 2003). Of these, one genotype has since become dominant – the so-called “Z” genotype (Li et al. 2004).

These “Z” viruses have continued to evolve so that H5N1 ‘Z’ genotype viruses isolated from the same location at different times, or those isolated from different countries at the same time have significant molecular and antigenic differences. Viruses in Thailand and Vietnam were very closely related, indicating a recent common origin, as were those found in South Korea and Japan (Li et al. 2004).

The 2003-04 epidemics in Southeast Asia were not due to the introduction and spread of a single virus but were caused by multiple viruses which were genotypically linked to the Goose/GD/96 lineage via the haemagglutinin gene (Sims et al. 2005; Chen et al. 2006). The range of genotypes and considerable variability within individual genotypes demonstrate the presence of a large pool of H5N1 HPAI viruses circulating in the region prior to and during the 2003-04 epidemic (Wan et al. 2005; Chen et al. 2006). Genetic characterization of isolates from southeast China, Vietnam, Thailand and Indonesia has shown that H5N1 HPAI viruses have been introduced in different South East Asian regions from southern China between 2001 and 2005 (Chen et al. 2006).

Genetic analysis of isolates from Mongolia (July 2005) show a close genetic relationship to wild bird isolates from Qinghaihu Lake outbreak (April/May, 2005). Genetic sequences from virus isolates obtained from 2005 wild bird outbreaks in Kazakhstan, Russia, Turkey, Romania and several EU countries have been shown to be very similar to the virus strain isolated in China around the Qinghaihu Lake (Brown et al. 2006 [abstract]).

Conclusions

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.

7.2. 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.

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

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

8.1.1. Introduction

This chapter provides a broad description of the major farming systems in geographical areas outside the EU affected by H5N1 HPAIV outbreaks in poultry and their relationship with poultry farming. These include areas in eastern European and central Asian countries, areas in South-East and East Asia, and in the African continent.

8.1.2. Eastern Europe and Central Asia

Data

The heterogeneity of agro-ecological, political, economic and social conditions in the region has resulted in the development of a variety of farming systems (Dixon et al. 2001). The map presented in Figure 8.1 shows the spatial distribution of the eleven major farming systems identified in this geographical area.

Figure 8.1. Farming systems in East European and Central Asian countries

Mixed Farming Systems are characterized by two dominant subsystems: (i) Small to medium scale private family farms and (ii) Medium to large corporate/ co-operative farms. Livestock production in small to medium scale private family farms often complements crop production so the produced crop is partly used as feeding material. Smaller farms are usually diversified, whilst the bigger ones tend to specialize in livestock production (World Bank Global Agricultural Systems study).

In Chechnya-Ingushetia a survey conducted to examine the livestock production status of in Chechnya and Ingushetia has shown that most farms are of mixed production and that the agricultural system consists mainly of family farms (FAO 2004a). The same study highlights that at present people keep poultry for satisfying their own needs with a small part of them for sale; priority is given to hens.

In Turkey where agriculture and farming are limited because of land shape or limited land and high number of population, households make their living with animals, especially in Eastern and Southeastern Anatolia (Akbay et al. 2005). In these regions, poultry are predominantly managed in backyard flocks.

Conclusions

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.

8.1.3. South-east Asia and East Asia

Data

The map in Figure 8.2 shows the geographical distribution of the farming systems of the region.

Figure 8.2. Farming systems in South-East and East Asian countries

The four Mekong countries Cambodia, Lao PDR, Thailand and Vietnam do not form a homogeneous group but rather show significant differences concerning living standards, economic performance, per capita income and population size. Agriculture remains an important part of the economies and societies of the Mekong countries with large shares in overall GDP and employment.

Conclusions

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.

8.1.4. African countries and Middle East

Data

Eight regional farming systems, based on criteria which include natural resources and climate, altitude, main crops, importance of livestock and access to supplementary or full irrigation can be defined in this area. Poultry farming in the Middle East and North Africa has been categorized as part of urban based farming system (Dixon et al. 2001). The farming systems in the Middle-Eastern and North African countries are shown in Figure 8.3.

Figure 8.3. Farming systems in the Middle Eastern and North African countries

For sub-Saharan Africa, fourteen broad farming system categories were defined on the basis of criteria such as natural resource base, dominant livelihoods, and main staple and cash income sources. Four farming systems support almost half of the agricultural population of the region which is the Tree Crop, the Maize Mixed, the Agro-pastoral Millet/ Sorghum Cereal- Root Crop Mixed and the Irrigated Farming Systems. The geographical location of these farming systems for sub-Saharan Africa can be seen in Figure 8.4.

Figure 8.4. Major farming systems in the sub-Saharan African countries

Conclusions

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

8.2. Geographical Distribution of Poultry Population outside the EU

8.2.1. Introduction

The density of poultry populations currently has to be predicted using statistical models that use various data sources.

For the production of the maps presented in this section for each country the most recently available sub-national livestock data and corresponding administrative boundaries have been collected and entered into a database. The components of the database include: a global network of providers of data on livestock and sub-national boundaries; an Oracle database in which these data are managed and processed; a system for predicting livestock distributions based on environmental data; and an interactive web application, the Global Livestock Production and Health Atlas, through which data are viewed and disseminated (http://www.fao.org/ag/aga/glipha/index.jsp).

The methodology has been described in “FAO Global livestock distribution atlas” and as been validated using the subnational FAOSTAT totals for the year 2000. This approach and its outputs have not been peer-reviewed.

The maps provided in this section are the outputs of the FAO prediction model for poultry (or chicken) density and the pixel values are actual densities (per square kilometre) multiplied by 10. Poultry represent chickens plus domestic production bird species.

8.2.2. Eastern Europe and the Middle East

Data

The map in Figure 8.5 presents the distribution of poultry density for eastern European countries and the Middle East. A high density of poultry is found in Turkey and countries surrounding the Black Sea as well as in the Saudi Arabia.

Figure 8.5. Estimated spatial distribution of poultry density for 2005 in Eastern European and Middle Eastern countries

FAO (2004a) conducted a livestock sector survey carried out in Chechnya and Ingushetia which indicates that poultry farming was the main means of livelihood among survey respondents (66%). Hens are the most common poultry being raised (54%) followed by turkeys (21%), ducks (14%) and geese (11%).

In Turkey, the information on the number and size of holdings are sourced from agricultural censuses, which are conducted every 10 years on the basis of large sample surveys (Togan et al. 2003). In contrast to the red meat sector, the number of poultry has steadily increased during the same period. Poultry products are gaining importance and account for a major share of animal products in the human diet in Turkey. By 2000, Turkey had 264.5 million heads of poultry, almost four times higher than the number in 1990. The majority of these poultry are reared by small farmers (<50 acres), which constitute 65% of all farmers (Akbay et al. 2005). Most village families own a few animals on land that lacks alternative use.

Conclusions

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.

8.2.3. Mekong region, Indonesia and China

Data

Between 1980 and 2000, poultry production has risen by a factor of three in all four countries in the Mekong region and is expected to continue to increase by factors from two for Thailand to 5.7 for Lao PDR. In most countries, average farm size continues to decline. Although signs of declining rural populations and land aggregation are occurring in some countries, for instance, Thailand and to a small extent in China, it is anticipated that even in 2030 the majority of farms in the region will still be smallholdings. Farms in the region are dominantly smallholder-based with widespread occurrence of subsistence production systems. Presently, more than 36% of chickens and waterbirds of the world are found in the region. Figure 8.6 shows the poultry density distribution in Asian countries.

Figure 8.6. Estimated spatial distribution of poultry density for 2005 in Asian countries

In Cambodia, traditional village chicken raising is carried out by about 90 - 95% of all farming households. Usually a few chicken of mainly local breeds are owned by families and raised with minimum input. Chickens are kept scavenging and are fed supplementary feeds such as rice or paddy (Knips 2004).

Chickens are the main type of poultry raised in Lao PDR with most poultry meat being produced by smallholders. Most households raise 20-30 chickens, predominantly in scavenging systems. Commercial poultry production in Lao PDR is found near centres of high population density such as Vientiane (Knips 2004).

Most poultry production in Thailand takes place in commercial operations with the industry being dominated by large multinational companies. The broiler industry is completely integrated with feed-milling companies and mainly produces for export markets. In Thailand production has overtaken consumption since 1980 allowing for the development of a significant export industry. Net trade in poultry has risen 15-fold between 1990 and 2000 (Knips 2004).

Poultry production plays a very important role for rural development in Vietnam. More than 80% of the poultry production in Vietnam is based on traditional production systems at the smallholder level, even though a number of families now keep flocks of between 1,000 and 10,000 birds. Some 70% of the chickens produced in Vietnam are local breeds raised outdoors with the remaining 30% divided amongst different foreign breeds. The main locations for chicken production are close to urban areas and provinces with large amounts of waste from food processing industries. Broiler chicken production is carried out by private farms, which are still financially weak and lack access to technology, health-care and marketing facilities (Knips 2004).

In China, poultry production is 20% of all livestock production with an estimated total of 5 billion heads of poultry in 2002 (FAO 2005a). This country’s annual growth rate in poultry production for the period between 1990 and 2000 was around 5% per year. Disaggregated data regarding poultry farm type is not available for this country (FAO 2005a).

In Indonesia, poultry production is 55% of all livestock production with an estimated total of 1,3 billion heads of poultry in 2002 (FAO 2005b). This country’s annual growth rate in poultry production for the period between 1990 and 2000 was around 4.1% per year. Disaggregated data regarding poultry farm type is not available for this country.

Conclusions

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.

8.2.4. African countries

Data

Data which characterizes livestock production in African countries was collected using the FAO - Livestock Sector Brief reports. Relevant information is available only for Zambia, Ethiopia, Kenya and Tanzania (Table 8.1).

Table 8.1. Characteristics of the poultry sectors in selected African countries

Country	*Total poultry heads in 2000*	*Annual sector growth rate (%)*	*Contribution of poultry to national livestock units (%)*
Zambia	29,000,000	6.3	18
Ethiopia	5,600,000	0.3	3
Tanzania	43,447,000	3.0	3
Kenya	457,000	2.4	4

Sources: FAO 2003a; FAO 2003b; FAO 2003c; FAO 2004b

The map in Figure 8.7 outlines the predicted chicken density for 2005 in the African continent.

Figure 8.7. Estimated spatial distribution of poultry density for 2005 in African countries

Conclusions

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

8.3. Poultry Trade

Data

Small-scale poultry production systems (Sector 3 and 4)

In low income countries, transport of eggs and poultry from the village to the city usually begins with a purchase by a middleman dealer, direct from the household, or from small locally, held weekly markets (FAO 2002). Baskets with layers of straw protect the eggs from breakage, and other types of baskets are used to carry live birds. Bullock carts are still used in many countries for transport of both live poultry and eggs to larger community centres. Poultry can also be transported on the roof of buses or trains. Marketing quality considerations for live birds are usually concerned with weight loss in the bird from dehydration during transport. These are easily resolved by providing drinking water during the trip, and travelling during the cool part of the day when possible (FAO 2002).

In Vietnam, small commercial farms buy day-old-chicks and sell finished live birds. The supply to small farms is made through other neighbouring family farms and retailer traders (46.7%) (Dinh Xuan et al. 2005). Less than one fifth of small commercial farms buy in chickens; only very small farms (<10 chickens) and in special occasions (Tet, birthdays and weddings) buy in chickens. When selling finished birds 60% of farms do so at markets in the commune (own or neighbouring) and the remaining 40% do so to unknown destinations (beyond their own district), via wholesalers. Much of what is produced is consumed locally through short market chains (Dinh Xuan et al. 2005).

Industrial poultry production systems (Sector 1 and 2)

While commercial poultry producers were (eg. Thailand, Indonesia) and are (eg. Nigeria) often involved during the early stages of outbreaks in countries, they are less likely to experience outbreaks during the later stages of the epidemics. This is considered to be a consequence of improved biosecurity, since they need to be able to continue to trade. This economic pressure can also have adverse consequences. As an example, it has been reported by the Washington Post (2005) that the poultry industry in Indonesia requested delayed reporting of outbreaks in their farms from the the government. Consequentially, the first outbreaks were first reported several months after the first occurrence.

A report produced by GRAIN, an international non-governmental organisation promoting the sustainable management and use of agricultural biodiversity, suggests that trade of live chickens is a more important source of infection than wild birds or backyard farming (Grain 2006). Olsen et al. (2006) also emphasize the importance of poultry trade for spread of the virus.

Conclusions

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.

8.4. 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.

9. Environmental Stability of Asian Lineage H5N1 HPAIV and Transmission

Inactivation of extracellular viral infectivity is a function of temperature, time of exposure and the existence of UV radition. Presence of stabilising agents, in particular proteins, may prolong survival times.

Direct and indirect transmission of Asian lineage H5N1 HPAIV is strongly influenced by the ability of the virus to survive in different environments.

Most of the data on stability of avian influenza viruses is on viruses other than Asian lineage H5N1 HPAIV. Table 9.1 summarizes the results form published studies on avian influenza stability in the environment. A recent tendency has been observed for H5N1 HPAIV for a development toward increased stability in the environment (Webster 2006).

Table 9.1. Stability of different influenza viruses in various environmental materials and heat-treated poultry products

Material	*Parameters*	*Time*	*Result ****	*Reference*
Environmental materials				
Aerosol, faeces	low temperature, low humidity	not specified	prolonged infectivity	Schaffer et al. 1976
Droppings of feces (H5N2)	4°C	35 days	retained infectivity	Beard et al. 1984
Droppings of feces (H5N2)	25°C	2 days	retained infectivity	Beard et al. 1984
Chicken manure (H5N2)	Ambient	105 days	retained infectivity	Fitchner 1987
Chicken manure (H5N2)	not specified	44 days	retained infectivity	Utterback 1984
Chicken manure (H7N2)	4°C	23 days*	retained infectivity	Lu et al. 2003
Chicken manure (H7N2)	Ambient	19 days*	infectivity present, full inactivation at day 23	Lu et al. 2003
Chicken manure (H7N2)	37°C	14 days*	infectivity present, full inactivation at day 16	Lu et al. 2003
Chicken faeces (H5N1 HP/Asia)	32-35°C, sunlight exposure	30 minutes	no infectivity retained	Songserm et al. 2005
Chicken faeces (H5N1 HP/Asia)	25-32°C, shade	4 days	no infectivity retained	Songserm et al. 2005
Lake water (H3N6)	0°C	>30 days	retained infectivity	Webster et al. 1978
Lake water (H3N6)	22°C	4 days	retained infectivity	Webster et al. 1978
Surface water, rice field (H5N1 HP/ Asia)	not specified	3 days	no infectivity retained	Songserm et al. 2005
Distilled water (five subtypes)	17°C	207 days*	retained infectivity	Stallknecht et al. 1990
Distilled water (five subtypes)	28°C	102 days*	retained infectivity	Stallknecht et al. 1990
Heat-treated poultry products				
Meat	70°C	30 minutes	full inactivation	AQIS 1991
Meat	75°C	5 minutes	full inactivation	AQIS 1991
Meat	80°C	1 minute	full inactivation	AQIS 1991
Meat (H5N1 HP/Asia)	70°C	3 minutes	no infectivity retained	Songserm et al. 2005
Dried egg white (H7N2 LP, H5N2 HP)	54.4°C	15.2 days	full inactivation	Swayne and Beck 2004
Dried egg white (H7N2 LP, H5N2 HP)	67°C	0.6 days	full inactivation	Swayne and Beck 2004
Whole egg (H7N2 LP, H5N2 HP)	60°C	3 minutes	full inactivation	Swayne and Beck 2004
Whole egg (H5N1 HP/Asia)	70°C	3 minutes	no infectivity retained	Songserm et al. 2005

* Measured in manure of SPF chickens; times were considerably shortened when “field manure“ was used (4 days at ambient temperature and 12 hours at 37°C).

** Estimates of linear regression models based on inactivation kinetics of $10^{6.0}$ $TCID_{50}$ ml^{-1}

*** The results were based on in-vitro conditions and the risk of infection depends upon whether the minimal infectious dose is reached

9.1. Stability at varying temperatures

Data

See Table 9.1.

Conclusions

Even in protein-rich matrices like meat and whole eggs, temperatures exceeding 60-65°C lead to complete viral inactivation (also for the Asian lineage H5N1 HPAIV) within a maximum of 5 minutes. However, when virus is protected by dried protein (Table 9.1: dried egg white), survival times may increase considerably even at elevated temperatures of 67°C.

9.2. Stability in faeces

Data

See Table 9.1. and previous EFSA report (EFSA 2005).

During an Asian lineage H5N1 HPAIV outbreak in a UK quarantine facility, the only bird species affected were those kept for almost one month in the same cage as the infected birds (Defra 2005). Other birds (incl. sentinel chickens) kept in the same air space but different cages were not infected.

Conclusions

Bird faeces comprise a complex and often chemically agressive matrix. The presence of uric acids leads to low pH values. Masses of the enteral bacterial flora provide potentially hazardous enzymes (proteases, neuraminidases, nucleases). Nevertheless, values given in Table 9.1 indicate a remarkable resistance of avian influenza viruses in faeces. This includes Asian lineage H5N1 HPAIV which required at least four days at ambient temperatures of 25-32°C in the shade in Thailand for its reduction beyond detection level by virus isolation. Other studies, which examined different AI strains, demonstrated longer survival times in droppings and chicken manure. Frequently, the infectivity was retained after more than three weeks, especially when stored at temperatures as low as 4°C.

The data indicates that contaminated faeces are likely to represent a significant mechanism for exposure of other birds.

9.3. Stability in water

Data

See Table 9.1 and previous EFSA report (EFSA 2005).

It has been postulated that influenza viruses are perpetuated in ducks nesting in Siberia (Okazaki et al. 2000) and that the viruses are preserved in frozen lake water during winter in the absence of ducks. During the following breeding season returning ducks or their (susceptible) offspring can become re-infected with viruses released by chance from melting ice (Ito et al. 1995). It has been further hypothesised that influenza viruses can be preserved in environmental ice for prolonged time periods (Smith et al. 2004), and that ancient viruses and genotypes can recycle from this reservoir (Rogers et al. 2004).

Asian lineage H5N1 HPAIV was shown to be inactivated after three days in surface water coming from rice fields in Thailand (Songserm et al. 2005). Webster et al. (1978) showed that an H3N6 AIV retained its infectivity for more than 30 days at 0°C and for a few days at ambient temperature.
Stallknecht et al. (1990) described strain- and subtype-specific differences in inactivation slopes when measuring the retention of infectivity in distilled water of five different LPAI influenza virus strains. They concluded that certain strains seem to be adapted to prolonged survival in water at given temperatures

although the (molecular) mechanisms involved remained obscure. However, compared with other LP avian influenza viruses, the stability of infectivity of Asian lineage H5N1 HPAIV in water still resides at the lowest range of the scale.

No data are available about virus survival in salt or brackish water which are the habitats of many water bird species.

Conclusions

The only data available on the stability of Asian lineage H5N1 HPAIV in water indicates that it was inactivated after 3 days in surface water coming from rice fields in Thailand. It is likely that the duration of stability will increase with reduced temperature. Survival in salt water and brakish water is unclear.

This suggests that indirect transmission via water is possible, to other waterbirds using or drinking contaminated water or through domestic poultry drinking unprocessed water from contaminated reservoirs.

9.4. Stability in aerosols

Data

For human influenza viruses, transmission via aerosols of 1-5 µm in size is generally believed to be the most effective mode of transmission, because such small droplets most effectively reach the lower respiratory tract in humans (Glezen and Couch 1989; Wright and Webster 2001). Evidence for transmission via aerosols has come primarily from studies of outbreaks where contact transmission could be excluded, such as outbreaks in a factory (Acheson and Hewitt 1952), or in an aeroplane where 72% of passengers were infected with influenza in 4.5 hours without proof of direct contact with the index case (Moser et al. 1979). In addition, it has been shown that the minimal infectious dose of influenza is ~100-fold lower when administered via the lower respiratory tract as compared to nasal administration (Couch et al. 1971; Couch et al. 1983; Knight et al. 1970). Transmission of influenza virus via aerosols has been proven experimentally in mice (Schulman and Kilbourne 1963). In humans, the effectiveness of aerosol transmission is further supported in vaccination experiments with live-attenuated vaccines via aerosols versus other routes (Roth et al. 2003).

During an Asian lineage H5N1 HPAIV outbreak in a UK quarantine facility, a variety of bird species, including sentinel chickens, kept in the same air space (but different cages) as the infected birds for almost one month did not get infected.

Conclusions

It is not clear whether aerosol transmission of influenza viruses represents an important transmission mode in poultry or wild birds. However, given that the physical and chemical composition of avian and human influenza virus particles is comparable, aerosol transmission between birds should be considered a possibility. Since Asian lineage H5N1 HPAI viruses have been reported to replicate to higher titres in trachea than in the intestinal tract of experimentally infected birds and their contacts (Sturm-Ramirez et al, 2005), aerosol transmission may be particularly relevant for this virus lineage.

The above contradicts the findings from the Asian lineage H5N1 HPAIV outbreak in a UK quarantine station which suggests that aerosol transmission is not a significant source of infection in other birds.

9.5. Stability in carcasses

Data

Viral loads in tissues of highly susceptible species often exceed 10^8 EID_{50} per gram.

In the case of the feeding of fresh chicken carcasses unknown to be infected with Asian lineage H5N1 HPAIV led to infection of large cats kept in a zoo in Thailand (Keawcharoen et al. 2004).

Contact with carcasses of infected wild birds is believed to be cause of natural H5N1 HPAIV infections in three cats and a stone marten on the island of Rugen, northern Germany. In addition, the substantial involvement in that outbreak of predatory or scavenging avian species such as common buzzards, several species of gulls and corvids, points in this direction. Climatic conditions (temperatures between –5°C and +2°C) during the period at the beginning of the Rugen outbreak are considered to have increased the stability of viral infectivity in carcasses (Harder, pers. comm.).

Composting of infected bird carcasses has been shown to lead to shortened periods of viral stability (Senne et al. 2005).

Conclusions

The virus can survive in carcasses of infected animals for a varying period of time, which will depend on environmental temperature. The period of infectivity will increase with decreasing temperature.

Infected carcasses represent a potential source of infection for scavenging animal species.

9.6. Overall conclusions and recommendations

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.

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

Background

The important parameters to consider are the sensitivity and specificity of the diagnostic methods together with their practicability, i.e. type of sample/tissue, cost and sample processing time required to obtain results.

When assessing test sensitivity and specificity for virus isolation or detection, isolation of virus in embryonated fowl's eggs is used as the historical gold standard. However, precise data for this method itself is lacking but the assumption is made that the presence of infectious virus in a specimen will be detected after two blind passages of any sample using this internationally defined methodology. Determinations therefore of relative sensitivity and specificity for molecular based methods are relative to virus isolation in embryonated fowl's eggs.

Data

Conventional RT-PCR using single step systems followed by analysis of product using gel-electrophoresis are up to 100 less sensitive with a specificity of 90% (Brown unpublished data). Real-time PCR for the M gene has an increased sensitivity compared to egg isolation with detection of 0.6 egg infectious doses 50%(EID50) where 1EID 50 is the limit of detection in embryonated fowl's eggs (Spackman et al., 2003). Subtype specific real-time PCR will vary depending on the system utilised and also relating to the degree of primer match to target. Assuming 100% primer match these assays have 110% sensitivity compared to embryonated fowl's eggs (Brown unpublished data).

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 2004b; EU 1992). 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]

---

[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

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

11.1. General Overview of Bird Migration Systems and Concepts

11.1.1. Basic concepts

Data

The migration of birds has long been a subject of speculation and research, although scientific research into migration largely commenced with the advent of bird ringing schemes in 1919 (Bairlein 2001). The individual marking of birds with metal rings has given information on movements between the different areas used by migratory birds during the course of their annual cycle.

Basic concepts in bird migration have recently been summarised by Alerstam (1993), Owen (1996), Bairlein et al. (2002) and Rees et al. (2005), whilst Marchant (2002) described the main methods used to gather data on bird movements.

There are many different types of bird movement and evaluation of risk needs to differentiate between these. The main types of movement are summarised in Table 11.1 and outlined in more detail in Annex 1.

Table 11.1. Definition of different types of bird migration or movement

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

Migration strategies of longer distant migrants vary according to the frequency and duration of stop-overs at staging areas. Piersma (1987) described these different migration flights as either 'hop, skip or jump' strategies (Figure 11.1).

Figure 11.1. Different types of migratory strategy shown by waders moving from coastal west Africa to (sub-)arctic breeding grounds: (from left to right) by turnstone Arenaria interpres ('hop'), dunlin Calidris alpina & Redshank Tringa totanus ('skip') and red knot Calidris canutus & bar-tailed godwit Limosa lapponica ('jump'). Source: Piersma 1987.

For some birds, typically some coastal waterbirds, migration is focussed in a narrow 'flyway'. Such flyways can be described either for individual species (*e.g.* Figure 11.2 and Figure 11.4) or be used as a concept to describe and summarise the broadly similar migration routes used by several species. Thus for waders, Figure 11.3 shows the main flyways at a global scale, whilst for Anatidae (ducks, geese and swans), Isakov (1967) summarised four main flyways in western Eurasia (Figure 11.5).

Not only do migration patterns vary between different coastal waders within, for example, the East Atlantic Flyway (*e.g.* Figure 11.4), but for many species such summary maps are not applicable at all. Thus, in Europe populations Common Snipe *Gallinago gallinago* and Eurasian Woodcock *Scolopax rusticola* migrate broadly from east to west across Eurasia, movements that are not described by the summary flyways in Figure 11.3. Stroud et al. (2004) found that a small number (14) of migratory wader populations in Africa and western Eurasia do not fit into these summary flyways[2].

Figure 11.2. Flyways for white storks Ciconia ciconia as described by the locations of ringing recoveries [Source: Bairlein et al. (2002) updating Fiedler 1998]

Figure 11.3. Summary map of the global, multi-species, wader flyways (Source: International Wader Study Group 1998)

Figure 11.4. Examples of three different species' flyways within the East Atlantic Flyway, showing broad migration routes from northern breeding areas to over-wintering sites in Europe and Africa (Left to right, kentish plover Charadrius alexandrinus, red knot Calidris canutus and sanderling Calidris alba; source: Smit and Piersma 1998)

Figure 11.5. The four major flyways for Anatidae in western Eurasia as described by Isakov (1967) (Northern White Sea/North Sea population; 2. European Siberia/Black Sea-Mediterranean population; 3. West Siberian/Caspian/Nile population; and 4. Siberian-Kazakhstan/Pakistan-India population; note that this excluded flyway linkages with Canada and Greenland - important for several goose populations)

Other birds migrate on a broad front across wider geographical areas. Such broad-front migrants still show strong geographical orientation but movement for the population as a whole is more diffuse (*e.g.* Figure 11.6).

---

[2] "These are largely wader populations that breed broadly across north-west and northern Europe, the majority of which migrate on a broad front south through Europe but some of which overwinter on the coastlines of western and eastern Africa. In all, seven Black Sea/Mediterranean flyway populations also occur on parts of the East Atlantic Flyway, and two on the West Asian/ East African Flyway. A smaller number of populations occur chiefly on the two predominantly coastal flyways but parts of which spread inland across Europe and Africa." (Stroud et al. 2004)

Figure 11.6. An example of broad-front migration of Wheatears Oenanthe oenanthe ringed as nestlings along parallel migration routes within Europe [lines join ringing and recovery sites; reproduced with acknowledgement from Bairlein et al. (2002)]

Whilst migration is typically thought of as a seasonal phenomenon, in reality, there are bird movements year-round (Figure 11.7), but most species show distinct periods when increased mobility is apparent.

Figure 11.7. Many birds undergo complex movements between different sites outside migratory periods: ringing has shown that Dunlin Calidris alpina move extensively between different European coastal areas within the non-breeding period. Summary of late autumn (post-moulting) movements for which ringing studies found direct evidence. (Lines do not indicate actual routes between areas (Source: Pienkowski and Pienkowski 1983).

Furthermore, even among longer-distance migrants, there are different strategies, with some species having populations that are wholly migratory (geographically separate breeding and wintering areas), whilst other species have populations which are resident (year-round presence in the same geographical area), or partially migratory (part of the population migrates and part of the population remains).

Further differences in the extent of movement may relate to sex or age of bird. For example, differential migration by age is widely found in gulls and in several species of shorebirds, the tendency being for young birds to migrate further from the breeding grounds than mature adults, for example Northern Lapwing *Vanellus vanellus* (Siriwardena and Wernham 2002). The reason for such variability stems from the evolutionary drive to balance over-winter survival and advantages in remaining close to the breeding grounds.

In attempting to describe migration systems, it is important to realise that there is even considerable variability between individuals of the same population related to issues such as the timing of migration (e.g. Ens et al. 1994). Such variation relates to trade-offs between the eco-physiological costs and benefits of arriving earlier or later at different locations along a flyway (Piersma 1994). A migration strategy that is successful in a season, say, when the arctic summer comes early may be less successful in a year when the arctic thaw on breeding areas comes later. Any population will contain individuals migrating at different times and possibly using different routes, which may in any case vary between years according to a range of environmental conditions such as wind-speed and direction. At best, it is only possible to describe migration systems in generality.

Conclusions

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.

11.1.2. Site fidelity and predictability of occurrence

Data

Many waterbird species are highly faithful to the sites they use throughout their annual cycle (both within and between years). The use of large individually engraved leg rings, neck collars or other markers is a technique that has allowed measurement of site fidelity for goose and swan species in particular (Rees et al. 2005). Some wader species which have been the subject of intensive study have also been shown also to return to the same individual nesting territories year after year. Such site fidelity can be explained as a result of various selective pressures that favour individuals which have an intimate knowledge of their environment. Its consequence is that certain locations not only hold large concentrations of waterbirds year after year (Section 11.2 below) but that these sites are repeatedly visited by the same birds.

Not all waterbirds show such strong site fidelity, and a range of strategies exist between species (*e.g.* Lappo 1996). However, processes such as female philopatry (Rohwer and Anderson 1988; Rees et al. 2005) also encourage the exchange of individuals between different groups, so that the dispersal of birds within a population fosters subsequent genetic mixing.

Typically, sites used by waterbirds hold similar numbers year after year, and the high predictability of numbers allows their formalised identification at key sites (Heath and Evans 2000) such as wetlands of international importance under the Ramsar Convention or as Special Protection Areas under the EC Birds Directive.

Some variation on numbers does occur, often as a result of varying numbers of young, thus inflating population size in some years. This is particularly the case in some waterbirds which breed in the high Arctic where the effects of variable weather and other factors can result in years of excellent or very poor productivity ('boom' or 'bust'). Productivity in some such species is linked to changes in relative predator abundance, itself a consequence of the three year Lemming cycle. For Brent Geese *Branta bernicla*, there is a well-established cycle of a year where no young are produced, followed by a year in which there can be either poor or good productivity, then followed by a year of consistently high productivity (Summers and Underhill 1987). Such cycles have been found for other species also (as reviewed by Newton 1998) and have consequences for the overall sizes of populations in the non-breeding season as well as for numbers at individual wetland sites.

Conclusions

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 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.

11.1.3. Factors which influence waterbird occurrence

Data

Periods of prolonged cold weather can significantly alter numbers of waterbirds present in their wintering areas (Ridgill and Fox 1990). The onset of frozen conditions can trigger significant population movements by some species as they disperse in search milder, more favourable conditions. Some examples are given in Annex 2. Under these cold conditions, numbers of waterbirds at sites in milder regions of Europe (typically the south and west) can be greatly inflated for short periods. Figure 11.8 shows those parts of Europe which received net influxes of nine species of ducks in severe cold weather periods between 1967 and 1986.

Figure 11.8. Square areas of 50 x 50 km that were identified as refuges in periods of severe cold weather (1967-1986) for Shelduck Tadorna tadorna, Wigeon Anas penelope, Teal Anas crecca, Mallard Anas platyrhynchos, Pintail Anas acuta, Shoveler Anas clypeata, Pochard Aythya ferina, Tufted Duck Aythya fuligula and Coot Fulica atra (Source: Ridgill and Fox 1990)

Notable refuge areas are southern Britain, Ireland, the coast and interior of NW France, Iberia (especially inland flood plains, Marshes of Guadalquivir, and the Ebro Delta), the Mediterranean coast of France (especially the Camargue), and estuarine areas of Italy (notably the Po Delta).

Periods of extreme dry weather can also cause significant movements of waterbirds and thus changes in numbers at key sites (Kingsford 1996). Whilst not typically a factor influencing waterbirds in Europe, shifting movements from drought areas or intermittent use of temporary wetlands in arid areas is typical of many African waterbirds (*e.g.* Harrison et al. 1997; Mullié et al. 1999). Patterns of such 'rains migration' are hard to predict. Periods of severe drought in southern Europe will result in waterbird dispersal from dried up wetlands.

Some wetlands vary significantly in **seasonal patterns of use**, especially the case for sites within continental Europe.

A range of local factors can also influence numbers of waterbirds at sites. Probably of the greatest significance is disturbance — which can occur from a number of sources including hunting (Madsen 1995; Madsen and Fox 1995). However, in the absence of positive conservation measures to influence site management, it is probable that disturbance levels will generally tend to be the same from year to year. Thus it is probable that a heavily disturbed site in one year will also tend to be heavily disturbed in the following year.

Conclusions

Factors such as those outlined above result in varied potential for mixing of birds between and within species at different times of the year (see Section 11.2 below).

11.1.4. Data on wild bird migrations and its interpretation

Data

A combination of bird census data and bird ringing data (for example Fransson and Pettersson 2001; Wernham et al. 2002; van Roomen et al. 2004; Collier et al. 2005) have been instrumental in identifying sites of importance for migratory birds of different species, the timing of their use, and the origins and destinations of migrating birds. These data sources have shown the broad distributions of species and their flyways.

Most information on movements comes from 'conventional' ringing which gives information only about the locations where the bird was ringed and where it subsequently was recovered or recaptured. Typically this can be many years later, and maps showing ringing and recovery locations should not be interpreted as indicating exact migration routes. For example, Figure 11.9 shows ringing recoveries for the Greenland White-fronted Goose *Anser albifrons flavirostris.* All birds in this population are known to visit Iceland on spring and autumn migration, yet misinterpretation of this ringing recovery map might suggest direct movements to and from the breeding and wintering areas.

Remote sensing, using radio or satellite telemetry, offers the great advantage of yielding detailed and precise information about the location (and sometimes also behaviour) of the individuals carrying transmitters.

Miniature data loggers, for recording the behaviour of individuals, are also likely to become more widely used in the future. Radio-telemetry has been used very successfully for interpreting long distance migrations of even small waterbirds, notably Western Sandpipers Calidris mauri (Iverson et al. 1996). There are currently some limitations to the technique, notably high costs, the high time cost of locating birds carrying transmitters, weight limitations for satellite transmitters (constraining their use on the smallest waterbirds, especially waders), and that generally results come from a few individuals that may not represent the behaviour of the population as a whole. However, costs and minimum size of transmitters are falling - increasing the number of individuals and species that can carry them. This will greatly increase the value of the technique.

Satellite telemetry involves larger transmitters and more powerful batteries and to date its use has been largely restricted to migratory geese and swans, typically to investigate the detailed migration ecology of populations using well known flyways. The high costs of satellite telemetry will restrict its used for the foreseeable future. However, even though one consequence of this is its restriction to a small number of individuals, its use may be the only realistic means of obtaining information on migratory flyways for birds migrating through regions with few birdwatchers, or in which political instability restricts the potential for other forms of field studies.

Figure 11.9. A typical map of locations of ringing and recovery sites for Greenland White-fronted Goose Anser albifrons flavirostris (Source: Wernham et al. 2002)

Conclusions

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).

11.1.5. Quality of information on bird migration

Data

Care needs to be exercised in interpreting summary information on populations and flyways. Although there has been a long history of collection of data on bird ringing, there has been little investment in necessary analysis and synthesis, especially at international scales. The African-Eurasian Waterbird Agreement recently noted:

"There have been few systematic reviews of waterbird population limits in recent years, despite the existence of a range of new methodologies that might be informative. Whilst some of these involve expensive technologies that are unlikely to be widely applied to large samples of birds, there are other approaches that could be readily applied and would be highly instructive with relatively limited investment. Simple consideration of existing, but un-analysed, data relating to waterbird ringing recoveries is capable of giving major new insights."[3]

Existing maps of flyways largely derive from activity undertaken by the International Waterbird Research Bureau in the 1970s, or earlier, and there have been few contemporary analyses at continental scale. Thus, Wetlands International's Anatidae Atlas (Scott and Rose 1996) obtained its population limits for Common Teal *Anas crecca* (Figure 11.10) from the earlier work of Monval and Pirot (1989), who in turn had in turn drawn from Atkinson-Willes' summarisation (in the 1970s) of the work of Isakov (1967). Isakov broadly defined two European flyways for ducks in Western Europe (Figure 11.5): a Northern White Sea/North Sea population and a European Siberia/Black Sea-Mediterranean population. However, recent analysis of Teal ringing recoveries (Guillemain et al. 2005; Figure 11.11) shows that there is actually little evidence for discrete populations of Common Teal but rather the European distribution should be considered as a continuum.

Conclusions

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 the Africa-Eurasian Waterbird Agreement (AEWA) MoP3 in October 2005.

Figure 11.10. Map of populations of Common Teal Anas crecca (Source: Scott and Rose 1996)

Figure 11.11. Map of recoveries of Common Teal Anas crecca ringed in the Camargue in Southern France (red dots show birds ringed in the Camargue and recovered within the putative limits of the Northwest European population and blue dots show recoveries within the putative limits of the Black/Sea /Mediterranean population; Guillemain et al conclude there is little evidence for population structuring for this species in Europe (Source: Guillemain et al. 2005)

---

[3] Proposal for guidance in the definition of biogeographical populations of waterbirds. AEWA/MOP 3.12. 3rd Session of the Meeting of the Parties to the Agreement on the Conservation of frican-Eurasian Migratory Waterbirds (AEWA), 23 – 27 October 2005, Dakar, Senegal.

11.2. Identifying Areas of Concentration or Mixing

Data

All wetland habitats (Figure 11.12) have the potential for mixing by waterbirds of different species, notably during migration and hence the potential for spread of infection by AIVs between different species should these be carried by one or more of the species occurring. However, there are networks of wetland sites that are of particular strategic importance for migratory waterbirds, providing essential stopovers where birds can refuel for onward flight, or safe areas for birds to moult and replace feathers (Sections 11.1.1, 11.1.2, Annex A). Many such sites are of regular importance, supporting large numbers of waterbirds each year (Heath and Evans 2000; Stroud et al. 2001; Stroud et al. 2004; Collier et al. 2005). These sites may support resident, passage, and summering or wintering waterbirds, at the relevant time of year. A list of published and other sources of information about such sites (including national inventories) is given in Table 13.2 for EU Member States.

Not all sites within any one flyway will be used by all of the birds that move along that flyway as flight distances between staging posts vary between species (hop, skip, jump migratory strategies, Piersma 1987, Section 11.1.1). Furthermore, some of these mixing areas will be used as migration stopovers by birds from different breeding and wintering areas, and different flyways (e.g. Scott and Rose 1996; Wernham et al. 2002). The timing of use also varies (e.g. Ens et al. 1994; Piersma 1994, Section 11.1.1), with some sites used only on the northbound spring migration or the southbound autumn, whilst others may be used on both migrations (Stroud et al. 2004, Section 11.1.1).

Figure 11.12. Global distribution of wetlands, based on a reclassification of the FAO-UNESCO Soil Map of the World combined with a soil climate map (Source: FAO-UNESCO, Soil Map of the World, digitized by ESRI. Soil climate map, USDA-NRCS, Soil Survey Division, World Soil Resources, Washington D.C. http://soils.usda.gov/use/worldsoils/mapindex/wetlands.html)

Two categories of concentration or mixing areas have been distinguished in Figure 11.13. These two categories, termed Primary and Secondary Sites, have been distinguished to highlight those locations known to consistently hold large concentrations of waterbirds, amongst the many wetland sites that constitute mixing areas for migratory waterbirds.

Primary Sites are congregations of ≥ 20,000 waterbirds. There is a comprehensive network of internationally important sites for birds, Important Bird Areas (IBAs), identified by BirdLife International on the basis of quantitative ornithological criteria (Heath and Evans 2000). IBAs are underpinned by data from the World Bird DataBase (BirdLife International 2005). Primary Sites shown on Figure 11.13 are those meeting the Global IBA criterion for congregations, A4iii, and the European Union criterion, C7, for Special Protection Areas (SPAs) and candidate SPAs (Directive 79/409/EEC on the Conservation of Wild Birds (*Birds Directive*).

- A4iii. Congregations: The site is known or thought to hold, on a regular basis, ≥ 20 000 waterbirds or ≥ 10 000 pairs of seabird of one or more species (Heath and Evans 2000).
- C7: The site has been designated as a Special Protection Area (SPA) or selected as a candidate SPA based on ornithological criteria in recognized use for identifying SPAs (Heath and Evans 2000).

Thus, these criteria do not distinguish higher risk waterbirds from other waterbirds. It is relatively easy to extract and exclude sites listed primarily for their (marine) seabird colonies, but is potentially misleading to apply further filters. Counts may exist only for certain species, so site entries are not necessarily comprehensive in terms of providing information on all the species that contribute to the congregation. Consequently, Figure 11.14 includes sites that hold important concentrations of waterbirds, but not necessarily primarily higher risk species of waterbird.

Secondary Sites are all the remaining wetlands identified by the World Birds DataBase (WBDB) to have waterbird species. Some of these sites also may have large concentrations of higher risk species of waterbirds, but for the same reasons as for primary sites, data are not available in the WBDB to reliably elucidate this point.

There are limitations to the data. Not all countries have contributed data. Data in the database vary from one site to another in terms of count-years available and submitted, completeness of data, and species for which counts have been undertaken. These facts, together with the paucity of information about detailed migration routes for many species, have limited the extent of filtering that can be undertaken to identify mixing sites just for higher risk species.

Consequently, all sites meeting the criteria have been included, not just those in outbreak regions or in mixing areas used by migrating birds that come to EU countries. Thus the figure illustrates the many, widely distributed concentration and mixing areas for waterbirds including those within regions presently of concern due to H5N1 HPAIV. The region encompassing the Black Sea and Caspian Sea in particular represents a mixing area for birds, notably species of *Anatidae*, from several flyways and a region in which flyway boundaries are indistinct, e.g. *Anas crecca*, or where dispersive movements occur (Scott and Rose 1996, Section 11.1.3 this report).

Figure 11.13. Areas of concentrations and mixing for waterbirds (Source: BirdLife International 2005).

The other key source of information on concentrations of waterbirds and mixing areas used by migrating birds is the International Waterbird Census (IWC) (Figure 11.13 to Figure 11.15) (Gilissen et al. 2002). The frequency of count coverage for sites varies from one site to another, as indicated by Figure 11.14 – Figure 11.15, and our knowledge is far less complete for some areas than for others, for example South West Asia. Nonetheless, the IWC database does contain relevant data to enable an assessment of species occurrence across most or all sites in the database, minimally for the single count month of January. This is a necessary next step towards determining concentrations and mixing areas for higher risk species.

Furthermore, analysis of EURING data (Baillie 1995) on movements by individually ringed birds of those species considered to be higher risk species (Section 11.2.2) will be necessary to elucidate those mixing and concentration areas utilised by higher risk species. These two necessary analyses, of IWC and EURING data, are the subject of a separate project being undertaken by Wetlands International and EURING under contract to the EuropeDG Environment of the European Commission (O'Briain pers. comm.).

An essential consideration in interpreting Figure 11.12 to Figure 11.15 is that the sites depicted are concentration and mixing areas for any waterbird species; not all will be used by higher risk species, as defined in Section 11.2.2. Currently, the information available does not permit the identification of just those sites used by higher risk species.

Figure 11.14. All sites in the IWC database for the East Mediterranean and Black Sea area (Gilissen et al. 2002; solid black dots are sites with data for 1999, open circles are sites with no data for 1999)

Figure 11.15. All sites in the IWC database for the Southwest Asian area (Gilissen et al. 2002; solid black dots are sites with data for 1999, open circles are sites with no data for 1999)

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.

11.3. Phenology of Waterbird Migration

Data

Migratory species occurring in EU countries include wintering birds from northern breeding areas, summering birds that winter further south, and passage migrants, as well as short distance migrants that remain within Europe. As described in Section 11.1.1, movements are often complex and the text here can offer only some broad generalisations. Summer visitors generally migrate southwards to overwinter, some migrating as far as South Africa. Passage migrants and winter visitors originate from breeding areas ranging from arctic Canada, Greenland, Fennoscandia and across to Siberia, southwards throughout the EU. The proportion of avifauna comprising summer visitors, i.e. migrant birds that occur during the breeding season in Europe, increases with increasing latitude (Newton and Dale 1996). This is because winter temperatures at higher latitudes make these areas unsuitable for overwintering, as illustrated by the isotherms in January indicating the extent of frozen wetlands (Figure 11.16), so birds are forced to migrate to warmer climes to improve their overwinter survival. Within Europe, there is a cline in winter distribution, consistent with generally warmer winters in the south and west. Wintering populations in these areas are augmented during periods of severe weather by birds making cold weather movements (Ridgill and Fox 1990, Section 11.1.3).

The timing of migration is dependent on species, their origin and destination. In reality, there is a spectrum of bird movements throughout the year, with peaks during spring migration to generally more northerly breeding areas and autumn migration in a mainly southerly direction, when the largest numbers across many species are on the move. Spring migration may commence as early as late February/early March, continuing until late May/early June, and autumn migration may commence in June and continue until November (e.g. Collier et al. 2005). Within these broad time periods, there are peaks of migratory activity, the timing of which varies with latitude. In the UK, for example, spring migration usually peaks in April/May, whilst autumn migration tends to peak during August to October.

Furthermore, the duration of stopover by passage migrants varies greatly from brief refuelling stops of a few days to longer stays of several weeks to moult and so renew flight feathers. At such times, there is particularly high turnover of individual birds as some depart to be replaced by others (e.g. Frederiksen et al. 2001). Counts are not adequate to describe the numbers of birds actually using a site; turnover can be measured effectively only by the use of mark-recapture techniques (Schaub et al. 2001).

DG Environment of the European Commission have collated data on the timing of onset of both spring (pre-nuptial) and autumn (post-breeding) migration for species listed under Annex II of the EC Birds Directive for each of the EU15 Member States. These data are given on the website of the Birds Directive [4].

Figure 11.16. Isotherms for the period 6 to 15 January 1999, with an interval of 5 degrees Celsius produced by NOAA-CIRES Climate Diagnostics Centre, Boulder, Colorado (Gilissen et al. 2002)

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.

---

[4] http://europa.eu.int/comm/environment/nature/nature_conservation/focus_wild_birds/species_birds_directive/index_en.htm#reprod

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

11.4.1. Methodology

A sequence of decision rules was devised based on expert opinion to identify the migratory bird species which are considered to be more likely to be exposed to H5N1 HPAIV.

Species were identified based on distribution, ecology and behaviour suggesting that they may be more likely to become infected by Asian lineage H5N1 HPAIV outside the EU. The factors considered are outlined in this section and applied in Section 11.5 to derive a list of species we consider are vulnerable to infection by H5N1 HPAIV.

The relative population sizes of birds were considered but not used as a formal selection crtierion in the assessment of risk. Population sizes of European waterbirds range across six orders of magnitude (from <10 Slender-billed Curlews *Numenius tenuirostris* to c. 7,500,000 Mallards *Anas platyrhynchos*). Intuitively, it is the more numerous species whose behaviour makes them more likely to come into frequent contact with domestic poultry in Europe that are of increased risk to poultry if they are carrying H5N1 HPAIV. However, population size is correlated with other factors considered below, notably gregariousness, bird density within flocks, and degree of mixing. Most abundant species are likely to be those that are the most gregarious, occur at the highest densities and show the most mixing with other species. This assumption has not been demonstrated formally (and should be a future analytical priority), but for the time-being we consider that a separate filter related to population size would provide little extra discriminatory power.

The following sections discuss the factors which form the basis of the decision rules.

11.4.1.1. Initial list of species considered

Data

Reports of infection in migratory birds mainly include those species included in the orders *Anatidae* (ducks, geese and swans) and *Charadriiformes* (waders and gulls) (see Section 6.3; Webster et al. 1992; Alexander 2000).

Conclusions

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

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

For each species selected as above, a range of data was assembled in the appended spreadsheet (Annex 2). Brief descriptions of the data in the spreadsheets (columns from left to right) are in Annex 5.

In this section, those data elements are summarised that have relevance in the application of filters to select species more likely to be carrying Asian lineage H5N1 HPAIV. Given the lack of field studies on the dynamics of Asian lineage H5N1 HPAIV in wild bird populations these assessments have been made solely on the basis of expert opinion.

11.4.1.2.1. Gregariousness during migration/wintering periods

Data

None available.

Conclusions

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.

Gregariousness has been indicated by two letters, which denote group size and within-group density, respectively. The following coding has been applied:

Code	*Explanation*
Group size	
L	Large: often several hundreds to thousands of individuals (Eurasian Wigeon *Anas penelope*)
M	Medium: often several tens to few hundred individuals (Whooper Swan *Cygnus cygnus*)
S	Small: often up to a few tens of birds (Purple Sandpiper *Calidris maritima*)
O	Usually solitary or a few birds together (Green Sandpiper *Tringa ochropus*)
Within-group density	
H	High density: often less than 2 m between individuals (Dunlin *Calidris alpina*)
M	Medium density: often between 2-5 m between individuals (Herring Gull *Larus argentatus*)
L	Low density: often more than 5 m between individuals (Common Snipe *Gallinago gallinago*)
O	(near) solitary

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.

11.4.1.2.2. 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.

Degree of mixing with other species (mixed foraging, mixed roosts, mixing at moulting areas, *etc*.) has been indicated as follows:

Code	*Explanation*
H	High degree (Eurasian Wigeon)
M	Medium degree (Northern Lapwing *Vanellus vanellus*)

Code	*Explanation*
L	Low degree (Temminck's Stint *Calidris temminckii*)
O	Hardly any mixing (Common Sandpiper)

11.4.1.2.3. 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.

The following coding has been used:

Code	*Explanation*
A	agricultural land
N	natural land habitat (usually marshes near wetlands; this coding has especially been used to distinguish purely freshwater species, which rarely come ashore (F), from those who also use non-agricultural land habitat (FN))
O	other habitat (variety of habitat types, including woodland, urban areas, *etc.*)
F	fresh water
M	marine
L	littoral
sal	salinas

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.

Examples of codes used are and their explanation listed below.

Code	*They should all be read as "the species mainly uses ……." :*
A	agricultural land (Rook *Corvus frugilegus*)
AN	agricultural land and natural land habitat (Eurasian Golden Plover *Pluvialis apricaria*)
FA	freshwater and agricultural land (Greater White-fronted Goose *Anser albifrons*)
FAL	freshwater, agricultural land, littoral zone (Black-headed Gull *Larus canus*)
F	freshwater (Tufted Duck *Aythya fuligula*)
FL	freshwater and littoral zone (Common Sandpiper *Tringa hypoleucos*)
FM	freshwater and marine (Common Goldeneye *Bucephala clangula*)
FN	freshwater and natural land habitat (Marsh Sandpiper *Tringa stagnatilis*)
L	littoral zone (Red Knot *Calidris canutus*)
LA	littoral zone and agricultural land (Brent Goose *Branta bernicla*)
M	marine (Common Scoter *Melanitta nigra*)
MA	marine and agricultural land (Mediterranean Gull *Larus melanocephalus*)
MF	marine and freshwater (Greater Scaup *Aythya marila*)

Code	*They should all be read as "the species mainly uses ...." :*
ML	marine and littoral (Glaucous Gull *Larus hyperboreus*)
O	other terrestrial habitat (Eurasian Woodcock *Scolopax rusticola*)
Sal	salinas (Greater Flamingo *Phoenicopterus ruber*)

(Note that potentially Whiskered Tern *Childonias hybridus* might have been selected on the basis of its occurrence in freshwater habitats, but owing to significant lack of knowledge concerning gregariousness and degree of mixing the species was excluded.)

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

In evaluating migratory bird species more likely to be exposed to H5N1 HPAIV we followed the steps described below (presented graphically in Figure 11.17).

From the initial list of all species of European *Anseriformes* and *Charadriiformes* (List 1), a selection was made of those that are migratory. The only European non-migratory waterbird species excluded at this step were Barrow's Goldeneye *Bucephala islandica* and the Harlequin *Histrionicus histrionicus*, both being North American ducks which, within Europe, are endemic to Iceland.

The further selection of species was conducted based on degree of mixing, gregariousness, and habitat use.

Species were not selected if they showed:

- hardly any (O), or a low (L) gregariousness (*i.e.* codes OL, OM, SL and SM), although species with code ML (low density but medium group size were not excluded); and/or
- least mixing with other species (showing either hardly any mixing (O) or a low degree of mixing (L); and/or
- they occurred mainly in marine (M), salinas (sal), littoral (L) environments or other habitats (O) (*i.e.* species whose habitat use codes begin with O, sal, L or M) since such species are expected to only occasionally use freshwater habitats.

The final criterion was whether the species was likely to have passed through a geographic region which currently is considered to have endemic Asian lineage H5N1 HPAIV infection in wild birds or domestic poultry (note that this criterion was not applied here, since the necessary data was not available).

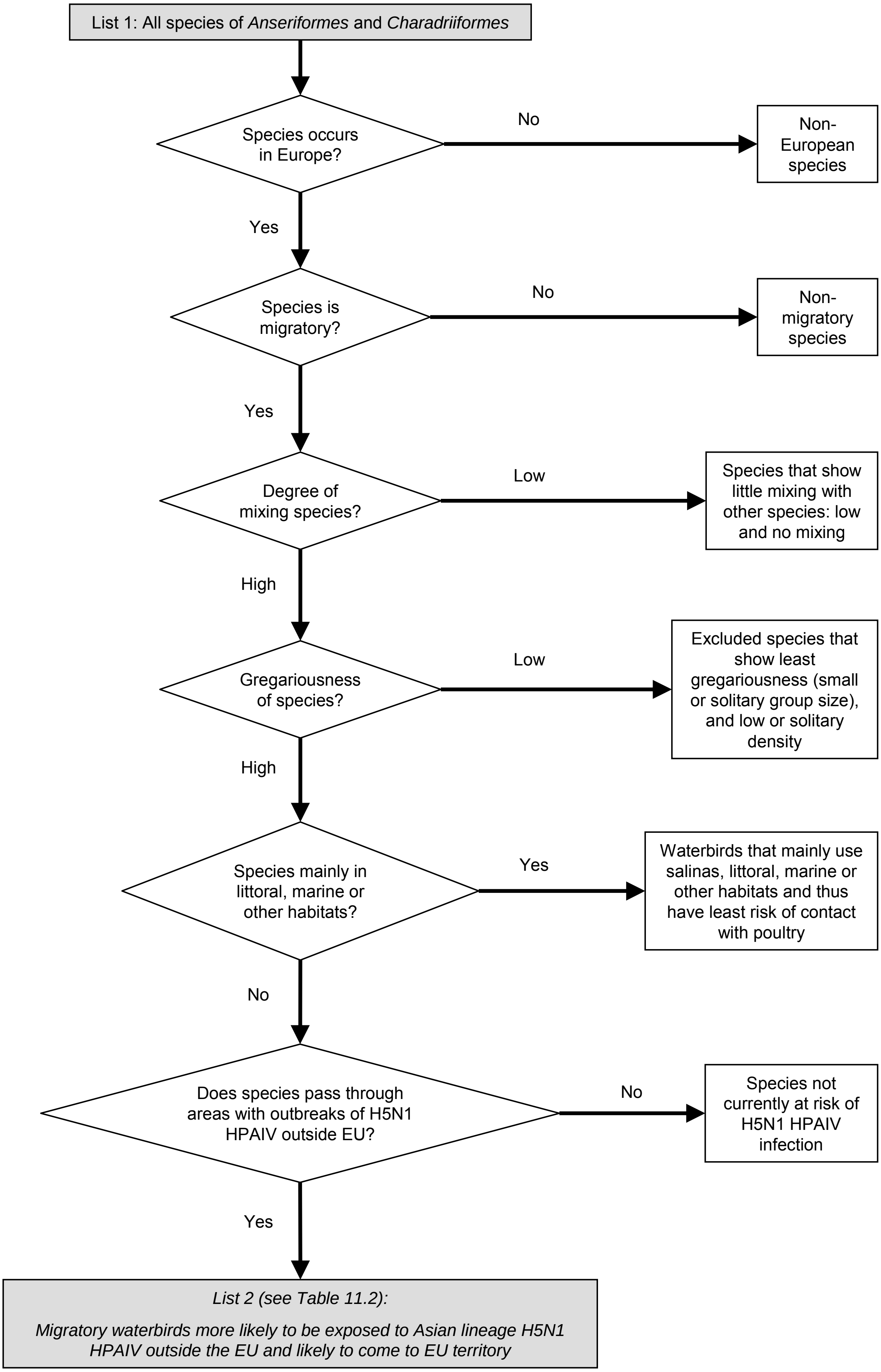


Figure 11.17. Decision tree for selection of migratory species more likely to be exposed to Asian Lineage H5N1 HPAIV outside Europe and to release it to the European Union

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 (called List 2 in Figure 11.17) is given in Table 11.2. 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).

Note that a significant number of additional species not currently included in the Table 11.2 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.

Table 11.2. Selection of waterbird species more likely to be exposed to Asian lineage H5N1 AIV on the basis of gregariousness or mixing and which may expose European poultry on the basis of shared habitats (see Section 13; see Section 11.4 and Annex 5 for explanation of codes. Y = yes, N = no)

Common name	*Scientific name*	*Occurs in Europe?*	*Migratory?*	*Well defined flyway system?*	*Potential direct migratory linkage Black or Aegean Seas to EU?*	*Potential direct migratory linkage Southern Urals to EU?*	*Potential direct migratory linkage Nigeria to EU?*	*Species migrates through the Baltic region*	*Species migrates through the Adriatic region*	*Main habitat during migration/wintering*	*Gregariousness during migration/winter*	*Degree of mixing during migration/winter*	*Consolidated risk of contact with poultry*	*Species identified as 'higher risk' in Commission Decision 2005-726*
<u>Swans</u>														
Bewick's Swan	*Cygnus columbianus*	Y	Y	Y	N	N	N	Y	N	FA	ML	M	**L**	
Mute Swan	*Cygnus olor*	Y	Y	N	Y	?	N	Y	Y	FA	ML	M	**M**	
<u>Geese</u>														
Pink-footed Goose	*Anser brachyrhnchus*	Y	Y	Y	N	N	N	N	N	FA	LH	M	**L**	
Bean Goose	*Anser fabalis*	Y	Y	Y	N	N	N	Y	N	FA	LM	H	**L**	Y
Greater White-fronted Goose (European race)	*Anser albifrons albifrons*	Y	Y	N	Y	Y	N	Y	Y	FA	LH	H	**M**	Y
Lesser White-fronted Goose	*Anser erythropus*	Y	Y	Y	Y	?	N	Y	N	FA	LH	M	**0**	
Greylag Goose	*Anser anser*	Y	Y	Y	Y	N	N	Y	Y	FA	LH	H	**M**	
Barnacle Goose	*Branta leucopsis*	Y	Y	Y	N	N	N	Y	N	FAL	LH	H	**L**	
Brent Goose	*Branta bernicla*	Y	Y	Y	N	N	N	Y	N	FAL	LH	M	**L**	
Red-breasted Goose	*Branta ruficollis*	Y	Y	Y	Y	Y	N	N	N	AL	MH	H	**L**	
Canada Goose	*Branta canadensis*	Y	Y	N	N	N	N	Y	N	FA	MM	H	**L**	
<u>Ducks</u>														
Eurasian Wigeon	*Anas penelope*	Y	Y	N	Y	Y	N	Y	Y	FAL	LH	H	**M**	Y
Common Teal	*Anas crecca*	Y	Y	N	Y	Y?	N	Y	Y	FAL	MH	H	**M**	Y
Mallard	*Anas platyrhynchos*	Y	Y	N	Y	N	N	Y	Y	FAL	MH	H	**H**	Y
Northern Pintail	*Anas acuta*	Y	Y	N	Y	Y?	N	Y	Y	FAL	MH	H	**L**	Y
Garganey	*Anas querquedula*	Y	Y	N	N	Y	Y	Y	Y	F	?	H	**L**	Y

Common name	*Scientific name*	*Occurs in Europe?*	*Migratory?*	*Well defined flyway system?*	*Potential direct migratory linkage Black or Aegean Seas to EU?*	*Potential direct migratory linkage Southern Urals to EU?*	*Potential direct migratory linkage Nigeria to EU?*	*Species migrates through the Baltic region*	*Species migrates through the Adriatic region*	*Main habitat during migration/wintering*	*Gregariousness during migration/winter*	*Degree of mixing during migration/winter*	*Consolidated risk of contact with poultry*	*Species identified as 'higher risk' in Commission Decision 2005-726*
Northern Shoveler	*Anas clypeata*	Y	Y	N	Y?	Y	N	Y	Y	FL	MH	H	**L**	Y
Marbled Teal	*Marmaronetta angustirostris*	Y	Y	N	N	N	N	N	N	F	MM	H	**0**	
Red-crested Pochard	*Netta rufina*	Y	Y	N	Y	N	N	Y	Y	F	MM	?	**L**	
Common Pochard	*Aythya ferina*	Y	Y	N	Y	Y	N	Y	Y	F	MH	H	**L**	Y
Tufted Duck	*Aythya fuligula*	Y	Y	N	Y	Y	N	Y	Y	F	MH	H	**L**	Y
Shorebirds														
Northern Lapwing	*Vanellus vanellus*	Y	Y	N	Y?	Y	N	Y	Y	FA	MH	M	**M**	Y
Eurasian Golden Plover	*Pluvialis apricaria*	Y	Y	Y	N	N	N	Y	Y	AN	LH	M	**L**	
Black-tailed Godwit	*Limosa limosa*	Y	Y	Y	N	N	N	Y	Y	FAL	MM	H	**L**	
Ruff	*Philomachus pugnax*	Y	Y	Y	N	N	Y?	Y	Y	FA	MM	M	**L**	Y
Gulls														
Black-headed Gull	*Larus ridibundus*	Y	Y	N	Y?	N	Y	Y	Y	FAL	LM	H	**H**	Y
Common Gull	*Larus canus*	Y	Y	N	N	N	N	Y	Y	FAL	MM	H	**L**	Y

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

Data

The mortality in 2005 of *about* 10% of the world population of bar-headed geese *Anser indicus* at Lake Qinghai (Chen et al. 2005) highlighted the significant possible consequences of H5N1 HPAIV spread for waterbirds with high conservation status.

European species of *Anseriformes* and *Charadriiformes* which are already globally threatened are listed in Table 11.3. The small population sizes of these species make them especially vulnerable to the consequences of significantly enhanced mortality from highly pathogenic avian influenza.

All these species are listed on Annex I of the EC Directive on the conservation of wild birds (EC 1979), and all have international action plans aimed at addressing the causes of their current unfavourable conservation status.

Table 11.3. Globally threatened species of European Anseriformes and Charadriiformes whose populations would be jeopardised by infection with H5N1 HPAIV

Common name	*Scientific name*	*IUCN Red-list status*
Lesser White-fronted Goose	*Anser erythropus*	Vulnerable
Red-breasted Goose	*Branta ruficollis*	Vulnerable
Marbled Teal	*Marmaronetta angustirostris*	Vulnerable
Ferruginous Duck	*Aythya nyroca*	Near threatened
White-headed Duck	*Oxyura leucocephala*	Endangered
Pygmy Cormorant	*Phalacrocorax pygmeus*	Near threatened
Sociable Plover	*Vanellus gregarius*	Critical
Great Snipe	*Gallinago media*	Near threatened
Slender-billed Curlew	*Numenius tenuirostris*	Critical
Audouin's Gull	*Larus audouinii*	Near threatened

Conclusion

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.

11.6. 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; 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."**

12. Surveillance of Wild Birds outside EU regarding Infection with the Asian lineage H5N1 HPAIV

Data

North America

Influenza viruses of subtypes H1-H12 have been isolated in waders in the *Charadriidae* and *Scolopacidae* families migrating through the eastern USA, with a high prevalence of certain H subtypes (H1, H2, H5, H7, H9- H12) and a larger variety of HA/NA combinations as compared to ducks in Canada (Krauss et al. 2004). Moreover, the seasonal prevalence of influenza viruses in waders seems to be reversed as compared to ducks, with high virus prevalence (~14%) during spring migration (Krauss et al. 2004).

Central Europe, Middle East and Africa

Field surveillance campaigns have been conducted in Central Europe, Middle East and African countries, before the migration of birds back to their original breeding areas under the FAO regional surveillance technical cooperation programmes (Martin, pers. comm.). A total of 13 key sites have been identified based on ecological considerations (rich and abundant wintering avifauna) (Table 12.1, Figure 12.1). A total of 4,540 samples have been collected between mid January and mid March. These include mostly Palaearctic ducks (36%, mostly garganey), African ducks (38%, mostly white-faced whistling duck), gulls and terns (12%), and shorebirds (10%) (Gaidet, pers. comm.). So far 1,646 samples have been analysed and no H5N1 HPAIV has been isolated in that sample subset. No data is available from Eastern European countries.

Table 12.1. List of key sites selected for HPAIV monitoring as part of an FAO initiative in 2006 (Source: FAO CIRAD/RVC TCP projects)

TCP	*Area*	*Country*	*Site*	*Period of year*	*Total samples collected*	*Laboratory (codes explained below)*
Middle East	Nile delta	Egypt	Nile delta	March	245	NAMRU3
Northern Africa	Northern Africa	Morocco	Bas Loukkos marshland	February	91	IZS
West Africa	Rift Valley	Ethiopia	Lake Awasa, Debre Zeit, Longano, Ziway	January	115	IZS
	Lake Chad Basin	Chad	Douguia	February	740	IZS
		Niger	Maradi and Zinder regions	February	129	IZS
	W Nat. Park	Niger	Gaya region	March	276	IZS
		Burkina Faso	Arly complex	February	349	IZS
	Niger Interior Delta	Mali	Mopti region	January	692	IZS
	Senegal delta	Mauritania	Aleg Lake, Diawling NP	February	462	IZS
		Senegal	Djoudj NP, Langue de Barbarie NP	March	460	IZS
	Banc d’Arguin NP	Mauritania	Banc d'Arguin NP	February	279	IZS

TCP	*Area*	*Country*	*Site*	*Period of year*	*Total samples collected*	*Laboratory (codes explained below)*
Eastern & Southern Africa	East Africa	Kenya	Lake Ol-Bolosot	February	286	OVI
	Southern Africa	Malawi	Lake Chilwa	February	416	OVI
Total					**4540**	

Laboratory codes: TCP (FAO Technical Cooperation Programme); NAMRU3 (Naval Medical Research Unit 3); IZS (Istituto Zooprofilattico Sperimentale delle Venezie, Padova, Italia); OVI (Onderstepoort Veterinary Institute, RSA)

Figure 12.1. Geographical distribution of sampling sites and numbers of animals sampled per site under the FAO/CIRAD/RVC regional active surveillance projects covering Central Europe, Africa and the Middle East as of March 2006

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.

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).

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

Chapter 11 described European waterbird migration systems and identified migratory species that could carry the Asian lineage H5N1 HPAIV into the EU. The current chapter more specifically aims to:

- further evaluate the risk of contact between wild bird species and domestic poultry; and
- identify information sources that describe the distributions and populations sizes of those species in Europe.

The selection of birds is done using two sets of criteria which are presented below.

- The list of bird species generated in Chapter 11 and presented as List 2 in Table 11.2 is further refined in Section 13.1 by assessing their probability of exposing poultry in the EU through the use of shared habitats. They may also be more likely to become exposed in outbreak areas to infection in poultry populations.
- An additional group of birds (see Section 13.2) is being selected from all bird species based on the degree to which any bird species are likely to come into close contact with poultry within the EU.

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

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

Data

Based on basic epidemiological principles and expert opinion, contact with domesticated poultry was assessed to be an important risk factor in the transmission of the Asian lineage H5N1 HPAIV from migratory birds to poultry.

On the basis of expert opinion in relation to knowledge about ecology and behaviour of waterbirds, the likelihood of close contact between the species concerned and domesticated/captive poultry has been assessed as:

0	Negligible or zero risk
L	Low risk
M	Medium risk
H	Higher risk

This assessment has considered risk as a function of contact intensity. Thus a scenario where small numbers of wild birds are potentially in contact with poultry for a long period is considered equivalent to a scenario where larger numbers are in contact for a shorter period. Expert opinion in relation to probability of contact was sought from the members of the Scientific Working Group of the EC Birds Directive's Ornis Committee. Responses were consolidated with those of this Working Group's ornithologists to produce a final evaluation, based on professional judgement and representing geographical variation in ecological and free-range conditions across Europe.

The resulting decision tree describing the selection process of birds starting from the species included in Table 11.2 is presented in Figure 13.1.

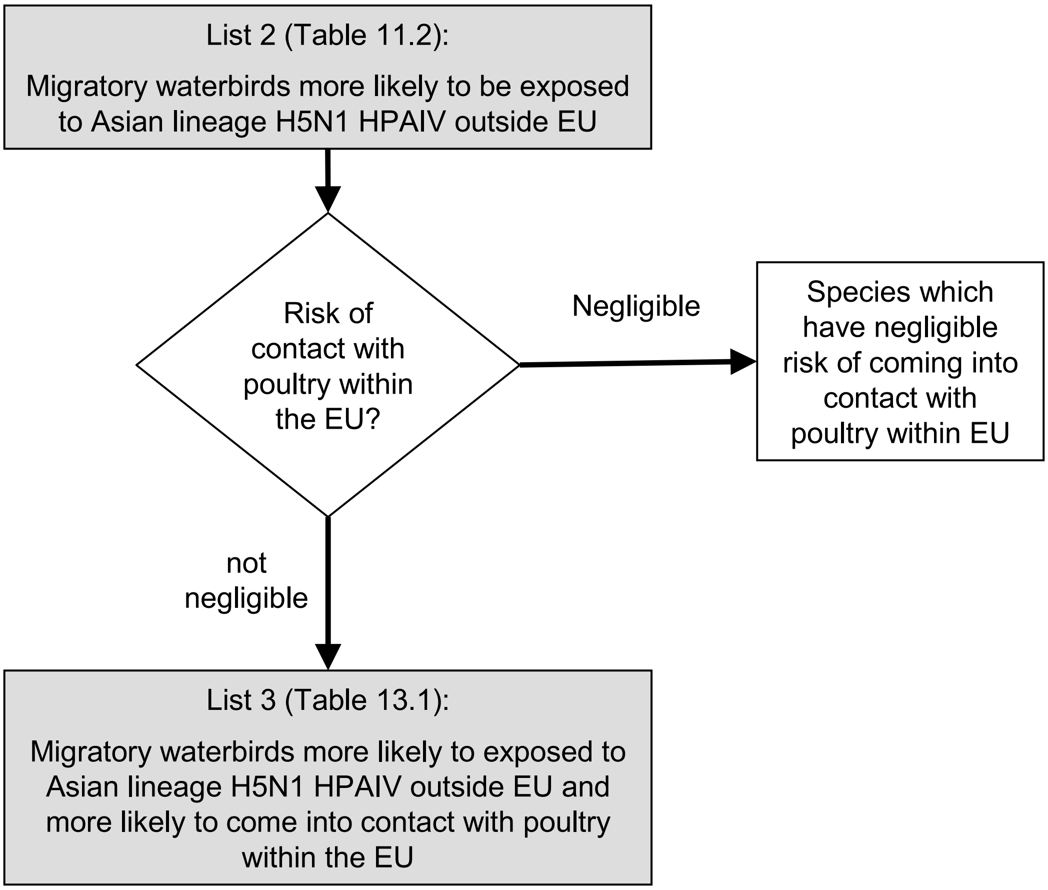


Figure 13.1. Decision tree defining bird species more likely to carry Asian lineage H5N1 HPAIV to European territories and to expose poultry (as a subset of Table 11.2)

Conclusion

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), both populations of which have small populations within the EU (see Section 11.4). All other species listed in Table 11.2 (a total of 25 species) were considered to have at least some probability of contact with domestic poultry within the EU.

Table 13.1. 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 (criteria described in Figure 13.1)

Common name	Scientific name	Occurs in Europe?	Migratory?	Well defined flyway system?	Potential direct migratory linkage Black or Aegean Seas to EU?	Potential direct migratory linkage Southern Urals to EU?	Potential direct migratory linkage Nigeria to EU?	Species migrates through the Baltic region	Species migrates through the Adriatic region	Main habitat during migration/wintering	Gregariousness during migration/winter	Degree of mixing during migration/winter	Consolidated probability of exposure to poultry in outbreak areas	Consolidated probability of contact with EU poultry	Species identified as 'higher risk' in Commission Decision 2005-726
Swans															
Bewick's Swan	*Cygnus columbianus*	Y	Y	Y	N	N	N	Y	N	FA	ML	M	**L**	**L**	
Mute Swan	*Cygnus olor*	Y	Y	N	Y	?	N	Y	Y	FA	ML	M	**M**	**M**	
Geese															
Bean Goose	*Anser fabalis*	Y	Y	Y	N	N	N	Y	N	FA	LM	H	**L**	**L**	Y
Greater White-fronted Goose (European race)	*Anser albifrons albifrons*	Y	Y	N	Y	Y	N	Y	Y	FA	LH	H	**M**	**M**	Y
Lesser White-fronted Goose	*Anser erythropus*	Y	Y	Y	Y	?	N	Y	N	FA	LH	M	**0**	**0**	
Greylag Goose	*Anser anser*	Y	Y	Y	Y	N	N	Y	Y	FA	LH	H	**M**	**M**	
Barnacle Goose	*Branta leucopsis*	Y	Y	Y	N	N	N	Y	N	FAL	LH	H	**L**	**L**	
Brent Goose	*Branta bernicla*	Y	Y	Y	N	N	N	Y	N	FAL	LH	M	**L**	**L**	
Red-breasted Goose	*Branta ruficollis*	Y	Y	Y	Y	Y	N	N	N	AL	MH	H	**L**	**L**	
Canada Goose	*Branta canadensis*	Y	Y	N	N	N	N	Y	N	FA	MM	H	**L**	**L**	
Ducks															
Eurasian Wigeon	*Anas penelope*	Y	Y	N	Y	Y	N	Y	Y	FAL	LH	H	**M**	**M**	Y
Common Teal	*Anas crecca*	Y	Y	N	Y	Y?	N	Y	Y	FAL	MH	H	**M**	**M**	Y
Mallard	*Anas platyrhynchos*	Y	Y	N	Y	N	N	Y	Y	FAL	MH	H	**H**	**H**	Y
Northern Pintail	*Anas acuta*	Y	Y	N	Y	Y?	N	Y	Y	FAL	MH	H	**L**	**L**	Y

Common name	*Scientific name*	*Occurs in Europe?*	*Migratory?*	*Well defined flyway system?*	*Potential direct migratory linkage Black or Aegean Seas to EU?*	*Potential direct migratory linkage Southern Urals to EU?*	*Potential direct migratory linkage Nigeria to EU?*	*Species migrates through the Baltic region*	*Species migrates through the Adriatic region*	*Main habitat during migration/wintering*	*Gregariousness during migration/winter*	*Degree of mixing during migration/winter*	*Consolidated probability of exposure to poultry in outbreak areas*	*Consolidated probability of contact with EU poultry*	*Species identified as 'higher risk' in Commission Decision 2005-726*
Garganey	*Anas querquedula*	Y	Y	N	N	Y	Y	Y	Y	F	?	H	**L**	**L**	Y
Northern Shoveler	*Anas clypeata*	Y	Y	N	Y?	Y	N	Y	Y	FL	MH	H	**L**	**L**	Y
Red-crested Pochard	*Netta rufina*	Y	Y	N	Y	N	N	Y	Y	F	MM	?	**L**	**L**	
Common Pochard	*Aythya ferina*	Y	Y	N	Y	Y	N	Y	Y	F	MH	H	**L**	**L**	Y
Tufted Duck	*Aythya fuligula*	Y	Y	N	Y	Y	N	Y	Y	F	MH	H	**L**	**L**	Y
Shorebirds															
Northern Lapwing	*Vanellus vanellus*	Y	Y	N	Y?	Y	N	Y	Y	FA	MH	M	**M**	**M**	Y
Eurasian Golden Plover	*Pluvialis apricaria*	Y	Y	Y	N	N	N	Y	Y	AN	LH	M	**L**	**L**	
Black-tailed Godwit	*Limosa limosa*	Y	Y	Y	N	N	N	Y	Y	FAL	MM	H	**L**	**L**	
Ruff	*Philomachus pugnax*	Y	Y	Y	N	N	Y?	Y	Y	FA	MM	M	**L**	**L**	Y
Gulls															
Black-headed Gull	*Larus ridibundus*	Y	Y	N	Y?	N	Y	Y	Y	FAL	LM	H	**H**	**H**	Y
Common Gull	*Larus canus*	Y	Y	N	N	N	N	Y	Y	FAL	MM	H	**L**	**L**	Y

13.1.2. Additional Information about Migratory Bird Species currently more likely to Expose Poultry in the EU to Asian Lineage H5N1 HPAIV

Population Sizes and Distribution

A wide range of information exists on the population sizes and distributions of European birds, sources of which are provided in Annex 5.

Movements

There has been a long history of the study of bird movements using, initially, metal rings and more recently other types of marker. More recently a number of national publications have sought to analyse the information derived from national ringing schemes, typically publishing this information in national ringing atlases. Recent publications which summarise movements of waterbirds migrating to or from Europe are summarised in Annex 6.

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

Data

Expert opinion indicates that in N & W Europe, in particular, contact between wild birds and domestic poultry is more likely to be restricted to those species, not exclusively waterbirds, that associate with man, or at least with farmland. Wild birds that live in close proximity to domestic poultry, perhaps sharing buildings or food and water sources, can be considered as 'bridge species' in that they may have the potential to transmit virus from other wild birds to domestic poultry, if they are carrying the virus. An example of the possible role of such bridge species was given by Alexander and Spackman (1981), who suggested that the Starlings *Sturnus vulgaris* may have been involved in an unprecedented series of outbreaks of highly pathogenic H7 infections in turkeys in eastern England in spring 1979. They noted that the severity of the preceding winter had damaged many of the turkey houses, allowing access to Starlings and other small birds searching for food in a period of scarcity. In this way, Starlings may have acted as a bridge for virus transmission from waterbirds in nearby wetlands to the turkey farms.

Virus has been isolated from some of these bridge species, *e.g.* House Sparrow *Passer domesticus* (Perkins and Swayne 2003). Kou et al. (2005) have recently highlighted the potential role of Tree Sparrows *Passer montanus* in transmission of H5N1 HPAIV between local poultry holdings in China.

The bird species which could act as ‘bridge species’ for transmission of H5N1 HPAIV transmission to domestic poultry were categorised into 3 groups, as described below.

Group 1: This comprises those feral birds which may be considered as domesticated poultry inasmuch as they are not of wild provenance.

Group 2: This comprises wild birds most likely to occur in habitats shared with domestic poultry, at least for part of the year. The list is not exhaustive and is based on the following criteria:

1. Habitat. A rapid review of *The EBCC Atlas of European Breeding Birds* (Hagemeijer and Blair 1997), to identify those species primarily associated with farmland.

2. Bird species observed to use areas also used by domestic poultry, based on direct, albeit limited, observations, relating to commercial free-range ducks and geese in a British context.
3. Gregarious species, at least outside the breeding season. Gregarious species, especially at higher density, are more likely to present opportunities for virus transmission than those species that tend to be solitary or occur in small numbers with little mixing or gregarious behaviour (see Section 11.4.3 above).
4. Mobility. Wild birds that range more widely in search of food are more likely to present opportunities for virus transmission than sedentary species.

Wild birds are attracted to land used by free-ranging domestic ducks and geese, mainly feeding in the compartments once the domestic birds have been harvested, but to varying degrees utilising these habitats when still occupied by domestic birds (R. Langston, pers. obs.). Food availability is largely invertebrates associated with these fields, presumably enhanced by eutrophication arising from high densities of domestic birds, and weed seeds from peripheral areas and planted cover for poultry. Puddling of the ground by poultry generally leaves a lot of bare ground available for foraging by wild birds.

Many candidate “bridge” species form flocks in winter, numbers ranging from several tens to hundreds, and flocks comprise both granivorous and insectivorous bird species. The extent to which flocks of farmland birds move around in winter varies, but some will range over several kms in search of good foraging opportunities (e.g. Calladine et al. 2006).

Knowledge of husbandry systems and situations, especially for free-range domestic poultry, will be essential for interpreting the most likely associated wild bird species. The regime at a commercial free-range poultry unit involves rotovating and seeding of paddocks following the harvesting of geese and ducks before the next cohort of poultry is introduced. There are fallow periods between cohorts of domestic birds. The wild birds using these areas include migratory species and may use a range of habitats, e.g. gulls (Table 13.1), including for example movement between wetlands and farmland, which may in fact be in close proximity.

Additionally, certain passerine species will enter poultry houses, if they can gain entry, in search of food, water, sheltered roost sites or nesting sites, notably starling *Sturnus vulgaris* and house sparrow *Passer domesticus,* which traditionally have a particularly close association with farm buildings.

These observations are based on the situation in the UK and are likely to reflect a similar situation elsewhere in northern Europe, although further south and east there are additional species that may associate with these commercial (particularly in the case of free-range) farming systems.

Group 3: In those areas where domestic poultry range widely, with no containment (non-commercial poultry), there is great potential for mixing with a wide range of resident wild birds, notably in the vicinity of freshwater wetlands, especially of *Anseriformes* and *Charadriiformes*. Some of these are given in this Group 3, although this again is not an exhaustive listing.

Figure 13.2 presents the decision tree used to select the bird ‘bridge’ species.

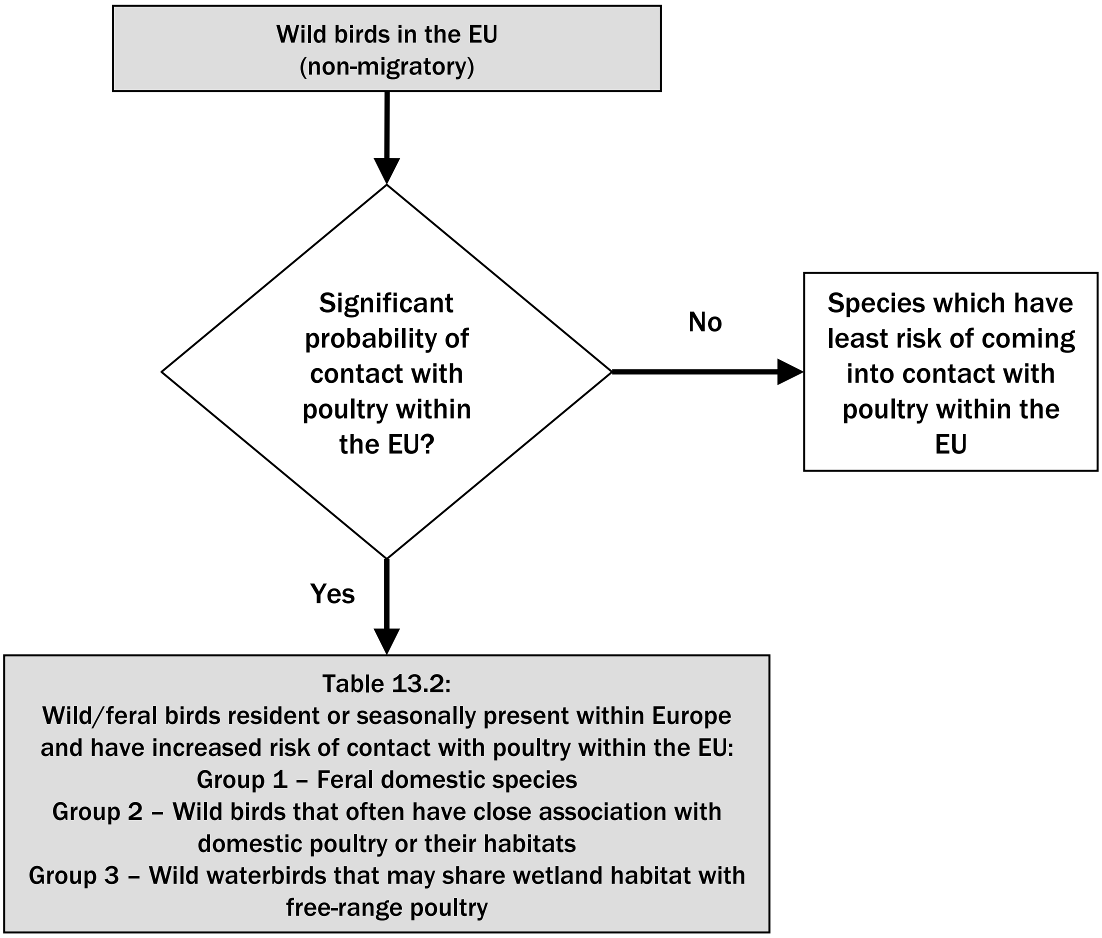


Figure 13.2. Decision tree for selecting potential bridge species of wild birds within the EU which could expose domestic poultry to Asian lineage H5N1 HPAIV

Conclusions

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, results in the three groups of bird "bridge" species presented in Table 13.2.

Table 13.2. European bird species that live in proximity to domestic poultryand could therefore be considered bridge species (selected on the basis of decision tree presented in Figure 13.2)

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

Common name	*Scientific name*	*Probability of contact with poultry*
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

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

Data

Very large numbers of waterbirds occur in, or pass through Europe during migration. Considering migratory waders alone, Stroud et al. (2004) calculated that 14.4 million waders use the East Atlantic Flyway and 25.9 million waders use the Black Sea Mediterranean Flyway. Further east, 22.8 million waders use the West Asian/East African Flyway and these birds mix to an unknown extent on breeding grounds and ultimate wintering areas with birds using the previous two flyways. To these should be added large populations of other waterbirds, notably ducks, geese and swans (Wetlands International 2002; Davidson and Stroud in press). Figure 11.12 maps the locations of the very large numbers of wetlands of importance for waterbirds in Europe. Probably some tens of thousands of additional sites exist which also support significant numbers of waterbirds at some stage of their annual cycle.

Europe's wetlands are linked both to each other and to similar habitats in Africa and Eurasia by a complex web of migratory movements of waterbirds (*e.g.* Figure 11.7).

The numbers of species using some of these sites is considerable. For example, the National Park of Doñana (RAMSAR, SPA, Biosphere Reserve) in the marsh system of the Guadalquivir, in the south-west part of Spain presents an annual average of about 313.000 of wintering birds of a high diversity (23 species) (Martí and del Moral, 2003). In eastern England, the Wash is a major estuarine system in eastern England that supports *c.*335,000 waterbirds in the non-breeding season and is either of national or international importance for 24 waterbird species (Collier et al. 2005). Long-term ringing at this site has shown that for (some) waders alone the exchange with other countries is very considerable. At least 41 countries are linked by the movements of 23 wader species (Wash Wader Ringing Group 2004). The movements of all the waterbird species that use the Wash probably link about 60 countries.

Conclusions

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.

13.4. 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 and Table 13.2.

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 11.2) will make a substantial contribution to extending our knowledge of bird migration across Europe.

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

Data

An approach to structured wild bird surveillance has been developed in the Netherlands and Sweden and been used since 2002 (Munster et al 2006 [abstract]).

Formal surveys for avian influenza in wild birds in EU Member States were first carried out in 2002-2003 under the Commission Decision 2002/649/EC (EC 2002). Initially surveillance was done on a voluntary basis in particular in those Member States which already had good co-operation with ornithological organisations or other bodies. The outcome of this surveillance was aimed at providing valuable information for an early warning system of strains that may be introduced to poultry from wild birds thereby contributing to knowledge of the threats to animal health from wildlife.

During 2004 sixteen Member States submitted results with a total of 8943 specimens examined. A further 933 samples were serologically examined. Preliminary results of samples indicated 15 were positive for subtype H5 and seven were positive for subtype H7. Three MSs, Denmark, Germany and Italy, reported H5 positive samples from wild birds. The number of H5 positive samples reported was 2, 1 and 12 respectively. All viruses were confirmed as LPAI. Three MSs, Sweden (1), Germany (1) and Italy (6), reported H7 positive samples from wild birds. All viruses were confirmed as LPAI.

These complimentary activities have resulted in the detection of a number of viruses in wild bird populations including some with high genetic similarity to newly detected viruses in poultry, including H7N3 in Italy and H7N7 in the Netherlands. Furthermore there is evidence for continued circulation of H5 and H7 viruses in wild *Anseriformes* thereby presenting a real and current threat for the introduction of viruses to domestic poultry especially those reared in outdoor production systems (Terregino et al. 2005; Munster et al. 2005).

To further strengthen surveillance aimed at providing definitive information on the potential role of wild birds in the spread of Asian lineage H5N1 HPAIV due to the developing epidemiological situation in Europe new programmes have been initiated. In October 2005 EU member states were required by Commission Decision 2005/464/EC (EC 2005d) to conduct mandatory surveillance of wild bird populations with the prime objective aimed at detection of Asian lineage H5N1 HPAI in healthy birds especially those in areas where poultry populations were free from infection with such viruses (currently all EU Member States at time of writing). These programmes are aimed at assessing the situation with regard to the possible relation between infection of wildlife with H5N1 subtype and the avian influenza outbreaks in domestic poultry. The decision provides broad guidelines for improved targeting and harmonisation. The focus is on Anseriformes but also include some other primarily aquatic species taking into account higher perceived risk of infection. A priority list of 15 waterbird species was specified for AIV sampling by Member States based on knowledge of migratory movements and perceived risk of transmission of H5N1 HPAIV from outbreak areas in Russia as in September 2005. Considerable flexibility is afforded to each member state to apply a locally appropriate programme.

To develop this programme further technical advice and some support was also provided to countries bordering the EU including some that have current infection in their poultry population.

All laboratory approaches based on validated methodology that are considered appropriate for AI surveillance are detailed in annexes to the previous EU directive (EC 1992) and have been incorporated into the new diagnostic manual that accompanies the newly adopted AI directive (EC 2005c). However, it must be considered that not all laboratories currently have facilities for use of molecular technology and therefore deploy virus isolation in embryonated fowl's eggs for which methods are well harmonised. The application of molecular diagnostics follows broad general principles but a standardised protocol although recommended in the new diagnostic manual has not been formally adopted. Trials to harmonise such testing and to evaluate local variation are currently in progress under the supervision of the Community Reference Laboratory.

Preliminary results were all negative for the detection of H5N1 HPAI in healthy wild bird populations.

Although there appears to be an increasing trend it is unclear whether this is due to enhanced surveillance in some countries or as a result of increased prevalence in bird populations including 'spikes' of circulation in wild aquatic species especially ducks. Surveys in wild birds in Northern Europe in 1999 to 2000 identified one H5 virus from a total of 8,500 birds sampled (Fouchier et al., 2003). This would appear to be lower than perceived prevalence in 2003-2004 in wild bird populations when fewer birds were sampled but from across a more diverse region of Europe.

Surveillance for AIVs at key wetlands where migratory flyways intersect, as well as major spring and autumn staging areas, would seem especially valuable. However, the reliability of the results of the monitoring activity in wild birds must be considered in relation to the sample size. The lack of a systematic approach with respect to temporal, spatial, species selection, location in relation to poultry outbreaks (if occurred), strategic location with respect to the migratory flyways of species of higher probability of being exposed, and diagnostic approaches may render difficulties in drawing firm conclusions.

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 13).

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).

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

15.1. Spatial Distribution of Poultry Population Density in the EU

The map in Figure 15.1 shows the output from a prediction model for poultry density in Europe for 2005 taking into account suitability and adjusted to match the observed totals. Details about the modelling procedures developed by FAO have been presented in Section 8.2.1. Based on these model predictions, the geographical areas in the European continent with the highest poultry densities occurring in Belgium and The Netherlands, the north-western region of France and Northern Ireland. Other areas of high poultry density are located in the north-western regions of Spain and Italy and in central regions of Portugal. The UK and the Republic of Ireland also show areas of high poultry density. Most of the Eastern European countries as well as the low land regions to the northwest of the Alpine mountains show moderate poultry densities.

Figure 15.1. Map of the spatial distribution of poultry density in Europe in 2005

15.2. Poultry Farming Systems in the EU

European poultry farming systems can be characterized by the type of poultry being reared and by farm size as measured by poultry heads. Data is available for all member states for farms containing laying hens and chicken broilers. Table 15.1 shows the number of holdings with laying hens in the EU25 member states stratified by farm size. Comparing totals within each size category, the highest number of farms with 1-99 heads of layer hens is observed in Romania, Poland, Hungary, Bulgaria and Greece. Each of these countries has more than 300,000 backyard farms. Countries such as the United Kingdom, Germany, Netherlands, Poland, Italy, Spain and France have the highest number of farms in the two size categories >= 10,000 laying hens. Each of these countries has more than 600 farms in this category.

Table 15.1. Number of holdings with laying hens stratified by agricultural size classes in each of the EU25 member states

EU Country	*Agricultural size classes (Number of laying hens per holding)*						
	1 - 99	*100 - 999*	*1000 - 2999*	*3000 - 4999*	*5000 - 9999*	*10000 - 29999*	*>30000*
Belgium	4310	130	50	40	120	200	160
Czech Republic	21690	110	40	10	10	30	60
Denmark	3410	140	20	40	60	90	40
Germany	81060	4610	1160	380	350	450	330
Estonia	14900	150	NA	0	0	0	10
Greece	320330	2820	200	70	110	70	30
Spain	182530	690	170	70	310	520	410
France	158000	1500	360	450	860	880	640
Ireland	7200	80	50	30	70	30	20
Italy	126740	1210	40	50	50	320	270
Cyprus	8610	100	0	0	0	10	10
Latvia	66100	90	0	NA	NA	0	10
Lithuania	185760	70	10	0	NA	0	10
Luxembourg	630	30	0	0	0	0	

EU Country	*Agricultural size classes (Number of laying hens per holding)*						
	1 - 99	*100 - 999*	*1000 - 2999*	*3000 - 4999*	*5000 - 9999*	*10000 - 29999*	*>30000*
Hungary	408710	1100	190	50	60	50	50
Malta	840	10	30	10	10	20	
Netherlands	260	180	80	80	200	540	350
Austria	62600	1190	460	160	130	80	20
Poland	989990	5460	480	270	470	430	290
Portugal	204340	240	0	30	10	60	80
Slovenia	47620	190	40	10	20	10	0
Slovakia	46330	50	10	0	0	10	30
Finland	960	260	310	130	120	90	20
Sweden	5030	170	60	40	90	100	50
United Kingdom	30050	1590	320	210	380	580	300
Bulgaria	475620	460	80	20	20	20	30
Romania	2924480	2710	90	20	20	30	50
Norway	1980	200	500	130	240	30	20

Source: EUROSTAT; Last update: Thu Nov 24 08:46:30 MET 2005; Date of extraction: Fri, 6 Jan 06 07:13:29; NA: Data not available

Table 15.2 shows the number of holdings with chicken broilers in the EU25 member states disaggregated by farm size. Within the size category 1-99 broilers, the highest number was reported in Romania, Bulgaria, Portugal, Poland and Greece. Each of these countries has more than 140,000 farms rearing between 1 and 99 heads of broiler chickens. The countries with the largest numbers of broiler farms with more than 50,000 heads include the United Kingdom, Poland, Netherlands, Italy, France and Spain. Each of these countries has more than 250 farms rearing more than 50,000 heads of chicken broilers.

Table 15.2. Number of holdings with broilers by agricultural size classes for each of the EU 25 member states

EU country	*Agricultural size classes (Agricultural size classes are in number of broilers per holding)*							
	1 - 99	*100 - 999*	*1000 - 2999*	*3000 - 4999*	*5000 - 9999*	*10000 - 49999*	*50000 - 99999*	*>100000*
Belgium	430	90	50	70	50	450	80	10
Czech	510	20	20		20	150	30	50
Denmark	150	20	0		0	70	60	30
Germany	10000	450	60	20	40	690	230	90
Estonia	370	10					:	0
Greece	170810	5010	120	50	250	450	70	30
Spain	65820	240	220	100	630	2750	350	80
France	77590	3620	1760	2060	2430	3060	500	70
Ireland	760	20	0	10	30	150	50	10
Italy	85480	2570	470	200	200	700	430	260
Cyprus	3860	100	10	0	10	40	10	10
Latvia	430	10				0		0
Lithuania	37150	170	0	0		0		0
Luxembourg	60	10	0		0			
Hungary	270	70	50	60	90	160	30	30
Malta	80	0	60	20	20	20		
Netherlands	0	0	10	10	10	400	250	90

EU country	*Agricultural size classes (Agricultural size classes are in number of broilers per holding)*							
	1 - 99	*100 - 999*	*1000 - 2999*	*3000 - 4999*	*5000 - 9999*	*10000 - 49999*	*50000 - 99999*	*>100000*
Austria	2840	100	60	20	60	180	20	
Poland	492660	6450	140	110	260	1820	320	260
Portugal	144510	470	10	130	470	360	30	30
Slovenia	4570	120	0	20	50	140	0	
Slovakia	1040	40	0	0	10	40	10	30
Finland		0	0		0	120	30	0
Sweden	150	10	0	0	0	30	30	10
United Kingdom	650	140	40	20	60	490	270	380
Bulgaria	163610	550	70	50	60	70	10	10
Romania	206100	710	20	0	10	40	10	30
Norway	70	0	0	10	60	240	30	0

Source: EUROSTAT; Last update: Tue Sep 06 15:47:04 MEST 2005; Date of extraction: Fri, 6 Jan 06 08:16:29

15.3. Statutory Measures in EU

15.3.1. Biosecurity of poultry production

Regulation (EC) No 2160/2003 on the control of salmonella and other specified food-borne zoonotic agents refers to guides for good animal husbandry practices requiring hygiene management at farms including for feed, drinking water, personnel, for animal transport and other measures to prevent incoming infections carried by animals (EC 2003).

Regulations (EC) No 852/2004 and No 853/2004 on the hygiene of foodstuffs and in particular for those of animal origin (EC 2004a, b) apply for all ‘food business operators’ (such as slaughterhouses), but also for the ‘primary production’, such as keeping poultry for slaughter or table egg production (EC 2004a, b).

Concerning primary production these require inter alia: a) measures to control contamination arising from air, soil, water, feed, fertilisers, veterinary medicinal products, plant protection products and biocides and from storage, handling and disposal of waste; b) animal health and welfare measures including programmes for the monitoring and control of zoonoses; c) to keep facilities including those for storage and handling of feed clean; d) to clean and where necessary, to disinfect facilities, equipment, containers, crates and means of transport; e) use of potable water, or clean water; f) to possibly prevent contamination from animals and pests and storage and handling of waste and hazardous substances; g) to prevent the introduction and spread of contagious diseases when introducing new animals and reporting of suspected outbreaks to the competent authority; h) to keep farm records.

Slaughterhouse operators may only accept poultry for slaughter, if the ‘food chain information’ has been received which includes the regional and the flock’s health status, production data and relevant reports about previous ante- and post-mortem inspections.

15.3.2. Trade with live poultry in the EU

Council Directive 90/539/EEC (EC 1990) contains specific animal health and biosecurity requirements for poultry breeding establishments and hatcheries before live poultry (mainly day-old chicks) and hatching eggs can be traded within the Community. Lay-out and sitting of facilities shall prevent disease introduction and must be protected against birds from outside and rodents. The 'all-in and all-out' principle, good separation of facilities and activities, effective cleaning and disinfection, protective clothing for personnel, record keeping, and hygienic measures for transport of day-old and hatching eggs must be observed. For holdings of other poultry categories, such as ready-to-lay pullets, poultry for restocking supplies of game and slaughter poultry less detailed facility requirements are laid down, but concentrate on official inspection and hygienic transport.

15.3.3. Dealing with AI outbreaks

Once an outbreak of AI is suspected and subsequently confirmed in poultry the control measures of Council Directive 92/40/EEC (EC 1992) apply aimed at limiting the spread of disease mainly by a) stamping-out of infected and suspected poultry; b) identifying possible contacts via epidemiological inquiries; c) restricting movements for live poultry, eggs, carcasses, waste, vehicles and persons; d) imposing zoning (protection and surveillance zones; e) cleaning and disinfection of infected premises, vehicles and equipment that are possible contaminated. Emergency vaccination of poultry flocks is possible under the current rules but has been rarely used due to related restrictions on trade with vaccinated birds.

While the scope of EC (1992) is limited to HPAI, the recently adopted Directive 2005/94/EC (EC 2005c) - applicable as from 1 July 2007 - includes surveillance and control measures for LPAI of H5 and H7 subtypes. It further also applies to other birds kept in captivity and foresees a broader use of emergency and preventive vaccination. More flexibility for extending control measures and granting derogations depending on the prevailing epidemiological situation are given.

Given the current situation with increasing findings of Asian lineage H5N1 HPAI in wildlife additional measures for trade of poultry and poultry products from affected Member States have been laid down in Decision 2006/115/EC. In case of an outbreak in poultry, as recently in a turkey flock in France (February 2006) additional safeguard measures are laid down in Decision 2006/135/EC by making use of regionalisation.

Following outbreaks of Asian lineage H5N1 HPAIV in non-EU countries and in wild birds in EU MS, starting in December 2003, the Commission has adopted several decisions with the goal of preventing the introduction of disease into the Community from the affected countries by banning imports of live poultry[5], captive birds and a range of poultry products including fresh poultry meat, eggs, untreated feathers and manure. An overview of legislation relevant for the current H5N1 HPAIV epidemic is given in Table 15.3.

---

[5] If previously authorised, as only for Croatia and Romania.

Table 15.3. Current EU legislation in relation to AI and in particular Asian lineage H5N1 HPAI (update as of 3/3/2006)

Objective	*Decisions by number in OJ*	*Countries*	*Specific remarks*
Safeguard measures Third Countries			import bans following notification of outbreaks
	2005/692/EC (repealing 2004/122/EC)	Asian countries	Cambodia, China including Hong Kong, Indonesia, Kazakhstan,Laos, Malaysia, Mongolia, North Korea, Pakistan, Thailand and Vietnam
	2005/693/EC	Russia	amended by 2005/740/EC and 2005/933EC
	2005/710/EC	Romania	regionalisation by 2006/24/EC
	2005/733/EC	Turkey	
	2005/758/EC	Croatia	only in wild birds; regionalisation 2006/11/EC
Untreated feathers	2005/883/EC	Ukraine	
	2006/7/EC	Georgia, Azerbaijan, Armenia, Iran, Irak and Syria	precautionary measure for countries bordering Turkey to the east
Pet Birds (accompanying their owner)	2005/759/EC	Worldwide with derogations for European third countries	harmonised import requirements including restriction to less than 5 birds, pre-export isolation, testing and quarantine and certification
Captive Birds	2005/760/EC	worldwide	prolonged by 2006/79/EC
Safeguard measures Member States (MS)	2006/86/EC	Greece	case in wild birds
	2006/90/EC	Italy	case in wild birds
	2006/91/EC	Slovenia	case in wild birds
	2006/94/EC	Austria	case in wild birds
	2006/104/EC	Germany	case in wild birds
	2006/105/EC	Hungary	case in wild birds
	2006/115/EC	EU 25	repealing previous MS decisions and applicable in case of positive findings of H5N1 HPAI in wild birds
	2006/135/EC	EU 25	in case of H5N1 HPAI outbreaks in EU poultry amended by 2006/175/EC: regionalisation for France following outbreak in turkey flock in Ain

Objective	*Decisions by number in OJ*	*Countries*	*Specific remarks*
Surveillance in poultry and wild birds	2005/464/EC	EU 25	guidelines for 2005 surveys; amended by 2005/726/EC (EC 2005e) defining 15 higher risk species
	2005/731/EC	EU 25	notification of wild bird morbidity/mortality by hunters and bird watchers, prolonged by 2006/52/EC
	EC 2005b	EU 25	approval of AI surveillance plans in poultry and wild birds July 05-January 06
	to be published	EU 25	approval of further surveillance programmes for 2006
Biosecurity and early detection systems	EC 2005a	EU 25	amended by 2005/745/EC and 2005/855/EC, details in section 15.1
Vaccination in zoos	2005/744/EC	voluntary upon submission of plan	preventive vaccination of zoo birds with restricted movements currently plans approved for BE, DK, FR, HU, LV, NL, PT, SE, SP
Approval of preventive vaccination of poultry	2006/147/EC	Netherlands	voluntary for not confined backyard poultry and certain free range layer systems
	2006/148/EC	France	free range ducks and geese in 3 departments (currently applied only in 1 department with approx. 300.000 birds)

Current EU legislation comprises a set of decisions that aim at the establishment of safeguard measures by third countries and member states surveillance in poultry and wild birds, biosecurity and early detection systems, vaccination in zoos and approval of preventive vaccination in poultry.

To specifically address the possible threat of wild birds introducing Asian lineage H5N1 HPAIV to EU poultry holdings and other captive birds **Commission Decision 2005/734/EC** (EC 2005a) provides for detailed biosecurity measures and early detection systems.

In line with the conclusions of the EFSA report on AI (EFSA 2005) risk factors for AIV introduction were identified such as: a) location of poultry holdings along migratory birds' flyways, in particular where birds are coming from HPAI affected areas; b) proximity of holdings to wet areas where migratory bird in particular water fowl gather; c) free range holdings or holdings in which contact between wild birds and poultry cannot be sufficiently prevented; d) areas with high densities of poultry holdings and intense movements promoting farm-to-farm virus spread after introduction. Based on these risk factors Member States have to define areas with a particular risk of AIV introduction in which the outdoor keeping of poultry is prohibited unless poultry are sufficiently screened from contacts with wild birds. In the latter case food and water must be supplied indoors or under a shelter, water may in any case not be sourced from surface water reservoirs, unless it was treated to ensure AIV inactivation. The use of birds of the orders *Anseriformes* and *Charadriiformes* as decoy during bird-hunting is prohibited (unless used for official surveillance purposes). The bringing-together of poultry and other birds at markets, shows, exhibitions and cultural events, including point-to-point races of birds, should be prohibited, unless specifically authorised based on favourable risk assessment. The national and regional assessments are constantly adapted to the changing epidemiological situation and national control measures can be viewed at the following links: National measures can be viewed by the following links:

http://europa.eu.int/comm/dgs/health_consumer/dyna/influenza/country_en.htm

http://europa.eu.int/comm/food/animal/diseases/controlmeasures/avian/qa_influenza_en.htm.

Member States have introduced early detection systems aimed at rapid reporting to the veterinary authorities of any sign of avian influenza infection in poultry by poultry keepers. Reporting is triggered by a drop in feed and water intake higher than 20 %, drop in egg production higher than 5 % for more than two days, mortality rate higher than 3 % in a week or any clinical sign or post-mortem lesion suggesting AI.

15.4. Overall Conclusions and Recommmendations

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 be 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 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 EC (1990).

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 thaht can also ne applied by backyard chicken producers.

16. Risk Assessment for Risk Question 1: Release Assessment

In Chapter 4, Risk Question 1 was defined as:

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.

16.1. Overview of Information Required

Table 16.1 lists the information required for this risk assessment and a judgement of the amount and type of data that was collected by the working group.

Table 16.1. Data required and type of data collected for the release assessment of Asian lineage H5N1 HPAIV in wild birds

Section of release assessment pathway	*Data required*	*Data obtained*
Exposure of wild birds in countries where Asian lineage H5N1 HPAIV is present	Infection status of domestic poultry, surveillance data, outbreak data. Prevalence data in ducks and poultry.	Reports on outbreaks in domestic chicken are available, but the amount of under-reporting is unknown. Only one peer-reviewed report on prevalence of Asian lineage H5N1 HPAIV in domestic ducks (China).
	Population data of wild birds by country and by species	Much data is collected by International Waterbird Census, but there is limited capacity to analyse and disseminate this. Ringing data, count data, flyway maps, may be incomplete and sometimes old.
	Prevalence of H5N1 in wild bird populations	Virtually no information about prevalence. The only paper reporting H5N1 HPAIV in wild duck populations does not indicate which species were carrying the virus.
	Management of factors leading to direct or indirect contact between infected poultry and wild birds by country, probability of contact, probability of transmission	Some data on poultry industries, but not for all countries. Limited empirical data on probability of transmission.
	Survival of Asian lineage H5N1 HPAIV in the environment	Experimental studies, but not conducted under standardised conditions nor using Asian lineage H5N1 HPAIV
	Infective dose of wild birds	Experimental data, only few studies using Asian lineage H5N1 HPAIV, only few bird species tested
	Pathogenicity of Asian lineage H5N1 HPAIV to wild bird species	Experimental data, only few studies using Asian lineage H5N1 HPAIV, only few bird species tested (nearly all not being wild bird species but poultry and domestic ducks) tested, small number of birds per experiment.

Section of release assessment pathway	*Data required*	*Data obtained*
	AIV Surveillance data of wild birds in countries with Asian lineage H5N1 HPAIV in domestic poultry	Very few systematic, published surveys. Some reports related to outbreaks in domestic poultry.
Exposure of wild birds at mixing and concentration areas	Survival of wild birds after infection with Asian lineage H5N1 HPAIV by species	Experimental data, only few studies using Asian lineage H5N1 HPAIV, only few bird species tested, small number of birds per experiment.
	Location of mixing and concentration areas	Good site inventory information, especially related to Important Bird Areas and areas where waterbirds are counted by the International Waterbird Census - but no capacity to analyse the later source of information. Classification of locations based on a number of criteria.
	Population data of wild birds at mixing and concentration areas	Much data collected by International Waterbird Census, but currently limited capacity to analyse these data. Considerable ringing data exists but no capacity to analyse at international scales. No good synthesized information on flyways based on recent information other than for geese and waders.
	Survival of Asian lineage H5N1 HPAIV in the environment	Experimental studies, but not conducted under standardised conditions nor using Asian lineage H5N1 HPAIV
	Surveillance data of wild birds at mixing and concentration areas	No published surveys, a few projects in progress.
Release of Asian lineage H5N1 HPAIV into the EU by wild birds	Migration patterns of wild birds by species	Considerable ringing data exists, but no capacity to analyse at international scales. No good synthesized information on flyways based on recent information other than for geese and waders.
	Population data for migratory birds by species	Much census data for specific sites collected by International Waterbird Census, but limited capacity to analyse and report these data.
	Survival of wild birds after infection with Asian lineage H5N1 HPAIV by species	Experimental data, only few studies using Asian lineage H5N1 HPAIV, only few bird species tested, small number of birds per experiment.

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

16.2.1. Factors influencing occurrence of Asian lineage H5N1 HPAIV

It is documented that HPAI H5 and H7 may arise *de novo* in poultry infected with H5 or H7 LPAI progenitor strains (EFSA 2005). The circulation of LPAI in domestic poultry is therefore a risk factor for the emergence of HPAIV strains. However, systematic investigations of domestic poultry with respect to LPAI are scarce.

The presence of free-grazing domestic ducks was identified to be a risk factor for the occurrence of Asian lineage H5N1 HPAIV in domestic poultry in Thailand

(Gilbert et al. 2006). This risk factor was associated with the presence of wetlands used for rice production, where the virus may be able to persist, but where there also is an interface with wild birds.

There is only one report of a systematic investigation of the prevalence of Asian lineage H5N1 HPAIV in domestic geese and ducks (Chen et al. 2006) demonstrating a low infection level, but higher than in other domestic poultry.

Seasonal patterns of virus isolation were observed in southern China. However, due to the lack of formal epidemiological investigations, it is impossible to exclude the possibility that factors not related to climate may have given rise to seasonal variability.

16.2.2. Presence of susceptible wild birds

Interpretation of data

Experimental and field data document that a considerable number of bird species across several Orders are susceptible to Asian lineage H5N1 HPAIV. However, only a limited number of species have so far been tested. And those studies that have undertaken such surveillance of wild species often do not clearly report results by species (e.g. Chen et al. 2006). Also, it is not clear which species can act as reservoirs of the virus, i.e. perpetuate Asian lineage H5N1 HPAIV over some time, and lead to exposure of other wild and/or domestic birds. There is anecdotal evidence that this may have occurred in a population of mute swans (*Cygnus olor*) in Poland (Polish CVO – Report on Actvities - File GIWz 400-258/06 of May 6 2006).

Under natural conditions, Asian lineage H5N1 HPAIV is more frequently isolated from waterbirds, but other birds such as crows (*Corvus spp.*), tree sparrows (*Passer montanus*) or raptors have have also been reported as having become infected. No systematic surveillance data across species exists.

Conclusion

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).

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

Interpretation of data

The probability of exposure of wild birds through infected domestic poultry depends on the management practices in the poultry industry of the region. In many regions affected by Asian lineage H5N1 HPAIV, significant numbers of chickens are raised at smallholder level in small flocks and free-range husbandry conditions. In South-East and East Asia these husbandry systems (FAO poultry productions sectors 3 and 4) also include domestic ducks and geese. These species are grazed on paddy fields where they have increased risk of contact with wild waterbirds. Data regarding the spatial distribution of poultry farm types are not available for China. Data on poultry production in Africa are scarce and not available at a detailed level. The probability is **very high** (low uncertainty) that poultry husbandry systems used in most low-income countries will contaminate the environment with Asian lineage H5N1 HPAIV after outbreaks in domestic poultry and there is likely to be direct or indirect contact between domestic and wild birds.

Particularly, free-grazing duck production systems allow for extensive direct and indirect contact between domestic ducks and wild waterbirds. Specifically domestic ducks may act as local reservoirs of Asian lineage H5N1 HPAIV from where the virus spills over into wild bird populations.

Indirect transmission of Asian lineage H5N1 HPAIV primarily depends on the environmental stability of the virus. Specific experiments regarding the stability of Asian lineage H5N1 HPAIV are scarce. Other AI viruses retain infectivity at room temperature from at least several days up to several weeks. Stability is extended at temperatures <20°C. Infectivity is retained in fresh surface water for several days. The survival of HPAI virus in salt water, soil and aerosols is not known. Given the physical and chemical composition of AIV particles, aerosol transmission between chicken and wild birds are considered possible, but there is currently only evidence which suggests that this transmission mechanism is less important than the faecal-oral route (Defra 2005).

Conclusion

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.

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

Interpretation of data

Based on experimental data, infection of mallards (*Anas platyrhynchos*) with Asian lineage H5N1 HPAIV results in very variable clinical manifestations. In the field, Asian lineage H5N1 HPAIV was isolated predominantly from dead wild birds. More systematic sampling of healthy birds, however, was shown to lead to the isolation of the virus.

Factors that may influence the pathogenicity in wild birds include: virus strain, species of bird, age of bird, infection dose. However, these factors have not yet been investigated systematically. There is some evidence related to LPAI that juvenile birds may exhibit an increased incidence of infection (EFSA 2005). Empirical data recently reported from several regions suggest an increased pathogenicity in mute swans (*Cygnus olor*). On the other hand, certain species, e.g. pigeons (*Colombia livia*), have been shown experimentally to have very low susceptibility to HPAIV. However, there has been reported evidence of field infection causing mortality (EFSA, 2005). In general, species-specific data on pathogenicity are lacking.

Asian lineage H5N1 HPAIV field isolates were shown to be a heterogeneous mixture of different pathotypes. Molecular determinants distinguishing between these different pathogenicity profiles in birds have not yet been identified.

It is well documented that some species of the Orders *Anseriformes* and *Charadriiformes* can act as reservoirs of LPAI viruses (Kaleta et al. 2005). Little is known, however, about the level of protection and longevity of specific immune response induced by LPAI virus. The prevalence of AI subtypes in wild ducks may be up to 60%. Partial humoral immunity against H5 in addition to cellular immunity could lead to an attenuated course of infection after exposure to Asian lineage H5N1 HPAIV, but is unlikely to prevent infection (i.e. sufficient immunity to prevent disease). This may indicate an increased probability of low pathogenicity of Asian lineage H5N1 HPAIV in these Orders of bird species.

Conclusion

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.

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

Interpretation of data

Survival of wild birds after experimental infection was documented in mallards (*Anas platyrhynchos*) for 10-17 days (Sturm-Ramirez et al. 2005; Hulse-Post et al. 2005; Chen et al. 2006). The amount of virus excreted and the duration of excretion was reduced for strains which exhibited low pathogenicity to ducks although retaining high pathogencity to chickens. In these experiments, some birds remained clinically healthy and surviving animals shed virus for up to 17 days post inoculation. Data on survival of wild birds after natural infection are not available, except for some anecdotal evidence about infected apparently healthy swans in Poland. However, based on molecular analyses of Asian lineage H5N1 HPAIV isolated from migratory birds in different regions of China and based on the chronological sequence of these isolations, it is possible that infected animals may migrate over considerable distances (Chen et al. 2006).

The fact that most isolates of Asian lineage H5N1 HPAIV from wild birds originated from individual birds that were found dead may be due to a high mortality caused in certain species, but it may also be due to sampling bias as dead birds are more accessible to sampling. Extensive surveillance of healthy migratory ducks in southern China provided both antigenic and serologic evidence of Asian lineage H5N1 HPAIV circulation (Chen et al. 2006). Extensive investigations in Russia led to the isolation of Asian lineage H5N1 HPAIV from both healthy and sick or dead water birds. Outbreaks of Asian lineage H5N1 HPAIV in wild birds were associated with high mortality in some wild bird populations, e.g. bar-headed geese *Anser indicus* at Lake Qinghaihu, China, 2005. This confirms a large variability of pathogenicity, the influential factors of which are largely unknown.

The analysis of the virus recently detected in dead wild birds in European countries showed very high similarity between the isolates (Brown et al 2006 [abstract]). This may indicate an adaptation of a distinct sublineage of the Asian lineage H5N1 HPAIV to wild birds, i.e. the H5N1 Z genotype.

A possible scenario for birds infected with Asian lineage H5N1 HPAIV to reach mixing and concentration areas is by relay transmission, i.e. when infected birds – before they die – pass on virus to other birds who then in turn continue migration. Whether infected birds will migrate normally is unknown. However, it seems likely that at least some birds infected with Asian lineage H5N1 HPAIV will reach mixing and concentration areas even if infected birds do not migrate normally.

Data on mixing and concentration areas are based on count data which are available over large geographical areas but vary spatially and temporally. Data on bird movements are generally based on re-sightings of individually ringed birds. Because continuing and systematic analysis of ringing data at international scales is lacking, maps of migration systems for individual species are either lacking or frequently based on outdated data. Additionally, migration patterns of birds are highly variable and influenced by species, age, sex, season and weather. Nevertheless, major flyways of birds, specifically ducks, geese, swans and waders have been described. For nearly all species, these maps are, however, not accurate enough to reliably predict the presence of certain species of specific origin on selected routes or sites. For some well-studied goose populations there is greater understanding of detailed spatial and temporal patterns of movement. They only allow for rough spatial and temporal descriptions of bird movements at a very general level. These general flyways show that currently infected areas in south-east Asia and Africa are covered by major flyways of waterbirds.

Conclusions

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.

16.4. Probability of Transmission at Mixing or Concentration Areas

Interpretation of data

Regarding waterbirds, all wetland habitats have the potential for mixing birds of different species and origins, notably during migration when different populations occur in the same areas. Mixing areas of waterbirds have been classified here into primary and secondary sites depending on the number of birds they hold. Primary sites are those sites that regularly hold >20,000 birds.

The classification is based on data of the World Bird Data Base (WBDB) and the International Waterbird Census (IWC). Both sources are incomplete and the quality of data varies considerably between sites, countries and count years. The number of birds present at any one site is influenced by weather conditions (cold, drought) and disturbance caused by human activities, as well as by time of year.

Some important mixing and concentration areas where several flyways converge, specifically of some species of Anatidae can be identified, e.g. the region encompassing the Black Sea and Caspian Sea.

Migratory flights larger than 5,000 km between South Europe and Asia, across Central Asia and Caspian Sea, as it has been confirmed for some wild bird species (Muñoz et al. 2006, *in press*), suggest the possibility of interchange, in some important mixing and concentration areas, between the populations from Europe and those from Asia (East, South and Central) by direct migration, misorientation or abmigration. These factors could contribute to the propagation of H5N1 HPAIV to currently virus-free areas.

These are also areas where there is potential mixing of poultry with wild birds and shared habitats. Comments made on migration patterns and their variability in Section 16.3 are equally applicable here.

By definition, mixing and concentration areas are those sites where large numbers of different wild bird species congregate for a variable time periods. The assessment of the number of species present at mixing and concentration areas, as well as the origins and destinations of birds using these sites, is based on data collected by IWC and EURING. These data are currently being analysed. At present, there is limited ability to identify all mixing and concentration areas used by specific bird species from a given flyway (i.e. for most species it is not possible to say that an individual bird using a flyway from A to B, uses sites C, D, E etc. – we do not know routes used except for a small number of species).

The density of birds at mixing and concentration areas enhances the probability of transmission both by direct and indirect pathways. Excretion of virus in experimentally infected mallards (*Anas platyrhynchos*) was consistently shown to last up to 17 days post infection (Hulse-Post et al. 2005). Data on excretion in other wild bird species are scarce. Excretion dose in mallards (*Anas platyrhynchos*) was assessed in only few experiments and reached 10^{4}-$10^{5.7}$ EID_{50}/ml. Such virus concentrations reliably led to infection under experimental conditions. Rapid transmission of Asian lineage H5N1 HPAIV within wild bird populations was confirmed during outbreaks in Hong Kong in 2002 where the incidence in certain species was >80% (Ellis et al. 2004). A high occurrence of infection was also found in recently observed outbreaks of Asian lineage H5N1 HPAIV in Germany.

The data by Globig et al. (2006) supports the hypothesis of significant levels of AIV transmission occurring for European migrating duck species at breeding grounds in the Northern part of Europe and Asia. It is of interest that during that particular 2-year study, no AIV were identified in ducks during periods of the year other than autumn/early winter, in mostly resident species (330 geese and 255 swans), or in migrating waders.

Regarding the probability of indirect transmission pathways, the same conclusions are drawn as in Section 16.2.3. Oropharyngeal excretion was found to be more significant than cloacal excretion in ducks experimentally infected with Asian lineage H5N1 HPAIV. Survival of the virus in the environment, eg. surface water, will be increased in geographical areas with lower temperatures, and thereby represent an increased risk of infection.

Conclusions

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.

16.5. Probability of Detection Given Infection

Interpretation of data

The probability of detection of infected wild birds at mixing or concentration areas will depend on the clinical signs, particularly mortality exhibited by the birds as well as on the level of vigilance and the existence of surveillance programmes and the presence of humans finding and reporting sick or dead birds.

Until recently, surveillance of wild birds for Asian lineage H5N1 HPAIV was introduced primarily in response to outbreaks, e.g. in Russia in 2005 (OIE report). Results of such programmes are rarely published in the scientific literature. Furthermore, there is a time lag before detailed analyses are carried out. Hardly any programmes with statistically sound sampling design have been conducted with the exception of extensive samplings conducted in southern China (Chen et al. 2006). Adequate taxonomic identification of species has been poor or lacking in some species, leading to considerable (ongoing) problems in identification of species being sampled (or dying).

Conclusion

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).

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

The two key factors to consider are the species migration patterns and following infection both the likelihood of survival and the ability to travel over long distances.

The species migration patterns are incorporated into the decision tree for species identification and the timing of migration described in the following two Sections 16.6.1 and 16.6.2. The survival and mobility are discussed in Section 16.6.3.

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

Interpretation of data

Many European bird species are migratory. Most long-distance migratory birds are likely to pass through mixing and concentration areas. As the occurrence of Asian lineage H5N1 HPAIV at mixing and concentration areas is largely unknown, it is not possible to identify migratory bird species that are at risk of carrying the virus. However, a series of risk factors can be identified that influence the probability of exposure to, infection with and subsequent introduction of Asian lineage H5N1 HPAIV into the EU for certain species:

Regarding the susceptibility of a European migratory bird species to Asian lineage H5N1 HPAIV, documented reports of virus isolation are available for some birds, although some are isolated observations (Annex 2). Additionally, the orders of *Anseriformes* and *Charadriiformes* are known to be highly susceptible to LPAI. Due to the lack of systematic data for all species, there is a very high uncertainty in relation to this factor.

Conclusions

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 in Chapter 16. Applying this approach, a list of wild bird species of higher significance in terms of transmission of Asian lineage H5N1 HPAIV was obtained (Table 16.2, summary based on Table 11.2). 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 16.2. 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)

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				

Common name	*Scientific name*	*Population name*	*Population size EU25*	*Units*
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
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

Common name	*Scientific name*	*Population name*	*Population size EU25*	*Units*
		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

16.6.2. Factors influencing time and location of introduction of Asian lineage H5N1 HPAIV via migratory wild birds

Previous studies have shown greater infection rates with AIVs in juvenile compared to adult ducks (e.g. Hinshaw et al. 1980) and that there is a peak of viral shedding activity in the autumn (Stallknecht et al. 1990a; De Marco et al. 2005). Given that flocks migrating in autumn will contain a significant proportion of juvenile birds (for arctic breeding species this proportion is variable according to the conditions during that year in the breeding areas), this suggests that the autumn migration period is of higher risk than spring migration.

Although migration activities are highly variable between and within bird species, general peaks of movements can be identified in autumn and in spring. Bird numbers during autumn migration from breeding sites to wintering areas tend to be higher and the proportion of young birds is higher. In autumn, migration movements tend to be spread over a longer time period and they are highly dependent on temperature conditions. In spring, migration back to the breeding sites tend to be more concentrated with fewer birds moving over a shorter time period (most notably for birds breeding at northern latitudes where the breeding season is short due to weather conditions). Further peaks of movement may occur in winter as a result of cold weather movements; the extent and timing of such movements are entirely dependent on weather conditions.

EU member states are situated over a large geographical area. The presence of migratory species at a given point in time is therefore variable between countries. No general statement can be made that is valid for all countries in terms of the probability of introduction of Asian lineage H5N1 HPAIV by species and season. Based on available data, it is not possible to accurately predict the time and location of the introduction of Asian lineage H5N1 HPAIV. However, an introduction via migratory waterbirds appears to be the most likely scenario if the virus was introduced by wild birds. Since the time when this assessment was performed (April 2006), this event has already happened.

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

Interpretation of data

Data on the survival of infected wild birds is limited, but for example duck species often suffer from asymptomatic infection. Anecdotal data exists reporting the presence of healthy but infected birds in Mute Swan (*Cygnus olor*) populations.

Conclusions

Currently available data suggests that the likelihood is **medium** (high uncertainty) for the species identified in Section 16.6.1.

16.7. 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 16.2 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 16.3). Using the interpretation given in Table 3.1, 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 16.3. 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 16.2.2)	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 16.2.3)	High – very high *	Medium
Infection of wild birds after exposure to Asian lineage H5N1 HPAIV (see Section 16.2.4)	High/very high	High
Infected wild birds reach mixing or concentration areas (see Section 16.3)	Low to high (Minority opinion: Medium)	High
Transmission of Asian lineage H5N1 HPAIV between wild birds at mixing and concentration areas (see Section 16.4)	Very high	Medium
Detection of infection (see Section 16.5)	Very low – low **	High
Infected wild birds reach staging, wintering or breeding areas inside EU after infection outside EU (see Section 16.6.3)	Medium ***	High
Summary: Conditional probability of some Asian lineage H5N1 HPAIV being released into the EU by migratory birds (in species listed in Section 16.6.1; see Section 16.7)	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 16.6.1; see Section 16.7)	Low (Minority opinion: Medium***)	High

* depending on whether free-grazing ducks are present
** depending on mortality caused
*** wild bird species identified in Section 16.6.1

16.8. 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.

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

In Chapter 4, Risk Question 2a is defined as:

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

17.1. Overview of Information Required

Table 17.1 lists the information required for this part of the risk assessment and an assessment of the amount and type of data that was collected by the Working Group.

Table 17.1. Data required and type of data collected with respect to the exposure and consequence assessment of Asian lineage H5N1 HPAIV in non-migratory wild birds in the EU

Section of exposure and consequence assessment pathway	*Data required*	*Data obtained*
Direct exposure of non-migratory wild bird populations	Behaviour, habitat data of non-migratory wild birds	Available but poorly synthesised
	Population data of non-migratory wild birds	Available from national organisations (see Chapter 13) but of variable quality
Indirect exposure of non-migratory wild bird populations	Behaviour, habitat data of non-migratory wild birds	Available but poorly synthesised
	Population data of non-migratory wild birds	Available from national organisations (see Chapter 13) but of variable quality
	Climate data	Available
Consequences of exposure in non-migratory wild birds	Susceptibility to H5N1 HPAIV of non-migratory wild birds	Unknown. Empirical data of recent outbreaks but poorly synthesised
	Data on survival post- H5N1 HPAIV infection for European non-migratory wild bird species	Unknown
	Population dynamics of Asian lineage H5N1 HPAIV in non-migratory wild birds	Unknown

17.2. Overview of Exposure Pathways for Wild Birds in EU

Conditional on the likelihood of Asian lineage H5N1 HPAIV introduction through migratory wild birds entering the EU, non-migratory birds could subsequently be infected via direct or indirect pathways. No data exist on transmission dynamics of Asian lineage H5N1 HPAIV within and between European wild bird species for Europe. Based on current epidemiological and ornithological knowledge, the probability of direct exposure of resident birds depends on the number of infected birds, the species involved, the habitat and behaviour of the infected species.

The mechanisms for exposure to Asian lineage H5N1 HPAIV in the EU of non-infected migratory birds are the same as discussed under Section 16.4 relating to behaviour at mixing and concentration areas, as well as other releant Sections of that same Chapter 16. These are not repeated here.

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

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

Considering the conclusions drawn under 16.2.2 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.

17.3.2. 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.

17.3.3. 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.

17.3.4. 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).

17.3.5. 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.

17.4. 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 16 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.

17.5. 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 16.7) 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 17.2). 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 16.7) 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 17.2). 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 17.2. 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 16.7)	Low to high (Minority opinion: Medium *)	High
Presence of susceptible non-migratory birds (see Section 17.3.1)	Very High	Medium
Direct exposure of non-migratory birds to migratory birds carrying Asian lineage H5N1 HPAIV (seee Section 17.3.2)	High	Medium
Indirect exposure of non-migratory birds to migratory birds carrying Asian lineage H5N1 HPAIV (see Section 17.3.3)	High	Medium
Infection of non-migratory wild birds after exposure to Asian lineage H5N1 HPAIV from migratory birds (see Section 17.3.4)	Medium – high *	High
Detection of infection in migratory and non-migratory wild birds (see Section 17.3.5)	Low or medium to high**	Low or High**
Persistence of infection in migratory and non-migratory bird populations (see Section 17.4)	Medium	High
Summary: Conditional probability of Asian lineage H5N1 HPAIV becoming endemic in non-migratory European wild birds is depending on the susceptibility 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-dependant environmental conditions (water, etc)	Low to high (Minority opinion: see below)	
Minority opinion: Summary: Conditional probability of Asian lineage H5N1 HPAIV becoming endemic in migratory and non-migratory European wild birds (see Section 17.5)	(Minority opinion: Medium)	High

* Depending on whether species is included in Section 16.6
**Depending on species, pathogenicity and level of surveillance

17.6. 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 16.2 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.

18. Risk Assessment for Risk Question 2b: Exposure and Consequence Assessment for Domestic Poultry as a Consequence of Wild Bird Infection

In Chapter 4, Risk Question 2b is defined as:

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)?

18.1. Overview of Information Required

Table 18.1 lists the information required for this part of the risk assessment and a judgement of the amount and type of data that was collected by the working group.

Table 18.1. Data required and type of data collected with respect to the exposure and consequence assessment of Asian lineage H5N1 HPAIV in poultry in the EU

Section of exposure and consequence assessment pathway	*Data required*	*Data obtained*
Direct exposure of poultry to wild birds	Habitat and behaviour data of migratory wild birds	Ornithological data available but of variable quality.
	Habitat and behaviour data of non-migratory wild birds	Ornithological data available but of variable quality.
	Infection status of migratory and non-migratory wild birds (surveillance data)	Empirical data of current outbreaks currently being collected but not available for analysis as part of this assessment.
	Population numbers of migratory and non-migratory wild birds	Ornithological data available but of variable quality.
	Spatial distribution of wild bird populations in EU	Ornithological data available but of variable quality and more limited for non-breeding season (other than for waterbirds).
Indirect exposure of poultry to wild birds	Virus stability in environment	Experimental studies, but not conducted under standardised conditions nor using Asian lineage H5N1 HPAIV
	Climate data	Meteorological data available
	Use of surface water in poultry production	Information available for some EU MS.
Transmission (consequence)	Number of farms present, husbandry systems (backyard flocks, free-range holdings, intensively reared poultry)	Farm statistics available, but primarily for intensively reared poultry, not specifying backyard and freerange holdings.
	Location of farms	Available at MS level, primarily for intensively reared poultry
	Susceptibility	Extensive data available from experiments and outbreaks involving Asian lineage H5N1 HPAIV
	Biosecurity measures	No detailed data available on level of implementation

18.2. Overview of Exposure Pathways for Domestic Poultry in the EU

Domestic poultry kept in the EU will be exposed to Asian lineage H5N1 HPAIV carried by wild birds under the assumption that either migratory birds infected with Asian lineage H5N1 HPAIV enter the EU or non-migratory birds within the EU are infected with Asian lineage H5N1 HPAIV from migratory birds. Exposure can be achieved by direct contact with these infected wild bird species or indirectly by contaminated environment (water or vegetation). As the possibility of poultry interacting with wild birds or with the environment is influenced by the husbandry system (e.g., free range vs. closed) and adherence to biosecurity measures, the probability of exposure needs to be considered separately for different husbandry systems.

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

18.3.1. 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 16.2). 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 18.2, summary based on Table 13.1).

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 18.2. 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)

Common name	*Scientific name*	*Population name*	*Population size EU25*	*Units*
Breeding populations				
Mute Swan	*Cygnus olor*	EU25 breeding population	68,000-92,000	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

Common name	*Scientific name*	*Population name*	*Population size EU25*	*Units*
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
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

Common name	*Scientific name*	*Population name*	*Population size EU25*	*Units*
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

18.3.2. 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 18.3, summary based on Table 13.2). 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 18.3. 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 13.2)

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

Common name	*Scientific name*	*Probability of contact with poultry*
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

18.3.3. 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.

18.3.4. 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.

18.3.5. 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).

18.4. 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).

18.5. 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).

18.6. 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 18.4. 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 16.6.1; see Section 16.7)	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 17.5)	Low to high (Minority opinion: Medium)	High
Exposure of free-range or backyard flocks (see Section 18.3.5)	High *	Medium
Exposure of intensively-reared or indoor flocks (see Section 18.3.5)	Negligible to very low **	Low
Transmission of Asian lineage H5N1 HPAIV to poultry (see Section 18.4)	High	Low
Detection of Asian lineage H5N1 HPAIV in poultry (see Section 18.5)	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 18.6)	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 18.6)	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 18.6)	Negligible **	Low

* Depending on proximity to wetlands

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

18.7. 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.

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).

19. References

Acheson F, Hewitt D, 1952. Spread of influenza in a factory. Br J Soc Med 6(1): 68-75.

Akbay C, Boz I, 2005. Turkey's livestock sector: Production, consumption and policies. Livestock Research for Rural Development 17(9): 14.

Alerstam T, 1993. Bird migration. Cambridge University Press, Cambridge, UK. 428pp.

Alexander DJ, 2000. A review of avian influenza in different bird species. Vet Microbiol 74(1-2): 3-13.

Alexander DJ, Allan WH, Parsons DG, Parsons G, 1978. The pathogenicity of four avian influenza viruses for fowls, turkeys and ducks. Res Vet Sci 24(2): 242-247.

Alexander DJ, Spackman D, 1981. Characterisation of influenza A viruses isolated from turkeys in England during March-May 1979. Avian Pathology 10: 281-293.

Allan WH, Alexander DJ, Pomeroy BS, Parsons G, 1977. Use of virulence index tests for avian influenza viruses. Avian Dis 21(3): 359-363.

AQIS, 1991. Discussion paper on the importation of fresh frozen and cooked chicken meat and products from the USA, Denmark, Thailand and New Zealand. Department of Primary Industries and Energy, Canberra, Australia.

Aubrecht G, Dick G, Prentice C, 1994. Monitoring of Ecological Change in Wetlands of Middle Europe. In Proc. International Workshop Linz, Austria 1993. IWRB Publication No. 30. Slimbridge UK. 55-60.

Baccetti N, Dall'Antionia P, Magagnoli P, Melega L, Serra L, Soldatini C, Zenatello M, 2002. Risultati dei censimenti degli uccelli acquatici svernanti in Italia: distribuzione stima e trend delle popolazioni nel 1991-2000 (Waterbirds in Italy: distributions trends). Biologia e Conservatione della Fauna 111: 1-240.

Baillie SR, 1995. Uses of ringing data for the conservation and management of bird populations: a ringing scheme perspective. Journal of Applied Statistics 22: 967-987.

Bairlein F, 2001. Results of bird ringing in the study of migration routes. Ardea 89 (Special Issue): 7-19.

Bairlein F, Elkins N, Evans P, 2002. Why and how do birds migrate? In: Wernham CV, Toms MP, Marchant JH, Clark JA, Siriwardena GM, Baillie SR (eds). The Migration Atlas: Movements of the Birds of Britain and Ireland. Poyser, London, UK. 23-43.

Bakken V, Runde O, Tjorve E, 2003. Norsk ringmerkings atlas. Vol. 1. Stavanger Museum, Stavanger, Norway. 431pp.

Beard CW, Brugh M, Johnson DC, 1984. Laboratory studies with the Pennsylvania avian influenza viruses (H5N2). Proc. 88th Ann Meeting U.S, Anim Health Assoc 88: 462-473.

Berrevoets CM, Strucker RCW, Arts FA, Meininger PL, 2002. Watervogels in de Zoute Delta 2001/2002. RIKZ Report 2003.001. Middelburg: Rijksinstitu ut voor Kust en Zee, The Netherlands.

BirdLife International, 2004. Birds in Europe: Population estimates, trends and conservation status. BirdLife Conservation Series No. 12. BirdLife International, Wageningen, The Netherlands.

BirdLife International, 2004a. Birds in the European Union: A status assessment. BirdLife International, Wageningen, The Netherlands. 50pp.

BirdLife International, 2005. BirdLife's World Bird Database. BirdLife International, Cambridge, UK. http://www.birdlife.org/datazone.

BirdLife Malta, (in prep.). An Atlas of the Breeding birds of Malta.

Blew J, Südbeck P (eds.), 2005. Migratory waterbirds in the Wadden Sea 1980-2000. Wadden Sea Ecosystem No. 20. Common Wadden Sea Secretariat Trilateral Monitoring and Assessment Group Joint Monitoring Group of Migratory Birds in the Wadden Sea, Wilhelmshaven, Germany. 200pp.

Blew J, Günther K, Südbeck P, 2005. Bestandsentwicklung der im deutschen Wattenmeer rastenden Wat- und Wasservögel von 1987/1988 bis 2001/2002. Vogelwelt 125: 99-125.

Bolton M, 1987. An Atlas of Wintering Birds in the Western Algarve. A Rocha Occasional Publication No.1. Merseyside, England.

Brader M, 1996. International Waterbird Census (IWC) in Upper Austria January 1996 (including census of November 1995 and March 1996). Vogelkundliche Nachrichten Oberösterreich - Naturschutz aktuell 4(2).

Brader M, et al, 2003. Atlas der Brutvögel Oberösterreichs (Atlas of Breeding Birds in Upper Austria), Denisia 7; Kataloge der Oberösterreichischen Landesmuseen, [Catalogues of the Upper Austrian Provincial Museums] Neue Folge Nr, 194.

Brown IH, Londt BZ, Shell W, Manvell RJ, Banks J, Gardner R, Outtrim L, Essen SC, Sabirovic M, Slomka M, Alexander DJ, 2006. First incursion of H5N1 highly pathogenic avian influenza viruses of the 'Asian' lineage into Europe. In: Brown I, Capua I (eds), 6th International Symposium on Avian Influenza, St. Johns College, Cambridge. Veterinary Laboratories Agency, Weybridge, UK. 37 [abstract]

Butler D, 2006. Thai dogs carry bird-flu virus, but will they spread it? Nature 439(7078): 773.

Calladine J, Robertson D, Wernham C, 2006. The ranging behaviour of some granivorous passerines on farmland in winter determined by mark-recapture and by radiotelemetry, Ibis 148 169-173.

Chan PK, 2002. Outbreak of avian influenza A(H5N1) virus infection in Hong Kong in 1997. Clin Infect Dis 34 Suppl 2: S58-64.

Chen H, Smith GJ, Zhang SY, Qin K, Wang J, Li KS, Webster RG, Peiris JS, Guan Y, 2005. Avian flu: H5N1 virus outbreak in migratory waterfowl. Nature 436(7048): 191-2.

Chen H, Smith GJ, Li KS, Wang J, Fan XH, Rayner JM, Vijaykrishna D, Zhang JX, Zhang LJ, Guo CT, Cheung CL, Xu KM, Duan L, Huang K, Qin K, Leung YH, Wu WL, Lu HR, Chen Y, Xia NS, Naipospos TS, Yuen KY, Hassan SS, Bahri S, Nguyen TD, Webster RG, Peiris JS, Guan Y, 2006. Establishment of multiple sublineages of H5N1 influenza virus in Asia: Implications for pandemic control. Proc Natl Acad Sci USA.

Chernichko I, Kostyushin V, 2003. Strategy for Waterbird Monitoring in the Black Sea Region, Wetlands International Kiev.

Colhoun K, Newton SF, 2000. Winter waterbird population on non-estuarine coasts in the Republic of Ireland: results of the 1997/98 Non-Estuarine Coastal Waterfowl Survey (NEWS), Irish Birds 6: 527-542.

Collier MP, Banks AN, Austin GE, Girling T, Hearn RD, Musgrove AJ, 2005. The Wetland Bird Survey 2003-04: Wildfowl and Wader Counts, BTO/ WWT/ RSPB/ JNCC Thetford.

Couch RB, Douglas RG, Jr., Fedson DS, Kasel JA, 1971. Correlated studies of a recombinant influenza-virus vaccine. 3. Protection against experimental influenza in man. J Infect Dis 124(5): 473-80.

Couch RB, Kasel JA, 1983. Immunity to influenza in man. Annu Rev Microbiol 37: 529-49.

Crowe O, 2005. Ireland's wetlands and their waterbirds: status and distribution, BirdWatch Ireland Dublin, 402 pp.

Crowe O, Boland H, 2004. Irish Wetland bird Survey: results of waterbird monitoring in Ireland in 201/02, Irish Birds 7: 313-326.

Davidson NC, Stroud DA, (in press), African-Western Eurasian Flyways: current knowledge population status and future challenges, Proceedings of the Waterbirds around the World Conference, The Stationary Office Edinburgh.

De Marco MA, Foni E, Campitelli L, Raffini E, 2003. Long-term Monitoring for Avian Influenza Viruses in Wild Bird Species in Italy, Veterinary Research Communications

Deceuninck B, 2005. Waterbirds censused in mid-January in France: importance of protected areas for wintering birds and trends over 1983-2002, Namur: Proceedings of the 28th French Conference for Ornithology November 28th-30th 2003.

Defra, 2005. Epidemiology Report on avian influenza in quarantine premises in Essex. National Emergency Epidemiology Group, November 2005

Devillers P, Roggeman W, Tricot J, Del Marmol P, Kerwijn C, Jacob JP, Anselin A. 1988. Atlas des oiseaux nicheurs de Belgique, [Atlas of Breeding Birds in Belgium], Institut Royal des Sciences Naturelles de Belgique Bruxelles, 395 pp.

Devos K, (in press). Numbers and population trends of waders along the Belgian North Sea coast, International Wader Studies 18.

Dimitrov M, Michev T, Profirov L, Nyagolov K, 2005. Waterbirds monitoring in Bourgas Wetlands. Pensoft Series Faunistica 44. 159pp.

Dinh Xuan T, Nguyen Thu T, Tran Cong T, 2005. Pork and Poultry markets in Vietnam. General Statistics Office - Vietnam: 50 pp.

Dixon J, Gulliver A, Gibson D, 2001. Global farming systems study: Challenges and priorities to 2030 - synthesis and global overview, Food and Agriculture Organization of the United Nations: 98 pp.

Dvorak M, Ranner A, Berg HM, 1993. Atlas der Brutvögel Österreichs, [Atlas of Breeding birds in Austria]. Ergebnisse der Brutvogelkartierung 1981-1985.

Dybbro T, 1976. De Danske Ynglefugles udbredlse, [Atlas of Breeding Birds in Denmark]. Kobenhavn Dansk Ornithologisk Forening.

EC, 1979. Council Directive 79/409/EEC of 2 April 1979 on the conservation of wild birds (OJ L 103 25.4.1979 p.1) [as ammended]

EC, 1990. Council Directive 90/539/EEC of 15 October 1990 on animal health conditions governing intra-Community trade in and imports from third countries of poultry and hatching eggs (OJ L 303 31.10.1990 p.6.).

EC, 1992. Council Directive 92/40/EEC1 of 19 May 1992 introducing Community measures for the control of avian influenza (OJ L 167 22.6.1992 p.14).

EC, 2002. Commission Decision 2002/649/EC of 5 August 2002 on the implementation of surveys for avian influenza in poultry and wild birds in the Member States (OJ L 213 9.8.2002 p, 3).

EC, 2003. Regulation of the European Parliament and of the Council (EC) No 2160/2003 of 17 November 2003 on the control of salmonella and other specified food-borne zoonotic agents OJ L 325 12.12.2003 p, 1).

EC, 2004a. Regulation (EC) No 852/2004 of the European Parliament and of the Council of 29 April 2004 on the hygiene of foodstuffs (OJ L 139 30.04.2004 p, 1) corrigendum by OJ L 226 25.06.2004 p, 3.

EC, 2004b. Regulation (EC) No 853/2004 of the European Parliament and of the Council of 29 April 2004 laying down specific hygiene rules for on the hygiene of foodstuffs (OJ L 139 30.04.2004 p, 55) corrigendum by OJ L 226 25.06.2004 p, 22.

EC, 2005a. Commission Decision 2005/734/EC of 19 October 2005 laying down biosecurity measures to reduce the risk of transmission of highly pathogenic avian influenza caused by Influenza virus A subtype H5N1 from birds living in the wild to poultry and other captive birds and providing for an early detection system in areas at particular risk (OJ L 274 20.10.2005 p, 105).

EC, 2005b. Commission Decision 2005/732/EC of 17 October 2005 approving the programmes for the implementation of Member States' surveys for avian influenza in poultry and wild birds during 2005 and laying down reporting and eligibility rules for the Community financial contribution to the implementation costs of those programmes (OJ L 274 20.10.2005 p, 95).

EC, 2005c. Council Directive 2005/94/EC of 20 December 2005 on Community measures for the control of avian influenza and repealing Directive 92/40/EEC (OJ L 10 14.1.2006 p.16).

EC, 2005d. Commission Decision 2005/464/EC of 21 June 2005 on the implementation of survey programmes for avian influenza in poultry and wild birds to be carried out in the Member States (OJ L 164 24.6.2005 p, 52).

EC, 2005e. Commission Decision 2005/726/EC of 17 October 2005 amending Decision 2005/464/EC on the implementation of survey programmes for avian influenza in poultry and wild birds to be carried out in the Member States (OJ L 273 19.10.2005 p, 21).

EFSA 2005. Opinion of the Scientific Panel on Animal Health and Welfare on Animal Health and Welfare Aspects of Avian Influenza. The EFSA Journal (2005) 266: 1-21.

Elias G, Reino L, Silva T, Tome R, Geraldes P, 1999. Atlas of the Wintering Birds of Baixo Alentejo, Sociedade Portuguesa para o Estudo das Aves.

Ellis TM, Bousfield RB, Bissett LA, Dyrting KC, Luk GS, Tsim ST, Sturm-Ramirez K, Webster RG, Guan Y, Malik Peiris JS, 2004. Investigation of outbreaks of highly pathogenic H5N1 avian influenza in waterfowl and wild birds in Hong Kong in late 2002. Avian Pathol 33(5): 492-505.

Ens BJ, Piersma T, Tinbergen JM, 1994. Towards predictive models of bird migration schedules: theoretical and empirical bottlenecks, NIOZ-Rapport Nederlands Instituut voor Onderzoek der Zee the Netherlands, 27pp

FAO, 2002. Small scale poultry production. Food and Agriculture Organization of the United Nations. AGAL: 119.

FAO, 2003a. Livestock Sector Brief - Tanzania, Food and Agriculture Organization of the United Nations: 16 pp.

FAO, 2003b. Livestock Sector Brief - Ethiopia, Food and Agriculture Organization of the United Nations: 15 pp.

FAO, 2003c. Livestock Sector Brief - Kenya, Food and Agriculture Organization of the United Nations: 16 pp.

FAO 2004. FAO Recommendations on the Prevention, Control and Eradication of Highly Pathogenic Avian Influenza in Asia. FAO Position Paper, September 2004. FAO, Rome Italy. 59 pages

FAO, 2004a. Livestock household needs survey - North Caucasus (Chechnya and Ingushetia). Food and Agriculture Organization of the United Nations: 46 pp.

FAO, 2004b. Livestock Sector Brief – Zambia. Food and Agriculture Organization of the United Nations: 15 pp.

FAO, 2005a. Livestock Sector Brief - China, Food and Agriculture Organization of the United Nations: 15 pp.

FAO, 2005b. Livestock Sector Brief-Indonesia. Food and Agriculture Organization of the United Nations: 15 pp.

Fiedler W, 1998. Joint Vogelwarte Radolfzell-EURING migration project: a large-scale ringing recovery analysis of the migration of European bird species, EURING Newsletter 2: 31-35.

Fitchner GJ, 1987. The Pennsylvania/Virginia experience in eradication of influenza H5N2. Proc 2nd Int Symp Avian Influenza U.S, Anim, Health Assoc Univ Wisconsin pp 33-38.

Fouchier RA, Bestebroer TM, Herfst S, Van Der Kemp L, Rimmelzwaan GF, Osterhaus AD, 2000. Detection of influenza A viruses from different species by PCR amplification of conserved sequences in the matrix gene. J Clin Microbiol 38(11): 4096-4101.

Fouchier RA, Olsen B, Bestebroer TM, Herfst S, van der Kemp L, Rimmelzwaan GF, Osterhaus AD, 2003. Influenza A virus surveillance in wild birds in Northern Europe in 1999 and 2000. Avian Dis 47(3 Suppl): 857-860.

Fransson T, Pettersson J, 2001. Svensk ringmärkningsatlas (Volym 1 Lommar-rovfåglar), [Swedish Bird Ringing Atlas (Volume 1 Divers-Raptors)], Naturhistoriska riksmuseet Sveriges Ornitologiska Forening Stockholm.

Frederiksen M, Fox AD, Madsen J, Colhoun K, 2001. Estimating the total number of birds using a staging site. Journal of Wildlife Management 65(2): 282-289.

Gabriel G, Dauber B, Wolff T, Planz O, Klenk HD, Stech J, 2005. The viral polymerase mediates adaptation of an avian influenza virus to a mammalian host. Proc Natl Acad Sci USA 102(51): 18590-18595.

Gibbons DW, Reid JB, Chapman RA, 1993. The new atlas of breeding birds in Britain and Ireland: 1988-1991. T., AD, Poyser London.

Gilbert M, Wint W, Slingenbergh JI, 2004. The ecology of Highly Pathogenic Avian Influenza in East and Southeast Asia: outbreak distribution, risk factors and policy implications, Food and Agriculture Organization of the United Nations: 43.

Gilbert M, Chaitaweesub P, Parakamawongsa T, Premashthira S, Tiensin T, Kalpravidh W, Wagner H, Slingenbergh J, 2006. Free-grazing ducks and highly pathogenic avian influenza, Thailand. Emerg Infect Dis 12(2): 227-234.

Gilissen N, Haanstra L, Delany S, Boere G, Hagemeijer W, 2002. Numbers and distribution of wintering waterbirds in the Western Palearctic and Southwest Asia in 1997 1998 and 1999. Results from the International Waterbird Census. Wetlands International Global Series No 11. Wageningen, The Netherlands.

Gjershaug JO, Thingstad PG, Eldøy S, Byrkjeland S, 1994. Norsk Fugleatlas, [Norwegian Bird Atlas]. Norsk Ornitologisk Forening. Klæbu.

Gleeson L, Selleck P, Bingham J, Lowther S, Trinidad L, Heine H, 2006. Transmission of H5N1 avian infleunza virus A/Muscovy duck/Vietnam/453/2004 to *Anas castanea* (chestnut teal), an Australian native duck. In Brown I, Capua I (eds) 6th International Symposium on Avian Influenza, St. Johns College, Cambridge. Veterinary Laboratories Agency, Weybridge, UK. 23 [abstract].

Glezen WP, Couch RB, 1989. Influenza viruses. In: Evans (ed). Viral infections in humans, Epidemiology and control., Chapter 15 pp 419-449 3rd edition Plenum Medical Book Company New York 1989. 15: 419-449

Globig A, Starick E, Werner O, 2006. Influenzavirus-Infektionen bei migrierenden Wasservögeln: Ergebnisse einer zweijährigen Studie in Deutschland. Berliner und Münchner Tierärztliche Wochenschrift 119(3-4):132-139.

Govorkova EA, Rehg JE, Krauss S, Yen HL, Guan Y, Peiris M, Nguyen TD, Hanh TH, Puthavathana P, Long HT, Buranathai C, Lim W, Webster RG, Hoffmann E, 2005. Lethality to ferrets of H5N1 influenza viruses isolated from humans and poultry in 2004. J Virol 79(4): 2191-2198.

GRAIN, 2006. Fowl play: the poultry industry's central role in the bird flu crisis. Grain briefing, February 2006. http://www.grain.org/briefings_files/birdflu2006-en.pdf

Guan Y, J, S, Peiris A, S, Lipatov T, M, Ellis K, C, Dyrting S, Krauss L, J, Zhang R, G, Webster and K, F, Shortridge, 2002. Emergence of multiple genotypes of H5N1 avian influenza viruses in Hong Kong SAR, Proc, Natl, Acad, Sci, USA 99 (13): 8950-8955.

Guan Y, Peiris M, Kong KF, Dyrting KC, Ellis TM, Sit T, Zhang LJ, Shortridge KF, 2002a. H5N1 influenza viruses isolated from geese in Southeastern China: evidence for genetic reassortment and interspecies transmission to ducks. Virology 292(1): 16-23.

Guan Y, Poon LL, Cheung CY, Ellis TM, Lim W, Lipatov AS, Chan KH, Sturm-Ramirez KM, Cheung CL, Leung YH, Yuen KY, Webster RG, Peiris JS, 2004. H5N1 influenza: a protean pandemic threat. Proc Natl Acad Sci USA 101(21): 8156-8161.

Guillemain M, Sadoul N, Simon G, 2005. European flyway permeability and abmigration in Teal Anas crecca an analysis based on ringing recoveries. Ibis 147: 688-696.

Hagemeijer WJM, Blair MJ, (eds) 1997. The EBCC Atlas of European Breeding Birds: Their Distribution and Abundance. T, AD, Poyser, London.

Hale WG, 1973. Waders. Collins London.

Harrison JA, Allan DG, Underhill LG, Herremans M, Tree AJ, Parker V, Brown CJ, (eds.) 1997. The Atlas of Southern African Birds, Vol, 1, BirdLife South Africa Johannesburg.

Hatta M, Gao P, Halfmann P, Kawaoka Y, 2001. Molecular basis for high virulence of Hong Kong H5N1 influenza A viruses. Science 293(5536): 1840-1842.

Heath M, Borggreve C, Peet N, 2000. European bird populations: estimates and trends. BirdLife Conservation Series No 10. BirdLife International Cambridge UK. 160 pp.

Heath MF, Evans MI, (eds), 2000. Important Bird Areas in Europe: Priority sites for conservation, 2 vols, Cambridge UK: BirdLife International (BirdLife Conservation Series No, 8), Volume 1: Northern Europe Volume 2 Southern Europe.

Helsinki Commission, 2004. Development of Baltic Waterbird Monitoring Strategy, 7th Meeting of Monitoring Assessment Group Talin.

Hinshaw VS, Webster RG, Turner B, 1980. The perpetuation of orthomyxoviruses and paramyxoviruses in Canadian waterfowl. Can J Microbiol 26(5): 622-9.

Hulse-Post DJ, Sturm-Ramirez KM, Humberd J, Seiler P, Govorkova EA, Krauss S, Scholtissek C, Puthavathana P, Buranathai C, Nguyen TD, Long HT, Naipospos TS, Chen H, Ellis TM, Guan Y, Peiris JS, Webster RG, 2005. Role of domestic ducks in the propagation and biological evolution of highly pathogenic H5N1 influenza viruses in Asia. Proc Natl Acad Sci U S A 102(30): 10682-10687.

International Wader Study Group, 1998. The Odessa Protocol on international co-operation on migratory flyway research and conservation., In: Hötker H, Lebedeva E, Tomkovich PS, Gromadzka J, Davidson NC, Evans J, Stroud DA, West RB, (eds.). Migration and international conservation of waders, Research and conservation on North Asian African and European flyways, International Wader Studies 10: 500 pp.

Isakov YA, 1967. MAR Project and conservation of waterfowl breeding in the USSR. In: Salverda Z, (ed.). Proceedings of the Second European Meeting on Wildfowl Conservation Noordwijk aan Zee. Ministry of Cultural Affairs Recreation and Social Welfare The Netherlands. 125-138

Ito T, Okazaki K, Kawaoka Y, Takada A, Webster RG, Kida H, 1995. Perpetuation of influenza A viruses in Alaskan waterfowl reservoirs. Arch Virol 140(7): 1163-1172.

Iverson GC, Warnock SE, Butler RW, Bishop MA, Warnock N, 1996. Spring migration of Western Sandpipers (Calidris mauri) along the Pacific Coast of North America: a telemetry study. Condor 98: 10-22.

Kaleta EF, Hergarten G, Yilmaz A, 2005. Avian influenza A viruses in birds - An ecological, ornithological and virological view. Deutsche Tierärztliche Wochenschrift 112:448-456.

Karesh WB, Cook RA, Bennett EL, Newcomb J, 2005. Wildlife trade and global disease emergence. Emerg Infect Dis 11(7): 1000-1002.

Kear J, (ed.) 2005. Ducks Geese and Swans, Oxford University Press Oxford, Two volumes, 908 pp,

Keawcharoen J, Oraveerakul K, Kuiken T, Fouchier RA, Amonsin A, Payungporn S, Noppornpanth S, Wattanodorn S, Theambooniers A, Tantilertcharoen R, Pattanarangsan R, Arya N, Ratanakorn P, Osterhaus DM, Poovorawan Y, 2004. Avian influenza H5N1 in tigers and leopards. Emerg Infect Dis 10(12): 2189-21991.

Kingsford RT, 1996. Wildfowl (Anatidae) movements in arid Australia, Gibier Faune Sauvage Game and Wildlife 13: 141-155.

Knight V, Couch RB, Landahl HD, 1970. Effect of lack of gravity on airborne infection during space flight. Jama 214(3): 513-518.

Knips V, 2004. Review of the Livestock Sector in the Mekong Countries. Livestock Sector Report – Cambodja, Lao PDR, Thailand, Vietnam. Food and Agriculture Organization of the United Nations: 38 pp.

Kou Z, Lei FM, Yu J, Fan ZJ, Yin ZH, Jia CX, Xiong KJ, Sun YH, Zhang XW, Wu XM, Gao XB, Li TX, 2005. New genotype of avian influenza H5N1 viruses isolated from tree sparrows in China. J Virol 79(24): 15460-15466.

Krauss S, Walker D, Pryor SP, Niles L, Chenghong L, Hinshaw VS, Webster RG, 2004. Influenza A viruses of migrating wild aquatic birds in North America. Vector Borne Zoonotic Dis 4(3): 177-189.

Kuiken T, Rimmelzwaan GF, Van Amerongen G, Osterhaus AD, 2003. Pathology of human influenza A (H5N1) virus infection in cynomolgus macaques (Macaca fascicularis). Vet Pathol 40(3): 304-10.

Kuiken T, Rimmelzwaan G, van Riel D, van Amerongen G, Baars M, Fouchier R, Osterhaus A, 2004. Avian H5N1 influenza in cats. Science 306(5694): 241.

Kwon YK, Joh SJ, Kim MC, Lee YJ, Choi JG, Lee EK, Wee SH, Sung HW, Kwon JH, Kang MI, Kim JH, 2005. Highly Pathogenic Avian Influenza in Magpies (Pica pica sericea) in South Korea. J Wildl Dis 41(3): 618-623.

Lack P, (ed.) 1986. The Atlas of Wintering Birds In Britain and Ireland, T AD Poyser London.

Lappo EG, 1996. Comparisons of breeding range structure for Dunlin Calidris alpina and Curlew Sandpiper Calidris ferruginea: conservative and nomadic waders, Wader Study Group Bulletin 80: 41-46.

Laursen K, Pihl S, Durinck J, Hansen M, Skov H, Frikke J, Danielsen F, 1997. Numbers and Distribution of Waterbirds in Denmark 1987-1989. National Environmental Research Institute, Department of Coastal Zone Ecology, Danish Review of Game Biology 15:181 pp.

Li K, S, Y, Guan J, Wang G, J, Smith K, M, Xu L, Duan A, P, Rahardjo P, Puthavathana C, Buranathai T, D, Nguyen A, T, Estoepangestie A, Chaisingh P, Auewarakul H, T, Long N, T, Hanh R, J, Webby L, L, Poon H, Chen K, F, Shortridge K, Y, Yuen R, G, Webster and J, S, Peiris, 2004. Genesis of a highly pathogenic and potentially pandemic H5N1 influenza virus in eastern Asia, Nature 430 (6996):209-213.

Lithuanian Ornithological Society (in prep.) Atlas of Breeding Birds in Lithuania.

Liu J, Xiao H, Lei F, Zhu Q, Qin K, Zhang XW, Zhang XL, Zhao D, Wang G, Feng Y, Ma J, Liu W, Wang J, Gao GF, 2005. Highly pathogenic H5N1 influenza virus infection in migratory birds. Science 309(5738): 1206.

Lu H, Castro AE, Pennick K, Liu J, Yang Q, Dunn P, Weinstock D, Henzler D, 2003. Survival of avian influenza virus H7N2 in SPF chickens and their environments. Avian Dis 47(3 Suppl): 1015-21.

Lyngs P, 2003. Migration and winter ranges of birds in Greenland, Dansk Ornitologisk Forenings Tidsskrift 97: 1-167.

Maclean IMD, Austin GE, Mellan HJ, Girling T, 2005. WeBS Alerts 2003/2004: Changes in numbers of wintering waterbirds in the United Kingdom its Constituent Countries Special Protection Areas (SPAs) and Sites of Special Scientific Interest (SSSIs), BTO Research Report No, 416 to the WeBS Partnership, BTO Thetford.

Madsen J, 1995. Impacts of disturbance on migratory waterfowl, Ibis 137: 67-74.

Madsen J, Fox AD, 1995. Impacts of hunting disturbance on waterbirds - a review, Wildlife Biology 1: 193-207.

Madsen J, Cracknell G, Fox AD, (eds) 1999. Goose populations of the Western Palearctic: a review of status and distribution, Wetlands International Publication No, 48/NERI Denmark, 343 pp.

Magnino S, Fabbi M, Moreno A, Sala G, Lavazza A, Ghelfi E, Gandolfi L, Pirovano G, Gasperi E, 2000. Avian influenza virus (H7 serotype) in a saker falcon in Italy. Vet Rec 146(25): 740.

Marchant J, 2002. Learning about bird movements: methods of study. In: Wernham CV, Toms MP, Marchant JH, Clark JA, Siriwardena GM, Baillie SR (ed.). The Migration Atlas: Movements of the Birds of Britain and Ireland. A. D, Poyser London UK. 1-13

Martí R, Del Moral JC, (eds.) 2002. La invernada de aves acuáticas en España, Dirección de Conservación de la Naturaleza-SEO/BirdLife, Ed, Organismo Autónomo Parques Nacionales Ministerio de Medio Ambiente Madrid, 309 pp + CD-ROM.

Martin V, Sims L, Lubroth J, Pfeiffer D, Slingenbergh J, Domenech J, 2006. Epidemiology and ecology of highly pathogenic avian influenza with particular emphasis on South East Asia. Dev Biol (Basel) 124: 23-36.

Mase M, Tsukamoto K, Imada T, Imai K, Tanimura N, Nakamura K, Yamamoto Y, Hitomi T, Kira T, Nakai T, Kiso M, Horimoto T, Kawaoka Y, Yamaguchi S, 2005. Characterization of H5N1 influenza A viruses isolated during the 2003-2004 influenza outbreaks in Japan. Virology 332(1): 167-176.

Meschini E, Frugis S, 1993. Atlante degli uccelli nidificanti in Italia, Suppl, Ric, Biol, Selvaggina 20: 1-344.

Michev T, Profirov L, 2003. Midwinter numbers of waterbirds in Bulgaria: results from 25 years of mid-winter counts carried out at the most important Bulgarian wetlands. Publ, House Pensoft Sofia. (In English with Bulgarian summary). 160 pp

Muñoz MJ, Sánchez-Vizcaíno JM, Peris S, 2006. Can highly pathogenic avian influenza (HPAI) reach the Iberian Peninsula from Asia by means of migratory birds?, Spanish Journal of Agricultural Research (in press).

Monval JY, Pirot JY, 1989. Results of the IWRB International Waterfowl Census 1967-1986. IWRB Special Publication No 8. Slimbridge UK.

Morris R, Jackson R, Stevenson M, Benard J, Cogger N, 2005. Epidemiology of H5N1 Avian Influenza in Asia and Implications for Regional Control, Food and Agriculture Organization of the United Nations: 254.

Moser MR, Bender TR, Margolis HS, Noble GR, Kendal AP, Ritter DG, 1979. An outbreak of influenza aboard a commercial airliner. Am J Epidemiol 110(1): 1-6.

Mullié WC, Brouwer J, Codjo SF, Decae R, 1999. Small isolated wetlands in the Central Sahel: a resource shared between people and waterbirds. In: Beintema A, van Vessem J, (eds). Strategies for conserving waterbirds, Proceedings of Workshop 2 of the 2nd International Conference on Wetlands and Development held in Dakar Senegal 8-14 November 1998, Wetlands International Publication No, 55. Wageningen The Netherlands. 30-38,

Munster VJ, Wallensten A, Baas C, Rimmelzwaan GF, Schutten M, Olsen B, Osterhaus AD, Fouchier RA, 2005. Mallards and highly pathogenic avian influenza ancestral viruses, northern Europe. Emerg Infect Dis 11(10): 1545-1551.

Munster VJ, Wallenstein A, Baas C, Rimmelzwaan GF, Olsen B, Osterhaus, ADME, Fouchier RAM, 2006. European influenza A virus monitoring in migratory fowl. In Brown I, Capua I (eds) 6th International Symposium on Avian Influenza, St. Johns College, Cambridge. Veterinary Laboratories Agency, Weybridge, UK. 61 [abstract]

NERI, 1995. Waterbird numbers in the Baltic Sea winter 1993, Ministry of the Environment and Energy National Environmental Research Institute Denmark.

Newton I, 1998. Population limitation in birds, Academic Press London, 597 pp.

Newton I. and Dale LC, 1996. Bird migration at different latitudes in Eastern North America. The Auk, Vol 113 (3) 626-635.

Nikolov SC, Vassilev VP, 2004. Breeding bird atlas of the Ponor Mountains Western Bulgaria, Sandgrouse 26: 7-22.

OIE, 2004. Manual of Diagnostic Tests and Vaccines for Terrestrial Animals: Chapter 2.1.14 Highly Pathogenic Avian Influenza, Fifth Edition, OIE Paris.

OIE 2004a. Handbook on Import Risk Analysis for Animals and Animal Products Volume 1, 2004 World Organisation for Animal Health.

OIE 2004b. OIE Manual of Diagnostic Tests and Vaccines for Terrestrial Animals: Chapter 2.1.14 Highly Pathogenic Avian Influenza., Fifth Edition 2004 OIE Paris.

OIE 2005. World Organisation for Animal Health Terrestrial Code 14th Edition 2005.

OIE, 2006. OIE Bulletin, ISSN: 1684-3770.

Okazaki K, Takada A, Ito T, Imai M, Takakuwa H, Hatta M, Ozaki H, Tanizaki T, Nagano T, Ninomiya A, Demenev VA, Tyaptirganov MM, Karatayeva TD, Yamnikova SS, Lvov DK, Kida H, 2000. Precursor genes of future pandemic influenza viruses are perpetuated in ducks nesting in Siberia. Arch Virol 145(5): 885-93.

Olsen B, Munster VJ, Wallensten A, Waldenstrom J, Osterhaus AD, Fouchier RA, 2006. Global patterns of influenza a virus in wild birds. Science 312:384-388.

Owen M, 1996. Review of the migration strategies of the Anatidae: challenges for conservation, Gibier Faune Sauvage Game and Wildlife 13: 123-139.

Perkins LE, Swayne DE, 2001. Pathobiology of A/chicken/Hong Kong/220/97 (H5N1) avian influenza virus in seven gallinaceous species. Vet Pathol 38(2): 149-164.

Perkins LE, Swayne DE, 2002 Susceptibility of laughing gulls (Larus atricilla) to H5N1 and H5N3 highly pathogenic avian influenza viruses. Avian Dis (4). 46: 877-885. 2002.

Perkins LE, Swayne DE, 2002a. Pathogenicity of a Hong Kong-origin H5N1 highly pathogenic avian influenza virus for emus, geese, ducks, and pigeons. Avian Dis 46(1): 53-63.

Perkins LE, Swayne DE, 2003. Varied pathogenicity of a Hong Kong-origin H5N1 avian influenza virus in four passerine species and budgerigars. Vet Pathol 40(1): 14-24.

Pfeiffer DU, 2005. Assistance in the geospatial analysis of HPAI outbreaks in Vietnam. Report based on Consultancy Mission OSRO/RAS/401/JPN. Food and Agriculture Organization of the United Nations, Rome, Italy. 8pp.

Pienkowski MW, Pienkowski A, 1983. WSG project on the movement of wader populations in western Europe eighth progress report, Wader Study Group Bulletin 38: 13-22.

Piersma T, 1987. Hink stap of sprong? Reisbeperkingen van arctische steltlopers door voedselzoeken vetopbouw en vliegsnelheid, [Hop skip or jump? Constraints on migration of arctic waders by feeding fattening and flight speed], Limosa 60: 185-194.

Piersma T, 1994. Close to the edge: energetic bottlenecks and the evolution of migratory pathways in Knots, Doctoral thesis Riksuniversiteit Groningen The Netherlands, 366 pp.

Priednieks J, Strazds M, Stradz A, Petrinš, 1989. Latvian breeding bird atlas 1980-1984, Zinâtne Riga Latvia (In Latvian, Russian and English).

Rees EC, Matthews GVT, Mitchell CR, Owen M, 2005. Movements and migrations. In: Kear J, (ed.) Ducks, Geese and Swans, Oxford University Press Oxford, 112-131,

Renno O, (ed.) 1993. Eesti Haudelindude Levikuatlas, Estonian Bird Atlas: The Atlas of Breeding Birds in Estonia, Vulgas Talin.

Ridgill S, Fox A.D, 1990. Cold weather movements of waterfowl in western Europe, IWRB Special Publication No, 13, IWRB Slimbridge, 87 pp.

Rimmelzwaan GF, van Riel D, Baars M, Bestebroer TM, van Amerongen G, Fouchier RA, Osterhaus AD, Kuiken T, 2006. Influenza A virus (H5N1) infection in cats causes systemic disease with potential novel routes of virus spread within and between hosts. Am J Pathol 168(1): 176-83; quiz 364.

Risberg L, 1990. Sveriges Faglar (Swedish Bird Atlas), Stokholm: Naturbokhandeln.

Rogers SO, Starmer WT, Castello JD, 2004. Recycling of pathogenic microbes through survival in ice. Med Hypotheses 63(5): 773-777.

Roggeman W, Huisseune D, Vangeluwe D, Vandenbulch P, Vandousselare P, 1995. Belgium Ringing Scheme Databank: Gavidae to Anatidae, Studiedocumenten van het Koninklijk Belgisch Instituut voor Naturwetenschappen Brussels Belgium.

Rohwer FC, Anderson MG, 1988. Female-biased philopatry monogamy and the timing of pair formation in migratory waterfowl, Current Ornithology 5: 187-221.

Roth Y, Chapnik JS, Cole P, 2003. Feasibility of aerosol vaccination in humans. Ann Otol Rhinol Laryngol 112(3): 264-270.

Rufino R, (ed.) 1989. Atlas das Aves que nidificam em Portugal Continental, Serviço Nacional de Parques Reservas e Conservação da Natureza Lisboa Portugal, 215 pp.

Rushton J, Viscarra R, Bleiche EG, McLeod A 2004. Impact of influenza outbreaks in the poultry sectors of five South east Asian countries (Cambodjia, Indonesia, lao PDR, Thailand, Viet Nam) outbreak costs, responses and potential long term control, FAO, Rome, Italy: 25.

Salomonsen F, 1968. The moult migration, Wildfowl 19: 5-24.

Schaffer FL, Soergel ME, Straube DC, 1976. Survival of airborne influenza virus: effects of propagating host, relative humidity, and composition of spray fluids. Arch Virol 51(4): 263-273.

Schaub M, Pradel R, Jenni L, Lebreton J-D, 2001. Migrating birds stop over longer than usually thought: an improved capture – recapture analysis, Ecology 82: 852-859.

Schmidt H, Luder R, Naef-Daenzer B, Graf N, Zbinden N, 1998. Schweizer Brutvogelatlas, Schweizerische Vogelwarte Sempach Switzerland.

Schulman JL, Kilbourne ED, 1962. Airborne transmission of influenza virus infection in mice. Nature 195: 1129-1130.

Scott DA, Rose PM, 1996. Atlas of Anatidae Populations in Africa and Western Eurasia, Wetlands International Publication No, 41, Wetlands International, Wageningen The Netherlands.

Senne DA, Panigrahy B, Kawaoka Y, Pearson JE, Suss J, Lipkind M, Kida H, Webster RG, 1996. Survey of the hemagglutinin (HA) cleavage site sequence of H5 and H7 avian influenza viruses: amino acid sequence at the HA cleavage site as a marker of pathogenicity potential. Avian Dis 40(2): 425-437.

Seo SH, Hoffmann E, Webster RG, 2004. The NS1 gene of H5N1 influenza viruses circumvents the host anti-viral cytokine responses. Virus Res 103(1-2): 107-13.

Shortridge KF, Zhou NN, Guan Y, Gao P, Ito T, Kawaoka Y, Kodihalli S, Krauss S, Markwell D, Murti KG, Norwood M, Senne D, Sims L, Takada A, Webster RG, 1998. Characterization of avian H5N1 influenza viruses from poultry in Hong Kong. Virology 252(2): 331-342.

Sims LD, Ellis TM, Liu KK, Dyrting K, Wong H, Peiris M, Guan Y, Shortridge KF, 2003. Avian influenza in Hong Kong 1997-2002. Avian Dis 47(3 Suppl): 832-8.

Sims LD, Guan Y, Ellis TM, Liu KK, Dyrting K, Wong H, Kung NY, Shortridge KF, Peiris M, 2003a. An update on avian influenza in Hong Kong 2002. Avian Dis 47(3 Suppl): 1083-6.

Sims LD, Domenech J, Benigno C, Kahn S, Kamata A, Lubroth J, Martin V, Roeder P, 2005. Origin and evolution of highly pathogenic H5N1 avian influenza in Asia. Vet Rec 157(6): 159-164.

Siriwardena G, Wernham C, 2002. Synthesis of the migration patterns of British Irish birds, In: Wernham CV, Toms MP, Marchant JH, Clark JA, Siriwardena GM, Baillie SR (Eds.). The Migration Atlas: Movements of the Birds of Britain and Ireland, T, AD, Poyser London UK, 70-102.

Smit C, Piersma T, 1989. Numbers midwinter distribution and migration of wader populations using the East Atlantic Flyway, In: Boyd H, Pirot J, (Eds.) Flyways and reserve networks for water birds, IWRB Special Publication No, 9: 24-63.

Smith AW, Skilling DE, Castello JD, Rogers SO, 2004. Ice as a reservoir for pathogenic human viruses: specifically, caliciviruses, influenza viruses, and enteroviruses. Med Hypotheses 63(4): 560-566.

Snow DW, Perrins CM, 1998. The Birds of the Western Palearctic, Volume 1: Non-Passerines, Concise Edition, Oxford University Press Oxford UK New York USA, 1008 pp.

Songserm T, Sae-Heng N, Jam-on R, Witoonsatient K, Meemak N, 2005. Clinical, gross-histopathologic and immunohistochemical finding of grazing ducks affected with HPAI H5N1 in Thailand [abstract 74]. In: Abstracts of the Office International des Epizooties/Food and Agricultural Organization International Conference on Avian Influenza, Paris, 7-8 April 2005.

Songserm T, Amonsin A, Jam-on R, Sae-Heng N, Meemak N, Pariyothorn N, Payungporn S, Theamboonlers A, Poovorawan Y, 2006. Avian influenza H5N1 in naturally infected domestic cat, Emerging Infectious Diseases, Vol. 12, N° 4, April 2006. Available from http://www.cdc.gov/ncidod/EID/vol12no04/05-1396.pdf

Sovinc A, 1994. The atlas of the wintering birds in Slovenia, DZS Ljubljana.

SOVON, 1992. All-year Atlas of Birds in the Netherlands in brief, SOVON Beek-Ubbergen The Netherlands.

SOVON, 2002. Atlas van de Nederlandse broedvogels 1998-2000. [Atlas of the Dutch breeding birds: 1998-2000] - Nederlandse Fauna 5, Nationaal Natuurhistorisch Museum Naturalis KNNV Uitgeverij European Invertebrate Survey-Nederland Leiden.

Spackman E, Senne DA, Bulaga LL, Myers TJ, Perdue ML, Garber LP, Lohman K, Daum LT, Suarez DL, 2003. Development of Real-Time RT-PCR for the Detection of Avian Influenza Virus. Avian Diseases, 47 (3):1079–1082.

St'astný K, Bejcek V, Hudec K, 1996. Atlas of Breeding Bird Distribution in the Czech Republic 1985-1989 (in Czech), Nakladatelstvi a vydavatelstvi H H.

Stallknecht DE, Shane SM, Kearney MT, Zwank PJ, 1990. Persistence of avian influenza viruses in water. Avian Dis 34(2): 406-11.

Stallknecht DE, Shane SM, Zwank PJ, Senne DA, Kearney MT, 1990a. Avian influenza viruses from migratory and resident ducks of coastal Louisiana. Avian Dis 34(2): 398-405.

Stallknecht DE, 1998. Ecology and epidemiology of avian influenza viruses in wild bird populations, In: Proceedings of the Fourth International Symposium on Avian Influenza Athens Georgia, US Animal Health Association. 61-69.

Stanevičius V, 2003. Monitoring of breeding waterbirds in Lithuania: organisation and sampling designs, Ornis Hungarica 12-13, 89-94.

Stroud DA, Chambers D, Cook S, Buxton N, Fraser B, Clement P, Lewis P, McLean I, Baker H, Whitehead S, (Eds), 2001. The UK SPA network: its scope and content, Joint Nature Conservation Committee, (www.jncc.gov.uk/page-1412).

Stroud DA, Davidson NC, West R, Scott DA, Haanstra L, Thorup O, Ganter B, Delany S, (compilers) on behalf of the International Wader Study Group, 2004. Status of migratory wader populations in Africa and Western Eurasia in the 1990s, International Wader Studies 15: 1-259.

Sturm-Ramirez KM, Ellis T, Bousfield B, Bissett L, Dyrting K, Rehg JE, Poon L, Guan Y, Peiris M, Webster RG, 2004. Reemerging H5N1 influenza viruses in Hong Kong in 2002 are highly pathogenic to ducks. J Virol 78(9): 4892-4901.

Sturm-Ramirez KM, Hulse-Post DJ, Govorkova EA, Humberd J, Seiler P, Puthavathana P, Buranathai C, Nguyen TD, Chaisingh A, Long HT, Naipospos TS, Chen H, Ellis TM, Guan Y, Peiris JS, Webster RG, 2005. Are ducks contributing to the endemicity of highly pathogenic H5N1 influenza virus in Asia? J Virol 79(17): 11269-11279.

Summers RW, Underhill LG, 1987. Factors related to breeding production of Brent Geese Branta b, bernicla and waders (Charadrii) on the Taimyr Peninsula, Bird Study 34: 161-171.

Švažas S, Balčiauskas L, Raudonikis L, 2003. Lithuanian wetlands database: the tool for bird monitoring and conservation in Lithuanian wetlands, Ornis Hungarica 12-13:95-103.

Swayne DE, Beck JR, 2004. Heat inactivation of avian influenza and Newcastle disease viruses in egg products. Avian Pathol 33(5): 512-518.

Terregino C, Cattoli G, De Nardi R, Beato MS, Capua I, Guberti V, Scremin M, 2005. Isolation of influenza A viruses subtype H7N7 and H7N4 from waterfowl in Italy. Vet Rec 156(9): 292.

Thorup O, (comp.) 2005. Breeding waders in Europe 2000, International Wader Studies 14, 142 pp.

Tiensin T, Chaitaweesub P, Songserm T, Chaisingh A, Hoonsuwan W, Buranathai C, Parakamawongsa T, Premashthira S, Amonsin A, Gilbert M, Nielen M, Stegeman A, 2005. Highly pathogenic avian influenza H5N1, Thailand, 2004. Emerg Infect Dis 11(11): 1664-1672.

Togan S, Bayaner A, 2003. Analysis of the impact on agricultural markets and incomes of EU enlargement to Turkey, Conference on Turkey: Towards EU Accession, Ankara.

Underhill LG, Tree AJ, Oschadleus HD, Parker V, 1999. Review of ring recoveries of waterbirds in southern Africa, Avian Demography Unit University of Cape Town Cape Town, 119 pp.

Utterback W, 1984. Update on avian influenza through February 21 1984 in Pensylvania and Virginia, Proc, 33rd Western Poultry Dis Conf pp 4-7.

Väisänen RA, Lammi E, Koskinnes P, 1998. Muuttuva pessimälinnusto [Distribution number and population changes of Finnish Birds], Otava Keuruu.

van Roomen M, van Winden E, Koffijberg K, Boele A, Hustings F, Kleefstra R, Schoppers J, van Turnhout C, SOVON Ganzen- en zwanenwerkgroep Soldaat L, 2004. Watervogels in Nederland in 2002/03, SOVON-monitoringrapport 2004/2 RIZA-rapport BM04/09 SOVON Vogelonderzoek Nederland Beek-Ubbergen, 235 pp.

van Roomen M, van Turnhout C, van Winden E, Koks B, Goedhart P, Leopold M, Smit C, 2005a, Trends in benthivorous waterbirds in the Dutch Wadden Sea 1975-2002: large differences between shellfish-eaters and worm-eaters, Limosa 78: 21-38.

Velasco T, Alberto LJ, 1993. Number main localities and distribution maps of waders wintering in Spain, Wader Study Group Bulletin, 70: 33-41.

Veterinaires Sans Frontieres 2004. Organization of avian production and description of HPAI epidemiological patterns in Vietnam - intermediate report, Veterinaires sans Frontiers/World Bank.

Vowles GA, Vowles RS, 1994. Breeding Birds of the Algarve, Centro de Estudos Ornitológicos no Algarve,

Wahl J, Sudfelt C, Naacke J, Mooij J, 2004. Rundbrief zum Wasservogelmoinitoring in Deutschland, Dachverband Deutscher Avifaunisten Muenster Germany.

Walasz, 2000. The Atlas of Wintering Birds in Malopolska (south east Poland).

Wan XF, Ren T, Luo KJ, Liao M, Zhang GH, Chen JD, Cao WS, Li Y, Jin NY, Xu D, Xin CA, 2005. Genetic characterization of H5N1 avian influenza viruses isolated in southern China during the 2003-04 avian influenza outbreaks. Arch Virol 150(6): 1257-1266.

Wash Wader Ringing Group 2004. Wash Wader Ringing Group, 2002-2003 Report, Wash Wader Ringing Group Thetford UK.

Washington Post, 2005. http://www.washingtonpost.com/wp-dyn/content /article/2005/10/19/AR2005101902147.html

Weber R, Munteanu D, Papadopol A, Kiss A, et al, 1994. Atlasul provizoriu al păsărilor clocitoare din România, [Provisional Atlas of Breeding Birds from Romania], Ed.I Publ.S.O.R, 2 Mediaş republicat sub titlul Atlasul păsărilor clocitoare din România Ed.II Publ.S.O.R, 16 Cluj-Napoca.

Webster RG, 1998. Influenza: an emerging disease. Emerg Infect Dis 4(3): 436-441.

Webster RG, Yakhno M, Hinshaw VS, Bean WJ, Murti KG, 1978. Intestinal influenza: replication and characterization of influenza viruses in ducks. Virology 84(2): 268-278.

Webster RG, Bean WJ, Gorman OT, Chambers TM, Kawaoka Y, 1992. Evolution and ecology of influenza A viruses. Microbiol Rev 56(1): 152-79.

Webster RG, Guan Y, Peiris M, Walker D, Krauss S, Zhou NN, Govorkova EA, Ellis TM, Dyrting KC, Sit T, Perez DR, Shortridge KF, 2002. Characterization of H5N1 influenza viruses that continue to circulate in geese in southeastern China. J Virol 76(1): 118-126.

Webster RG, Peiris M, Chen H, Guan Y, 2006. H5N1 outbreaks and enzootic influenza. Emerg Infect Dis 12(1): 3-8.

Wernham CV, Toms MP, Marchant JH, Clark JA, Siriwardena GM, Baillie SR, 2002. The Migration Atlas: Movements of the Birds of Britain and Ireland, T, AD, Poyser London UK, 884 pp.

Wetlands International, 2002. Waterbird Population Estimates - Third Edition, Wetlands International Global Series No, 12, Wageningen The Netherlands, 226 pp,

Wetlands International. International Wader Study Group (in prep), Atlas of wader populations in Africa and western Eurasia, Wetlands International and International Wader Study Group.

Whaley DJ, Dawes JC, 2003. Cyprus Breeding Bird Atlas, BirdLife Cyprus Cyprus.

Wolf PU, Uhl W, Gerst S, Wolf C, Gerst K, Klopries M, Teifke JP, Klopfleisch R, Harder T, Werner O, Hoffmann B, Starick E, Mundt E, Beer M, Mettenleitner T, 2006. Letal verlaufende Influenza bei Hauskatzen nach natürlicher Infektion mit H5N1/Asia in Deutschland. Deutsches Tierärzteblatt 54(4): 426-431.

Wright PF, Webster, RG Orthomyxoviruses, In: Knipe DM Howly PM eds, Fields Virology, Fourth edition Philadelphia: Lippincott Williams, Wilkins 2001, 47:1533-1579.

Xu X, Subbarao, Cox NJ, Guo Y, 1999. Genetic characterization of the pathogenic influenza A/Goose/Guangdong/1/96 (H5N1) virus: similarity of its hemagglutinin gene to those of H5N1 viruses from the 1997 outbreaks in Hong Kong. Virology 261(1): 15-19.

Yeatman-Berthelot D, 1991. Atlas des Oiseaux de France en Hiver, [Atlas of birds in France in winter], Paris France.

Yeatman-Berthelot D, Jarry G, 1994. Nouvel Atlas des Oiseaux Nicheurs de France 1985-1989. [New Atlas of Breeding Birds in France], Société Ornithologique de France Paris France.

20. Authors

The members of the Working Group which authored this report were:

Dirk U. Pfeiffer (Chairman)
Royal Veterinary College,
University of London,
London, United Kingdom

Ian Brown
Community Reference Laboratory for Avian influenza,
Central Veterinary Laboratory,
New Haw, Addlestone,
Surrey, United Kingdom

Ron A.M. Fouchier
Department for Virology,
Erasmus MC,
Dr. Molewaterplein,
Rotterdam, The Netherlands

Nicolas Gaidet
CIRAD EMVT,
Agricultural Research Centre for International Development,
Gestion intégrée de la faune,
Campus international de Baillarguet,
Montpellier, France

Vittorio Guberti
Istituto Nazionale Fauna Selvatica,
Via Ca' Fornacetta 9,
Ozzano E.,
Bologna, Italy

Timm Harder
Friedrich-Loeffler-Institut,
Boddenblick 5a,
Greifswald – Insel Riems, Germany

Rowena Langston
Conservation Science Department,
Royal Society for the Protection of Birds (RSPB),
The Lodge,
Sandy, Bedfordshire, United Kingdom

Ricardo Jorge Soares Magalhaes
Royal Veterinary College,
University of London,
London, United Kingdom

Vincent Martin
Food and Agriculture Organisation (FAO),
AGAH-FAO Animal Production and Health Service,
Viale delle Terme di Caracalla,
Rome, Italy

James Michael Sharp
Department of Pathology,
Veterinary Laboratories Agency,
Penicuik, United Kingdom

Katharina Stärk
Swiss Veterinary Service,
Bern, Switzerland

David Stroud
UK Joint Nature Conservation Committee,
Monkstone House, City Road,
Peterborough, United Kingdom

Bogdan Szewcyk
Department of Molecular Virology Intercollegiate Faculty of Biotechnology,
University of Gdansk & Medical University of Gdansk,
Ulica Kladki,
Gdansk, Poland

Jan Veen
Wetlands International,
Wieselseweg 110,
Wenum Wiesel, The Netherlands

Jonas Waldenström
Department of Animal Ecology
Ecology Building,
Lund University,
Lund, Sweden

21. Acknowledgments

The scientific co-ordination for this Scientific Report 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.

DG Environment, in particular Mr Michael O'Briain, is specifically acknowledged for collaborating closely during the preparation of chapters 11 and 13.

The following experts are also acknowledged for having contributed to the work of the Working Group:

Ward Hagemeier
Wetlands International

François Moutou
AFSSA LERPAZ,
Epidemiology Unit,
22 rue Pierre Curie,
Maisons-Alfort Cedex,
France

Bjorn Olsen
Biology and environmental Sciences,
Institute for Zoonotic Ecology and Epidemiology,
Kalmar University,
Sweden

Thanks to Mirzet Sabirovic (Department for Environment, Food and Rural Affairs, UK), Peter Cranswick and Rebecca Lee (Wildfowl & Wetlands Trust, UK) for permission to further develop their initial listings of high risk species (Chapter 11/Annex 2) and Andy Musgrove (BTO, UK) initially assessed risk of contact for UK waders. Thanks to Ian Fisher (RSPB, UK) for extracting data from the BirdLife International World Bird DataBase and produced Figure 11.13 depicting mixing and concentration areas.

We gratefully acknowledge the British Trust for Ornithology for permission to reproduce figures from the BTO's Migration Atlas (Wernham et al. 2002).

We are grateful to a number of the members of the Ornis Committee's Scientific Working Group who kindly provided assessments of the risk of contact between wild birds and poultry. These include David Lacina (Czech Republic), Philip Buckley (Ireland) and Andres Kuresoo (Estonia) and to Micheal O'Briain for facilitating this.

Ilya Maclean (British Trust for Ornithology) kindly collated the information on national information sources presented in Table 13.2.

22. AHAW Scientific Panel Members

This Scientific Report was peer-reviewed by the Members of the European Food Safety Authority's Scientific Panel for Animal Health and Welfare (AHAW) and used as the basis for a Scientific Opinion. The Members of the AHAW Scientific Panel were:

Bo Algers
Department of Animal Environment and Health,
Swedish University of Agricultural Sciences,
Skara,
Sweden

Harry J. Blokhuis
Animal Sciences Group,
Wageningen University and Research Centre,
Lelystad,
The Netherlands

Donald Maurice Broom
Department of Clinical Veterinary Medicine,
University of Cambridge,
Cambridge,
United Kingdom

Ilaria Capua
Istituto Zooprofilattico Sperimentale delle Venezie,
Legnaro, Padova,
Italy

Stefano Cinotti
Facolta di Medicina Veterinaria Alma Materstudiorum,
Università di Bologna,
Bologna,
Italy

Michael Gunn
Department of Agriculture and Food,
Veterinary Research Laboratory,
Dublin,
Ireland

Jörg Hartung
Institute for Animal Hygiene, Animal Welfare and Behaviour of Farm Animals,
University of Veterinary Medicine Hanover,
Hanover,
Germany

Per Have
Danish Institute for Food and Veterinary Research,
Copenhagen,
Denmark

Xavier Manteca Vilanova
School of Veterinary Science,
Universitat Autònoma de Barcelona,
Barcelona,
Spain

David B. Morton
Biomedical Services Unit,
University of Birmingham,
Birmingham,
United Kingdom

Michel Pépin
Laboratoire d'Etudes et de Recherches sur les Petits Ruminants et les Abeilles, Agence
Française de Securité Sanitaire des Aliments (AFSSA),
Sophia Antipolis,
France

Dirk Udo Pfeiffer
Royal Veterinary College,
University of London,
London,
United Kingdom

Ronald John Roberts
University of Stirling,
Stirling,
United Kingdom

José Manuel Sánchez Vizcaino
Facultad de Veterinaria,
Universidad Complutense de Madrid,
Madrid,
Spain

Alejandro Schudel
Office International des Epizooties,
Paris,
France

James Michael Sharp
Department of Pathology,
Veterinary Laboratories Agency,
Penicuik,
United Kingdom

Georgios Theodoropoulos
Department of Anatomy and Physiology of Farm Animals,
Faculty of Animal Science,
Agricultural University of Athens,
Athens,
Greece

Philippe Vannier
Poultry and Swine Research Laboratory,
Agence Française de Securité Sanitaire des Aliments (AFSSA),
Ploufragan,
France

Marina Verga
Facoltà di Medicina Veterinaria,
Università di Milano,

Milano,
Italy

Martin Wierup
Department of Biomedical Sciences and Veterinary Public Health,
Swedish University of Agricultural Sciences,
Uppsala,
Sweden

Marion Wooldridge
Centre for Epidemiology and Risk Analysis,
Veterinary Laboratories Agency,
Weybridge,
United Kingdom

23. Annexes

Annex 1 - Different types of bird movements

Seasonal migration is the annual movement between breeding areas and those areas, typically more southerly, that are used at other times of the year. Northwards movements peak in spring (the return to breeding grounds) and autumn (post-breeding migration to wintering areas). The exact timing and stopover sites used vary between species, although often broad migration flyways are recognised. Within these broad flyways, there may be differences in the routes taken in autumn and spring (**loop-migration**).

Leap-frog migration entails the overflight of more southerly breeding populations by more northerly breeding populations to reach their wintering grounds. In some cases there may be a body size difference linked to the different latitudes at which breeding occurs. This is well-illustrated by the Redshank in that the Icelandic race *Tringa totanus robusta* which winters furthest north in north-western Europe is larger than the race that breeds in northern Fennoscandia *T. t. totanus,* but occupies the most southerly wintering grounds extending to west Africa (Clark in Wernham et al. 2002; Figure 23.1).

Figure 23.1. An example of leap-frog migration. Winter ranges of Redshank Tringa totanus from (1) Iceland, (2) Britain and Ireland, (3) Denmark, Germany, the Netherlands and Belgium, (4) Sweden and Norway, and (5) Hungary, showing leap-frog migration of northern populations of larger birds. Source Hale 1973 (reproduced with acknowledgement from Bairlein et al. 2002).

Among migratory species there are different strategies, geese and swans usually migrate from their breeding grounds as family groups and remain together on the wintering grounds. In most waders (shorebirds), adults migrate before juveniles and there are differences in the timing of migration by the adult male and adult female, one of the pair remaining to care for dependent chicks (this parental care is undertaken by the male in some and by the female in other wader species).

Migration to breeding areas is often highly synchronised, especially in those species which breed in the high arctic, where the short breeding season makes time a critical commodity. The return migration to wintering grounds is staggered, with failed breeders often leaving early, whilst recently fledged juveniles leave later than breeding adults, for example in the case of shorebirds. Juvenile dispersal often entails, what are considered to be, exploratory flights by young birds, providing them with information that will enhance their future survival and productivity. Furthermore, immature birds may remain on the wintering grounds during the breeding season, or migrate to intermediate sites along the flyway, not returning to the breeding areas until ready to breed.

In waterbirds, it takes several years for birds to reach breeding maturity, for example up to five or more years in the Greenland White-fronted Goose *Anser albifrons flavirostris*. There may be only a very short period of time at the wintering locations when migratory birds are absent or occur in very low numbers. Although interchange between sites occurs, there is a high degree of site fidelity to wintering and breeding areas in particular, by many species, once young birds have selected a site.

Migration flights may be on a broad front, with many parallel migration streams over a large geographical area, as is generally considered to be the case for passerines. For large, soaring species in particular, migratory bottlenecks occur, narrow corridors where birds concentrate to take advantage of a short sea crossing or mountain pass to facilitate crossing a physical barrier along their route. Migration may be undertaken in a single flight, or a series of flights, with stopover sites along the way used to refuel. The strategy used depends on the distance, species and ability to carry fat reserves to fuel flight.

Inter-annual and seasonal fluctuations in food availability may trigger large-scale movements or irruptions, most notably in many seed or fruit-eating passerines, but also in birds of prey that feed on small mammals that undergo population cycles, *e.g.* lemmings.

Moult migrations are undertaken by some bird species, notably waterbirds such as Shelduck *Tadorna tadorna* (Salomonsen 1968; Figure 23.2). During the annual moult of the wing feathers, these species become flightless and so more vulnerable to predation, necessitating a safe moulting site and rich food supply. Typically, these are either at higher latitudes, or sometimes higher altitudes.

Figure 23.2. An example of moult migration. Movements (lines and recovery locations (points) of Canada Geese Branta canadensis that have been present in the Beauly Firth north-east Scotland. Many moulting birds in the Beauly Firth breed in North Yorkshire, England, but birds also migrate to the Firth to moult from other locations in Britain. (Source: BTO data, reproduced with acknowledgement from Bairlein et al. 2002).

Cold-weather movements are triggered by cold weather, for example freezing conditions that make food incessible, as birds move in search of less severe conditions (Ridgill and Fox 1990). Several species, notably wildfowl and shorebirds, that are noted for making cold weather movements, for example Eurasian Wigeon *Anas penelope*, Common Teal *Anas crecca*, Mallard *Anas platyrhynchos*, Tufted Duck *Aythya fuligula* and Northern Lapwing. Such movements are entirely dependent on periods of severe weather to trigger them and so, although associated with winter, the precise timing and frequency in any one winter varies. Cold weather movements are characterised by influxes of large numbers of birds to milder climes (*e.g.* Figure 23.3).

Figure 23.4 shows those European regions (50 x 50 km squares) that showed net influxes of nine species of waterbirds in severe cold winters (Ridgill and Fox 1990).

Figure 23.3. Areas of 50 x 50 km squares that were identified as refuges in periods of severe cold weather (1967-1986) for Shelduck Tadorna tadorna, Wigeon Anas penelope, Teal Anas crecca, Mallard Anas platyrhynchos, Pintail Anas acuta, Shoveler Anas clypeata, Pochard Aythya ferina, Tufted Duck Aythya fuligula and Coot Fulica atra. Source: Ridgill and Fox 1990.

Figure 23.4. An example of cold weather movements (Ridgill and Fox 1990). European distribution of Shoveler Anas clypeata in two contrasting winters. January 1984 (left map) was mild and there were major concentrations in The Netherlands and Brittany. January 1985 (right map) was severely cold and major shifts of distribution from these areas to Spain occurred.

Annex 2 – Reported recoveries of Asian lineage H5N1 HPAIV in selected wild bird orders

DAS_HRS trial 04 -
DAS 23 Feb 06.xls

Annex 3 - Sampling for laboratory testing

To prepare samples for influenza virus detection, a clean cotton swab is inserted approximately 5 mm into the cloaca of a bird, and then gently turned to moisture the cotton swab. Even if there is no visible sign of faeces, the sample may contain sufficient material for analysis. The swab is then inserted into a vial of storage media and broken just above the cotton tip; this can be done easily by bending (plastic swab) or using scissors (metal swab). The vial with the cotton tip can now be closed properly, and labelled. Alternatively, faecal samples may be used for diagnostics if it is impossible or difficult to collect cloacal swabs. For liquid faeces from birds (e.g. from gulls) a cotton swab may be used to transfer faeces to the vials, and the tip of the cotton swab broken off as described above. For more solid faeces (e.g. from geese) it may be more convenient to transfer a piece of faeces using the tube and the lid itself. The swabs should be stored in appropriate storage media (e.g. Hanks balanced salt solution containing 10% glycerol, 200 U/ml penicillin, 200 mg/ml streptomycin, 100 U/ml polymyxin B sulfate, and 250 mg/ml gentamycin and immediately after collection stored at –70ºC. An unbroken cold chain from the sampling site to the laboratory is important. If this is not possible, storage at +4 C for a few days is acceptable. Repeated freeze-thawing must be avoided.

Annex 4 - Explanation of data fields used in Annex 2 spreadsheet

Order

Taxonomic Order within which the species occurs.

Common name

Most common English name of species.

Scientific name

Scientific name of species.

Occurs in Europe?

Denotes whether the species occurs in Europe: Y = yes; N = no. Europe has been defined as the EU together with immediately adjacent countries (*i.e.* including Norway, Switzerland, Romania, but excluding Turkey, Belarus, Ukraine and Russia).

Migratory?

Denotes whether the species is migratory in the sense that it crosses EU borders or otherwise moves between countries within the EU: Y = yes, N = no.

Information on migratory status and flyways is drawn principally from Scott & Rose (1996), Madsen *et al.* (1999) and Kear (2005) for Anatidae, from both Stroud et al. (2004) and Wetlands International and International Wader Study Group (in prep.) for waders, and from Snow and Perrins (1998) for gulls.

Well defined flyway system?

Distinguishes between species with a well defined migratory route and those with a more diffuse migratory pathway: Y = yes, N = no.

The assessment of degree of definition of flyway migration systems for any individual species (or population) is an expert judgement, based on the sources given above and other information, as to whether specific linkages may be made between breeding, staging and wintering areas with reasonable confidence. Such assessments are largely informed by information from ringing (*e.g.* the national ringing atlases listed in Table 13.2 or other types of marking such as the use of satellite telemetry for some species.

Gregariousness during migration/wintering

Gregariousness has been indicated by two letters, which denote group size and group density, respectively. The following coding has been applied:

Group size

L = Large: often several hundreds to thousands of individuals (Eurasian Wigeon *Anas penelope*)

M = Medium: often several tens to few hundred individuals (Whooper Swan *Cygnus cygnus*)

S = Small: often up to a few tens of birds (Purple Sandpiper *Calidris maritima*)

O = Usually solitary or a few birds together (Green Sandpiper *Tringa ochropus*)

Density

H = High density: often less than 2 m between individuals (Dunlin *Calidris alpina*)

M = Medium density: often between 2-5 m between individuals (Herring Gull *Larus argentatus*)

L = Low density: often more than 5 m between individuals (Common Snipe *Gallinago gallinago*)

O = (near) solitary

Degree of mixing during migration/wintering

Degree of mixing with other species (mixed foraging, mixed roosts, mixing at moulting areas, *etc.*) has been indicated as follows:

H = High degree (Eurasian Wigeon)

M = Medium degree (Northern Lapwing *Vanellus vanellus*)

L = Low degree (Temminck's Stint *Calidris temminckii*)

O = Hardly any mixing (Common Sandpiper)

Main habitat during migration/wintering

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.

Examples of codes used are listed below. They should all be read as “the species mainly uses ....” :

A = agricultural land

N = natural land habitat (usually marshes near wetlands; this coding has especially been used to distinguish purely freshwater species, which rarely come ashore (F), from those who also use non-agricultural land habitat (FN))

O = other habitat (variety of habitat types, including woodland, urban areas, *etc.*)

F = fresh water

M = marine

L = littoral

sal = salinas

As a rule codes indicate the “main habitat” used. In case various habitats are used multiple coding has been applied. Examples of codes used are listed below. They should all be read as “the species mainly uses ....” :

A - agricultural land (Rook *Corvus frugilegus*)
AN - agricultural land and natural land habitat (Eurasian Golden Plover *Pluvialis apricaria*)
FA - freshwater and agricultural land (Greater White-fronted Goose *Anser albifrons*)
FAL - freshwater, agricultural land, littoral zone (Black-headed Gull *Larus canus*)
F - freshwater (Tufted Duck *Aythya fuligula*)
FL - freshwater and littoral zone (Common Sandpiper *Tringa hypoleucos*)
FM - freshwater and marine (Common Goldeneye *Bucephala clangula*)
FN - freshwater and natural land habitat (Marsh Sandpiper *Tringa stagnatilis*)
L - littoral zone (Red Knot *Calidris canutus*)
LA - littoral zone and agricultural land (Brent Goose *Branta bernicla*)
M - marine (Common Scoter *Melanitta nigra*)
MA - marine and agricultural land (Mediterranean Gull *Larus melanocephalus*)
MF - marine and freshwater (Greater Scaup *Aythya marila*)
ML - marine and littoral (Glaucous Gull *Larus hyperboreus*)
O - other land habitat (Eurasian Woodcock *Scolopax rusticola*)
Sal - salinas (Greater Flamingo *Phoenicopterus ruber*)

Risk of contact with domesticated poultry in the EU

On the basis of knowledge of ecology and behaviour of waterbirds, the likelihood of close contact between the species concerned and domesticated/captive poultry has been assessed as:

0	Zero or virtually zero risk
L	Theoretical but low risk
M	Medium risk species
H	Higher risk species

This assessment has considered risk as a function of contact intensity. Thus a scenario where small numbers of wild birds are potentially in contact with poultry for a long period is considered equivalent to a scenario where larger numbers are in contact for a shorter period. Independent assessments of risk of contact were sought from the members of the Scientific Working Group of the EC Birds Directive's Ornis Committee. Responses were consolidated with those of this Working Group's ornithologists to produce a final evaluation.

Species defined as "higher risk" in Commission Decision 2005-726

Species which were included in a preliminary list of "higher risk species" for Europe, related to the outbreak areas in SW Siberia, Northern Kazakhstan and the area south of the Urals, in September 2005 and which were adopted by the European Commission (Decision 2005-726).

H5N1 confirmed

Species, from all over the world, for which H5N1 HPAIV has been confirmed. The status of the infected individuals has been indicated in different columns (Wild, Domestic, Captive, Experimental) and references have been given. Codes in columns: Y = H5N1 HPAIV confirmed, no further details; dead = infected bird found dead; live = infected bird found/shot alive.

Note that many of the species listed as having been infected by Asian lineage H5N1 relate to single instances of birds having been found dead. There remains no good information as to the extent of infection of wild birds with H5N1 HPAIV in SE Asia or elsewhere.

Information was taken largely from the listing of the US Geological Service1 developed and updated by Mirzet Sabirovic (Department for Environment, Food and Rural Affairs, UK), Peter Cranswick and Rebecca Lee (Wildfowl & Wetlands Trust, UK).

Annex 5 - Information on population sizes and distribution of migratory species currently more likely to expose poultry in the EU to H5N1 HPAIV

A wide range of information exists on the population sizes and distributions of European birds. Distributions of all European breeding bird species are mapped by Hagemeijer and Blair (1997), whilst Snow and Perrins (1998) present maps showing year-round distributions of all species. For Anatidae, Scott and Rose (1996) show breeding and non-breeding distributions together with key sites. More detailed data and information are presented for each European goose population by Madsen et al. (1999).

Population data are tabulated by country for all European bird species by Heath et al. (2000), updated by BirdLife International (2004). Detailed information on the population sizes (by country) of wader populations in Africa and Western Eurasia is given by Stroud et al. (2004), whilst Thorup (2005) presents updated population estimates for some European breeding waders.

Most recent information on the sizes of biogeographic (international) population sizes of waterbirds is collated by Wetlands International and published in *Waterbird Population Estimates* (most recently in Wetlands International 2002).

Sources of information on key sites for species more likely to expose poultry in the EU to H5N1 HPAIV

Heath and Evans (2000) presented summary information on all Important Bird Areas in Europe with listings of the major species occurring on each site (see also section 11.2 on concentration and mixing areas).

Most European countries publish periodic (often annual) summaries of national waterbird monitoring schemes. These typically summarise important sites for each waterbird species. Most recent national sources of data and information are given in Table 23.1.

Table 23.1. Recent national sources of information on the distribution of breeding birds and important sites for non-breeding waterbirds in Europe

Country	*National breeding bird atlas*	*Most recent waterbird monitoring review and/or site inventory*	*Web sources*
Austria	Brader et al. 2003 Dvorak et al. 1993	Brader 1996	http://www.robbsnet.com/rbwintee.htm
Belgium	Devillers et al. (eds). 1988	Devos in press	http://www.natuurpunt.be/ http://www.aves.be/atlas_brux/atlasbrux.htm http://www.aves.be/surbru.html
Bulgaria	Nikolov and Vassilev 2004	Michev and Profirov 2003 Dimitrov et al. 2005 Chernichko and Kostyushin 2003	http://www.pomonet.bg/bourgaslakes/en/monitoring.html http://www.bspb.org/
Cyprus	Whaley and Dawes 2003		http://www.birdlifecyprus.org/
Czech Republic	Sťastný et al. 1996	Aubrecht et al. 1994	http://www.birdlife.cz/
Denmark	Dybbro 1976	International Wadden Sea: Blew & Südbeck 2005 Laursen et al. 1997 NERI 1995 Helsinki Commission 2004	http://www.dmu.dk/International/ http://www.waddensea-secretariat.org
Estonia	Renno 1993	Helsinki Commission 2004 NERI 1995	http://www.eoy.ee/atlas/index.html http://www.eoy.ee/
Finland	Väisänen *et al.* 1998	Helsinki Commission 2004 NERI 1995	http://www.birdlife.fi/
France	Yeatman-Berthelot and Jarry 1994 Yeatman-Berthelot 1991	Deceuninck 2005	http://www.oncfs.gouv.fr/ http://www.lpo.fr/
Germany	Baur et al. (in prep.) A Breeding Bird Atlas for Germany	International Wadden Sea: Blew & Südbeck 2005 Blew et al. 2005 Wahl et al. 2004 Helsinki Commission 2004 NERI 1995	http://www.vogelmonitoring.de/ http://www.nabu.de/ http://www.waddensea-secretariat.org
Greece			http://www.ornithologiki.gr/en/enmain.htm
Hungary			http://www.mme.hu/

Country	***National breeding bird atlas***	***Most recent waterbird monitoring review and/or site inventory***	***Web sources***
Ireland	Lack 1986 (winter) Gibbons et al. 1993	Colhoun and Newton 2000 Crowe and Boland 2004 Crowe 2005	www.birdwatchireland.ie
Italy	Meschini & Frugis 1993	Baccetti et al. 2002	http://www.lipu-uk.org/
Latvia	Priednieks et al. 1989	Helsinki Commission 2004 NERI 1995	http://www.lob.lv/
Lithuania	Lithuanian Ornithological Society (in prep.)	NERI 1995 Švažas et al. 2003 Stanevičius 2003) Helsinki Commission 2004	http://www.birdlife.lt/
Malta	BirdLife Malta (in prep.)		http://www.birdlifemalta.org/
Norway	Gjershaug et al. 1994 Bakken et al. 2003		http://folk.uio.no/csteel/nof/
Poland	Walasz 2000	NERI 1995 Helsinki Commission 2004	http://www.otop.org.pl/
Portugal	Bolton 1987 Rufino 1989 Elias et al. 1999 Vowles and Vowles 1994		http://www.spea.pt/
Romania	Weber et al. 1994	Chernichko and Kostyushin 2003	http://www.sor.ro/
Slovakia			http://www.birdlife.org/worldwide/national/slovakia/index.html
Slovenia	Sovinc 1994		http://www.ptice.org/
Spain	Martí (2003)	Velasco and Alberto 1993	http://www.seo.org/
Sweden	Risberg 1990 Fransson and Pettersson 2001	NERI 1995 Helsinki Commission 2004	http://www.nrm.se http://www.sofnet.org/
Switzerland	Schmidt et al. 1998		http://www.vogelwarte.ch/ http://www.birdlife.ch/

Country	*National breeding bird atlas*	*Most recent waterbird monitoring review and/or site inventory*	*Web sources*
The Netherlands	SOVON 2002 SOVON 1992	International Wadden Sea: Blew and Südbeck (2005) van Roomen et al. 2005 van Roomen et al. 2004 Berrevoets et al. 2002	http://www.waddensea-secretariat.org http://www.sovon.nl/ http://www.rikz.nl/home/NL/
United Kingdom	Lack 1986 (winter) Gibbons et al. 1993	Collier et al. 2005 Maclean et al. 2005	http://www.bto.org/survey/webs/index.htm http://blx1.bto.org/webs/alerts/index.htm

Annex 6 - Information on movements of migratory species currently more likely to expose poultry in the EU to H5N1 HPAIV

Recent publications which summarise movements of waterbirds migrating to or from Europe are summarised in Table 23.2.

Table 23.2. Atlases of movements of birds to or from Europe[6]

Country or region	*National atlas*
Belgium	Roggeman et al. 1995
Greenland	Lyngs 2003
Ireland	Wernham et al. 2002
Norway	Bakken et al. 2003
Southern Africa	Underhill et al. 2002
Sweden	Fransson and Pettersson 2001
United Kingdom	Wernham et al. 2002

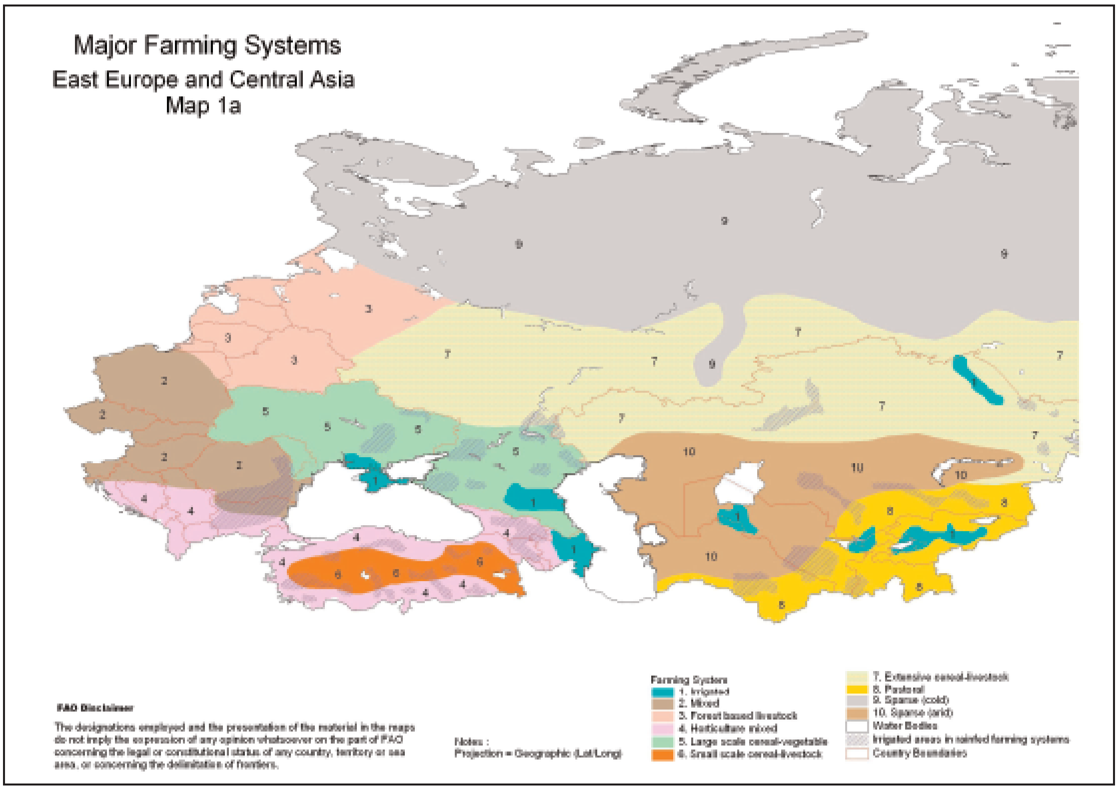
EURING is an international federation of European national ringing schemes. It established and continues to harmonise the standards for national ringing schemes in order to aid the ready exchange and analyses of bird ringing data at European scale. It maintains a database of all European bird ringing recoveries, which is currently hosted by the British Trust for Ornithology.

The European Commission (DG Environment) has contracted to EURING the analysis of data holdings so as to provide information related to the movements of species more likely to expose poultry in the EU to H5N1 HPAIV. These analyses will be published in spring 2006 and the current document could then be updated.

---

[6] Information on planned atlases is given at http://www.euring.org/research/migration_atlases/index.htm

Figure 8. 1. *Farming systems in East European and Central Asian countries*

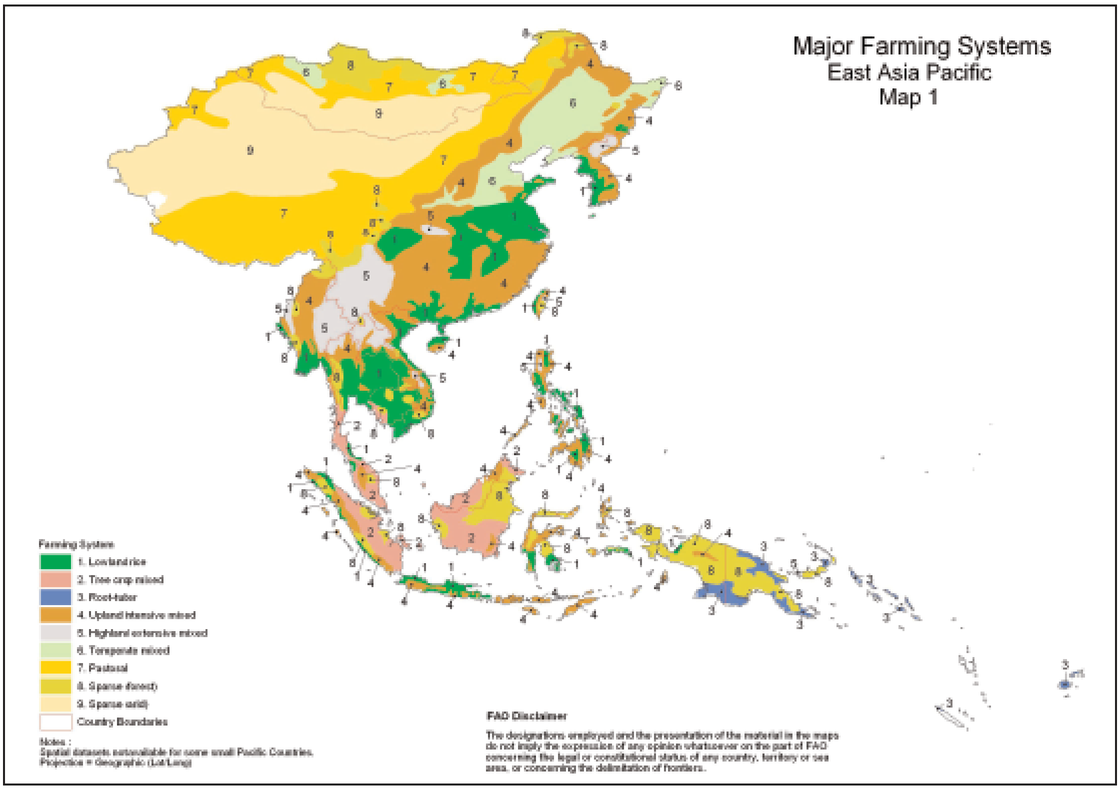


FAO Disclaimer

The designations employed and the presentation of the material in the maps do not imply the expression of any opinion whatsoever on the part of FAO concerning the legal or constitutional status of any country, territory or sea area, or concerning the delimitation of frontiers.

Notes :
Projection = Geographic (Lat/Long)

Figure 8.2. *Farming systems in South-East and East Asian countries*



Notes :
Spatial datasets notavailable for some small Pacific Countries.
Projection = Geographic (Lat/Long)

FAO Disclaimer

The designations employed and the presentation of the material in the maps do not imply the expression of any opinion whatsoever on the part of FAO concerning the legal or constitutional status of any country, territory or sea area, or concerning the delimitation of frontiers.

Figure 8.3. Farming systems in the Middle Eastern and North African countries

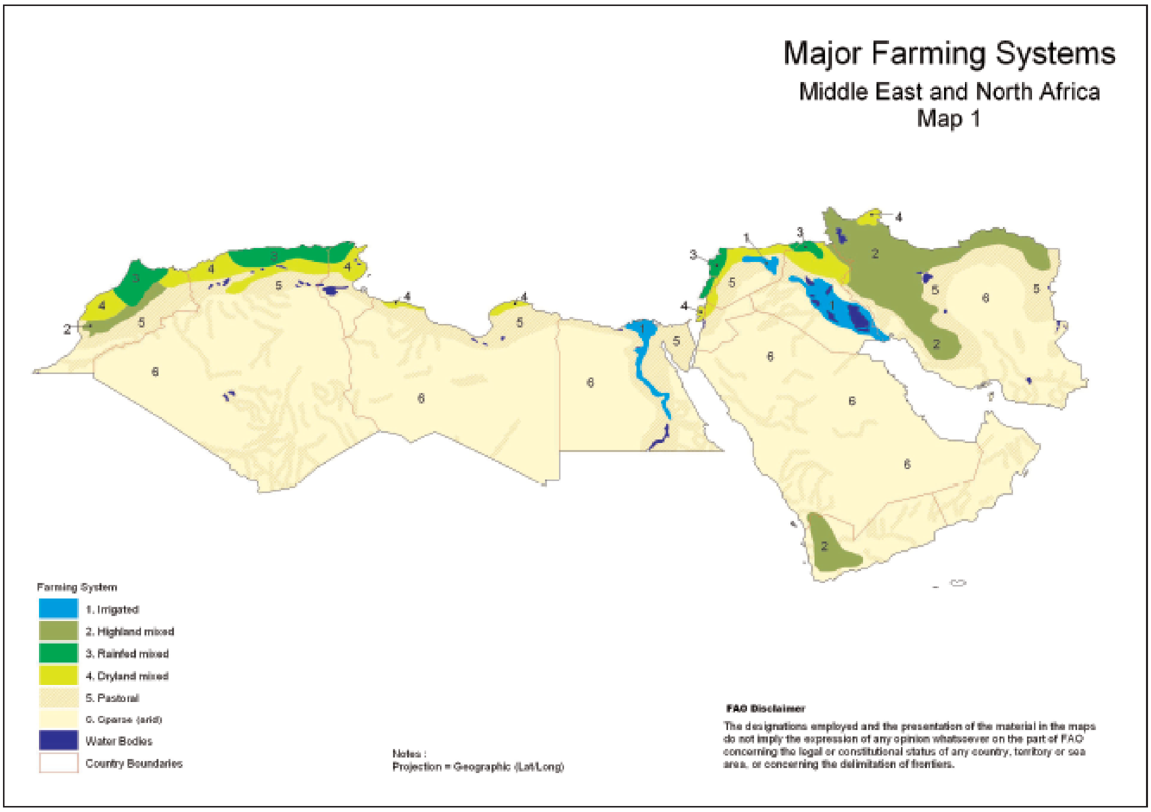


Figure 8.4. Major farming systems in the sub-Saharan African countries

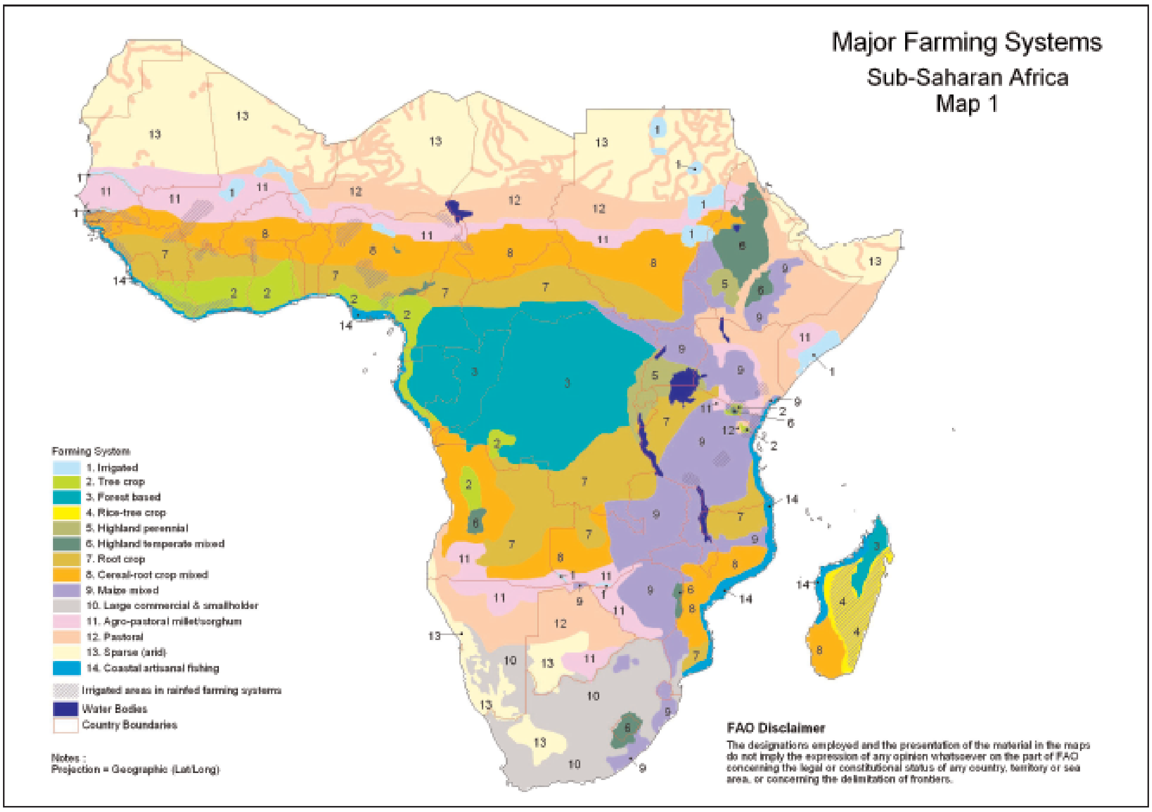


***Figure.8.5** Estimated spatial distribution of poultry density for 2005 in eastern European and Middle Eastern countries*

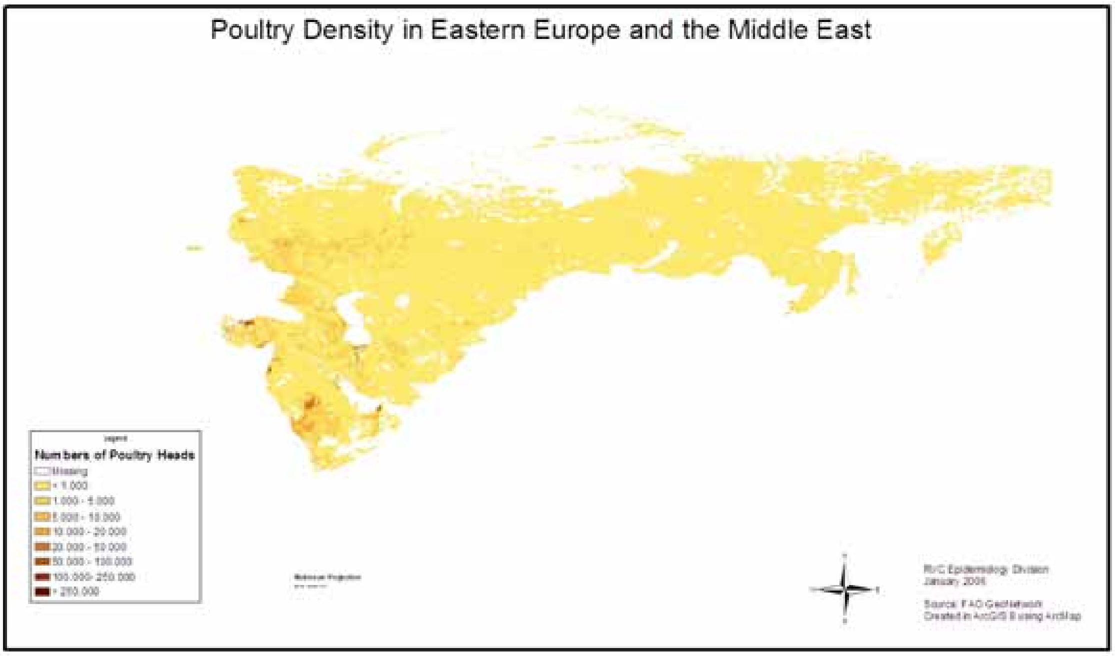


***Figure 8.6** Estimated spatial distribution of poultry density for 2005 in Asian countries*

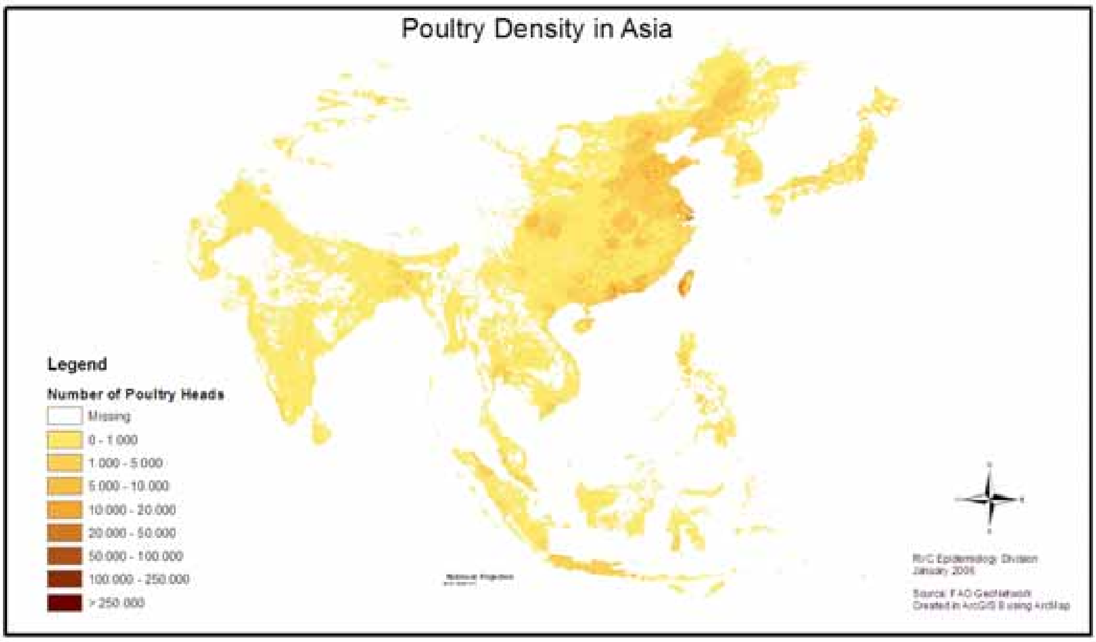


Figure 8.7. Estimated spatial distribution of poultry density for 2005 in African countries

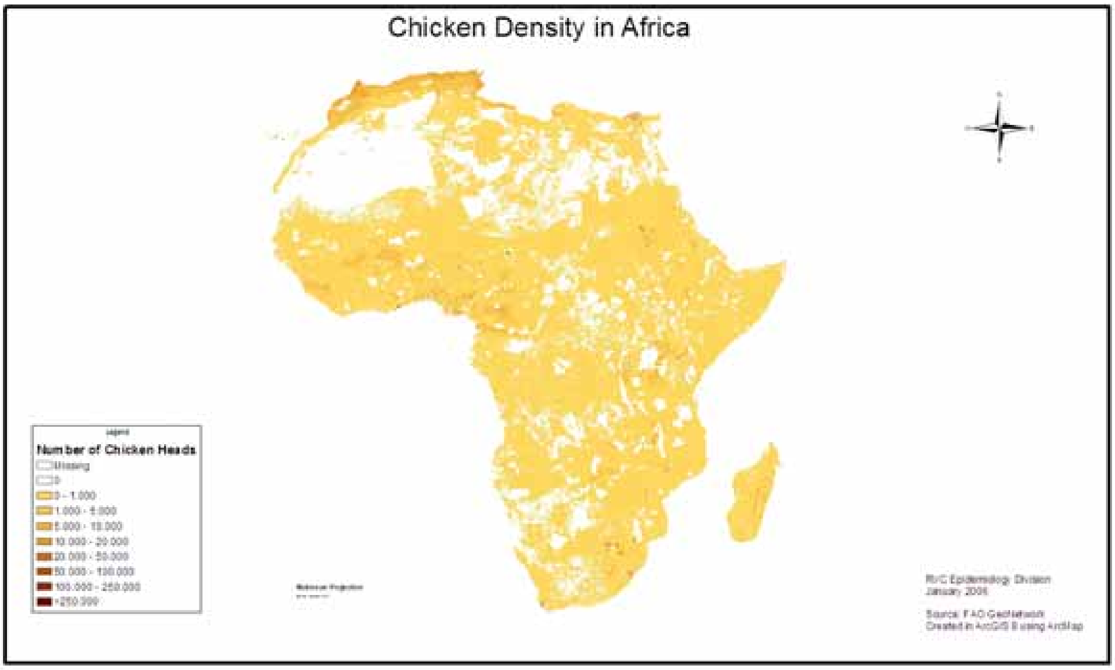


Figure 11.1. Different types of migratory strategy shown by waders moving from coastal west Africa to (sub-)arctic breeding grounds: (from left to right) by turnstone Arenaria interpres ('hop'), dunlin Calidris alpina & Redshank Tringa totanus ('skip') and red knot Calidris canutus & bar-tailed godwit Limosa lapponica ('jump'). Source: Piersma 1987.

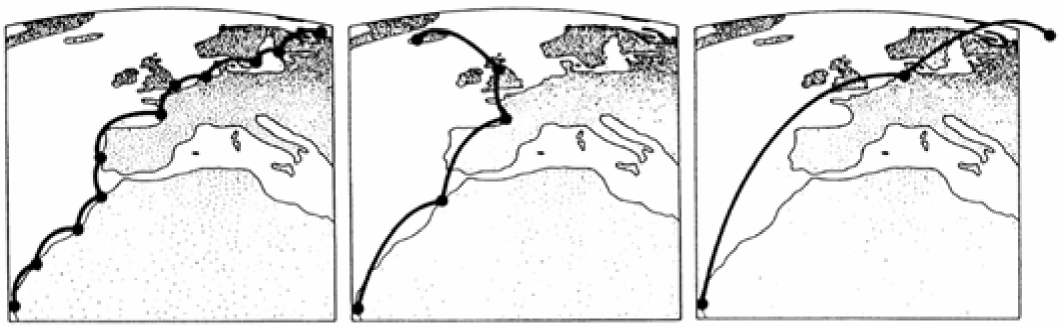


Figure 11.2. *Flyways for white storks Ciconia ciconia as described by the locations of ringing recoveries. (Source: Bairlein et al. (2002) updating Fiedler 1998).*

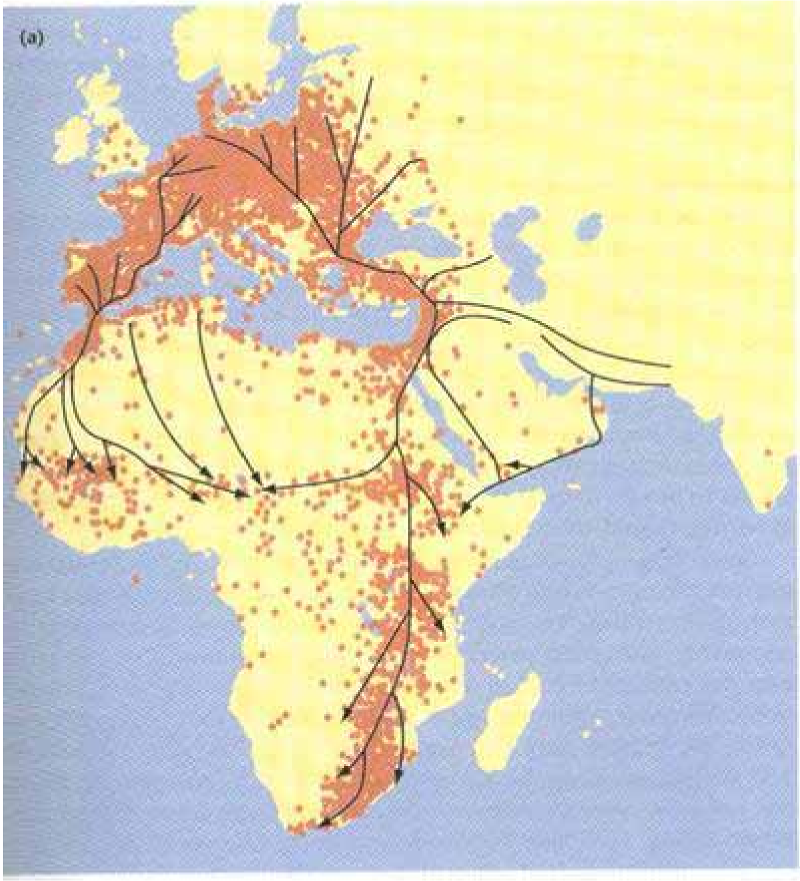


Figure 11.3. *Summary map of the global, multi-species, wader flyways. (Source: International Wader Study Group 1998).*

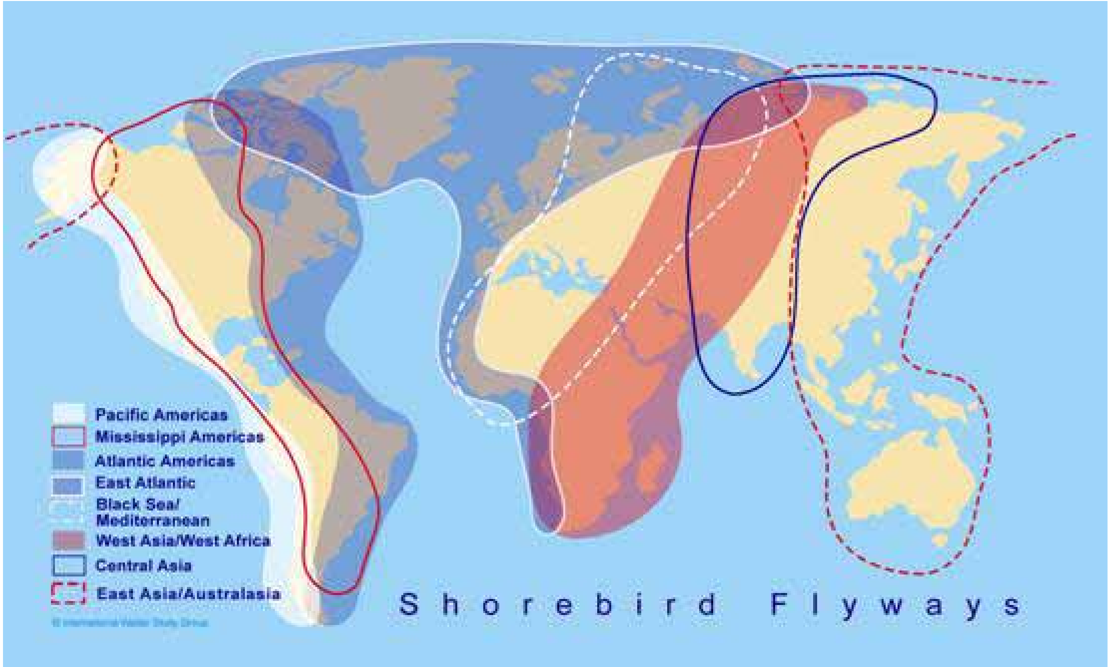


***Figure 11.4.** Examples of three different species' flyways within the East Atlantic Flyway, showing broad migration routes from northern breeding areas to over-wintering sites in Europe and Africa. Left to right, kentish plover Charadrius alexandrinus, red knot Calidris canutus and sanderling Calidris alba. Source: Smit and Piersma (1998).*

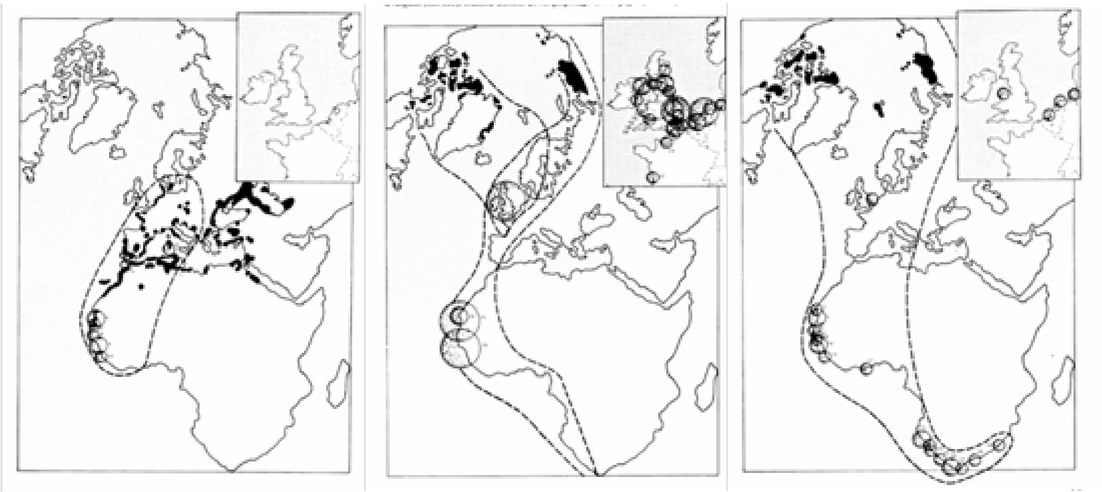


***Figure 11.5.** The four major flyways for Anatidae in western Eurasia as described by Isakov (1967). 1. Northern White Sea/North Sea population; 2. European Siberia/Black Sea-Mediterranean population; 3. West Siberian/Caspian/Nile population; and 4. Siberian-Kazakhstan/Pakistan-India population. Note that this excluded flyway linkages with Canada and Greenland - important for several goose populations.*

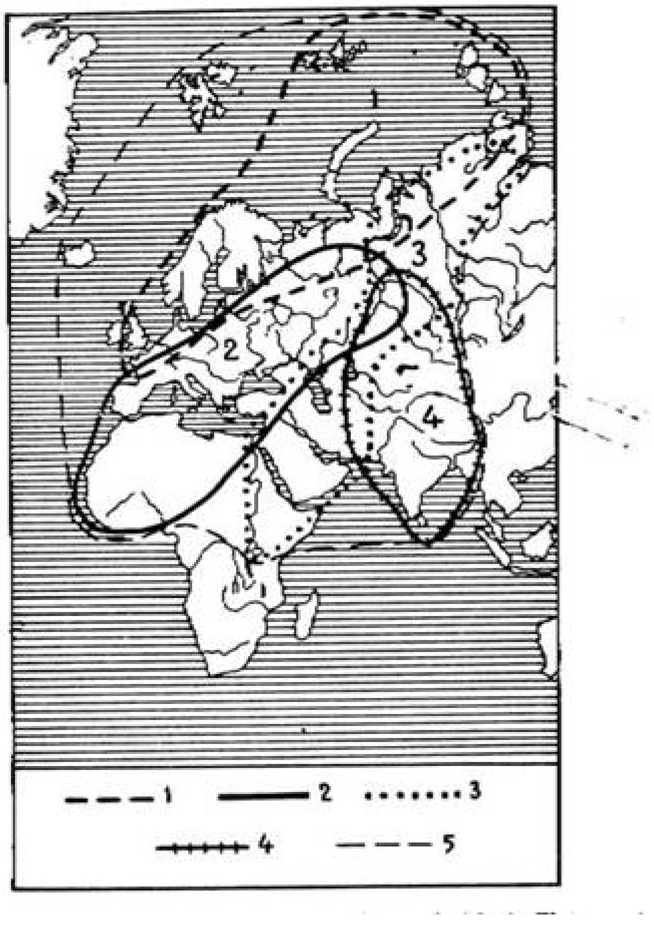


Figure 11.6. An example of broad-front migration of Wheatears Oenanthe oenanthe ringed as nestlings along parallel migration routes within Europe. Lines join ringing and recovery sites. Reproduced with acknowledgement from Bairlein et al. (2002).

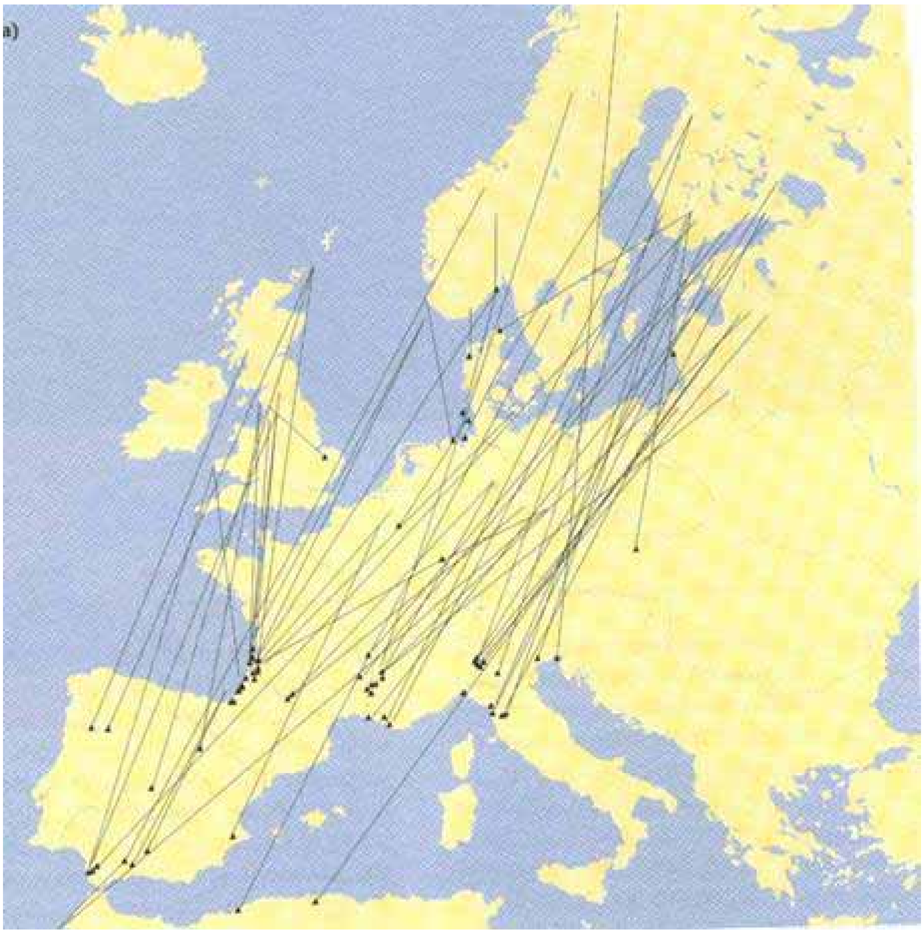


Figure 11.7. *Many birds undergo complex movements between different sites outside migratory periods: ringing has shown that Dunlin Calidris alpina move extensively between different European coastal areas within the non-breeding period. Summary of late autumn (post-moulting) movements for which ringing studies found direct evidence. (Lines do not indicate actual routes between areas. (Source: Pienkowski and Pienkowski 1983).*

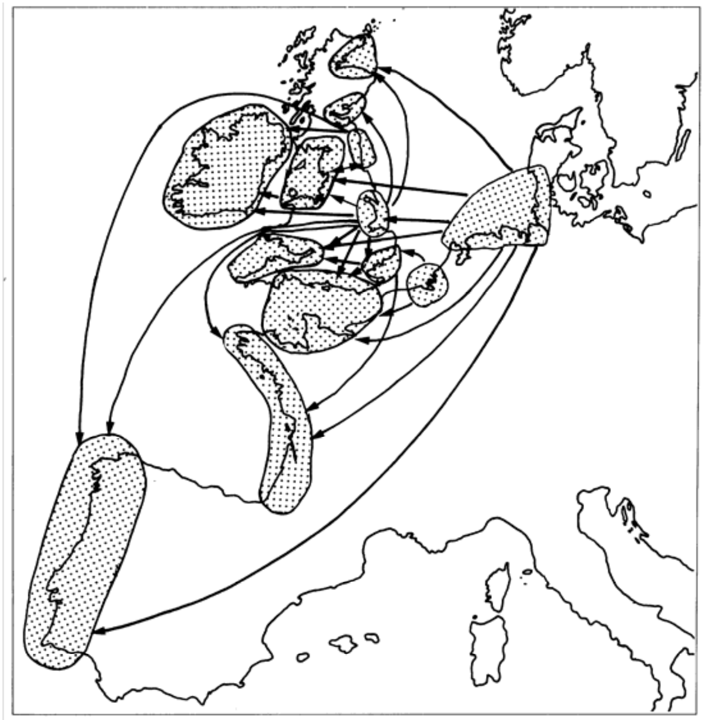


Figure 11.8. *Square areas of 50 x 50 km that were identified as refuges in periods of severe cold weather (1967-1986) for Shelduck Tadorna tadorna, Wigeon Anas penelope, Teal Anas crecca, Mallard Anas platyrhynchos, Pintail Anas acuta, Shoveler Anas clypeata, Pochard Aythya ferina, Tufted Duck Aythya fuligula and Coot Fulica atra. (Source: Ridgill and Fox 1990).*

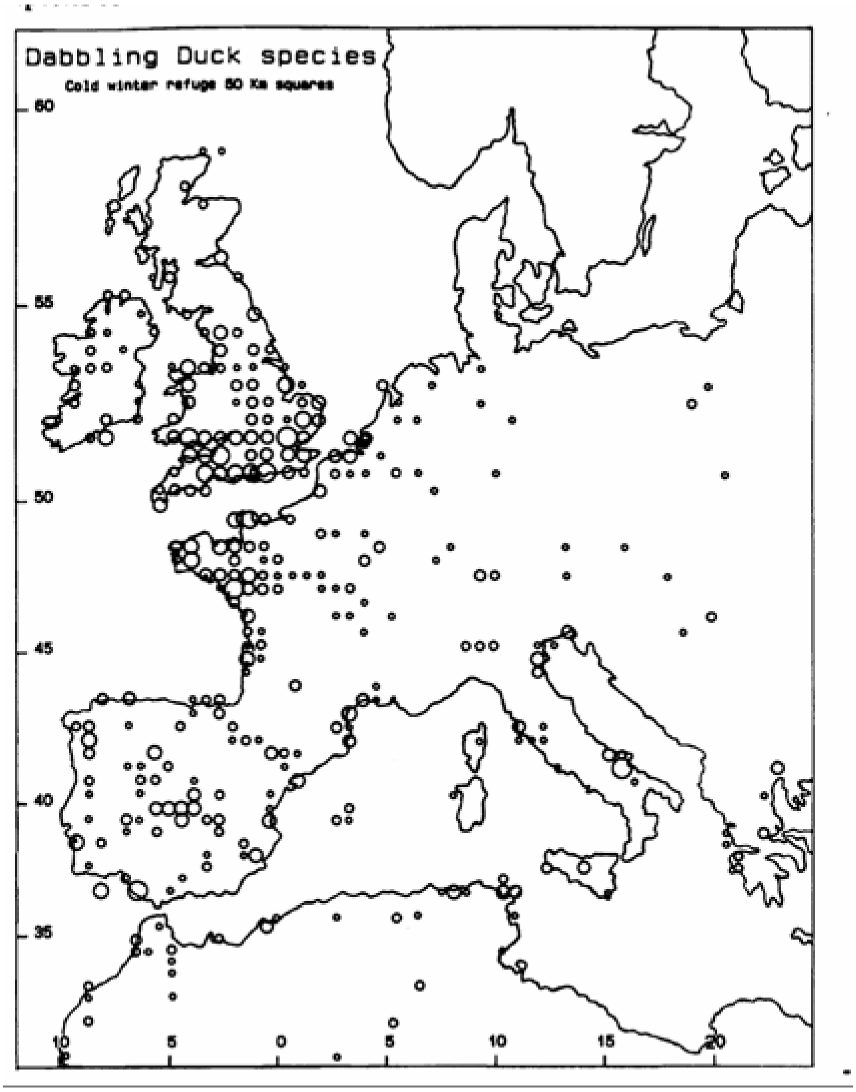


Figure 11.9. A typical map of locations of ringing and recovery sites for Greenland White-fronted Goose Anser albifrons flavirostris (Source: Wernham et al. 2002).

Figure 11.10. Map of populations of Common Teal Anas crecca (Source: Scott and Rose 1996).

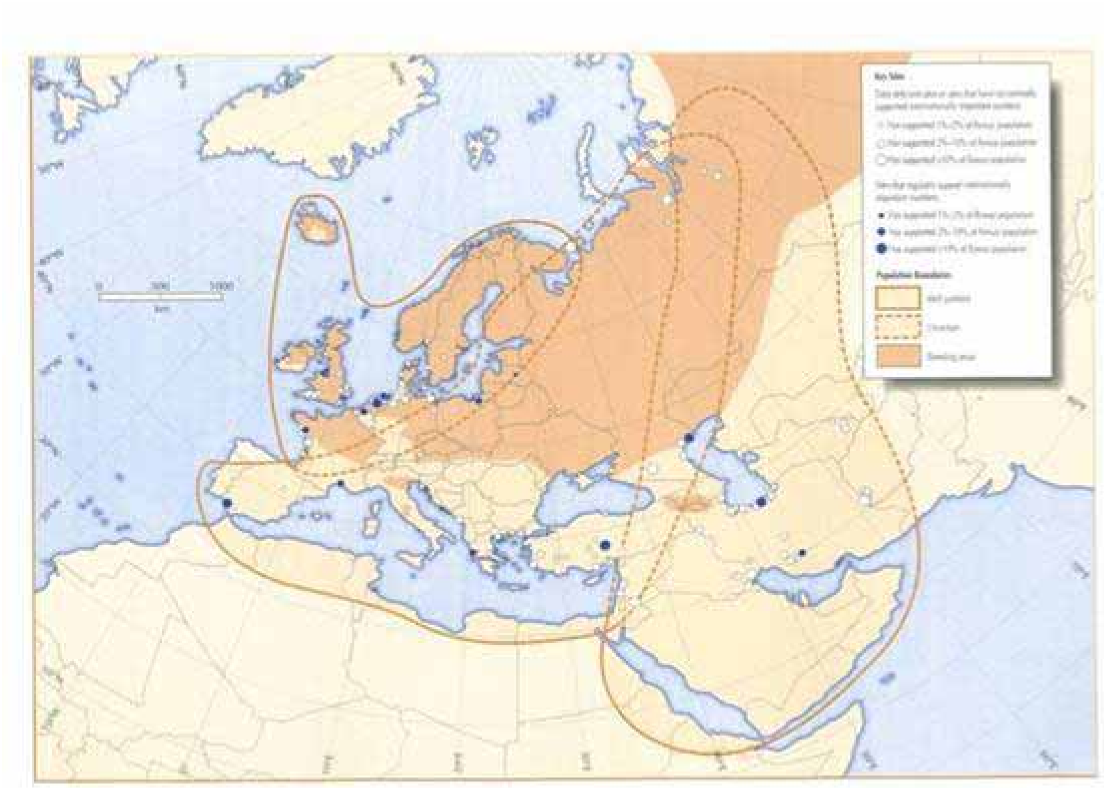


Figure 11.11. *Map of recoveries of Common Teal Anas crecca ringed in the Camargue in Southern France. Red dots show birds ringed in the Camargue and recovered within the putative limits of the Northwest European population and blue dots show recoveries within the putative limits of the Black/Sea /Mediterranean population. Guillemain et al conclude there is little evidence for population structuring for this species in Europe. Source: Guillemain et al. (2005).*

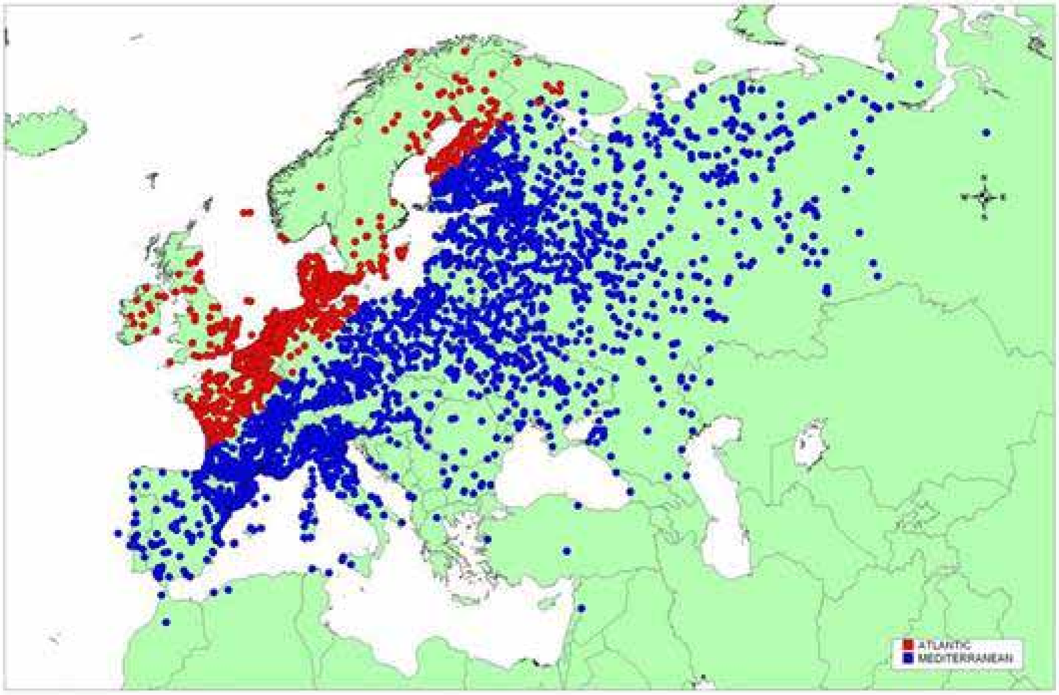


Figure 11.12*. Global distribution of wetlands, based on a reclassification of the FAO-UNESCO Soil Map of the World combined with a soil climate map. (Source: FAO-UNESCO, Soil Map of the World, digitized by ESRI. Soil climate map, USDA-NRCS, Soil Survey Division, World Soil Resources, Washington D.C. http://soils.usda.gov/use/worldsoils/mapindex/wetlands.html)*

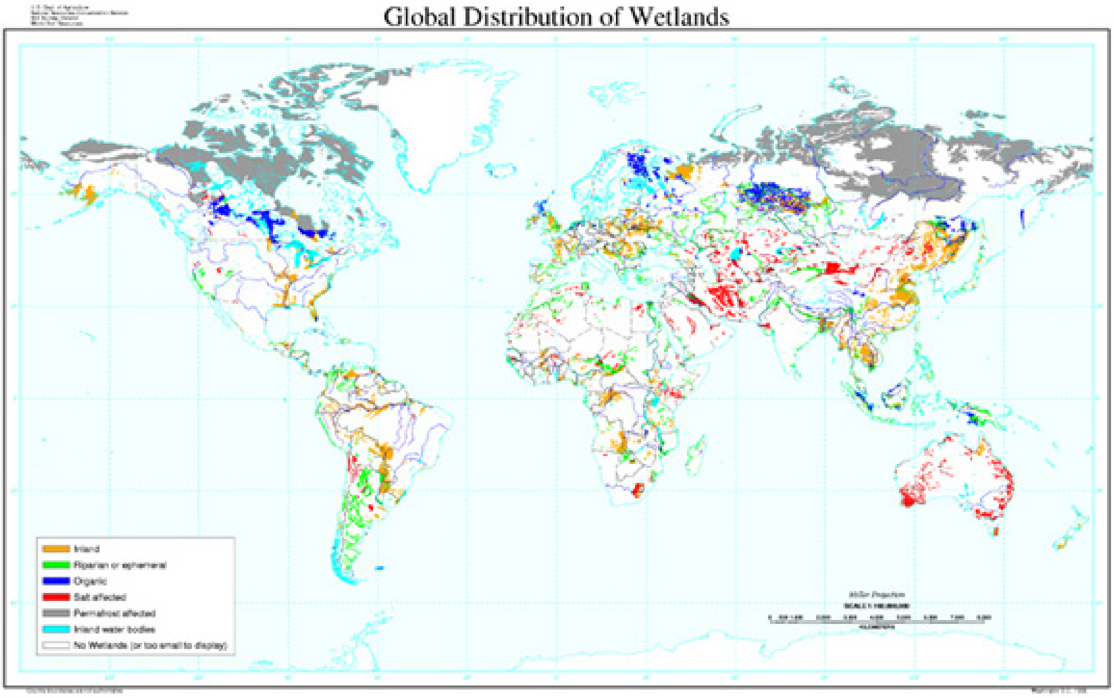


Figure 11.13*. Areas of concentrations and mixing for waterbirds, from the WBDB (Source: BirdLife International 2005).*

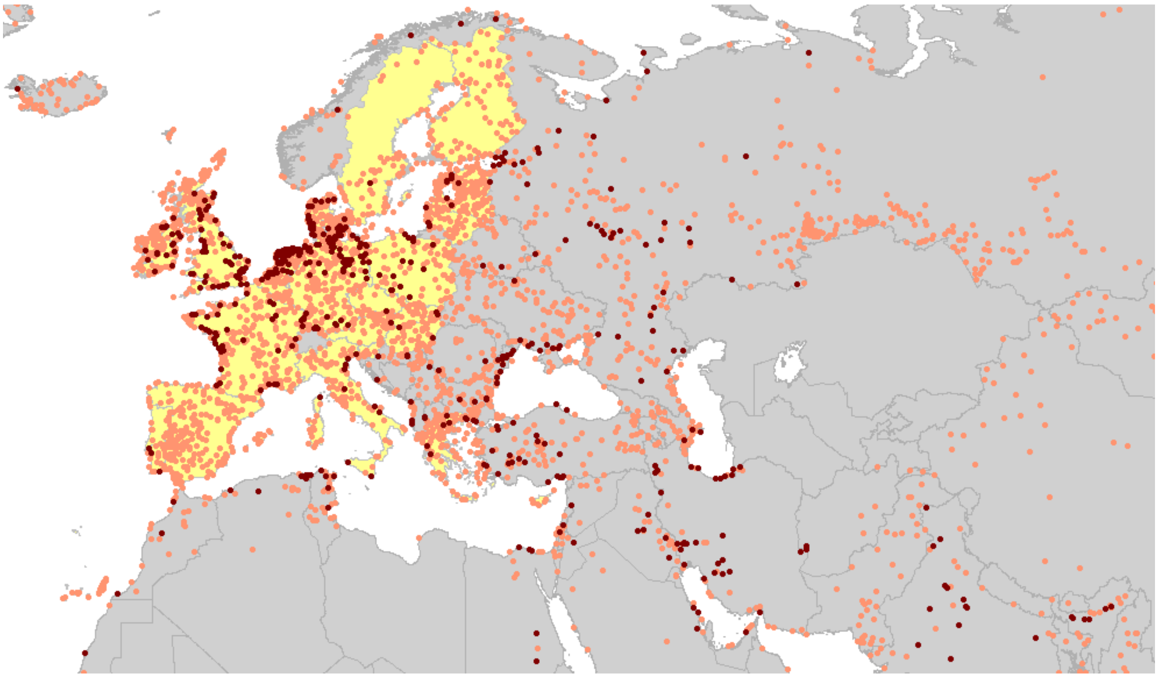


Figure 11.14. All sites in the IWC database for the East Mediterranean and Black Sea area (Gilissen et al. 2002). Solid black dots are sites with data for 1999, open circles are sites with no data for 1999.

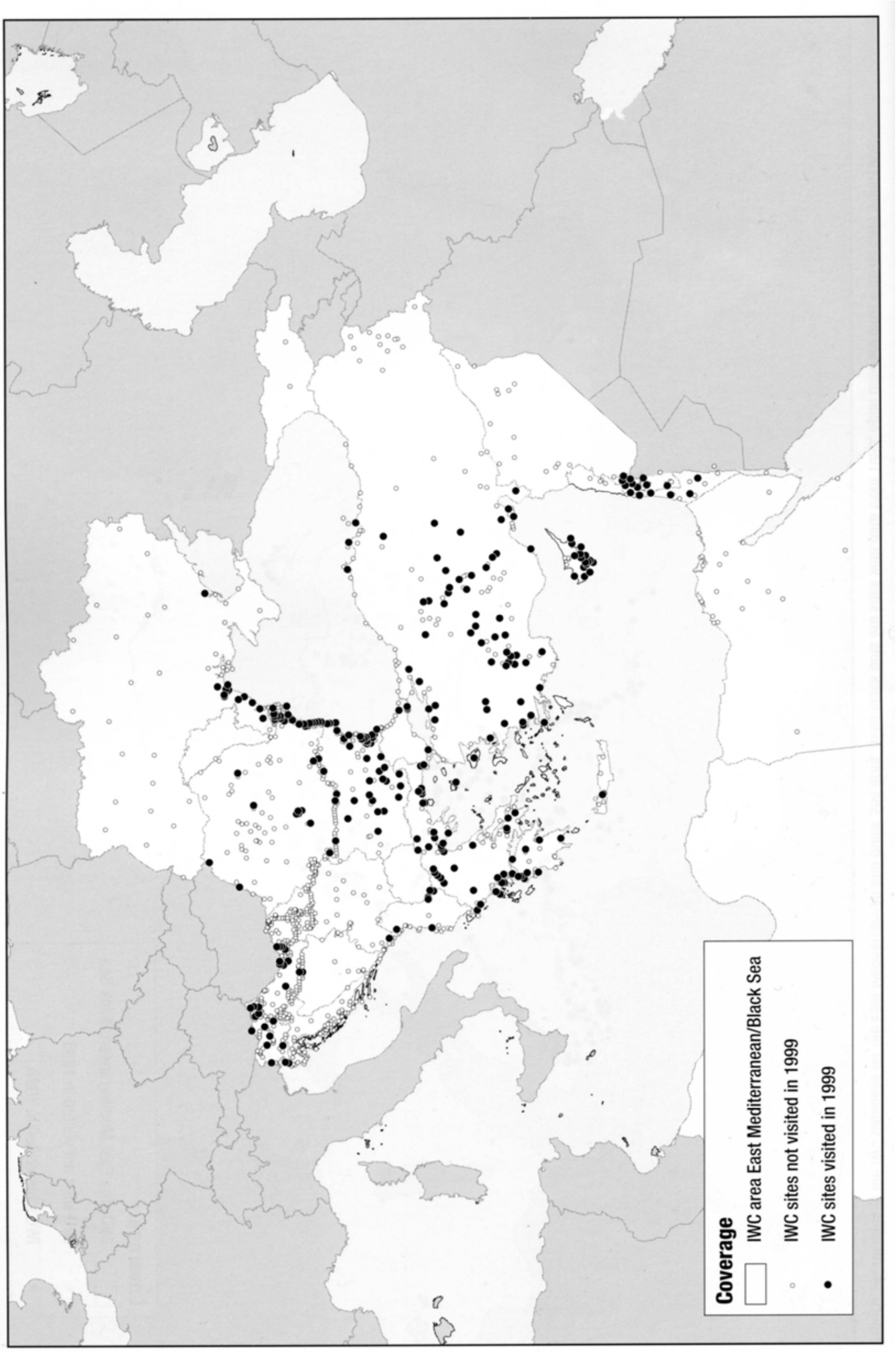


***Figure 11.15**. All sites in the IWC database for the Southwest Asian area (Gilissen et al. 2002). Solid black dots are sites with data for 1999, open circles are sites with no data for 1999.*

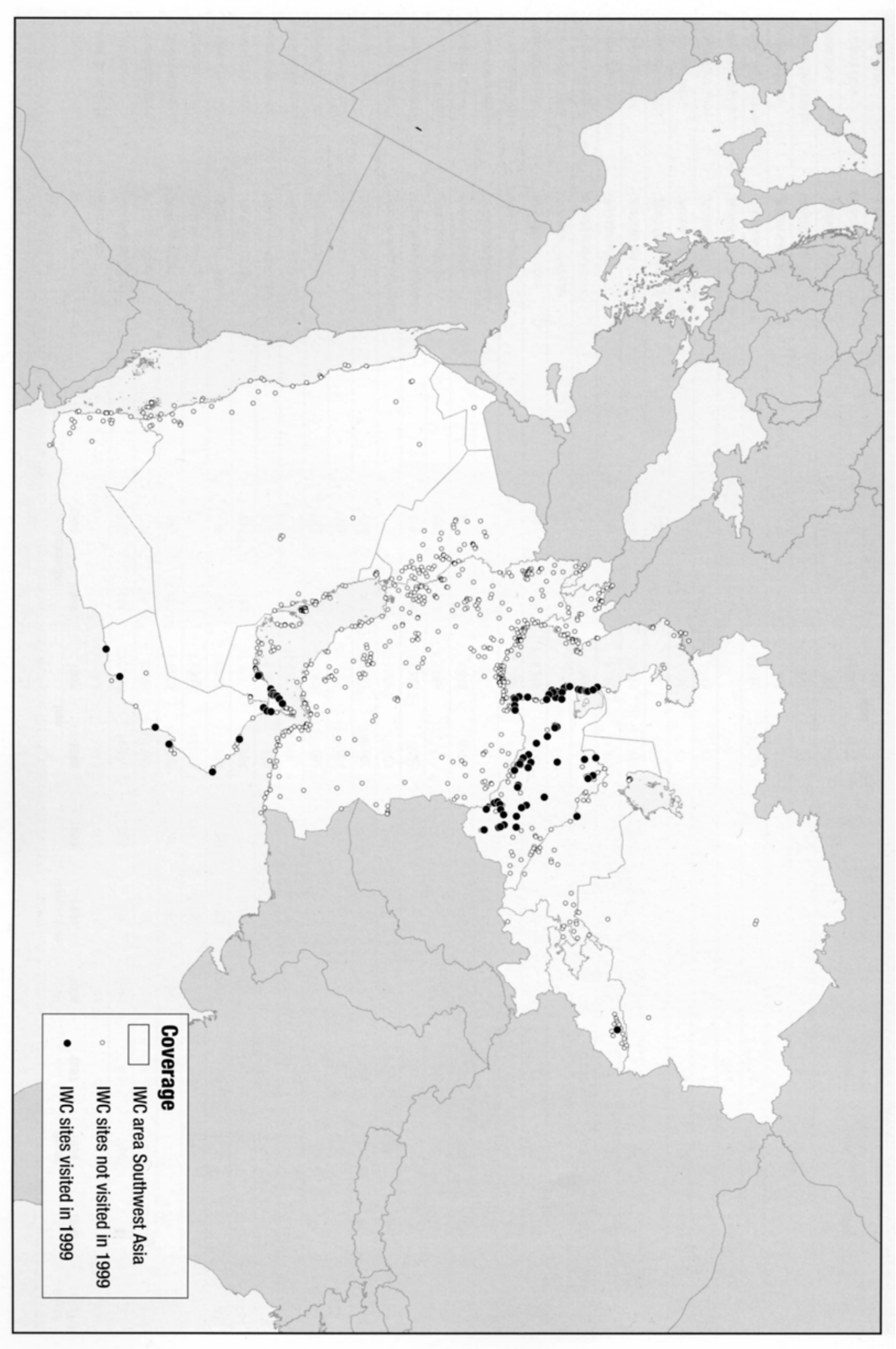


Figure 11.16. Isotherms for the period 6 to 15 January 1999, with an interval of 5 degrees Celsius produced by NOAA-CIRES Climate Diagnostics Centre, Boulder, Colorado (Gilissen et al. 2002).

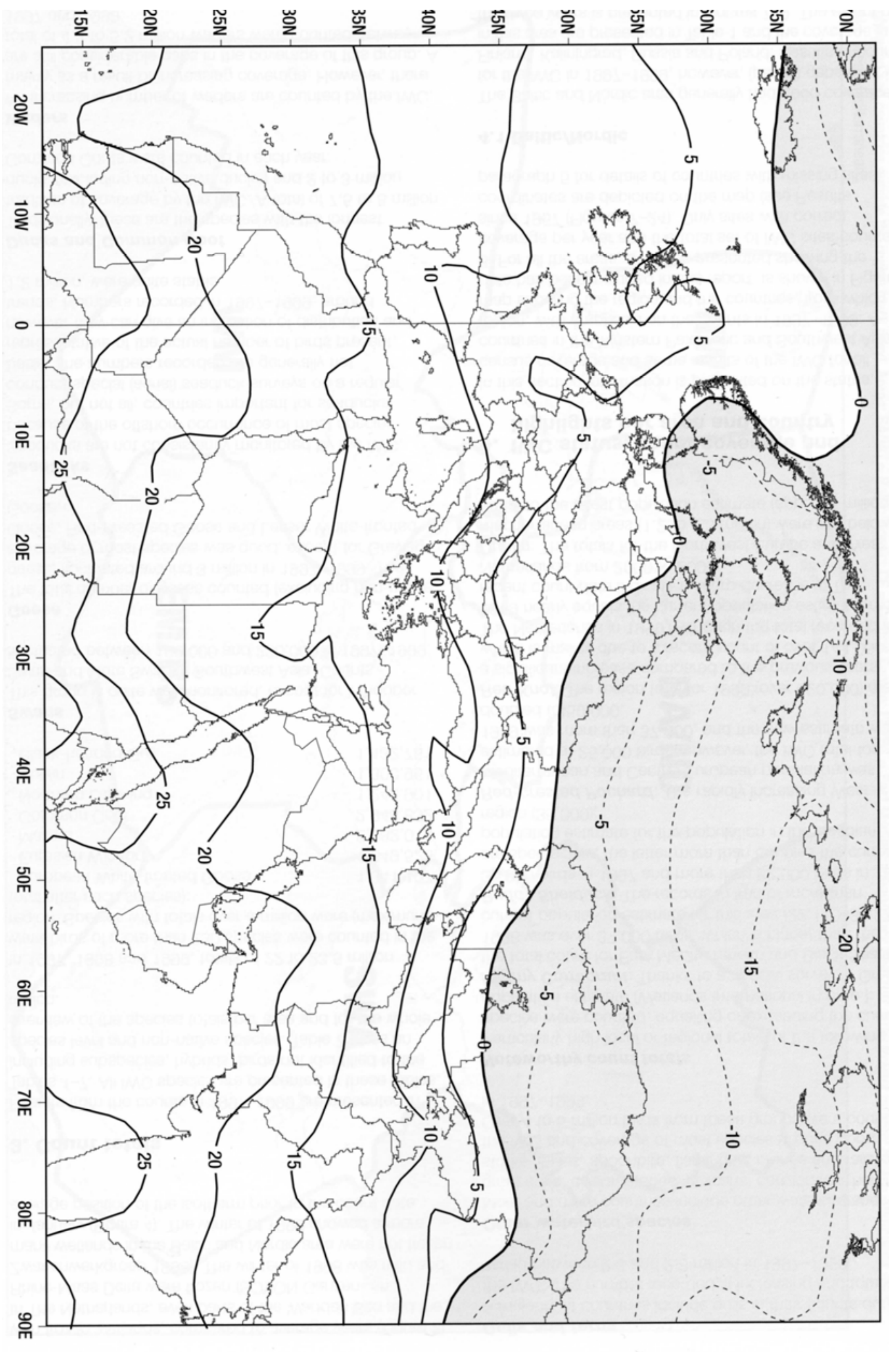


Figure 12.1 *Geographical distribution of sampling sites and numbers of animals sampled per site under the FAO/CIRAD/RVC regional active surveillance projects covering Central Europe, Africa and the Middle East as of March 2006*

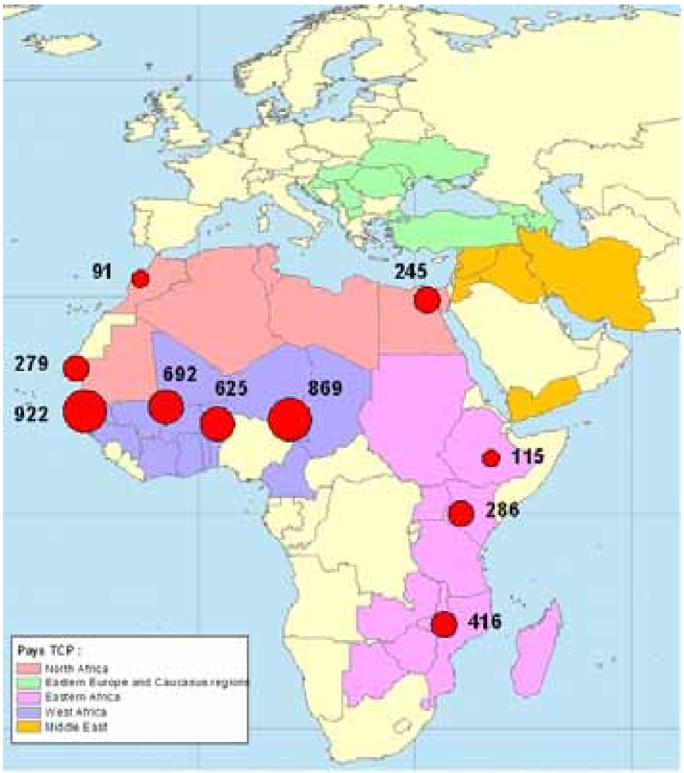
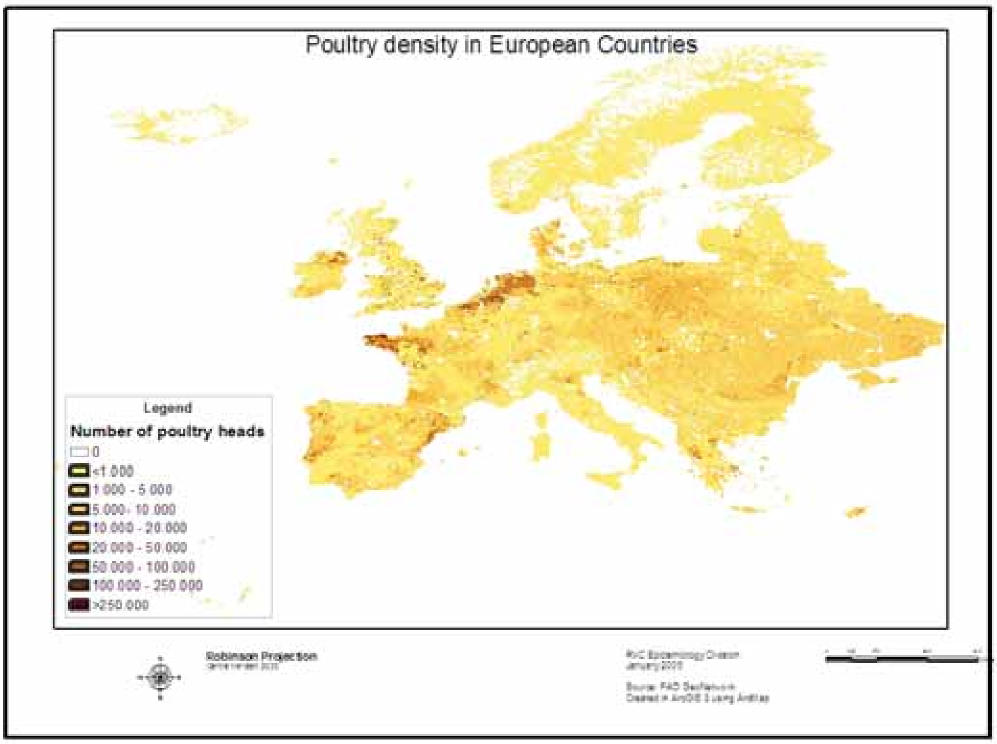


Figure 15.1. *Map of the spatial distribution of poultry density in Europe in 2005*



.

Annexes

Figure 23.1. *An example of leap-frog migration. Winter ranges of Redshank Tringa totanus from (1) Iceland, (2) Britain and Ireland, (3) Denmark, Germany, the Netherlands and Belgium, (4) Sweden and Norway, and (5) Hungary, showing leap-frog migration of northern populations of larger birds. Source Hale 1973 (reproduced with acknowledgement from Bairlein et al. 2002).*

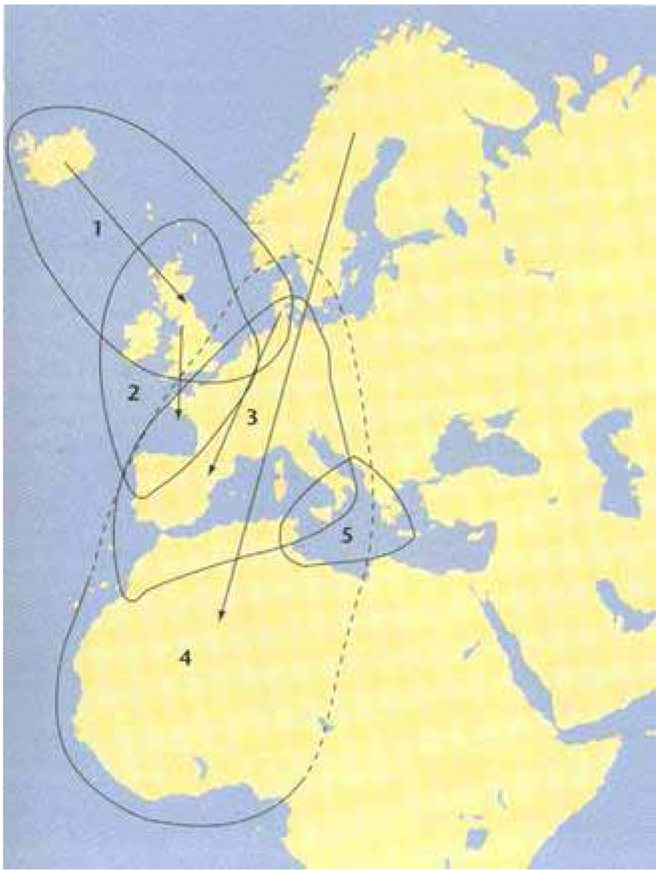


***Figure 23.2**. An example of moult migration. Movements (lines and recovery locations (points) of Canada Geese Branta canadensis that have been present in the Beauly Firth north-east Scotland. Many moulting birds in the Beauly Firth breed in North Yorkshire, England, but birds also migrate to the Firth to moult from other locations in Britain. (Source: BTO data, reproduced with acknowledgement from Bairlein et al. 2002).*

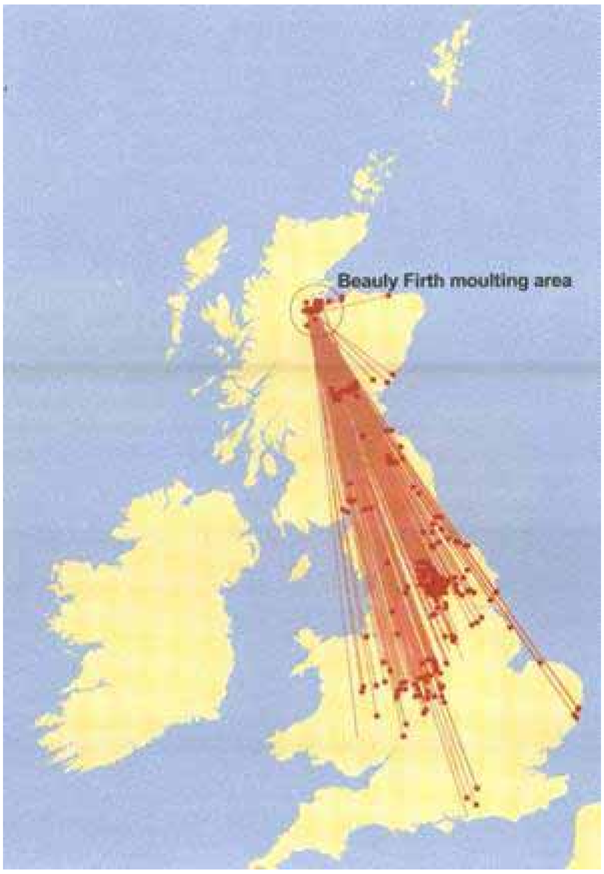


Figure 23.3. *Areas of 50 x 50 km that were identified as refuges in periods of severe cold weather (1967-1986) for Shelduck Tadorna tadorna, Wigeon Anas penelope, Teal Anas crecca, Mallard Anas platyrhynchos, Pintail Anas acuta, Shoveler Anas clypeata, Pochard Aythya ferina, Tufted Duck Aythya fuligula and Coot Fulica atra (Source: Ridgill and Fox 1990).*

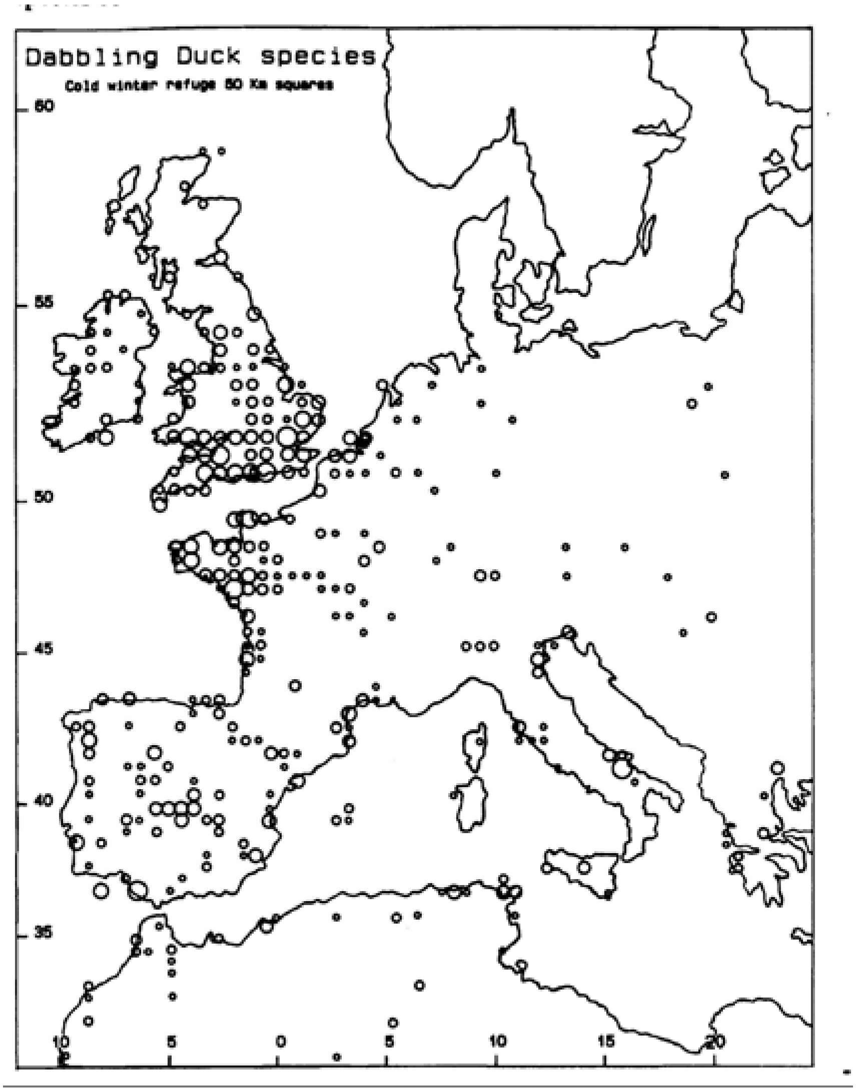
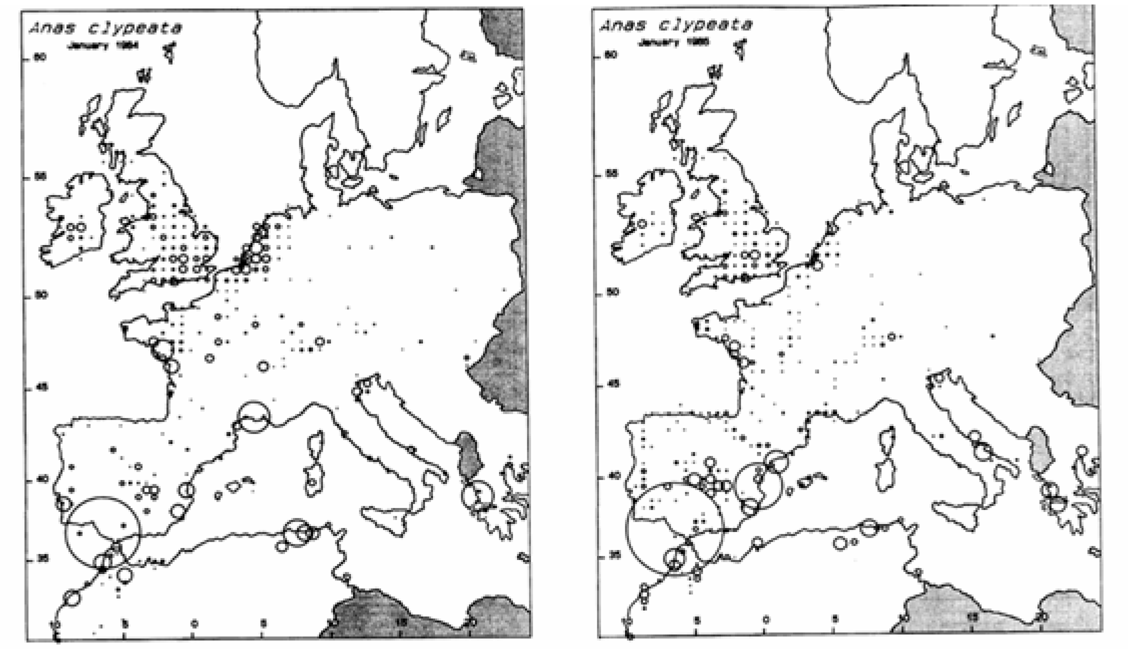


Figure 23.4. An example of cold weather movements (Ridgill and Fox 1990). European distribution of Shoveler Anas clypeata in two contrasting winters. January 1984 (left map) was mild and there were major concentrations in The Netherlands and Brittany. January 1985 (right map) was severely cold and major shifts of distribution from these areas to Spain occurred.



Annex to *The EFSA Journal* (2006) 357, 1-18, *Addendum* to the Scientific Opinion on "Migratory birds and their possible role in the spread of highly pathogenic Avian Influenza (EFSA-Q-2005-243)"

Addendum to the

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

Adopted on 11/12/2006

Table of Contents

1. Introduction and approach

The EFSA Scientific Opinion on migratory birds and their possible role in the spread of highly pathogenic avian influenza was adopted on May 12, 2006 (EFSA, 2006). From May to October 2006, no further cases of HPAI Asian lineage H5N1 in wild birds in Europe were reported except for one case in Spain in July.

In the meantime, scientific work on the role of migratory wild birds in the introduction and spread of HPAI Asian lineage H5N1 has continued in various areas. Specifically, work commissioned by DG Environment and conducted by Wetlands International and EURING was published in an extensive report (Delany et al., 2006). The report contains relevant information which previously had been unavailable and which allows for more specific recommendations on surveillance.

Further work was conducted by various groups in relation to susceptibility and pathogenicity of HPAI Asian lineage H5N1 in selected wild bird species. Also, diagnostic sampling was conducted in healthy wild birds during summer and data on cases in wild birds from last winter are being analysed. Only part of the results from these investigations have so far been published. It is expected that additional relevant information will become available in the coming months. In addition, further research has been commissioned in response to the call issued by DG Research. In October 2006, a total of €28.3 million was allocated to 17 new research projects into avian and pandemic influenza (http://ec.europa.eu/research /press/2006 /pr1710en.cfm). The projects cover human and animal health and address research needs identified by organisations such as the World Health Organisation, the World Organisation for Animal Health, and the UN Food & Agriculture Organisation. The projects addressing animal health will cover vaccines, better diagnosis and early warning systems, increased knowledge of the avian influenza virus, technology transfer to third countries, and a network for monitoring migratory birds[1].

1.1. Approach

Based on new reports and published scientific articles, previous recommendations were specified and updated. Using information on wild bird species with a higher probability of being exposed to and/or carrying HPAI Asian lineage H5N1 (such bird species are sometimes referred to as “higher-risk species”) and information on the geographic location and population size of these species over time, the recommendations on wild bird surveillance can be further developed towards the adoption of a risk-based approach. Risk-based surveillance is a targeted surveillance informed by the results of risk assessments (Stärk et al., 2006). Risk-based surveillance is specifically suitable for the surveillance of rare events. The efficiency can be increased by targeting sub-populations, areas or time windows where there is a higher probability of detecting cases.

---

[1] http://europa.eu/rapid/pressReleasesAction.do?reference=MEMO/06/381&format=HTML&aged=0&language=EN&guiLanguage=fr]

1.2. Objectives

- To assess new information on risk factors such as species, location, population size etc. with respect to surveillance
- To identify areas for developing risk-based surveillance in wild birds
- To update aspects of previous recommendations on surveillance using all available information

2. Differences between high risk species assessments

In August 2006, the European Commission published the results of an assessment of ornithological data relevant to the spread of Asian lineage HPAI H5N1 in Europe undertaken by Wetlands International and EURING (Delany et al., 2006). This extensive report summarised large amounts of data on mid-winter distributions of waterbirds collected by the International Waterbird Census and curated by Wetlands International, and large volumes of information related to the movements of birds drawn from EURING's international database of bird ringing recoveries. The three parts of the report:

- identified higher risk species;
- identified and mapped concentrations and movements of waterbirds with potential to spread avian influenza; and
- developed a rapid assessment format for the collection and interpretation of ornithological data in the event of an outbreak of H5N1.

Although published in August, the report by Delany *et al.* (2006) was submitted to the DG Environment in May and work on this report was being undertaken simultaneously with inputs by the same individuals to the EFSA Working Group's report (Pfeiffer et al., 2006) which was finalised in April, and adopted and published in May 2006.

There are minor differences in species listings between the two reports. The differences are as follows:

Species included in EFSA report but not in DG Environment report

Canada Goose	*Branta canadensis*

Species included in DG Environment report but not in EFSA report

Pink-footed Goose	*Anser brachyrhynchus*
Lesser White-fronted Goose	*Anser erythropus*
Marbled Teal	*Marmaronetta angustirostris*

The background and implications of these differences are outlined below:

Canada Goose

Canada Goose was added to draft lists of species assessed as higher risk at a late stage in drafting the EFSA report on the basis that, whilst populations throughout much of the EU are non-migratory (or only undertaken short-distance movements), some populations are migratory, especially in Scandinavia (Snow and Perrins, 1998; Andersson et al., 1999).

The decision tree in Fig. 11.17 distinguishes between migratory species and non-migratory species, but does not further distinguish between those species that migrate within Europe from those that migrate into or through Europe. Following discussion amongst the Working Group's ornithologists it was decided to exclude Canada Goose at this second filter stage, given that its movements are confined within (parts of) Europe and thus in the context of Risk Question 1 (the risk of HPAI release within the EU), this is not a species of importance. It is of course relevant in the context of Risk Question 2 (establishment of subsequent endemic infection within the EU) [see Table 13.2 in the original EFSA opinion].

Pink-footed Goose[2]

Lesser White-fronted Goose and Marbled Teal

Lesser White-fronted Goose and Marbled Teal were identified in EFSA Table 11.2 as being of higher risk on the basis of mixing, gregariousness and other factors. However, they are not listed in EFSA Table 13.1 because of expected zero contact risk with poultry. This results in a difference with the DG Environment report since these two species are retained in Table 1.6 of that report (although still indicating no contact risk with poultry). Thus the difference arises because of additional contact risk considerations for these (rare) species.

Evaluation of differences in listings

Canada Goose	In the context of the original Risk Question (entry of HPAI to the EU) the correct approach was to deselect Canada Geese, since they do not migrate into the EU from external regions where HPAI was/is present. However, the species is clearly a potential reservoir in the context of risk assessments related to the spread/establishment of H5N1 within the EU. **Working Group conclusion**: Canada Geese are not high risk in the context of Risk Question 1 but are potentially high(er) risk in the context of establishment of endemic infection within the EU (Risk Question 2).
Pink-footed Goose	**Working Group conclusion**: Pink-footed Geese are higher risk species in the context of the EFSA selection process[2]
Lesser White-fronted Goose and Marbled Teal	**Working Group conclusion**: Whilst features of Lesser White-fronted Goose and Marbled Teal ecology indicate a theoretical higher risk of transmission of HPAI H5N1, the assessed zero contact risk with poultry (and their small and geographically restricted populations) means that these species do not present significant risks to poultry.

Consideration of this issue, especially the case of the Canada Goose, highlights the fact that the original Risk Questions (posed by DG SANCO in October 2005)

---

[2] Pink-footed Goose was incorrectly omitted in the list of higher risk species (Table 13.1 of the EFSA Scientific Opinion), and this has now been rectified.

were rapidly overtaken by arrival and spread of HPAI H5N1 in the EU in February–May 2006 (the period when the report was being finalised).

3. Identification of key issues for developing risk-based surveillance in wild birds

3.1. Use of new and relevant sources of information

The Wetlands International/EURING report (Delany et al., 2006) provides a considerable wealth of information relevant to focussing surveillance on areas of potentially higher risk. In particular, summary maps showing the location of concentrations of waterfowl and of higher risk species are valuable. Figure 1 [Delany *et al.* Figure 2.1] shows the distribution of all waterbirds counted in mid-winter, whilst Figure 2 [Delany et al., Figure 2.2] presents peak counts of 17 higher risk species in January. Figure 3 [Delany et al., Figure 2.3] identifies those areas with multiple numbers of higher risk species (*i.e.* are concentration areas with a high risk of inter-species mixing), and Figure 4 [Delany *et al.* Figure 2.3] shows those sites where there are the greatest numbers of higher risk species.

Unpublished analyses (Stroud unpublished) highlight the main waterbird migration routes and flyways within and passing through Europe. This has used information on biogeographic population sizes of migratory waterbirds (from Wetlands International 2002), and proportionately mapped the movements of these species for ducks (Figure 5), geese and swans (Figure 6) and waders (Figure 7).

Unsurprisingly, both analyses highlight similar areas of the EU as being of key importance for large numbers of waterbirds in Europe, both in migration periods and mid-winter (Figure 8). These are:

- the White Sea/Baltic Sea corridor leading to the international Wadden Sea and southern North Sea;
- the coastal wetlands of the northern Mediterranean including the coasts of eastern Spain, southern France and the Adriatic coast of Italy;
- the coastal wetlands of the northern Aegean and Black Seas; and
- the Caspian Sea.

It is highly desirable that sites within these regions are included within national surveillance programmes, whilst, in the current absence of European-scale information on the dynamics and movements of avian influenza viruses in waterbirds, not diminishing the value of collection of data from other areas. Areas where concentrations of waterbirds occur in proximity to poultry production centres should be given priority for the development of surveillance schemes.

3.2. Constraints

A major constraint on developing a more strategic approach to AI surveillance is the current lack of a co-ordinated, pan-European analysis or reporting of surveillance for 2005/6. Whilst gross totals (from 1 July 2005 to 31 January 2006 only) have been reported on DG-SANCO's web-site, no information is readily available about numbers of different species sampled, locations within countries where sampling was undertaken, or results (other than at the crudest scales). The lack of this necessary data and information greatly constrains the refinement and adaptation of existing surveillance activity at Member State level.

National totals until December 2005 (of all birds, not restricted to waterbirds), indicate that there was possibly significantly greater sampling effort in the Baltic/North Sea corridor and possibly in northern Italy than in the important Aegean and Black Sea regions (the latter being currently outside the EU, of course).

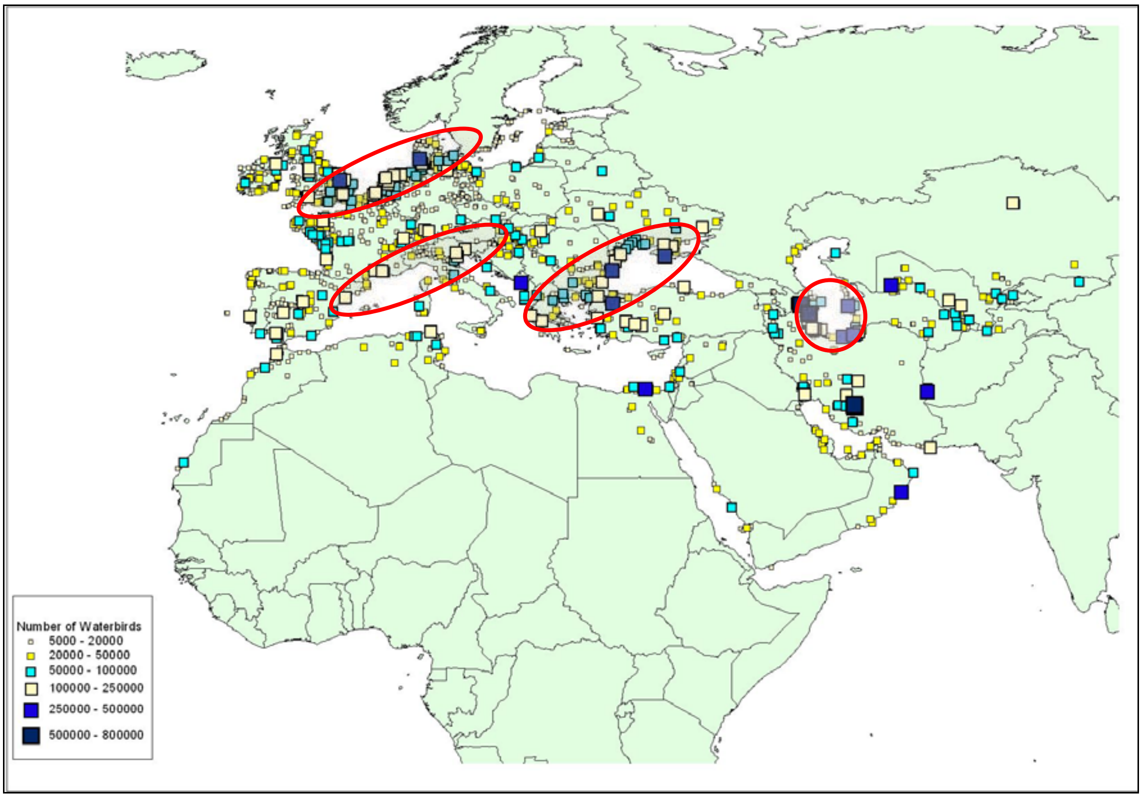


Figure 1. Peak January counts between 1990 and 2005 of all waterbird species combined, the peak counts of each waterbird species at each site in this period have been summed to produce site totals. No appropriate data are available for sub-Saharan Africa. Figure 2.1 from Delany *et al.* 2006.

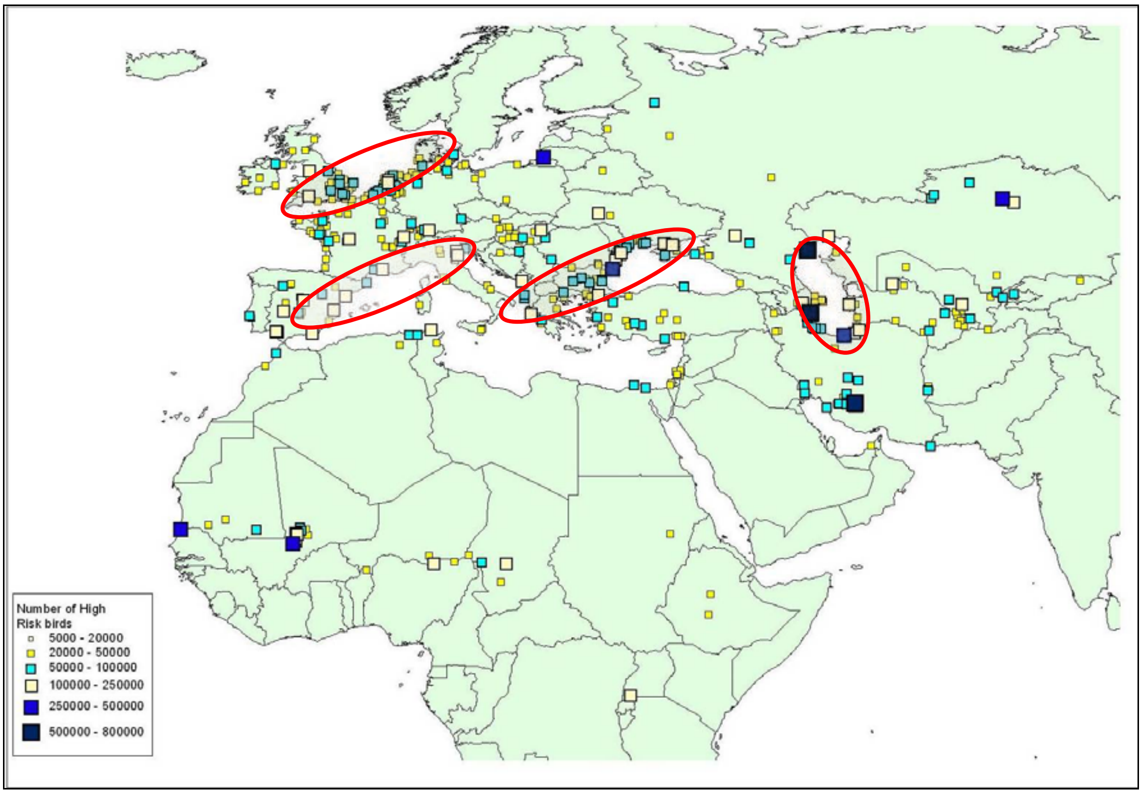


Figure 2. Peak January counts between 1990 and 2005 of 17 "Higher Risk" waterbird species. The peak counts of each of 17 waterbird species considered to pose a high risk of transmitting Avian Influenza at each site in this period have been summed to produce site totals. Figure 2.2 from Delany *et al.* 2006.

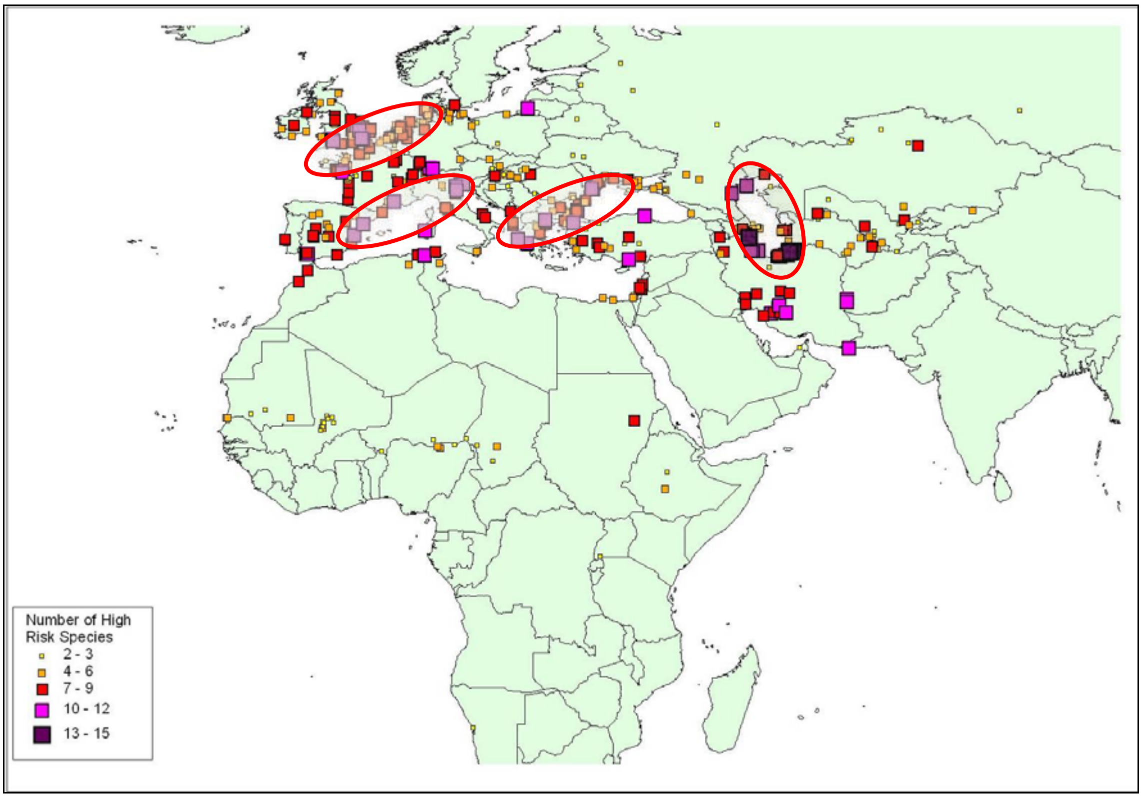


Figure 3. The number of 17 higher risk waterbird species recorded at each IWC site during January counts between 1990 and 2005 in Europe, Africa, West and Central Asia. **Figure 2.3 from Delany *et al.* 2006.**

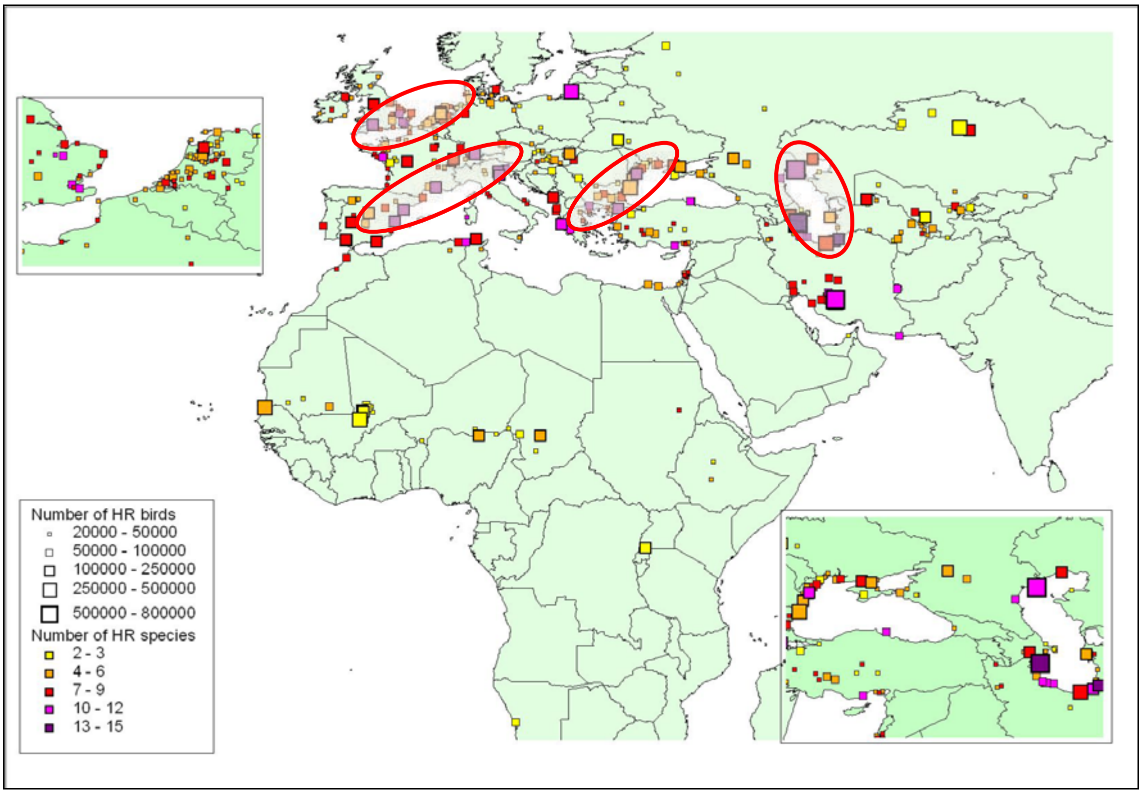


Figure 4. All sites where combined counts of higher risk waterbird species exceeded 20,000 between 1990 and 2005, and where two or more of these species occurred in numbers exceeding thresholds of 100, 250 or 500, (depending on species – see Delany *et al.* 2006). Figure 2.4 from Delany *et al.* 2006.

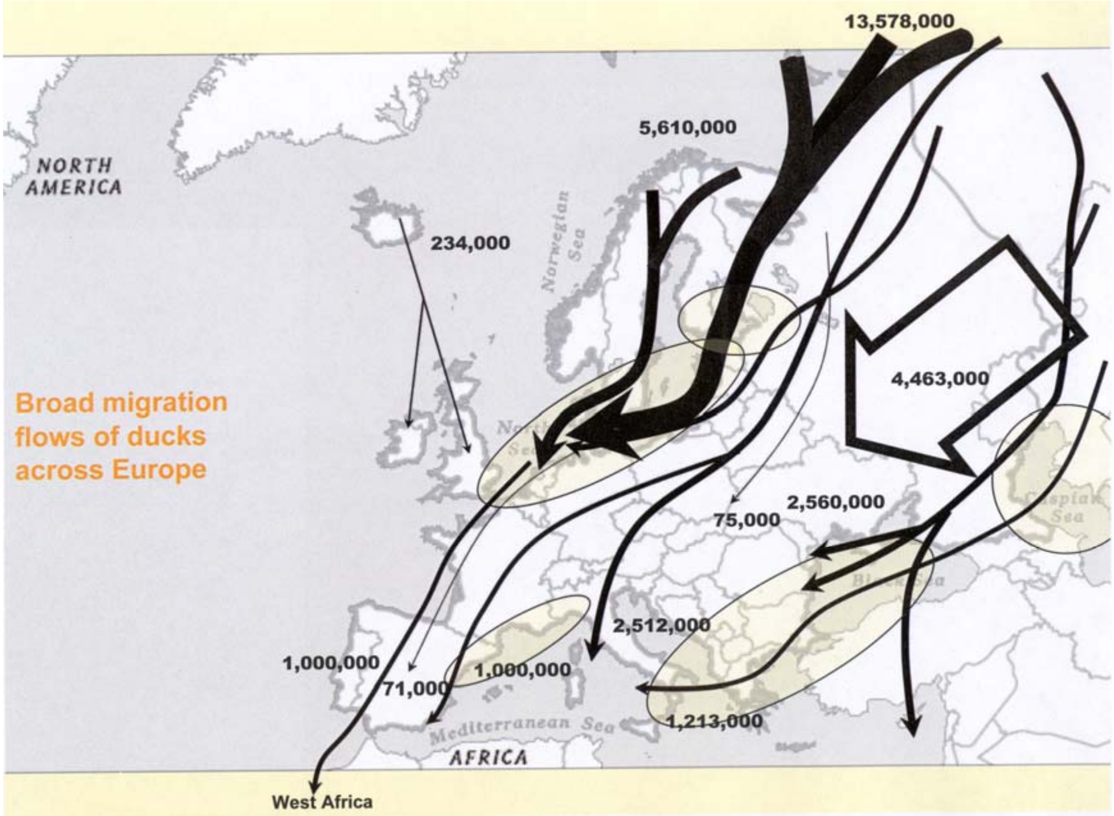


Figure 5. The main migratory corridors and flyways for ducks moving to or through Europe at the end of the breeding season. Data on population sizes drawn from Wetlands International 2002. The size of the arrows is proportionate to the number of birds using specific flyways or migration routes. (Stroud unpublished).

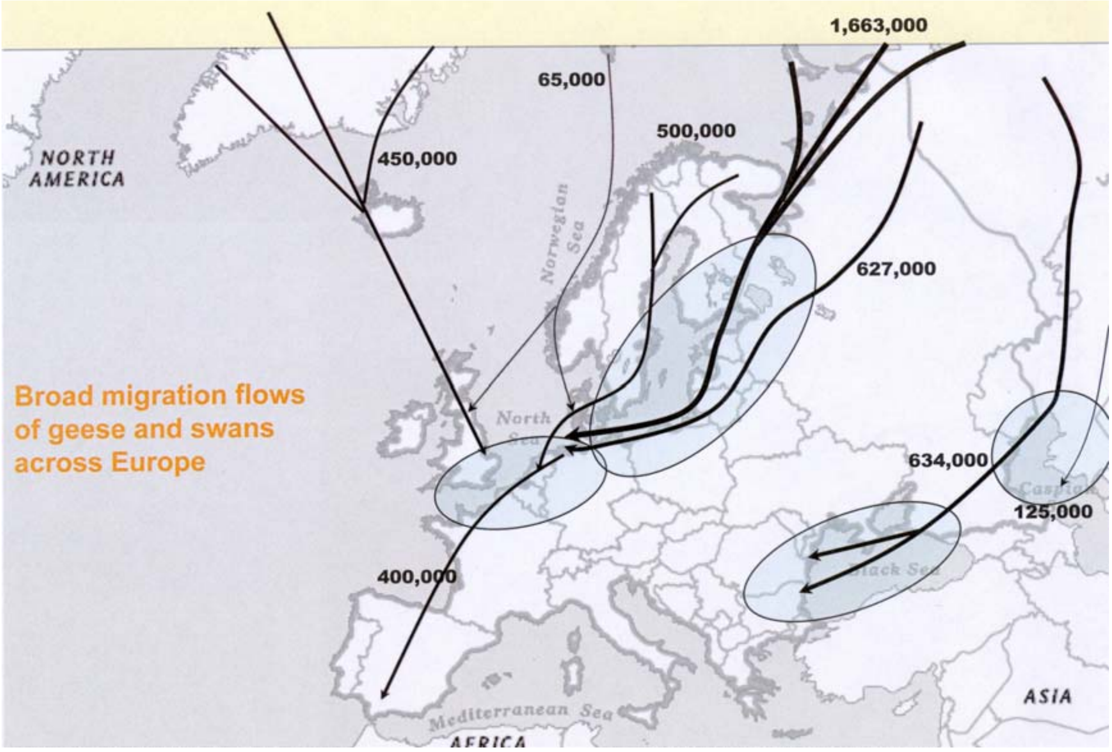


Figure 6. The main migratory corridors and flyways for geese and swans moving to or through Europe at the end of the breeding season. Data on population sizes drawn from Wetlands International 2002. The size of the arrows is proportionate to the number of birds using specific flyways or migration routes. (Stroud unpublished).

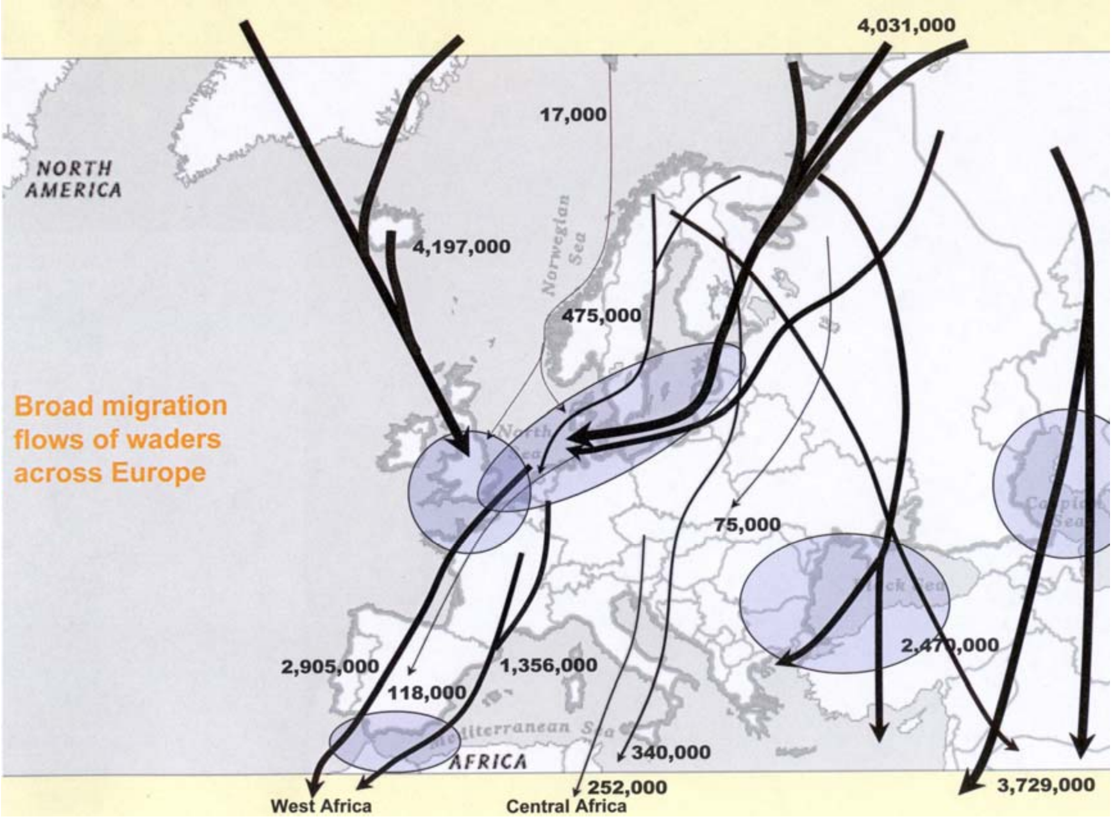


Figure 7. The main migratory corridors and flyways for waders moving to or through Europe at the end of the breeding season. Data on population sizes drawn from Wetlands International 2002. The size of the arrows is proportionate to the number of birds using specific flyways or migration routes. (Stroud unpublished).

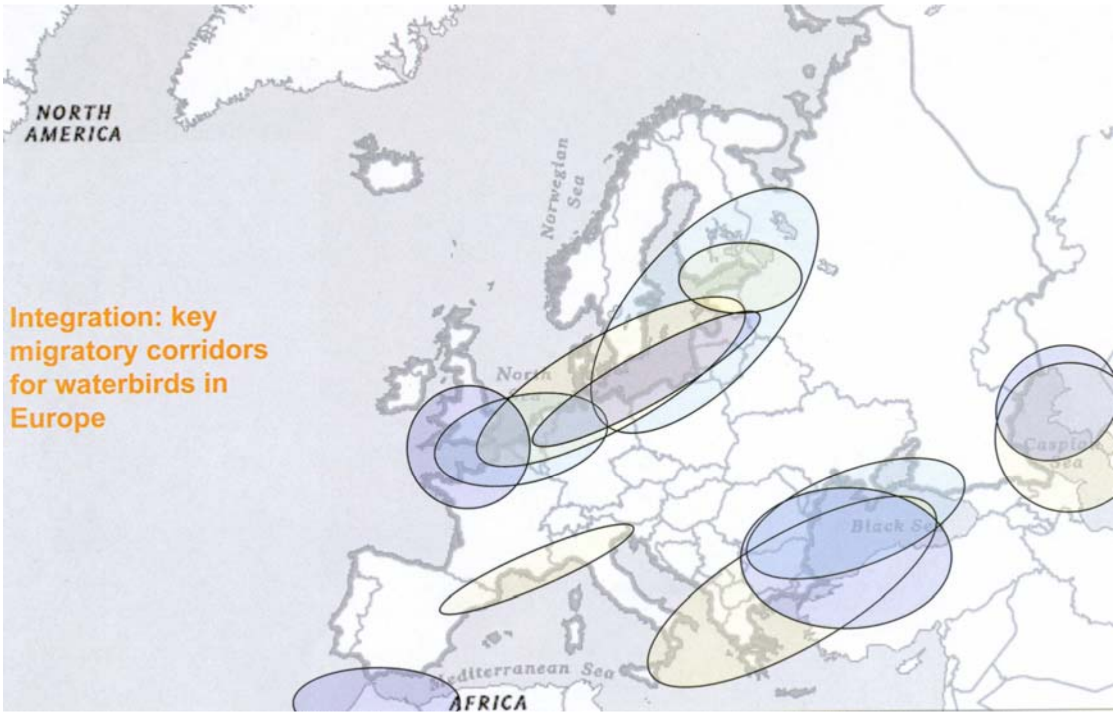


Figure 8. Core European regions through which there are major migratory movements of ducks, geese, swans and waders at the end of the breeding season, summarised from Figures 5-7.

3.3. Factors to be considered when designing a surveillance programme

The objective of surveillance of HPAI in wild birds is the early detection. In order to achieve this, both active and passive surveillance approaches need to be combined since they can reveal different epidemiological patterns. Passive surveillance is defined as any activity aimed at detecting the infection from reported mortality cases. Active surveillance is defined as any activity related to the sampling of healthy birds (even not alive, e.g. hunted birds).

Type of sampling	Assumptions	Approach	Limitation	Sensitivity
Passive sampling of any dead individual belonging to "higher risk species"	H5N1 has high lethality rate in higher risk species	Since H5N1 lethality rate is high, the probability of detecting a dead infected individual is higher when compared with any other type of sampling	Endemic H5N1 can be underestimate or unnoticed; The probably of detecting dead individuals is biased because of the clumped human distribution and the different ecological characteristics of both the surveyed areas and the selected bird species. Higher risk species are mainly determined on their ecological characteristics since intrinsic determinants of H5N1 are unknown in the wild .	Very high if H5N1 retains its lethality rate; Fully applicable in an early detection strategy.

Type of sampling	Assumptions	Approach	Limitation	Sensitivity
Passive sampling of mortality clusters in any bird species (or group of species) not considered at higher risk	H5N1 retains its lethality rate in *non* higher risk species	If H5N1 spreads outside wetlands, it will be easily detected in dead infected individuals not belonging to the waterfowl bird group; This type of sampling is mainly addressed in detecting secondary outbreaks in possible bridge species;	Difficult definition of mortality cluster; Huge amount of samples obtained from urban - anthropized areas	Very high if H5N1 retains its lethality rate in species not considered at higher risk Partially applicable in an early detection strategy
Active sampling in randomly selected areas and bird species	H5N1 is endemic in some bird species (or population) and its lethality rate is low or null. The sampled areas are selected randomly but bird population size serves as a trade off. In the selected areas all the individuals live in an homogenous mixing (e.g. same probability of being infected irrespectively of species, age and gender)	The presence of H5N1 in unaffected species has been suspected. This type of sampling will reveals the endemic presence of H5N1 when showing a low or null lethality rate in some susceptible bird species (LPAI-like behaviour)	Areas and species are likely to be selected with an opportunistic approach or combining other risk factors (e.g. poultry density); The size of the sampling unit and the H5N1 expected prevalence are unknown, as a consequence many basic assumption of this type of sampling are violated.	High in detecting certain level of H5N1 prevalence and when the size of sampling unit is known ; Low or null if H5N1 shows a sporadic behaviour Not applicable in an early detection strategy if not combined with other type of sampling
Active sampling in all areas and individuals considered at risk	H5N1 shows a sporadic/unpredictable behaviour	Each wetland and its ornithocenoses is considered at risk	Practically inapplicable due to the excessive quantity of samples needed	Very high if properly done; Fully applicable in an early detection strategy.
Sentinel birds	Sentinel bird species are in locations where they at high risk of being exposed to infection and they are susceptible to infection	Susceptible domestic bird species are kept in high risk areas and their infection status is monitored	Requires possibility for effective transmission given the presence of the virus	Depends on method of exposure. If aerosol is important, could be sensitive

H5N1 = H5N1 HPAI Asian lineage

3.3.1. Target population and sampling units

The correct identification of the target population and its sampling units will increase the sensitivity and the cost/efficacy of the surveillance. From the theoretical point of view the sampling unit can be defined as the group of animals in which (Beaglehole et al., 1993):

a) Each individual has the same probability of being positive (or negative);
b) Each individual has the same probability of being sampled;

Units can be sampled according to several strategies and a range of risk factors (e.g. poultry density) can be taken into account.

3.3.2. Timing of surveillance

Birds migrate according to a seasonal pattern and the phenology of migration can be broadly divided in a) breeding period; b) autumnal migration; c) wintering period and d) spring migration (Rees et al., 2005). The large-scale epidemiology of the AIV shows a decreasing prevalence linked to the timing of migration. Prevalence of AIVs in any species is generally higher during the post-breeding season and lowest during spring migration (Olsen et al., 2005). As prevalence decreases during the months following the end of the breeding season, it tends to have highest prevalence in species in those areas of migratory flyways that are closest to the breeding grounds (typically in either more northerly and/or easterly directions) and is lowest in areas further from breeding areas that are visited later in the non-breeding season (i.e. generally in more southerly and/or westerly areas). The probability of detecting the virus in Northern latitudes, during summer, is relatively high in comparison with the probability of detecting the same virus during winter in South latitudes (e.g. Sub Saharan Africa or Mediterranean Basin).The sampling intensity should consider the described, rather different, probabilities. Data on timing of migration is available at country level (Delany et al., 2006).

3.3.3. Location

Surveillance should focus on locations considering the available scientific information on the number of individuals belonging to the high risk species and their possible geographical origins, as well as the mixing areas (stopovers) that permit further mixing between populations of different origins. At present, data on locations of important bird areas and relevant mixing points are available at country level (Delany et al., 2006).

3.3.4. Sample size

Many practical and methodological issues related to sample size have not been resolved and need to be further evaluated.

Specifically, lack of knowledge on lethality rate and contact rate between subgroups within species at a given location are limiting the validity of traditional methods for sample size calculation.

4. Update on diagnostic approach for the detection of Asian Lineage H5N1 HPAIV in Wild Bird Populations

4.1. New and relevant data

In 2006, several EU member states have reported the detection of Asian lineage H5N1 HPAIV in wild birds. In most instances, numerous organs were collected from dead birds and tested for H5N1 virus using the diagnostic methods described in the Scientific Report (EFSA-Q-2005-243). From these analyses it was concluded that the H5N1 virus was frequently detected in tissues of the respiratory tract. In addition, oropharyngeal swabs were found to be a reliable indicator for the presence of H5N1 virus in wild birds (Harder unpublished data). To reduce the workload in the laboratories and to enable the screening of larger numbers of dead wild birds, several laboratories used oropharyngeal swab testing as the primary diagnostic test following the initial investigations on multiple organs. Tissues containing high viral loads were found in the lung and in the central nervous system correlating also with immunohistochemical investigations in diseased wild swans (Teifke et al., unpublished data).

Experimental infections of several species of ducks belonging to the *Anas* and *Aythya* genera have been performed (Fouchier unpublished data). Under these experimental conditions, the Asian lineage H5N1 HPAIV (A/Turkey/Turkey/1/05) was detected primarily in pharyngeal swabs, and rarely in cloacal swabs. Virus shedding from the respiratory tract occurred for 2-6 days at titres of $10^{3.5}$ to $10^{6.2}$ TCID50. In contrast, virus shedding from the digestive tract occurred only for 1 or 2 days, only in very few animals, and at titres of $10^{2.2}$ to $10^{3.2}$ TCID50. None of 32 ducks belonging to 4 *Anas* species (*A. platyrhynchos, A. penelope, A. strepera, A. crecca*) developed clinical signs whereas 3/7 Pochards (*Aythya ferina*) and 4/7 Tufted ducks (*Aythya fuligula*) displayed reduced activity. In addition, 1/7 of these Pochards and 3/7 Tufted ducks were moribund or died. Similar data were obtained by Brown et al. (2006) using North American ducks and laughing gulls infected with influenza viruses A/Whooper Swan/Mongolia/244/05 and A/Duck meat/Anyang/01, although these viruses were detected in cloacal swabs more frequently than in the Dutch study. Whereas Blue-winged teals (*Anas discors*), Redhead ducks (*Aythya americana*), Mallards (*Anas platyrhynchos*) and Northern Pintails (*Anas acuta*) did not show signs of disease, whereas Wood ducks (*Aix sponsa*) and Laughing gulls (*Larus atricilla*) did (4/6 and 6/6 respectively) and a large proportion of the animals died from the infection (3/6 and 4/6 respectively). In experimentally infected birds, the brain, lung, and kidney were positive for influenza virus most frequently and generally had the highest virus load (Brown et al., 2006).

Despite the intense EU-wide surveillance efforts aimed at detecting Asian lineage H5N1 HPAIV in wild migrating birds, the virus has not been detected in live birds areas distant from where the virus was found in dead birds. Because it is possible that the testing of cloacal swabs alone is not sufficient to detect the H5N1 virus, no firm conclusions can be drawn about potentially infected species. While serological testing in general provides a relatively simple opportunity to estimate the prevalence of pathogens in host populations, serological surveys for the presence of Asian lineage HPAI H5N1 virus in wild birds have not been conducted. The primary reason is that serological assays that can discriminate between birds exposed to LPAI (H5) viruses and birds exposed to the Asian lineage HPAI H5N1 virus are not yet available. Recently, it has become clear that the antigenic properties of Asian lineage HPAI H5N1 viruses are changing rapidly (http://www.who.int/csr/disease/avian_influenza/guidelines/recommendationvaccine.pdf). It is possible that, based on the differences in antigenic properties between LPAI and Asian lineage HPAI H5N1 viruses, serological tests can be designed that will be useful for serological surveys in wild birds. Such studies would then allow the rapid identification of previously exposed wild bird populations and subsequent intensified targeting of these populations in virus surveillance studies. These studies should be conducted by reference laboratories that have extensive experience in the use of serology for influenza virus.

5. Recommendations

5.1. Differences between high risk species assessments

- The Working Group's original report and the Panel opinion be amended to resolve minor differences in species listings as described above.

- An updated assessment is made of the risks of the spread of infection within the EU using information on the species involved in the spring 2006 outbreaks (and the results from surveillance programmes in 2005/06).

- That, as time did not permit the assessment of the potential role of waterbirds other than *Anatidae* and waders in EFSA's earlier published assessment, assessments are now undertaken for other waterbirds (*e.g.* herons, gallinules and Coot *Fulica atra*, and some others) [see Chapter 13 in the original EFSA opinion]. Herbivorous species such as Moorhen (*Gallinula gallinula)* and Coot are potentially likely to have high contact rates with poultry but have not formally been assessed through the filter process set-out in either the EFSA or DG Environment reports.

- Field studies should be urgently undertaken on the behaviour of so-called bridge-species (*e.g.* sparrows, starlings, crows, pigeons *etc*. [see chapter 13 of original opinion]) that associate with man and may act as a bridge between waterbirds and poultry. This should include consideration of bird behaviour with the aim of developing practical guidance on ways and means of reducing this risk. Such work should also analyse data for such species from outbreaks and surveillance in 2005 and 2006 to help understand the rôle of bridge species as local vectors of avian influenza viruses.
- In the event of future outbreaks of HPAI H5N1 it will be important to assess the infection status of potential bridge species to better understand their actual or potential rôle as local vectors of avian influenza viruses.

5.2. Identification of key issues for developing risk-based surveillance in wild birds

- A pan-European assessment of surveillance data collected since 2005 needs to be undertaken as a matter of urgency. As well as summarising and analysing results by species, this should attempt to summarise sampling effort by location and thus (to the extent possible) against the different biogeographical populations of the waterbirds concerned, and thus the different flyways used by these populations.
- Given the expressed desire of the EU to establish ‘early warning systems’, future analysis and reporting of AIV surveillance data needs to be much more rapid and responsive, as previously recommended, the current development of on-line systems of data-capture and reporting of AI surveillance results by the Community Reference Laboratory (CRL) is a welcome development. It is important that this work is completed by the CRL’s and implemented by EU Member States as soon as possible.
- The critical importance of correct identification of sampled birds to at least the relevant species continues to require strong reinforcement with Member State authorities responsible for AIV surveillance, as does the value of collecting ancillary data such as that related to age and sex of the birds so as better to develop an understanding of the apparently unique epidemiology of Asian lineage HPAI H5N1. To this end, we recommend that close co-operation between the national veterinary authorities and non-governmental organisations with specialist ornithological expertise should continue to be strongly encouraged.
- It is highly desirable to better develop wider international perspectives in the collection and analysis of data on avian influenza viruses along migratory flyways, especially in those areas from where birds will migrate into the European Union. To this end, the development of the Global Network for Avian Influenza Surveillance (GAINS) as an international initiative (and

NEWFLUBIRD in western Eurasia and Africa as a possible regional component of GAINS) should be encouraged.

- The information provided in Delaney et al. (2006) provides a summary of extensive data-holdings and should be used by Member States to develop better targeted (risk-based) surveillance programmes.
- Whilst there is now a clear understanding of the distribution of higher-risk waterbirds in Europe, further work is desirable to overlay this information on main centres of poultry production as an important next step in European risk assessment. Work by the British Trust for Ornithology (BTO), presented at the British Ornithologists' Union (BOU) conference on bird diseases (20 & 21 Nov 2006, Peterborough), provides one approach, albeit considering a larger suite of wild birds than just waterbirds, for the UK.
- Guidelines for avian influenza surveillance in 2007 published by the European Commission in May 2006 (DG SANCO 2006) have responded to a number of problems apparent from surveillance of wild birds conducted in 2005. We recommend that these guidelines be reviewed in the light of the recommendations of this addendum, in particular the need for more co-ordinated and strategic approaches at a European scale. We envisage that this will require co-ordinated approaches between neighbouring Member States, especially those located on similar flyways, in particular to produce regional samples, as outlined in section 3.1.

5.3. Factors to be considered when designing a surveillance programme

- Research on the ecology of H5N1 HPAI Asian lineage and in general on AIV in wild birds is needed. Analytical methods to estimate the size of the sampling units and its species composition need to be developed
- Research on methodological developments for sample size calculation is needed (incorporating demographic and epidemiological parameters such as lifespan, lethality, intra and infra groups/species contact rate)

5.4. Update on diagnostic approach for the detection of Asian Lineage H5N1 HPAIV in Wild Bird Populations

- Based on the recent results from experimental infections of ducks and diagnostic tests performed on infected wild birds found dead in the field, it is recommended that where practically possible, selected tissues (e.g. lung, brain, kidney) are tested since they offer the most sensitive tool. However, oropharyngeal swabs provide a valuable alternative in times of heavy demand placed upon veterinary and laboratory resources.
- It is recommended that oropharyngeal and cloacal swabs should be collected from live healthy birds for the presence of both HPAI and LPAI. Any sampling of live birds should minimise suffering and adhere to regulations of the national animal ethics guidelines including the provision of training as necessary.

5.4.1. Recommendations for future research

- Antigen cartography should be investigated to determine its potential to reveal epitopes that may discriminate between LP and H5N1 HPAI viruses of the Asian Lineage.
- The dynamics of the immune response in exposed wild birds should be defined.
- Serological investigations at the research level should be initiated to obtain broad estimates of infection levels in wild bird populations, taking into account parameters of the animal sampled, specifically the species, age and virus heterogeneity.
- Detailed validation data should be collected on the use of different sample types for H5N1 virus detection in dead wild birds together with the sensitivity of post sampling handling of such specimens.

6. References

Andersson, Å., Madsen, J., Mooij, J. & Reitan, O., 1999. Chapter 16. Canada Goose *Branta canadensis* Fennoscandia/continental Europe. Pp. 236-245. In: Madsen, J., Cracknell, G. & Fox, A.D. (eds.) *Goose Populations of the Western Palearctic. A review of status and distribution.* Wetlands International Publ. 48, Wetlands International, Wageningen, The Netherlands. National Environmental Research Institute, Rønde, Denmark. 344 pp.

Beaglehole, R., Bonita, R., Kjellesatrom, T., 1993. Basic Epidemiology. WHO

Brown J. D., Stallknecht D. E., Beck J.R., Suarez D. L., Swayne D. E., 2006. Susceptibility of North American Ducks and Gulls to H5N1 Highly Pathogenic Avian Influenza Viruses, Emerging Infectious Diseases 12:1663-70.

Delany, S., Veen, J., Clark, J. (eds.), 2006. *Urgent preliminary assessment of ornithological data relevant to the spread of Avian Influenza in Europe.* Report from Wetlands International and EURING to the European Commission. 343 pp. (At: http://ec.europa.eu/environment/nature/nature_conservation/focus_wild_birds/avian_influenza/index_en.htm)

DG SANCO 2006. *Guidelines on the implementation of survey programmes for avian influenza in poultry and wild birds to be carried out in the Member States in 2007.* European Commission, SANCO/10268/2006.

EFSA, 2006. Scientific Opinion on “Migratory birds and their possible role in the spread of highly pathogenic Avian Influenza (EFSA-Q-2005-243)”. Adopted on 12th May 2006. The EFSA Journal (2006) 357, 1-46. http://www.efsa.europa.eu/en/science/ahaw/ahaw_opinions/1484.html

Olsen B., Munster, V.J., Wallensten, A., Waldenstrom, J., Osterhaus, A.D.M.E., Fouchier, R.A.M., 2006. Global patterns of Influenza A virus in Wild Birds. Science 312(5772):384-388.

Pfeiffer, D.U., Brown, I., Fouchier, R.A.M., Gaidet, N., Guberti, V., Harder, T., Langston, R., Soares Magalhaes, R.J., Martin, V., Sharp, J.M., Stärk, K., Stroud, D.A., Szewcyk, B., Veen, J. & Waldenström, J. 2006. *Scientific*

Report on migratory birds and their possible role in the spread of highly pathogenic avian influenza. 155 pp + 20 pp figures. [Annex to: Migratory birds and their possible role in the spread of highly pathogenic avian influenza. *The European Food Safety Authority Journal* 357: 1-46.] http://www.efsa.europa.eu/en/science/ahaw/ahaw_opinions/1484.html

Rees, E.E.C., Matthews, G.V.T., Mitchell, C.R., Oven, M., 2005. Movements and Migrations in: J. Kear (Ed.) – Ducks, Geese and Swans. Oxford University Press.

Snow, D.W. and Perrins, C.M., 1998. *The Birds of the Western Palearctic.* Volume 1: Non-Passerines. Concise Edition. Oxford & New York, Oxford University Press.

Stärk K.D.C., Regula, G., Hernandez, J., Knopf, L., Fuchs, K., Morris, R.S., Davies P., 2006. Concepts for risk-based surveillance in the field of veterinary medicine and veterinary public health: A review. BMC Health Services Research, 6:20 www.biomedcentral.com

Wetlands International 2002. *Waterbird Population Estimates – Third edition.* Wetlands International Global Series No. 12. Wageningen, The Netherlands.

7. 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 this Addendum to the Scientific Opinion.

The scientific co-ordination for this Addendum has been undertaken by the EFSA AHAW Panel Scientific Officers, J. Serratosa and O. Ribó.

8. AHAW Scientific Panel Members

The Scientific AHAW Panel adopted this Addendum to the Scientific Opinion on 11/12/2006. Members of the AHAW Panel are:

Bo Algers, Harry J. Blokhuis, Donald M. Broom, Patrizia Costa, Mariano Domingo, Mathias Greiner, Daniel Guemene, Jörg Hartung, Trevor Hastings, Per Have, Frank Koenen, Christine Muller-Graf, David B. Morton, Albert Osterhaus, Dirk U. Pfeiffer, Moez Sanaa, Mo Salman, J. Michael Sharp, Philippe Vannier, Martin Wierup, Marion Wooldridge.