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## Avian influenza overview – update on 19 November 2020, EU/EEA and the UK

European Food Safety Authority,  
European Centre for Disease Prevention and Control and  
European Union Reference Laboratory for Avian Influenza

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### Abstract

Since 16 October 2020, outbreaks of highly pathogenic avian influenza (HPAI) viruses have been reported in several EU/EEA countries – Belgium, Denmark, France, Germany, Ireland, the Netherlands, and Sweden as well as in the United Kingdom. As of 19 November, 12pm, 302 HPAI A(H5) detections have been reported, with the majority of the detections referring to wild birds (n=281), and a few related to outbreaks in poultry (n=18) and captive birds (n=3). Most of the detections in wild birds were in wild waterbirds, being barnacle goose the most affected species (n=110), followed by greylag goose (n=47), Eurasian wigeon (n=32), mallard (n=14), and common buzzard (n=13). Three HPAI virus subtypes were identified, A(H5N8), A(H5N5) and A(H5N1), with A(H5N8) being the most reported subtype (n=284). Phylogenetic analysis indicated that the viruses evolved from a single progenitor virus that went through multiple reassortment events. Based on the ongoing autumn migration of wild waterbirds to their wintering areas in Europe, there is a continued risk of further introduction of HPAI A(H5) viruses into Europe. Furthermore, given the expected movements of both migratory, and resident wild birds in Europe during winter, there is a high risk of further spread of HPAI A(H5) viruses within Europe. No genetic markers indicating adaptation to mammals have been identified in the viruses analysed so far, and no human infection due to avian influenza viruses detected in the recent outbreaks has been reported. For that reason, the risk to the general population remains very low. However, following the precautionary principle, people should avoid touching sick or dead birds unprotected to minimise any potential risk.

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## 1. Background

On 21 October 2020, the Netherlands notified highly pathogenic avian influenza (HPAI) virus A(H5N8) in two mute swans found dead in a wetland area (OIE, 2020a). This was the first HPAI detection in an EU/EEA country since June 2020, when HPAI was notified in poultry in Hungary. As of 19 November, 12pm, 302 HPAI A(H5) detections in wild birds and outbreaks in poultry and captive birds have been reported from Belgium (n=3), Denmark (n=17), France (n=1), Germany (n=223), Ireland (n=3), the Netherlands (n=46), Sweden (n=1), and the United Kingdom (UK; n=8). The majority detected in wild birds (n=281), although a few outbreaks in poultry (n=18) and captive birds (n=3) were also observed. The following wild bird species were mostly reported to be affected: barnacle goose (n=110), greylag goose (n=47), Eurasian wigeon (n=32), mallard (n=14) and common buzzard (n=13). The reported detections in wild birds in Germany and the Netherlands (Table A.4 in Annex A) are only a small proportion of the sick and dead wild birds observed, and the overall numbers therefore do not reflect the scale of mortality in wild birds in those countries. Furthermore, the virus is spreading rapidly and it is expected that the current situation will change significantly in the coming days with increasing number of detections. Genetic analysis of the current outbreaks revealed that the identified viruses differ from the HPAI A(H5N8) and A(H5N2) viruses that were observed in east-central Europe from December 2019 to June 2020. In their latest avian influenza overview published in September, EFSA, ECDC and EURL raised an early alert to increase awareness of the possible introduction of HPAI virus into Europe via wild birds migrating to their wintering areas (EFSA et al., 2020). This alert followed the detection of HPAI A(H5N8) virus in areas in western Russia and in north Kazakhstan (OIE, 2020b, c, d) over the summer period that are spatially associated with the autumn winter migration routes of wild waterbirds into Europe. The number of HPAI reported detections in EU/EEA countries are rapidly increasing and, in contrast to the 2019-2020 HPAI A(H5N8) epidemic, several HPAI virus subtypes have so far been identified: A(H5N8), A(H5N5) and A(H5N1). EFSA, ECDC and EURL have been issuing quarterly reports on the avian influenza situation within Europe and worldwide since 2017. Due to the currently rapidly evolving situation in Europe, the mass mortality observed in wild birds, and the significant changes in the observed epidemiology of the infection in comparison to the 2019-2020 (previous) season, the European Commission (SANTE) requested EFSA to rapidly update the 'overview of avian influenza' in the EU/EEA and the UK. This scientific report gives an update of the situation up to 19 November 2020 12 pm, with the aim to providing insight into the risk of further spread of avian influenza within the wild bird and poultry populations across Europe, and assesses the zoonotic potential of the virus strains currently circulating.

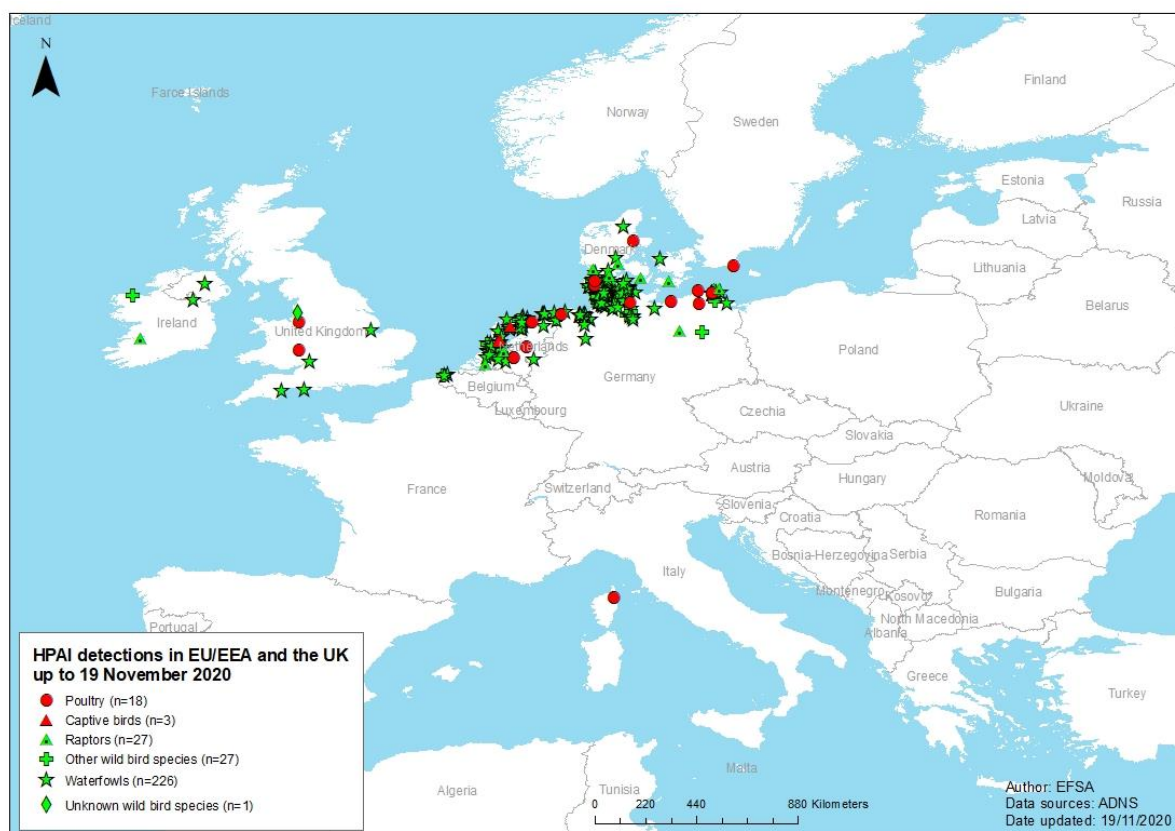
### 1.1. Overview of HPAI detections in EU/EEA and the UK

As of 19 November 2020, 12pm, 302 HPAI A(H5) virus detections in wild birds (n=281) and outbreaks in poultry (n=18) and captive birds (n=3) were notified from EU/EEA countries and the UK, as presented in Table 1. The HPAI viruses were subtyped as: 284 A(H5N8), five A(H5N5), four A(H5N1), eight A(H5) with missing NA-subtype, and one virus with missing HA- and NA-subtype. The hemagglutinin gene of all the identified subtypes belongs to a single genetic group within clade 2.3.4.4b, indicating a single progenitor virus that underwent multiple reassortment events. The timeline, location and affected bird categories of the outbreaks are presented in Figures 1 and 2. Data presented in this section originates from the Animal Disease Information System (ADNS); for a single HPAI notification in wild birds one or more than one wild bird species might have been found infected. The data has some limitations: the number of cases and reported type of bird species in wild birds could reflect a single dead bird, but in areas with mass mortality events in wild bird populations, the total number of wild bird cases for each event reported to ADNS represents the number of tests performed on selected dead birds and does not reflect the scale of wild bird mortality in those areas as e.g. currently communicated from the Netherlands and Germany (pers. communication from Thijs Kuiken and Christoph Staubach).

**Table 1:** Number of highly pathogenic avian influenza virus detections in wild birds and outbreaks in poultry and captive birds in EU/EEA and the UK, by country and virus subtype, 19 November 2020

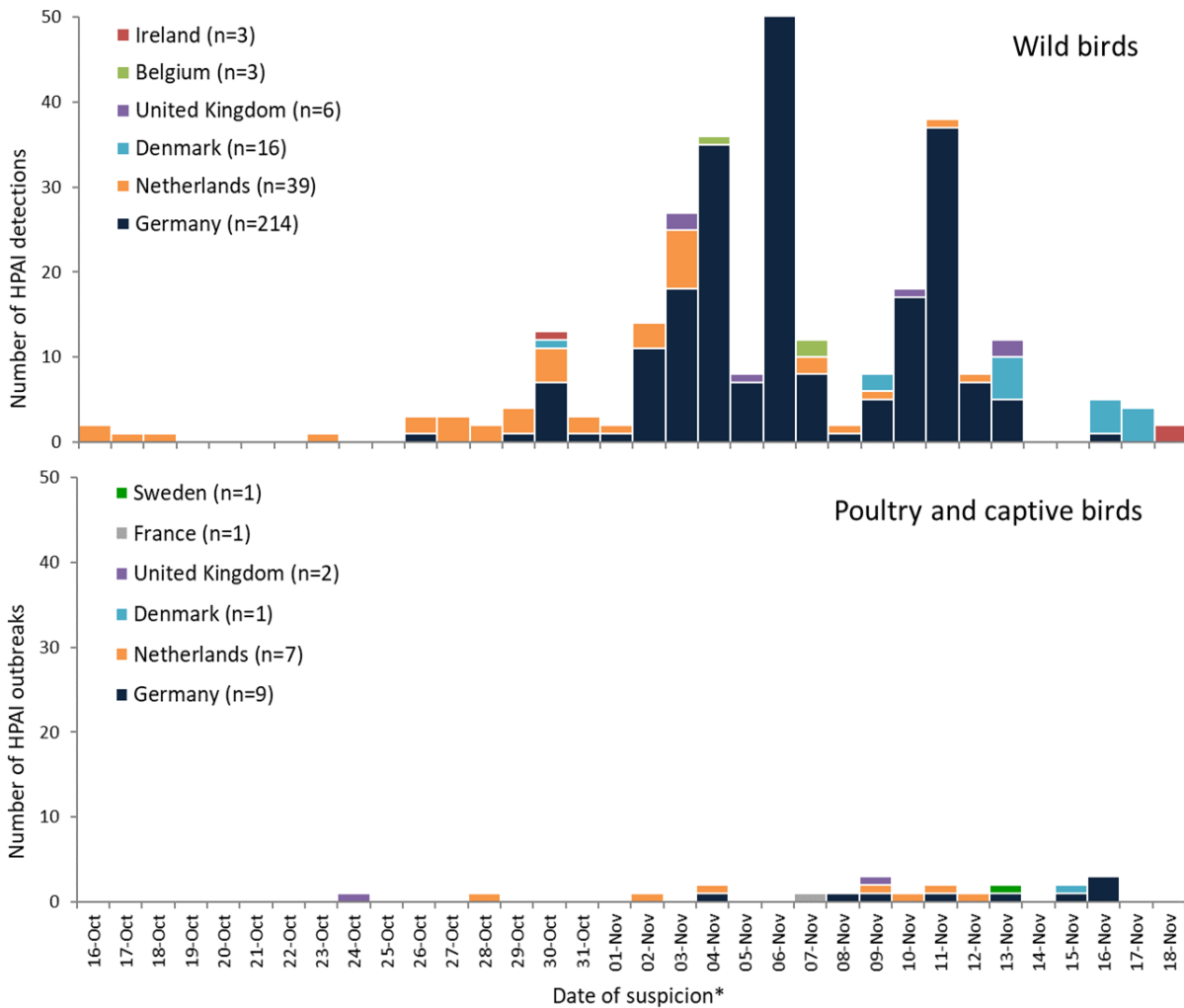
Country	Wild Birds					Poultry			Captive Birds	Total
	A(H5N1)	A(H5N5)	A(H5N8)	A(H5)	No info	A(H5N5)	A(H5N8)	A(H5)	A(H5N8)	
Belgium			3							3
Denmark		1	14	1			1			17
France							1			1
Germany		2	205	6	1	1	8			223
Ireland			3							3
Netherlands	4	1	34				3	1	3	46
Sweden							1			1
United Kingdom			6				2			8
<b>Total</b>	<b>4</b>	<b>4</b>	<b>265</b>	<b>7</b>	<b>1</b>	<b>1</b>	<b>16</b>	<b>1</b>	<b>3</b>	<b>302</b>

Data source: ADNS (19.11.20 at 12pm).



\* This designation is without prejudice to positions on status and is in line with United Nations Security Council Resolution 1244 and the International Court of Justice Opinion on the Kosovo Declaration of Independence.

**Figure 1:** Geographical distribution, based on available geocoordinates, of highly pathogenic avian influenza virus detections in EU/EEA and the UK by affected bird category, 19 November 2020 (n=302)



\* When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion. Data source: EFSA and ADNS (17.11.20). Date of suspicion for the Belgian cases was communicated by Mieke Steensels (SCIENSANO)

**Figure 2:** Distribution of the HPAI A(H5) reported detections in Europe, by date of suspicion and affected subpopulation, in wild birds (n=281) and poultry and captive birds (n=21), 19 November 2020

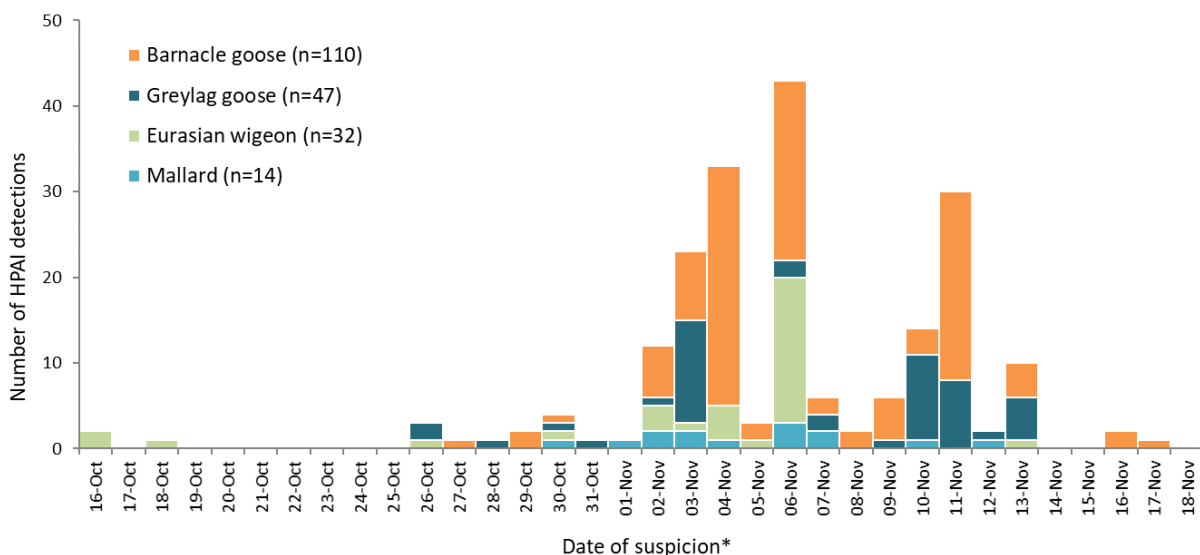
In the Netherlands, Germany, and Denmark, HPAI A(H5) virus was detected in wild birds several days or weeks before outbreaks occurred in poultry or captive birds (Figure 2). In the UK, France (Corsica), and Sweden, HPAI A(H5) outbreaks were reported first in poultry or captive birds.

As of 19 November, 12pm, 27 wild bird species were reported as infected, mostly waterfowl species (13 species; 226 detections), followed by raptors (8 species; 27 cases) and other aquatic wild bird species (7 species; 27 cases) (see Table A.1, Annex A for the full data). The wild bird species most often reported were barnacle goose (*Branta leucopsis*) (n=110), greylag goose (*Anser anser*) (n=47), Eurasian wigeon (*Mareca penelope*) (n=32), mallard (*Anas platyrhynchos*) (n=14) and common buzzard (*Buteo buteo*) (n=13). The majority of the ADNS reported detections of wild birds indicated that the birds had been found dead or moribund, apart from two Eurasian wigeons that were sampled in a duck decoy for scientific research in the Netherlands on 16 October 2020. These two Eurasian wigeons were the first infected wild birds found in Europe (Figure 3). The birds showed no clinical signs when they were sampled, although they developed clinical signs of HPAI infection a few days later; one wigeon tested positive for A(H5N1) and one for A(H5N8) virus. Neurological clinical signs were observed in these birds prior to death. Clinical signs of neurological disease (e.g. torticollis, loss of balance, swimming or walking in circles) were also commonly observed in infected wild birds in Belgium, Germany and the Netherlands (pers. communication). The presence of these neurological clinical signs was also a feature commonly observed during the HPAI A(H5N1) epidemic in Europe in 2005 – 2006.

The bird species described above were reported via ADNS, however, this does not exclude the possibility that other bird species are also affected<sup>1</sup>. Also apparently healthy birds have been found to be infected, e.g. in a sample of approximately 100 birds hunted on the island of Rügen in the Baltic Sea, 17 birds tested positive for HPAI virus, although no clinical signs were observed in these birds (FLI, online). Among these healthy infected birds, several bird species listed above such as Eurasian wigeons, greylag goose, and bean goose were described. Furthermore, at the North Sea coastal area some samples from apparently healthy birds tested positive for HPAI virus.

Figure 3 shows the date of suspicion and the number of HPAI reported detections in wild birds where barnacle goose, greylag goose, Eurasian wigeon and mallard were involved.

Of the large number of reported detections of HPAI in geese (n=160), the most affected species was the barnacle goose, which was not commonly detected in previous HPAI outbreaks and was not included in the list of target species compiled by EFSA (EFSA et al., 2017a). Raptors have been reported infected in previous epidemics (e.g. 2016-2017) and are normally detected at a later phase of the epidemic, as they are likely to acquire the infection via hunting or scavenging infected wild waterfowl. Currently, infected raptors have been reported in Denmark (n=6), Germany (n=16), Ireland (n=1) and the Netherlands (n=4) at an early stage.



\* When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.  
Data source: EFSA and ADNS (17.11.20).

**Figure 3:** Number of reported detections of highly pathogenic avian influenza virus A(H5) in wild birds of the four most affected wild bird species in EU/EEA and the UK, by date of suspicion, 17 November 2020 (n=198)

## 1.2. Relevant information on plausible further incursions

Based on the available evidence, further incursions of HPAI viruses in the EU/EEA and the United Kingdom are plausible in the coming weeks/months. However, it is uncertain which wild bird species might introduce the virus into Europe.

Information on the migratory flyways for the wild bird species with the largest number of detections is shown in Figure 4.

The population of Barnacle goose in Russia, Germany and the Netherlands consists of three Management Units (MUs): the Arctic Russian (migratory), the temperate Baltic (migratory) and the

<sup>1</sup> The detection and reporting of dead wild birds found via passive surveillance to ADNS, is determined by factors such as: human presence where the birds are located, the size and other phenotypic characteristics of the birds, etc. Therefore, it is not possible to know what other species are affected by these HPAI viruses if the species do not show clinical signs (including mortality), or if the deaths of these birds occurred in areas not frequented by humans.

temperate North Sea breeding populations, with this last population made up of birds breeding in the Netherlands, Belgium, Germany and south-west Denmark (considered sedentary)<sup>2</sup>. In the Netherlands, there is a resident population of about 19,000 breeding pairs. Between the end of September and the beginning of November, the numbers increased more than 10-fold, to around 800,000 birds, by Arctic Russian migrants, which have the Netherlands as their final wintering destination (van der Jeugd 2018).

Around this time of year, greylag geese are mainly moving south from Scandinavia (or are relatively local birds). In contrast, Eurasian wigeon are migrating birds from more eastwards breeding areas, with many birds having recently returned from breeding and passage areas in northern Russia and Eastern Europe.

The mallard population has a mixture of such eastward migratory birds and more sedentary individuals.

Based on this information and on capture-recapture data from EURING<sup>3</sup> (coordinating organization for European bird ringing schemes), further incursions and movements of the migratory birds of some of these species are plausible in the coming weeks/months (e.g. see Table A.2, Annex A). Table A.2 shows recapture data in different countries of wigeons captured in the area of Russia and Belarus between September and November (EURING). Recapture data of these species show that, particularly in the Netherlands, and the United Kingdom, recoveries of wigeons lasted until the end of March/ beginning of April. Further, other species not detected to date in Europe may be involved in further incursions. To illustrate, from 1 July to 17 November, 10 detections in wild birds in the area of Russia and Kazakhstan were reported from FAO Empres-i involving: mute swan, tufted duck, mallard, crows, common pochard, garganey, gadwall, and unspecified Anatidae<sup>4</sup>.

Real time distribution of the Eurasian wigeon and greylag goose (citizen science data) can be observed on the EuroBird Portal<sup>5</sup> website.



Data source: Critical Site Network Tool 2.0 (flyways for barnacle goose; flyways for wigeon; flyways for greylag goose; flyways for mallard). Wetlands International/BirdLife International.

**Figure 4:** Migratory flyways with population boundaries for A barnacle goose, B Eurasian wigeon, C mallard and D greylag goose

<sup>2</sup> <https://egmp.aewa.info/species-info/barnacle-geese-1>

<sup>3</sup> <https://euring.org/data-and-codes/euring-databank>

<sup>4</sup> <http://empres-i.fao.org/ei3gmapcomp/?MAPREQUEST=d8d601da-a2c3-4077-b7a1-cde4e676b1fa>

<sup>5</sup> <https://eurobirdportal.org/ebp/en/#home/HIRRUS/r52weeks/CUCCAN/r52weeks/>



### 1.3. Relevant information for plausible HPAI virus spread

Following the incursion of the HPAI viruses into Europe, further spread within and among the Member States is expected. Due to the mixing habits, and the long and short-distance migratory routes of wild birds, further detections in wild birds will follow over the next months. Further, based on previous HPAI incursions, and on the expected increase of the virus circulation in the wild bird population, the risk of new introductions of HPAI in poultry will remain high in already affected countries and will become high for other regions across Europe as the season evolves. Nonetheless, due to this mixing of wild bird species present in Europe in this season it is difficult to predict where the next outbreaks will occur.

As barnacle geese are expected to breed in Belgium, south-west Denmark the Netherlands, and Germany and not to move further, they might be a source of infection for other wild species that share the same habitat. In contrast, some of the other waterbird species reported as infected might move around.

Links to the dynamic maps for Eurasian wigeon, mallard, and greylag goose showing individual ringing recovery locations and kernels containing 50% (red) and 95% (blue) of the recoveries, for birds ringed in the different months of the year in both, the area of Belgium/the Netherlands, and in Germany/Denmark, respectively, are shown below:

[https://www.efsa.europa.eu/sites/default/files/scientific\\_output/avian-influenza-nov2020/Wigeon\\_Germany\\_and\\_Denmark\\_08\\_anim\\_WN.gif](https://www.efsa.europa.eu/sites/default/files/scientific_output/avian-influenza-nov2020/Wigeon_Germany_and_Denmark_08_anim_WN.gif)

[https://www.efsa.europa.eu/sites/default/files/scientific\\_output/avian-influenza-nov2020/Wigeon\\_Belgium\\_Netherlands\\_07\\_anim\\_WN.gif](https://www.efsa.europa.eu/sites/default/files/scientific_output/avian-influenza-nov2020/Wigeon_Belgium_Netherlands_07_anim_WN.gif)

[https://www.efsa.europa.eu/sites/default/files/scientific\\_output/avian-influenza-nov2020/Mallard\\_Germany\\_and\\_Denmark\\_08\\_anim\\_MA.gif](https://www.efsa.europa.eu/sites/default/files/scientific_output/avian-influenza-nov2020/Mallard_Germany_and_Denmark_08_anim_MA.gif)

[https://www.efsa.europa.eu/sites/default/files/scientific\\_output/avian-influenza-nov2020/Mallard\\_Belgium\\_Netherlands\\_07\\_anim\\_MA.gif](https://www.efsa.europa.eu/sites/default/files/scientific_output/avian-influenza-nov2020/Mallard_Belgium_Netherlands_07_anim_MA.gif)

[https://www.efsa.europa.eu/sites/default/files/scientific\\_output/avian-influenza-nov2020/Greylag\\_Goose\\_Germany\\_and\\_Denmark\\_08\\_anim\\_GJ.gif](https://www.efsa.europa.eu/sites/default/files/scientific_output/avian-influenza-nov2020/Greylag_Goose_Germany_and_Denmark_08_anim_GJ.gif)

[https://www.efsa.europa.eu/sites/default/files/scientific\\_output/avian-influenza-nov2020/Greylag\\_Goose\\_Belgium\\_Netherlands\\_07\\_anim\\_GJ.gif](https://www.efsa.europa.eu/sites/default/files/scientific_output/avian-influenza-nov2020/Greylag_Goose_Belgium_Netherlands_07_anim_GJ.gif)

An example of these maps can be seen in Figure 5. As Eurasian wigeons have been observed infected in Germany and the Netherlands, Figure 5 shows the recoveries (individual and kernels of these recoveries containing 50% and 90% of the recoveries) of Eurasian wigeon ringed in the month of November in Belgium and the Netherlands (left) and in Germany and Denmark (right), respectively<sup>6</sup>.



Data source: EURING <sup>6</sup>

<sup>6</sup> Data obtained from the Migration Mapping Tool developed by EURING. <https://eurring.org/research/migration-mapping-tool>

**Figure 5:** Individual recoveries and kernels containing 50% (red) and 95% (blue) of the recoveries of Eurasian wigeon ringed in the month of November in Belgium and the Netherlands (left), and in Germany and Denmark (right), respectively

These dynamic maps are shown for illustrative purposes and are not intended to suggest that these would be the only species that may be involved in the spread within Europe. Rather, it is expected that multiple species are involved in the spread. For example, although very few infected mallards have been recovered dead in the affected countries to date, the mixing dynamics of these birds could lead to the spread of HPAI virus from both Germany and the Netherlands towards the South of Germany, North West of France, Switzerland, Italy and other countries within the EU (see links to dynamic maps for mallards above and Table A.3, Annex A). Table A.3 shows the recoveries of mallards in different countries by month after having been captured between September and November in the Germany/Denmark area.

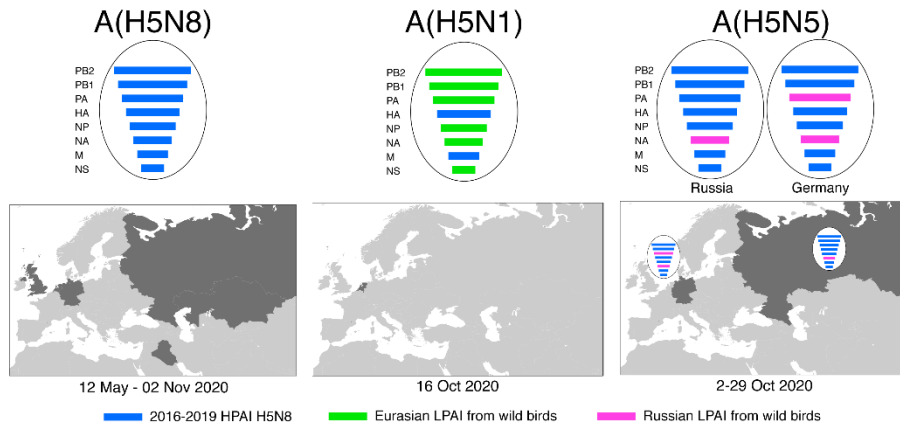
#### 1.4. Genetic characterisation of avian influenza viruses circulating in the EU/EEA and the UK

Complete genome sequences of eight HPAI A(H5) viruses collected from wild and domestic birds in the Netherlands, Germany and the UK were deposited in the GISAID EpiFlu database by Member States. These European virus sequences were analysed together with 12 HPAI A(H5) viruses identified between May and November 2020 in Iraq, the Russian Federation and Kazakhstan from wild and domestic birds (sequence data available in GISAID, accessed on 18 November 2020) (Table B.1, Annex B).

The analysis performed so far, showed that there is no evidence of mutations associated with mammalian adaptation in any of the investigated viruses at the EURL.

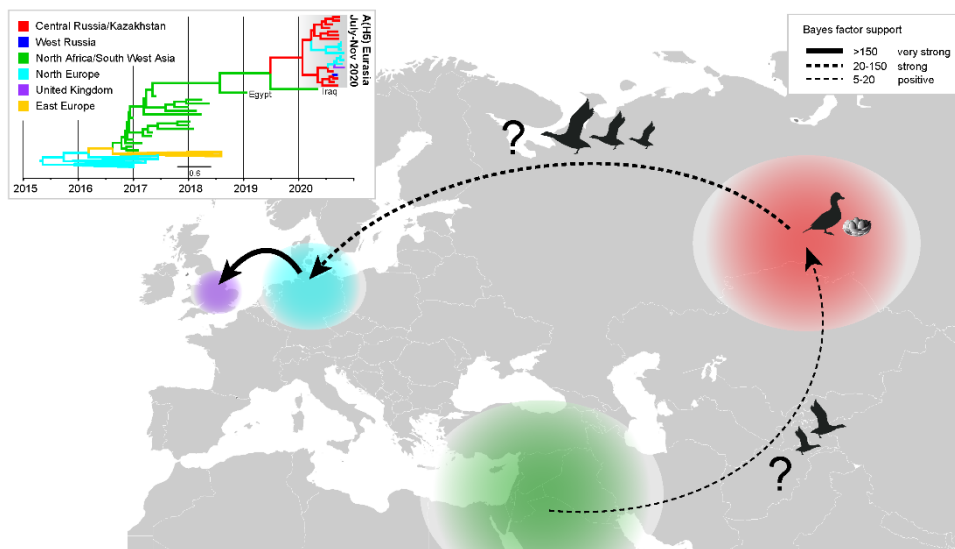
The publicly available HA gene sequences of all these viruses indicated that they originate from a single genetic group within clade 2.3.4.4b and cluster separately from the HPAI A(H5) viruses detected in Europe during the first semester of 2020. All the virus sequences analysed (Table B.1, Annex B) show the highest identity with HPAI A(H5N8) strains that have been circulating in Egypt since 2017. However, the long branch that separates these viruses from their potential ancestors underlines the existence of an important gap in genetic data from North Africa/South-West Asia and the need to perform further analyses to confirm this observation.

Analyses of the remaining gene segments identified four distinct genotypes – one A(H5N8), one A(H5N1) and two A(H5N5) – originating from multiple reassortment events with low pathogenic avian influenza (LPAI) viruses circulating in wild birds in Eurasia (Figure 6). Specifically, the A(H5N8) genotype possesses the same gene constellation of the A(H5N8) viruses introduced into Europe, South-West Asia and North Africa during the 2016-2017 epidemic season; the A(H5N1) genotype shares the HA and M genes with the A(H5N8), while the remaining gene segments have been acquired through reassortment events with LPAI viruses circulating in wild birds in Eurasia. This strain is not related to A(H5N1) viruses circulating in south-east Asia that have caused human infections. The A(H5N5) viruses identified in the Russian Federation and Germany belong to two different genotypes: i) the A(H5N5) from the Russian Federation has the same gene constellation as A(H5N8), except for the NA gene which shows the highest identity with the NA gene of a LPAI virus detected in wild birds in Central Russia while ii) the A(H5N5) from Germany differs from the Russian strain for the PA gene segment, which is closely related to the PA of a LPAI virus collected from a wild bird in Central Russia (Figure 6).



**Figure 6.** HPAI A(H5) genotypes identified in Eurasia since May 2020 and their geographic detection based on the available sequences. We gratefully acknowledge the authors, originating and submitting laboratories of the sequences from GISAID’s EpiFlu™ Database on which this analysis is based.

To shed light on the origin of the European A(H5) viruses, a discrete Bayesian phylogeographic analysis was performed. The results based on the currently available HA gene sequences indicate that North African/Middle Eastern/South-West Asian strains are the most likely progenitors of these viruses, which subsequently spread – apparently through wild migratory birds – to Russia/Kazakhstan and then westward to Northern Europe. Acquiring additional genetic data, in particular from North Russia and Siberia, which are the main breeding areas from which migratory species like Eurasian wigeons and the Arctic Russian population of barnacle geese fly in large numbers to North Europe, will help to better elucidate the spatial spread of these strains (Figure 7).



**Figure 7.** Hypothetical spatial spread of the HPAI A(H5) strain based on the currently available genetic data. Data generated through discrete Bayesian phylogeographic analyses of the HA gene sequences performed in BEAST v10.4. The map shows the virus transmission dynamics into Europe (statistically supported non-zero rates with Bayes Factor >5). The lack of recent viral gene sequences, in particular from the South-West Asia and North Russia/Siberia, hampers an accurate reconstruction of the history of the spread (dashed arrows). The thickness of the arrows representing the rates is proportional to the relative strength by which rates are supported. On the top-left – maximum clade credibility (MCC) tree of the HA gene segment of clade 2.3.4.4b H5 viruses collected in Eurasia between 2016 and 2020. The colour of each branch indicates the geographic area where the analysed viruses were collected. Topology of the MCC tree identifies North Africa/South West Asia (green area) as the most likely origin of the virus identified in summer 2020 in Central Russia/Kazakhstan (red area). From Central

Russia/Kazakhstan or from an unsampled location in Russia the virus subsequently spread westward to North Europe (light blue and blue areas). We gratefully acknowledge the authors, originating and submitting laboratories of the sequences from GISAID's EpiFlu™ Database on which this analysis is based.

### 1.5. Human cases due to avian influenza A(H5N1), A(H5N2), A(H5N5) or A(H5N8) viruses detected in Europe

No human infection with avian influenza viruses described in this report, and currently detected in wild birds and poultry in Europe, has been reported so far. No virus genetic markers indicating adaptation to mammal receptor binding and increased risk of human transmission have been identified. A risk assessment on A(H5N8) is available from WHO stating that the likelihood of human infection with A(H5N8) virus is low (WHO, online).

## 2. Conclusions

- The risk of zoonotic transmission of avian influenza viruses to the general population in Europe remains very low. The evolution of the viruses and recent reassortment events need to be closely monitored in order to assess the ongoing risk of emerging reassorted viruses to transmit to humans.
- Given the low zoonotic potential of these viruses and the strict control measures implemented in poultry holdings related to HPAI viruses (Council Directive 2005/94/EC<sup>7</sup>), the risk of transmission to humans by eventually contaminated poultry products is considered negligible as outlined also in a previous EFSA assessment (EFSA AHAW Panel, 2017).
- Phylogenetic analysis of the currently circulating HPAI viruses shows that they were different from those that circulated in previous 2019-2020 season. The HA genes of all the identified subtypes belongs to a single genetic group within clade 2.3.4.4b, indicating a single progenitor virus with the highest similarity to North African/Middle Eastern/South-West Asian strains. The different genotypes likely emerged through reassortment events with LPAI viruses circulating in wild birds before arriving in Northern Europe, but the exact location where this occurred cannot be assessed from the currently available data.
- As the southward and westward movements of some waterbird species towards their wintering area continues as part of the autumn migration, there is a high risk of further introduction of HPAI A(H5) viruses to other European countries. The long-distance virus carriers are not known, but possible candidates might include barnacle geese and Eurasian wigeons, given their far eastern breeding range and high frequency of infection (based on the reported data).
- Once introduced into a European country, there is a high risk that HPAI A(H5) viruses can further spread in different directions due to shorter-distance movements of infected birds. Multiple species may be involved in this.
- Besides waterbirds, raptors and other carrion-eating birds are at risk of infection from feeding on contaminated bird carcasses. These species, in particular peregrine falcons and Eurasian buzzards, may be sensitive sentinels for the presence of HPAI A(H5) virus in the environment even when waterbird mortality is low and possibly below detection limit.
- The risk of further spread to unaffected areas via wild bird migrations (and by local movements of residential birds) is high and ongoing. Autumn migration from breeding and staging sites to wintering sites is ongoing and may depend on the weather conditions. The low temperatures of autumn and winter may facilitate the environmental survival of avian influenza viruses. Aggregation during autumn migrations, as well as the mixing of wild birds from different geographic origins during migration, will increase the risk of the infection spreading. Residential

<sup>7</sup> Council Directive 2005/94/EC of 20 December 2005 on Community measures for the control of avian influenza and repealing Directive 92/40/EEC.

infected wild birds (e.g. scavengers) are a sign of an already contaminated environment (e.g. Ireland) and may contribute to disease spread within their range.

- The risk of virus spread from wild birds to poultry is high; Member States should carefully evaluate, also by means of the assessment on avian influenza risk carried out at a national level, the option to enforce in 'high risk areas' of their territories the measures provided for in Commission Implementing Decision (EU) 2018/1136<sup>8</sup> to: i) adopt appropriate AI risk mitigating measures for outdoor poultry; ii) increase disease awareness among stakeholders, and their level of information on biosecurity; iii) strengthen biosecurity in poultry holdings (commercial and rural) with a focus to prevention/reduce the risk of direct/indirect contacts with wild birds; iv) reinforce AI early detection systems in poultry; v) adopt appropriate AI risk reduction measures for the use of decoy birds of the order *Ansariformes* and *Charadriiformes* and the release of poultry for restocking supplies of game birds; and vi) guarantee the collection and testing of dead/sick targeted species of wild birds (primarily ducks, geese, swans, gulls and birds of prey) at higher risk of AI.

### 3. Options for response

- Continued surveillance of avian influenza virus in wild birds and poultry in Europe, combined with timely generation and sharing of complete viral genome sequences are crucial. This will enable to follow virus evolution and to promptly detect the emergence of novel reassortant viruses, or of genetic mutations, resulting in changes in viral properties relevant for animal and public health.
- People should avoid touching sick or dead birds or bird droppings unprotected. Wearing personal protection equipment when directly exposed to birds, their products or droppings, which may potentially be infected or contaminated with avian influenza viruses will minimise any residual risk. National guidelines might detail the required level of protection and equipment.
- Characterised viruses so far have not shown markers for human adaptation and are assessed as having low risk for human transmission. However, the high genetic variability of the viruses identified and the multiple reassortment processes with local LPAI viruses, underlines the possibility of the emergence of viruses that might have increased potential to infect humans. Following the precautionary principle, people such as hunters, bird ringers, ornithologists or others handling wild birds or involved in processes like defeathering and preparing hunted wild birds should consider wearing personal protective equipment.
- People exposed unprotected to infected birds, e.g. during culling operations, should be actively monitored or at least self-monitor for respiratory symptoms or conjunctivitis for 10 days following exposure and immediately inform local health authorities to initiate testing and follow-up. Antiviral pre- or post-exposure prophylaxis should be considered for exposed people according to national recommendations.
- Member States should use the opportunity to test hunted birds or at least a proportion of them for avian influenza viruses at local laboratories.
- In local areas where avian influenza viruses have been detected in wild birds, human access should be regulated or restricted to avoid further dispersal of the virus.
- It should be considered to remove contaminated bird carcasses from those locations where high densities of wild birds congregate to feed or rest, or where there is a high risk of scavenging by raptors or other carrion-eating birds, in order to avoid extra risk of infection of wild birds. It is highly recommended to carry on this operation implementing all the available measures to avoid further dispersal of the virus in the environment.

<sup>8</sup> Commission Implementing Decision (EU) 2018/1136 of 10 August 2018 on risk mitigation and reinforced biosecurity measures and early detection systems in relation to the risks posed by wild birds for the transmission of highly pathogenic avian influenza viruses to poultry (notified under document C(2018) 5243).

- The observation in some affected areas of relatively high prevalence of HPAI A(H5) viruses in healthy wild waterfowl suggests that active surveillance can also be implemented, to increase the sensitivity of the avian influenza detection system. In addition to testing captured and hunted wild birds, faecal droppings and plumage swabs might be collected in target areas. In particular, targeted observations and testing waterfowl (e.g. geese, wigeons, mallard) should be carried out in bird sanctuaries/rehabilitation/rescue centres to evaluate local risk.
- Re-evaluation of risk assessments performed by Member States should take into account the local situation, particularly the presence and abundance of HPAI virus in wild birds in the area and other risk factors, such as the proximity to wet areas sites of wintering birds, for the introduction of HPAI viruses into establishments listed in the Commission Implementing Decision (EU) 2018/1136 of 10 August 2018.
- To improve early detection of infections in poultry, enhanced awareness of farmers to monitor and report increases in daily mortality and drops in production parameters (EFSA Opinion on Avian Influenza 2017) such as egg production and food and water intake are recommended. Circulating HPAI A(H5) viruses have been able to induce high mortality not only in gallinaceous poultry but also in anseriform poultry.
- Particular attention is warranted for the 0° C isotherm, which was shown to be associated with significantly higher frequency of HPAI A(H5) detection in wild birds both in the 2005-2006 and the 2016-2017 epidemics (Reperant et al., 2010; EFSA et al., 2017b), especially because some waterbird species choose to winter just south of the 0° C isotherm. Prediction of the 0° C isotherm up to several days in advance (available at various weather forecasting sites<sup>9</sup>) might be used to predict high risk period for potentially infected wild birds to further move and aggregate, facilitating the virus spread.
- Close cross-sectorial cooperation and communication between animal, public and occupational health authorities is recommended (One Health approach) to initiate rapid response and control measures.

<sup>9</sup> An example of website forecasting the 0° C isotherm is <https://www.theweatheroutlook.com/twodata/datmdlout.aspx> (click on 'Eur temp' button)

## Annex A – Data on wild bird

**Table A.1:** Wild birds species reported to ADNS as HPAI detection up to 19 November 2020, 12 pm

Category of wild bird species	Wild bird specie	Country from where the HPAI detection in the wild bird species where reported (NL: observed mortality in one week: 31 October to 6 November; raw data; source: working group AImpact2021)	Number of HPAI detections where the wild bird species was reported*	Total number of HPAI detections where the wild bird species was reported*
<b>Waterfowls</b>	Barnacle goose ( <i>Branta leucopsis</i> )	Denmark (n=9), Germany (n=95), Netherlands (n=6)	110	230
	Greylag goose ( <i>Anser anser</i> )	Denmark (n=1), Germany (n=34), Netherlands (n=10), United Kingdom (n=2)	47	
	Eurasian wigeon ( <i>Mareca penelope</i> )	Germany (n=27), Netherlands (n=4), United Kingdom (n=1)	32	
	Mallard ( <i>Anas platyrhynchos</i> )	Germany (n=11), Netherlands (n=3)	14	
	Mute swan ( <i>Cygnus olor</i> )	Belgium (n=1), Ireland (n=1), Netherlands (n=7), United Kingdom (n=1)	10	
	Bean goose ( <i>Anser fabalis</i> )	Germany (n=3), Netherlands (n=2)	5	
	Canada goose ( <i>Branta canadensis</i> )	Germany (n=1), United Kingdom (n=2)	3	
	Greater white-fronted goose ( <i>Anser albifrons</i> )	Belgium (n=1), Netherlands (n=1)	2	
	Cygnus sp	Germany (n=2)	2	
	Black swan ( <i>Cygnus atratus</i> )	United Kingdom (n=1)	1	
	Brent Goose ( <i>Branta bernicla</i> )	United Kingdom (n=1)	1	
	Common eider ( <i>Somateria mollissima</i> )	Germany (n=1)	1	
	Eurasian teal ( <i>Anas crecca</i> )	Germany (n=1), Netherlands (n=1)	2	
<b>Raptors</b>	Common buzzard ( <i>Buteo buteo</i> )	Denmark (n=3), Germany (n=7), Netherlands (n=3)	13	27
	Peregrine falcon ( <i>Falco peregrinus</i> )	Denmark (n=2), Germany (n=3), Ireland (n=1)	6	
	Eurasian sparrowhawk ( <i>Accipiter nisus</i> )	Denmark (n=1), Germany (n=1)	2	
	Accipitriformes	Germany (n=1)	1	
	Common kestrel ( <i>Falco tinnunculus</i> )	Germany (n=1)	1	
	Eurasian eagle-owl ( <i>Bubo bubo</i> )	Germany (n=1)	1	
	Falco sp	Germany (n=1)	1	
	Short-eared owl ( <i>Asio flammeus</i> )	Netherlands (n=1)	1	
	White-tailed eagle ( <i>Haliaeetus albicilla</i> )	Germany (n=1)	1	
<b>Other wild bird species</b>	Laridae	Germany (n=7)	7	27
	Numenius sp	Germany (n=6)	6	
	Curlew ( <i>Numenius arquata</i> )	Belgium (n=1), Ireland (n=1), Netherlands (n=1)	3	
	European herring gull ( <i>Larus argentatus</i> )	Germany (n=3)	3	
	Great black-backed gull ( <i>Larus marinus</i> )	Germany (n=3)	3	
	Black-headed gull ( <i>Chroicocephalus ridibundus</i> )	Germany (n=2)	2	
	Crane ( <i>Grus grus</i> )	Germany (n=1)	1	
	Eurasian oystercatcher ( <i>Haematopus ostralegus</i> )	Germany (n=1)	1	

	Great cormoran ( <i>Phalacrocorax carbo</i> )	Netherlands (n=1)	1	
<b>Unknown wild bird specie</b>	Unknown	United Kingdom (n=1)	1	1
<b>Total</b>				285

Data source: ADNS (19 Novembre, 12 pm).

\* Note that on one single reported detection of HPAI in wild birds more than one wild bird species can be

**Table A.2:** Seasonal movements to and from Russia and Belarus for Eurasian wigeon. This table shows where ringed birds present in Russia and Belarus between September and November have been found by country and month.

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
<b>Belgium</b>	1	2	4	.	.	.	.	.	.	.	1	1
<b>Denmark</b>	.	.	.	1	.	.	2	.	2	8	3	.
<b>Finland</b>	.	.	.	.	.	.	1	.	.	.	.	.
<b>France</b>	.	2	.	.	.	.	.	.	.	.	.	1
<b>Great Britain &amp; Ireland</b>	39	43	13	1	1	.	.	2	5	12	10	27
<b>Ireland</b>	2	1	.	.	.	.	.	.	.	1	.	.
<b>Italy</b>	1	.	.	.	.	.	.	.	.	.	2	.
<b>Sweden</b>	.	.	.	.	.	.	.	1	4	.	.	.
<b>Switzerland</b>	.	.	.	.	.	.	.	.	.	.	.	1
<b>The Netherlands</b>	53	39	19	4	.	.	.	2	5	41	86	68

**Table A.3:** Seasonal movements to and from Germany & Denmark for mallard (*Anas platyrhynchos*). This table shows where ringed birds present in Germany & Denmark between September and November have been found by country and month.



	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
Austria	.	.	.	.	.	1	.	.	.	.	1	.
Belarus	.	.	.	.	.	.	.	2	1	.	.	.
Belgium	24	10	7	2	2	2	10	16	10	9	12	33
Czech Republic	.	.	.	.	.	.	.	.	1	1	.	.
Denmark	631	432	289	184	197	1484	2521	1831	2147	1595	1146	417
Finland	.	.	1	3	12	16	30	131	53	16	2	1
France	49	15	5	.	.	.	1	.	2	3	16	20
Germany	154	154	41	11	33	123	173	142	57	45	78	87
Great Britain & Ireland	133	93	38	9	11	22	18	43	124	89	108	144
Hungary	.	.	.	.	.	.	.	.	.	.	1	.
Ireland	3	.	.	.	.	.	.	1	1	1	1	.
Italy	25	1	1	1	.	.	.	.	2	9	15	10
Kazakhstan	2	.	.	.	.	.	1	.	.	1	.	.
Latvia	.	.	1	.	6	9	1	.	2	.	.	.
Lithuania	.	.	.	.	.	2	12	4	.	1	.	.
Luxembourg	.	.	.	.	.	.	.	.	.	.	.	1
Norway	.	1	.	1	.	1	4	4	13	8	.	.
Poland	7	1	2	2	6	92	179	7	.	5	4	4
Portugal	2	.	.	.	.	.	.	.	.	.	.	1
Romania	.	1	.	.	.	.	.	.	1	.	.	2
Russian Federation	2	.	.	15	15	2	2	32	17	10	2	1
Spain	5	1	.	.	.	1	.	.	.	.	4	3
Sweden	28	21	21	11	39	85	110	117	129	139	95	48
Switzerland	10	6	1	1	1	3	2	3	1	.	2	7
The Netherlands	78	39	9	.	.	1	10	37	29	20	50	89
Ukraine	.	.	.	.	.	.	.	.	.	1	1	.

**Table A.4:** Observed mortality in the Netherlands in the week 31 October – 6 November (raw data).  
Data source: working group AImpact2021

Category of wild bird species	Wild bird species	Observed mortality in the Netherlands in the week 31 October – 6 November, raw data
<b>Waterfowls</b>	Barnacle goose ( <i>Branta leucopsis</i> )	314
	Eurasian wigeon ( <i>Mareca penelope</i> )	15
	Greylag goose ( <i>Anser anser</i> )	54
	Mallard ( <i>Anas platyrhynchos</i> )	8
	Mute swan ( <i>Cygnus olor</i> )	10
	Canada goose ( <i>Branta canadensis</i> )	6
	Greater white-fronted goose ( <i>Anser albifrons</i> )	6
	Cygnus sp	57
	Laridae	3
	Numenius sp	11
	European herring gull ( <i>Larus argentatus</i> )	2
	Great black-backed gull ( <i>Larus marinus</i> )	8
	Black-headed gull ( <i>Chroicocephalus ridibundus</i> )	20
	Great cormorant ( <i>Phalacrocorax carbo</i> )	5
<b>Raptors</b>	Peregrine falcon ( <i>Falco peregrinus</i> )	1
	Common buzzard ( <i>Buteo buteo</i> )	10
	Common kestrel ( <i>Falco tinnunculus</i> )	2
<b>Total</b>		532

## Annex B – Genetic data

**Table B.1:** Complete genome sequences of eight HPAI A(H5) viruses collected from wild and domestic birds available from GISAID EpiFlu database on 18 November

Country	Collecti on date	Species	EpiFlu accession numbers	H5N8	H5N5	H5N1	TOTAL
The Netherlands	16-17 Oct	Eurasian wigeon Mute swan	EPI1806856- EPI1806863 EPI1807236- EPI1807267	2		3	5
Germany	29-30 Oct	Barnacle goose Buzzard	EPI1811564- EPI1811579	1	1		2
United Kingdom	2 Nov	Chicken	EPI1811697- EPI1811704	1			1
Iraq	12 May	Chicken	EPI1811625- EPI1811632	1			1
The Russian Federation	31 July – 2 Oct	Chicken Goose Duck	EPI1811657- EPI1811696 EPI1812530- EPI1812537	4	2		6
Kazakhstan	19-23 Sept	Mute swan Domestic goose	EPI1811580- EPI1811581 EPI1811583- EPI1811588 EPI1811590- EPI1811623	5			5
<b>TOTAL</b>				14	3	3	20

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## Abbreviations

ADNS	Animal Disease Notification System
ECDC	European Centre for Disease Prevention and Control
EFSA	European Food Safety Authority
EEA	European Economic Area
EU	European Union
EURL	European Union Reference Laboratory
FAO	Food and Agriculture Organization
HPAI	Highly pathogenic avian influenza
LPAI	Low pathogenic avian influenza
WHO	World Health Organization