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Surveillance for avian influenza in wild birds carried out by Member States

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Newcastle disease*

**ANNUAL REPORT OF THE EU AVIAN
INFLUENZA SURVEILLANCE IN WILD BIRDS
2006**



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SUMMARY

This report provides information on the surveillance of wild birds for Avian Influenza in European Member States (MS) and Switzerland. In 2006, all EU MS including Bulgaria tested a total of 144, 805 birds and in addition Romania tested approximately 5103 birds. Switzerland sampled from 1529 birds in 2006 (excluded from EU total).

This total number of birds tested was treble the number of wild birds tested in 2005. Half of the total number of birds tested were sampled in just three Member States (Germany, the Netherlands and Spain).

There was a large variation between Member States in respect to their focus on active or passive surveillance and also in the degree of targeting risk species. Data from Spain and Romania could not be included in the report as it was provided at an aggregated level and therefore has not been included in the figures below. (Switzerland also not included in EU total)

- Overall the majority of birds (55% in the EU) were tested between February and May. Exceptions were Belgium and Latvia, where the highest number of samples was taken between June and August 2006 and Denmark, Italy and Sweden where the highest number of samples were taken between September and December 2006.
- Most MS increased the active surveillance of live and hunted birds in the course of the year and 61% of all live or hunted birds were sampled between September and December.
- Passive surveillance decreased both in terms of the numbers and the proportion of the total sampled birds in most MS and 84% of all dead and diseased birds were tested between February and May 2006.
- Overall the proportion of risk species amongst the sampled birds increased in the course of the year.
- A large heterogeneity occurred between MS in respect to their surveillance programmes and especially the number of birds tested. Whilst some Member States focused on the active surveillance of live birds, others focused on passive surveillance of dead or diseased birds. The degree of targeting of risk species and sample types also varied between Member States. As these factors impact on the probability of obtaining positive results, **the proportion of birds that were found to be positive for avian influenza cannot be directly compared either between species or countries.**
- The proportion of samples that yielded a positive result cannot be interpreted as indicating prevalence of avian influenza in a country or species for the following reasons:

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- The sampled birds of a particular species are unlikely to be representative of the wild bird population of that species
 - As previously mentioned, there is considerable heterogeneity in the surveillance methodologies amongst Member States
 - The probability of any bird of a particular species being sampled is not equal
 - The probability that a sample from a particular species yields a positive result is not equal
 - Finally, wild bird populations are dynamic, so a sample taken at a particular place and time is not representative of that place and time at some future date.
- In total, 590 cases of H5N1/ H5 HPAI were reported in the period between February and May 2006 from 13 Member States. However, an additional 270 (plus 4 from mammalian species) cases occurred in Germany that could not be included in the report due to the format of the data. One additional case of H5N1 was reported in the period between September and December from Spain.
 - Most MS found a much higher proportion of H5N1/ H5 HPAI positive birds through the surveillance of dead or diseased risk species, indicating that this was the most valuable surveillance source for the detection of H5N1.
 - Overall, the proportion of swans (*Cygnus spp.*) positive for H5N1/ H5 HPAI out of the swans tested in February – May was 6.1%, which is very high when compared to the proportion of positive samples in all other species (excluding swans) in which 0.3% of tested birds gave a positive result. Overall 71% of all reported H5N1 infections were detected in swans.
 - Between February and May 2006, 13% of the total sampled diving ducks (*Aythya spp.*) tested positive for H5N1/ H5 HPAI. The proportion of H5N1/ H5 HPAI infected Tufted Ducks (*Aythya fuligula*) was especially high in Denmark (66%) (72% between February and May) and Sweden (19.7% (24% between February to May), where most of the positive diving ducks originated from this species. In these two countries, Tufted Ducks accounted for 57% (Denmark) and 45% (Sweden) of the total H5N1 infections.
 - All infections were detected in several raptor species such as Buzzards, Falcons and Owls. Since these birds get infected through feeding on dead or diseased infected birds they are also a potentially valuable additional surveillance source for avian influenza.

In total, 1616 birds in 18 MS (excluding 4 positives from CH) tested positive for subtypes other than H5N1/ H5 HPAI or the subtype was not determined or was still pending at the time of reporting. For the majority of these (62%) the subtype could not be determined. LPAI H5 was detected in 136 birds from eight MS: DK (8), FR (49), DE (8), IT (1), NL (38), PL (1), SE (19) and UK (12). Most (88%) LPAI

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H5 infections were found through the surveillance of live or hunted birds of risk species. More LPAI H5 infections (66%) were identified in the last reporting period (after the 1st of September). Most (92%) of these H5 LPAI infections were detected in dabbling ducks. No HPAI H7 was reported in 2006. 26 cases of LPAI H7 were identified in five Member States: AT (6), DE (2), IT (11), NL (6) and PT (1). Similarly to LPAI H5, the large majority of the LPAI H7 infections (85%) occurred in dabbling ducks, however the majority of infections (85%) were detected in the first reporting period.

Conclusions:

- For detection of H5N1, passive surveillance through the testing of dead and diseased birds, especially swans, diving ducks and mergansers has been shown to be the most valuable surveillance source and almost all H5N1 outbreaks were discovered through a positive test result of dead swans. Consequently the maintenance of a good functional passive surveillance system appears very important for the early detection of H5N1. If practically and ecologically feasible the placement of sentinel swans (if not already present) for observation in high-risk areas might be a cost efficient surveillance method.
- For the detection of other subtypes, the surveillance of live or hunted birds, especially of dabbling ducks appeared to be the best surveillance source.

INTRODUCTION

Wild birds have been known to be a reservoir of low pathogenic avian influenza viruses and much more rarely highly pathogenic avian influenza viruses (Alexander, 2000). The main value of surveillance in wild birds for the poultry industry is the detection of infection with H5/H7 avian influenza strains, which could lead to outbreaks of highly pathogenic avian influenza in poultry after mutation in the poultry host. Since the emergence and establishment of the highly pathogenic avian influenza virus subtype H5N1 of the Asian lineage in Asia and Africa, this aspect has become of increased importance, as wild birds are one of the possible routes of introduction of the virus in to the European Union.

In 2002 the European Commission decision 2002/649/EC included the surveillance of wild birds for avian influenza by means of a preliminary survey, especially in Member States (MS) that had already established wild bird surveillance. The first guidelines for the surveillance of avian influenza were established: The implementation of the survey was to be carried out in cooperation with bird conservation/ ornithological research institutions and hunters. Sampling was recommended to be carried out through cloacal swabs and to include 70% waterfowl, 20% shorebirds and 10% other free-living birds. The outcome of this surveillance was aimed to provide an early warning system for strains that could be introduced into poultry flocks as well as to contribute to the knowledge of the threat of avian influenza to animal health.

In 2004, sixteen MS submitted 7482 samples from wild birds for virological examination, of which 15 were positive for the H5 subtype and 7 for the H7 subtype; positives for H5 occurred in Denmark (2), Germany (1) and Italy (12) (Jordan and Brown,).

In 2005 Decision 2005/464/EC was adopted by the European Commission, which included revised guidelines with further recommendations such as focusing sampling on birds that were migrating south during autumn and early winter. Due to the evolution of the H5N1 epidemic in Asia, it was decided to intensify the planned wild bird surveillance and the decision was amended by Decision 2005/726/EC. Guidelines were much more specific and included separate recommendations for active and passive surveillance, which were advised to be risk based and to target higher risk species based on their origin, migratory flyways, numbers and their likelihood of contact with poultry. Sampling was advised to take place in locations where mixing of migratory birds occurs, that are in proximity to poultry farms or located along flyways. A provisional list of 15 wild bird species that were thought to present a higher risk in relation to avian influenza was introduced with the proviso that this will be updated with new scientific evidence. It was also recommended that tissue samples were collected from dead birds.

In 2005, 47232 birds were tested, which was almost 6 times the number tested in the previous year and all 25 MS participated. 165 samples tested positive for subtypes H5/H7. The H5 subtype was

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found in 10 MS namely: Denmark, France, Germany, Greece, Italy, Latvia, The Netherlands, Spain, Sweden and the UK (Cooke, Powell et al.).

Surveillance in wild birds, which so far had been conducted on a voluntary basis, became compulsory with the adoption of Decision 2006/101/EC in February 2006. The decision kept the guidelines for surveillance described in Decision 2005/464/EC, but added that serological surveillance should not be carried out in wild birds.

In May 2006 the European Food Safety Authority (EFSA) produced an updated list of risk species (EFSA, 2006). This list was established using the following criteria: gregariousness during migration/wintering periods (group size and group density), degree of mixing during migration wintering periods, main habitat during migration/ wintering and degree of mixing with other species. It included 14 of the 15 species listed in Decision 2005/464/EC, as well as a group of 13 additional species, and was integrated in the new guidelines on avian influenza surveillance in 2007 in the Commission Document SANCO/10268/2006 Rev.5 (SANCO, 2006).

The actual surveillance programmes conducted in MS were very diverse in many aspects, including the sampling method, the relative importance of active surveillance compared to passive surveillance and the actual number of birds collected. This diversity in programmes and the reporting of aggregated data had an impact on the interpretation of the results, which is considered in the discussion section of this report.

In principle three types of wild bird surveillance were implemented across MS:

- Active surveillance, focusing on the testing of live birds, most of times targeted towards higher risk species and/or risk areas
- Passive surveillance monitoring increased morbidity and mortality
- Sentinel surveillance, most frequently using ducks kept in high-risk areas that were submitted to regular testing

In 2006, the information collection was extended and data were collected in a harmonised manner allowing more detailed analysis than in the previous years. Furthermore, the European Epidemiology Working Group for Surveillance of Avian Influenza in Wild Birds was established to discuss results of wild bird surveillance for avian influenza and to continuously improve data analysis. This process is intended to provide an increased insight into the epidemiology of avian influenza and outputs of the analysis may contribute to the optimisation of targeting of wild bird surveillance, keeping in mind the two main objectives of wild bird surveillance:

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1) To ensure early detection of HPAI H5N1 by investigating especially the increased incidence of mortality in wild birds, in particular in selected higher risk species.

2) To continue a baseline surveillance of different species of free-living migratory birds as part of a continuous monitoring of LPAI viruses. Waterfowl and shorebirds (Anseriformes and Charadriiformes) are considered as the main target to determine potential carriage of LPAI H5/H7 viruses (SANCO, 2006).

Within this report the results of the 2006 wild bird surveillance will be presented and discussed in relation to the above objectives.

OBJECTIVES

- Present the 2006 wild bird surveillance data reported by MS in a comparative manner
 - Present a descriptive analysis of these data
 - Discuss relevant findings
-

MATERIALS AND METHODS

This report was produced by the EU Community Reference Laboratory (the Veterinary Laboratories Agency – Weybridge) in close collaboration with the European Epidemiology Working Group for Avian Influenza.

The survey programmes

Details of the survey programmes for each MS are available on the Internet at http://ec.europa.eu/food/animal/diseases/eradication/2006_314_ec.pdf

The testing of samples

Details regarding the specific surveillance programmes are presented in Appendix 1.

Laboratory tests were carried out in accordance with the avian influenza diagnostic manual. As laid down by Commission Decision 2006/437/EC (EU Commission), member states that wished to use alternative tests were obliged to submit the necessary validation data to the Community Reference Laboratory (CRL) for approval. It was recommended that all tests should be carried out at National Reference Laboratories for avian influenza or by other laboratories authorised by competent authorities and under the control of the National Laboratories. Results were sent to the CRL for Avian Influenza for collation.

It was recommended that samples should initially be tested using M gene PCR (to detect presence of avian influenza virus), with rapid testing of positives for H5 and that analysis of the haemagglutinin cleavage site should be undertaken to determine the pathogenicity of the avian influenza virus (EU Commission).

Data processing and completeness

All data records were submitted from the MS to the CRL via the European Commission. This report is restricted to data that were collected and submitted to the EU commission under EU decision 2006/101/EC. Consequently the data may differ from other reporting systems such as the ADNS to which outbreaks of avian influenza in wild birds are reported. Records were checked for data quality and completeness. If deemed necessary, queries were sent out to MS and their responses were integrated before the data were uploaded into the database and combined with species information from the EURING database (<http://www.euring.org/>). Species information was then evaluated by ornithologists from the European Epidemiology Working Group for Surveillance of Avian Influenza in Wild Birds for potential data errors or reports of captive birds and if identified, these were then excluded from the analysis. Records of samples collected on dates outside the relevant reporting period (for example records collected in the February to May period but reported in June and vice versa), were included in this report and are reported under the appropriate period for their sampling date, which may lead to discrepancies in sample numbers compared to other reports.

- Data from Spain were reported in an aggregated format that precluded inclusion in this report and are therefore only described in summaries and are not included in most graphs.
- In addition to EU MS, data was also received from Bulgaria, Romania and Switzerland and these have been integrated into this report: Whilst Bulgaria is integrated into the EU total numbers, as it became a MS in 2007, Romania was not due to formatting problems and Switzerland has not been included as it is not a part of the EU.
- The following MS sent amended data following an opportunity to review the annual report, and as such, their amended data has been integrated into this report: Austria, Belgium, Cyprus, Denmark Italy and Slovenia.
- Denmark – Some of the positive findings were found in pools of five birds, which could not be separated at the laboratory.

For the creation of tables of risk species (species with a higher probability to contribute to the transmission of Asian lineage H5N1 HPAI inside the EU due to their susceptibility, habitat and behaviour (EFSA 2006)) and bridge species (species that have either a low, medium or high probability of contact with poultry or that share wetlands or farmlands (EFSA 2006)), 3 sources of information were used:

- The risk species listed in the SANCO document SANCO/10268/2006 Rev.5 (SANCO 2006)
- The EFSA Scientific Opinion on “Migratory birds and their possible role in the spread of highly pathogenic avian influenza” adopted by the Animal Health and Welfare Panel of EFSA on 12 May 2006 (EFSA, 2006) and

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- The work carried out by the ORNIS Committee and contractors to DG Environment

The proportion test function in the statistical software package R (Ihaka and Gentleman 1996) was used to test for differences between the overall proportion of positive samples and the proportion of positive samples detected by each surveillance activity (e.g. live birds, dead birds, etc).

Definitions:

Positive/ Infected: For the purpose of this report, a positive/ infected case of avian influenza is defined as a bird, from which at least one sample tested positive on either PCR or virus isolation.

Risk Species: Species listed as those with an increased probability to contribute to the transmission of the Asian -lineage H5N1 viruses within Europe as defined in the scientific report by EFSA (EFSA, 2006) and the 2007 guidelines(SANCO, 2006) (in total 29 species). The EURING codes corresponding to these species are listed in Annex 5

Bridge species: Species listed as those that may provide contact between risk species and poultry through sharing of wetlands or farmlands with poultry EFSA. Categorisation of the risk into high, medium and low was also used from the EFSA Scientific Opinion (EFSA, 2006), (SANCO, 2006)).

Passive surveillance: For the purpose of this report, passive surveillance will be used as an equivalent to the surveillance of dead or diseased birds

Active surveillance: For the purpose of this report, active surveillance will be used as an equivalent to the surveillance of live or hunted birds.

Origin: Relates to the collected information on the status of the bird when sampled. The four categories are: live, hunted, diseased and found dead.

Data completeness (EU 24 + Bulgaria):

Species of birds:

Species information was complete for 94% of the birds' records. For 6.40% no EURING code was provided, 1.1% of the records had unknown EURING codes (00000) and for 11.36% of the records information was only supplied at genus level.

Origin of birds:

All Member States except one, provided information on the origin of birds sampled. Eighteen Member States gave complete information on the origin of birds sampled. Overall this information was complete for 96.5% of the submitted data. Information on this parameter improved throughout the year and in the last quarter 98% of records had this information provided.

Subtype information:

This was complete for all positive samples from all MS throughout the year.

Date:

Date information was 100% complete for 21 out of 25 MS (including BG). The lowest percentage of completed date information reported from a member state was 88.2% (IT). Completion of this field improved significantly throughout the year and information was basically complete for the second and third quarter.

Spatial information:

Spatial information (either geographical coordinates or ADNS codes) was provided for 58.6% of the sampled birds. Ten MS were able to provide spatial information for their complete data set.

Abbreviation	Country
AT	Austria
BE	Belgium
BG	Bulgaria
CH	Switzerland
CY	Cyprus
CZ	Czech Republic
DE	Germany
DK	Denmark
EE	Estonia
EL	Greece
ES	Spain
FI	Finland
FR	France
HU	Hungary
IE	Ireland
IT	Italy
LT	Lithuania
LU	Luxembourg
LV	Latvia
MT	Malta
NL	Netherlands
PL	Poland
PT	Portugal
RO	Romania
SE	Sweden
SI	Slovenia
SK	Slovak Republic
UK	United Kingdom

Table 1 Key to Member State abbreviations

Phylogenetic tree

Samples were received by the EU Community Reference Laboratory (CRL) at the Veterinary Laboratories Agency (VLA), Weybridge, UK in the form of tissue or allantoic fluid from 9-10 day-old SPF embryonated chicken eggs used for virus isolation. RNA was extracted using QIAamp RNA extraction kits (QIAGEN, UK). The HA1 fragment of the haemagglutinin gene was amplified with the use of QIAGEN One-step RT-PCR kits (QIAGEN, UK). The HA1 PCR amplicons were visualised by Ethidium bromide staining after electrophoresis through 2% agarose gel (Invitrogen, UK) and purified using QIAquick gel extraction kits (QIAGEN, UK). RT-PCR products were sequenced by cycle-sequencing reactions using ABI Terminator cycle sequencing V3.1 chemistry on a Perkin-Elmer ABI Prism™ 3130xl Genetic Analyser (Applied Biosystems, UK). Sequence data was assembled, edited and aligned using the Lasergene SEQMAN and MEGALIGN v7.1 software (DNASTAR Inc, USA). Additional Asian-like H5N1 sequences, used for comparison, were obtained from the National Centre for Biotechnology Information (NCBI). Phylogenetic and molecular evolutionary analyses were performed using MEGA version 3.1 (Kumar, Tamura, Nei 2004) using the Minimum Evolution (ME) algorithm with 1000 bootstrap replicates.

RESULTS

Unless specified otherwise, all totals and overall proportions refer to 24 EU MS (excl Spain and Romania) and including accession state Bulgaria.

During 2006, 144, 805 birds were sampled in the EU 25 plus accession state Bulgaria (Figure 1). Accession state Romania tested approximately 5103 additional birds (see explanation below) and Switzerland sampled a total of 1529 birds in 2006 (Switzerland excluded from EU total).

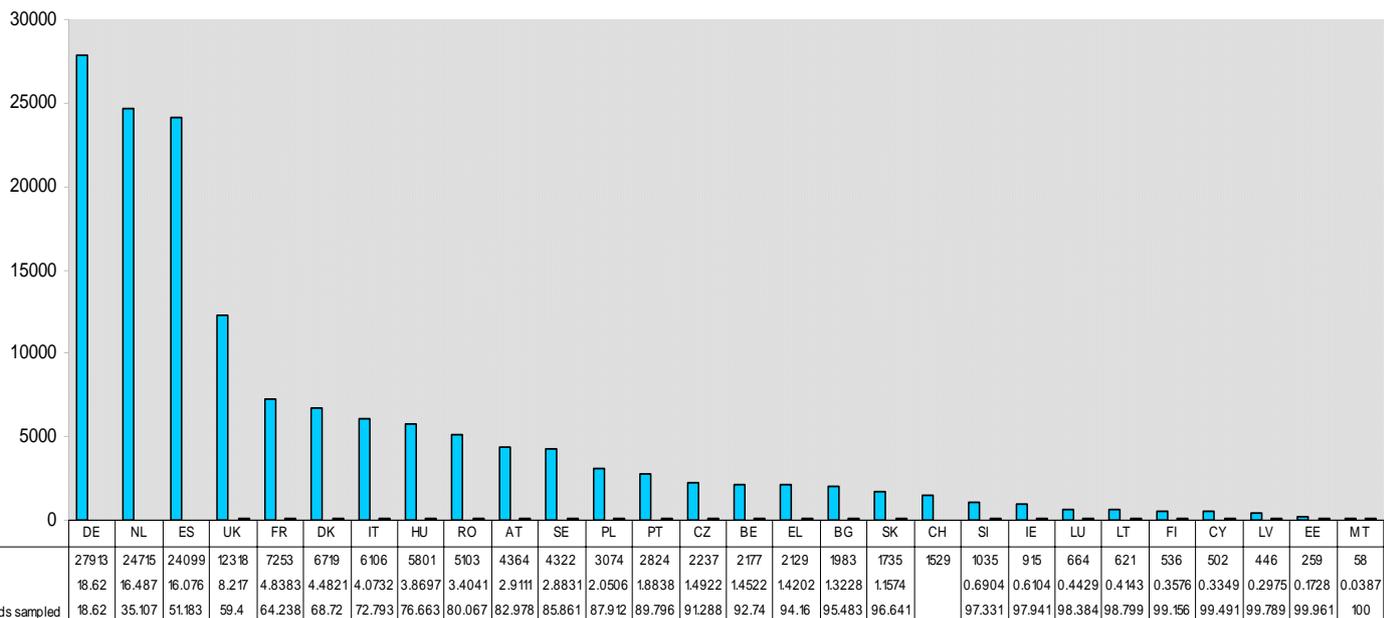


Figure 1 Total number of birds sampled in 2006 by MS including Bulgaria, Romania and Switzerland

Detailed Figures regarding the number of birds sampled by MS in each quarter are displayed in Annex 1.

Most of the birds tested in 2006 originated from five Member States: Germany, Spain, Netherlands, United Kingdom, France and Denmark. Eight Member States sampled fewer than 1000 birds throughout the year. These large differences in sampling numbers should be taken into consideration when interpreting the results of the surveillance.

The data received from Romania and Spain was reported in a format incompatible with further analysis and are therefore reported in Annex 6.

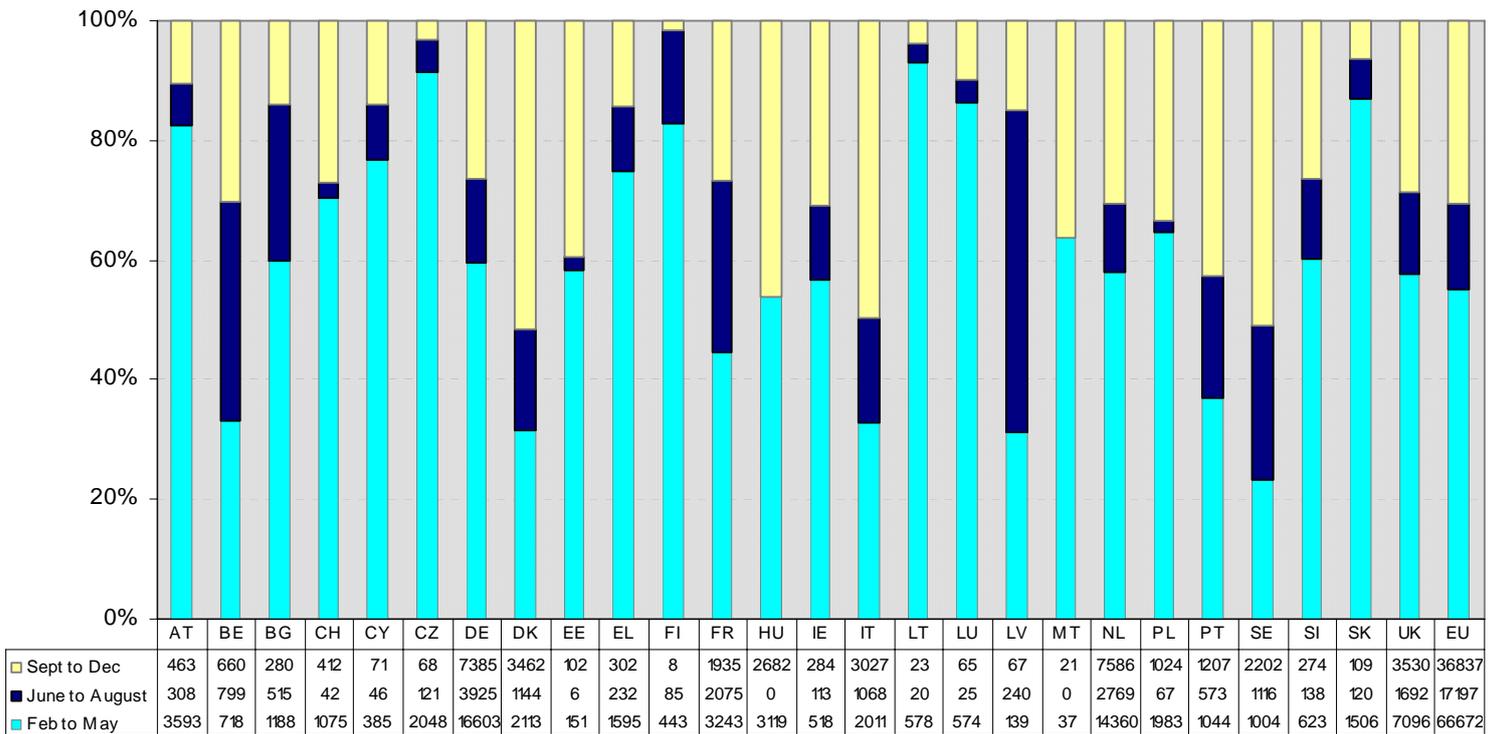


Figure 2 Number and proportion of all birds sampled by season and MS (EU total = EU 24 + Bulgaria)
 *EU total excludes CH

Most birds (55% in the EU 24 + Bulgaria) were tested between February and May due to outbreaks of H5N1 in 14 MS (including Bulgaria) (Figure 2). Exceptions were Belgium and Latvia, where the highest number of samples were taken between June and August and Denmark, Italy and Sweden where the highest number of samples were taken between September and December.

A large variation amongst MS occurred with respect to their focus on active or passive surveillance (Figure 3). While some MS focused on active surveillance in live birds as for example, Belgium, Denmark and Sweden, others focused on passive surveillance of dead birds, for example the Czech Republic, Slovakia and Lithuania. The importance of these two surveillance components also changed throughout the year (Figure 4): In the first quarter a large number of dead birds were sampled, probably because of the outbreaks of H5N1, associated heightened public awareness and harsh weather conditions, that led to an unusually elevated mortality. The proportion of dead birds collected amongst the birds sampled decreased considerably in the remainder of the year. The reverse is true for active surveillance in live birds, where not only the proportion of this category amongst all birds sampled, but also the absolute numbers sampled increased throughout the year with almost 61% of all live birds being sampled between September – December (Table 2).

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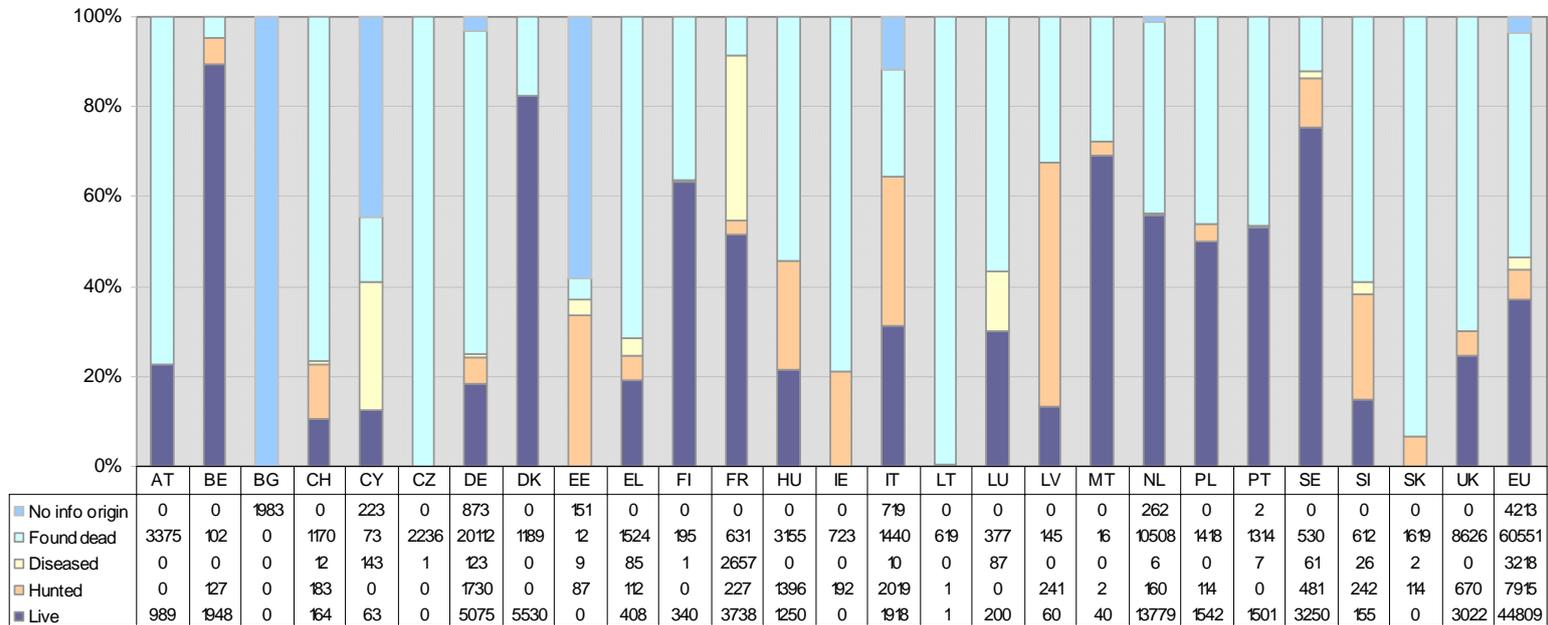


Figure 3 Number and proportion of birds sampled by origin and MS (EU total = EU 24 + Bulgaria)

*EU total excludes CH

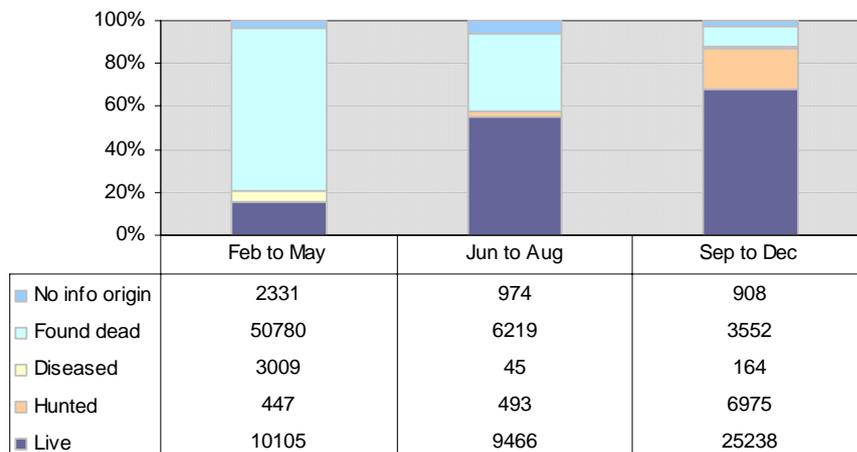


Figure 4 Number and proportion of total birds sampled by origin and season (EU 24+Bulgaria)

*Total excludes CH (RO and ES not included)

More detailed graphs displaying the distribution of origin categories amongst sampled birds for each MS and each reporting period can be found in Annex 2.

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Table 2 Number of birds tested in active surveillance by country (live and hunted birds)

Member State	Feb - May 2006	Jun - Aug 2006	Sep - Dec 2006	Total *
AT	585	55	349	989
BE	664	772	639	2075
BG*	0	0	0	0
CH	0	0	347	347
CY	32	9	22	63
CZ	0	0	0	0
DE	114	1078	5613	6805
DK	1102	1017	3411	5530
EE	0	0	87	87
EL	165	107	248	520
ES	NI	NI	NI	0
FI	312	26	2	340
FR	588	1720	1657	3965
HU	0	0	2646	2646
IE	0	0	192	192
IT	851	611	2475	3937
LT	2	0	0	2
LU	200	0	0	200
LV	17	239	45	301
MT	21		21	42
NL	4099	2436	7404	13939
PL	596	50	1010	1656
PT	278	275	948	1501
RO	NI	NI	NI	0
SE	485	1087	2159	3731
SI	56	91	250	397
SK		21	93	114
UK	385	365	2942	3692
EU 24 + Bulgaria	10552	9959	32213	52724

Table 3 Number of birds tested in passive surveillance by country (diseased and dead birds)

Member State	Feb - May 2006	Jun - Aug 2006	Sep - Dec 2006	Total *
AT	3008	253	114	3375
BE	54	27	21	102
BG*	NI	NI	NI	0
CH	1075	42	65	1182
CY	141	27	48	216
CZ	2048	121	68	2237
DE	16427	2660	1148	20235
DK	1011	127	51	1189
EE	0	6	15	21
EL	1430	125	54	1609
ES	NI	NI	NI	0
FI	131	59	6	196
FR	2655	355	278	3288
HU	3119	0	36	3155
IE	518	113	92	723
IT	442	457	551	1450
LT	576	20	23	619
LU	374	25	65	464
LV	122	1	22	145
MT	16	0	0	16
NL	10261	71	182	10514
PL	1387	17	14	1418
PT	766	298	257	1321
RO	NI	NI	NI	0
SE	519	29	43	591
SI	567	47	24	638
SK	1506	99	16	1621
UK	6711	1327	588	8626
EU 24 + Bulgaria	53789	6264	3716	63769

* Excluding any records where information on the origin of birds was unavailable or where the sampling date was unknown (Spain and Romania). CH also not included in the EU total.

Table 2 and Table 3 display the numbers of birds collected for active and passive surveillance respectively by MS and reporting period. Samples for which the origin of the birds or the sampling date was not reported were not included in this table. Most Member States increased their active surveillance significantly in the course of the year. The numbers of dead or diseased birds tested decreased in most MS and in most Member States the lowest number of dead or diseased birds was collected between September and December. Eighty four percent of all dead or diseased birds were tested between February and May 2006.

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A large variation between Member States also occurred in respect of targeting towards the high risk species as listed by EFSA (EFSA, 2006) and SANCO (SANCO, 2006). The proportion of all birds sampled in the EU in 2006 that were higher risk species was 51%, although this varied from as little as 4% (Bulgaria) to 70% (UK), as shown in Figure 5.

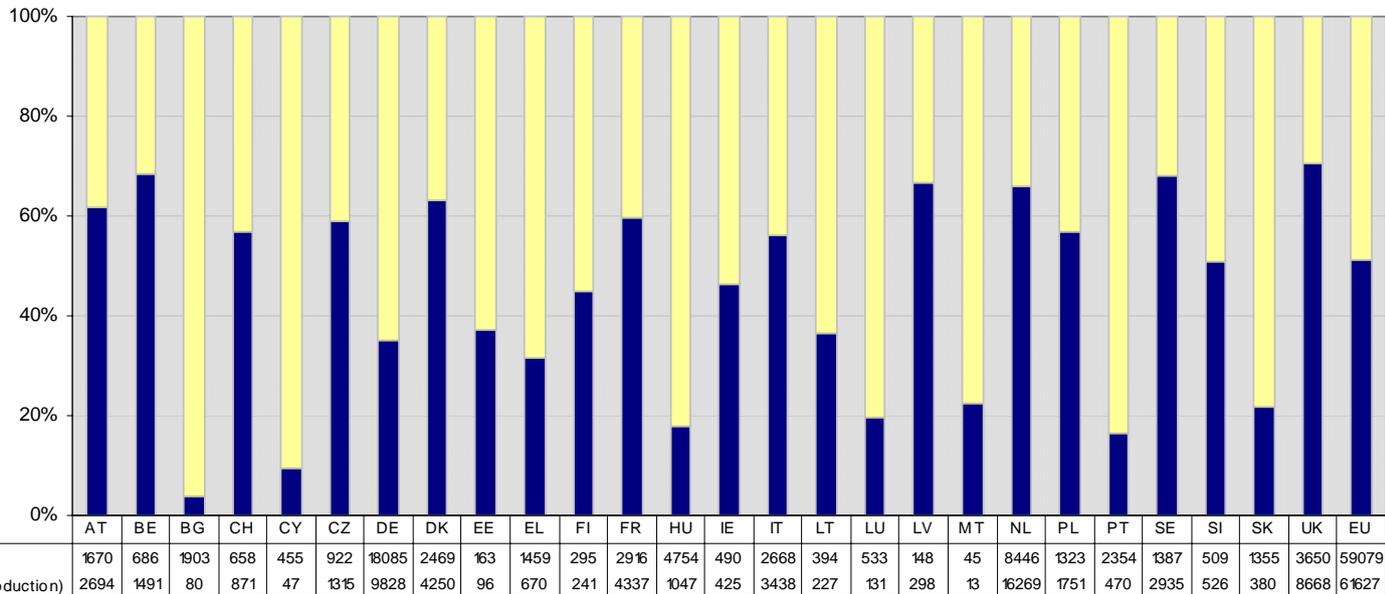


Figure 5 Number and proportion of birds sampled by risk species and MS (EU total = EU 24 + Bulgaria)

*EU total excludes CH

Most MS increased the amount of targeting of risk species in the course of the year, leading to an increase in the proportion of risk species sampled amongst the total (Figure 6).

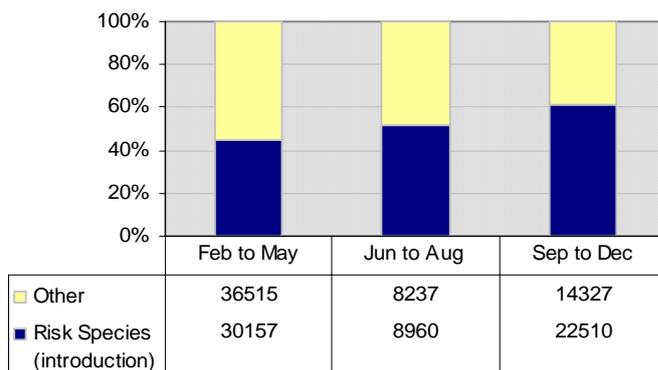


Figure 6 Number and proportion of birds sampled by risk species and season (EU 24 + Bulgaria)

More detailed graphs, displaying the proportion of risk species among the sampled birds by MS and reporting period are displayed in Annex 3.

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Figure 7 displays the number and proportion of bridge species (EFSA, 2006) sampled by MS. Figure 8 shows the proportion of bridge species in the three reporting periods. In the interpretation of these graphs it should be kept in mind that some species may be listed amongst the risk species and also be represented among the bridge species, for example Mallards (*Anas platyrhynchos*).

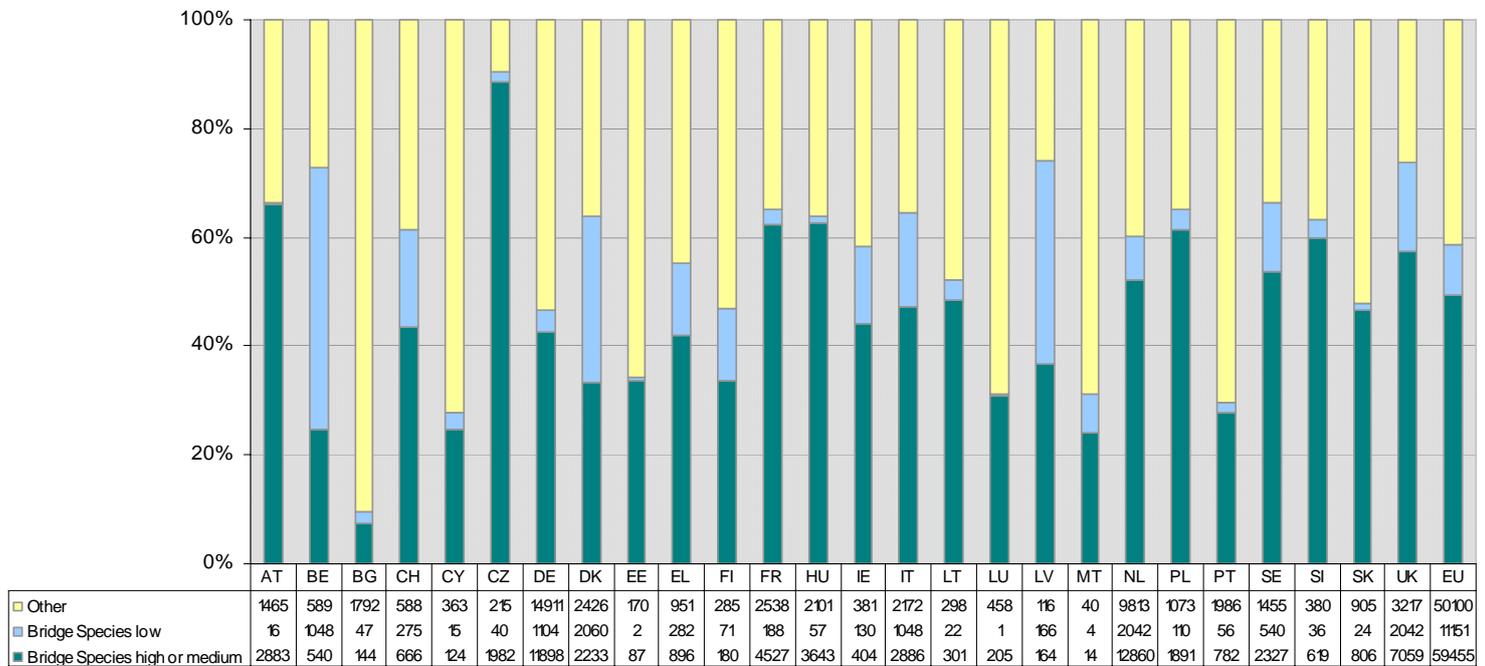


Figure 7 Number and proportion of birds sampled by bridge species and MS (EU total = EU 24 + Bulgaria)

*EU total excludes CH

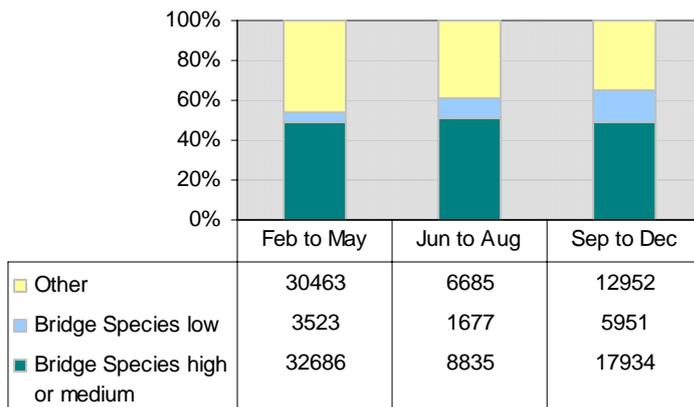


Figure 8 Number and proportion of birds sampled by bridge species and season (EU 24 + Bulgaria)

More detailed graphs, displaying the proportion of bridge species among the sampled birds by MS and reporting period are displayed in Annex 4.

POSITIVES

A differentiation is made between H5N1/ H5 HPAI infections and all other subtypes reported. Subtypes that were reported as not determined or pending are included in the category of all other subtypes. All H5N1 cases mentioned in this report are HPAI.

H5N1/ H5 HPAI positives

In the first reporting period between February and May 2006, 13 MS and Bulgaria reported a total of 590 birds infected with H5N1/ H5 HPAI. Romania reported two infected swans, one H5 HPAI and one H5N1, but no further details such as dates were available. H5N1 and H5 HPAI are reported together in this report, as many birds reported as H5 HPAI were likely to be H5N1, but due to the number of infected birds the neuraminidase was not always determined. In MS experiencing H5N1 infections, the proportion of H5N1/ H5 HPAI positive birds ranged from 0.01% (UK) to 7.38% (SI) (Table 4).

In addition to the 71 H5N1/ H5HPAI infected birds, Germany reported a further 270 H5N1/H5HPAI infected birds. These birds were not included in the tables and graphs of this report as the denominator data (data on the number of birds sampled) of the federal states these birds originated from was not available. It was therefore felt by the authors of this report that this would portray a skewed picture of the results and therefore these birds are only summarized at this point: The H5N1/H5HPAI positive samples originated from 41 different species the majority of those were taken from *Cygnus* species (137 birds, 51%). Ten percent of the total number of positive birds were from *Buteo spp.*, 9.6% from *Aythya spp.*, 7% *Anas spp.* and 3.7% *Larus spp.* In addition to the wild birds sampled, Germany also detected 2 mammalian species positive for H5N1: 3 cats and 1 Stone Marten.

In the second and third reporting period only one H5N1/ H5 HPAI case was detected; one H5N1 positive Great Crested Grebe (*Podiceps cristatus*) from Spain (date not available). Table 4 presents the overall proportion of H5N1/H5 HPAI positive birds for MS that did experience cases of H5N1 between February to May and according to four surveillance types (dead/diseased birds of risk species, dead/ diseased birds of other species, live/hunted birds of risk species and live/hunted birds of other species). Differences in the proportion of positive results in these surveillance types compared with the overall proportion by Member State are highlighted (red if the relevant proportion lies significantly above the overall mean and in blue if below).

Most MS found a much higher proportion of H5N1/ H5 HPAI positive birds through the surveillance of dead or diseased risk species, indicating that this was the most valuable surveillance source for the detection of H5N1. In Poland a total of 39 H5N1 infected mute swans were reported as live and not diseased. These swans belonged to a group of 113 swans that were quarantined in an aviary in the Torunski region. The first H5N1 positive swan of these 39 live mute swans was sampled on the 10th

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of March, a further six positive swans were tested on the 11th of March and the remaining 32 live positive swans were sampled on the 29th of March.

Table 4 Proportion of sampled positive by surveillance type and country, for countries that did experience H5N1 cases for H5N1/ H5 HPAI Feb-May 06

Member State Excl. Spain	Total number sampled a	Total number positive b	Total positive proportion b/ a	Proportion positive of dead or diseased risk species n= number sampled	Positive proportion in live or hunted risk species n= number sampled	Positive proportion in dead or diseased other species n= number sampled	Positive proportion in live or hunted other species n= number sampled
SI	623	46	7.38%	18.41% n=239	0.00% n=31	0.61% n=328	0.00% n=25
SE	1004	42	4.18%	8.87% n=282	0.00% n=88	7.17% n=237	0.00% n=397
PL	1983	70	3.53%	4.38% n=640	8.61% n=453	0.40% n=747	0.00% n=143
AT	3593	120	3.31%	5.18% n=2084	0.00% n=197	1.19% n=924	0.00% n=388
CH	1075	32	2.98%	2.91% n=515	Not sampled n=0	3.04% n=560	Not sampled n=0
DK	2113	45	2.13%	16.92% n=188	0.00% n=967	1.04% n=823	2.63% n=135
FR	3243	65	2.00%	5.62% n=978	0.00% n=145	0.60% n=1677	0.00% n=443
HU	3119	61	1.96%	18.35% n=327	Not sampled n=0	0.04% n=2792	Not sampled n=0
EL	1595	31	1.94%	6.38% n=470	0.00% n=100	0.10% n=960	0.00% n=65
IT	2011	19	0.94%	8.25% n=206	0.00% n=598	0.85% n=236	0.00% n=253
CZ	2048	14	0.68%	1.21% n=1157	Not sampled n=0	0.00% n=891	Not sampled n=0
DE	16603	71	0.43%	1.03% n=5070	0.00% n=53	0.17% n=11357	0.00% n=61
BG	1188	4	0.34%	No info	No info	No info	No info
SK	1506	2	0.13%	0.00% n=284	Not sampled n=0	0.16% n=1222	Not sampled 0
UK	7096	1	0.01%	0.02% n=4340	0.00% n=365	0.00% n=2371	0.00% n=20
TOTAL *	47725	590	1.24%				

* EU member states which reported birds positive for Avian influenza + Bulgaria for which origin of bird was known

Legend	No statistically significant difference to total proportion	Statistically significantly lower than total proportion p<0.05	Statistically significantly higher than total proportion p<0.05
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Phylogenetic tree

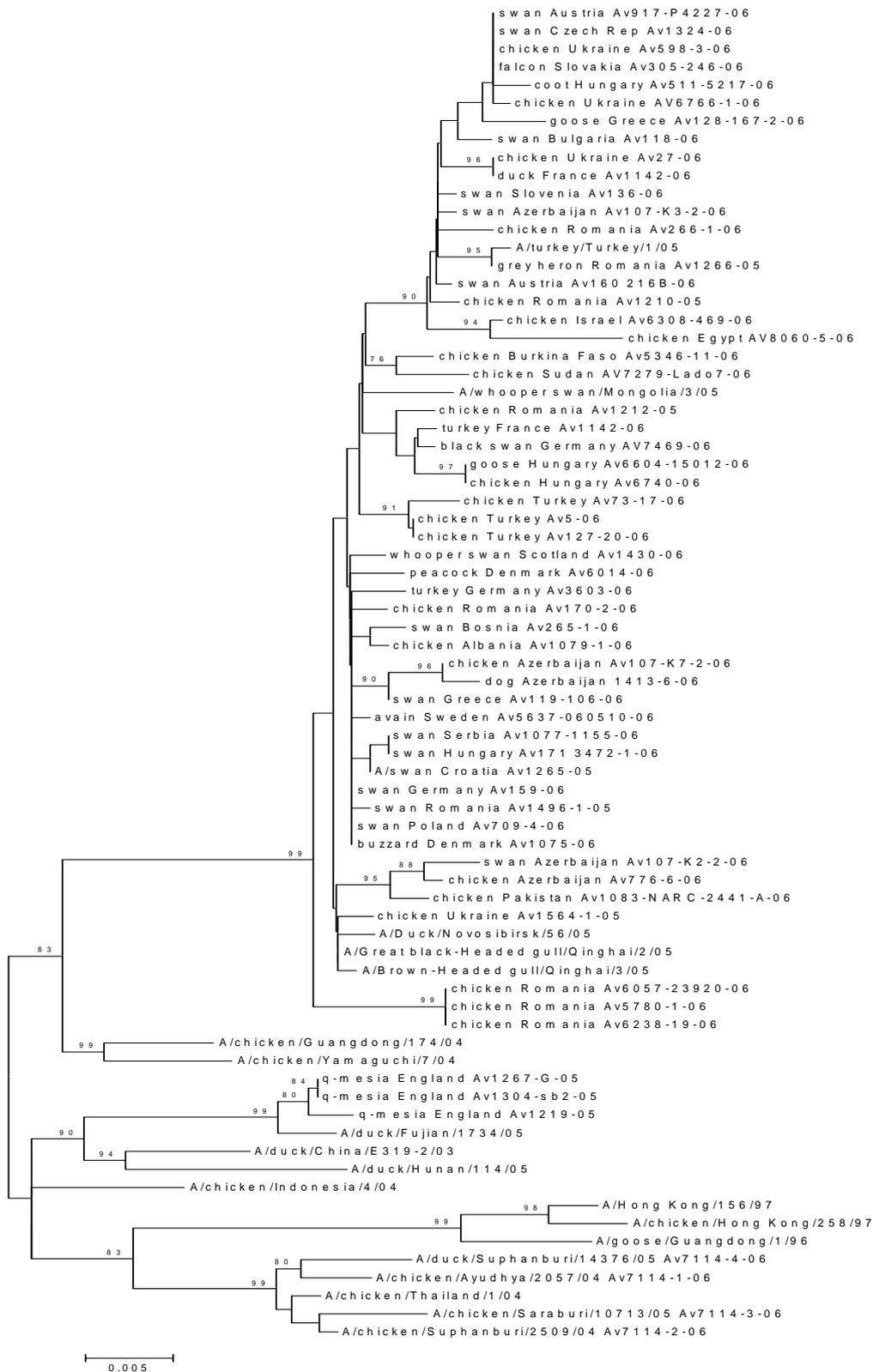


Figure 9 Phylogenetic tree of samples sent to VLA, Weybridge and incorporated reference sequences

Figure 9 displays the phylogenetic tree of all samples sent to the CRL in Weybridge and inserted reference sequences. Phylogenetic analyses of HA1 have placed these isolates within a phylogenetic grouping that has recently been classified as Clade 2 of the Asian-like H5N1 avian influenza viruses. What is immediately evident is the significant amount of evolution that has occurred during the spread of this H5N1 from its origin in South-East Asia, across Asia and into and across Europe and Africa. Several countries including Romania, Greece, Turkey, Azerbaijan and the Ukraine appear to have had simultaneous introductions of phylogenetically distinct isolates. It is also likely that two separate introductions have occurred in Romania as shown by the significant amount of evolution seen in viruses isolated in late 2006 in Romania (Av5780/06, Av6057/06 and Av6238/06) such that an entirely separate cluster has formed.

All Other Subtypes (excluding H5N1 H5 HPAI)

Infections with subtypes other than H5N1/ H5 HPAI were found in 1616 birds from 18 MS. For the majority of these (62%) the subtype could not be determined. LPAI H5 was detected in 136 birds from eight MS: DK (8), FR (49), DE (8), IT (1), NL (38), PL (1), SE (19) and UK (12). Most (88%) LPAI H5 infections were found through the surveillance of live or hunted birds of risk species. More LPAI H5 infections (65%) were identified in the last reporting period (after the 1st of September). Most (91.2%) of these infections were detected in dabbling ducks (*Anas spp.*). No HPAI H7 was reported in 2006. Twenty-six cases of LPAI H7 were identified in five Member States: AT (6), DE (2), IT (11), NL (6) and PT (1). Similar to LPAI H5, the large majority of the LPAI H7 infections (85%) occurred in dabbling ducks, but in contrast to LPAI H5, the majority of LPAI H7 infections (85%) were detected in the first reporting period. Table 4 displays the total and seasonal proportion of positives and number sampled by Member State.

The highest proportion of positives of subtypes other than H5N1 H5 HPAI in 2006 was found in Latvia, where 44 out of 446 birds tested positive for AI (subtype not determined). Most (31) of these positive birds in Latvia were detected within three days in August and 19 of those were sampled at the same location. All of the positive birds in Latvia (except one bird of the diving duck genus *Aythya* that was sampled live) were hunted dabbling ducks (genus *Anas*). Details on the species tested positive in Latvia can be found in the relevant MS section. A very high proportion of positive birds were found in Cyprus in the summer. Most of the 13 cases were detected in the first two weeks of August and all were of the same subtype (H1N1). Species involved included mainly mallards (*Anas platyrhynchos*) but also three Kestrels (*Falco tinnunculus*).

The increased proportion of positives birds found in Austria in the second reporting period (Jun - Aug) is mainly due to the finding of a group of gulls that were found dead that were infected with the H6 subtype. Apparently most of these birds died due to infection with Botulism, as were the birds infected with H1N1 in Cyprus (see below). Several MS detected a higher proportion of positives (when compared to the overall proportion of positives) (highlighted in red in Table 5) in the period from September to December 2006. This was especially true for Latvia, the Netherlands, Ireland, Slovenia,

UK, Germany and Poland, where the proportion of positive birds in the final sampling period (Sep - Dec) was more than double the overall annual proportion of positive birds.

Table 6 presents the overall proportion of positive birds for subtypes other than H5N1/ H5 HPAI according to four surveillance types (dead/ diseased birds of risk species, dead/ diseased birds of other species, live/ hunted birds of the risk species and live/ hunted birds of other species). Differences in the positive proportion in these surveillance types compared with the overall proportion by MS are highlighted (red if the relevant proportion lies above the overall mean and in blue if below). In contrast to the surveillance of H5 HPAI, active surveillance of live or hunted birds appears to result generally in a higher proportion of positives for subtypes other than H5N1 HPAI than passive surveillance of dead or diseased birds. Targeting risk species resulted, with a few exceptions, in a higher proportion of positives than not targeting high-risk species. There appear to be three exceptions to this: Sweden, Cyprus and Portugal, where a higher proportion of positives were found through passive surveillance of dead or diseased birds. However, many cases in Sweden occurred during the time of the H5N1 outbreak and at the time of reporting the subtype results were still pending. These birds are presented in this section but were in fact likely to be H5N1 affected birds. The positive samples in Cyprus were all of the H1N1 subtype and were taken from birds that died of an outbreak of Botulism. The number of positive birds in Portugal was very low and only 2 birds were positive in the category of dead or diseased risk species, which could be a possible explanation for this apparent difference to other MS.

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Table 5 Annual and seasonal number sampled and proportion positive in 2006 (excl. H5 HPAI) by country, plus Bulgaria and Switzerland for countries that detected AI infections of subtypes other than H5N1 H5 HPAI (Total = MS with positive birds + Bulgaria)

Member State	Total number sampled	Total number positive 2006	Proportion positive of sampled annual	Proportion positive Feb - May (n=number sampled)	Proportion positive June - August (n=number sampled)	Proportion positive Sep - December (n=number sampled)
LV	446	44	9.87%	0.00% n=139	13.33% n=240	17.91% n=67
FR	7253	344	4.74%	2.28% n=3243	9.59% n=2075	3.67% n=1935
SE	4322	189	4.37%	4.58% n=1004	2.69% n=1116	5.13% n=2202
IT	6106	190	3.11%	2.73% n=2011	0.00% n=1068	4.46% n=3027
CY	502	13	2.59%	0.00% n=385	28.26% n=46	0.00% n=71
NL	24715	438	1.77%	0.36% n=14360	1.70% n=2769	4.48% n=7586
IE	915	13	1.42%	0.77% n=518	0.00% n=113	3.17% n=284
SI	1035	14	1.35%	0.32% n=623	1.45% n=138	3.65% n=274
UK	12318	127	1.03%	0.54% n=7096	0.53% n=1692	2.27% n=3530
AT	4364	38	0.87%	0.78% n=3593	2.27% n=308	0.65% n=463
DK**	6719	57	0.85%	0.04% n=2113	0.00% n=1144	1.62% n=3462
BG	1983	9	0.45%	0.76% n=1188	0.00% n=515	0.00% n=280
DE	27913	115	0.41%	0.13% n=16603	0.38% n=3925	1.06% n=7385
PT	2824	10	0.35%	0.67% n=1044	0.35% n=573	0.08% n=1207
PL	3074	8	0.26%	0.00% n=1983	0.00% n=67	0.78% n=1024
CH	1529	4	0.26%	0.00% n=1075	0.00% n=42	0.97% n=414
BE	2177	5	0.23%	0.00% n=718	0.00% n=799	0.76% n=660
EL	2129	1	0.05%	0.00% n=1595	0.00% n=232	0.33% n=302
CZ	2237	1	0.04%	0.05% n=2048	0.00% n=121	0.00% n=68
TOTAL *	111032	1616	1.46%			

* EU member states which reported birds positive for Avian influenza + Bulgaria

Legend	no difference to total proportion	Higher than total proportion	Lower than total proportion
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**DK – Some of the positive findings noted in Table 5 were found in pools of five birds, which could not be separated at the laboratory.

Table 6 Positive proportions of sampled birds by surveillance type and MS in 2006 excluding H5N1/ H5 HPAI for all MS plus Bulgaria and Switzerland Total = MS with positive birds + Bulgaria)

Member State	Total number sampled	Total number positive	Total positive proportion	Proportion positive in dead or diseased risk species n= number sampled	Proportion positive of live or hunted risk species n= number sampled	Proportion positive of dead or diseased other species n= number sampled	Proportion positive of live or hunted other species n= number sampled
LV	446	44	10%	0% n=2	15% n=294	0% n=141	0% n=7
FR	7253	344	5%	3% n=1328	8% n=3009	3% n=1960	1% n=956
SE	4322	189	4%	10% n=310	5% n=2625	5% n=281	0% n=1106
CY	500	13	3%	11% n=46	0% n=1	2% n=170	6% n=62
IT	6106	190	3%	2% n=446	6% n=2736	0% n=1004	2% n=1201
NL	24715	438	2%	0% n=6065	4% n=10202	0% n=4449	2% n=3737
IE	915	13	1%	0% n=200	5% n=165	1% n=463	0% n=27
SI	1035	14	1%	1% n=255	3% n=271	0% n=383	2% n=126
UK	12318	127	1%	0% n=5296	3% n=3372	0% n=3330	1% n=320
DK**	6719	57	1%	0% n=245	1% n=4005	0% n=944	2% n=1525
AT	4364	38	1%	1% n=2263	1% n=431	1% n=1112	0% n=558
BG	1983	9	0.45%	No info No info	No info No info	No info No info	No info No info
DE	27913	115	0.41%	0% n=6354	2% n=2839	0% n=13881	1% n=3966
PT	2824	10	0.35%	4% n=47	0.24% n=423	0% n=1274	0.65% n=1078
PL	3074	8	0.26%	0% n=648	1% n=1103	0% n=770	0.36% n=553
CH	1529	4	0.26%	0% n=391	1.49% n=269	0% n=791	0% n=78
BE	2177	5	0.23%	0% n=82	0% n=1409	0% n=20	0% n=666
EL	2129	1	0.05%	0% n=490	1% n=180	0% n=1119	0% n=340
CZ	2237	1	0.04%	0% n=1315	Not sampled n=0	0.1% n=922	Not sampled n=0
TOTAL*	111032	1616	1.46%				
* EU member states which reported birds positive for Avian influenza + Bulgaria for which origin of bird was known							
Legend				No statistically significant difference	Statistically significantly lower than total proportion p<0.05	Statistically significantly higher than total proportion p<0.05	

**DK – Some of the positive findings noted in Table 5 were found in pools of five birds, which could not be separated at the laboratory.

Positive species

Table 7 displays the test results for the 29 risk species according to SANCO (SANCO, 2006) and EFSA (EFSA, 2006). Two species (Lesser White-fronted Goose *Anser erythropus* and Marbled Teal *Marmaronetta angustirostris*) are not displayed, as they were not sampled in any of the MS.

A green cell indicates that the species was sampled in the relevant MS and also contains the number sampled. A red cell indicates that the species tested positive for H5N1 or H5 HPAI. The number displayed in the cell refers to the number positive out of the number sampled. A yellow cell indicates that the species tested positive for avian influenza, other than subtype H5 (including pending results and unknown subtypes). The aim of the table is to put the proportion of positives into the context of the sampling frame, taking into account the number of birds sampled and the number of MS that sampled this species and did, or did not detect positives.

Risk species

H5N1/ H5 HPAI infection was detected in 11 of the risk species in 12 MS. Infections with avian influenza of subtypes other than H5N1/ H5 HPAI were detected in 23 of the risk species in 17 MS.

An approximate estimate of the proportion of birds in each of the higher risk species was made. National totals of birds sampled were allocated to different bio-geographical populations of waterbirds based on the population ranges given by Scott and Rose (1996) (wildfowl), Stroud, Davidson *et al.*, (2004) (waders) and Wetlands International (2006) (gulls and rails). Most recent estimates of the size of each waterbird population were taken from Wetlands International 2006, with minimum population sizes used in the cases where population ranges are given.

The five populations that had the highest proportions sampled (either actively or passively) for avian influenza were all populations of either Mute (*Cygnus olor*) or Whooper Swans (*Cygnus cygnus*). Over 6% of the British Mute Swan population were sampled with 2.3% of the North West and Central European, and 1.9% of the Irish populations of this species also sampled. Over 2% of both the Northern mainland Europe and Icelandic populations of Whooper Swans were sampled. About 1.8% of the Central European population of White-fronted Geese *Anser albifrons albifrons* were sampled.

No other populations were sampled for avian influenza at a rate exceeding 1%. Fourteen populations were apparently sampled at frequencies from 0.1-0.99%, ten populations at between 0.01-0.099%, and six populations at less than 0.01%. Two higher risk species were not sampled at all.

Despite the total population size (4.5m) the significant total numbers of NW European Mallard *Anas platyrhynchos* sampled resulted in over 0.5% of the population being tested for avian influenza.

Such calculations make many assumptions, and are necessarily crude, but the results serve to indicate — albeit roughly — which populations were sampled at relatively higher frequencies in 2006. Most of the infrequently sampled populations of higher risk species (<0.1% of total populations

sampled) were those populations occurring in the Black Sea/ Mediterranean region, reflecting the smaller national surveillance programmes for MS in that region compared to MS in NW Europe. Also included amongst those populations most infrequently sampled are most of the populations of higher risk gulls and waders – in many cases reflecting methodological difficulties of capture (for active surveillance).

Swans (*Cygnus olor*, *Cygnus cygnus* and *Cygnus columbianus*) tested positive for H5N1/H5 HPAI in all MS experiencing an outbreak of this subtype with the exception of the Slovak Republic, where only two H5N1 cases in total were detected. With the exception of France, Slovak Republic and Denmark, swans were the first species to be detected positive in the H5N1 outbreaks. Seventy one percent of the detected H5N1/ H5 HPAI infections were found in swans. Throughout the year 8239 Mute swans (*Cygnus olor*) were tested in 21 MS and overall 372 Mute swans, 4.5%, (6.97% between February and May) tested positive for H5N1 H5 HPAI. Forty-four (0.5%) of the tested swans were positive for subtypes other than H5N1 H5 HPAI. However, in the majority of these infections (68%), the subtype was not determined. The large majority (69%) of the sampled Mute swans were either dead or diseased. With the exception of 39 mute swans in Poland that were kept in confinement after the detection of a positive case and that were live without clinical signs at the time of sampling, all mute swans were either dead (333) or diseased (20).

Whooper Swans (*Cygnus cygnus*) were sampled in 14 MS of which four MS (DK, FR, UK and EL) detected H5N1/H5 HPAI infections and 5 MS (DK, DE FR, SE and UK) detected infections other than H5N1/ H5 HPAI in this species. Overall 2.5% (6.1% between February and May) of the tested Whooper Swans were found infected with H5N1/ H5 HPAI and 1.26% was infected with other types of avian influenza, where in almost half of these the subtype could not be determined. The large majority of H5N1/H5 HPAI infected Whooper Swans (39 out of 44) were found in France. Two Whooper Swans tested positive for LPAI H5, one in the UK and one in Denmark.

Overall the proportion of all swan species positive for H5N1/ H5 HPAI out of the swans tested in February – May was 6.1%, which is very high when compared to the positive proportion to all other species, excluding swans in this period, which was 0.3% of the tested birds.

Diving ducks (Tufted duck *Aythya fuligula* and Pochard *Aythya ferina*): Pochard's (*Aythya ferina*) were sampled in 14 MS in relatively low numbers (1-67). One H5N1 positive Pochard was found in France, and two birds infected with AI other than H5N1/ H5 HPAI were found in Italy (1) and the Netherlands (1).

Fourteen MS sampled Tufted Ducks (*Aythya fuligula*) in varying numbers (1-132). Five MS found tufted ducks positive for AI and H5N1/ H5 HPAI infection in this species was found in 3 MS. Of this species, a total of 9.7% (19.8% between February and May) tested positive for H5N1/ H5 HPAI and 5.8% for other types of AI. The proportion of H5N1/ HPAI infected Tufted Ducks was especially high in Denmark (66%) (72% between February and May) and Sweden (19.8%) (24% between February and May). In these two countries Tufted Ducks accounted for 57% (Denmark) and 45% (Sweden) of

the total H5N1 infections, which was much higher than in other MS, where swans were the predominantly affected genus. The proportion of H5N1 infections in Sweden may have been even higher, as for 25 birds reported infected with subtypes other than H5N1 H5 HPAI, the subtype was not available at the time of reporting and as other cases of H5N1 occurred at that time, these ducks may have been infected with H5N1. One LPAI H5 and one LPAI H7 infected Tufted Duck were found in Sweden and Portugal respectively.

Dabbling ducks (Pintail *Anas acuta*, Shoveler *Anas clypeata*, Teal *Anas crecca*, Wigeon *Anas penelope*, Mallard *Anas platyrhynchos*, Garganey *Anas querquedula*): Mallards (*Anas platyrhynchos*) were the most frequently sampled species with 28313 birds tested. Six MS out of 14 that experienced cases of H5N1 H5 HPAI in 2006 found H5N1/ H5 HPAI infected mallards. All of the H5N1/ H5 HPAI infected Mallards were found dead. A very low proportion (0.26%) of all mallards tested between February and May were positive for H5N1/ H5 HPAI, this proportion ranged from below 0.5% (IT, DE, SE) to 1.7% (AT).

Overall, mallards accounted for 61% of all positive cases of subtypes other than H5N1/H5 HPAI while accounting for only 5.6% of all positive H5N1/H5 HPAI cases. Infections with subtypes other than H5N1/ H5 HPAI were found in 16 MS. The proportion of non H5N1/ H5 HPAI positive mallards amongst those sampled ranged from 0.4% in Portugal (2/ 465) to 25% (4 /16) in Cyprus. Overall 3.5% of the mallards were infected with AI other than H5N1. Mallards infected with LPAI H5 (total 109) were detected in 7 MS (DK, FR, DE, IT, NL, SE, UK). The infected proportion varied from 0.05% (IT) to 1.3% in France. Almost all (107) of these LPAI H5 cases were detected after the first week of August. LPAI H7 was detected in 17 mallards in NL (4), IT (7), DE (1) and AT (5). Of a total of 202 sampled shovelers (*Anas clypeata*), 26 (12.87%) tested positive in five Member States. The proportion of infected birds amongst sampled varied from 2% in the Netherlands to 54% (13 out of 24) in Latvia, which was the origin of half of the total number of shovelers (*Anas clypeata*) found positive.

Relatively low numbers (565) of Pintails *Anas acuta* were tested in 11 Member States. One MS (SI) detected H5N1 infection in one out of three tested ducks. Overall 1.6% of the tested Pintails were positive for any AI ranging from 0.4% in the UK to 11% in Italy.

Eighteen MS sampled birds of the species *Anas crecca* in variable numbers (1-694) of which eight MS detected AI infections in this species (88 AI positive). No H5N1/ H5 HPAI was found, but a total of eight cases of LPAI H5 were detected in the UK (5) and DK (3). The overall proportion positive was 4.6% ranging from 0.9% (DE) to 26% (LV).

Wigeon's (*Anas penelope*) were sampled in 13 MS, of which six detected AI positive birds of subtypes other than H5N1/ H5 HPAI. 1.45% of the sampled Wigeons tested positive, ranging from around 1% (UK, SE, DK) to 8.7% (LV).

Anas querquedula were tested in very low numbers (143) in 14 MS. Thirteen birds (9%) tested positive in 3 MS.

Table 7 Number sampled and number positive of risk species (SANCO 2006, EFSA 2006) Total = EU24 + Bulgaria)

123	Number sampled	1/20	Those tested positive are shown as number positive/ number sampled ** Totals exclude Switzerland																				* Those member states, which tested positive for avian influenza where all subtypes, were '8' (no subtype info/ not determined)							
HPAI H5/ H5N1 positive	Other positive	Member States**																						**HPAI H5 +ves	**Total other +ves	**Total Birds Sampled				
Species	AT	BE	BG	CY	CZ	DK	EE	FI	FR	DE	EL	HU	IE	IT	LV	LT	LU	MT	NL	PL	PT	SK	SI	SE	CH	UK				
Anas acuta		38							3	5	15		2	3*/27	1*/7				3/197				1/3	2		1*/266	1	8	565	
Anas clypeata		1		1					3*/20	4	1/9			8*/76	13*/24				1/50					1		16	0	26	202	
Anas crecca		9	3	4	4	6/314	1			1*/116	49	13	1*/67	26/383	11*/43			3	5*/108		1		2	6/88	3	32/694	0	88	1902	
Anas penelope		2	1		2	7*/597		1		99	24		36	8/279	2*/23				15*/1076						1/94	2	3/251	0	36	2485
Anas platyrhynchos	16/1783 26/1783	5/250	8/66	4/16	732	8/290		47	261/3217	54/4429 3/4429	70	1/758	7*/111	105/1863 1/1863	11/138	34	74	1	322/7064	6/651	2/465	226	8/372	123/1850	4/243	48/3806	33	988	28313	
Anas querquedula	1		2	1					4*/64	28	4	1		4*/21	5*/11		1	1		4		2		2			0	13	143	
Anser albifrons albifrons																			4/734								0	4	734	
Anser anser	1/73	4		1	12	1/314	19	47		2*/452 1/452		10	1	1		1			2*/502	61		2		96	5	2/172	3	6	1769	
Anser brachyrhynchus						215				1									2/103							2/108	0	4	427	
Anser fabalis			3				12			7*/350		9							3/132	68	1			3/103		1	0	13	679	
Aythya ferina		67			3	1			1/40	38	24	2		1*/66	11	5			1/4	1	2				6/109	46	1	2	310	
Aythya fuligula	4	127			20	26/39	1			1*/132 3/132	1		3	6	1*/24				1/9		1/1			25/96 19/96	6/150	30	48	29	493	
Branta bernicla	11					122				4									1/89				2		43	0	1	271		
Branta canadensis		581				123		4	1/9	219		1							3/71					2/199 1/199	2*/647	2	7	1854		
Branta leucopsis						366	1	4		171	45								2053					3	1	28	0	0	2671	
Branta ruficollis			1							1/4	1/1																1	1	6	
Cygnus columbianus		1				1				2	2			1/39												7	0	1	52	
Cygnus cygnus		3				2/212 3/212	47	66	9/445 39/445	3/404	1/8		2			6	9		3			7		1/89		7/439 1/439	44	22	1741	
Cygnus olor	3*/564 81/564	51		1	14/358	5*/326 4/326	14		4/282 14/282	3*/1576 45/1576	28/329	57/177	1*/190	16/161	1	112	43		7/828	67/832		119	3/125 42/125	4*/216 4/216	1/125	14*/1935	372	44	8239	
Fulica atra	4*/251	113	3	1*/18	92	29		1	1*/90	3/1158	50	1/48	1	2*/195	2	10		1	269	33		17	4	27	4/211	82	1	11	2494	
Larus canus		7				2*/570	14	74		86	24					48			162	36			1	1/10		16	0	3	1048	
Larus ridibundus	2	71		4	92	399	16	23	78	2/342	8	1/28	9	8*/190	14	10	3	7	3/2793	60		7	19	8/48	12	80	1	21	4303	
Limosa limosa											1						1										0	0	2	
Netta rufina									13	144	1								20						7		0	0	178	
Philomachus pugnax		3	1							32	1			5		1					5			5			0	0	53	
Pluvialis apricaria		131				150							3	1*/60													0	1	344	
Vanellus vanellus	5	32				182		19	2	32	4			1*/66					2					4	3	1	0	1	349	

Grey geese (*Anser spp.*)

European White-Fronted Goose *Anser albifrons albifrons*: This species was only tested in the Netherlands where four out of 734 birds tested positive (0.5%).

Greylag Geese (*Anser anser*) were included in the surveillance in 17 MS. Three MS (AT, DE, DK) detected H5N1/ H5 HPAI infected geese, but all of them only in a single bird. Low numbers of positives for subtypes other than H5N1/ H5 HPAI (two per MS) were found in NL, DE and UK. Overall 0.16% of collected birds were positive for H5N1/ H5 HPAI and 0.3% for other AI subtypes.

Pink-footed Geese *Anser brachyrhynchus* were sampled in Denmark, The Netherlands, Germany and the UK. In the Netherlands and the UK two of the sampled birds, 1.9% and 1.8% respectively, tested positive for subtypes other than H5N1/H5 HPAI.

Bean Geese *Anser fabalis* were tested in nine MS, of which three MS (all that tested more than 100 birds of this species in 2006) found positives. Overall 1.9% of these birds tested positive for avian influenza other than H5N1/ H5 HPAI, ranging from 2% (DE) to 2.9% (SE). Two Bean Geese (*Anser fabalis*) tested positive for LPAI H5; one in the Netherlands and one in Sweden.

Black geese (*Branta spp.*)

Branta bernicla was tested in low numbers in six northern European MS and one LPAI positive (1.1%) was detected in the Netherlands.

Canada Geese (*Branta canadensis*) were tested in nine MS. France and Sweden each detected a single H5N1/ H5 HPAI infections in this species. AI infections other than H5N1/ H5 HPAI were detected in three MS (NL, SE and UK). Overall 0.38% were positive for subtypes other than H5N1/ H5 HPAI, ranging from 0.3% (UK) to 4.2% in the Netherlands.

Barnacle Geese *Branta leucopsis* were sampled in eight MS (plus one sampled in Switzerland) and especially in the Netherlands which was the origin of almost 80% of the total sampled birds of this species. None of the sampled birds tested positive for avian influenza.

Only 6 Red-breasted Geese *Branta ruficollis* were tested, as this is an endangered species. Two positive birds were found: One LPAI infected live bird in Germany and one H5N1 positive bird in Greece.

Seagulls (*Larus*)

Black headed gulls (*Larus ridibundus*) were tested in most MS (23/ 24 EU MS) and a low proportion (0.5%) of positives for subtypes other than H5N1/ H5 HPAI were found in five MS. The highest proportion of positives was found in Sweden where eight out of 48 (16.6%) tested were positive. One dead black-headed gull infected with H5 HPAI was found in Hungary.

Common Gulls (*Larus canus*) were tested in 12 MS. Two MS (DK and SE) found birds positive for subtypes other than H5N1/H5 HPAI. The overall positive proportion of tested birds was 0.3%.

Other risk species:

The remaining risk species were tested in generally very low numbers in a number of MS (see Table 7). One Golden Plover *Pluvialis apricaria* and one Northern Lapwing *Vanellus vanellus* tested positive for AI other than H5N1/H5 HPAI in Italy, but no other birds in the remaining risk species tested positive.

Other species

Table 8 below displays the number sampled and positive by MS for species that were not listed among the risk species but in which positive birds were detected.

Only 13 Greater Scaup *Aythya marila* were sampled in 4 MS, and 4/9 (55%) tested positive in Sweden. With the exception of one bird, which was found diseased, all were found dead. Active surveillance of live and hunted Ferruginous Ducks *Aythya nyroca* was increased in Germany after May 2006 and led to the finding of one H5 HPAI infected bird and nine other infected birds of this species. In 8/9 of these birds the subtype was not determined. One case of other LPAI was found.

Positives for H5N1 were detected in several raptor species: Common Buzzards (*Buteo buteo*) were sampled in seventeen MS (plus CH) and HPAI H5 positives were found in five MS (Table 8). A low number (9) of positive falcons (Peregrine Falcon *Falco peregrinus* (1), *Falco sp.* (1) and Kestrel *Falco tinnunculus* (7)) were detected in several MS (CY, DK, DE, SK and SE). The 3 falcons, which tested positive in Cyprus, were infected with the H1N1 subtype and reported as live not diseased.

Sawbills of the genus *Mergus* were tested in very low numbers (105 Goosander *Mergus merganser* and eight Smew *Mergus albellus*) and a high proportion of positives were found: 15.2% in Goosander and 25% in Smew. All cases were either H5N1/ H5 HPAI, or the subtype was still pending at the time of reporting.

Gulls were tested in many MS and 63 Gulls tested positive in 8 MS (excluding Common Gull *Larus canus* and Black-headed Gull *Larus ridibundus*, as discussed in the section on risk species (Table 6)). The proportion of tested birds in which infection was detected ranged among species from 0.65% in Great Black-backed Gull (*Larus marinus*) to 3.85% (1 out of 26) in the slender billed gull (*Larus genei*). For the majority of birds (56%) the subtype was not determined, 36% of the positives were infected with subtypes classified as "other LPAI".

Table 8 Number sampled and positive of birds of species not classified as risk species (SANCO 2006, EFSA 2006) Total = EU24 + Bulgaria

1	Sampled	Anas Strepera = Bridge Species																								1/20	Number positive/ Number sampled				** Totals exclude Switzerland				**HPAI H5 +ves	**Total other +ve	**Total Birds Sampled
HPAI H5/ H5N1 positive	*	Those member states, which tested positive for avian influenza where all subtypes, were '8' (no subtype info/ not determined)																																			
Other positive	MEMBER STATES																																				
SPECIES	AT	BE	BG	CY	CZ	DK	EE	FI	FR	DE	EL	HU	IE	IT	LV	LT	LU	MT	NL	PL	PT	SK	SI	SE	CH	UK											
Unknown species	2/ 435 5/ 435	36	493	223	1	1*/ 1	90		2/ 383 4/ 383	12/ 2456 6/ 2456	7	95	2*/ 118	145		6	27	5	11/ 3447	61	389	8	10	1	2	5*/ 648	15	35	9085								
Accipiter gentilis		44			5	15	2			1/ 185		11				1	11					4		1/ 10			0	2	288								
Accipiter sp.										637			1		4	2				1/ 82		21					1	0	747								
Alopochen aegyptiacus		24							1	150									3*/ 103		4		3			6	0	3	291								
Anas sp.	2*/ 61		137	13	1	19		1	32/ 578 3/ 578	9/ 1907 1/ 1907	121	28	66	1*/ 404	18	86	38	24		1/ 461	6/ 565		1*/ 44		8/ 126	317	4	52	4889								
Anas strepera		1							1	1/ 8	6		1	4*/ 88	5				2/ 147							18	1	6	275								
Anser albifrons	1*/ 150		46			1*/ 136	1		3/ 41	2/ 570	21	35							27*/ 1266	11				42		5	0	34	2324								
Anser cygnoides										1*/ 41						1								1	1	1	0	1	44								
Anser sp.	1/ 39		1/ 8			2				1*/ 341	5	98	1	155		2	67			47	52		7				2	1	822								
Ardea cinerea	93	1	6	10	1*/ 355	24	1		2/ 120 1/ 120	831	16	55	13	13	2	2	9		984	1/ 22		14	2/ 69	11	17	1*/ 19	4	4	2670								
Ardea sp.	1/ 187		14			4				17				102			5		454		23	53	11				1	0	870								
Asio otus				3	2	2				29	6	23		1					1	2					1/ 9		0	1	78								
Aythya marila										1													1	1/ 9 4/ 9	2	2	4	1	13								
Bubo bubo					2				1	2/ 21	7				2		1				2	2		2/ 12 2/ 12			4	2	50								
Buteo buteo				6	58	6/ 223		1	1/ 50	3/ 2496	47	46		1/ 16			127		428	43	4	21	1	2/ 13	16	17	13	0	3597								
Buteo lagopus					2	1/ 14				2																	1	0	18								
Cairina moschata	1/ 16				2																						1	0	18								
Carduelis chloris									1/ 36	29	2	36	3								1	19	1	1	1	134	0	1	262								
Ciconia ciconia				1/ 5	7		1		14	49	43	4		3	17	17				20	47	15	14	1	2		0	1	257								
Clangula hyemalis						1	5			1/ 2										8				2		3	0	1	21								
Columba oenas									2/ 246										1							1	0	2	248								
Cygnus sp.	8		1/ 264 3/ 264			103	14			1/ 400	2			23	2	3					11	28	92	1/ 4	1/ 168	7/ 303	4	9	1257								
Falco peregrinus		20		1		1/ 1				14			1						2	5		5					7	1	0	56							
Falco sp.	16	3	14							25	29			13		1	2				10	1/ 34			4	1	1	0	148								
Falco tinnunculus				3/ 20	29	39		1	10	1/ 502 1/ 502	6	11		5			23			13	1	16		2/ 8	4	3	1	6	687								
Fringilla coelebs								1	19	46	4	11	3			1						1				1*/ 52	0	1	138								
Gallinago gallinago									5	26	4	2	13	19						8	2	1		1*/ 1	11	2	0	1	94								

Table 8 Number sampled and positive of birds of species not classified as risk species (SANCO 2006, EFSA 2006) Total = EU24 + Bulgaria

1	Sampled	Anas Strepera = Bridge Species																				1/20	Number positive/ Number sampled				** Totals exclude Switzerland				**HPAI H5 +ves	**Total other +ve	**Total Birds Sampled
HPAI H5/ H5N1 positive	*	Those member states, which tested positive for avian influenza where all subtypes, were '8' (no subtype info/ not determined)																															
Other positive	MEMBER STATES																																
SPECIES	AT	BE	BG	CY	CZ	DK	EE	FI	FR	DE	EL	HU	IE	IT	LV	LT	LU	MT	NL	PL	PT	SK	SI	SE	CH	UK							
Gallinula chloropus	1*/12	8		2/8	5				14	99	15	4	3	1*/156			5	2	26	4	19	1	5		1	48	0	4	434				
Himantopus himantopus				1/3					1																		0	1	4				
Larus argentatus		90	18			24*/834 1/834		65		8/181		2	15	2					11*/341	66				2/48		71	3	38	1579				
Larus fuscus		12				22		4	5/48	1									69				1		5	0	8	168					
Larus genei														1*/26													0	1	26				
Larus marinus						1/95		10		5			2						32	1			2		8	0	1	155					
Larus sp.	9/282 1/282	21		19		37		13		498	139	7	53	91	27	12	1			1/58	1/217	8	1		41	57	1	11	1541				
Locustella naevia									1										3/36								0	3	37				
Mergus albellus										5		1										1/1		1/1			2	0	8				
Mergus merganser						3	1		1	5/36					4					1/16			1	5/35 5/35	1/23	8	11	5	105				
Oxyura jamaicensis													1*/1													3	0	1	4				
Parus caeruleus									2/23	9		19		3					24			1				5	0	2	90				
Pelecanus sp.			30							1/1																	0	1	31				
Phalacrocorax carbo	75		22	11	134			1	35	545	1/32	1/12	12	33		2	5		4	25		4		1/32	23	52	2	1	1036				
Phalacrocorax sp.						160				16				4						15	14	17	1*/23				0	1	249				
Pica pica			21	6		1/27	9	1	8	274	24	18	11	12		1	1		3	1	4	7	2	5		30	1	0	465				
Podiceps cristatus	2/76	2	1		10	1/2		1	3/48 1/48	68			2	5	1	4			2	6		1	22	4	1/66	6	4	3	261				
Porphyrio porphyrio														1/1													1	0	1				
Scolopax rusticola	6		3		4	9			1*/21	97	12	5	10	3		1	1		15	2	1	1		1		3	0	1	195				
Somateria mollissima						14		85		23									8/98					10	67	0	8	297					
Sterna albifrons											3			33						1				1/59			0	1	96				
Sterna hirundo		193				8		1	1				5	3*/94		1				4	2			221		3	0	3	533				
Streptopelia decaocto				11	7	1			2/82	6	67	231	2	1			5			11	107	13				29	0	2	573				
Streptopelia turtur				1	1				2/95					23								4					0	2	124				
Sturnus vulgaris			2		32	11		1	101	82	48	62	2	19		9				6		17	3		2	1*/139	0	1	534				
Tachybaptus ruficollis				1	5					3	1			1		1							11		2/10	3	0	0	26				
Tadorna tadorna		130	2			1			6	16	22			12/23					17		3			1/51		1*/103	0	19	574				
Tyto alba				1/3	9	5			5	86	1	6		1							23	5				7	0	1	151				
Uria aalge									2/24				1*/29						7					1		165	0	3	226				

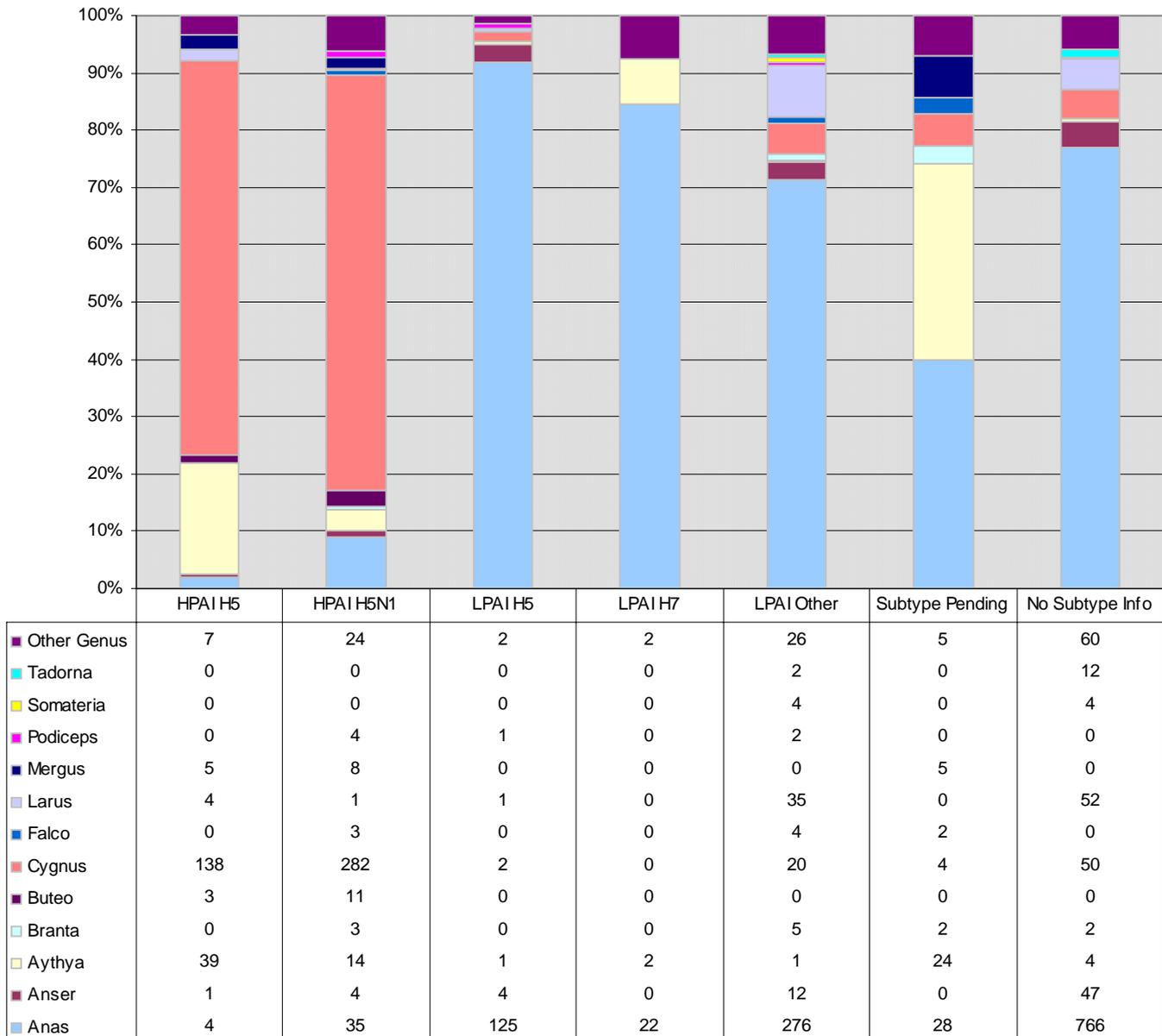


Figure 10 Number of positive birds by subtype and genus (EU 24 + Bulgaria)

*Total excludes CH

Figure 10 shows the number and proportion of positive birds by subtype and genus of birds. Swans (*Cygnus spp.*) made up the highest proportion (71%) amongst the positives for H5N1/ H5 HPAI. Another large proportion of the other HPAI H5 proportion was diving ducks (*Aythya spp.*). Dabbling ducks (*Anas spp.*), although also making up a large proportion of the total number of birds sampled (32%), were predominantly the most represented genus for other subtypes (especially LPAI H5), but were less strongly represented amongst the positive H5N1/ H5 HPAI birds.

DISCUSSION

Triggered by the outbreak of H5N1 in wild birds in early 2006, a massive increase of the surveillance in wild birds occurred and most MS sampled a multiple of the planned sample numbers submitted in the surveillance programmes to the European Commission. In 2006, a total of 144805 birds were tested for AI in the EU 25 plus Bulgaria (excluding CH and RO). This was approximately three times greater than the number of birds tested in the EU MS in 2005. The absence (with the exception of one case in Spain) of the occurrence of further H5N1 cases indicates that the virus did not establish itself successfully at a large scale in EU wild birds. Two potential reasons for this are, that either the virus did not survive in sufficient concentrations in the environment to infect further birds or that it was maintained at very low level in the European wild bird population and was thus not detected at existing sample levels. In addition, the virus did not establish in local poultry populations so the potential for spill over to wild birds was reduced.

A large heterogeneity occurred between MS in respect to their surveillance programmes and especially the number of birds tested. While some MS focused on the active surveillance of live birds, others focused on passive surveillance of dead or diseased birds. The degree of targeting of risk species and sample types are also variable between MS. As these factors impact on the probability of obtaining positive results, **the positive proportion of birds cannot be directly compared.**

Due to the inability to assess whether the sampled population is representative of the wild bird population, the fact that this population is dynamic, the non-equal probability of a bird to be selected for sampling and to be positive and the mentioned heterogeneity of the surveillance amongst Member States, the results cannot be interpreted as prevalence of avian influenza in either a particular species or in a country. Comparison and interpretation of positive proportions is further complicated by the absence of a batch number, which makes it impossible to differentiate in the majority of the cases between positive birds sampled on one occasion (same time and location) and positive birds identified on multiple sites and dates.

However, in spite of these differences some results are the same or similar across MS. For example, in the case of H5N1, testing of dead birds, especially swans, diving ducks and mergansers was the most likely way of detecting infection with this subtype. This might be taken as a sign of pathogenicity of the H5N1 strain, but the finding of 39 live swans in Poland kept in confinement after the finding of the first positive case and repetitively tested that were reportedly found positive without being clinically diseased, requires for caution before making assumptions without a strong evidence base. Furthermore it is possible that the H5N1 strain was present in another species, but that it was not detected and only became apparent when other more susceptible species became infected.

Another finding that was reflected in the majority of the MS was that testing of live or hunted birds of the risk species, especially of dabbling ducks was the most likely way to detect

infections of other AI subtypes. Although there is no single explanation for this finding, several factors are likely to play a role. Firstly, active surveillance in live birds is frequently highly targeted to increase the probability of detecting the virus. Targeting high risk areas, risk species, and the time in the year when the detection of infection with avian influenza virus is most likely, as well as potential targeting towards other risk factors such as juvenile birds may have increased the proportion of infected birds for birds that were sampled live. Birds are often caught in batches and if the virus is present at a particular time and place, then it is likely that more positive birds will be detected in a batch than if the same total number of birds had been sampled from multiple locations. This cluster effect is a well-recognised feature of infectious disease epidemiology in general. Moreover detected infections may be less frequent in dead birds as LPAI infections do not normally lead to morbidity and mortality in wild birds. In addition, tissue samples are frequently used in the testing of dead birds and as in low pathogenic avian influenza the virus load in the tissue is much lower than for highly pathogenic avian influenza, or absent given the different virus tropisms, so the detection of LPAI infections through this sample type is less likely. The relative importance of each of these factors cannot be evaluated with purely descriptive analysis and should be explored.

Most of the infrequently sampled populations of higher risk species (<0.1% of total populations sampled) were those populations occurring in the Black Sea/ Mediterranean flyway, reflecting the smaller national surveillance programmes for MS in that region (Central and Eastern Mediterranean and Black Sea) compared to MS in North-West Europe.

Since the introduction of H5N1 HPAI viruses into Europe, West Asia, the Middle East and Africa a number of distinguishable subgroups have emerged, indicating a dynamic situation in which the viruses continue to evolve. The so called 'clade 2' viruses that derive directly from viruses associated with spread from Northern China through Mongolia and the Russian Federation in late 2005 are the progenitors for all of the strains detected in Europe to date. Further subdivisions within this clade are possible and reflect the closely related but heterogenous population of H5N1 HPAI viruses (Salzberg *et al* 2007; Brown 2007). Detailed analysis of the data can lead to the conclusion that there have been several independent introductions before local spread within wild bird populations. The presence of virus in wild birds in many countries in the absence of reports of disease in poultry provided further evidence for probable introduction of virus to countries via wild birds.

Ecosystems where there is close functional connection between domestic poultry, higher risk migratory species and endemic populations of wild birds that are susceptible to the virus continue to pose higher risk for further virus introduction and may also contribute to the future rates of virus evolution that may have consequences for future control approaches. The current safeguard measures would therefore appear highly appropriate given the continued risk and key knowledge gaps about the virus ecology and epidemiology in wild bird populations.

The number of dead birds tested has decreased substantially during the course of the year 2006. This decrease could be caused by decreased public awareness due to less media attention and a general lower mortality of birds, which was aggravated in early 2006 due to harsh weather

conditions. Considering that all outbreaks of H5N1 in wild birds in the EU were detected through the discovery of infected dead birds, this type of surveillance appears very important for the detection of H5N1. As dead birds are obtained through reporting by the public or voluntary participants of ornithological societies or conservation bodies, it is important to maintain awareness and encourage the reporting of dead birds. Swans were the most frequently identified species with H5N1 infection in most EU MS in 2006, an explanation for this could be that these birds are clinically very susceptible to the infection and aided by high visibility are consequently easily detected. Dabbling ducks were the most frequent source for the detection of infections other than H5N1 and even though birds of this genus were the most frequently sampled genus; it was still much more likely for a bird infected with a subtype different to H5N1 HPAI to be of this genus.

Wild birds are now recognised as having played a role in the long distance spread of H5N1 HPAI, although, the relative contributions of migratory birds and anthropogenic factors associated with the poultry industry remain unclear. This uncertainty is compounded by limited knowledge of wild bird host factors including the range of susceptible species, infection dynamics in these birds and precise details of their migratory and other movement patterns.

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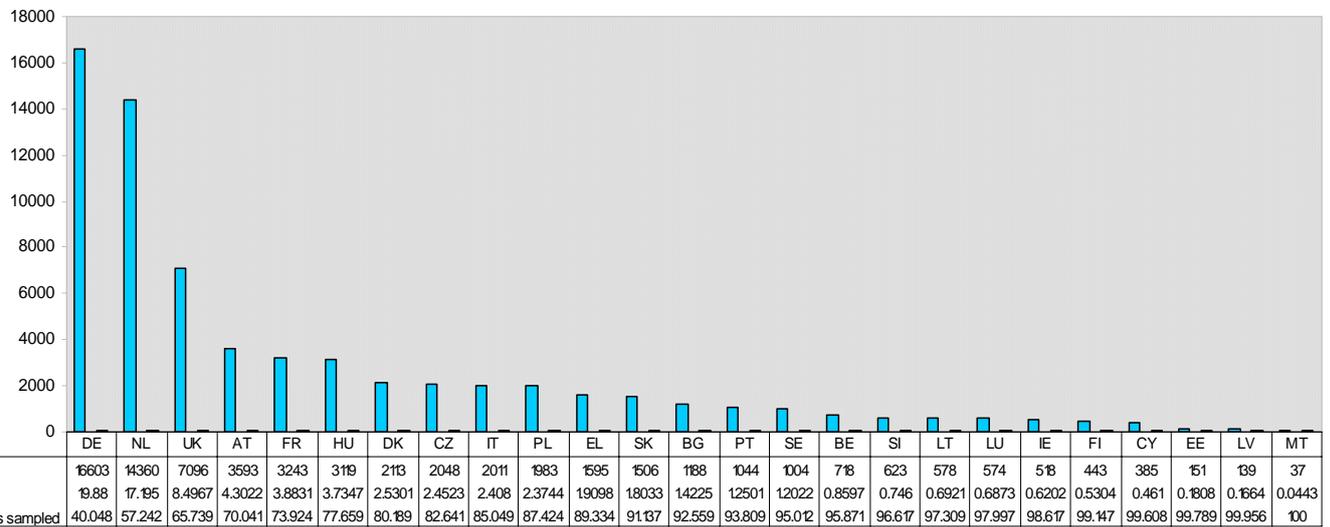
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Stroud, D.A., Davidson, N.C., West, R., Scott, D.A., Hanstra, L., Thorup, O., Ganter, B. & Delany, S. (compilers) on behalf of the International Wader Study Group (2004). Status of migratory wader populations in Africa and Western Eurasia in the 1990s. *International Wader Studies* 15: 1-259. <http://web.uct.ac.za/depts/stats/adu/wsg/iws15.html>

Wetlands International 2006. *Waterbird Population Estimates – Fourth Edition*. Wetlands International, Wageningen, The Netherlands. 239 pp.

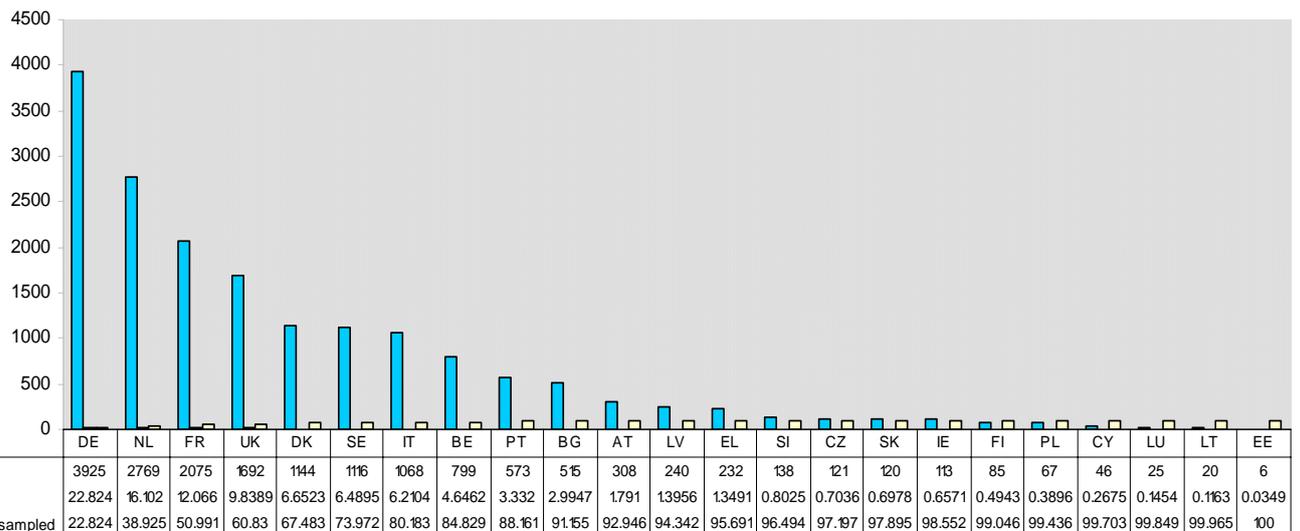
ANNEX 1 BIRDS SAMPLED BY MEMBER STATES, BY SEASON

February - May 2006



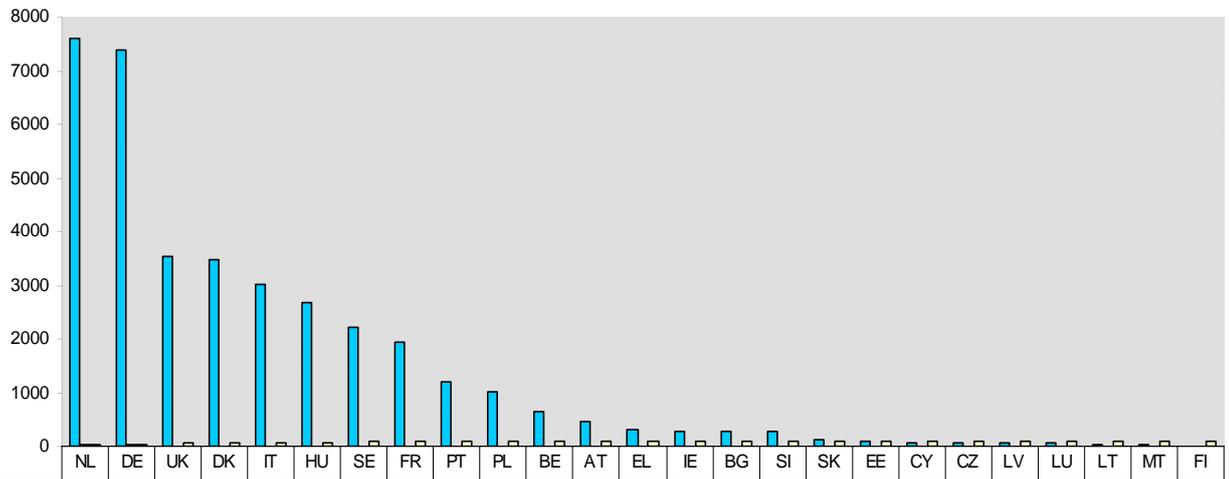
During February to May 2006, 83515 birds were sampled in the EU (25 MS plus accession state Bulgaria).

June - August 2006



During June to August 2006, 17197 birds were sampled in the EU (24 MS excluding Spain) plus accession state Bulgaria. Spain is not included in this total, as they did not provide a total number of birds for this sampling period.

September – December 2006

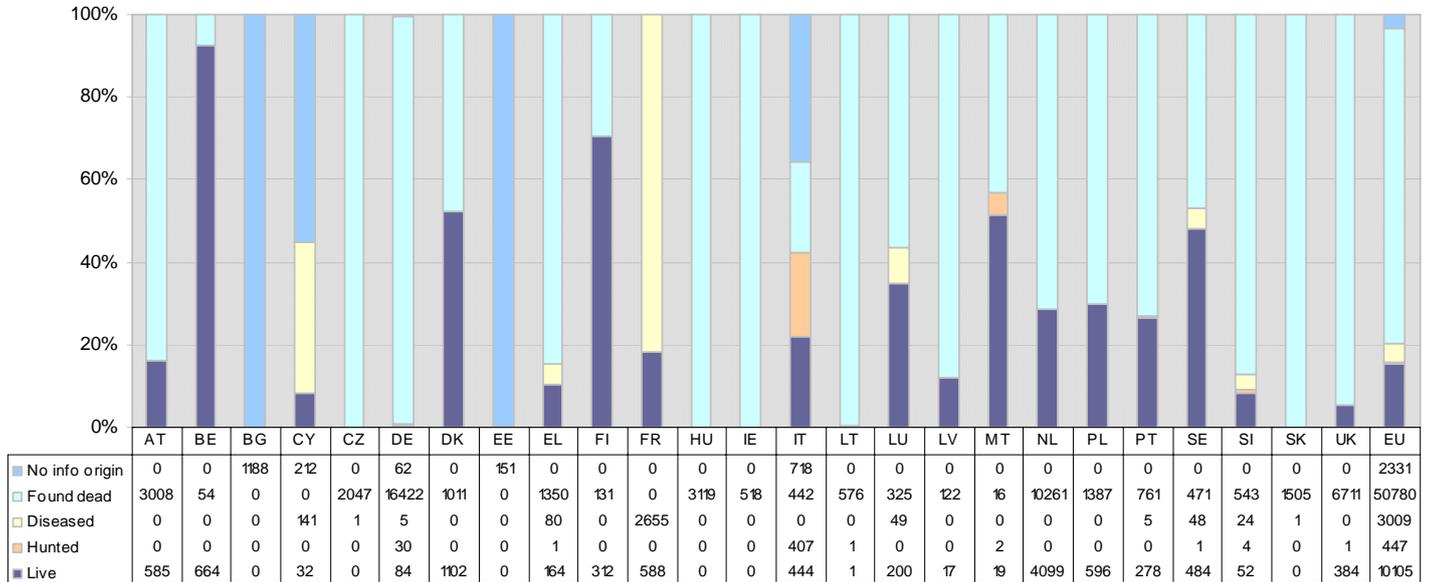


	NL	DE	UK	DK	IT	HU	SE	FR	PT	PL	BE	AT	EL	IE	BG	SI	SK	EE	CY	CZ	LV	LU	LT	MT	FI
Member State Total	7586	7385	3530	3462	3027	2682	2202	1935	1207	1024	660	463	302	284	280	274	109	102	71	68	67	65	23	21	8
% of total birds sampled	20.6	20	9.58	9.4	8.22	7.28	5.98	5.25	3.28	2.78	1.79	1.26	0.82	0.77	0.76	0.74	0.3	0.28	0.19	0.18	0.18	0.18	0.06	0.06	0.02
Accumulative % of total birds sampled	20.6	40.6	50.2	59.6	67.8	75.1	81.1	86.4	89.6	92.4	94.2	95.5	96.3	97	97.8	98.6	98.8	99.1	99.3	99.5	99.7	99.9	99.9	100	100

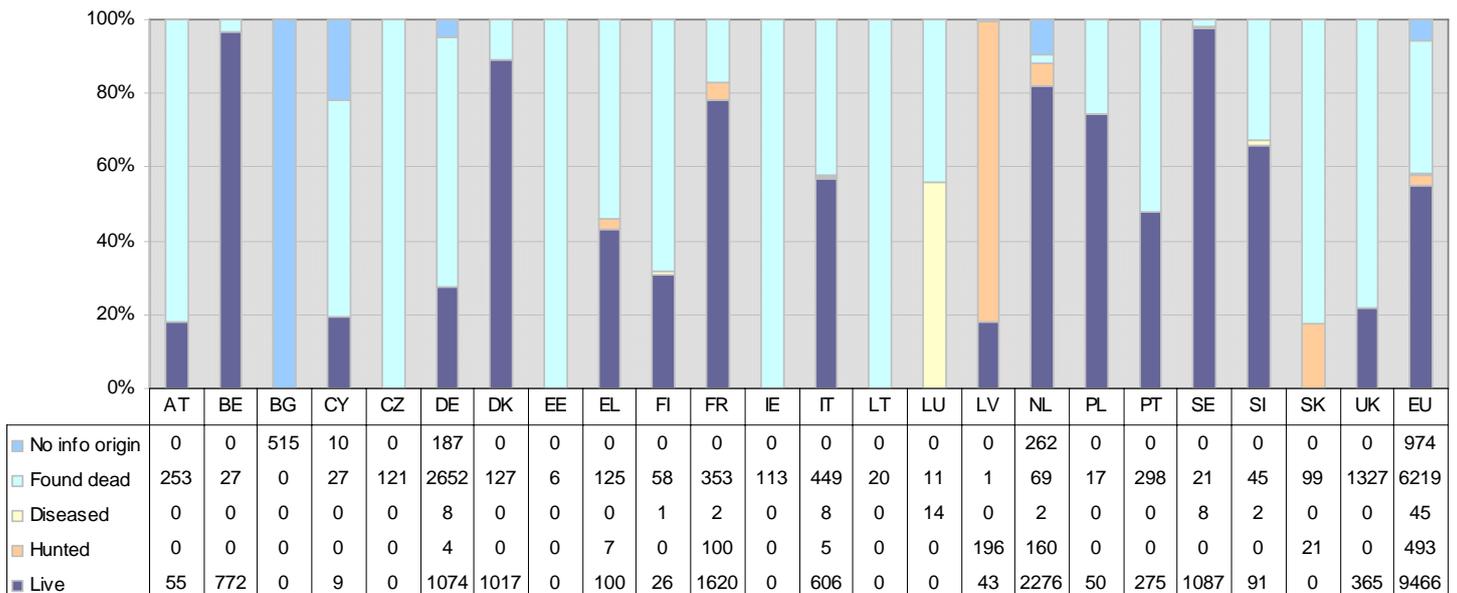
During September to December 2006, 36837 birds were sampled in the EU (24 MS excluding Spain) plus accession state Bulgaria. Spain is not included in this total, as they did not provide a total number of birds for this sampling period.

ANNEX 2 ORIGIN OF BIRDS BY MS AND TIME

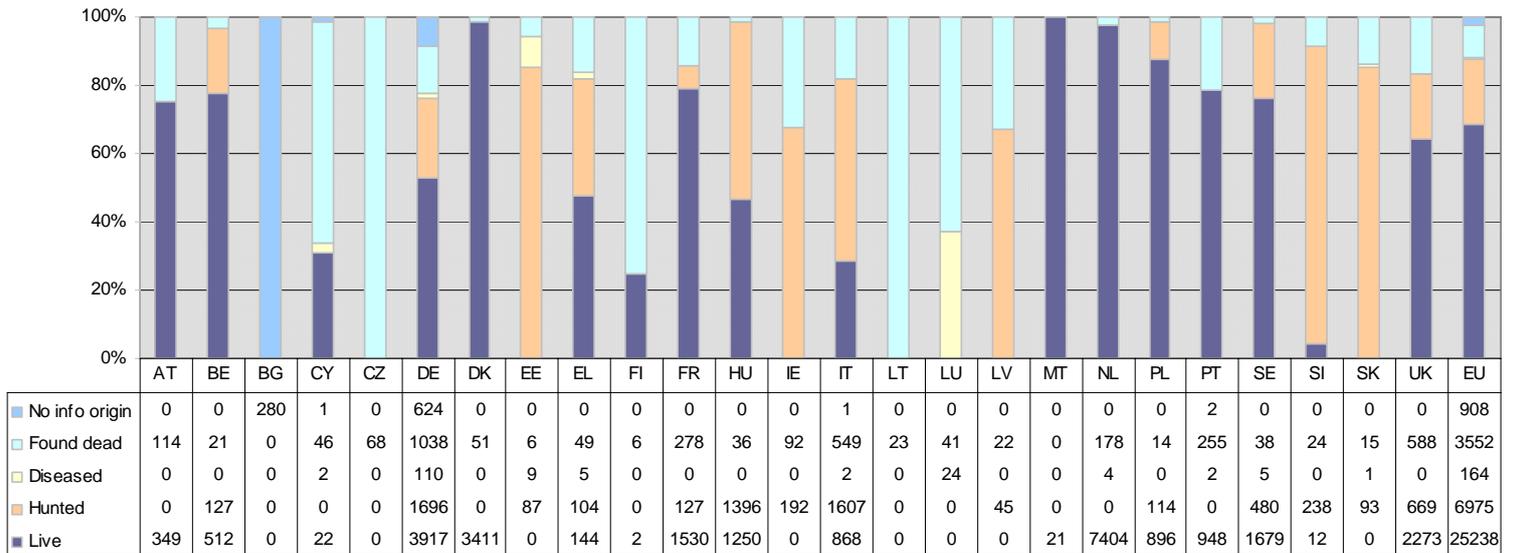
February - May 2006 - Origin of sampled birds



June to August 2006 - Origin of sampled birds

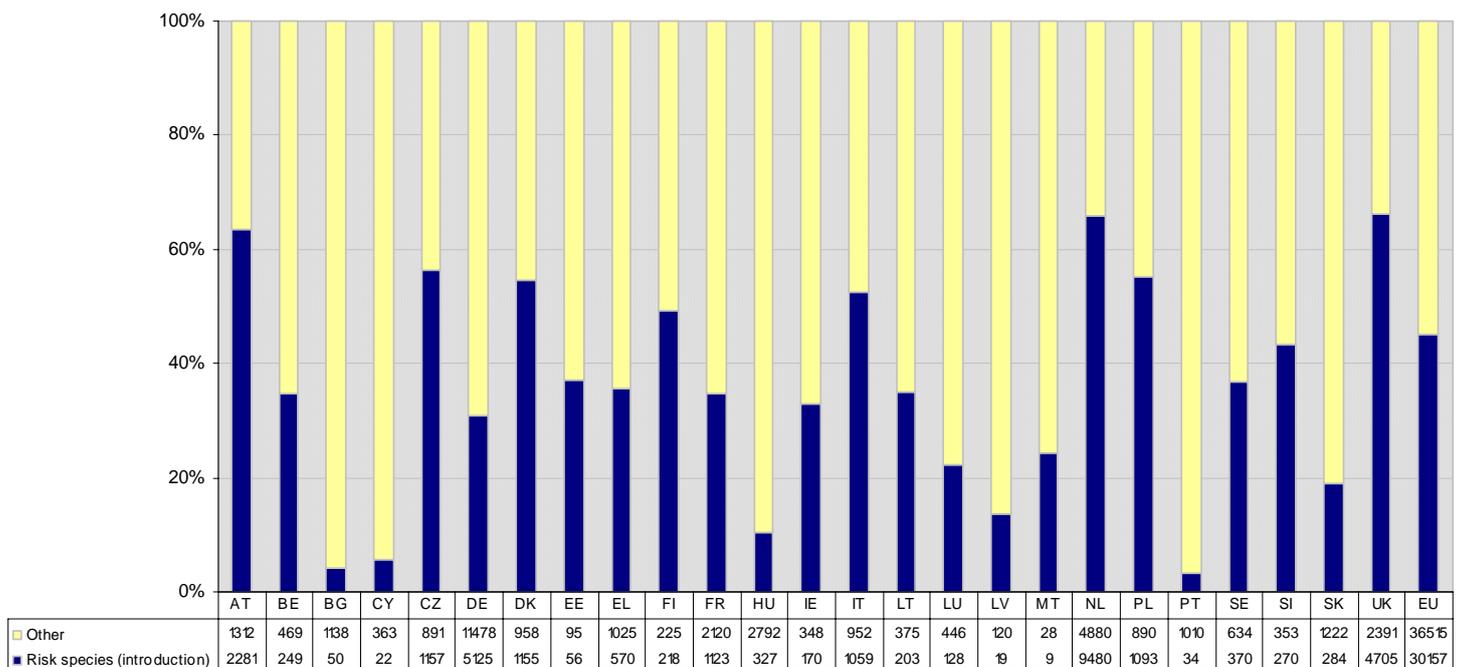


September to December 2006– Origin of sampled birds

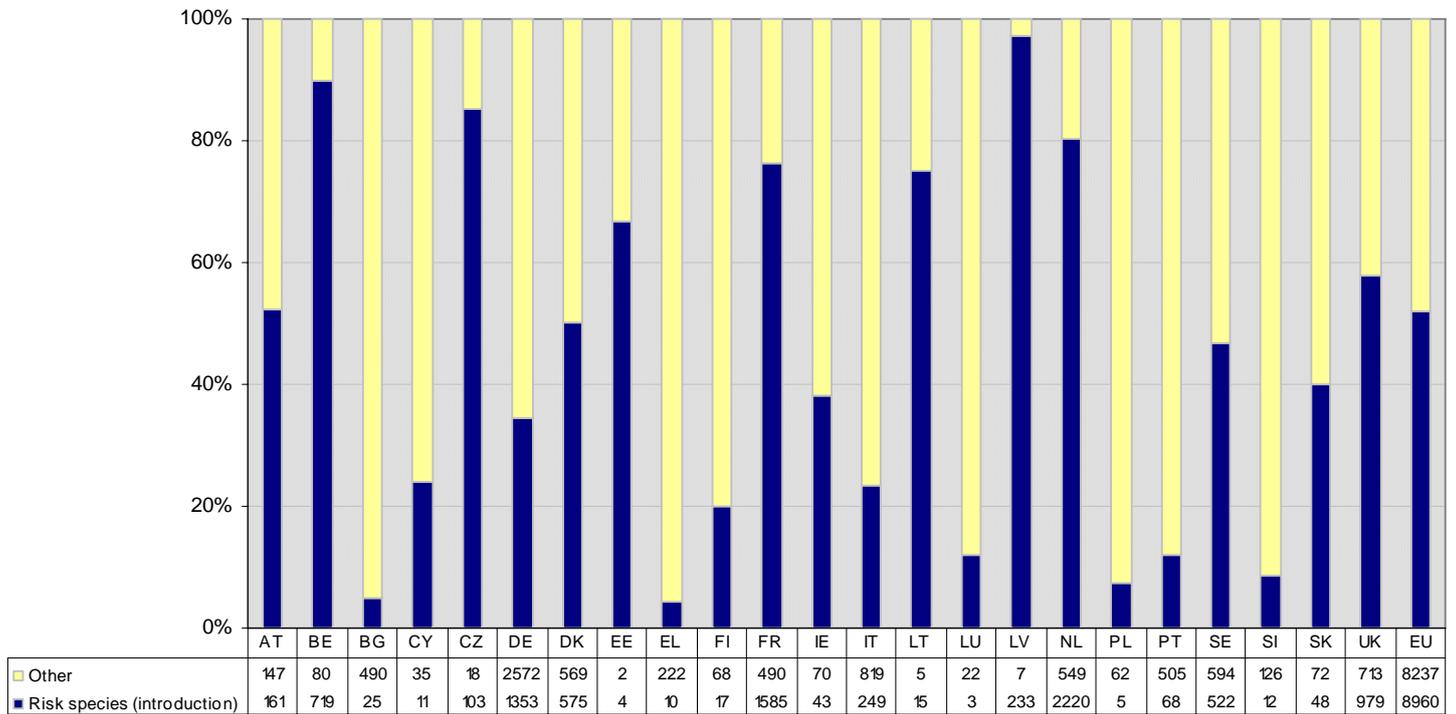


ANNEX 3 PROPORTION OF RISK SPECIES (SANCO 2006, EFSA 2006) AMONGST BIRDS SAMPLED BY MS AND TIME PERIOD

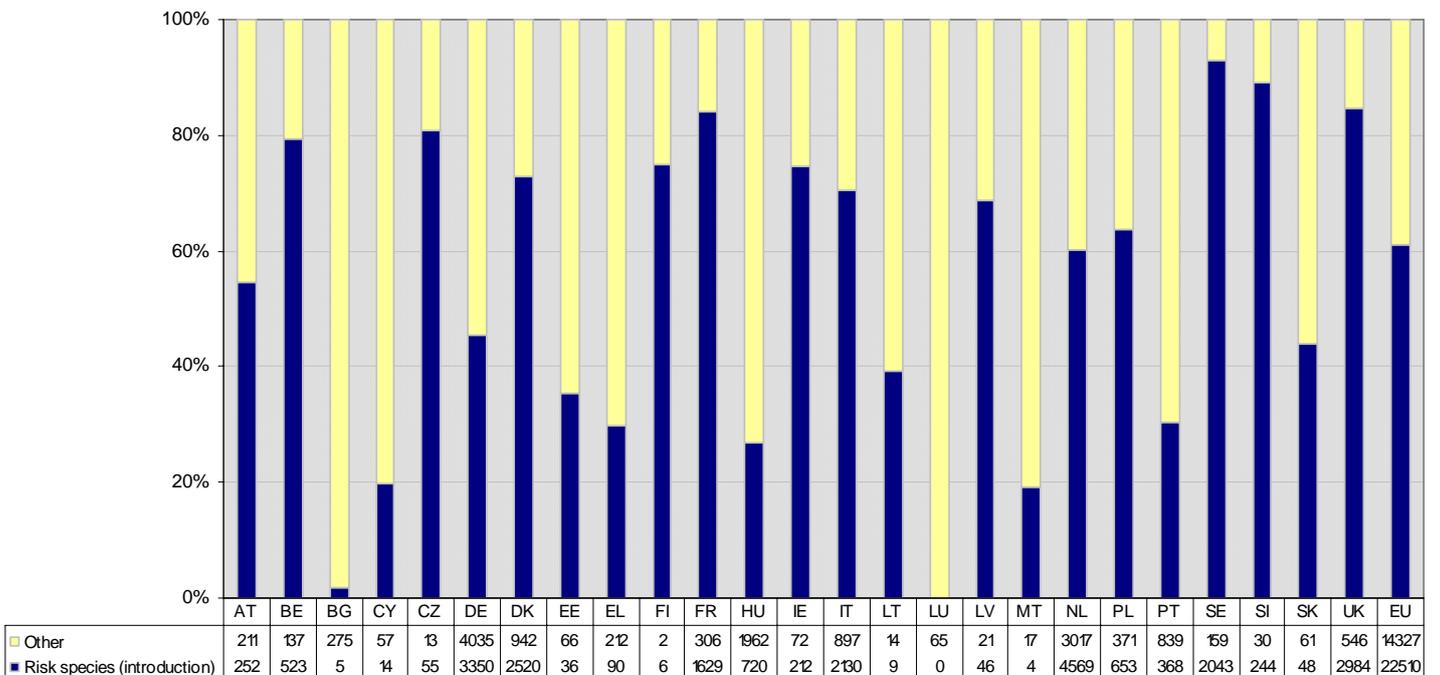
February to May 2006 – Risk species – sampled birds



June to August 2006 – Risk species – sampled birds

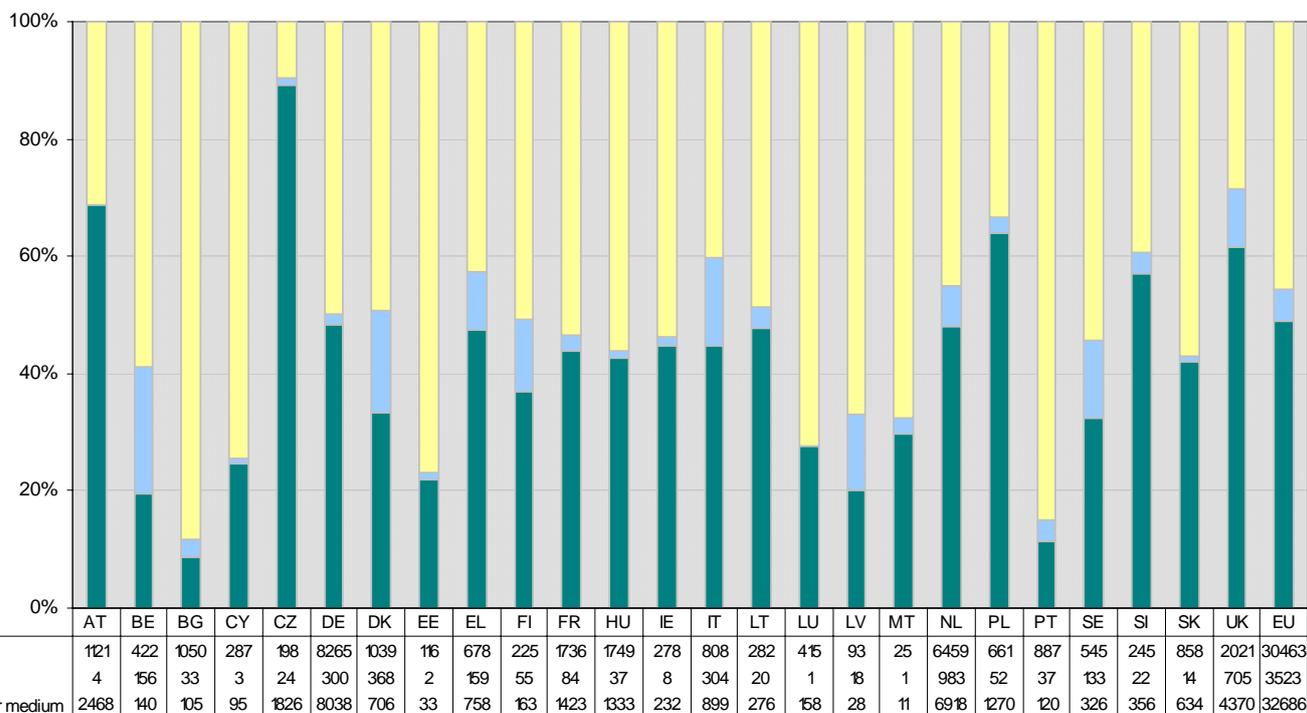


September to December 2006 – Risk species – sampled birds

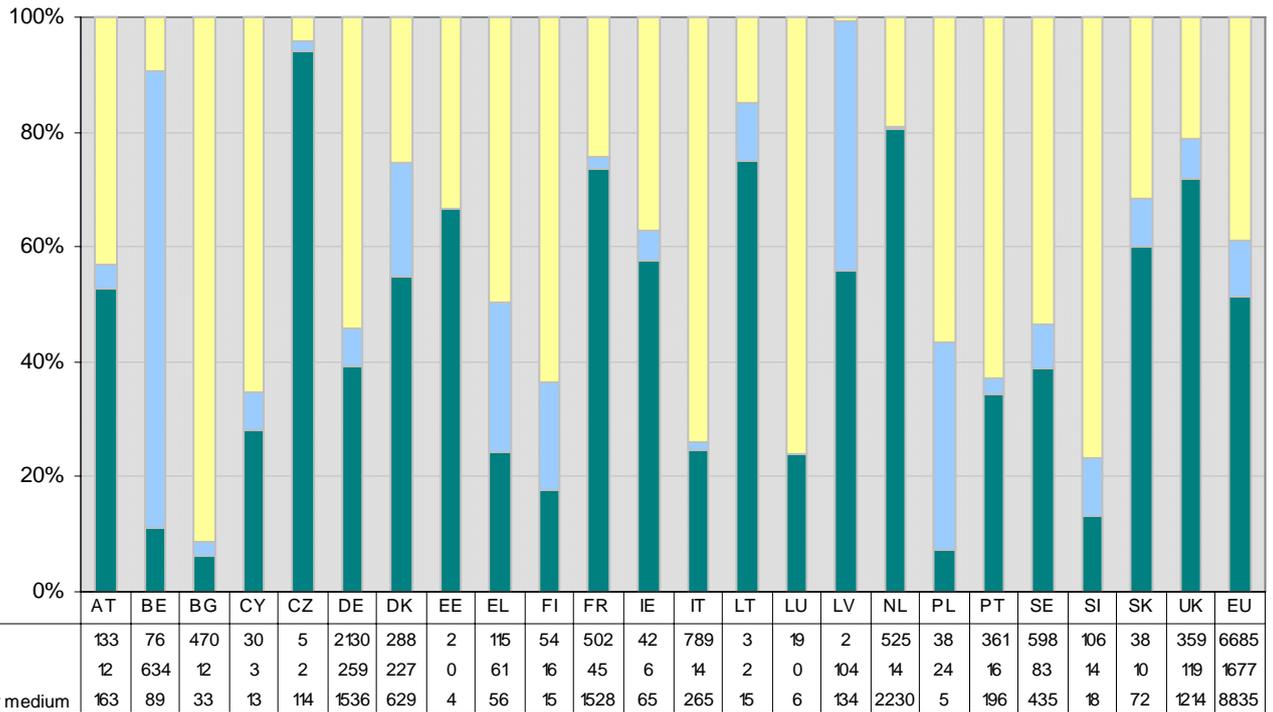


**ANNEX 4 PROPORTION OF BRIDGE SPECIES (EFSA 2006)
AMONGST BIRDS SAMPLED BY MS AND TIME PERIOD**

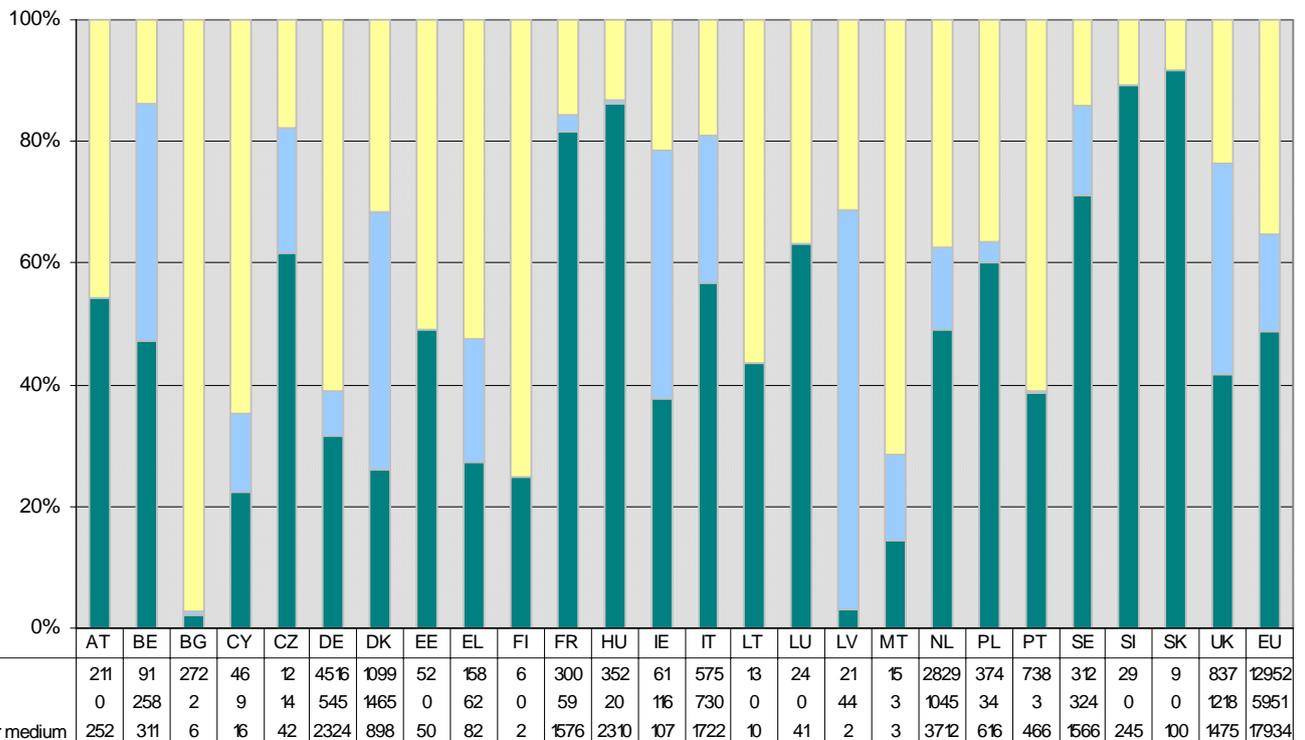
February to May 2006 – Bridge species- sampled birds



June to August 2006 – Bridge species- sampled birds



September to December 2006 – Bridge Species – Sampled birds



ANNEX 5 EURING CODES FOR RISK SPECIES AND SUBSPECIES

Code	Species	Genus	Family	Order
01890	<i>Anas acuta</i>	<i>Anas</i>	Anatidae	Anseriformes
01940	<i>Anas clypeata</i>	<i>Anas</i>	Anatidae	Anseriformes
01840	<i>Anas crecca</i>	<i>Anas</i>	Anatidae	Anseriformes
01842	<i>Anas crecca carolinensis</i>	<i>Anas</i>	Anatidae	Anseriformes
26570	<i>Anas crecca carolinensis</i>	<i>Anas</i>	Anatidae	Anseriformes
01841	<i>Anas crecca crecca</i>	<i>Anas</i>	Anatidae	Anseriformes
01843	<i>Anas crecca nimia</i>	<i>Anas</i>	Anatidae	Anseriformes
01790	<i>Anas penelope</i>	<i>Anas</i>	Anatidae	Anseriformes
01860	<i>Anas platyrhynchos</i>	<i>Anas</i>	Anatidae	Anseriformes
01910	<i>Anas querquedula</i>	<i>Anas</i>	Anatidae	Anseriformes
01591	<i>Anser albifrons albifrons</i>	<i>Anser</i>	Anatidae	Anseriformes
01610	<i>Anser anser</i>	<i>Anser</i>	Anatidae	Anseriformes
01580	<i>Anser brachyrhynchus</i>	<i>Anser</i>	Anatidae	Anseriformes
01600	<i>Anser erythropus</i>	<i>Anser</i>	Anatidae	Anseriformes
01570	<i>Anser fabalis</i>	<i>Anser</i>	Anatidae	Anseriformes
01980	<i>Aythya ferina</i>	<i>Aythya</i>	Anatidae	Anseriformes
02030	<i>Aythya fuligula</i>	<i>Aythya</i>	Anatidae	Anseriformes
01680	<i>Branta bernicla</i>	<i>Branta</i>	Anatidae	Anseriformes
01681	<i>Branta bernicla bernicla</i>	<i>Branta</i>	Anatidae	Anseriformes
01682	<i>Branta bernicla hrota</i>	<i>Branta</i>	Anatidae	Anseriformes
01660	<i>Branta canadensis</i>	<i>Branta</i>	Anatidae	Anseriformes
01665	<i>Branta canadensis asiatica</i>	<i>Branta</i>	Anatidae	Anseriformes
01661	<i>Branta canadensis canadensis</i>	<i>Branta</i>	Anatidae	Anseriformes
01664	<i>Branta canadensis hutchinsii</i>	<i>Branta</i>	Anatidae	Anseriformes
01662	<i>Branta canadensis occidentalis</i>	<i>Branta</i>	Anatidae	Anseriformes
01663	<i>Branta canadensis parvipes</i>	<i>Branta</i>	Anatidae	Anseriformes
01670	<i>Branta leucopsis</i>	<i>Branta</i>	Anatidae	Anseriformes
01690	<i>Branta ruficollis</i>	<i>Branta</i>	Anatidae	Anseriformes
01530	<i>Cygnus columbianus</i>	<i>Cygnus</i>	Anatidae	Anseriformes
01532	<i>Cygnus columbianus bewickii</i>	<i>Cygnus</i>	Anatidae	Anseriformes
01531	<i>Cygnus columbianus columbianus</i>	<i>Cygnus</i>	Anatidae	Anseriformes
01540	<i>Cygnus cygnus</i>	<i>Cygnus</i>	Anatidae	Anseriformes
01520	<i>Cygnus olor</i>	<i>Cygnus</i>	Anatidae	Anseriformes
04290	<i>Fulica atra</i>	<i>Fulica</i>	Rallidae	Gruiformes
05900	<i>Larus canus</i>	<i>Larus</i>	Laridae	Charadriiformes
05901	<i>Larus canus canus</i>	<i>Larus</i>	Laridae	Charadriiformes
05902	<i>Larus canus heinei</i>	<i>Larus</i>	Laridae	Charadriiformes
05820	<i>Larus ridibundus</i>	<i>Larus</i>	Laridae	Charadriiformes
05320	<i>Limosa limosa</i>	<i>Limosa</i>	Scolopacidae	Charadriiformes
05322	<i>Limosa limosa islandica</i>	<i>Limosa</i>	Scolopacidae	Charadriiformes
05321	<i>Limosa limosa limosa</i>	<i>Limosa</i>	Scolopacidae	Charadriiformes
01950	<i>Marmaronetta angustirostris</i>	<i>Marmaronetta</i>	Anatidae	Anseriformes
01960	<i>Netta rufina</i>	<i>Netta</i>	Anatidae	Anseriformes
05170	<i>Philomachus pugnax</i>	<i>Philomachus</i>	Scolopacidae	Charadriiformes
04850	<i>Pluvialis apricaria</i>	<i>Pluvialis</i>	Charadriidae	Charadriiformes
04852	<i>Pluvialis apricaria altifrons</i>	<i>Pluvialis</i>	Charadriidae	Charadriiformes
04851	<i>Pluvialis apricaria apricaria</i>	<i>Pluvialis</i>	Charadriidae	Charadriiformes
04930	<i>Vanellus vanellus</i>	<i>Vanellus</i>	Charadriidae	Ciconiiformes

ANNEX 6 RESULTS FROM ROMANIA AND SPAIN

Romania

It was not possible to differentiate between sample numbers and birds. The total number of samples taken is as follows; 4639 cloacal swabs, 41 faecal swabs, 2106 tracheal swabs, 804 tissue samples, and 41 blood samples. To approximate the total number of birds sampled, it was assumed that one cloacal swab was collected per bird, and if no cloacal swab was collected then samples from another category were counted, the approximate total equalling: 5103 (4639 cloacal swabs, 405 tracheal swabs and 59 tissue samples). The date of sampling was not provided with the data. Birds were sampled from all origin categories; it was not possible to determine exactly how many samples were taken from which category of origin. From a total of 507 reports (approximately 5103 birds), 12 records (134 birds) were live birds, 32 records (294 birds) were hunted birds, 3 records (7 birds) were diseased and 384 records (3291 birds) were taken from birds that were found dead. For the remaining 76 (14.99% of total) records (1377 (26.98%) birds), it was not possible to distinguish how many birds were sampled from which category of origin, as more than one category was in each record (e.g. live and diseased, live and dead). 14 out of 124 (11.29%) species sampled in Romania (including unknown species) were risk species; *Cygnus olor*, *Cygnus cygnus*, *Anser albifrons albifrons*, *Anser anser*, *Branta ruficollis*, *Anas Penelope*, *Anas crecca*, *Anas platyrhynchos*, *Anas clypeata*, *Fulica atra*, *Vanellus vanellus*, *Philomachus pugnax*, *Limosa limosa* and *Larus canus*. 29 out of 124 species (23.39%) were bridge species of high or medium risk; 10 (8.06%) were of low risk and 85 (68.45%) were categorized as 'other'. However the number of birds and proportion of birds in these categories could not be determined.

Positives:

Three cloacal swabs were taken from diseased *Cygnus olor*, and tested positive for H5 (it is not clear whether this was HPAI or LPAI). A further 11 cloacal swabs sampled from *Cygnus olor* tested positive for HPAI H5. It is not clear from how many birds these samples were taken: Two of these samples appear to be taken from dead birds; the other 9 were of unknown origin and all were sampled outside of a restricted area.

One live bird, a "shearwater" was categorized as subtype HPAI H5, however the results columns do not indicate a positive result therefore it is difficult to determine if this was a possible data entry error.

Spain

In 2006, a total of 24099 birds were sampled. HPAI H5N1 was only identified in one bird, the Great Crested Grebe, *Podiceps cristatus* between June and December 2006.

16843 wild birds from 158 species were sampled between February and May 2006. This represented 20.48% of birds sampled across the European Union (excluding Romania and Switzerland) during this sampling period. Sixty-two birds tested positive for LPAI and no detections of HPAI were reported between February and May 2006.

Between June and December 2006, 7256 wild birds (excluding captive birds) from 193 species were sampled. Sixteen percent of the birds tested were of risk species. No information was available on sample date, sample type, origin or location of birds. It was not possible to differentiate between samples and birds, consequently the number of positive birds for June- December cannot be stated. 20666 RT-PCR tests were conducted on samples taken from these birds (multiple samples collected from a number of birds) between June and December. One hundred and forty five samples tested by RT-PCR were found positive for avian influenza, ten of which were H5 positive of which one sample was H5N1 positive. The following LPAI subtypes were isolated from 6 species including unidentified species: H1N1 (*Tadorna tadorna* and unidentified species), H1N6 (*Anas platyrhynchos*), H3N1 (*Anas platyrhynchos*), H3N2 (*Anas platyrhynchos* and Order Anatidae), H3N8 (*Anas platyrhynchos* and Order Anatidae), H4N6 (*Himantopus himantopus* and unidentified birds), H10N4 (*Anas platyrhynchos*), H10N7 (*Phoenicopus ruber*).

3 further species tested positive for avian influenza, however the subtype was not determined (*Anas querquedula*, *Tringa nebularia* and *Larus audouinii*).

ANNEX 7 ADDITIONAL INFORMATION BREAKDOWN FOR EACH MEMBER STATE

Due to the size of the file this Annex has been published as a separate document.

This Annex includes country level graphs displaying data, by season, for each member state on the origin of samples for sampled and positive wild birds, risk of sampled and positive wild birds, and bridge species. A species table displaying all data is also included for each member state.