



EUROPEAN COMMISSION
HEALTH & CONSUMERS DIRECTORATE-GENERAL

Directorate D – Animal Health and Welfare
D1 - Animal Health and Standing Committees
04 – Veterinary control programmes

SANCO/2181/2008 – Rev.1

Annual Report on surveillance for avian influenza in wild birds in the EU during 2007



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GLOSSARY AND ABBREVIATIONS

Animal Disease Notification System	ADNS
Avian Influenza	AI
Community Reference Laboratory	CRL
European Food Safety Authority	EFSA
European Union	EU
Highly Pathogenic Avian Influenza	HPAIV
Highly Pathogenic	HP
Higher-Risk Species	HRS
Low Pathogenic Avian Influenza	LPAIV
Member State	MS
National Reference Laboratory	NRL
Nomenclature of Units for Territorial Statistics	NUTS

Abb.	Country
AT	Austria
BE	Belgium
BG	Bulgaria
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

Active surveillance: For the purpose of this report, active surveillance will be used as an equivalent to the surveillance birds that were live without clinical signs, hunted without clinical signs and hunted with clinical signs.

Bird Origin: Relates to the collected information on the origin of the bird when sampled. The six categories are: live without clinical signs, live with clinical signs, injured, hunted without clinical signs, hunted with clinical signs and found dead. Birds sampled with no information on their origin were reported in the first quarter (Jan-Mar) prior to the onset of online submission.

Bridge Species: Species listed as those that may provide contact between risk species and poultry through sharing wetlands or farmlands with poultry (EFSA, 2006).

DG SANCO: Directorate General for Health and Consumers.

EU 27: Refers to the 27 Member States of the European Union.

EURING code: European Union for Bird Ringing; A 5-digit number allocated to a species or subspecies of bird.

Higher-Risk Species (HRS): Species listed as those with an increased probability to contribute to the transmission of the Asian-lineage H5N1 HPAIV viruses within Europe as defined in the scientific report by EFSA (EFSA, 2006) and the guidelines for programmes carried out in 2007 (EC, 2007) (in total 29 species). The EURING codes corresponding to these species can be found at: http://www.euring.org/data_and_codes/euring_code_list/euring_exchange-code_2000.pdf

Incident: For the purpose of this report H5N1 HPAIV cases were grouped into incidents based on proximity of 10km radius, which is equivalent to the size of monitoring areas (EC, 2006a).

LPAIV H5: birds positive for LPAIV of subtype H5

LPAIV H7: birds positive for LPAIV of subtype H7

LPAIV other: birds reported as LPAIV of other subtypes

NUTS 3: Nomenclature of Units for Territorial Statistics. At NUTS 3 level this refers to, for example, a region, district, county, municipal or unitary authority (depending on the MS).

Other positives: birds positive for Avian Influenza but that were not clearly reported as either LPAIV or HPAIV.

Passive surveillance: For the purpose of this report, passive surveillance will be used as an equivalent to the surveillance of birds that were live with clinical signs, injured and found dead.

PCR: Polymerase chain reaction is a generic term for laboratory methodology that acts through the amplification of specific viral nucleic acid from clinical specimens.

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

VI: Virus isolation is a laboratory methodology that enables the propagation of infectious virus directly from clinical specimens.

SUMMARY¹

Avian Influenza (AI) is a highly contagious viral infection which can affect all species of birds. AI infections in birds are divided in two groups on the basis of the ability of the virus to cause disease. Highly Pathogenic Avian Influenza (HPAI) spreads rapidly causing serious disease with high mortality in almost all bird species and has so far been restricted to H5 and H7 subtypes. Low Pathogenic Avian Influenza (LPAI) belonging to H1-H16 subtypes usually causes a mild disease in poultry. LPAI strains of the H5 and H7 subtypes have the potential to mutate into HPAI. Wild waterfowl are recognised as the natural reservoir of LPAI viruses. Although previously HPAIV infections were rarely observed in wild birds and if so only in connection with poultry outbreaks, since the continuing outbreaks of H5N1 HPAI in Asia, wild birds have been thought to be implicated in the long distance spread of that virus. Therefore wild bird surveillance and the reporting of the results have become compulsory since 2005 in the European Union. The surveillance three main objectives are: The early detection of H5N1 HPAIV in wild birds, the investigation of possible carrier or bridge species following an incident of H5N1 HPAIV and baseline monitoring of circulation of LPAIV H5 and H7 strains in wild birds. The surveillance results reported here were collected between January and December 2007 according to EU harmonised guidelines.

All 27 Member States of the European Union have reported results and a total of 79 392 wild birds were tested during 2007. In contrast to 2006 where cases in wild birds were reported from 14 Member States, H5N1 HPAIV incidents in 2007 were reported from only four Member States and were limited in time and locations. A total of 329 cases of H5N1 HPAIV were reported from nine incidents in the four Member States of Czech Republic (1), Germany (318), France (7) and Poland (3). With the exception of three H5N1 HPAIV cases of captive wild birds reported from Poland that occurred in December, all incidents occurred during the summer months between June and September outside the main migration period.

Most incidents were detected through the finding of dead swan *spp.* With the exception of one apparently healthy swan that was shot in the area of an incident, all H5N1 HPAIV infected birds were either dead (326) or showed clinical signs (2). In one incident, larger scale mortalities occurred within a short time frame, whilst in other incidents the findings of H5N1 HPAIV extended over longer periods of time without apparently increased mortalities. Most incidents involved swan *spp.* In one incident in DE high mortalities occurred in Black-necked Grebes (*Podiceps nigricollis*) and Great Crested Grebes (*Podiceps cristatus*). In total at least 14 species tested positive for H5N1 HPAIV in 2007. With the exception of a little grebe (*Tachybaptus ruficollis*) and a White stork (*Ciconia ciconia*) (which was a captive bird though), all of the H5N1 HPAIV positive species also had H5N1 HPAIV positives identified

¹**DISCLAIMER: on data completeness please see page 10.**

in 2006. Two findings of the 2007 data suggest that the occurrence of H5N1 HPAIV incidents in 2007 were the result of a new introduction rather than a continuous circulation of the virus at a low level. Firstly, the weekly number of reported cases of wild birds in 2006 as well as in 2007, display two epidemic curves typical of an infectious disease, which are clearly separated. Secondly, phylogenetic analysis showed that the viruses found in 2007 could be clearly differentiated from those associated with previous outbreaks/ incidents in poultry and wild birds in the EU. It would appear that the viruses had derived as a result of a further and independent spill-over potentially from infected poultry populations in the Middle Eastern or wider region back into wild birds.

LPAIV of H5 was detected in 105 birds from ten Member States: Germany (9), Denmark(6), Finland(1), France(16), Ireland(2), Italy(7), Netherlands(2), Portugal (3), Sweden (55) and the United Kingdom (4). LPAIV H7 was found in seven birds derived from six Member States: Germany (1), Denmark (2), Hungary (1), Italy (1), Poland (1) and Sweden (1). Consistent with previous years, the large majority of LPAI H5/H7 infections in 2007 were identified through active surveillance of HRS, especially dabbling ducks (*Anas spp.*) and swans (*Cygnus spp.*).

The detection of incidents in wild birds without outbreaks in poultry illustrated the value and role of wild bird surveillance as a potential early warning system for the presence of H5N1 HPAI virus in a country.

INTRODUCTION

Wild bird surveillance in the EU is aimed at identifying the risk of introduction of AI viruses (LPAIV and HPAIV) into domestic poultry (EC, 2007).

Voluntary Surveillance for AI in wild birds in EU MS was first carried out in 2002-2003 under Commission Decision 2002/649/EC (EC, 2002), although several MS had already been conducting wild bird surveillance prior to this.

In response to the cases in wild birds and outbreaks in poultry and the evolving epidemiological situation of H5N1 HPAIV in Asia, activities with regard to wild bird surveillance were increased. Wild bird surveillance became compulsory in 2005 for all MS and information collection on wild birds was extended and harmonised.

In 2006, EFSA completed a scientific opinion on migratory birds and their possible role in the spread of HPAIV (EFSA, 2006). This included an assessment of birds of predominantly the orders Anseriformes and Charadriiformes regarding their likelihood to introduce H5N1 HPAIV following the criteria of 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. This opinion has led to an inclusion of a “higher risk species” (HRS) list into the guidelines for targeting of surveillance.

OBJECTIVES

The main objective of this report is to present the surveillance results of 2007 in a comparative manner to 2006 (SANCO, 2007) and to discuss the main findings.

The objectives of the EU wild bird AI surveillance are (EC, 2007):

“Ensuring early detection of H5N1 HPAIV by investigating increased incidence of morbidity and mortality in wild birds, in particular in selected “higher risk” species.

In the event that H5N1 HPAIV is detected in wild birds, then surveillance of live and dead wild birds shall be enhanced to determine whether wild birds of other species can act as asymptomatic carriers or “bridge species”.

Continuing a “baseline” surveillance of different species of free-living migratory birds as part of continuous monitoring of LPAIV viruses. Anseriformes (water fowl) and Charadriiformes (shorebirds and gulls) shall be the main sampling targets to assess if they carry LPAIV viruses of H5 and H7 subtypes (which would in any case also detect H5N1 HPAIV and other HPAIV, if present). “Higher risk species” must be targeted in particular”

MATERIALS AND METHODS

THE SURVEY PROGRAMMES

Details of the survey programmes for MS's are available on the website of the Directorate General of the European Commission (DG SANCO) under the following links:

AI Surveillance programmes of Member States (25) before the accession of BG and RO:

http://ec.europa.eu/food/animal/diseases/eradication/programme2007/2006_875_ec.pdf

AI Surveillance programmes of BG and RO:

http://ec.europa.eu/food/animal/diseases/eradication/programme2007/2006_876_ec.pdf

THE TESTING OF SAMPLES

Laboratory tests were carried out in accordance with the avian influenza diagnostic manual. It was recommended that samples should initially be tested using M gene PCR (to detect presence of AI 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 AI virus (EC, 2006b).

DATA COMPLETENESS (EU 27)

The data presented in this report is limited to data collected under surveillance programmes according to Commission Decision 2007/268/EC (EC, 2007).

It must be noted that some MS experienced difficulties with the introduction of the online reporting system. Consequently some further data collected by **Austria, Denmark, Germany, Italy and Romania** could not be included in this report. The most common reasons for that being: a) data submitted with duplicate bird identifiers, b) data submitted after the reporting deadline and c) programming errors.

Data from **Malta** are not included in this report since they were not submitted.

Note: Graphs and tables in this report were created using the information that was available and records where no information was available were omitted in some instances. Since with the exception of missing subtype/pathotype information this only concerned a very low proportion of records this is not thought to have impacted on the overall results but should be kept in mind when comparing tables that made use of this information and where it was impractical for reasons of readability and interpretability to display the proportion of missing data.

DATA PROCESSING

Maps were produced using the ArcMap function of Arc GIS version 9.2.

Samples are displayed at NUTS 3 level, unless less than 80% of the reported records contained valid spatial information (IT, EE, BG and RO). In this case sample numbers were displayed at a randomized national level. Since data of the first quarter (Q1) was reported in a different format, such data is displayed at randomized national level rather than a specific location and was clearly distinguished through use of a different colour in the display.

SPECIES OF BIRDS:

Species information was of high quality and almost complete (97.6%).

Assumptions:

Since it could not be clarified in time whether birds reported from FR as Black-chinned hummingbirds (*Archilochus alexandri*) with EURING code (08160) were the result of a data entry error, these birds were assumed to be to be Mallards (*Anas platyrhynchos*) instead (01860).

BIRD ORIGIN

Information on the origin of the bird at sampling was almost complete and only 0.008% of the total birds sampled for the year had no information about the origin of the bird.

SUBTYPE / PATHOTYPE INFORMATION:

Of the 1814 birds testing positive, 90% had subtype information supplied and 31% were clearly identified either as LPAIV or HPAIV.

DATE OF SAMPLING:

For birds sampled between April and December 2007, all MS provided a localisation date (from when the bird was sampled in the field). In the first quarter, 7338 birds from 14 MS did not have date information (9.24% of the total number sampled in 2007).

SPATIAL INFORMATION:

Of the submitted spatial information for Quarters 2 to 4, 49969 (90% of birds sampled during this period) could be located at the NUTS 3 level for mapping, either via NUTS codes or coordinates provided. A further 5020 (9%) birds from Quarters 2 to 4 were mapped at NUTS 0 (BG, EE, IT and RO) as less than 80% of the data submitted by these MS were able to be mapped at NUTS 3 level. A total of 440 (1%) birds were unable to be mapped due to errors in the spatial information submitted by the MS. The total number of birds mapped for Quarters 1 to 4 at both NUTS0 and NUTS3 level was 78952.

Assumptions

An incident was defined in this report as H5N1 HPAIV infected bird(s) that were found within 10 km (size of the monitoring area (EC, 2006a) of another H5N1 HPAIV infected bird.

PHYLOGENETIC ANALYSIS

Minimum analysis involved generation of haemagglutinin gene sequences of H5 viruses submitted to the CRL. This was then compared using the programme MEGA (Tamura *et al.*, 2007) to reveal phylogenetic relationships. This comparison was done with data generated at the CRL and that available in the public domain (including some deposited by National Reference Laboratories (NRLs) from MS).

RESULTS

SAMPLING

OVERVIEW

During 2007, 79392 birds were sampled in the EU in all 27 MS (Figure 1). Detailed figures regarding the number of birds sampled by MS in each quarter are displayed in Annex I a. Most of the birds tested in 2007 originated from DE (n=23949), where nearly three times the number of birds were sampled than the next highest sample number from NL (n=8446). Seventeen MS sampled fewer than 1000 birds throughout the year. Table 2 displays the number of birds sampled in 2007 by type of surveillance. All MS conducted active and passive surveillance, although the proportion of each varied highly, reflecting results of the 2006 surveillance.

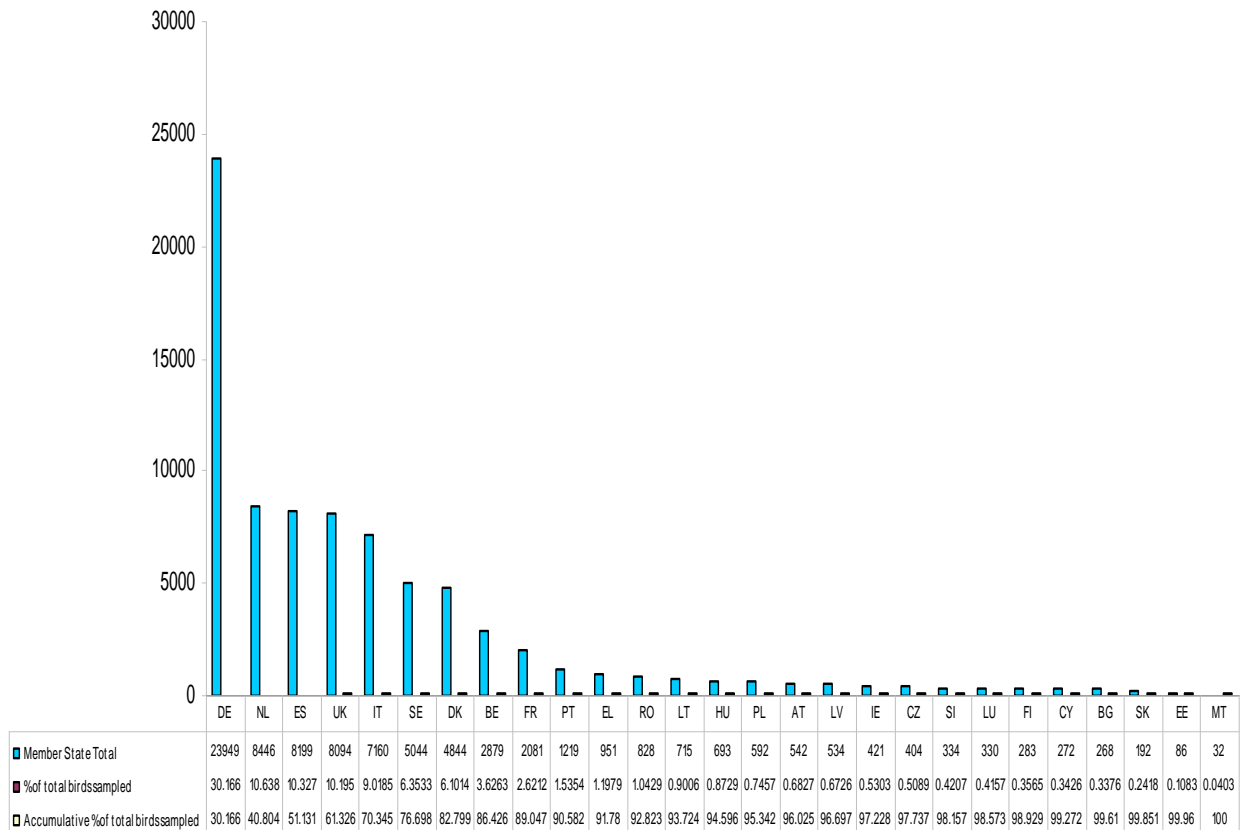


Figure 1 Total number of birds sampled in 2007 by EU MS

Table 2 Number and proportion of birds sampled in 2007 by surveillance type and MS					
Member State	Number of Birds Sampled	Proportion of HRS sampled	Proportion of Active Surveillance	Proportion of Passive Surveillance	Proportion of Surveillance Type Unknown
AT	542	50.6%	38.9%	60.1%	0.9%
BE	2879	67.4%	97.5%	2.5%	0.0%
BG	268	21.6%	64.6%	33.2%	2.2%
CY	272	4.4%	32.0%	54.4%	13.6%
CZ	404	84.2%	1.0%	99.0%	0.0%
DE	23949	54.5%	68.8%	30.1%	1.1%
DK	4844	70.1%	94.8%	5.2%	0.0%
EE	86	66.3%	68.6%	31.4%	0.0%
EL	951	23.6%	53.1%	46.9%	0.0%
ES	8199	26.6%	69.9%	27.9%	2.2%
FI	283	51.9%	81.3%	18.7%	0.0%
FR	2081	79.9%	55.7%	44.3%	0.0%
HU	693	58.4%	77.3%	22.7%	0.0%
IE	421	77.9%	61.5%	38.5%	0.0%
IT	7160	61.1%	88.4%	11.6%	0.0%
LT	715	92.6%	88.0%	12.0%	0.0%
LU	330	14.5%	79.7%	20.3%	0.0%
LV	534	93.6%	95.5%	2.4%	2.1%
MT	32	87.5%	93.8%	6.3%	0.0%
NL	8446	61.2%	92.5%	7.5%	0.0%
PL	592	41.7%	66.2%	18.4%	15.4%
PT	1219	18.0%	66.8%	33.2%	0.0%
RO	828	12.9%	89.0%	10.9%	0.1%
SE	5044	64.1%	93.2%	6.8%	0.1%
SI	334	65.3%	68.9%	31.1%	0.0%
SK	192	33.3%	57.3%	42.7%	0.0%
UK	8094	79.6%	75.9%	24.1%	0.0%
EU	79392	57.2%	77.5%	21.7%	0.8%

GEOGRAPHICAL TARGETING

Figure 2 and 3 aim to illustrate the distribution of active and passive surveillance respectively on a spatial scale by displaying the number of birds sampled.

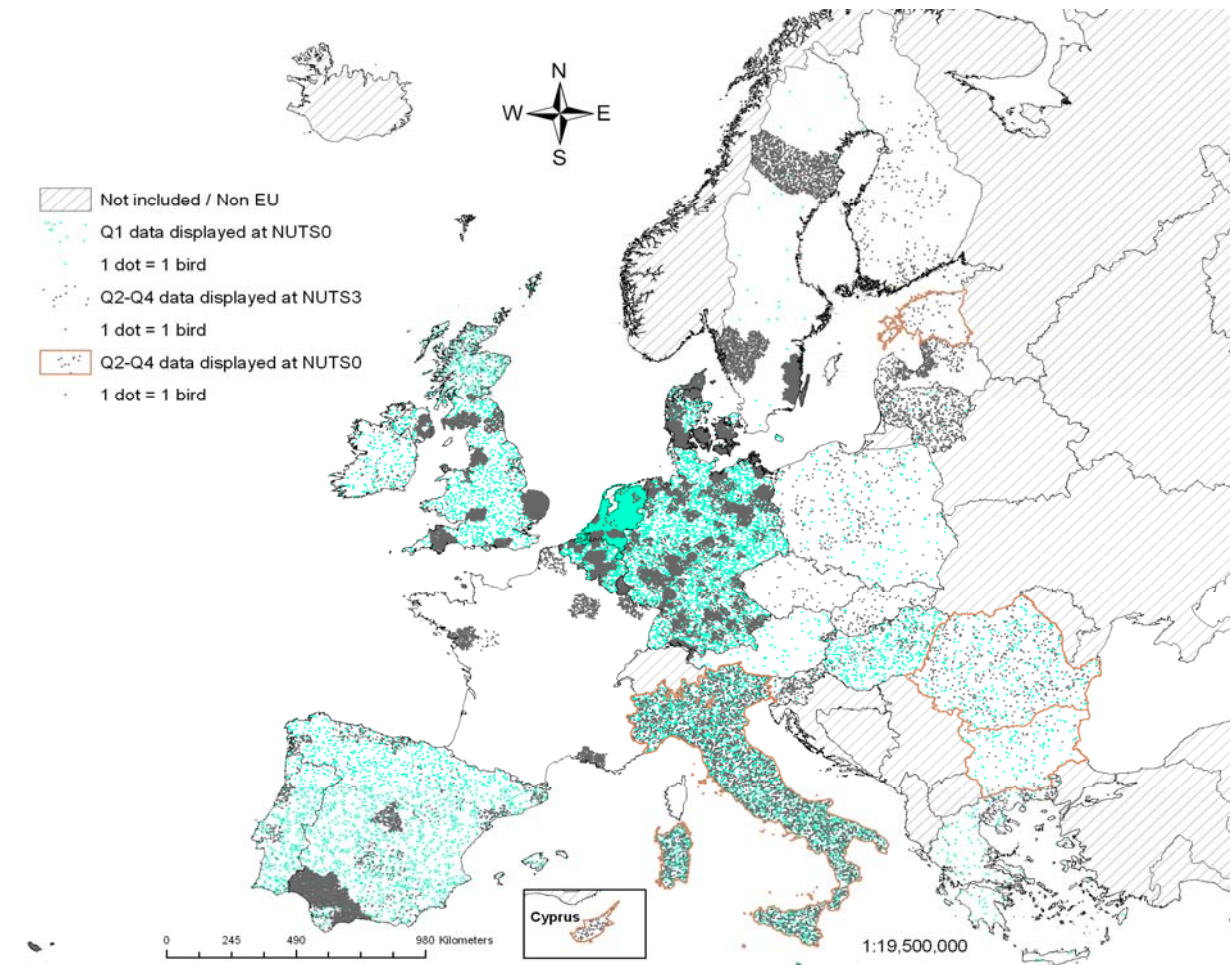


Figure 2 Number of wild birds sampled in active surveillance (live and hunted birds) in EU MS in 2007 (Quarter 1 randomized at NUTS 0 level).

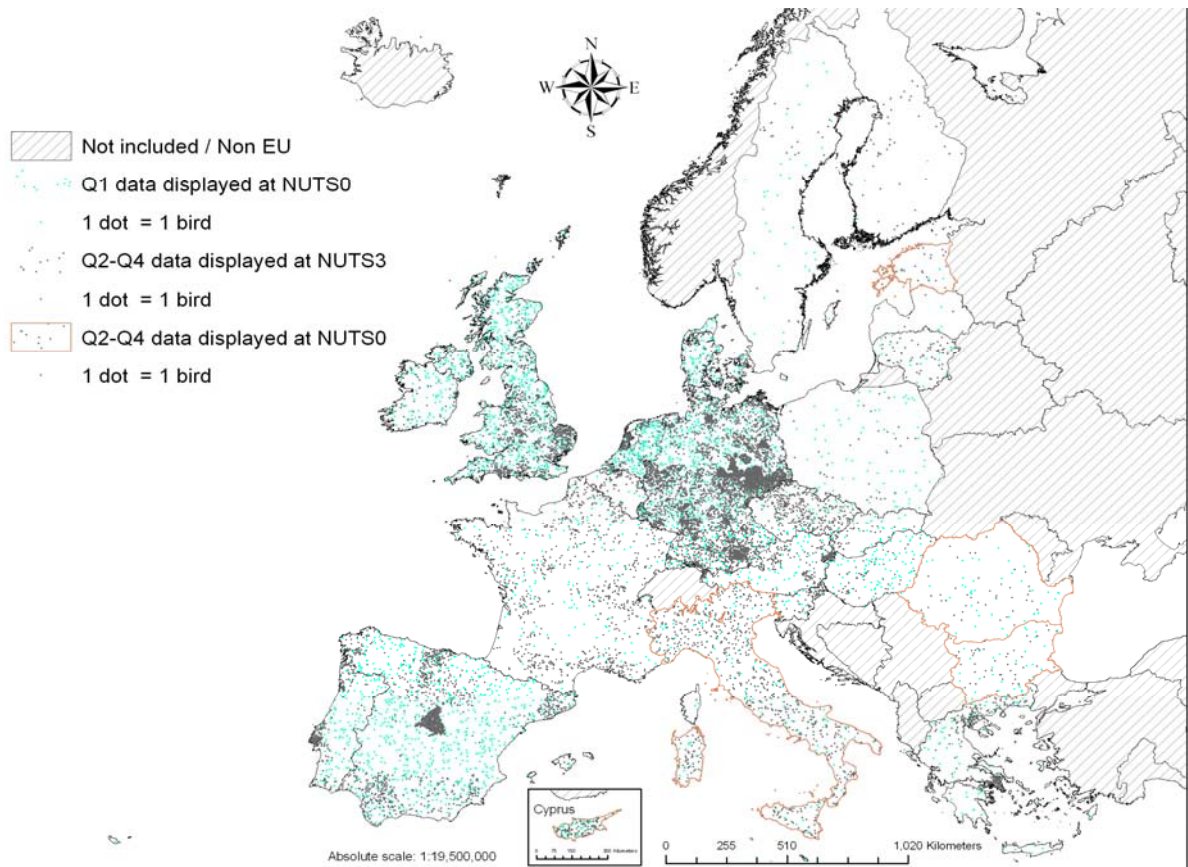


Figure 3 Number of wild birds sampled in passive surveillance (birds found dead, injured or live with clinical signs) in EU MS in 2007 (Quarter 1 randomized at NUTS 0 level)

SEASONAL TARGETING

Figure 4 displays the number of birds sampled by MS and quarter. Overall similar numbers of birds were tested in each quarter. Temporal targeting of sampling varied among MS and while some MS increased the number of birds tested throughout the year other MS decreased the numbers whilst others sampled the largest proportion of birds during the time of the H5N1 HPAIV incidents in the summer months.

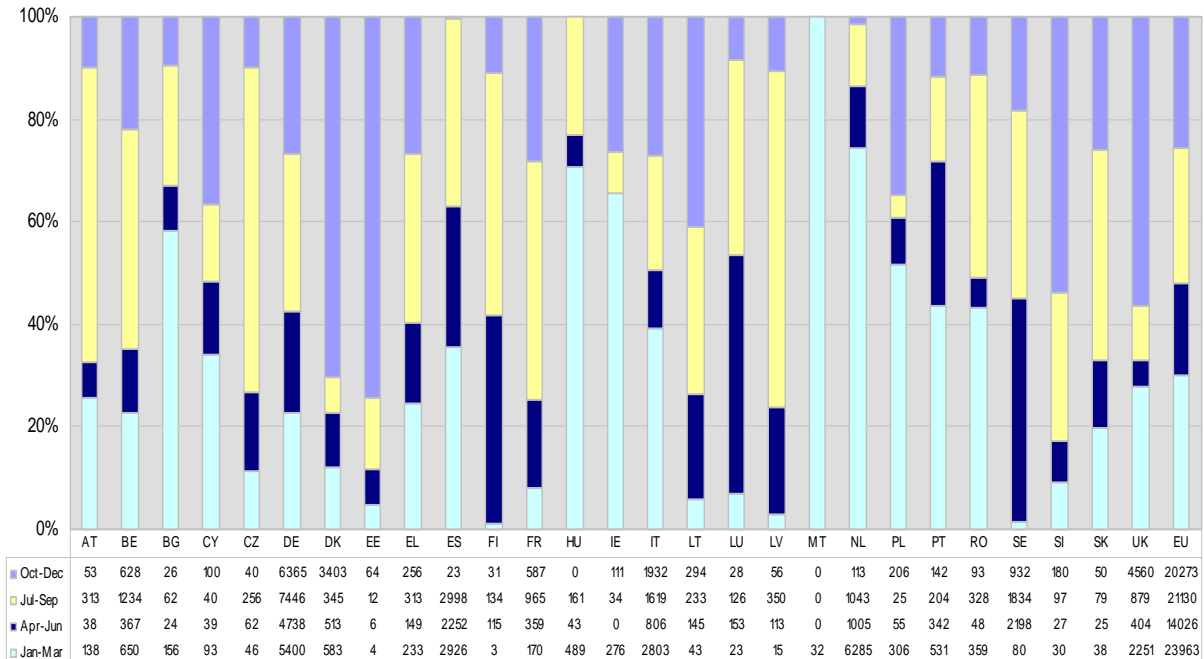


Figure 4 Number and proportion of all birds sampled by quarter and MS

Figure 5 displays the overall number of birds sampled in EU MS in 2006 and 2007 by surveillance type. Active surveillance of HRS was increased in the late summer to late autumn months in 2006 as well as in 2007, but overall numbers in 2007 stayed below those of 2006. Active surveillance of birds other than HRS peaked in the summer months in response to the incidents in DE and CZ and in the time period between May and July birds not considered HRS exceeded the number of HRS birds tested in active surveillance. Passive surveillance of higher risk and other species also increased in the summer months of 2007 in response to the incidents. Outbreaks in poultry that occurred between November and December in DE, PL and RO did not trigger an overall increase in passive surveillance of wild birds, while probably being the reason for an increased active surveillance of non-HRS birds during this time period. However even during incident/outbreak times, the number of birds tested through passive surveillance was lower than the number of birds tested during the incidents in early 2006. Tables displaying the number of birds sampled according to surveillance type and MS are displayed in Annex I b.

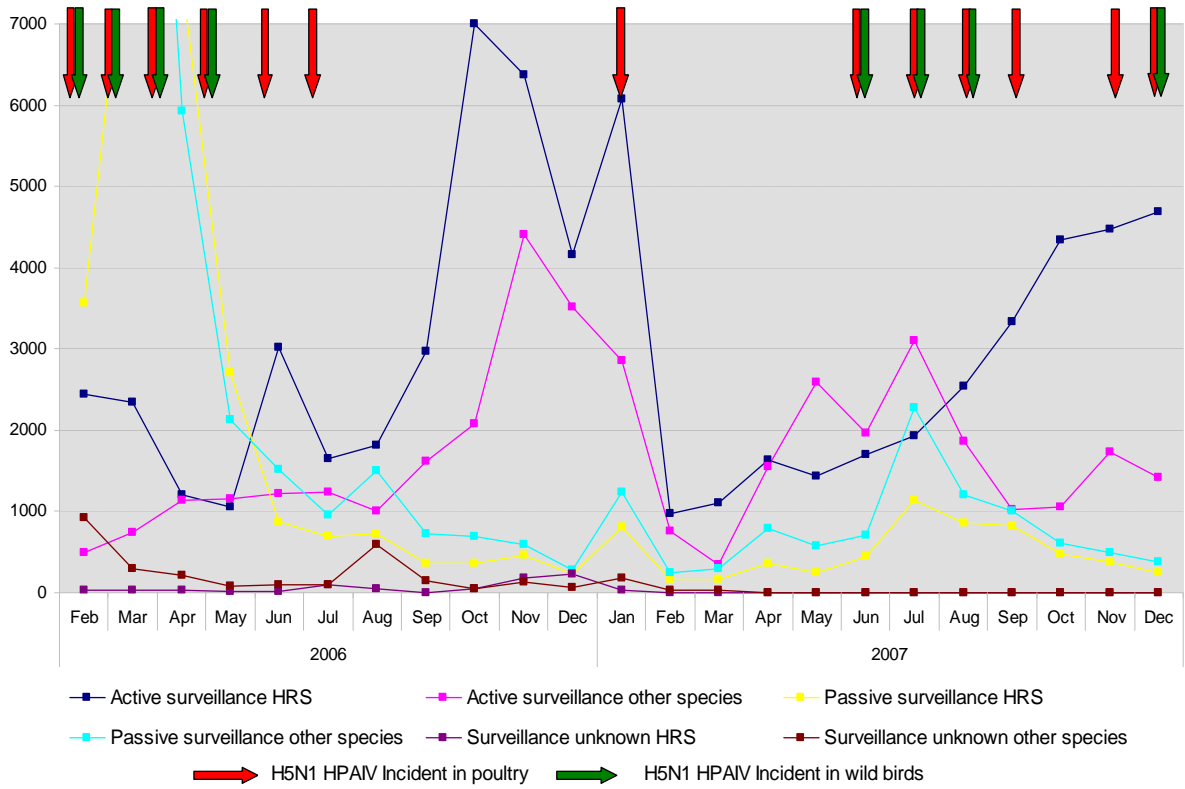


Figure 5 Total number of birds sampled by surveillance type and month in 2006/07

TARGETING OF HRS

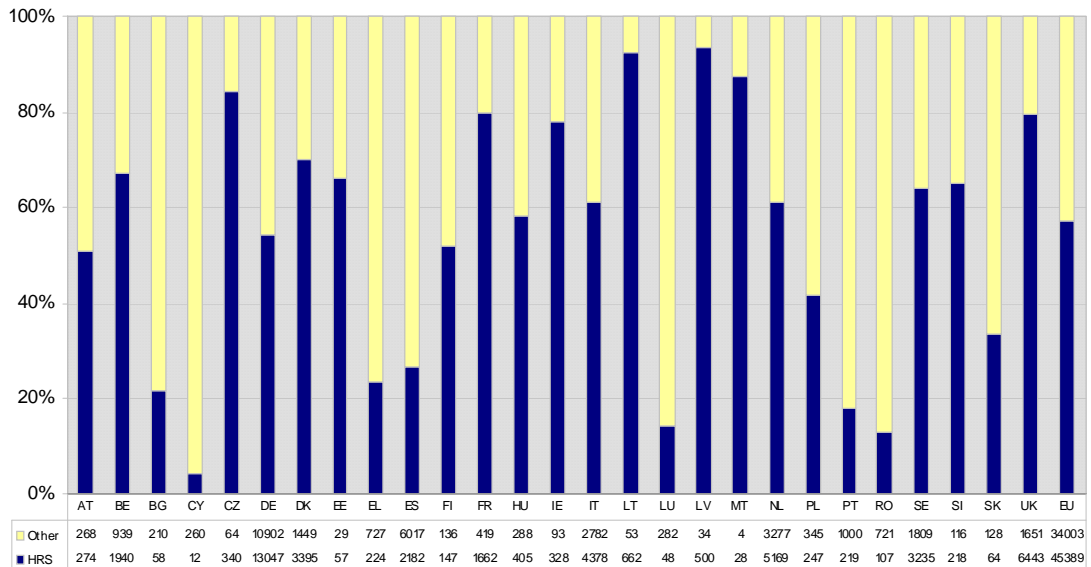


Figure 6 Number and proportion of HRS and non-HRS sampled in the 2007 EU AI wild bird surveillance

A large variation between MS occurred in respect of targeting HRS. The EU proportion of HRS is 57%, (Range among MS 4.4% - 93%) which was similar to 2006 (51%) (Figure 6).

Targeting of HRS peaked at the start and end of the year. Most MS increased the amount of targeting of HRS in the course of the year, leading to an increase in the proportion of HRS sampled amongst the total at the end of 2007 (71%) (Figure 7). More detailed graphs, displaying the proportion of HRS among the sampled birds by MS and reporting period are displayed in Annex I c.

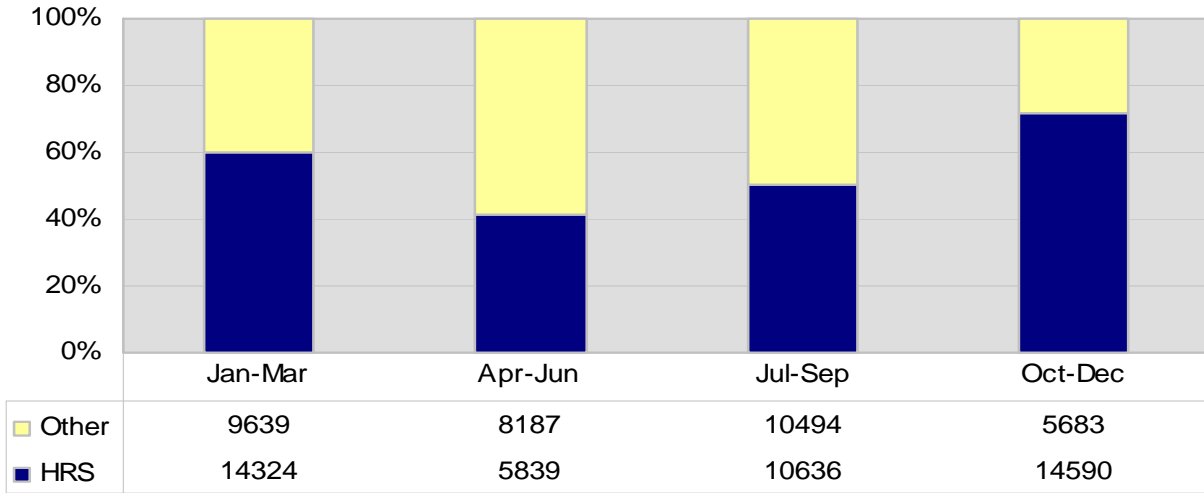


Figure 7 Number of birds and proportion of HRS sampled in 2007 by quarter

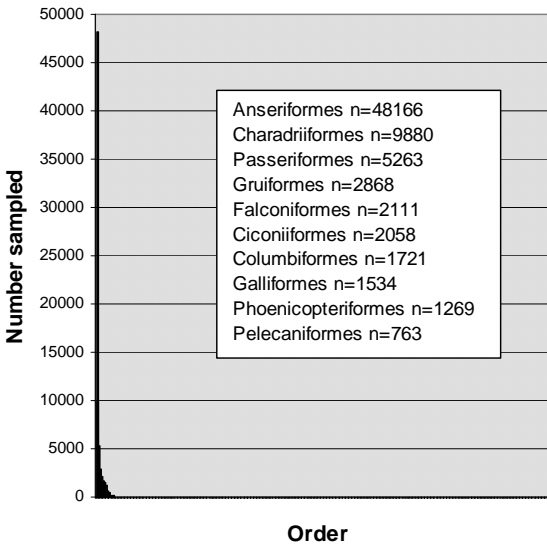


Figure 8 Top ten orders sampled in 2007 in EU MS

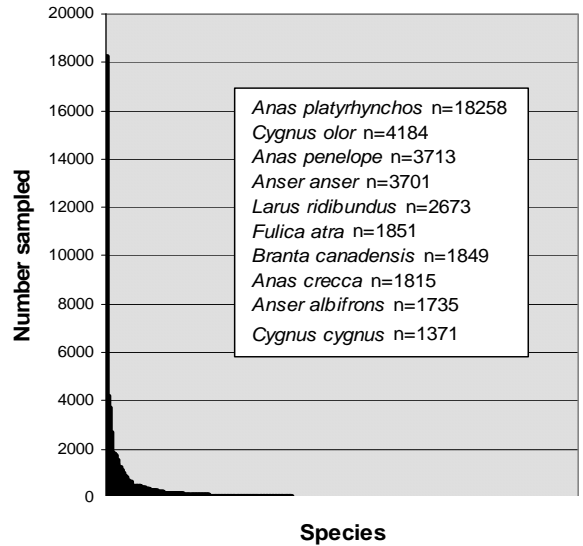


Figure 9 Top ten species sampled in 2007 in EU MS

In total 79392 birds of 22 orders and at least 398 species were sampled. Figure 8 displays the ten most frequently sampled orders. As in 2006, the three Orders in which most birds were sampled were: Anseriformes (Ducks, Geese and Swans), Charadriiformes (Gulls and waders) and Passeriformes (perching/ songbirds).

Figure 9 displays the top 10 species sampled in 2007 throughout MS. Mallards (*Anas platyrhynchos*) were the most frequently sampled species in 2007 (n=18258) as in 2006. Mute Swans (*Cygnus olor*) (n=4184) and Wigeons (*Anas penelope*) (n=3713) were also sampled in high numbers. All of the ten most frequently sampled species were HRS. Figure 9 also indicates that the top ten species were sampled in high numbers, accounting for 52% of all birds tested in 2007, and a large majority of species were sampled in very low numbers.

H5N1 HPAIV POSITIVES

A differentiation is made between H5N1 HPAIV infections and LPAIV. Unless otherwise stated, all references made to H5N1 refer to highly pathogenic H5N1. In total 329 cases of H5N1 HPAIV infections were observed in 2007 in four MS. Overall 0.41% of the sampled birds tested positive for H5N1 HPAIV. In MS experiencing H5N1 infections, the proportion of H5N1 HPAIV positive birds ranged from 0.25% (CZ) to 1.33% (DE) (Table 3).

Member State	Number of birds sampled	Number of birds H5N1 HPAIV positive	Proportion of sampled birds positive for H5N1 HPAIV
CZ	404	1	0.25%
DE	23949	318	1.33%
FR	2081	7	0.34%
PL	592	3	0.51%
EU Total	79392	329	0.41%

DESCRIPTIVE OVERVIEW OF H5N1 HPAIV INCIDENTS IN WILD BIRDS

After outbreaks in poultry holdings in the UK and Hungary in January / February of 2007, no further poultry outbreaks or incidents in wild birds were observed until the second half of June when almost simultaneously reports of H5N1 HPAIV detections came from the Czech Republic, Germany and France:

Czech Republic:

In CZ the finding of H5N1 HPAIV in one mute swan (*Cygnus olor*) in the south of the country on 25/06/2007 was preceded by an outbreak in commercial turkeys in the central part of the country on 21/06/2007 and in broilers on 27/06/2007. Further outbreaks in poultry occurred on the 09/07/2007 in two breeding hen holdings.

France:

On 28/06/2007 three dead juvenile H5N1 infected Whooper swans (*Cygnus cygnus*) were found in FR in the vicinity of the Luxembourg border. Two Mute swans (*Cygnus olor*) were found in the monitoring area of the first incident, one month after the discovery of the first two swans and two further infected dead mallards (*Anas platyrhynchos*) were found in the beginning of August in the same location.

Germany:

In DE wild bird cases were first observed in the city of Nurnberg in the south of the country (Bavaria) on 19/06/2007. The incident was detected through the finding of several dead Mute swans (*Cygnus olor*). The incident lasted until 08/07/2007 and a total of 13 Mute swans, one Canada goose (*Branta Canadensis*), one Mallard (*Anas platyrhynchos*) and one Greylag goose (*Anser anser*) were infected with H5N1 HPAIV. After the first incident, several locally limited incidents occurred in four German states: In the city of Nuremberg, Aschheim in the vicinity of Munich, the lake of Kelbra in Thuringia, the dam of Windischleuba in Saxony and Ebeleben in Thuringia. At lake Kelbra a large number of dead Grebes (Black-necked and Crested) tested positive for H5N1 HPAIV and it was estimated that two thirds of the local grebe population of 500 birds were affected by the infection (FLI, 2007). The last infection was reported on the 25/07/2007 and concerned a Black-necked Grebe from lake Kelbra.

Poland:

Following on from five outbreaks of H5N1 HPAIV in poultry (turkeys, ducks and layers) in late November/ early December of 2007, H5N1 HPAIV was found in three birds kept at a wild bird rehabilitation centre.

Therefore this incident cannot be truly regarded as concerning wild birds but is reported in this report for completeness.

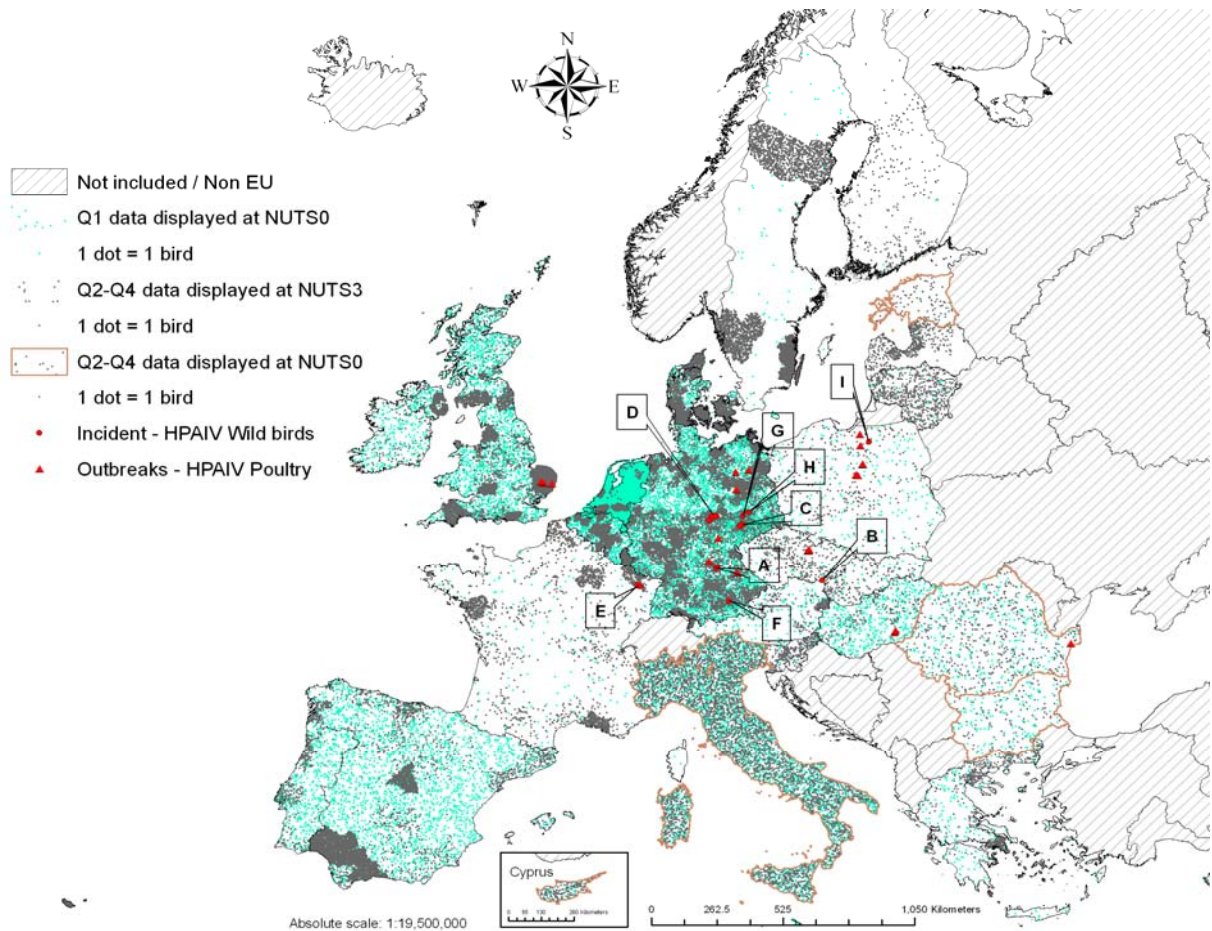


Figure 10 H5N1 HPAIV incidents in wild birds and H5N1 outbreaks in poultry in EU MS in 2007 (Q1 data randomized at NUTS 0 level)

Figure 10 above displays the location of the H5N1 HPAIV incidents in wild birds and poultry. Cases of wild birds were grouped into an incident if they were located within 10 km of each other. Nine incidents in wild birds occurred. More detailed information regarding how they were detected; the number of birds tested during and after an incident is displayed in Table 4.

Timing of H5N1 wild bird incidents

The timing of the H5N1 HPAIV outbreaks in poultry and incidents in wild birds is presented in Figure 11 and Figure 12 shows the number of wild bird H5N1 HPAIV cases as well as the number of birds tested in the EU in 2007 by week. The observed peak of number of birds sampled in the first week of January is due to a number of birds reported in this week that were in fact sampled during 2006 but were not reported then and therefore included in the first week of 2007.

Table 4 Details of H5N1 HPAIV incidents in 2007

MS	Incident	Incident duration	Detection through	Number and species of birds H5N1 HPAIV positive (Bird origin) L = live no clinical signs D= dead H= Hunted healthy LCS = live with clinical signs HCS= Hunted with clinical signs	Number and species of additional birds tested during incident (in affected NUTS 4/5 zone and/ or monitoring and control areas) PNK = positive pathotype not known/ pending LP= Positive for LPAIV	Number and species of birds tested in follow up in affected NUTS 4/5 zone and/or monitoring and control areas (until the end of the year) PNK = positive pathotype not known/ pending LP= Positive for LPAIV
Germany	A	19/06/2007-08/07/2007	Mute Swan	1 <i>Anas platyrhynchos</i> (HCS); 13 <i>Cygnus olor</i> (12 D; 1 LCS) 1 <i>Anser anser</i> (D); 1 <i>Branta canadensis</i> (D);	25 <i>Anas platyrhynchos</i> ; 1 <i>Anas</i> sp.2 <i>Cygnus olor</i> 1 <i>Anser</i> sp. 5 unknown; 1 <i>Alcedo atthis</i> ; 1 <i>Apus apus</i> ; 1 <i>Aythya ferina</i> ; 5 <i>Aythya fuligula</i> ; 1 <i>Carduelis carduelis</i> ; 4 <i>Columbus</i> sp.; 3 <i>Corvus corone corone</i> ; 3 <i>Corvus</i> sp.; 1 <i>Falco tinnunculus</i> ; 11 <i>Fulica atra</i> ; 2 <i>Garrulus glandarius</i> ; 1 <i>Netta rufina</i> ; 1 <i>Numida meleagris</i> ; 2 <i>Phalacrocorax carbo</i> ; 3 <i>Pica pica</i> ; 1 <i>Strix aluco</i> ; 2 <i>Turdus merula</i> ; 1 <i>Tyto alba</i>	20 <i>Anas platyrhynchos</i> ; 3 <i>Anas</i> sp.5 <i>Cygnus olor</i> ; 1 <i>Cygnus</i> sp.1 <i>Anser</i> sp. 5 unknown; 1 <i>Accipiter</i> sp.; 5 <i>Anser anser</i> ; 1 <i>Asio otus</i> ; 3 <i>Aythya ferina</i> ; 1 <i>Aythya fuligula</i> ; 4 <i>Columbus</i> sp.; 4 <i>Corvus</i> sp.; 2 <i>Falco</i> sp.; 5 <i>Fulica atra</i> ; 3 <i>Larus ridibundus</i> ; 5 <i>Parus</i> sp.; 1 <i>Phasianus colchicus</i> ; 4 <i>Pica pica</i> ; 1 <i>Picus viridus</i> ; 1 <i>Podiceps cristatus</i> ; 1 <i>Turdus merula</i>
Czech Republic	B	25/06/2007-25/06/2007	Mute Swan	1 <i>Cygnus olor</i> (D)	1 <i>Cygnus olor</i> 4 <i>Anas platyrhynchos</i> ;	6 <i>Cygnus olor</i> 14 <i>Anas platyrhynchos</i> 1 <i>Ardea cinerea</i> ; 1 <i>Ciconia ciconia</i> ; 2 <i>Columba livia</i> ; 2 <i>Larus ridibundus</i>
Germany	C	25/06/2007-04/07/2007	Mute Swan	1 <i>Cygnus</i> sp. (D) 4 <i>Cygnus olor</i> (D) 1 <i>Anas platyrhynchos</i> (D)	1 <i>Cygnus</i> sp. 2 <i>Cygnus olor</i> 1 <i>Anas</i> sp.	1 <i>Cygnus</i> sp. 6 <i>Anas</i> sp. 1 <i>Columba</i> sp.; 1 <i>Dendrocopos major</i> ; 1 <i>Turdus merula</i>

Table 4 Details of H5N1 HPAIV incidents in 2007						
MS	Incident	Incident duration	Detection through	Number and species of birds H5N1 HPAIV positive (Bird origin) L = live no clinical signs D= dead H= Hunted healthy LCS = live with clinical signs HCS= Hunted with clinical signs	Number and species of additional birds tested during incident (in affected NUTS 4/5 zone and/ or monitoring and control areas) PNK = positive pathotype not known/ pending LP= Positive for LPAIV	Number and species of birds tested in follow up in affected NUTS 4/5 zone and/or monitoring and control areas (until the end of the year) PNK = positive pathotype not known/ pending LP= Positive for LPAIV
Germany	D	28/06/2007-27/07/2007	Black-necked Grebe	3 <i>Cygnus olor</i> (2 D; 1 H). 2 <i>Larus</i> sp. (D) 37 <i>Podiceps cristatus</i> (D) 246 <i>Podiceps nigricollis</i> (D) 2 <i>Tachybaptus ruficollis</i> (D)	1 <i>Cygnus olor</i> ; 28 <i>Cygnus</i> sp. 9 <i>Larus</i> sp. 2 <i>Podiceps cristatus</i> (PNK) 33 <i>Podiceps nigricollis</i> (16 PNK; 10 PNK (SubtypeH5)) 5 <i>Fulica atra</i> (1 PNK (Subtype H5)) 29 unknown; 39 <i>Accipiter</i> sp.; 1 <i>Anas platyrhynchos</i> ; 2 <i>Anas</i> sp.; 1 <i>Hirundinidae</i> ; 30 <i>Milvus</i> sp.; 2 <i>Turdus merula</i> ; 1 <i>Turdus philomelos</i> ; 20 <i>Spizaetus nipalensis</i>	40 <i>Cygnus olor</i> ; 14 <i>Cygnus</i> sp. 40 <i>Larus</i> sp. 4 <i>Podiceps cristatus</i> 9 <i>Podiceps nigricollis</i> (1 PNK (subtype H5)) 3 <i>Fulica atra</i> 25 unknown; 4 <i>Alopochen aegyptiacus</i> ; 4 <i>Anas platyrhynchos</i> ; 6 <i>Anas</i> sp.; 6 <i>Ardea cinerea</i> ; 30 <i>Milvus</i> sp.; 1 <i>Pica pica</i> ; 1 <i>Riparia riparia</i>
France	E	28/06/2007-08/08/2007	Whooper Swan	2 <i>Cygnus olor</i> (D) 2 <i>Anas platyrhynchos</i> (D) 3 <i>Cygnus cygnus</i> (D)	2 <i>Cygnus olor</i> 4 <i>Anas platyrhynchos</i> ; 1 <i>Anas</i> sp.	61 <i>Cygnus olor</i> 52 <i>Anas platyrhynchos</i> (24 LPAI (2 subtype H5)) 3 <i>Cygnus cygnus</i> 75 <i>Aythya ferina</i> (20 LPAI) 1 <i>Podiceps cristatus</i>
Germany	F	06/07/2007-06/07/2007	Great Crested Grebe	1 <i>Podiceps cristatus</i> (D)	No further birds tested on same day as H5N1 HPAIV incident	1 <i>Passer</i> sp.; 1 <i>Phylloscopus collybita</i>
Germany	G	06/07/2007-06/07/2007	Swan	1 <i>Cygnus</i> sp. (D)	2 <i>Anas platyrhynchos</i>	3 <i>Cygnus</i> sp. 72 <i>Anas platyrhynchos</i> 1 <i>Anas crecca</i> ; 2 <i>Ardea cinerea</i> ; 7

Table 4 Details of H5N1 HPAIV incidents in 2007

MS	Incident	Incident duration	Detection through	Number and species of birds H5N1 HPAIV positive (Bird origin) L = live no clinical signs D= dead H= Hunted healthy LCS = live with clinical signs HCS= Hunted with clinical signs	Number and species of additional birds tested during incident (in affected NUTS 4/5 zone and/ or monitoring and control areas) PNK = positive pathotype not known/ pending LP= Positive for LPAIV	Number and species of birds tested in follow up in affected NUTS 4/5 zone and/or monitoring and control areas (until the end of the year) PNK = positive pathotype not known/ pending LP= Positive for LPAIV
						<i>Columba</i> sp.; 1 <i>Falco</i> sp.; 3 <i>Fulica atra</i> ; 4 <i>Larus</i> sp.; 1 <i>Phalacrocorax carbo</i>
Germany	H	26/07/2007-26/07/2007	Diving Duck	2 <i>Aythya</i> sp. (D)	1 <i>Aythya</i> sp. PNK (Subtype H5)	4 <i>Tachybaptus ruficollis</i> ; 2 <i>Podiceps nigricollis</i> ; 2 <i>Aythya fuligula</i> ; 1 <i>Anas clypeata</i> (PNK); 1 <i>Anas platyrhynchos</i>
Poland	I	07/12/2007-09/12/2007	White Stork and Common Buzzard	2 <i>Buteo buteo</i> (D) 1 <i>Ciconia ciconia</i> (D)	In monitoring area: 1 <i>Anas platyrhynchos</i> ; 1 <i>Anas querquedula</i> and 1 <i>Cygnus</i> sp.	1 <i>Ciconia ciconia</i> In monitoring area: 11 <i>Anas platyrhynchos</i> ; 10 <i>Anas</i> sp.; 3 <i>Anser anser</i> ; 5 <i>Anser</i> sp.; 2 <i>Columba livia</i> ; 1 <i>Cygnus olor</i> ; 11 <i>Cygnus</i> sp.; 2 <i>Egretta</i> sp.; 1 <i>Grus grus</i> ; 1 <i>Larus marinus</i> (PNK); 2 <i>Phasianus colchicus</i>

ORIGIN OF THE H5N1 INFECTED BIRDS

As in 2006, all incidents in 2007 were detected through passive surveillance and most birds were found dead. The exceptions were two Mute swans in DE, one of which was shot without showing clinical signs. The other Mute swan showed clinical signs as well as one Mallard. All these cases occurred in connection with the incidents previously identified through the finding of dead birds.

ORDER AND SPECIES OF BIRDS AFFECTED BY H5N1 HPAIV INFECTIONS

Table 5 shows the orders of birds in which H5N1 HPAIV cases were found in 2007 and the apparent prevalence in these. Podicipediformes were the order with the highest apparent prevalence. This reflects the surveillance results from 2006 although a high uncertainty was associated with that proportion as this concerned only four birds out of the order Podicipediformes testing positive (out of 310 sampled). All orders in which positives were found in 2007 also had positives identified in 2006.

Order	2006			2007		
	Total number of birds tested	Total number of birds positive for H5N1 HPAIV	Apparent sample prevalence of H5N1 HPAIV	Total number of birds tested	Total number of birds positive for H5N1 HPAIV	Apparent sampled prevalence of H5N1 HPAIV
Podicipediformes	310	4	1.29%	473	286	60.47%
Falconiformes	6845	18	0.26%	2111	2	0.09%
Anseriformes	64487	535	0.83%	48166	36	0.07%
Gruiformes	3714	2	0.05%	2868	2	0.07%
Ciconiiformes	4550	5	0.11%	2058	1	0.05%
Charadriiformes	12527	5	0.04%	9880	2	0.02%

Table 6 below displays the apparent overall prevalence by species. Black-necked grebes (*Podiceps nigricollis*) were the species with the highest apparent prevalence observed in 2007. Although the apparent prevalence in swans is quite low, the majority of incidents were detected through the finding of a dead swan. The lowest apparent prevalence of 0.02% for species with positive results was observed in Mallards (*Anas platyrhynchos*). Detailed information regarding the number of birds tested and positive birds by MS and species that were either of the HRS or tested positive for H5N1 HPAIV or LPAIV H5/H7 is displayed in Annex II a.

Species	2006			2007		
	Total number of birds tested	Total number of birds positive for H5N1 HPAIV	Apparent overall prevalence of H5N1 HPAIV	Total number of birds tested	Total number of birds positive for H5N1 HPAIV	Apparent overall prevalence of H5N1 HPAIV
<i>Podiceps nigricollis</i>	4	0	0.00%	304	246	80.92%
<i>Podiceps cristatus</i>	261	4	1.53%	145	38	26.21%
<i>Aythya</i> sp.	19	0	0.00%	9	2	22.22%
<i>Tachybaptus ruficollis</i>	26	0	0.00%	20	2	10.00%
<i>Cygnus olor</i>	8239	372	4.52%	4184	23	0.55%
<i>Buteo buteo</i>	3597	13	0.36%	510	2	0.39%
<i>Larus</i> sp.	1541	1	0.06%	639	2	0.31%
<i>Ciconia ciconia</i>	257	0	0.00%	343	1	0.29%
<i>Cygnus cygnus</i>	1741	44	2.53%	1371	3	0.22%
<i>Cygnus</i> sp.	1257	4	0.32%	1071	2	0.19%
<i>Fulica atra</i>	2494	1	0.04%	1851	2	0.11%
<i>Branta canadensis</i>	1854	2	0.11%	1849	1	0.05%
<i>Anser anser</i>	1769	3	0.17%	3701	1	0.03%
<i>Anas platyrhynchos</i>	28313	34	0.12%	18258	4	0.02%

PHYLOGENETIC ANALYSIS OF H5N1 VIRUSES RELEVANT TO THIS SURVEY

The analysis presented in Figure 13 shows the phylogenetic relationships based on the HA1 portion of the haemagglutinin gene. All of the viruses analysed were grouped in clade 2.2 consistent with all other H5N1 HPAIV Asian-lineage viruses isolated in Europe and Africa since late 2005.

Based upon the analyses, two broad epidemiological events occurred during the year. Firstly, limited outbreaks in poultry apparently linked, in HU and the UK during January and February were caused by viruses very closely related to those associated with widespread incidents during 2006. Secondly, in contrast to all viruses isolated prior to June 2007 in Europe, the viruses associated with incidents in wild birds or outbreaks in poultry after this period formed a distinct subgroup within clade 2.2 (putatively sub-sub clade 2.2.3) and were therefore clearly distinguishable. The closest progenitor viruses to this group were viruses isolated from poultry in the Middle East during winter-spring 2007, consistent with dispersal of such viruses over a wider geographical area. A number of sub groupings were identified, reflective of different events temporally and geographically. Close similarity was detected in viruses isolated simultaneously or in a similar time frame from both wild birds and poultry. This is demonstrated by the close relationship of a virus from a Mute swan (*Cygnus olor*) in the CZ and postulated incursion into the poultry sector that had a close temporal relationship. It should also be noted that close similarity to other poultry viruses such as isolated from the UK in November 2007 could also be demonstrated to show close relationships to these wild bird precursors although despite enhancement of surveillance, virus was not detected in local wild bird populations in spite of strong epidemiological evidence to the contrary. In conclusion, further and perhaps unexpected incursions of H5N1 viruses derived from clade 2.2 of the Asian-lineage occurred during mid 2007 with subsequent occasional detection both in wild birds and poultry to the year-end. These viruses could be clearly differentiated from those associated with previous outbreaks/ incidents in poultry and wild birds in the EU. It would appear that the viruses had derived as a result of a further and independent

spill over potentially from infected poultry populations in the Middle Eastern or wider region back into wild birds. Viruses then appeared to subsequently spread via wild birds (in the absence of other detailed epidemiology ruling out poultry origins) and were detected in several MS during this period. A number of outbreaks with similar and closely related viruses occurred in poultry populations in several MS particularly in the period October to December. Since the dynamic of infection is complicated between both wild birds and poultry species particularly those reared outdoors in abundance, it underlines the risk to the EU from viruses that may be imported from beyond or close to our borders where the virus may be less controlled and potentially endemic.

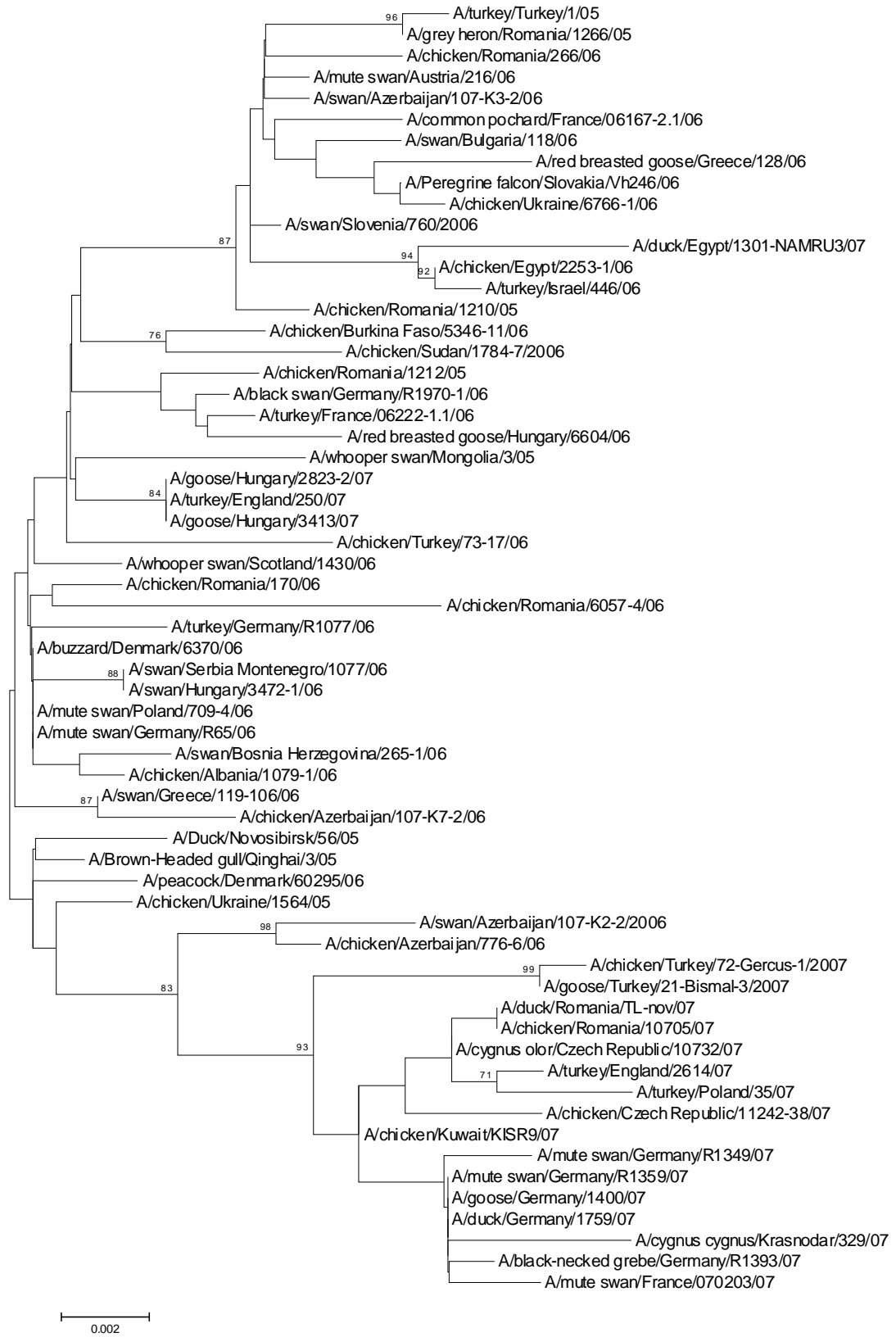


Figure 13 Minimum Evolution phylogenetic tree of a 967bp HA1 fragment of H5

LPAIV

INTRODUCTION

It should be noted that this section focuses on the analysis of H5/H7 LPAIV unless specifically mentioned.

Since many positive birds were reported with pathotype “unknown”, “pending”, “missing” etc, birds that tested positive on PCR or virus isolation are reported in four groups in this section:

- 1) “LPAIV H5” are birds positive for LPAIV H5
- 2) “LPAIV H7” are birds positive for LPAIV H7
- 3) “LPAIV other” are birds reported as LPAIV of other subtypes
- 4) “Other positives” are birds positive for influenza A but that were not clearly reported as either LPAIV or HPAIV.

OVERVIEW OF LPAIV RESULTS

In total 1485 birds tested positive for subtypes other than H5N1 HPAIV.

LPAIV H5 was detected in 105 birds from ten MS: DE (9), DK (6), FI (1), FR (16), IE (2), IT (7), NL (2), PT (3), SE (55) and the UK (4).

LPAIV H7 was identified in seven birds of six MS: DE (1), DK (2), HU (1), IT (1), PL (1) and SE (1).

LPAIV of other subtypes was detected in 123 birds. “Other positives” were detected in 1250 birds.

Table 7 indicates the total number and proportion of wild birds testing positive for LPAIV H5 and H7 in those MS that detected these subtypes and Figure 15 maps the geographical distribution of LPAIV H5 and H7 positives.

Overall a very low apparent prevalence of LPAIV H5 of 0.13% was detected, which reflects, in spite of minor variations at MS level, the findings of 2006 when an overall LPAIV H5 prevalence of 0.11% was observed (Annex 2 b). The highest apparent prevalence of LPAIV H5 was found in SE. All but one of the Swedish positive birds originated from the same location and was sampled between 15/10/2007 and 12/11/2007 and are therefore subject to cluster effects. During this time 605 Mallards (*Anas platyrhynchos*) (of which 50 (8%) tested positive for LPAIV H5) and 21 Wigeons (*Anas penelope*) (of which four (19%) tested positive) were sampled at this location.

Hardly any cases of LPAIV H7 were found in 2007 in the EU, which also reflects the finding of a very low apparent prevalence of 0.02% in 2006.

Table 7: Total number and proportion of birds testing positive for LPAIV H5, H7 and other subtypes for MS that detected LPAIV H5 or H7

MS	Birds Sampled	Birds LPAIV H5 Positive	Positive Proportion (LPAIV H5)	Birds LPAIV H7 Positive	Positive Proportion (LPAIV H7)	Birds other LPAIV Positive	Positive Proportion other LPAIV	Birds positive "other positives"	Total Positive Proportion "Other positives"
SE	5044	55	1.09%	1	0.02%	1	0.02%	127	2.52%
FR	2081	16	0.77%	-	-	-	-	265	12.73%
DE	23949	9	0.04%	1	<0.01%	10	0.04%	168	0.70%
DK	4844	6	0.12%	2	0.04%	6	0.12%	35	0.72%
IT	7160	7	0.10%	1	0.01%	17	0.24%	137	1.91%
UK	8094	4	0.05%	-	-	7	0.09%	26	0.32%
FI	283	1	0.35%	-	-	4	1.41%	7	2.47%
IE	421	2	0.48%	-	-	-	-	3	0.71%
NL	8446	2	0.02%	-	-	34	0.40%	79	0.94%
PT	1219	3	0.25%	-	-	5	0.41%	2	0.16%
AT	542	-	-	-	-	-	-	19	3.51%
BE	2879	-	-	-	-	38	1.32%	189	6.56%
BG	268	-	-	-	-	-	-	1	0.37%
CZ	404	-	-	-	-	-	-	3	0.74%
ES	8199	-	-	-	-	1	0.01%	64	0.78%
HU	693	-	-	1	0.14%	-	-	-	-
LT	715	-	-	-	-	-	-	48	6.71%
LU	330	-	-	-	-	-	-	1	0.30%
LV	534	-	-	-	-	-	-	27	5.06%
PL	592	-	-	1	0.17%	-	-	30	5.07%
SI	334	-	-	-	-	-	-	19	5.69%
EU Total	79392	105	0.13%	7	0.01%	123	0.15%	1250	1.58%

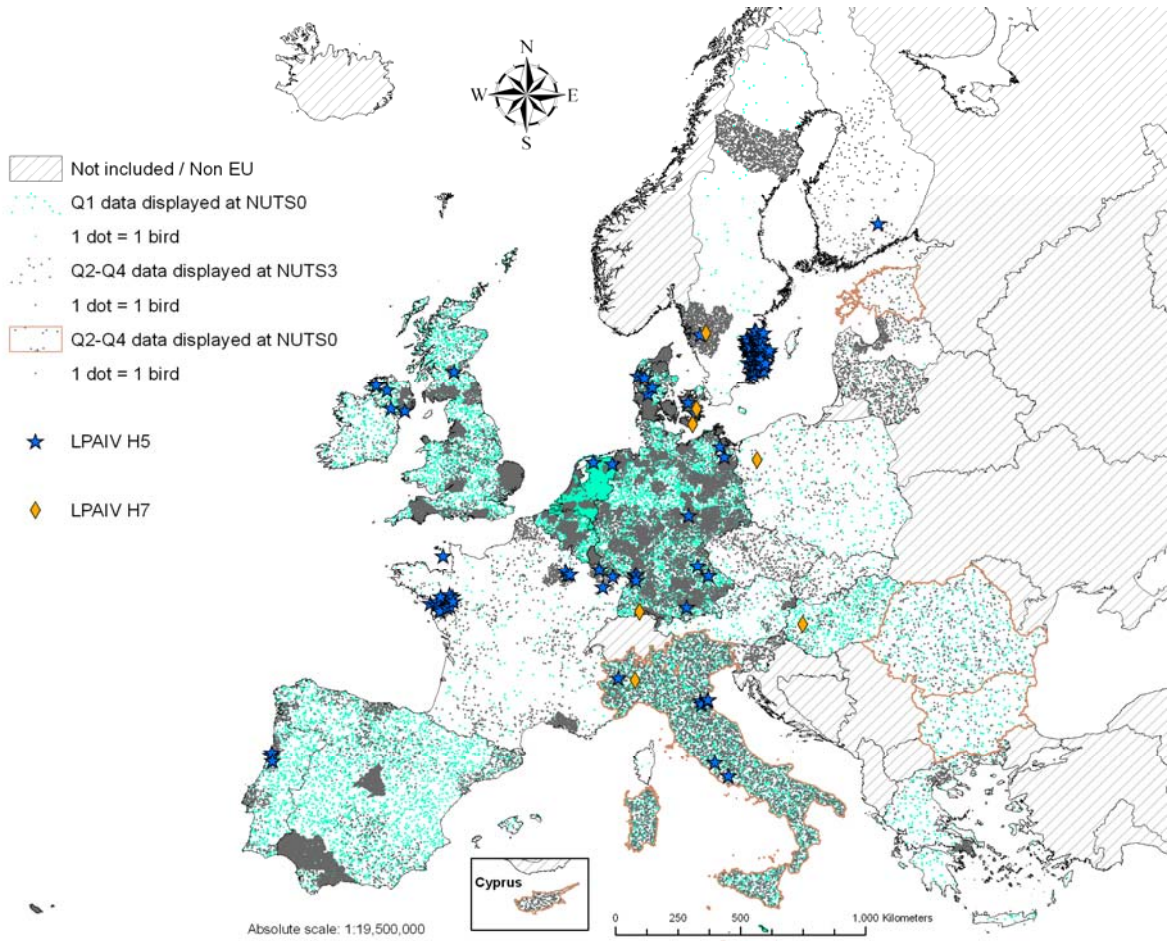


Figure 14 Sampling density and geographical location of LPAIV H5 and H7 positive birds in EU MS in 2007

TIMING OF LPAIV H5/H7 DETECTIONS

Figure 15 displays the calendar week of LPAIV H5 and H7 detections by MS. Figure 16 displays the number of LPAIV H5/H7 detections and the number of birds sampled by week. LPAIV H5 was mainly found between late summer and winter, while LPAIV H7 infections did not show a particular pattern.

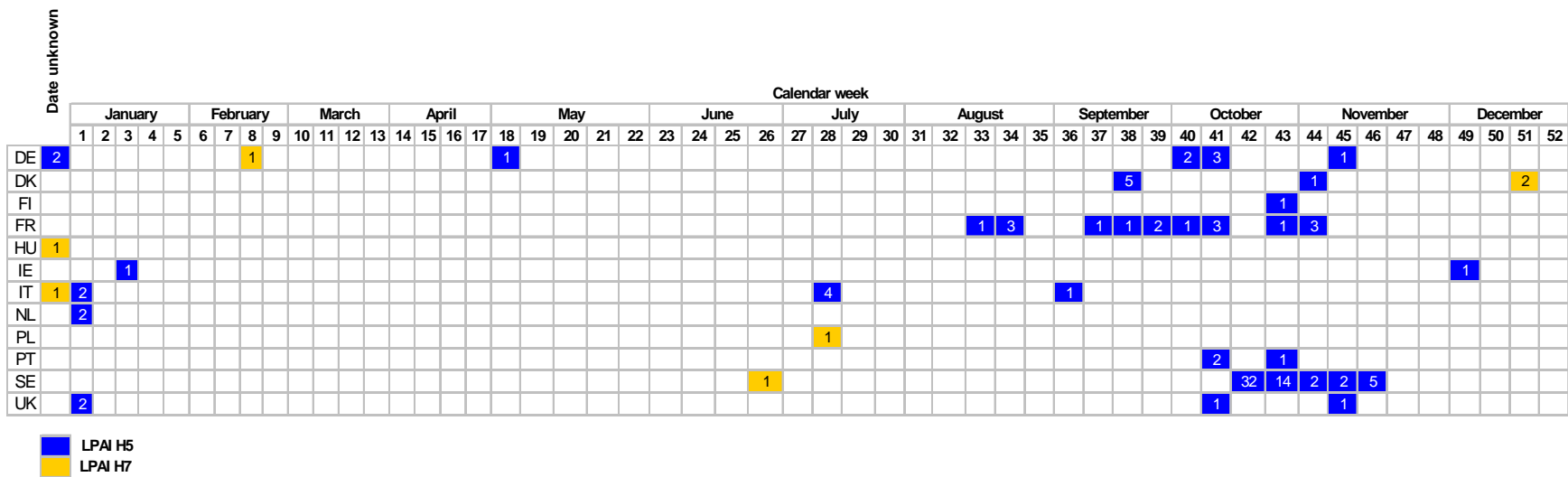


Figure 15 Number and week of detection of LPAIV H5/ H7 positive birds by MS

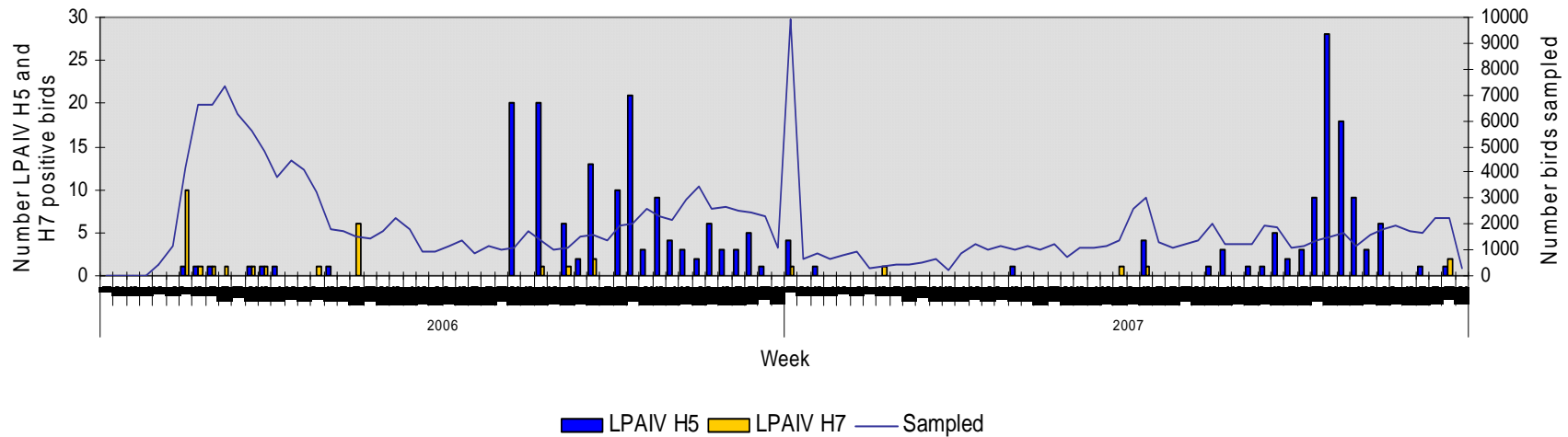


Figure 16 Number of LPAIV H5 and H7 detections in wild birds and number of wild birds sampled in the EU by week in 2006 and 2007

ORIGIN OF LPAIV H5/H7 POSITIVE BIRDS

Table 8 below displays the apparent prevalence of LPAIV H5/H7 by surveillance type. Hardly any LPAIV H5/H7 birds were identified through passive surveillance and the highest apparent prevalence at EU level was observed in birds of HRS that were sampled through active surveillance. In this surveillance type the apparent prevalence was around double that of the total EU apparent prevalence of LPAIV H5/H7.

Member State	Total Sampled	Total LPAIV H5/H7 Positive	Total LPAIV H5/H7 Apparent prevalence	Apparent LPAIV H5/ H7 prevalence Active surveillance HRS n= number of birds sampled	Apparent LPAIV H5/ H7 prevalence Active surveillance other sp. n= number of birds sampled	Apparent LPAIV H5/ H7 prevalence Passive surveillance HRS. n= number of birds sampled	Apparent LPAIV H5/ H7 prevalence Passive surveillance other sp. n= number of birds sampled	Apparent LPAIV H5/ H7 prevalence Surveillance type unknown n= number of birds sampled
SE	5044	56	1.11%	1.78% n=3145	0.00% n=1554	0.00% n=89	0.00% n=252	0.00% n=4
FR	2081	16	0.77%	1.33% n=1127	0.00% n=33	0.19% n=535	0.00% n=386	N/A n=0
IE	421	2	0.48%	0.84% n=237	0.00% n=22	0.00% n=91	0.00% n=71	N/A n=0
FI	283	1	0.35%	0.82% n=122	0.00% n=108	0.00% n=25	0.00% n=28	N/A n=0
PT	1219	3	0.25%	1.53% n=196	0.00% n=618	0.00% n=23	0.00% n=382	N/A n=0
PL	592	1	0.17%	0.00% n=234	0.00% n=158	7.69% n=13	0.00% n=96	0.00% n=91
DK	4844	8	0.17%	0.21% n=3279	0.08% n=1314	0.00% n=116	0.00% n=135	N/A n=0
HU	693	1	0.14%	0.00% n=351	0.00% n=185	1.85% n=54	0.00% n=103	N/A n=0
IT	7160	8	0.11%	0.14% n=4144	0.00% n=2188	0.00% n=234	0.34% n=593	0.00% n=1
UK	8094	4	0.05%	0.06% n=5174	0.00% n=966	0.08% n=1269	0.00% n=685	N/A n=0
DE	23949	10	0.04%	0.06% n=10212	0.05% n=6266	0.04% n=2795	0.00% n=4404	0.00% n=272
NL	8446	2	0.02%	0.02% n=4903	0.03% n=2913	0.00% n=266	0.00% n=264	N/A n=0
EU Total	79392	112	0.14%	0.26% n=38697	0.02% n=22837	0.08% n=6629	0.02% n=10622	0.00% n=607

ORDER AND SPECIES OF BIRDS POSITIVE FOR LPAIV H5 H7

Order

LPAIV H5 was exclusively found in Anseriformes, while LPAIV H7 was also observed in Charadriiformes. Other positives were observed in a variety of orders (Table 9).

Order	Total Sampled	Birds LPAIV H5 Positive	Apparent prevalence LPAIV H5	Birds LPAIV H7 positive	Apparent prevalence LPAIV H7	Birds 'other LPAIV' positive	Apparent prevalence 'other LPAIV'	Birds 'other positives'	Apparent prevalence 'other positives'
Anseriformes	48166	105	0.22%	6	0.01%	95	0.20%	1056	2.19%
Charadriiformes	9880			1	0.01%	27	0.27%	122	1.23%
Ciconiformes	2058							4	0.19%
Columbiformes	1721							2	0.12%
Galliformes	1534							3	0.20%
Gruiformes	2868							22	0.77%
Passeriformes	5263							3	0.06%
Pelecaniformes	763							2	0.26%
Phoenicopteriformes	1269							4	0.32%
Podicipiformes	473							29	6.13%
Species Unknown	1537					1	0.07%	3	0.20%
TOTAL	79392	105	0.13%	7	0.01%	123	0.15%	1250	1.58%

Species

Further details and tables regarding sampling and results for high-risk and other species by MS can be found in Annex 2a. With the exception of two species (*Anser albifrons* and *Aythya fuligula*) all observations of LPAIV H5 in 2006 and 2007 were made in dabbling ducks and swans (Table 10).

Most observations of LPAIV H5 were made in Mallards (*Anas platyrhynchos*). In most species in both years the observed prevalence was below one percent. The two species with the highest observed apparent prevalence in 2007 were also sampled in the lowest numbers; therefore a larger uncertainty is associated with the result.

With the exception of one detection in a black-headed gull (*Larus ridibundus*), all detections of LPAIV H7 were also made only in dabbling ducks and swans in 2007 (Table 11).

Table 10: Apparent prevalence of LPAIV H5 by species in EU MS in 2007

Species	2006			2007		
	Total birds sampled	Total LPAIV H5 positive	Apparent prevalence of LPAIV H5	Total birds sampled	Total LPAIV H5 positive	Apparent prevalence of LPAI H5
<i>Cygnus atratus</i>	4	0	0.00%	16	2	12.50%
* <i>Anas querquedula</i>	143	0	0.00%	143	4	2.80%
* <i>Anas platyrhynchos</i>	28313	109	0.38%	18258	80	0.44%
* <i>Anas acuta</i>	565	0	0.00%	470	2	0.43%
* <i>Anas crecca</i>	1902	8	0.42%	1815	5	0.28%
* <i>Anas clypeata</i>	202	0	0.00%	490	1	0.20%
* <i>Cygnus cygnus</i>	1741	2	0.11%	1371	2	0.15%
* <i>Anas penelope</i>	2485	0	0.00%	3713	4	0.11%
* <i>Anser albifrons</i>	734	2	0.27%	1779	2	0.11%
<i>Cygnus sp.</i>	1257	0	0.00%	1071	1	0.09%
<i>Anas sp.</i>	4889	8	0.16%	1811	1	0.06%
<i>Cygnus olor</i>	8239	0	0.00%	4184	1	0.02%
* <i>Aythya fuligula</i>	493	1	0.20%	445	0	0.00%
Legend	* = HRS					

Table 11 Apparent prevalence of LPAIV H7 by species in EU MS in 2007

Species	2006			2007		
	Total birds sampled	Total LPAIV H7 positive	Apparent prevalence of LPAIV H7	Total birds sampled	Total LPAIV H7 positive	Apparent prevalence of LPAIV H7
<i>Cygnus sp.</i>	1257	0	0.00%	1071	1	0.09%
* <i>Anas crecca</i>	1902	1	0.05%	1815	1	0.05%
* <i>Larus ridibundus</i>	4303	0	0.00%	2673	1	0.04%
* <i>Anas platyrhynchos</i>	28313	17	0.06%	18258	3	0.02%
* <i>Cygnus olor</i>	8239	0	0.00%	4184	1	0.02%
* <i>Anas clypeata</i>	202	3	1.49%	490	0	0.00%
* <i>Aythya ferina</i>	310	1	0.32%	471	0	0.00%
* <i>Aythya fuligula</i>	493	1	0.20%	445	0	0.00%
Legend	* = HRS					

DIAGNOSIS

This section of the reports aims to analyse the samples collected and associated test results. The following data is limited to the period of April to December 2007 as this level of information was not available in the data submitted for the first quarter.

Sampling

The guidelines recommend oro-pharyngeal and cloacal swabs to be collected from healthy free living birds and cloacal and oro-pharyngeal and/ or tissues from dead or shot birds. Table 12 shows the number and proportion of samples collected according to the origin of the birds in 2007.

Samples Taken	Live & Injured Birds		Hunted Birds		Dead Birds	
	Count	%	Count	%	Count	%
Cloacal	10724	30%	2178	29%	1238	10%
Faecal	13345	38%	86	1%	558	4%
OP	1045	3%	1015	13%	2588	21%
Tissue	54	0%	577	8%	3428	28%
Blood	490	1%	56	1%	-	-
Other	1146	3%	94	1%	206	2%
Cloacal Faecal OP Blood	-	-	-	-	1	0%
Cloacal OP Other	4	0%	-	-	4	0%
Cloacal OP Blood	109	0%	-	-	74	1%
Cloacal OP Tissue	-	-	9	0%	86	1%
Cloacal Blood Other	1	0%	-	-	-	-
Cloacal + OP	7443	21%	3506	46%	4044	33%
Cloacal + Blood	14	0%	-	-	6	0%
Cloacal + Other	1029	3%	6	0%	31	0%
Cloacal + Faecal	48	0%	1	0%	99	1%
Cloacal + Tissue	2	0%	-	-	9	0%
Faecal + OP	9	0%	23	0%	10	0%
OP + Tissue	5	0%	-	-	11	0%
OP + Other	1	0%	-	-	1	0%
OP + Blood	1	0%	-	-	-	-
Tissue + Blood	-	-	-	-	14	0%
Total (Birds)	35470	100%	7551	100%	12408	100%
Total Samples Taken	51983		12469		20419	
Legend	OP = Oro-pharyngeal					

The majority of live birds were sampled either by cloacal swab or faeces; only a fifth of the birds were sampled with cloacal and oro-pharyngeal swabs. In hunted birds around half of the samples were cloacal and oro-pharyngeal swabs. Ten percent of dead birds were tested by cloacal sample only, however the majority of samples were cloacal and oro-pharyngeal samples and/or tissue.

H5N1

Table 13 displays the H5N1 diagnostic test results for each sample type collected for dead birds. With the exception of one sample, all samples on which virus isolation was performed tested positive on virus isolation as well as on PCR.

Sample type / Number of positives		Sample 1 Test results (proportion) + = positive - = negative NA=not performed			Sample 2 Test results (proportion) + = positive - = negative NA=not performed		
Sample type	Total positives	PCR + VI +	PCR - VI -	PCR + VI NA	PCR + VI +	PCR - VI -	PCR + VI NA
OP	263			100.0%	NA	NA	NA
Cloacal only	1			100.0%	NA	NA	NA
Tissue only	36	8.3%	2.8%	88.9%	NA	NA	NA
Faecal only	16			100.0%	NA	NA	NA
Cloacal + OP	10	70.0%		30.0%	70.0%		30.0%
Legend	OP = Oro-pharyngeal						

Other positives (LPAIV, pathotype not reported, unidentifiable and pending)

Table 14 shows the test results of samples collected from live birds that were positive for other subtypes (data limited to April – December 2007). Table 15 and 16 display the test results for hunted and dead birds respectively. In all categories for a relatively high proportion of birds that were positive on PCR, virus isolation was negative when both PCR and virus isolation were performed. Just over a tenth (12.6%) of live birds that had oro-pharyngeal and cloacal swabs collected, only tested positive on the oro-pharyngeal swab. Just over 40% of live birds that had an oro-pharyngeal and cloacal swab taken only tested positive on the cloacal swab.

Table 14 Test-results and samples taken for live birds without clinical signs positive to subtypes other than H5N1 HPAIV (data April – September)

Sample type / Number of positives		Sample 1 Test results (proportion) + = positive - = negative NA=not performed				Sample 2 Test results (proportion) + = positive - = negative NA=not performed			
Sample type	Total positives	PCR + VI +	PCR + VI -	PCR + VI NA	PCR - VI NA	PCR + VI +	PCR + VI -	PCR + VI NA	PCR - VI NA
OP only	29	6.9%		93.1%					
Faeces only	164	6.1%	14.6%	79.3%					
Cloacal only	213	8.9%	34.7%	56.3%					
Cloacal (1) + OP (2)	135	8.1%	30.4%	48.9%	12.6%	2.2%	10.4%	46.7%	40.7%
Cloacal (1)+ faeces (2)	4			100.0%				100.0%	
Cloacal + other	8	12.5%	75.0%	12.5%			12.5%		87.5%
Other	18	55.6%	33.3%	11.1%					
Legend	OP = Oro-pharyngeal								

Table 15 and 16 display the test results for collected samples in hunted and dead birds that tested positive for AI for other subtypes than H5N1 HPAIV.

Table 15 Test-results and samples taken for hunted birds with and without clinical signs positive to subtypes other than H5N1 HPAIV

Sample type / Number of positives		Sample 1 Test results (proportion) + = positive - = negative NA=not performed				Sample 2 Test results (proportion) + = positive - = negative NA=not performed			
Sample type	Total positives	PCR + VI +	PCR + VI -	PCR + VI NA	PCR - VI NA	PCR + VI +	PCR + VI -	PCR + VI NA	PCR - VI NA
OP only	77		1.3%	98.7%					
Cloacal only	324	1.5%	38.9%	59.6%					
Tissue only	2	100.0%							
Cloacal + OP	130	18.5%	59.2%	15.4%	6.9%	1.5%	8.5%	16.2%	73.8%
OP + Faecal	3	100.0%							100.0%
Cloacal + other	1	100.0%				100.0%			
Legend	OP = Oro-pharyngeal								

Sample type / Number of positives		Sample 1 Test results (proportion) + = positive - = negative NA=not performed				Sample 2 Test results (proportion) + = positive - = negative NA=not performed			
Sample type	Sample type	PCR + VI +	PCR + VI -	PCR + VI NA	PCR - VI NA	PCR + VI +	PCR + VI -	PCR + VI NA	PCR - VI NA
OP only	33			100.0%					
Faeces only	2			100.0%					
Cloacal only	19	5.3%	10.5%	84.2%					
Tissue only	34	82.4%	17.6%						
Cloacal + OP	58	3.4%	5.2%	89.7%	1.7%	1.7%	1.7%	84.5%	12.1%
Cloacal + faeces	9	88.9%		11.1%				100.0%	
Cloacal + other	1			100.0%				100.0%	
Legend	OP = Oro-pharyngeal								

DISCUSSION

H5N1 HPAIV incidents in 2007 were limited in time and affected fewer MS and locations. The smaller scale of the incidents compared to 2006 is probably best explained by their occurrence outside the main migration periods and therefore likely limited further spread by wild birds. The timing of the incidents outside the main migration period may appear to suggest that the virus may have continued to circulate in the EU wild bird population at a low level without being detected. However there are several observations made from the surveillance data that do suggest that this event is less likely than a new introduction of the virus into the EU via wild birds:

Firstly, although most birds only move locally or over short distances, moult migrations occur during this time. Moulting migrations can also involve substantial international movements (Defra, 2007). Other movements can also not be excluded. For example, ringing studies have found some Mute swans present in DE between June and August have spent time in the CZ and PL between April and June (see Annex III for table copied from the BTO migration mapping tool website (BTO mapping tool (<http://blx1.bto.org/ai-eu/>)).

In the incident in 2007 in FR, Pochard's were observed at the location before the detection of the dead swans. These birds are thought to have arrived from Eastern Europe and are known to occur at the location for autumn moult. Two weeks before the incident that affected a large number of grebes in DE, a large congregation of swans was observed that moved off before mortalities in the grebes commenced (T. Harder pers. Comm.).

Secondly, the weekly number of reported cases of wild birds in 2006 as well as in 2007, display two distinct epidemic curves. Although summarizing this information at EU level is somewhat simplified, the shape of these curves are typical for an infectious disease. In view of the intensity of surveillance conducted after the incidents in 2006, it could have been expected to find more occasional incidents of H5N1 HPAIV between the periods of incidents if the virus was maintained at a level other than very low within the wild bird population.

The final indicator supporting a new introduction of the virus rather than continued and persistent circulation of '2006' like viruses in the wild bird population is the results of the phylogenetic analysis: The viruses found in 2007 could be clearly differentiated from those associated with previous outbreaks/ incidents in poultry and wild birds in the EU. It would appear that the viruses had derived as a result of a further and independent spill-over potentially from infected poultry populations in the Middle Eastern or wider region back into wild birds.

As in 2006 most of the incidents in wild birds were detected through the finding of a dead swan. However, the incident in lake Kelbra was detected through the finding of dead Grebes. Grebes, due to their behavioural characteristics are not listed as one of the HRS. However they were the most strongly affected species in this incident. This finding highlights that the apparent prevalences observed in 2006 and 2007 are more an indication of clinical susceptibility of a species rather than an indication for the risk of infection and are affected by cluster effects. The original list of HRS was established based on their likelihood of introducing and/or propagating the spread of the virus (EFSA, 2006). Species displaying mortalities are not necessarily those species that brought the virus to a specific location. Therefore to increase the probability of detection of incidents, passive surveillance of dead or diseased birds should include a variety of species and not be limited to HRS. However since contact with birds that have introduced the virus is necessary for birds to become infected, targeting passive surveillance to waterbirds, which share habitats with HRS and raptors/scavengers, which are likely to feed on dead HRS would allow a degree of targeting and is more likely to detect H5N1 HPAIV positives, than for example surveillance of Passeriformes.

In recently reported clinical experiments Mallards did not show clinical signs upon infection with H5N1 HPAIV (Keawcharoen *et al.*, 2008), (Brown *et al.*, 2007), (EFSA , 2008). However, during the EU incidents in 2006 and 2007, Mallards were always found dead or with clinical signs when infected with H5N1 HPAIV and the overall apparent prevalence of H5N1 was very low compared to other species. Although the active sampling of Mallards in response to incidents was variable, in two German incidents large numbers of Mallards were tested in response to the incidents without positive results whilst in FR 56 Mallards were shot in the monitoring zone following the incident, and while a high prevalence of LPAIV was observed, no H5N1 HPAIV infections were detected. However, infection in live birds may have been present but may not have been detected. Therefore the actual role of Mallards in the epidemiology of H5N1 HPAIV still remains unclear.

Within the actual incidents, two types of scenarios with reference to mortalities were observed: Firstly a scenario where large scale mortalities were observed, as was the case in DE at lake Kelbra, where a large part of the grebe population died over a short period of time - and secondly an observation of a low number of cases occurring over an extended period of time in the absence of increased mortalities as for example in FR in 2007. Experimental infections showed that swans, that were serologically positive to LPAIV of a subtype other than H5 showed no clinical signs when consequently infected with H5N1 HPAIV (Kalthoff *et al.*, in press). Although many factors such as bird density and conditions for virus survival are likely to influence the scale of observed mortalities, pre-infection with an unrelated LPAIV could be another important influential factor. For example in FR several species of birds were shot for surveillance purposes in response to the incidents and a high prevalence of LPAIV infections was observed in Mallards and Pochards. For passive surveillance this may mean that in areas where a high exposure to LPAIV is to be expected, increased mortalities are less likely. However levels of uncertainty exist and more knowledge is required on the level of clinical cross-protection provided by different LPAIV strains for infection with H5N1 HPAIV.

The first objective of AI surveillance in the EU in wild birds is to ensure early detection of H5N1 HPAIV through the investigation of increased mortalities. The detection of incidents in wild birds without the outbreaks in poultry illustrated the value and role of wild bird surveillance in the early detection of H5N1 HPAIV presence in a country. Detections of such infections are important to maintain and raise vigilance amongst the poultry sector, especially keepers of free-range poultry. However, as discussed above, incidents in the EU have not always been associated with increased mortalities in wild birds.

Consequently, to increase the probability of early detection, the initiation of collection of samples from dead birds should not be dependent on increased mortalities and passive surveillance and may need to be intensified in areas of increased risk. Thereby risk is referred to in the risk analysis context of defining risk as a product of the likelihood of occurrence of an adverse event and the likely magnitude of the consequences (OIE, 2004). For improved targeting, detection of H5N1 HPAIV infections in wild birds in remote areas that are not linked through any bird movements with areas of intensive poultry production should be assigned a lower priority than detection in higher density poultry areas where migratory wild birds may occur. Risk factors for consideration have been laid out in Commission Decision 2005/734/EC (EC, 2005). A further action to improve targeting of passive surveillance could be to use existing migratory information in conjunction with outbreak/ incident data to identify priority areas for surveillance. If, for example, an outbreak occurs in an area neighbouring the EU or within the EU, migratory data such as available through the BTO migration mapping tool (Atkinson *et al.*, 2007) can be used to identify areas of increased vigilance for passive surveillance, based upon the areas and times migratory species are likely to arrive from affected regions.

It is also important to consider that some migratory species introducing the virus into the EU may not display clinical signs and so may not be detected through passive surveillance. Therefore active surveillance in theory appears to be the best tool for early detection to target species of birds more likely to introduce the virus and to detect infection before it spills over to other species. However substantial numbers of birds of HRS sampled through targeted active surveillance in 2006 and 2007 could not fulfil such a function. This may be because the prevalence was too low to be detectable

even with such large sample sizes, or that the virus was only present in the wild bird population for a limited period of time. Therefore it appears that at present active surveillance is not efficient with regard to resources for the early detection of H5N1 HPAIV, although this may change with evolving knowledge of H5N1 HPAIV epidemiology in wild birds. A current EU research project NewFlubird (<http://www.new-flubird.eu>) is implementing targeted active surveillance for early detection and will provide further insights into this type of surveillance.

The second objective of EU wild bird surveillance relates to the investigation of asymptomatic carriers and bridge species in the event of H5N1 HPAIV detection.

In surveillance in response to one German incident, an H5N1 HPAIV infected swan not exhibiting clinical signs was shot. In several of the incidents large numbers of Mute swans, Mallards, Gulls and Pochards were tested with negative results for H5N1 HPAIV and several “bridge species” were tested in varying numbers. However evaluation of the importance of carrier and bridge species is better assessed through epidemiological investigations and assessments in collaboration with ornithologists and epidemiologists, since such reports can better evaluate factors such as sizes of local populations, local movements and functional links with the affected site, all of which are crucial to the theoretical principle of bridge species. Information collection and dissemination on the epidemiology of wild bird incidents and influential factors such as details of residential wild bird populations and environmental sampling could play an important role in furthering the knowledge gain on the epidemiology of H5N1 HPAIV in wild birds.

The final objective of the EU surveillance, the baseline surveillance of LPAIV H5/H7 surveillance appears to be best addressed through active surveillance of live birds, as consistent with previous years, in 2007 the large majority of LPAIV infections in 2007 were identified through active surveillance of HRS, especially dabbling ducks and swans.

The joint reporting and analysis of EU AI surveillance has been greatly facilitated through the use of an online reporting system. The collected information has allowed some important conclusions to be made about H5N1 surveillance in wild birds and provides a valuable dataset for further extended analysis and research. There are several aspects though that should be considered when interpreting the results: Cluster effects occur and were not accounted for in the analysis. Clusters influence reported results, for example the apparent high prevalence of H5N1 HPAIV in Grebe *spp.* or the apparent higher prevalence of LPAIV H5 in SE, where most of the positive birds were identified at the same location over a limited period of time. In addition when small sample numbers are collected for a MS or for a species, the uncertainty around a proportion/ apparent prevalence increases. Also, surveillance programmes were quite variable between MS in respect to a number of parameters including sample size, weighting between active and passive surveillance and targeting. Therefore, as with most surveillance data collected through various sources with heterogeneous design, no direct comparisons can be made regarding the prevalence between MS and the apparent prevalence observed in a species cannot be assumed to be the true underlying prevalence. The analyses conducted to date have evaluated each potential influencing factor (such as species, origin of the bird) separately. To further evaluate the interaction between these factors and ranking their importance more extensive multivariable analysis is required.

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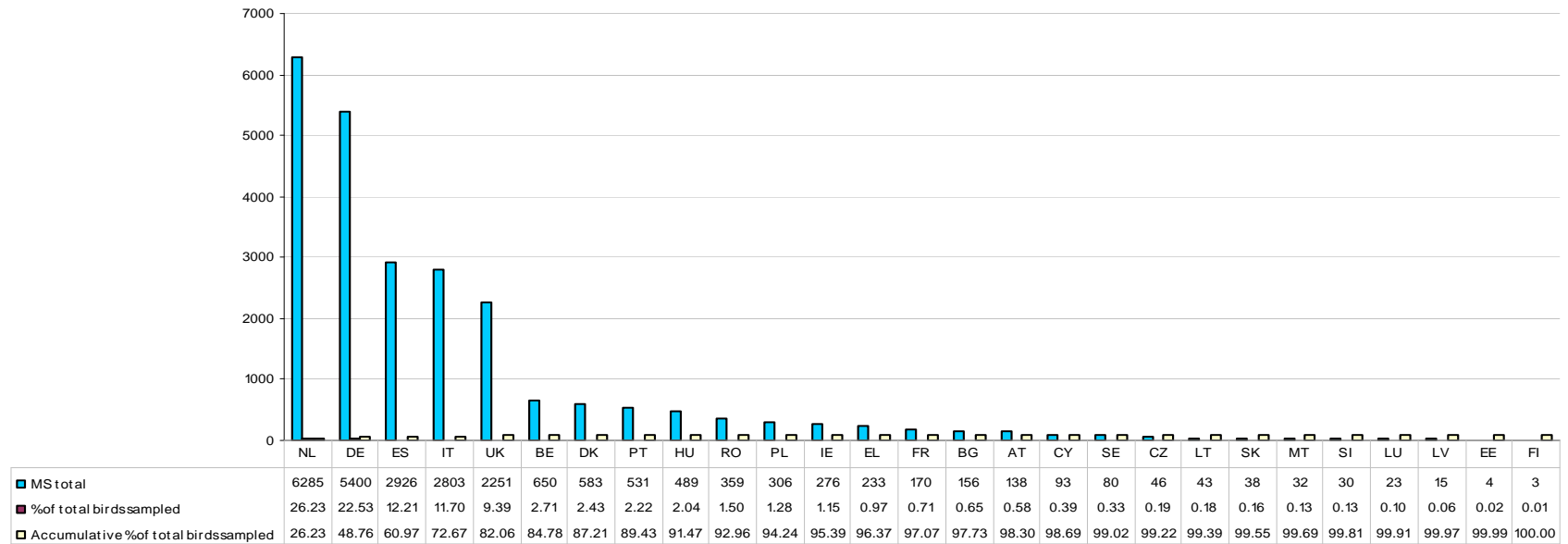
SANCO(2007) SANCO/10554/2007 Rev.1 Annual Report of the EU avian influenza surveillance in wild birds 2006
http://ec.europa.eu/food/animal/diseases/controlmeasures/avian/annrepres_surv_wb_02-12-2006_en.pdf

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ANNEXES

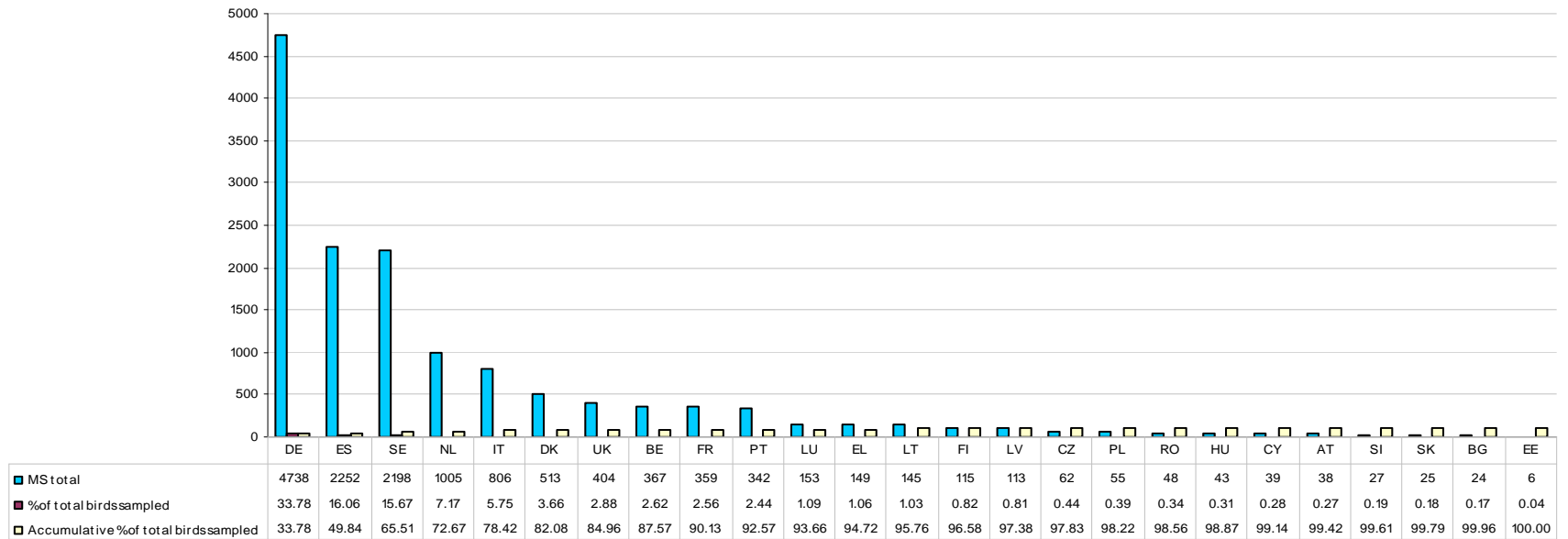
ANNEX I A – NUMBER OF WILD BIRDS SAMPLED BY QUARTER

January - March 2007



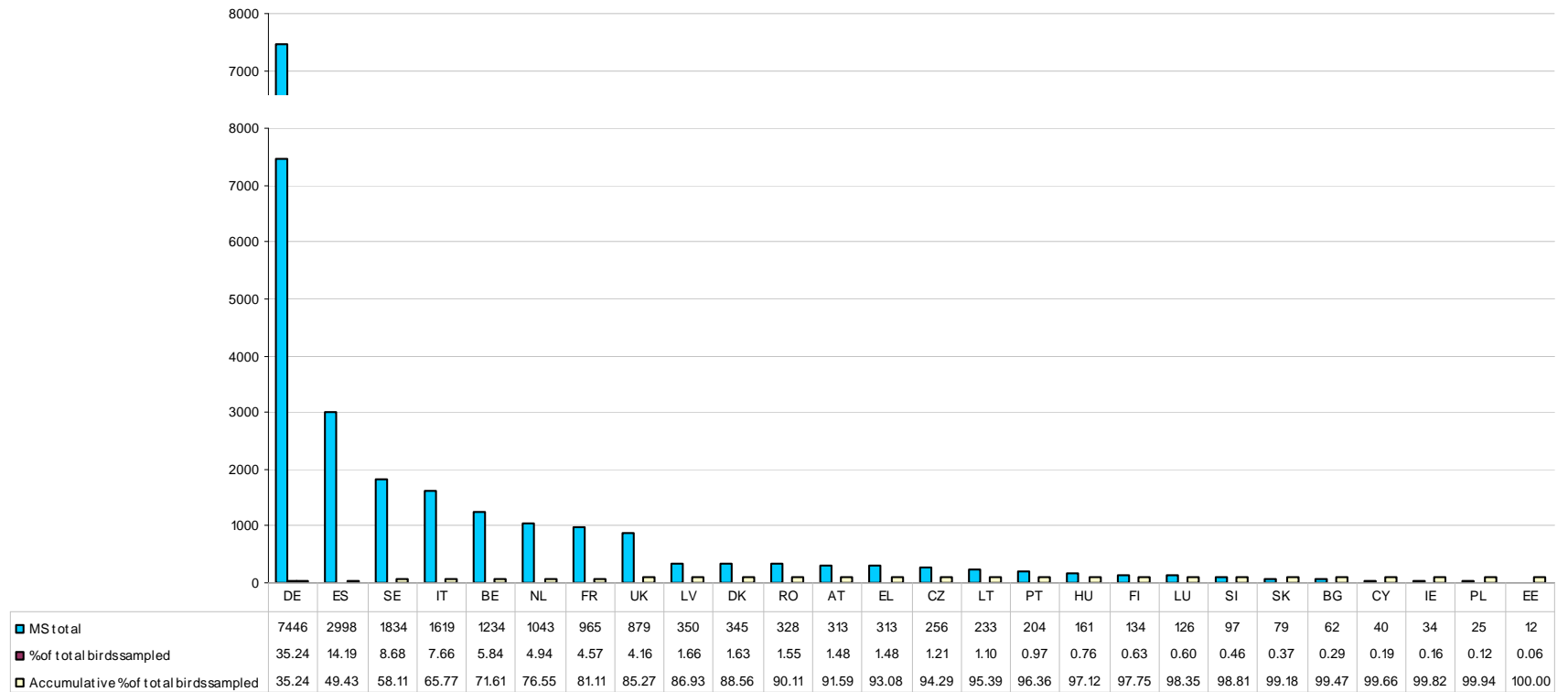
Between January and March 2007, a total of 23963 birds were sampled in 27 EU MS.

April - June 2007



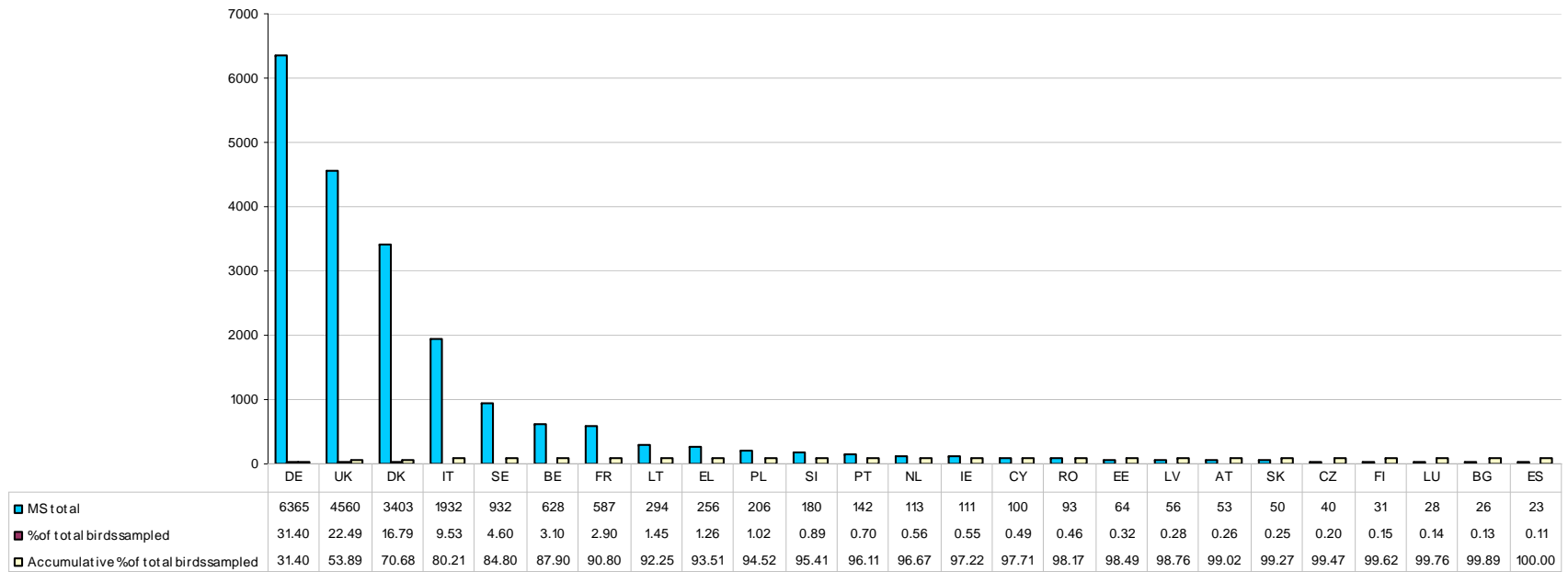
Between April and June 2007 a total of 14026 birds were sampled in 25 EU MS (excluding Ireland and Malta).

July - September 2007



Between July and September 2007 a total of 21130 birds were sampled in 26 MS (excluding Malta).

October - December 2007



Between October and December 2007 a total of 20273 birds were sampled in 25 MS (excluding Hungary and Malta)

ANNEX I B – TYPE OF SURVEILLANCE BY QUARTER

The following tables I and II display the number of birds sampled in 2006 and 2007, by both passive and active surveillance. This excludes birds sampled where the status or surveillance type was unknown

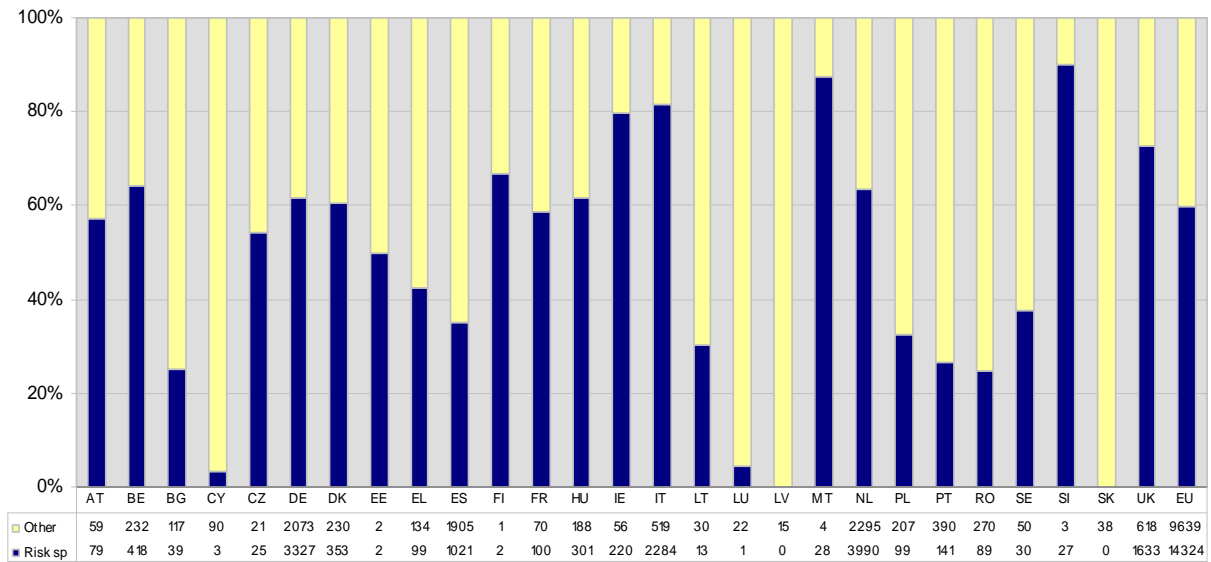
MS	Feb - May 2006	Jun - Aug 2006	Sep - Dec 2006	2006 Total	Jan - Mar 2007	Apr - Jun 2007	Jul - Sep 2007	Oct - Dec 2007	2007 Total
AT	585	55	349	989	70	0	93	48	211
BE	664	772	639	2075	643	356	1185	622	2806
BG	0	0	0	0	116	17	21	19	173
CY	32	9	22	63	0	7	14	66	87
CZ	0	0	0	0	0	0	4	0	4
DE	114	1078	5613	6805	4150	3717	3527	5084	16478
DK	1102	1017	3411	5530	450	473	324	3346	4593
EE	0	0	87	87	0	2	3	54	59
EL	165	107	248	520	143	57	160	145	505
ES	NI	NI	NI	0	1883	1606	2219	23	5731
FI	312	26	2	340	0	94	113	23	230
FR	588	1720	1657	3965	0	293	400	467	1160
HU	0	0	2646	2646	391	19	126	0	536
IE	0	0	192	192	172	0	1	86	259
IT	851	611	2475	3937	2670	613	1262	1787	6332
LT	2	0	0	2	22	113	217	277	629
LU	200	0	0	200	0	139	104	20	263
LV	17	239	45	301	0	107	347	56	510
MT	21	0	21	42	30	0	0	0	30
NL	4099	2436	7404	13939	6087	849	880	0	7816
PL	596	50	1010	1656	140	51	20	181	392
PT	278	275	948	1501	387	238	118	71	814
RO	NI	NI	NI	0	311	43	304	79	737
SE	485	1087	2159	3731	31	2064	1734	870	4699
SI	56	91	250	397	12	3	45	170	230
SK	0	21	93	114	10	17	45	38	110
UK	385	365	2942	3692	1433	0	553	4154	6140
EU	10552	9959	32213	52724	19151	10878	13819	17686	61534
All birds sampled for which the origin was known									

Table II Number of birds tested in passive surveillance by country (injured, live and diseased and dead birds)

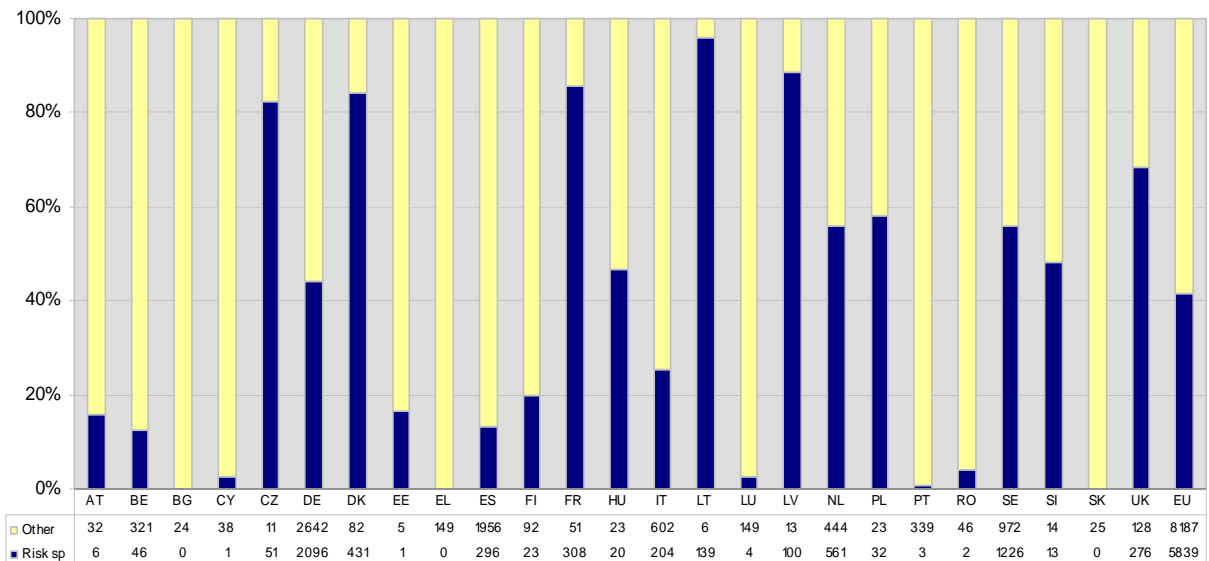
MS	Feb - May 2006	Jun - Aug 2006	Sep - Dec 2006	2006 Total	Jan - Mar 2007	Apr - Jun 2007	Jul - Sep 2007	Oct - Dec 2007	2007 Total
AT	3008	253	114	3375	63	38	220	5	326
BE	54	27	21	102	7	11	49	6	73
BG	NI	NI	NI	0	34	7	41	7	89
CY	141	27	48	216	56	32	26	34	148
CZ	2048	121	68	2237	46	62	252	40	400
DE	16427	2660	1148	20235	978	1021	3919	1281	7199
DK	1011	127	51	1189	133	40	21	57	251
EE	0	6	15	21	4	4	9	10	27
EL	1430	125	54	1609	90	92	153	111	446
ES	NI	NI	NI	0	864	646	779	0	2289
FI	131	59	6	196	3	21	21	8	53
FR	2655	355	278	3288	170	66	565	120	921
HU	3119	0	36	3155	98	24	35	0	157
IE	518	113	92	723	104	0	33	25	162
IT	442	457	550	1449	132	193	357	145	827
LT	576	20	23	619	21	32	16	17	86
LU	374	25	65	464	23	14	22	8	67
LV	122	1	22	145	4	6	3	0	13
MT	16	0	0	16	2	0	0	0	2
NL	10261	71	182	10514	198	156	163	113	630
PL	1387	17	14	1418	75	4	5	25	109
PT	766	298	257	1321	144	104	86	71	405
RO	NI	NI	NI	0	47	5	24	14	90
SE	519	29	43	591	45	134	100	62	341
SI	567	47	24	638	18	24	52	10	104
SK	1506	99	16	1621	28	8	34	12	82
UK	6711	1327	588	8626	818	404	326	406	1954
EU	53789	6264	3716	63769	4205	3148	7311	2587	17251
All birds sampled for which the origin was known									

ANNEX I C PROPORTION OF HIGHER-RISK SPECIES SAMPLED BY MS AND QUARTER

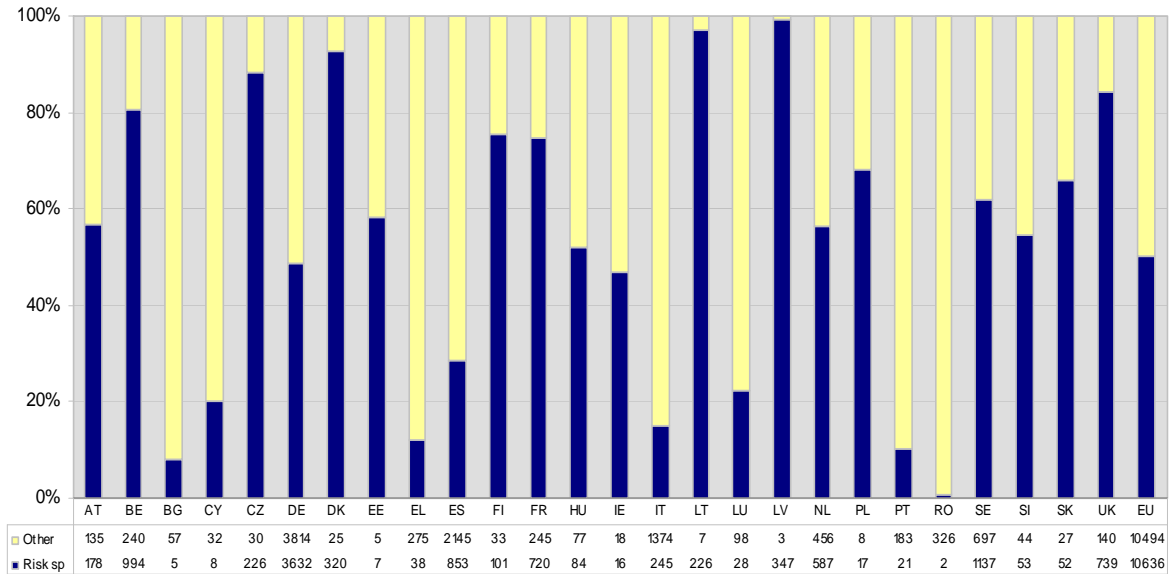
January - March 2007 – HRS – sampled birds



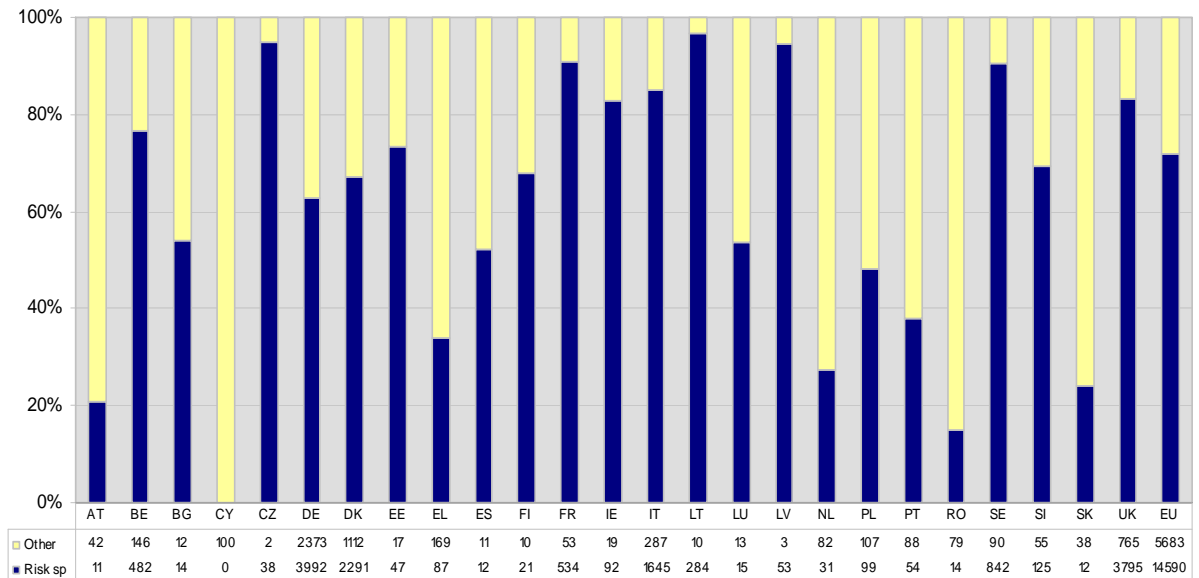
April - June 2007 – HRS – sampled birds



July - September 2007 – HRS– sampled birds



October - December 2007 – HRS – sampled birds



ANNEX IIA OVERVIEW OF RESULTS FOR HIGHER-RISK AND OTHER SPECIES SAMPLED AND POSITIVE BIRDS

Table I and III display the test results for the 29 higher-risk species according to the guidelines (EC, 2007) and EFSA (EFSA, 2006). Tables II and IV display those species where Avian Influenza was detected but which are not considered higher-risk species.

Table I indicates for each MS, the number of HRS sampled, and the number of positive birds detected. A green cell indicates an MS sampled the relevant species, but avian influenza was not detected. A red cell indicates that the species tested positive for H5N1 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 LPAI H5 and an orange cell indicates that the species tested positive for LPAI H7. Table II displays bird species where H5N1 HPAI, LPAI H5 or LPAI H7 was detected, in those species not considered higher-risk.

Table III displays data on sampling and positives for HRS, but the positive birds are split into H5N1 HPAI positives, and all other positive birds (all LPAI and other positives).

Table IV displays data on sampling and positives for birds not listed as HRS, but the positive birds are split into H5N1 HPAI positives, and all other positive birds (all LPAI and other positives).

Table V indicates for 2007, which species (HRS and other bird species) were positive for other LPAI subtypes excluding H5 and H7.

The aim of these tables 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.

Table I Number sampled and positive by MS for birds listed as higher-risk species

Species	MEMBER STATE																								Total HPAI H5	Total LPAI H5	Total LPAI H7	Total Bin Sam				
	AT	BE	BG	CY	CZ	DE	DK	EE	EL	ES	FI	FR	HU	IE	IT	LT	LU	LV	MT	NL	PL	PT	RO	SE					SI	SK	UK	
	1/20 Number positive/ Number sampled																															
<i>Anas acuta</i>		24					25	2	6	19	3		2		72			4	1	17		3		2			2/290	0	2	0	4	
<i>Anas clypeata</i>					1	4		1	16	236	3	1/8		2	175	1		16		17			2				8	0	1	0	4	
<i>Anas crecca</i>		9	4			75	3/195	3	67	14	20	15		2/138	525	3		38	1	28	1	51	9	1/40		1	578	0	5	1	18	
<i>Anas penelope</i>		28				128	292	2	19	1	9	2		36	731	1		17		1365		22		4/42			1018	0	4	0	37	
<i>Anas platyrhynchos</i>	187	757	44	2	176	2/5094 7/5094	1/477 2/477		28	67	810	1/64 10/1019	2/1019 1/2278	352	74	5/2278 1/2278	597	2	328	22	1/1708	123	3/124	54	51/215 2	176	61	1/1482	4	80	3	182
<i>Anas querquedula</i>			1			5			16	3		4/69			10	1		31			4		2	1				0	4	0	14	
<i>Anser albifrons</i>			1			1/491	5	3	1	44		2	11	1				1		1/1206			11				2	0	2	0	17	
<i>Anser anser</i>	3	1			1	1/2714	172	4		221	1	16			16					165	15	11	5	190	1		165	1	0	0	37	
<i>Anser brachyrhynchus</i>						11					1									3							111	0	0	0	12	
<i>Anser erythropus</i>										2													1					0	0	0	3	
<i>Anser fabalis</i>						382	251	10			2		23							124	23			2				0	0	0	8	
<i>Aythya ferina</i>		42				46			1	20		84		1	88	4			13		2		2	5			163	0	0	0	4	
<i>Aythya fuligula</i>		115				165	1				2	3		4	2		1	21		11		1	2	76			41	0	0	0	4	
<i>Branta bernicla</i>						1	146				1	2								43				1			53	0	0	0	3	
<i>Branta canadensis</i>		479				1/634	243			4	2									16	8			19			444	1	0	0	18	
<i>Branta leucopsis</i>		27				248	396	1			5									446		2		1			151	0	0	0	12	
<i>Branta ruficollis</i>						48														2			1					0	0	0	5	
<i>Cygnus columbianus</i>						8									11						6						38	0	0	0	6	
<i>Cygnus cygnus</i>						54	1/334			8	11	3/156 1/156		48	16	3	40			1	1		10	14			675	3	2	0	13	
<i>Cygnus olor</i>	72	57	9		1/137	20/1836	190	2	3	7	6	2/209	1/16	16	22	48	5	3	2	399	49	1	4	24	40		1/1027	23	1	1	41	
<i>Fulica atra</i>	6	142		2	3	2/695	5		12	539		59	3		184	2			1	103			12		1	2	80	2	0	0	18	
<i>Larus canus</i>						129	102	1			5	12		5	1					25	2			128			20	0	0	0	4	
<i>Larus ridibundus</i>	1	87		2	22	709	268	3	13	215	11	7	7	4	238	2		29		688	1/15			254			98	0	0	1	26	
<i>Limosa limosa</i>																				1								0	0	0	1	
<i>Marmaronetta angustirostris</i>										3					3													0	0	0	6	
<i>Netta rufina</i>				6		32				32			2							1		2						0	0	0	7	
<i>Philomachus pugnax</i>	5	8								1	1				1									131				0	0	0	14	
<i>Pluvialis apricaria</i>		114					80								1									71				0	0	0	20	
<i>Vanellus vanellus</i>		50				29	118		4	3		1			4					5				87			1	0	0	0	30	
TOTAL																												34	101	6	47	

The following tables only display the positive results for HPAI H5N1, LPAI H5 and H7 (All HRS and only those species not considered higher-risk where a positive result was detected).

Table II Number sampled and positive by MS for birds not listed as higher-risk species, where HPAI H5N1, LPAI H5 or H7 was detected

Species	MEMBER STATE																				HPAI H5N1	LPAI H5	LPAI H7	Total Birds Sampled							
	AT	BE	BG	CY	CZ	DE	DK	EE	EL	ES	FI	FR	HU	IE	IT	LT	LU	LV	MT	NL					PL	PT	RO	SE	SI	SK	UK
	Number positive/ Number sampled																														
<i>Anas sp.</i>	6		22	5		1060	1/43		3	166		125		2	61	24	24	3			70	135					62	0	1	0	1811
<i>Aythya sp.</i>	1					2/3				1												4						2	1	0	9
<i>Buteo buteo</i>		1	1	4		262	11		65	55	1		14	1	46		7			33	2/2	1		3			3	2	0	0	510
<i>Ciconia ciconia</i>			14	1	9	52			49	162		4	10		3	5		1		1	1/2	16			12	2		1	0	0	343
<i>Cygnus atratus</i>		1				5									2/3					2							5	0	2	0	16
<i>Cygnus sp.</i>	64					2/816				1	7				21			5			46	8	1	4		26	72	2	1	1	1071
<i>Larus sp.</i>	41			4		2/262			87	33				2	29	2		2			4	56		2			115	2	0	0	639
<i>Podiceps cristatus</i>	14	1			1	38/93			1	25		3			1					5							1	38	0	0	145
<i>Podiceps nigricollis</i>						246/302			1						1													246	0	0	304
<i>Tachybaptus ruficollis</i>						2/10			1	7					1												1	2	0	0	20
TOTAL																												295	4	1	32268

Table III Number sampled and positive by MS for birds listed as risk species

Species	MEMBER STATE																						Total HPAI H5	Total other +ves	Total Bird Sampled						
	AT	BE	BG	CY	CZ	DE	DK	EE	EL	ES	FI	FR	HU	IE	IT	LT	LU	LV	MT	NL	PL	PT				RO	SE	SI	SK	UK	
	1/20 Number positive/ Number sampled																														
<i>Anas acuta</i>		14/24					25	2	6	1/19	3		2		4/72			4	1	17		3		2			3/290	0	22	470	
<i>Anas clypeata</i>					1	1/4		1	16	236	3	7/8		2	7/175	1		16		17			2				8	0	15	490	
<i>Anas crecca</i>		9	4			3/75	14/195	3	67	14	20	6/15		5/138	30/525	3/3		2/38	1	1/28	1	51	9	1/40		1	8/578	0	73	1815	
<i>Anas penelope</i>		28				1/128	4/292	2	19	1	9	2		36	7/731	1		17		5/1365		22		8/42			2/1018	0	27	3713	
<i>Anas platyrhynchos</i>	4/187	118/757	1/44	2	3/176	2/5094 109/5094	13/477	28	67	21/810	8/64	2/1019 201/1019	352	74	102/2278	44/597	1/2	22/328	22	52/1708	123	6/124	54	174/2152	15/176	3/61	16/1482	4	913	1825	
<i>Anas querquedula</i>			1			5			16	3		24/69			1/10	1		3/31			4		2	1				0	28	143	
<i>Anser albifrons</i>			1			2/491	5	3	1	44		2	11	1				1		30/1206			11				2	0	32	1775	
<i>Anser anser</i>	3	1			1	1/2714 3/2714	172	4		1/221	1	16			16					1/165	15	2/11	5	190	1	1/165	1	8	3701		
<i>Anser brachyrhynchus</i>						11					1										3						111	0	0	126	
<i>Anser erythropus</i>										2													1					0	0	3	
<i>Anser fabalis</i>						3/382	1/251	10			2		23							1/124	23			2				0	5	817	
<i>Aythya ferina</i>		7/42				46			1	20		20/84		1	1/88	4		13		2		2	5				1/163	0	29	471	
<i>Aythya fuligula</i>		4/115				3/165	1				2	3		4	2		1	21		11		1	2	76			1/41	0	8	445	
<i>Branta bernicla</i>						1	146				1	2									43			1			53	0	0	347	
<i>Branta canadensis</i>		4/479				1/634 2/634	243			4	2									16	8			19			1/444	1	7	1849	
<i>Branta leucopsis</i>		27				248	396	1			5									1/446		2		1			151	0	1	1277	
<i>Branta ruficollis</i>						48															2		1					0	0	51	
<i>Cygnus columbianus</i>						8																							0	0	63
<i>Cygnus cygnus</i>						54	1/334			8	11	3/156 4/156		48	1/16	3	40			1	1		10	14			1/675	3	7	1371	
<i>Cygnus olor</i>	72	7/57	9		1/137	20/1836 7/1836	1/190	2	3	7	6	2/209 11/209	1/16	16	22	1/48	5	3	2	1/399	49	1	4	1/24	3/40		2/1027	23	35	4184	
<i>Fulica atra</i>	6	8/142		2	3	2/695 3/695	5		12	4/539		59	3		1/184	2			1	103			12		1	2	80	2	16	1851	
<i>Larus canus</i>						129	102	1			5	12		5	1					25	2			128		20	0	0	430		
<i>Larus ridibundus</i>	1	25/87		2	22	709	1/268	3	13	5/215	11	7	7	4	1/238	2		29		19/688	1/15			254		98	0	52	2673		
<i>Limosa limosa</i>																			1									0	0	1	
<i>Marmaronetta angustirostris</i>										3					3													0	0	6	
<i>Netta rufina</i>				6		1/32				32			2							1		2						0	1	75	
<i>Philomachus pugnax</i>	5	8								1	1				1										131			0	0	147	
<i>Pluvialis apricaria</i>		114					80								1										71			0	0	266	
<i>Vanellus vanellus</i>		50				29	118		4	3		1			4					5				87		1	0	0	302		

Table IV Number sampled and positive by MS for birds not listed as risk species, for those species where positives were found

Species	MEMBER STATE																							Total HPAI H5	Total other types	Total Birds Sampled				
	AT	BE	BG	CY	CZ	DE	DK	EE	EL	ES	FI	FR	HU	IE	IT	LT	LU	LV	MT	NL	PL	PT	RO				SE	SI	SK	UK
<i>Anas sp.</i>	6		22	5		9/1060	4/43		3	4/166		6/125	2	61	24	24	3			70	1/135					62	0	24	1811	
<i>Anas strepera</i>	2	30				23			2	21				2/131			7		1/112			30				25	0	3	383	
<i>Anser spp.</i>	9/48		8	1		354			3	2/27	1			15													0	11	501	
<i>Arenaria interpres</i>		1/57				1				1										1			11				0	1	71	
<i>Aythya sp.</i>	1					2/3				1											4						2	1	9	
<i>Buteo buteo</i>		1	1	4		262	11		65	55	1		14	1	46		7			33	2/2	1		3		3	2	0	510	
<i>Calidris minuta</i>						1									1/104								1				0	1	106	
<i>Ciconia ciconia</i>			14	1	9	52			49	162		4	10		3	5	1		1	1/2	16			12	2	1	0	343		
<i>Columba livia</i>		1	2	1	10	38		10	18	1/460		32	19	1	21	10				2	30	8	37	2		44	0	1	746	
<i>Columba palumbus</i>				1		26	15	2		1/19				12	10					7			6	2		4	0	1	104	
<i>Corvus sp.</i>				1		144				3													6	14		1/84	0	1	252	
<i>Coturnix coturnix</i>	1		13	2		5				18					1/127							15	19				0	1	200	
<i>Cygnus atratus</i>		1				5									2/3					2							5	0	2	16
<i>Cygnus sp.</i>	5/64					2/816				1	7				21		5			46	8	1	4		26	72	2	7	1071	
<i>Fulica cristata</i>										1/85																	0	1	85	
<i>Gallinula chloropus</i>		2/10	1	2	1	27			6	192		23	7	2	156		1		1	14		1				13	0	2	457	
<i>Haematopus ostralegus</i>		5/94																		1	21			1		2	0	5	119	
<i>Lanius senator</i>										1/7																	0	1	7	
<i>Larus argentatus</i>		22/131	1			7/299	6/134	3	6	4/116	3/15	3		5	4					355	6			69		49	0	42	1196	

Table IV Number sampled and positive by MS for birds not listed as risk species, for those species where positives were found

Species	MEMBER STATE																					Total HPAI H5	Total other types	Total Birds Sampled						
	AT	BE	BG	CY	CZ	DE	DK	EE	EL	ES	FI	FR	HU	IE	IT	LT	LU	LV	MT	NL	PL				PT	RO	SE	SI	SK	UK
<i>Larus argentatus cachinnans</i>									30	8/139					2					1					1/5			0	9	177
<i>Larus argentatus michahellis</i>						1			25	2/83					164													0	2	273
<i>Larus fuscus</i>		68				2				22	1/1	13	1							383			1				3	0	1	494
<i>Larus marinus</i>						72	1/71			3			1							33	1/1			7			2	0	2	190
<i>Larus sp.</i>	1/41			4		2/262 1/262			87	33			2	29	2		2				4	1/56		2			115	2	3	639
<i>Limosa lapponica</i>		2/10				4				3		2								27								0	2	46
<i>Luscinia megarhynchos</i>						3				2/52					2		1					4						0	2	62
<i>Numida meleagris</i>		4				1/8																						0	1	12
<i>Passer domesticus</i>			2	6		174	3		3	1/69	1	6			1		2					2		2			6	0	1	277
<i>Phalacrocorax carbo</i>	2	1	2			304	1/101		12	1/157	1	1		4	68	4				5	2				1		5	0	2	670
<i>Phasianus colchicus</i>	2		23		2	174	607			2	1	1/7	99	8	26					5	8		151	1		1/36	2	0	2	1154
<i>Phoebastria immutabilis</i>				8					7	4/685		1			562							2						0	4	1265
<i>Platalea leucorodia</i>						1			1	4/195										1								0	4	198
<i>Plegadis falcinellus</i>									2	10/463																		0	10	465
<i>Podiceps cristatus</i>	14	1			1	38/93 2/93			1	25		3			1					5							1	38	2	145
<i>Podiceps nigricollis</i>						246/302 27/302			1						1													246	27	304
<i>Rallus aquaticus</i>		3/55				12			2	3					40		1											0	3	113
<i>Somateria mollissima</i>						26	2/99				3									15				9			11	0	2	163

Table IV Number sampled and positive by MS for birds not listed as risk species, for those species where positives were found

Species	MEMBER STATE																								Total HPAI H5	Total other positives	Total Birds Sampled			
	AT	BE	BG	CY	CZ	DE	DK	EE	EL	ES	FI	FR	HU	IE	IT	LT	LU	LV	MT	NL	PL	PT	RO	SE				SI	SK	UK
<i>Sterna hirundo</i>		21	1			31	1			35				38						22	29/39			201			5	0	29	394
<i>Streptopelia decaocto</i>			1	3		2			13	1/28		17	15	1	7							8	32	2			1	0	1	130
<i>Sylvia atricapilla</i>				19		40			10	1/59		2				104									18			0	1	252
<i>Tachybaptus ruficollis</i>						2/10			1	7					1												1	2	0	20
<i>Tadorna tadorna</i>		5/233				11			7	17		1/2			23					19				77	1		604	0	6	994
<i>Uria aalge</i>						9				1/97		1		4						3				6			48	0	1	168
<i>Species unknown</i>	2		22	46		428	3			2/238	3	54	13		1/101			11		3/572	92	269	43	2		22	242	0	6	2163

Species	Total birds sampled	Total 'LPAI other' positive birds	Apparent prevalence of 'LPAI Other' positive birds
* <i>Anas acuta</i>	470	5	1.06%
* <i>Anas clypeata</i>	490	1	0.20%
* <i>Anas crecca</i>	1815	4	0.22%
* <i>Anas penelope</i>	3713	4	0.11%
* <i>Anas platyrhynchos</i>	18258	63	0.35%
* <i>Anas querquedula</i>	143	1	0.70%
<i>Anas</i> sp.	1811	2	0.11%
* <i>Anser albifrons</i>	1779	1	0.06%
* <i>Anser anser</i>	3701	2	0.05%
* <i>Anser fabalis</i>	817	1	0.12%
* <i>Branta leucopsis</i>	1277	1	0.08%
* <i>Cygnus cygnus</i>	1371	1	0.07%
* <i>Cygnus olor</i>	4184	3	0.07%
<i>Larus argentatus</i>	1196	2	0.17%
<i>Larus marinus</i>	190	1	0.53%
* <i>Larus ridibundus</i>	2673	23	0.86%
<i>Larus</i> sp.	639	1	0.16%
<i>Luscinia megarhynchos</i>	62	2	3.23%
<i>Passer domesticus</i>	277	1	0.36%
<i>Phasianus colchicus</i>	1154	1	0.09%
<i>Somateria mollissima</i>	163	1	0.61%
Species unknown	2163	1	0.05%
<i>Tadorna tadorna</i>	994	5	0.50%
TOTAL	79392	127	0.16%
* HRS			

**ANNEX II B TOTAL NUMBER AND PROPORTION OF
LPAI POSITIVE BIRDS IN 2006**

MS	Total birds sampled	Total birds LPAI H5 Positive	Total Positive Proportion (LPAI H5)	Total LPAI H7 Positive	Total Positive Proportion (LPAI H7)	Total birds Positive (LPAI Other)	Total Positive Proportion (LPAI other)	Total number of 'Other positive' birds	Total Positive Proportion 'Other Positive' birds
FR	7253	49	0.68%	-	-	83	1.14%	212	2.92%
SE	4322	19	0.44%	-	-	126	2.92%	44	1.02%
NL	24715	38	0.15%	6	0.02%	97	0.39%	297	1.20%
DK	6719	8	0.12%	-	-	-	-	49	0.73%
UK	12318	12	0.10%	-	-	9	0.07%	106	0.86%
DE	27913	8	0.03%	2	0.01%	10	0.04%	95	0.34%
PL	3074	1	0.03%	-	-	7	0.23%	-	-
IT	6106	1	0.02%	11	0.18%	20	0.33%	158	2.59%
AT	4364	-	-	6	0.14%	5	0.11%	26	0.60%
BE	2177	-	-	-	-	5	0.23%	-	-
BG	1983	-	-	-	-	1	0.05%	8	0.40%
CY	502	-	-	-	-	13	2.59%	-	-
CZ	2237	-	-	-	-	-	-	1	0.04%
EL	2129	-	-	-	-	1	0.05%	-	-
IE	915	-	-	-	-	1	0.11%	12	1.31%
LV	446	-	-	-	-	-	-	44	9.87%
PT	2824	-	-	1	0.03%	9	0.32%	-	-
SI	1035	-	-	-	-	-	-	14	1.35%
EU Total	120706	136	0.11%	26	0.02%	387	0.32%	1066	0.88%

ANNEX III BTO OFFPRINT FROM MIGRATION MAPPING TOOL

Migration Mapping Tool - Microsoft Internet Explorer provided by Internet Explorer - VLA

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Address <http://bx1.bto.org/ai-eu/>

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Seasonal movements to and from Germany & Denmark for Mute Swan (*Cygnus olor*)

This table will show you where ringed birds present in Germany & Denmark at different times of year have been found (by country and month).

Select the season in which the species is present in Germany & Denmark **Jun - Aug**

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
Austria	8	9	4	1	1	4
Belgium	.	3	1	1	.	.
Croatia	1	.	.
Czech Republic	92	109	38	27	24	20	25	21	13	25	51	112
Denmark	2	.	1	1	1	1	.	.	1	.	.	.
Finland	2
France	1	1	.
Germany	862	1162	765	592	652	487	1220	1707	1234	571	375	642
Great Britain & Ireland	.	1	1	.	.	1
Hungary	2	1	1	.
Lithuania	20	14	25	5	1	2	.	2	17	9	2	3
Luxembourg	.	.	2	1	.	.
Norway	.	.	.	1
Poland	287	254	180	67	32	7	33	37	29	71	97	206
Slovakia	2	1
Sweden	7	19	11	.	.	.	13	27	9	1	1	1
Switzerland	1
The Netherlands	33	22	22	7	.	3	9	63	21	3	1	7
Ukraine	.	1

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Sites

For EU Countries, sites refer to **Natura 2000** data held by the EU. For other countries data are from International Waterbird Census Counts. All sites in the country will be shown.

Select the country you wish to view

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