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Avian influenza overview September–December 2023

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Abstract

Between 2 September and 1 December 2023, highly pathogenic avian influenza (HPAI) A(H5) outbreaks were reported in domestic (88) and wild (175) birds across 23 countries in Europe. Compared to previous years, the increase in the number of HPAI virus detections in waterfowl has been delayed, possibly due to a later start of the autumn migration of several wild bird species. Common cranes were the most frequently affected species during this reporting period with mortality events being described in several European countries. Most HPAI outbreaks reported in poultry were primary outbreaks following the introduction of the virus by wild birds, with the exception of Hungary, where two clusters involving secondary spread occurred. HPAI viruses identified in Europe belonged to eleven different genotypes, seven of which were new. With regard to mammals, the serological survey conducted in all fur farms in Finland revealed 29 additional serologically positive farms during this reporting period. Wild mammals continued to be affected mostly in the Americas, from where further spread into wild birds and mammals in the Antarctic region was described for the first time. Since the last report and as of 1 December 2023, three fatal and one severe human A(H5N1) infection with clade 2.3.2.1c viruses have been reported by Cambodia, and one A(H9N2) infection was reported from China. No human infections related to the avian influenza detections in animals in fur farms in Finland have been reported, and human infections with avian influenza remain a rare event. The risk of infection with currently circulating avian H5 influenza viruses of clade 2.3.4.4b in Europe remains low for the general population in the EU/EEA. The risk of infection remains low to moderate for occupationally or otherwise exposed people to infected birds or mammals (wild or domesticated); this assessment covers different situations that depend on the level of exposure.

Keywords: avian influenza, captive birds, HPAI, humans, monitoring, poultry, wild birds

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[1] 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.

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1. Introduction

This Scientific Report provides an overview of highly pathogenic avian influenza (HPAI) virus detections in poultry[2], captive birds[3], wild birds and mammals that occurred in and outside Europe between 2 September and 1 December 2023, as well as human cases due to avian influenza viruses up until 1 December 2023.

The background, Terms of Reference and interpretation thereof are described in Appendix A, whereas the data and methodologies used are reported in Appendix B.

Scientific species names of wild birds and mammals mentioned in this report are listed in Table A.3 (Annex A) and Table 3, respectively.

2. Assessment

2.1 HPAI virus detections in birds

2.1.1 HPAI virus detections in birds in Europe

Figure 1 shows all HPAI outbreaks in birds that were reported via the European Union (EU) Animal Disease Information System (ADIS) or the World Organisation for Animal Health (WOAH) World Animal Health Information System (WOAH-WAHIS) in Europe for the last seven and the current epidemiological years[4] by month of suspicion. For the current epidemiological year 2023–2024, starting on 1 October 2023, data reported are truncated on 1 December 2023.

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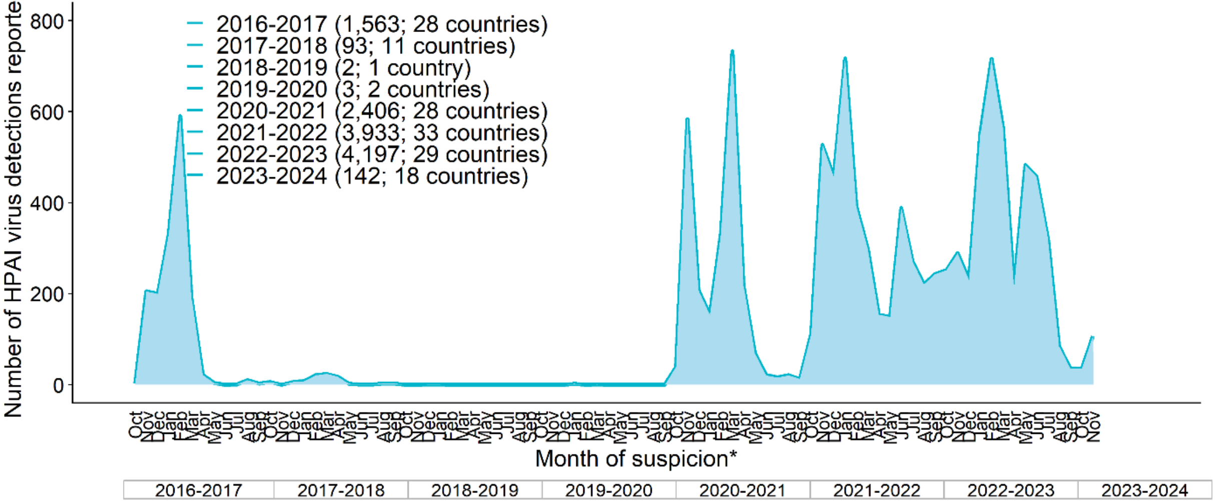
[2] According to Regulation (EU) 2016/429 of the European Parliament and of the Council of 9 March 2016, point (9), 'poultry' means birds that are reared or kept in captivity for: (a) the production of: (i) meat; (ii) eggs for consumption; (iii) other products; (b) restocking supplies of game birds; (c) the purpose of breeding of birds used for the types of production referred to in points (a) and (b).

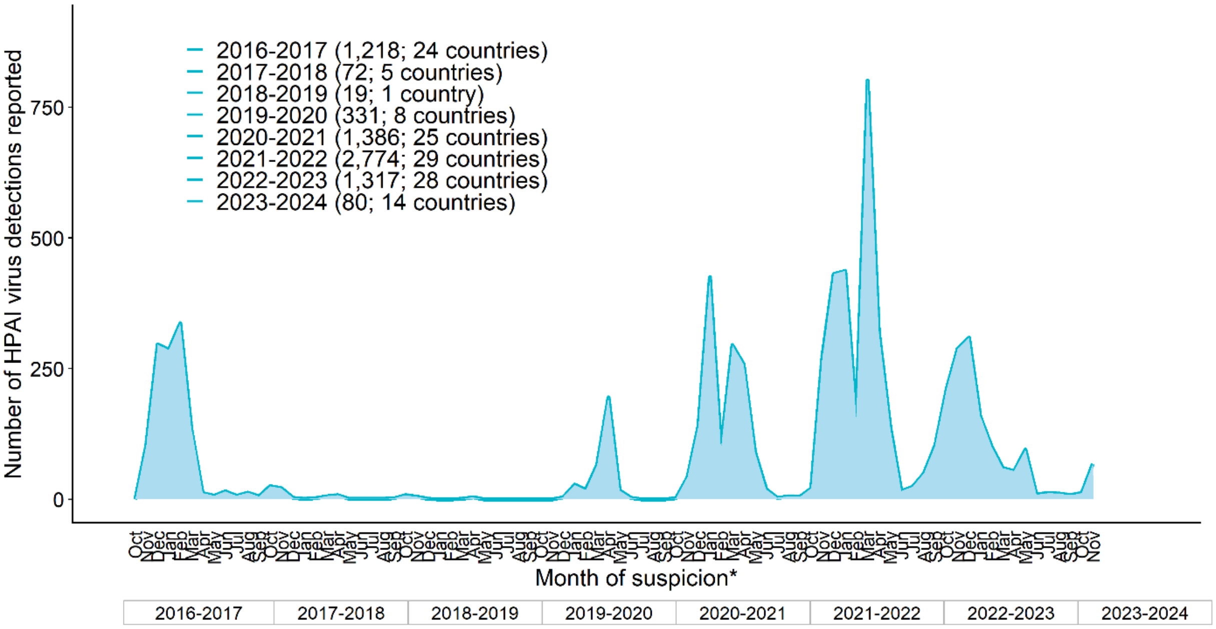
[3] According to Regulation (EU) 2016/429 of the European Parliament and of the Council of 9 March 2016, point (10), 'captive birds' means any birds other than poultry that are kept in captivity for any reason other than those referred to in point (9), including those that are kept for shows, races, exhibitions, competitions, breeding or selling.

[4] In this document an 'epidemiological year' refers to the period starting in week 40 (the beginning of October) and ending in week 39 (the end of September) of the following year, based on the dates on which the first HPAI virus detections were observed in wild birds in Europe in 2016–2017, 2020–2021 and 2021–2022.

(a) Wild birds



(b) Domestic birds



*If the date of suspicion was not available, the date of confirmation was used to assign the week of suspicion. United Kingdom data are from the Animal Disease Notification System (ADNS, former ADIS) up until 31 December 2020. From 1 January 2021 onwards, the data source was WOAH for the United Kingdom (excluding Northern Ireland) and ADNS/ADIS for the United Kingdom (Northern Ireland)[5].
Source: ADNS/ADIS and WOAH (data extraction carried out on 1 December 2023).

Figure 1: Distribution of the number of HPAI virus detections in wild (12,339) (a) and domestic (7,197) (b) birds reported in Europe during eight epidemiological years by month of suspicion, from 1 October 2016 to 1 December 2023 (19,536)

After a decline in HPAI virus detections during summer (July–September) 2023, particularly in domestic birds, the number of HPAI virus detections in both domestic and wild birds began to rise again steeply at the end of October 2023, a few weeks after the start of the new epidemiological year. This rise in HPAI virus detections occurred later than in 2022 and 2021 (Figure A.3 in Annex A), and is expected to continue in the coming weeks. The later rise in HPAI virus detections in wild birds may be due to a later autumn migration of several wild waterbird species following a relatively warm autumn period (Reperant et al.,

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[5] In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Protocol on IE/NI, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).

2010). For example, autumn migration of Eurasian wigeons to the Netherlands peaked about 2–3 weeks later in 2023 than in the previous three years, based on citizen science data from waarneming.nl.

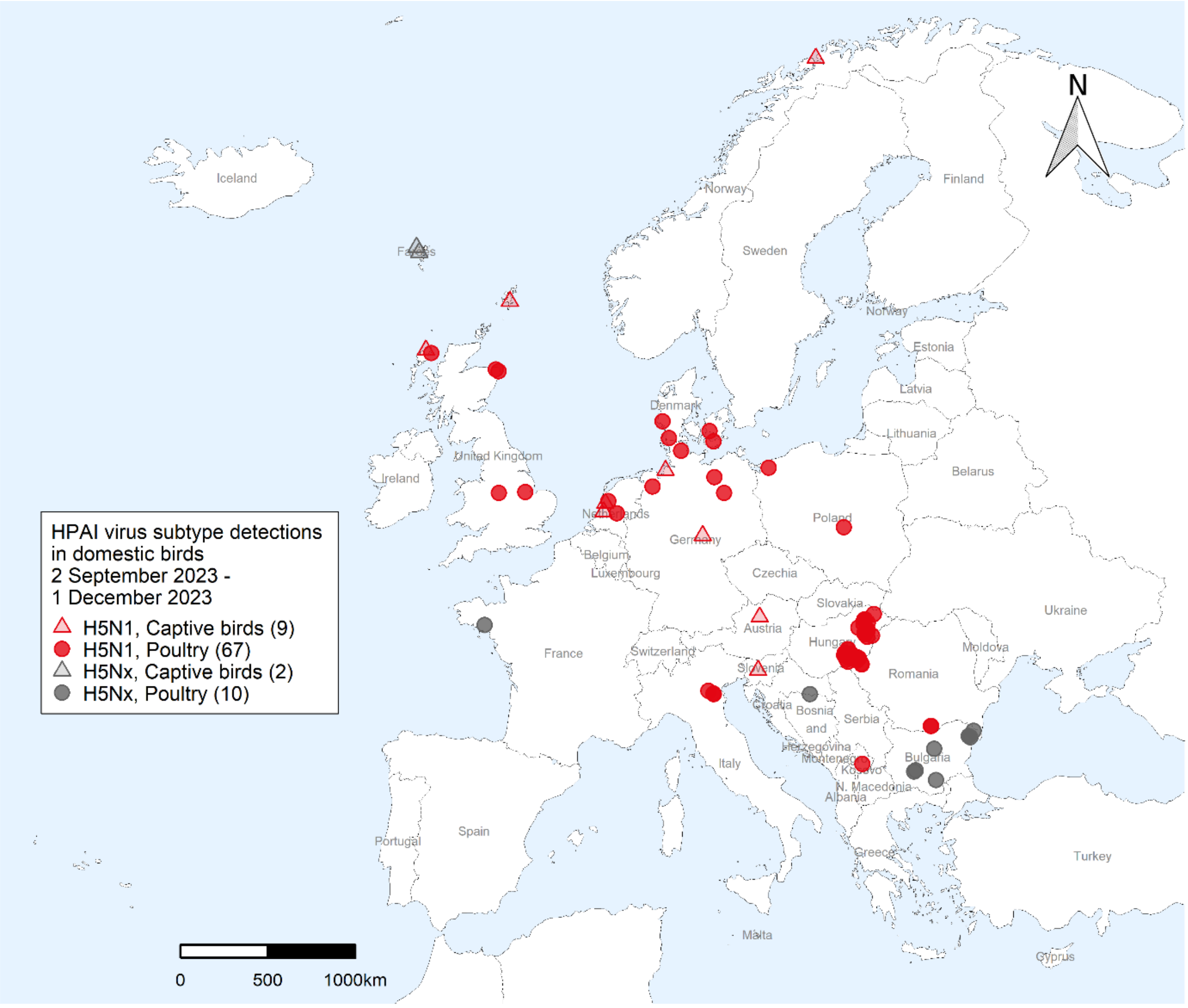
The HPAI epidemic observed in the 2022–2023 epidemiological year surpassed the previous epidemiological year (2021–2022) in terms of total number of HPAI virus detections reported in wild birds (4,197 vs 3,933), whereas a lower number of domestic birds (1,317 vs 2,774) were affected by HPAI viruses in the 2022–2023 epidemiological year (Figure 1, Table 1).

Table 1: Number of HPAI outbreaks reported in Europe, by country, virus subtype and affected sub-population, from 2 September to 1 December 2023. Cumulative numbers since the start of the 2023–2024 epidemiological year are reported in parentheses (1 October to 1 December 2023)

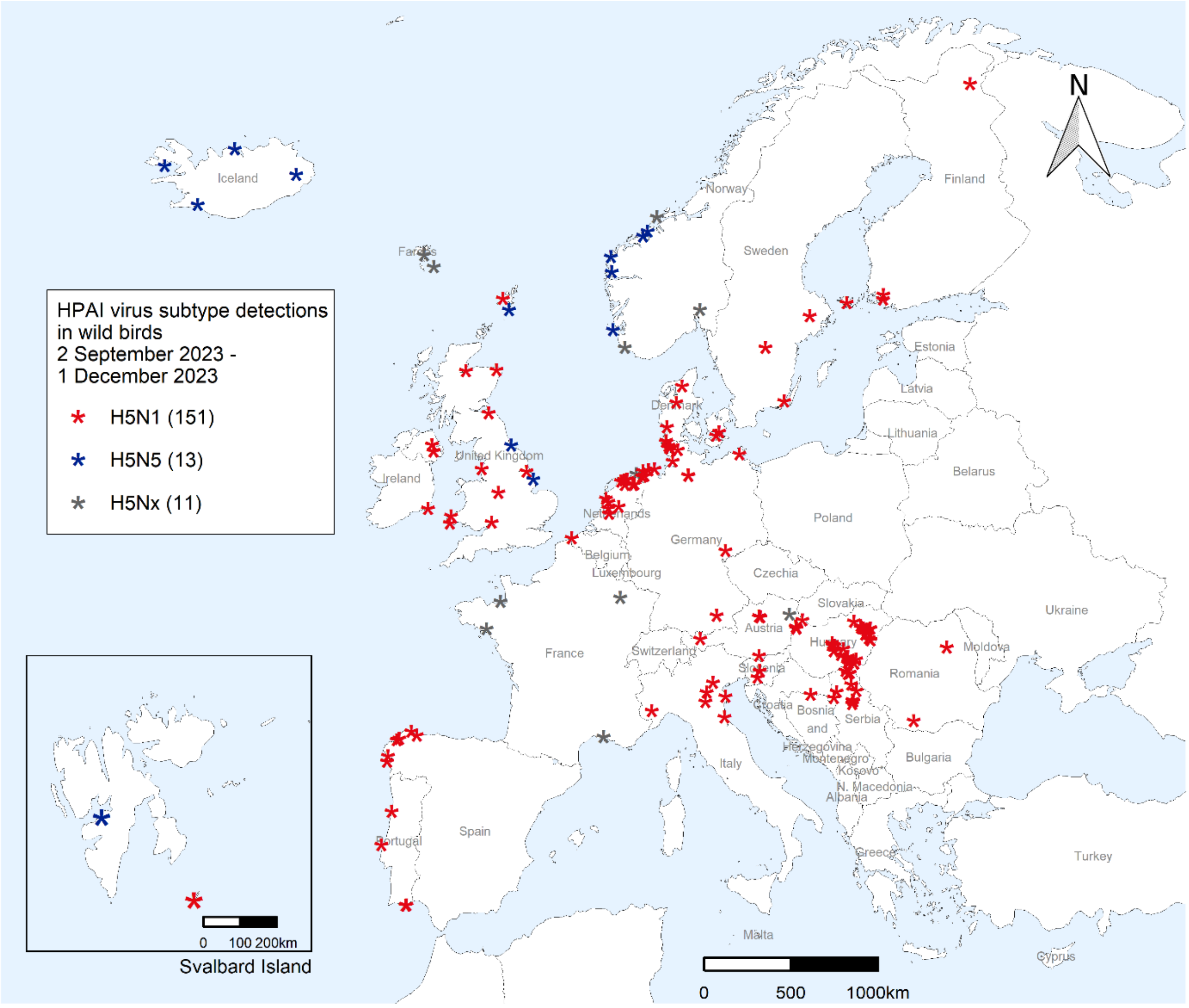
Reporting country	**Captive birds**		**Poultry**		**Wild birds**			**Total**
	H5Nx	H5N1	H5Nx	H5N1	H5Nx	H5N5	H5N1	
Austria	-	1 (1)	-	-	1 (1)	-	10 (10)	12 (12)
Belgium	-	-	-	-	-	-	1	1 (0)
Bulgaria	-	-	8 (8)	-	-	-	-	8 (8)
Croatia	-	-	1 (1)	-	-	-	1 (1)	2 (2)
Denmark	2 (1)	-	-	4 (3)	2	-	5 (3)	13 (7)
Finland	-	-	-	-	-	-	4 (2)	4 (2)
France	-	-	1 (1)	-	4 (4)	-	-	5 (5)
Germany	-	2 (2)	-	4 (4)	1 (1)	-	27 (20)	34 (27)
Hungary	-	-	-	43 (43)	-	-	35 (34)	78 (77)
Iceland	-	-	-	-	-	4 (2)	-	4 (2)
Ireland	-	-	-	-	-	-	1	1 (0)
Italy	-	-	-	4 (4)	-	-	7 (7)	11 (11)
Kosovo[*]	-	-	-	1 (1)	-	-	-	1 (1)
Netherlands	-	2 (2)	-	2 (2)	-	-	12 (12)	16 (16)
Norway	-	1 (1)	-	-	3 (3)	6 (3)	1	11 (7)
Poland	-	-	-	2 (2)	-	-	-	2 (2)
Portugal	-	-	-	-	-	-	4 (4)	4 (4)
Romania	-	-	-	2 (2)	-	-	7 (7)	9 (9)
Serbia	-	-	-	-	-	-	10 (9)	10 (9)
Slovenia	-	1	-	-	-	-	3 (1)	4 (1)
Spain	-	-	-	-	-	-	6 (6)	6 (6)
Sweden	-	-	-	-	-	-	3 (3)	3 (3)
United Kingdom	-	2	-	5 (2)	-	3 (1)	14 (8)	24 (11)
Total	**2 (1)**	**9 (6)**	**10 (10)**	**67 (63)**	**11 (9)**	**13 (6)**	**151 (127)**	**263 (222)**

[*] 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.

Considering the current reporting period, from 2 September to 1 December 2023, 263 HPAI virus detections were reported in poultry (77), captive (11) and wild birds (175) (Table 1, Figure 2).



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 01/12/2023



Author: EFSA
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Date updated: 01/12/2023

*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.
United Kingdom data are from ADNS up until 31 December 2020. From 1 January 2021 onwards, the data source was WOAH for the United Kingdom (excluding Northern Ireland) and ADNS/ADIS for the United Kingdom (Northern Ireland)[6].
Source: ADIS, EFSA and WOAH (data extraction carried out on 1 December 2023).

Figure 2: Geographic distribution, based on available geocoordinates, of HPAI virus detections in poultry and captive birds (88) (upper panel), and in wild birds (175) (lower panel) reported by virus subtype in Europe from 2 September to 1 December 2023

HPAI virus detections in domestic birds (poultry and captive birds) occurred in a northwest–southeast orientation in large parts of Europe, with the exception of the Iberian Peninsula and the majority of Scandinavia. In all of those detections, HPAI A(H5) viruses were identified. Two clusters of HPAI virus detections in poultry were present in the south and east of Hungary, which overlapped with clusters of detections in wild birds in the same areas. Almost all (151 out of 175) HPAI virus detections in wild birds were due to A(H5N1) viruses, whereas 13 detections in Iceland and along the British and Norwegian coastlines, including the Svalbard Islands, were attributed to A(H5N5) viruses. A(H5Nx) viruses were identified in another 11 detections. Dynamics of the A(H5N5) subtype, which had only occurred in Norway (and once in Finland) since the 2021–2022 epidemiological year up until

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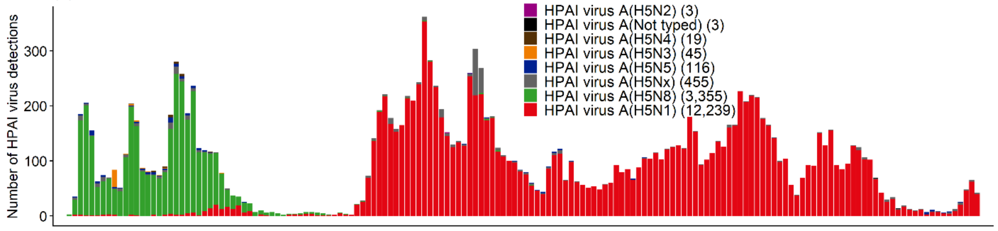
[6] In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Protocol on IE/NI, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).

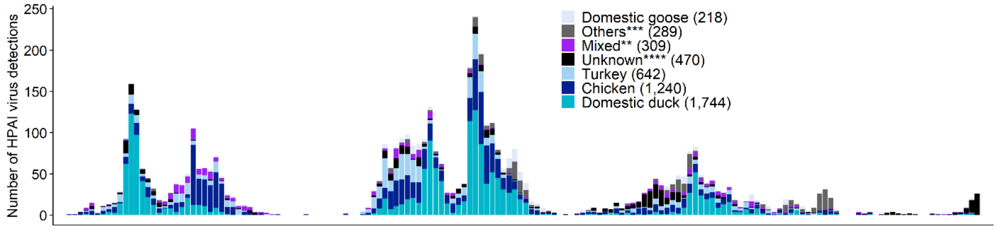
this reporting period, appear to be separate from the dynamics of other HPAI viruses in terms of geographical expansion. During this reporting period, also Portugal reported HPAI virus detections in wild birds after many months of absence. At the European level, HPAI virus detections in wild birds still occurred along coastlines, as described in the previous report (EFSA, ECDC and EURL, 2023), but they were increasingly found also inland, particularly in southern and central Europe.

The low number of HPAI virus detections reported in colony-breeding seabirds at the end of the previous reporting period, coinciding with their dispersal from breeding sites, continued in the current reporting period (Figure 3). However, from the second half of October 2023, there has been an increasing number of HPAI virus detections reported in waterfowl and the 'other' wild bird categories (mostly common cranes), coinciding with their autumn migration and arrival at wintering and/or stopover sites in Europe (Figure 3).

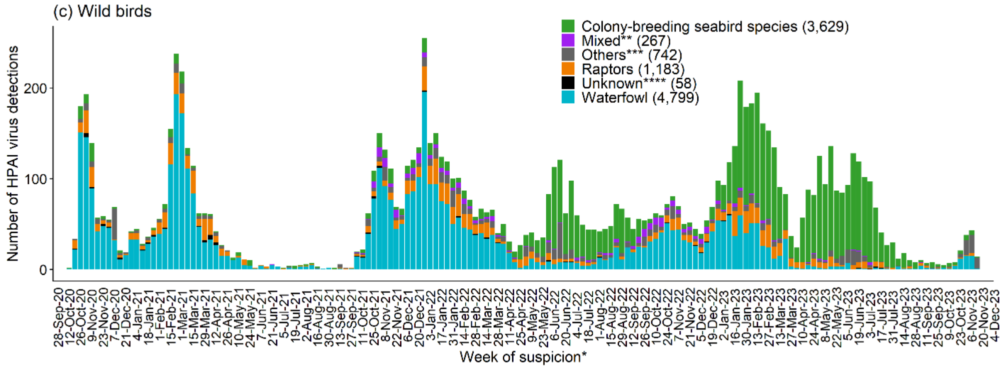
(a) All birds



(b) Poultry



(c) Wild birds



United Kingdom data are from ADNS up until 31 December 2020. From 1 January 2021 onwards, the data source was WOAH for the United Kingdom (excluding Northern Ireland) and ADNS/ADIS for the United Kingdom (Northern Ireland)[7].
*If the date of suspicion was not available, the date of confirmation was used to assign the week of suspicion.
**'Mixed' refers to outbreaks in which multiple species or categories were involved.
***'Others' groups all other affected categories that are not indicated in the legend.
****'Unknown' refers to affected categories that were not further specified during reporting.
Source: ADNS/ADIS, EFSA and WOAH (data extraction carried out on 1 December 2023).

Figure 3: Distribution of the total number of HPAI virus detections reported in Europe by week of suspicion (dates indicate the first day of the week) and virus subtype (16,235) (a), affected poultry categories (4,912) (b) and affected wild bird categories (10,678) (c), from 1 October 2020 to 1 December 2023

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[7] In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Protocol on IE/NI, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).

As of 13 December 2023, 43 HPAI virus detections have been notified to ADIS since the end of the current reporting period (after 1 December 2023). Of those, 18 have been reported in poultry in Hungary (7), France (4), Germany (3), Poland (2), Belgium (1) and the Netherlands (1); 1 in captive birds in Slovakia (1); and 24 in wild birds in the Netherlands (8), Germany (5), Italy (5), Denmark (2), Sweden (2), Austria (1) and Belgium (1).

Spatio-temporal information on all HPAI virus detections reported in Europe since October 2016 is available via EFSA's interactive dashboard[8].

Domestic birds

HPAI outbreaks in poultry were all identified as HPAI A(H5) and reported in Hungary (43), Bulgaria (8), the United Kingdom (5), Denmark (4), Germany (4), Italy (4), the Netherlands (2), Poland (2), Romania (2), Croatia (1), France (1) and Kosovo[9] (1) (Table 1, Figure 4). Overall, more than 2.5 million birds died or were culled in the HPAI-affected poultry establishments with Bulgaria accounting for 49% of the birds that died or were culled (corresponding to 10% of the affected establishments) (Figure 4).

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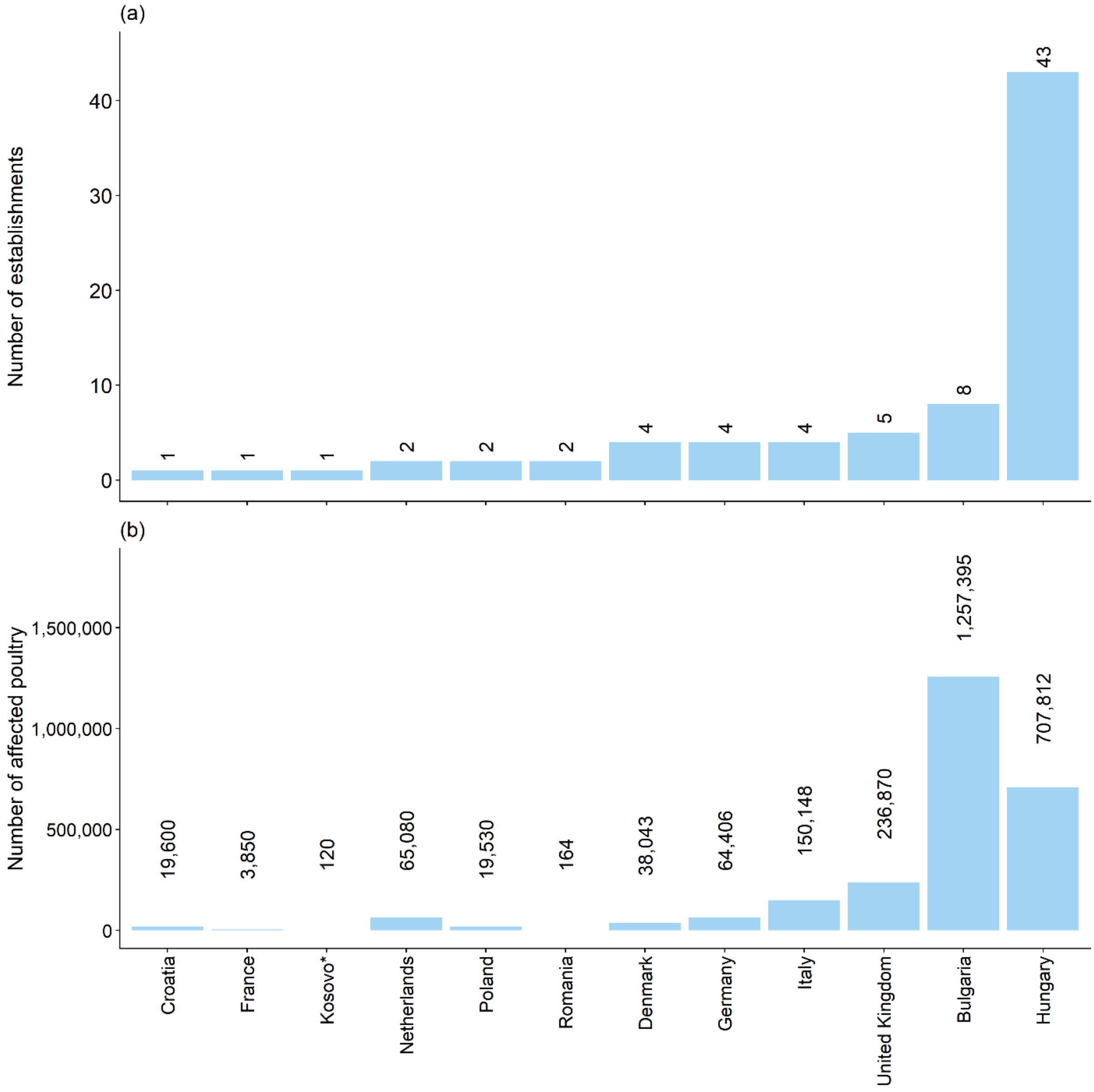
[8] http://hpai.efsa.aus.vet/

[9] 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.



The number of affected poultry for Croatia was later corrected to 19,497, leading to a total number of 2,562,915 poultry in the HPAI-affected establishments.

Figure 4: Number of HPAI-affected establishments (77) (a) and number of poultry in the HPAI-affected establishments (2,563,018) (b) in Europe between 2 September and 1 December 2023

In the following, a brief description of HPAI outbreaks in poultry is given by country. This description is based on information collected by EFSA from ADIS, WOAH-WAHIS, reporting countries (in form of additional data submitted and personal communications) and media reports. In the time period 2 September to 1 December 2023, 77 HPAI outbreaks in poultry were reported in Europe via ADIS. Additional data (see Appendix B) on poultry outbreaks occurred during this reporting period were collected for 23 of those 77 outbreaks from Bulgaria, Denmark, Hungary, Kosovo*, the Netherlands, Norway, Poland and Romania. Those data on the characteristics of the affected poultry establishments and poultry species reared are presented in Annex B. The remaining 54 outbreaks in poultry occurred too close to the time of production of this report, which is why additional data on those outbreaks will only be collected from reporting countries for the next report.

Bulgaria

During the current reporting period from 2 September to 1 December 2023, 8 outbreaks in poultry were reported in Bulgaria via ADIS. Seven of those 8 outbreaks occurred in commercial establishments rearing laying hens, whereas one outbreak occurred in a commercial establishment keeping Pekin ducks for breeding. Outdoor access for birds was not provided by any of the 8 establishments. For all 8 outbreaks, the most likely source of introduction was unknown. An epidemiological link between two technologically connected establishments located in Dobrich region was reported. Increased mortality was observed in 7 of the 8 establishments, but for all 8 outbreaks, the presence of clinical signs was unknown. Information on the number of exposed people was only available for 4 of the 8 outbreaks. Twenty-one people were reported as exposed.

Croatia

During the current reporting period from 2 September to 1 December 2023, 1 primary outbreak in poultry was reported in Croatia via ADIS. HPAI A(H5N1) virus was detected in a commercial establishment keeping turkeys for fattening (n = 19,497) in mid-November. The establishment did not provide outdoor access for birds. Increased mortality and clinical signs (lack of appetite, decreased food and water intake, and decreased activity) were observed. Dead wild birds and waterbodies in the vicinity of the establishment were indicated as possible source of infection. No information on the number of exposed people was available at the time of production of this report.

Denmark

During the current reporting period from 2 September to 1 December 2023, 4 outbreaks in poultry were reported in Denmark via ADIS. At the end of September 2023, an HPAI A(H5N1) outbreak was confirmed in a non-commercial establishment housing laying hens and ducks (n = 43) which had outdoor access. Direct contact with wild birds was the most likely source of introduction. Another outbreak occurred in a commercial turkey establishment (n = 33,000) at the beginning of November, in which 900 birds had died before culling. Information on the most likely source of introduction and number of exposed people for this outbreak was unknown at the time of production of this report. In mid-November, HPAI A(H5N1) virus was detected in an organic free-range establishment (n = 2,300) rearing laying hens in mobile homes, broilers, geese, turkeys, pigs and sheep. The establishment also owned a small slaughterhouse on its premises for which control measures applied. The slaughterhouse sourced animals only from the same and a neighboring establishment, and supplied products only to the local Danish market. Clinical signs and increased mortality were only observed in laying hens. Other poultry species as well as the pigs tested negative (European Commission, online). One week later, another outbreak was detected in an establishment rearing pheasants (n = 2,700), in which 300 birds died and the remainder were culled. This establishment was close to the Wadden Sea and major wild bird flyways. Introduction of the virus by wild birds was the most probable source of introduction for these two establishments (Eriksen, online).

France

During the current reporting period from 2 September to 1 December 2023, 1 primary outbreak in poultry was reported in France via ADIS. The outbreak occurred in a commercial establishment keeping 3,850 turkeys for fattening in the Brittany region at the end of November. Birds had no outdoor access. A drop in feed and water intake associated with an increase in mortality triggered a suspicion report on 26 November: reported daily mortality was less than 10 birds at that point in time. The affected poultry appeared lethargic and silent, while a few birds also showed neurological signs. Pathological findings in dead birds included non-specific congestion and hemorrhages, hepatomegaly, splenomegaly, pericarditis and limited aerosacculitis. The HPAI A(H5N1) virus identified from this poultry outbreak belonged to the BB genotype, which had also been extensively detected in infected wild birds before summer 2023 and was more recently associated with several sporadic detections in dead wild birds (mostly gull species) along the northern French coastline since July 2023. Given the available information, the most likely source for the poultry outbreak would appear to be indirect introduction from the contaminated environment into the establishment. No information on the number of exposed people was available at the time of production of this report. Since the beginning of October 2023, preventive vaccination against HPAI A(H5) viruses in poultry is being implemented in France (mainland territory, excluding Corsica) and is planned to be performed all year round. Vaccination of ducks (Pekin, Muscovy and Mulard ducks) is compulsory, at the production stage, for all poultry establishments keeping more than 250 birds; establishments keeping breeding ducks may implement vaccination only if all their products (hatching eggs and day-old ducklings) are intended for the French domestic market. Vaccination is forbidden for all other domestic ducks and all other poultry species (GOVFR, online-a). By 19 November 2023, more than 6.8 million domestic ducks had already been vaccinated: the most prominent regions for duck production in France (Pays-de-la-Loire, Nouvelle-Aquitaine, Occitanie and Britanny, all situated in western France) were accounting for more than 94% of this total (GOVFR, online-b). Compliant with Commission Delegated Regulation (EU) 2023/361[10], active surveillance (virological testing of 60 vaccinated ducks every 30 days) and enhanced passive surveillance (virological testing of a weekly sample of collected dead vaccinated birds) is implemented in all establishments keeping vaccinated ducks: no HPAI virus circulation has been detected so far.

Germany

During the current reporting period from 2 September to 1 December 2023, 4 outbreaks in poultry were reported in Germany via ADIS. Three of the 4 outbreaks occurred in commercial establishments rearing turkeys for fattening, whereas one outbreak affected a commercial free-range establishment rearing laying hens. The latter was the only establishment for which both clinical signs and an increase in mortality were reported. For the other three outbreaks, an increase in mortality but the absence of specific clinical signs were reported. Information on the most likely source of introduction or number of exposed people was not available for any of the outbreaks at the time of production of this report.

Hungary

During the current reporting period from 2 September to 1 December 2023, 43 outbreaks in poultry were reported in Hungary via ADIS. The majority of the 43 outbreaks were secondary (n = 36), and almost all of them (n = 40) occurred in commercial establishments. All those commercial establishments were mono-species establishments keeping ducks (9) or geese (4) for foie gras production, ducks (5), geese (2) or turkeys (3) for fattening, ducks (2), geese (7), turkeys (3) or hens (1) for breeding, and broilers (4). For the 3 non-commercial establishments, the poultry species kept were unknown. Of the 10 outbreaks for

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[10] Commission Delegated Regulation (EU) 2023/361 of 28 November 2022 supplementing Regulation (EU) 2016/429 of the European Parliament and the Council as regards rules for the use of certain veterinary medicinal products for the purpose of prevention and control of certain listed diseases. OJ L 52, 20.2.2023, p. 1–42.

which additional information was available (raising ducks, geese, turkeys and broilers), 2 establishments keeping geese provided outdoor access. Dead common cranes infected with HPAI viruses were found around 9 of those establishments. The most likely source of introduction was indirect contact with wild birds. As the last establishment was located close to a primary outbreak, the most likely source of introduction was indirect contact with poultry. In 9 of the 10 outbreaks for which additional information was available, an increase in mortality was reported, and in 6 of those 9, also clinical signs were observed. Comparable information was not available for the other 33 outbreaks, as they were too close to the time of production of this report. No information on the number of exposed people was available for all 43 outbreaks at the time of production of this report.

Italy

During the current reporting period from 2 September to 1 December 2023, 4 outbreaks in poultry were reported in Italy via ADIS, all of them in the Veneto region. The first 3 outbreaks were confirmed within 3 days in mid-November in poultry establishments located in the same municipality in the province of Padua. The establishments involved were a commercial establishment housing turkeys for fattening (n = 21,500, of which 18,995 alive on the day of suspicion), an establishment housing guineafowl for fattening (n= 18,600, of which 17,256 alive) and an establishment rearing broiler chickens (n = 150,250, of which 85,592 alive). The fourth outbreak was detected in the last week of November in an establishment housing turkeys for fattening located in the province of Verona (n = 14,000, of which 13,392 alive). The first HPAI virus detection in wild birds in Italy was confirmed at the beginning of November, 50 km away from the first poultry outbreak. Increased mortality and clinical signs (neurological signs and reduced feed and water intake) were observed in turkeys. Only a slight increase in mortality was observed in guineafowl and none in broilers, for which HPAI viruses were only detected at the time of testing for pre-movement to the slaughterhouse. Environmental samples taken from the surface of feeders, drinkers and air fans in the broiler establishment one day after the official confirmation were negative to virological tests. No information on the number of exposed people was available at the time of production of this report. Phylogenetic analysis of the viruses involved in those poultry outbreaks showed that they belonged to a new variant of A(H5N1) virus, which likely originated through multiple reassortments among European HPAI and low pathogenic avian influenza (LPAI) viruses (genotype DA). These viruses show a high similarity to A(H5N1) viruses that have been isolated from the HPAI outbreaks in wild birds in the Veneto region since November. These results, together with findings of the epidemiological investigations, suggest that the most likely source of introduction into poultry establishments was indirect contact with wild birds. However, given the high genetic similarity of the viruses detected in the first three outbreaks in the province of Padua, secondary spread among those establishments cannot be completely excluded.

Kosovo[11]*

During the current reporting period from 2 September to 1 December 2023, 1 outbreak in poultry was reported in Kosovo[11] via ADIS. The outbreak occurred in a non-commercial establishment keeping chickens, geese, ducks and turkeys (n = 200). The establishment provided outdoor access for birds and the most likely source of introduction was unknown. Increased mortality and clinical signs such as drop in egg production, and drop in feed and

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[11] 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.

water intake were reported. No information on the number of exposed people was available at the time of production of this report.

The Netherlands

During the current reporting period from 2 September to 1 December 2023, 2 outbreaks in poultry were reported in the Netherlands via ADIS. One of the affected establishments was a care farm keeping 180 birds, for which increased mortality (sudden death of 6 chickens) and clinical signs were reported. The second outbreak occurred in a laying hen establishment (n = 64,000), in which increased mortality and a drop in feed and water intake were observed. Affected hens appeared drowsy, limp and stood with their eyes closed (European Commission, online). Genetic analysis of the virus identified a new variant of A(H5N1) virus containing gene segments derived from an LPAI virus. No information on the most likely source of introduction or number of exposed people was available at the time of production of this report.

Poland

During the current reporting period from 2 September to 1 December 2023, 2 outbreaks in poultry were reported in Poland via ADIS. The first outbreak occurred at the beginning of October in a laying hen establishment (n = 19,450), in which increased mortality and the occurrence of clinical signs were observed. The number of exposed people was 2. Genomic analysis showed that the virus involved was closely related to the A(H5N1) viruses found in a white stork and a non-commercial establishment in June 2023. Although the farm did not provide outdoor access, the most likely source of introduction was indirect contact with wild birds. A week later, HPAI virus was again detected in a non-commercial farm keeping laying hens, ducks, pigeons and pheasants. Genomic analysis and the presence of outdoor access led to the conclusion that the most likely source of infection was wild birds. Five people were reported as exposed.

Romania

During the current reporting period from 2 September to 1 December 2023, 2 outbreaks in poultry were reported in Romania via ADIS. The first outbreak occurred in a non-commercial establishment keeping chickens, ducks, turkeys and geese (n = 120). This establishment provided outdoor access and the most likely source of introduction was direct or indirect contact with wild birds. One week later, another outbreak was confirmed in a neighboring non-commercial establishment keeping ducks and chickens (n = 44). This outbreak was considered secondary, as there was an epidemiological link to the first affected establishment. Clinical signs and increased mortality were observed in both establishments. For both outbreaks, the number of exposed people was 1.

United Kingdom

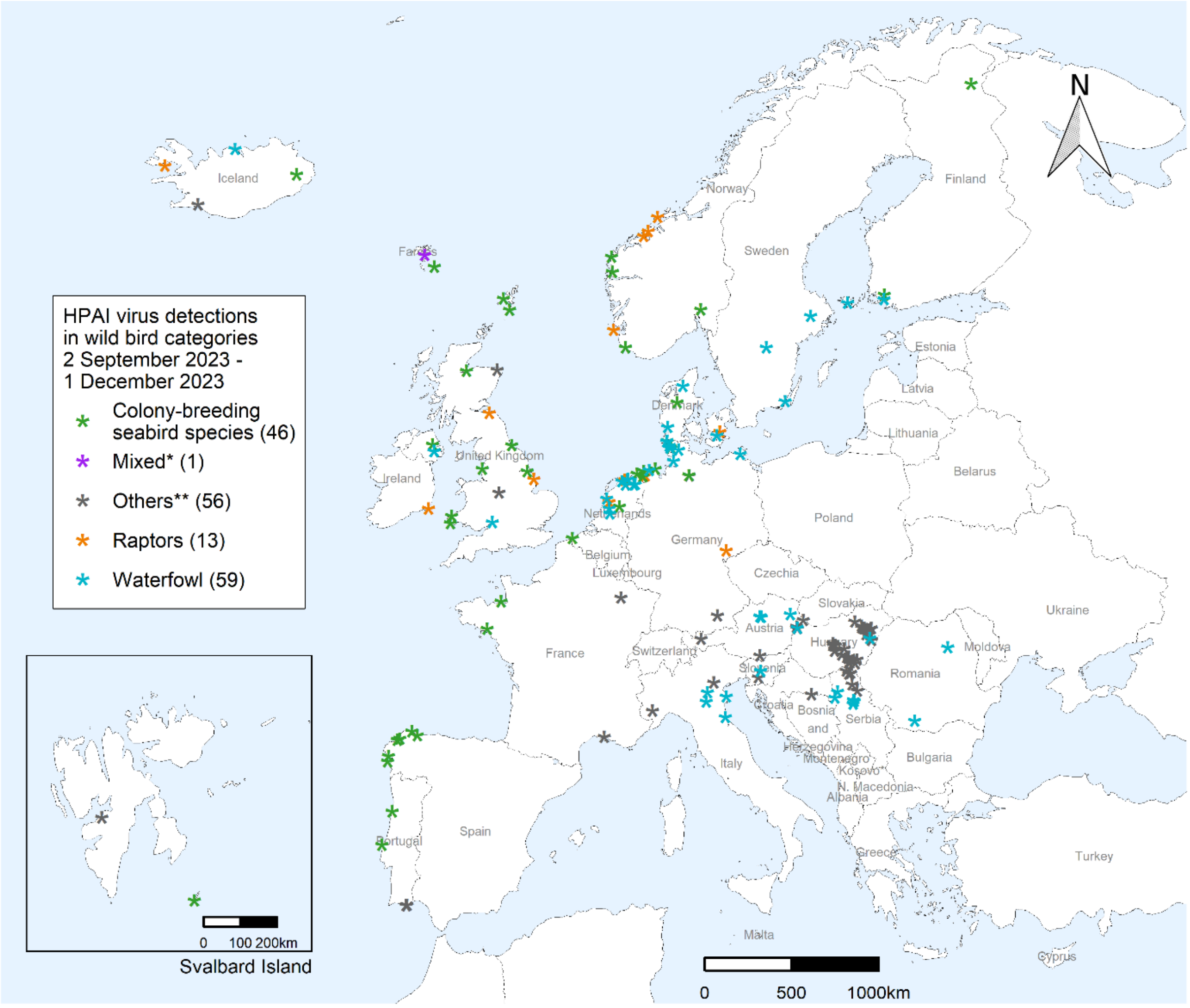
During the current reporting period from 2 September to 1 December 2023, 5 outbreaks in poultry were reported in the United Kingdom via WOAH-WAHIS. Three of those outbreaks occurred in Scotland (1 commercial establishment rearing 221,000 laying hens; 2 non-commercial establishments housing 10 chickens and 4 geese, and 15 chickens, respectively) and 2 in England (2 commercial establishments housing 1,400 pheasants for game purposes and 14,000 turkeys, respectively) (GovUK, online, a). Additional outbreaks (not yet notified via WOAH by 1 December 2023) in commercial establishments rearing pheasants for game purposes (n = 1,300), broiler breeders (n = 30,000) and ducks (n = 3,500) were confirmed in England at the end of November 2023. No information on the presence of outdoor access, the most likely source of introduction or the number of exposed people was available at the time of production of this report.

HPAI virus detections in captive birds, all due to A(H5) viruses, were reported in Denmark (Faroe Islands) (2), Germany (2), the Netherlands (2), the United Kingdom (2), Austria (1), Norway (1) and Slovenia (1) (Figure 2, Table 1).

In Austria, the outbreak involved a dead grey crowned crane in a zoo (Noen, online). In the Netherlands, one of the outbreaks in captive birds occurred in a petting farm keeping poultry as well as finches and parakeets. In Norway, the outbreak occurred in a non-commercial establishment keeping chickens (n = 19). The birds had outdoor access and the most likely source of introduction was direct contact with wild birds. Increased mortality and the presence of clinical signs were reported. The number of exposed people was 6. The outbreak was handled in accordance with the regulations.

Wild birds

During the time period 2 September to 1 December 2023, a total of 151 A(H5N1), 13 A(H5N5) and 11 A(H5Nx) virus detections were reported in Hungary (35), Germany (28), the United Kingdom (17), the Netherlands (12), Austria (11), Norway (10), Serbia (10), Denmark (including Faroe Islands) (7), Italy (7), Romania (7), Spain (6), Finland (4), France (4), Iceland (4), Portugal (4), Slovenia (3), Sweden (3), Belgium (1), Croatia (1) and Ireland (1) (Figure 2, Figure 5, Table 1).



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 01/12/2023

[*] 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.
Note that the unit reported is the number of HPAI virus detections in different wild bird categories and not the number of HPAI virus detections in wild birds (as more than one species can be involved in one single HPAI virus detection reported).
[*] ‘Mixed’ refers to outbreaks in which multiple categories were involved.
[**] ‘Others’ groups all other affected categories that are not indicated in the legend.
Source: ADIS, EFSA and WOAH (data extraction carried out on 1 December 2023).

Figure 5: Geographic distribution, based on available geocoordinates, of HPAI virus detections in different categories of wild birds in Europe, by species category, from 2 September to 1 December 2023

The overall picture of HPAI in wild birds during this reporting period was characterised by four distinct aspects. First, the high rate of HPAI virus detections in migrating common cranes at the important Hortobágy stopover site in Hungary in November, associated with high mortality, is evidence of HPAI severely affecting a new species of wild birds in Europe. Second, the low rate of HPAI virus detections in colony-breeding seabirds along coastlines in Europe is the tail of an epidemic that peaked in spring and summer 2023, when those seabirds were aggregated in their breeding colony sites (Figure 3). Third, the similarly low but increasing rate of HPAI virus detections in waterfowl, centered around the Baltic and Mediterranean/Black Sea migration routes, is possibly the start of an epidemic that will peak in the coming months, when high numbers of waterfowl aggregate at stopover and wintering sites in Europe. Evidence for continued increase in HPAI detections comes from data after the current reporting period: 9 HPAI detections in waterfowl (barnacle goose, graylag goose, mallard and unspecified Anserinae) in Europe in the period from 2 to 13 December 2023. Fourth, the low rate of HPAI virus detections in raptors reflects their predation and scavenging on waterfowl, seabirds and other wild bird species, in which the overall rate of detection is also low.

The overall number of HPAI virus detections in wild birds (including detections in mixed species) (175) was 67% lower than the one of the previous reporting period (530 from 24 June to 1 September 2023), mainly due to a lower number of HPAI virus detections affecting the category of colony-breeding seabirds (46 in the current vs 452 in the previous reporting period). The number of HPAI virus detections in the categories of raptors (13 vs 34) and mixed species (1 vs 5) were also lower, while those in waterfowl (59 vs 11) and other wild bird species (56 vs 24) were higher (Figure 5).

The top three waterfowl identified to species in which HPAI virus detections were reported were the mute swan (17 in the current vs 5 in the previous reporting period), greylag goose (8 vs 1) and mallard (8 vs 1) (Annex A).

The main species in the 'other' wild bird category was the common crane (48 in the current vs 0 in the previous reporting period), with the remaining individuals in this category comprising unspecified birds in the order Gruiformes, to which the common crane belongs (Annex A). The majority of those HPAI virus detections were from November 2023 in Hungary (33), but there were also smaller numbers of detections in common cranes or unspecified Gruidae from Serbia (5), Austria (3), Italy (3), France (2), Germany (2), Croatia (1) and Slovenia (1). The European population of the common crane is estimated at 309,000–423,000 mature individuals (IUCN, online-a). HPAI-associated mortality in Hungary was initially concentrated at crane roosting sites in the Hortobágy region and subsequently spread to roosting sites in the Southern Great Plain and Western Transdanubia. These sites are part of the Baltic-Hungarian route, one of the main migration routes that have been identified for the European population of common cranes. Two other important routes are the West European and East European routes (Leito et al., 2015). As of 6 December 2023, the number of dead common cranes was estimated at 20,000–30,000 in Hungary (Natuurpunt, online), where carcasses have been collected and disposed of, and 600 in Serbia (Ekapija, online). A link between HPAI virus detections in common cranes and poultry in Hungary is expected. Preliminary genetic characterisation shows that the HA gene of one virus from a common crane and one virus from a domestic duck are identical, supporting the hypothesis of common cranes as a possible source of the virus for poultry, although it is more likely that very similar viruses circulate in other wild birds (e.g. wild ducks) more commonly associated with introductions of HPAI viruses into poultry. This is the first time that HPAI has been recorded to cause high-level mortality in common cranes in Europe. The only previously known die-off in common cranes from HPAI was in Israel in autumn 2021, when an estimated 10,000 common cranes on their migration along the East European route from Russia and Scandinavia to Ethiopia and Sudan died from A(H5N8) virus infection in and around the Hula Valley in Israel (Lublin et al., 2023).

The top three raptors identified to species in which HPAI virus detections were reported were the white-tailed eagle (4 in the current vs 5 in the previous reporting period), peregrine falcon (3 vs 14) and Eurasian buzzard (2 vs 0) (Annex A). Mostly raptors and scavenging species were involved in the A(H5N5) virus detections during this reporting period.

The complete list of wild bird species found as HPAI virus-infected from 2 September to 1 December 2023 is reported in Figure A.1 in Annex A. The number of HPAI virus-affected wild birds that were not identified to species was 29/175 (16.6%), a substantial improvement compared to the previous reporting period (133/587, 22.7%) (Figure A.2 in Annex A). HPAI virus detections in wild birds are generally underestimated. Therefore, the numbers provided are not representative of the number of wild birds that actually died from A(H5) virus infection.

Note that Figure 5 and Figures A.1-A.2 in Annex A provide information on the numbers of wild bird categories/families/species that were detected as HPAI virus-infected at single bird level, as more than one bird can be involved in one single HPAI virus detection reported.

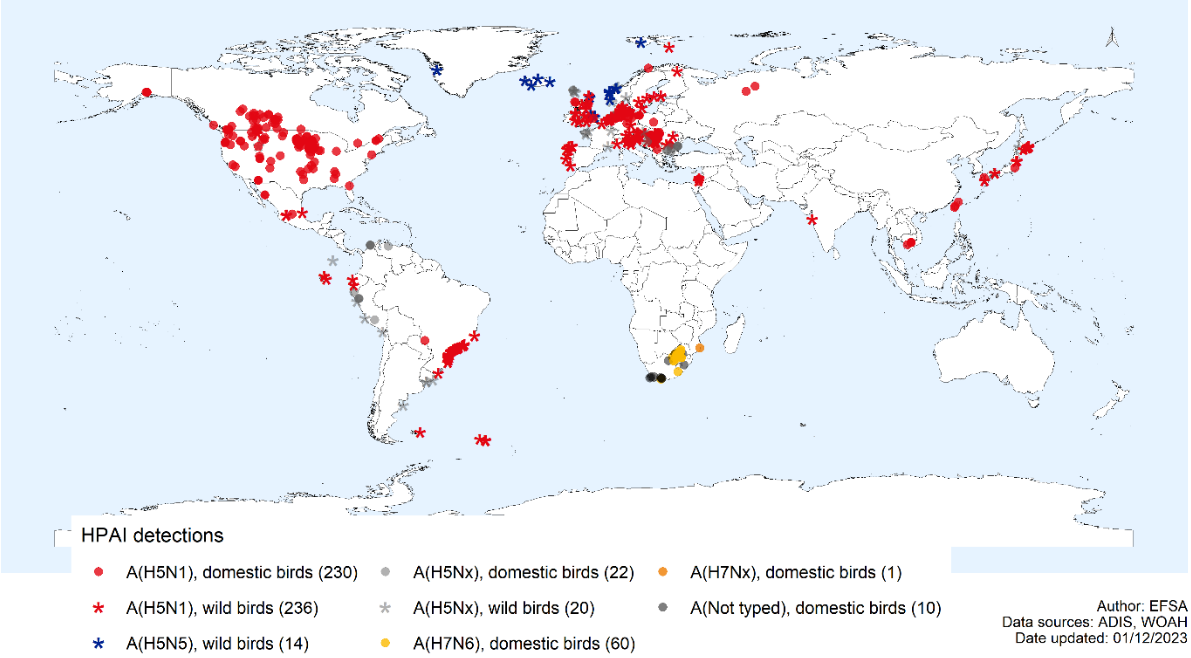
2.1.2 HPAI virus detections in birds outside Europe

An overview of the HPAI virus detections in birds that were notified from other countries not reporting via ADIS but via WOAH from 2 September to 1 December 2023 is presented in Table 2 and Figure 7.

Table 2: Number of HPAI virus detections in non-European countries, by virus subtype and country, from 2 September to 1 December 2023

Region	**Country**	**Domestic birds**					**Wild birds**			**Total**
		H7Nx	H7N6	H5N1	H5Nx	A(Not typed)	H5N1	H5N5	H5Nx	
Africa (71)	Mozambique	1	-	-	-	-	-	-	-	1
	South Africa	-	60	-	-	10	-	-	-	70
Americas (226)	Argentina	-	-	-	-	-	-	-	1	1
	Brazil	-	-	1	-	-	50	-	-	51
	Canada	-	-	40	-	-	-	-	-	40
	Colombia	-	-	-	4	-	-	-	-	4
	Costa Rica	-	-	-	-	-	-	-	1	1
	Ecuador	-	-	-	-	-	5	-	-	5
	Falkland Islands	-	-	-	-	1	-	-	-	1
	Greenland	-	-	-	-	-	-	1	-	1
	Mexico	-	-	3	-	-	3	-	-	6
	Peru	-	-	-	5	-	-	-	3	8
	United States of America	-	-	96	-	-	1	-	1	98
	Uruguay	-	-	-	-	-	-	-	2	2
	Venezuela	-	-	-	1	-	-	-	-	1
Antarctica (5)	South Georgia and the South Sandwich Islands	-	-	-	-	-	4	-	-	4
Asia (34)	Cambodia	-	-	4	-	-	-	-	-	4
	India	-	-	-	-	-	1	-	-	1
	Israel	-	-	3	-	-	2	-	-	5
	Japan	-	-	2	-	-	18	-	1	21
	Taiwan	-	-	3	-	-	-	-	-	
Europe (2)	Russia	-	-	2	-	-	-	-	-	2
Total		**1**	**60**	**154**	**10**	**10**	**85**	**1**	**9**	**330**

'-' means that no HPAI outbreaks were notified to WOAH.
Source: WOAH (data extraction carried out on 1 December 2023).



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 01/12/2023

Figure 7: Geographic distribution, based on available geocoordinates, of HPAI virus detections reported worldwide in domestic (323) and wild (270) birds by virus type, from 2 September to 1 December 2023

In the tables and figures of the present report, only data extracted from WOAH on 1 December 2023 are presented. However, HPAI virus detections in poultry and wild birds are also reported to the public via different means. This additional information on HPAI virus detections available from sources other than WOAH-WAHIS has been integrated in the text below.

In comparison to the previous reporting period (EFSA, ECDC and EURL, 2023), an increasing number of HPAI outbreaks in poultry and wild birds (330 vs 99) were notified from a higher number of countries (22 vs 12) worldwide, especially from the Americas and Asia. Furthermore, HPAI virus detections in seabirds on the Falkland Islands and in the Antarctic region were reported from 2 September to 1 December 2023. In the Americas, HPAI A(H5) virus continued to be detected in poultry and wild birds in previously affected countries, but in contrast to the last report, Canada, Greenland, Mexico, Peru, Uruguay and Venezuela notified outbreaks to WOAH after a longer period of absence. In Asia, the number of affected countries increased with reports from Cambodia, India, Israel, Japan and Taiwan, but no additional outbreaks were reported from China. In Africa, the number of affected countries has remained stable, but in contrast to the last report, only southern Africa was affected. Overall, HPAI outbreaks in poultry increased dramatically (235 vs 45) and almost twice the number of cases in wild birds were reported to WOAH (95 vs 54) in the current reporting period.

The devastating outbreak of HPAI A(H7N6) in South Africa was notified to WOAH and continued on poultry farms of all sizes, but especially in large to very large poultry farms near the Indian Ocean coast (CBS News, online-a; IOL, online; WattPoultry, online-a). Media reports have already mentioned shortages in egg and poultry meat supply after 20–30% of the country's chicken stock had been destroyed (CBS News, online-a; WattPoultry, online-a). In contrast to the previous reporting period, no outbreaks of HPAI A(H5N1) or cases of HPAI A(5) in wild birds were reported to WOAH. Furthermore, Mozambique notified the detection of the A(H7) subtype in a large poultry establishment at the end of September

2023. The large outbreak of A(H5N1) in the United States of America and Canada accounted for almost half of the reported outbreaks in domestic birds worldwide. Poultry species affected included turkeys, chickens, geese and ducks in poultry farms of all sizes. With exception of some wild birds and mammal cases, no outbreaks in poultry were detected since April up until the beginning of October 2023. In the current reporting period, the United States of America notified also cases in wild waterfowl, specifically in canvasbacks and mallards. Furthermore, media reports mentioned affected wild geese in an area in California, where geese, mallards and other migratory waterfowl gather as they travel along the Pacific Flyway (CBS News, online-b; The Sacramento Bee, online). The situation is comparable to the situation in Europe 2021 with an adapted virus spreading in a naïve wild waterbird population. In contrast to the previous reporting period, Argentina did not confirm any HPAI outbreaks in poultry but reported A(H5Nx) virus detections in James's flamingo, a bird species of the high Andes (listed as near-threatened by the International Union for Conservation of Nature with a population of 106,000 individuals based on coordinated census in 2010 (IUCN, online-b) with 220 deaths (MDZ, online). In addition to Argentina, also Costa Rica (in great frigatebird), Ecuador (in great frigatebird, magnificent frigatebird and red-footed booby), Greenland (in northern fulmar and glaucous gull) and Uruguay (in royal and South American tern) reported HPAI virus detections in wild birds but no poultry outbreaks during the current reporting period. Furthermore, the large outbreak in wild birds on the Brazilian Atlantic coast continued, accounting for more than half of the wild bird cases. Several species, such as common tern, royal tern, South American tern, Cabot's tern, great egret, snowy egret, Antarctic prion, American golden-plover, white-chinned petrel, Manx shearwater and brown booby, and one outbreak in backyard poultry were notified to WOAH. Colombia, Mexico, Peru and Venezuela detected A(H5N1) and A(H5Nx) mainly in backyard farms and in wild birds, such as in Eurasian teal, cinnamon teal, great skua, waved albatross, Peruvian booby and falcons. Media reported that the outbreak in Humboldt penguins in Chile has continued and up to 3,000 animals have died of A(H5N1) virus infection by October 2023. Therefore, the actual situation in the Americas is continuously evolving with new HPAI virus detections in wild and domestic birds as well as in mammal species. Until now, A(H5) has resulted in the death of high numbers of seabirds (and other animals) in the Northern Hemisphere, the south of Africa, around the Atlantic and Pacific Oceans, and throughout South America. Identifying HPAI viruses in brown skua, also known as sub-Antarctic skua on South Georgia (Bird Island) inside of the Antarctic convergence, the marine belt encircling the Antarctic region, and in the southern fulmar on the Falkland Islands in the sub-Antarctic region, indicates that HPAI virus has been introduced to new population groups that had not been exposed to it previously. It may be argued that such expansion is a consequence of an increased risk of transmission and spread in the adjacent source zone, which seems consistent with increased numbers of HPAI virus detections in neighboring South America, as predicted in the last report (EFSA, ECDC and EURL, 2023). Furthermore, sequences from Bird Island clustered with sequences from South America, particularly Uruguay, Peru and Chile. They all belong to the B3.2 genotype, a reassortant of the original Eurasian A(H5N1) virus introduced into North America in late 2021, and local North American avian influenza viruses (FluGlobalNet, online). Bennison et al. (2023) outlined that discrete trait analysis based upon the country of origin suggested that the source of HPAI virus for both South Georgia and the Falkland Islands was Chile. In Asia, Cambodia reported outbreaks of HPAI A(H5N1) to WOAH from a region where human cases of A(H5N1) belonging to clade 2.3.2.1c have occurred (KhmerTimes, online). They were caused by a viral clade that has been circulating in poultry in Cambodia since 2014 (ECDC, online). As no sequence information from the outbreaks in poultry is publicly available yet, a more precise analysis and differentiation from the worldwide more common clade 2.3.4.4b is currently not possible.

The outbreaks of A(H5N1) in poultry farms in Taiwan continued and new outbreaks of A(H5N1) clade 2.3.4.4b in domestic birds were detected in Japan this season (TellerReport, online), which had been preceded by many cases in Japanese wild birds, such as in northern pintail, Eurasian wigeon, whooper swan, red-crowned crane, Eastern buzzard, Eurasian goshawk, Japanese sparrow hawk and large-billed crow. Furthermore, India reported cases of A(H5N1) in black swan and silver pheasant in a non-poultry bird establishment on the western coast. Also Israel notified the first HPAI outbreaks in poultry and migrating wild birds (marbled duck and black stork) since April 2023 during this reporting period (JPost, online). Russia detected A(H5N1) virus in a very large poultry and a backyard farm in Komi republic, west of the Ural Mountains (ProMed, online; UH 50, online).

The list of wild bird species that have been reported to WOAH as HPAI virus-infected from 2 September to 1 December 2023 is presented in Table A.1 in Annex A.

2.1.3 Genetic characteristics of HPAI viruses of the A(H5N1) subtype circulating in Europe in avian species

Details on the nomenclature of the HPAI A(H5) viruses used in this section are reported in Appendix B.

Genetic diversity of HPAI A(H5N1) viruses in avian species

From February 2023, there was a rapid increase in the frequency of the BB (H5N1-A/Herring_gull/France/22P015977/2022-like) genotype, which in the period April–August 2023 reached a frequency > 80%. This genotype, which has circulated mainly among Laridae, has been detected in 20 European countries, in the Leningrad region as well as in West Africa. Since September 2023, with the decreased number of cases in seabirds and the increased prevalence in wild Anseriformes and other wild bird species, such as common cranes, there has been a sharp decline in the frequency of detection of the BB genotype, and the emergence of novel genotypes has been observed. Specifically, based on the data available, in the current reporting period eleven different genotypes were identified: four genotypes which persistently circulated in Europe from the previous epidemiological years, namely BB, AB (H5N1 A/duck/Saratov/29-02/2021-like), CH (H5N1-A/Mallard/Netherlands/18/2022-like) and I (H5N5 A/whooper_swan/Romania/10123_21VIR849-1/2021-like), and seven new A(H5N1) genotypes which emerged from novel reassortment events with LPAI viruses circulating in wild birds, namely DA (H5N1-A/mute_swan/Slovenia/PER1486-23TA_23VIR10323-22/2023-like), DB (H5N1- A/herring_gull/Germany-NI/2023AI08764/2023-like), DC (H5N1-A/Common_Buzzard/Netherlands/23023642-002/2023-like), DD (H5N1-A/Pheasant/England/113705/2023-like), DE (H5N1-A/Chicken/Scotland/114176/2023-like), DF (H5N1-A/Sparrowhawk/Scotland/131359/2023-like) and DG (H5N1-A/chicken/Germany-NI/2023AI08838/2023-like). Whether these new genotypes originated in Europe or represent new virus introductions cannot be assessed given the limited data available from other countries outside Europe. Among the genotypes characterised in the current reporting period, five (AB, BB, DA, DB and I) were identified in multiple countries. The new DA genotype has been detected in wild and captive birds (zoo) as well as in poultry in eastern and southern Europe (Austria, France, Italy, Germany, Romania and Slovenia). Of note, based on the available genetic data, all viruses collected from common cranes in Europe (Austria, France, Germany and Italy) during this reporting period (n = 9) belong to the DA genotype. Differently, the DB genotype has been isolated from the wild and domestic bird population in northern Europe (Denmark, Germany and the Netherlands). Subtype A(H5N5), genotype I, which emerged in Europe in 2021, has been persistently detected in

Norway since the 2021–2022 epidemiological year. In September 2023, viruses of this genotype, highly related to the Norwegian viruses, were identified in Iceland and the United Kingdom, suggesting a geographic expansion of this variant.

Of note, one of the A(H5N1) viruses from poultry outbreaks reported in Poland in October 2023 belonged to the same genotype, namely CH, collected in the country in June and July 2023 in a white stork, a chicken establishment, in domestic cats and a caracal. Similarly to these viruses circulating in birds and mammals during summer, it possessed the mutation PB2-E627K. This finding indicates a persistent circulation of viruses containing a mutation associated with mammalian adaptation in the bird population of the country. To date this variant (CH with PB2-627K) has not been identified in other European countries.

Mutations identified in HPAI A(H5N1) viruses from avian species

Molecular analyses of the HPAI A(H5N1) viruses circulating in birds in Europe during the 2022–2023 epidemiological year indicate that they continue to be well-adapted to avian species, as they retain a preferential binding for avian-like receptors. However, several mutations, previously described in literature (Suttie et al., 2019), have been identified as being associated with i) enhanced polymerase activity and replication in mammals or mammalian cells, ii) increased virulence, iii) increased/conferred resistance towards antiviral drugs, iv) increased in vitro binding to human-type receptors alpha2,6-SA, v) decreased antiviral response in ferrets, vi) evasion of human butyrophilin subfamily 3 member A3 (BTN3A3) and vii) disruption of the second sialic acid (SIA) binding site in the neuraminidase protein, with a frequency varying by the distinct mutations. The net effect of these mutations on the biological characteristics of the viruses is still unknown and further studies are needed to improve existing knowledge. Mutations associated with virus adaptation in mammals have been detected in 14 A(H5N1) viruses collected from wild birds (n = 4 with PB2-627K, n = 4 with PB2-526R) in five European countries and from domestic birds (n = 2 with PB2-E627K, n = 1 with PB2-D701N, n = 1 with PB2-T271A, n = 1 with PB2-526R-627K and n = 1 with 526R) in four European countries since October 2022. Among the mutations in the HA protein that have proved to increase in vitro binding to human-type receptors, some (i.e. S133A, S154N, T156A and H5 numbering) have been identified in the majority of the A(H5N1) viruses circulating in Europe since October 2022, while others (i.e. D94N, S155N and V210I) have only been sporadically observed. The impact of these HA mutations on the biological characteristics of the circulating viruses is still unknown; however, none of them have been demonstrated to cause a shift from avian-like to human-like receptor binding preference. Moreover, almost all the A(H5N1) viruses belonging to the BB genotype (H5N1 A/gull/France/22P015977/2022-like) contain mutations NP-Y52N and NA-S369I, which may increase their zoonotic potential. Mutations associated with antiviral resistance have been occasionally identified in the circulating strains.

2.2 HPAI virus detections in non-human mammals

2.2.1 HPAI virus detections in non-human mammals worldwide

From 2 September to 1 December 2023, HPAI A(H5N1) and A(H5Nx) viruses were reported in farmed and wild mammals in Europe and South America. Data were collected from WOAH-WAHIS and supplemented with additional information provided by Member States and retrieved from media reports (Table 3).

In response to the A(H5N1) outbreaks in fur farms in Finland during summer 2023, Finland initiated a serological survey in all 400 fur farms of the country. Since September and up until mid-November 2023, 29 new fur farms with ongoing or past HPAI virus infection were detected by either RT-PCR or serological tests. Three farms with clinical signs were found by passive surveillance: one of those farms at the beginning of September had recently reported severe clinical signs and was RT-PCR-positive, but for the other two farms, diagnosis was based on serology. Following the serological surveillance in all fur farms, 3 out of 115 (2.5%) farms keeping American mink were found serologically positive to HPAI A(H5) viruses, and a few farms with American mink are still under investigation. In addition, of the farms keeping foxes and/or common raccoon dogs, around 110 had been serologically investigated up until mid-November 2023. Twenty-three out of those 110 farms (20.9%) were found serologically positive. Since part of the fur farms keep both American mink and foxes or raccoon dogs, these farms have been surveyed twice and included in both counts. In surveyed farms, the number of serologically positive animals out of 60 tested in most cases ranged between 1–5 (1.7–8.3%), with a maximum of 17 (28.3%) positive animals in a surveyed farm. Control measures such as culling of all animals present in positive farms were applied whenever clinical signs and/or an epidemiological link to another positive farm or wild birds was evident. Among those 29 farms, 14 kept only Arctic foxes, 1 kept only American mink, and 14 were mixed-species farms keeping red and Arctic foxes, American mink, common raccoon dogs and sables. All 29 farms are located in the west and southwest of Finland. Direct contact with wild birds was the suspected source of introduction, as all of the animals kept had outdoor access. Increased mortality was reported in 3 (10%) of those farms (1 keeping only Arctic foxes, 1 keeping Arctic foxes and American mink, 1 keeping red and Arctic foxes). Clinical signs were present in 2 (7%) of those farms (1 keeping Arctic foxes and American mink, 1 keeping only Arctic foxes). Follow-up samples were only taken in the farm having PCR-positive primary samples, which were collected during the culling of animals, but those follow-up samples turned out negative.

No HPAI virus detections in pet mammals were reported during this reporting period. In the United States of America, however, four A(H5N1) virus detections in feral cats (three in South Dakota and one in Montana) were reported to WOAH. One of the cats from South Dakota tested positive in an HPAI-affected poultry farm, while the cat from Montana lived in a non-commercial poultry establishment and was euthanised after showing neurological signs (Nation World, online). In a region in Spain in which HPAI virus detections in wild birds were reported, a serological study conducted in feral cats between March 2022 and March 2023 revealed the presence of antibodies to influenza A viruses in 4 out of 183 (2.2%) cats tested (Villanueva-Saz et al., 2023).

In wild mammals, in Europe, A(H5N1) virus detections were reported in Eurasian lynx and Eurasian otter in Finland, and in harbor seals in Denmark. Outside Europe, high rates of A(H5) virus detections were reported in South America: in South American sea lions in Argentina (> 70, (Río Negro, online)), Brazil (> 900, (Reuters, online)) and Uruguay (> 400 animals, (Lansi-Savo, online)); in South American fur seals in Brazil and Uruguay; and in southern elephant seals in Argentina (>2,400, (Ambientales, online; Big.AZ, online)). Particularly high mortality was reported in southern elephant seals: 40–70% in adults and up to 100% in juveniles (Ambientales, online; Big.AZ, online) on the Valdés Peninsula in Argentina. It was the first time that HPAI virus detections in mammals were reported from Brazil, with mass mortality events taking place along the coastlines of Rio Grande do Sul. Numerous carcasses were also found along the coastlines of Uruguay, many of which were buried (MercoPress, online-a). After the first HPAI virus detections in wild birds in the Antarctic region, also southern elephant seals were found positive in eight different locations across the region. Some of those animals were reported to have shown respiratory signs (The Guardian, online). The relative contribution of A(H5) viruses to those mass mortality events in South American sea lions and other seal species, compared to different factors such as the El Niño phenomenon, remains unclear (El Tipografo, online; MercoPress, online-b).

Table 3: Avian influenza A(H5Nx) virus detections in mammal species other than humans related to circulating viruses worldwide, 2016–2023

Virus	Animal (order, family, species)			Country	Reference
A(H5N1) or A(H5Nx) clade 2.3.4.4b	Artiodactyla	Suidae	Domestic pig (*Sus scrofa*)*	Italy	Rosone et al. (2023)
	Carnivora	Canidae	Arctic fox (*Vulpes lagopus*)	Finland	WOAH
			Bush dog (*Speothos venaticus venaticus*)	United Kingdom	WOAH
			Common raccoon dog (*Nyctereutes procyonoides*)	Finland, Japan	WOAH
			Coyote (*Canis latrans*)	United States of America	WOAH
			Dog (*Canis lupus familiaris*)	Canada, Italy*	WOAH Moreno et al. (2023)
			Japanese raccoon dog (*Nyctereutes viverrinus*)	Japan	FAO
			Red fox (*Vulpes vulpes*)	Belgium, Canada, Denmark, Estonia, Finland, France, Germany, Ireland, Italy, Japan, Latvia, Netherlands, Norway, United Kingdom (Northern Ireland), United Kingdom, United States of America, Sweden	WOAH, SVA Liang et al. (2023), USDA (online)
		Felidae	Amur leopard (*Panthera pardus*)	United States of America	USDA (online)
			Amur tiger (*Panthera tigris*)	United States of America	WOAH
			Bobcat (*Lynx rufus*)	United States of America	WOAH
			Caracal (*Caracal caracal*)	Poland	WOAH
			Cat (*Felis catus*)	Canada, France, Italy*, Korea (Rep. of), Poland, United States of America	WOAH Briand et al. (2023)
			Eurasian lynx (*Lynx lynx*)	Finland	WOAH FFA (online)
			Lion (*Panthera leo*)	Peru	WOAH
			Mountain lion (*Puma concolor*)	United States of America	WOAH
		Mephitidae	Striped skunk (*Mephitis mephitis*)	Canada, United States of America	WOAH CTV News (online), USDA (online)
		Mustelidae	American mink (*Neovison vison*)	Canada, Finland, Spain	WOAH Xunta de Galicia (online)
			Beech marten (*Martes foina*)	Netherlands	GISAID
			Eurasian otter (*Lutra lutra*)	Netherlands, Finland	WOAH, WUR
			European badger (*Meles meles*)	Netherlands	WUR

Virus	Animal (order, family, species)			Country	Reference
			European pine marten (*Martes martes*)	Germany	WOAH
			European polecat (*Mustela putorius*)	Belgium, Netherlands	WUR
			Ferret (*Mustela furo*)	Belgium, Slovenia	WOAH
			Fisher (*Pekania pennanti*)	United States of America	WOAH
			Marine otter (*Lontra felina*)	Chile	WOAH
			North American River otter (*Lontra canadensis*)	United States of America	WOAH
			Sable (*Martes zibellina*)*	Finland	WOAH
			Southern river otter (*Lontra provocax*)	Chile	WOAH
		Otariidae	Northern fur seal (*Callorhinus ursinus*)	Russia	WOAH
			South American fur seal (*Arctocephalus australis*)	Argentina, Brazil, Peru, Uruguay	WOAH, FAO
			South American sea lion (*Otaria flavescens*)	Argentina, Brazil, Chile, Peru, Uruguay	WOAH Cruz et al. (2023), Gamarra-Toledo et al. (2023), Leguia et al. (2023)
		Phocidae	Caspian seal (*Pusa caspica*)	Russia	FAO
			Grey seal (*Halichoerus grypus*)	Canada, Germany, Netherlands, Poland, United Kingdom, United States of America	WOAH AMMI (2022), Mirolo et al. (2023)
			Harbour seal (*Phoca vitulina*)	Canada, Denmark, Germany, United Kingdom, United States of America	WOAH Agriland (online)
			Southern elephant seal (*Mirounga leonina*)	Argentina	infobae (online)
		Procyonidae	Raccoon (*Procyon lotor*)	Canada, United States of America	WOAH
			South American coati (*Nasua nasua*)	Germany, Uruguay	WOAH
		Ursidae	American black bear (*Ursus americanus*)	Canada, United States of America	WOAH Healthy Wildlife (online), KTOO (online)
			Asian black bear (*Ursus thibetanus*)	France	WOAH GISAID
			Brown bear (*Ursus arctos*)	United States of America	Kiniradio (online), USDA (online)
			Kodiak grizzly bear (*Ursus arctos horribilis*)	United States of America	FAO
	Cetacea	Delphinidae	Bottlenose dolphin (*Tursiops truncatus*)	Peru, United States of America	WOAH UFHealth (online)

Virus	Animal (order, family, species)			Country	Reference
			Chilean dolphin (*Cephalorhynchus eutropia*)	Chile	FAO Sernapesca (online)
			Common dolphin (*Delphinus delphis*)	Peru, United Kingdom	WOAH Leguia et al. (2023)
			White-sided dolphin (*Lagenorhynchus acutus*)	Canada	Avian Flu Diary (online-a)
		Phocoenidae	Burmeister’s porpoise (*Phocoena spinipinnis*)	Chile	FAO
			Harbour porpoise (*Phocoena phocoena*)	Sweden, United Kingdom	SVA
	Didelphimorphia	Didelphidae	Virginia opossum (*Didelphis virginiana*)	United States of America	WOAH USDA (online)
A(H5N5) clade 2.3.4.4b	Carnivora	Canidae	Red fox (*Vulpes vulpes*)	Canada	WOAH
		Procyonidae	Raccoon (*Procyon lotor*)	Canada	WOAH
A(H5N6) clade 2.3.4.4b	Carnivora	Canidae	Dog (*Canis lupus familiaris*)	China	Yao et al. (2023)
A(H5N8) clade 2.3.4.4b	Artiodactyla	Suidae	Domestic pig (*Sus scrofa*)*	France	Herve et al. (2021)
			Wild boar (*Sus scrofa*)*	Germany	Schülein et al. (2021)
	Carnivora	Canidae	Red fox (*Vulpes vulpes*)	United Kingdom	Floyd et al. (2021)
		Phocidae	Grey seal (*Halichoerus grypus*)	Poland, Sweden, United Kingdom	SVA Shin et al. (2019), Floyd et al. (2021) Personal communication by Siamak Zohari (Sweden)
			Harbour seal (*Phoca vitulina*)	Denmark, Germany, United Kingdom	Floyd et al. (2021), Ärzteblatt (online), Avian Flu Diary (online-b), Outbreak News (online), SSI (online)

*Serological detection.

2.2.2 Genetic characteristics of HPAI viruses of the A(H5N1) subtype circulating in Europe in non-human mammals

Details on the nomenclature of the HPAI A(H5) viruses used in this section are reported in Appendix B.

Genetic diversity of HPAI A(H5N1) viruses in non-human mammals in Europe

Since October 2020, the complete genome sequences of about 250 HPAI A(H5) viruses of clade 2.3.4.4b collected from 16 European countries from 18 distinct mammalian species (i.e. American mink, Arctic fox, Asian black bear, beech marten, bush dog, caracal, cat, common raccoon dog, European badger, Eurasian lynx, Eurasian otter, European polecat, ferret, grey seal, harbor porpoise, harbor seal, red fox and South American coati) have been generated. The characterised viruses belong to 8 different A(H5N1) and A(H5N8) genotypes previously identified in birds. During the 2022–2023 epidemiological year, most of the mammalian infections were caused by the 3 most widespread genotypes in birds, namely BB (H5N1-A/gull/France/22P015977/2022-like), AB (H5N1-A/duck/Saratov/29-02/2021-like) and CH (H5N1-A/Eurasian_Wigeon/Netherlands/3/2022-like). Most of the infections reported in wild mammals during the summer months were caused by the BB genotype. In contrast, the last cases reported in wild mammals (Eurasian lynx, Eurasian otter and harbor seals) in Finland and Denmark in September–October 2023 belonged to the AB genotype.

In pets or reared mammals, the infections reported during the 2022–2023 epidemiological year were caused by the BB genotype, which infected fur farms (American mink, Arctic and red foxes, and common raccoon dogs) in Spain in October 2022 (n = 1) and in Finland in July–September 2023 (number of genetically characterised farms = 26), by the CH genotype, which infected 30 domestic cats in Poland in June–July 2023, and by the AB genotype, which infected a domestic cat in France in December 2022.

Most of the A(H5N1) viruses collected from fur farms in Finland are highly related to each other and to viruses collected from gulls in the same geographic area, making it difficult for most of the cases to assess the virus origin (wild bids vs other fur farms vs within-farm virus transmission).

About 43% of the characterised viruses contain at least one of the adaptive markers associated with an increased virulence and replication in mammals in the PB2 protein (E627K, D701N, T271A or K526R) (Suttie et al., 2019). These mutations have rarely been identified in the HPAI A(H5) viruses of clade 2.3.4.4b collected in birds in Europe since October 2020. This observation suggests that these mutations with potential public health implications have likely emerged upon transmission to mammals.

2.3 Avian influenza virus infections in humans

2.3.1 Most recent human infections with avian influenza A(H3N8), A(H5N1), A(H5N6) and A(H9N2) viruses

Since the last report and as of 1 December 2023, five new human cases with avian influenza infection were reported from Cambodia (four A(H5N1)) and China (one A(H9N2)) (Table 4). All were reported to have had exposure to poultry or live poultry markets prior to avian influenza virus detection or onset of illness.

Table 4: Most recent human cases due to avian influenza viruses, by virus subtype

Subtype	New cases reported	Number of reports with disease onset or detection in 2023	Total cases (deaths)	Countries reporting human cases
A(H3N8)	-	1 case	3 (1) Since 2022	China
A(H5N1)	4 new cases in Cambodia (clade 2.3.2.1c)	12 cases/detections	882 (461) Since 2004	23 countries reported cases; EU/EEA: Spain with virus fragment detections in two poultry workers considered contamination and no productive infections
A(H5N6)	-	4 cases	88 (34) Since 2014	China (87), Laos (1)
A(H9N2)	1 new case in China	7 A(H9N2) cases	128 (2) Since 1998	No EU/EEA country; China (115), Egypt (4), Bangladesh (3), Cambodia (2), Oman (1), Pakistan (1), India (1), Senegal (1)

Source: ECDC line list and WHO.

2.3.2 Human A(H3N8) cases, summary

No new human infections have been reported since the previous report and as of 1 December 2023. During 2022 and 2023, in total three infections have been reported from China with two in children (4 and 5 years old) and one in an adult (56-year-old female) exposed to either infected backyard poultry or live poultry markets. The infections were mild in one case and more severe or critical in the other two, including one death (Bao et al., 2022; Sit et al., 2022). The reported death from A(H3N8) virus was in a patient with multiple myeloma who was undergoing immunosuppressive treatment. She presented with pyrexia, sore throat and a cough. The patient developed myelosuppression and pneumonia and, despite intensive treatment, died following acute heart failure 22 days after the onset of illness (Zhuang et al., 2023). Human-to-human transmission has not been reported and all three cases were considered sporadic spill-over events.

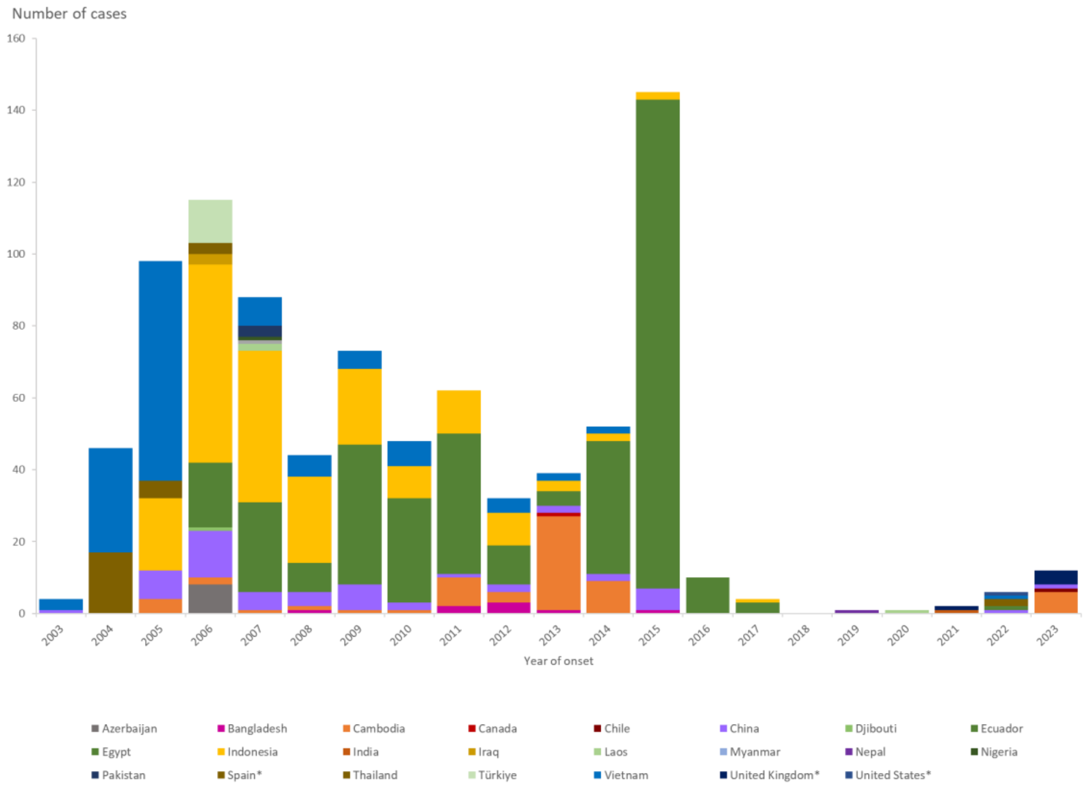
2.3.3 Human A(H5N1) cases, summary

Cambodia reported four new human infections with A(H5N1) of clade 2.3.2.1.c in individuals who had contact with sick and dead chickens in their villages before onset of symptoms (WHO, online-a). The first case was reported in October 2023 in a 50-year-old male who developed symptoms on 3 October and died four days after onset of symptoms, and the second infection was identified through severe acute respiratory infection (SARI) surveillance in a 2-year old girl admitted to hospital one day after the identification of the first case. The girl died three days after onset of symptoms on 6 October (WHO, 2023a, e; Cambodia TMoHo, online-a, b).

In November 2023, an outbreak of avian influenza in a village in Kampot province, Cambodia, caused an additional two human infections, one in a 21-year-old woman who developed fever, cough and shortness of breath on 19 November 2023, was admitted to hospital on 23 November, and died three days after admission. The second infection was detected in a 4-year-old girl, through active contact tracing of contacts of the 21-year-old woman. The girl was admitted to hospital with severe conditions. Both had contact to sick or dead infected chickens before onset of symptoms (WHO, 2023b, online-a).

In 2022, five countries reported six human cases/detections (Figure 8): China (1), Ecuador (1), Spain[12] (2), United States of America (1) and Vietnam (1). In 2023, four countries reported 12 cases/detections: Cambodia (6, clade 2.3.2.1c), Chile (1), China (1) and the United Kingdom (4).

As of 1 December 2023, there have been 882 human cases including 461 deaths with A(H5N1) infection notified to the World Health Organization (WHO) from 23 countries (Azerbaijan, Bangladesh, Cambodia, Canada, Chile, China, Djibouti, Ecuador, Egypt, Indonesia, India, Iraq, Laos, Myanmar, Nepal, Nigeria, Pakistan, Spain[12], Thailand, Türkiye, Vietnam, United Kingdom, United States of America; Figure 8).



*Includes detections due to suspected environmental contamination and no evidence of infection reported in 2022 from Spain (2) and the United States (1), and in 2023 from the United Kingdom (3, 1 inconclusive).

Figure 8: Distribution of confirmed human cases of A(H5N1) virus infection by year of onset and country, 2003–2023 (data as of 1 December 2023, n = 882)

2.3.4 Human A(H5N6) cases, summary

Since the last report, no additional cases have been reported.

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[12] A(H5N1) virus detections in two Spanish poultry workers involved in culling activities are considered contaminations and not productive infections.

As of 1 December 2023 and since 2014, China (87) and Laos (1) reported a total of 88 human infections with A(H5N6) (Figure 9), including 34 (39%) with fatal outcome according to notifications to WHO. Since 2021, the majority of A(H5N6) viruses identified in humans belong to clade 2.3.4.4b, although sequence information is not available for all viruses. After the modification of the H5 component in the vaccine used for poultry in China in January 2022, the number of human cases declined. However, with the available information it is not possible to make any further conclusions on whether the vaccination caused the observed decline (Chen et al., 2022; Cui et al., 2022; Gu et al., 2022; Zhu et al., 2022).

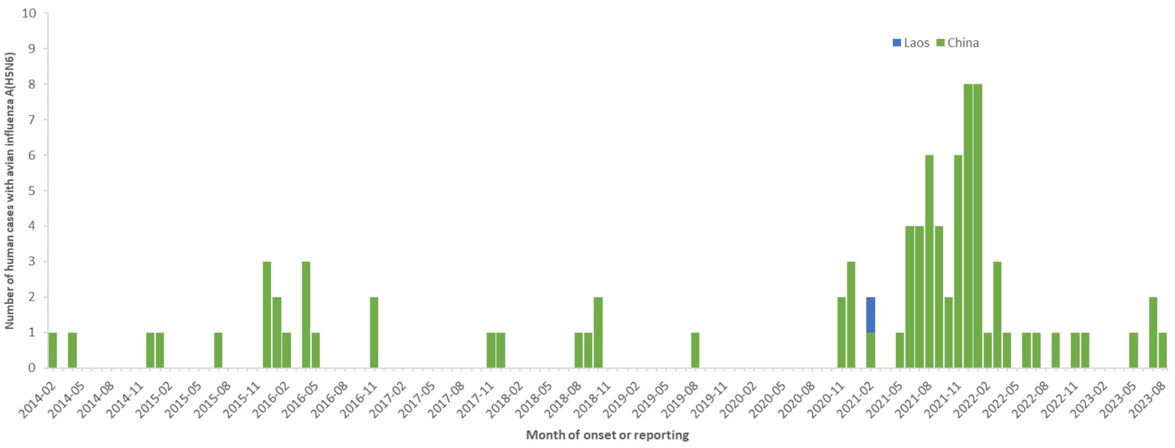

Figure 9: Distribution of confirmed human cases of A(H5N6) virus infection by month and year of onset and country, 2014–2023 (data as of 1 December 2023, n = 88)

2.3.5 Human A(H9N2) cases, summary

Since the last report and as of 1 December 2023, one new human case with A(H9N2) infection has been reported by China. The A(H9N2) case is from Sichuan province with date of symptom onset on 1 October 2023 (GovHK, 2023).

As of 1 December 2023 and since 1998, a total of 128 human infections, including two fatalities, with A(H9N2) have been reported from eight countries, all outside the EU (Figure 10): Bangladesh (3), China (115), Cambodia (2), Egypt (4), Pakistan (1), Oman (1), India (1) and Senegal (1). The majority of infections were identified in children up to 9 years of age (96; 76%) and women were more affected than men (74 vs 52; 2 of unknown sex).

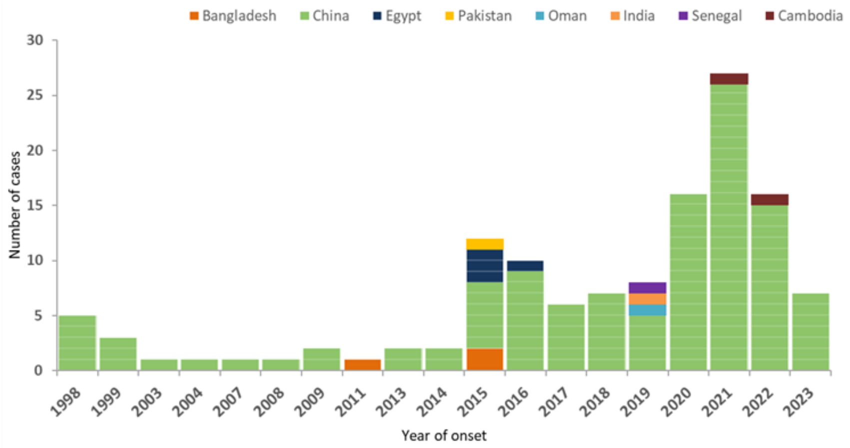

Figure 10: Distribution of confirmed human cases of A(H9N2) virus infection by month and year of onset and country, 1998–2023* (as of 1 December 2023, n = 128)

2.3.6 Genetic characteristics of HPAI viruses of the A(H5Nx) subtype from humans

Based on the data available from the GISAID's EpiFlu™ Database[13], since 2020 human infections have been caused by four different A(H5) clades of the A/goose/Guangdong/1/1996-lineage, namely 2.3.2.1c (Laos, 2020 and Cambodia, 2023), 2.3.2.1a (India, 2021), 2.3.4.4h (China, 2020–2021) and 2.3.4.4b (China, Europe, North America, South America, 2020–2023).

Mutation Q226L was identified in two A(H5N6) viruses of clade 2.3.4.4b collected in China in 2021 (Zhu et al., 2022). This mutation is associated with the switch in the receptor specificity from avian-type to human-type receptor (Stevens et al., 2006; Chutinimitkul et al., 2010; Russell et al., 2012). This mutation was previously detected in two A(H5N1) viruses of clade 1 collected from human infections in Cambodia in 2013 (Rith et al., 2014) and, based on the available sequence data, it is not present in the clade 2.3.4.4b A(H5Nx) viruses currently circulating in the avian population in Europe. Moreover, six clade 2.3.4.4b A(H5N6) viruses collected from human infections in China in 2021 possessed one of the adaptive markers in the PB2 protein (Q591K, E627K or D701N) associated with an increased virulence and replication in mammals (Zhu et al., 2022).

Available sequence information from the virus A/Chile/25945/2023 detected from the human case in Chile in March 2023 shows that the 2.3.4.4b clade virus carries two amino acid substitutions in PB2, indicative of mammalian adaptation, Q591K and D701N. Q591K has been associated with increased polymerase activity and replication in mammalian cell lines and increased virulence in mice, while D701N was also associated with increased virulence and contact transmission in guinea pigs (Li et al., 2005; Gao et al., 2009; Le et al., 2009; Steel et al., 2009; Yamada et al., 2010; Taft et al., 2015; Suttie et al., 2019).

Available sequence data from the six human cases detected in Cambodia in 2023 show that all the viruses belong to clade 2.3.2.1c and they all carry HA mutation S155N which is associated with increased mammalian receptor-binding (Wang et al., 2010).

Within the sequences there are four (EPI_ISL_18373263, EPI_ISL_18540514, EPI_ISL_18366401, EPI_ISL_18543643) that additionally carry HA mutations D94N, associated with increased mammalian receptor binding (Su et al., 2008), and N154D, which is associated with decreased virulence in mice (Jin et al., 2019). These four sequences additionally carry K142N in PA (for the 3 out of 4 sequences where the PA segment sequence is available), which is associated with increased virulence in mice (Kim et al., 2010). They further carry E627K in PB2 (PB2 segment available for 2 out of 4 sequences), which is associated with increased transmissibility in mammals (Herfst et al., 2012).

The remaining two sequences (EPI_ISL_17024123 and EPI_ISL_17069010) instead carry the HA mutation K189R, which is associated with increased human receptor binding (Wang et al., 2010). They also carry the PA mutations K142R and A343S, which are associated with increased polymerase activity in mammalian cell lines (Leung et al., 2010; Zhong et al., 2018). These two sequences further carry PB2 mutations I147T, K339T and A588T, which are associated with increased polymerase activity in mammalian cell lines and increased virulence in mice (Fan et al., 2014). In addition, they also have the M2

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[13] https://gisaid.org/

mutation S31N, which is associated with increased resistance to amantadine and rimantadine (Suttie et al., 2019).

Overall, the viruses carry a combination of several different mammalian adaptation mutations, with all of these individual adaptation mutations being rare in animal A(H5N1) sequences. It is challenging to assess the effect of the combined mutations of the genotype of a virus and translate this to the phenotype. The referenced studies investigate a single mutation or a combination of few mutations but do not assess the genotype to phenotype association for many different mutations combined.

2.3.7 Additional information and international risk assessments

Additional information from recent publications relevant for public health

In a review of avian influenza detections globally in 2013–2022, 2,000 human infections and 10 different subtypes of avian influenza viruses were reported (Szablewski et al., 2023). The majority (90%) of human avian influenza virus cases occurred between December and May. Across all virus subtypes, 75% of human cases had known exposure to animals before the onset of illness. There were 58 (3%) reports of possible or confirmed human-to-human transmission over the whole period.

A(H3N8)

The A(H3N8) virus causing infections in humans (Cheng et al., 2022; Tan et al., 2022; Zhuang et al., 2023) is believed to have resulted from reassortment between avian H3 and N8 viruses present in ducks and A(H9N2) virus endemic in poultry in China (Chen et al., 2023; Yang et al., 2023). Avian influenza A(H3N8) viruses were isolated from clinically healthy poultry in China (Chen et al., 2023; Cui et al., 2023), suggesting asymptomatic circulation in poultry populations.

In experimentally infected mice, A(H3N8) viruses were able to replicate and weight loss was observed in several mice (Cui et al., 2023). Ferrets experimentally infected with A(H3N8) virus displayed clinical signs of respiratory disease and weight loss. Transmission between ferrets occurred following direct contact but was less efficient through airborne exposure (Chen et al., 2023). In guinea pigs, several A(H3N8) viruses assessed were transmissible to animals in proximity via respiratory droplets (Cui et al., 2023). In experimental infection of human lung and bronchial tissue ex vivo, the A(H3N8) virus replicated inefficiently, indicating it is unlikely to transmit effectively between humans (Hui et al., 2023). Inhibition studies suggest the two A(H3N8) viruses from humans in 2022 are sensitive to oseltamivir (Zhu et al., 2023).

No detectable antibodies against A(H3N8) virus were identified in individuals vaccinated against seasonal influenza viruses, suggesting a susceptible human population to A(H3N8) infection (Zhu et al., 2023). Seasonal influenza vaccines are not protective against A(H3N8) infection. However, serological surveillance in healthy individuals found 3–6% were seropositive to A(H3N8) viruses. A higher prevalence (8–13%) of seropositive individuals above 50 years of age suggested presence of cross-reactive antibodies to A(H3N8) viruses in those born before 1968. In contrast, only 0.6–1% of individuals were seropositive among 18–49-year-olds (Chen et al., 2023).

A(H5N1)

The first documented human case of HPAI A(H5N1) in Chile, which was reported in March 2023, was a 53-year-old man who presented with a cough and sore throat (Godoy et al., 2023; WHO, online-c). He was hospitalised with severe disease progression but recovered. Comparison of the genomic sequence of the virus from the human case with avian influenza viruses in marine mammals noted two mutations in the PB2 segment, which were also present in a sea lion from the same region in March 2023 (Godoy et al., 2023). The source of infection remains unclear. There has been no evidence of human-to-human transmission.

An experimental transmission study assessed the potential for airborne transmission between mammals of HPAI A(H5) viruses of clade 2.3.4.4b obtained from American mink. Ferrets in close proximity but without direct contact with experimentally infected ferrets did not become infected or seroconvert, suggesting the virus does not transmit between ferrets through respiratory droplets (Maemura et al., 2023).

Antivirals can have a part in control and preparedness strategies for avian influenza in humans. A study of the antiviral susceptibility of the HPAI A(H5N1) viruses circulating globally in 2022–2023 found that most current HPAI A(H5N1) viruses remain susceptible to antiviral drugs. Presence of neuraminidase (NA) substitutions associated with reduced inhibition by NA inhibitors, such as oseltamivir and peramivir, or baloxavir was low overall (Andreev et al., 2023).

International risk assessments

The United States Centers for Disease Control and Prevention (US CDC) published a Technical Report summarising the situation and risk related to avian influenza A(H5N1) viruses in the United States of America and elsewhere (CDC, 2023). The previously issued risk assessment using the Influenza Risk Assessment Tool (IRAT) of the US CDC placed the risk of clade 2.3.4.4b viruses in the lower moderate category (CDC, 2021). The risk of the A(H5N1) clade 2.3.4.4b viruses currently circulating in the United States of America's bird and poultry populations, which are closely related to European viruses, was assessed by the US CDC to be low for human health in the general population and higher for people occupationally or recreationally exposed to birds (CDC, online-a, c). An updated IRAT assessment for the A(H5N1) clade 2.3.4.4.b virus from the American mink farm outbreak in Spain in 2022 scored slightly higher in some risk elements than the virus of clade 2.3.4.4.b previously assessed overall indicating a comparable 'moderate' risk level (CDC, online-b).

The WHO assessed the risk related to the recent A(H5N1) viruses infecting humans as low for the general public and low to moderate for occupationally exposed people (WHO, 2022, online-b). WHO previously assessed the risk for A(H5N6) as follows: 'the zoonotic threat remains elevated due to spread of the viruses in birds, based on evidence available so far, the overall pandemic risk is considered not significantly changed in comparison to previous years'. The UK Health Security Agency (UKHSA) assesses the situation to remain at level 3 (with limited mammalian transmission that excludes humans but with low confidence) on a scale ranging between 0–6 similar to the previous assessment (GovUK, online-b, c, d). Additional information is also available in the Joint ECDC/EFSA/EURL/EU-OSHA document on 'Testing and detection of zoonotic influenza virus infections in humans in the EU/EEA, and occupational safety and health measures for those exposed at work' (ECDC, 2022b).

2.3.8 ECDC risk assessment

Overall, the risk of infection of humans with avian influenza viruses of the currently circulating clade 2.3.4.4b A(H5) viruses in Europe for the general public in EU/EEA countries remains low.

The risk to occupationally or otherwise exposed groups to avian influenza infected birds or mammals including infected cats remains at low to moderate level. This assessment covers different situations that depend on the level of exposure.

More information on the methodology used for the assessment of the risk can be found at the published ECDC operational tool on rapid risk assessment methodology (ECDC, 2022a).

With the autumn migration of birds from northern to more central and southern areas in Europe, avian influenza detections in wild birds and outbreaks in poultry farms have been reported in central and southern European countries. This means a change of the avian influenza situation on the animal side from large outbreaks with mass mortality events in colony-breeding sea birds along coastlines, water bodies and in northern regions to single wild bird detections and poultry outbreaks across Europe. This shifts the exposure of humans geographically away from wild bird mortality close to urban areas, which is associated with exposure of a larger number of people in the general population and occupational groups, towards outbreaks in poultry farms where trained and specialised occupational groups such as cullers are exposed. Reassortment events have been observed and will likely continue globally leading to a more complex situation. Viruses currently circulating in bird populations in Europe are considered to be avian-adapted viruses, e.g. they bind to avian-like receptors, transmit and replicate best in bird species. However, mutations associated with mammalian adaptation have been identified sporadically in birds and more frequently in infected mammals. Despite the occurrence of mutations associated with mammalian adaptation, the viruses analysed retain preferential binding to avian receptors. Additional studies are required to better understand the impact of the different mutations that particularly evolved in the mammalian hosts. The newly introduced reassorted viruses and the various identified mutations associated with mammalian adaptation, which could increase the transmission to and replication in humans, will continue to be monitored for the emergence of any evidence that would change the overall risk assessment.

Despite indications of mammal-to-mammal transmission, no mammal-to-human transmission of clade 2.3.4.4b viruses has been observed. No transmission to exposed people has been identified during the investigation related to infected cats in Poland, nor has any human infection been detected in relation to the outbreaks in fur farms in Finland. Further, despite the large number of human exposure events to clade 2.3.4.4b viruses in EU/EEA over the last three years, e.g. exposure to poultry during culling operations or wild bird findings, no symptomatic or productive infection has been identified and reported. This underlines that the virus does not easily transmit from animals to humans and remains adapted to avian-like receptors despite gaining some increased ability to better replicate in mammals as indicated by mutations outlined earlier. Avian influenza transmission from animals to humans is a rare event, nevertheless, transmission to humans cannot be excluded when people without protection are in direct contact with infected animals or contaminated environment. To reduce the remaining risk of infection, people are recommended to wear protective equipment when in contact with sick or dead animals as well as contaminated environment.

A(H5N1) viruses of clade 2.3.2.1c have caused six human infections in Cambodia in 2023, four of those fatal, and are an older virus clade circulating in the region, but are not present in Europe and do not represent a risk to the general EU/EEA population. Exposure in the Cambodian cases was reported to sick and dead backyard chickens before onset of symptoms. Travelers to this region need to be aware of the risk of infection related to outbreaks in chickens in those rural areas and should avoid any contact to birds, their blood, feathers, droppings or other material in such places.

Outside the EU, human infections with severe disease progression and fatal outcomes have been observed, however, and such severe infections cannot be excluded should infections in the EU occur. The majority of human cases developing symptoms after infection with clade 2.3.4.4b viruses were reported to have had unprotected exposure to infected sick or dead poultry mostly in backyard settings but also exposed to contaminated environment. Special attention should be given to such settings to raise awareness and remind people to inform authorities when birds show acute symptoms and die as well as wear personal protective equipment when in contact with sick and dead birds.

Based on the analyses of known molecular markers associated with resistance towards antiviral drugs in the available sequences, the majority of the circulating A(H5N1) viruses in Europe remain susceptible to licensed antivirals for use in seasonal influenza virus infections as well as for pandemic use (NAIs: oseltamivir, zanamivir), M2 blockers (adamantanes), and cap-dependent endonuclease blocker (baloxavir marboxil). Antivirals are available as treatment options and post-exposure prophylaxis.

The proposed candidate vaccine viruses prepared for pandemic preparedness (to develop H5 vaccines for humans) are considered to be antigenically similar to the currently circulating clade 2.3.4.4b viruses in Europe. During the September 2023 Vaccine Composition meeting a new Candidate Vaccine Virus (CVV) for H9 (antigenically like A/Anhui/ Tianjiaan/11086/2022) was proposed (WHO, 2023d).

Vaccines against A(H5) viruses for the use in humans are not available at the moment. However, the A(H5N1) vaccine with market authorisation in the EU is currently being updated to include an avian influenza virus strain to match the circulating virus/clade, and it is expected to be authorised and available in early 2024.

For the winter period, when the annual respiratory virus epidemic typically occurs, ECDC suggests a risk-based targeted surveillance approach that focusses on outbreaks and severe respiratory or unexplained neurological disease in hospitalised patients:

- People admitted to hospitals with respiratory symptoms should be asked about exposure to sick or dead birds, wild or other animals in the two weeks prior to symptom onset or before admission (if symptom onset date cannot be defined), and should be tested according to an assessment of risk by the clinician. Specimens from hospitalised patients with very severe influenza virus infections could be considered for subtyping, particularly if believed to be part of a nosocomial outbreak.

- Hospitalised patients with unexplained viral encephalitis/meningoencephalitis should be considered for testing for seasonal influenza virus, and type A virus-positive specimens should be further subtyped for seasonal influenza viruses and therefore rule out avian influenza virus.
- Clusters of severe respiratory infections requiring hospitalisation should be investigated and testing for avian and other influenza viruses should be considered if routine testing for respiratory pathogens is inconclusive.

The surveillance guidance for the influenza season 2023/34 'Targeted surveillance to identify human infections with avian influenza virus during the influenza season 2023/24, EU/EEA' is available here: https://www.ecdc.europa.eu/en/publications-data/avian-influenza-infections-surveillance-eu-eea

This document complements the earlier published guidance that covered the summer period 2023: Enhanced surveillance of severe avian influenza virus infections in hospital settings in the EU/EEA (europa.eu)

3. Conclusions

3.1 Birds

- Compared to previous epidemiological years, a delay in the increase in number of HPAI virus detections in waterfowl, usually expected to occur after the summer period, is observed. In previous epidemiological years this increase was already observed at the beginning of October, whereas this year the increase has only taken place from November. The delay observed is possibly due to a delayed wild bird migration associated with warm autumn weather.
- The steep increase in HPAI virus detections in waterfowl observed since the end of October 2023, both along the Baltic and Black Sea/Mediterranean migration routes, is likely to result in increased levels of the virus present in the environment, leading to further increase in HPAI virus detections in wild birds, poultry and mammals. It is too early to predict whether a similarly high number of HPAI virus detections as in the previous years or a reduction due to development of some level of immunity in previously affected wild bird species would be observed.
- There was an incursion of HPAI virus into common cranes along the Baltic-Hungarian migration route, causing high mortality in this species for the first time in Europe. All the genetically characterised viruses from common cranes were highly related to each other.
- In line with an increase in HPAI virus detections in wild birds, there is an ongoing increase in the number of outbreaks in poultry, with most outbreaks being reported at the end of this reporting period. Following the trends of previous epidemiological years, a medium to high risk of incursion in poultry establishments is expected for the coming winter months.
- With the exception of two clusters of HPAI outbreaks in Hungary due to secondary spread, most outbreaks detected in poultry during this reporting period were reported as primary outbreaks with most likely source of

introduction being contact with wild birds. A range of different poultry species and production systems has been affected since the beginning of the new epidemiological year 2023–2024.

- Since the beginning of October 2023, preventive vaccination against HPAI A(H5) viruses has been implemented in France, targeting certain categories of poultry. By 19 November 2023, more than 6.8 million domestic ducks had already been vaccinated. So far, no HPAI virus circulation has been detected in the vaccinated population.
- A sharp decline in detections of the A(H5N1) BB genotype, which circulated extensively in Europe (mainly in seabirds) during the summer months, was observed. Since October, there has been an increase in the number of other circulating genotypes, several of which had never been detected in Europe before. The change in the prevalence of detected genotypes and the increase in the genotype diversity is likely due to the decreased number of cases in seabirds and the increased prevalence in wild Anseriformes and other wild bird species. The limited availability of genetic data from countries outside Europe makes it impossible to determine whether these new genotypes were newly introduced or generated within Europe.
- The detection in a poultry outbreak in Poland of a virus containing a marker of mammalian adaptation in the PB2 protein (E627K), similar to the viruses responsible of several infections in domestic cats during the summer months, indicates a persistent circulation in the bird population of a virus with an increased zoonotic potential.
- The A(H5N1) viruses currently circulating in Europe retain a preferential binding for avian-like receptors; however, several mutations associated with increased zoonotic potential have been detected. Their effects on the biological characteristics of the viruses need to be further investigated.
- Subtype A(H5N5), genotype I, which has been persistently detected in Norway since the 2021–2022 epidemiological year, spread to Iceland and the United Kingdom. A(H5N5) was also detected in Greenland during this reporting period.
- Compared to the previous reporting period (EFSA, ECDC and EURL, 2023), HPAI outbreaks in poultry increased by five times worldwide and almost twice the number of HPAI virus detections in wild birds were reported from a higher number of countries to WOAH, especially from the Americas and Asia.
- The HPAI situation in North America has been severe with a large number of HPAI outbreaks in poultry being reported from the United States of America (and increasingly also from Canada). In contrast, the number of HPAI virus detections notified in wild birds during this reporting period was low. However, HPAI virus detections in both poultry and wild birds in South America may indicate continuous circulation of HPAI viruses among migratory wild bird species on the continent.
- HPAI virus detections in seabirds in the sub-Antarctic and Antarctic regions, on the Falkland Islands and South Georgia, were reported during this reporting period. There is concern for high mortality in the many wild bird populations on

those islands, including penguins, albatrosses and petrels. There is also concern for HPAI spreading to wild birds elsewhere in the Antarctic region.

3.2 Mammals

- The ongoing serological survey in all fur farms in Finland resulted in 29 additional serologically positive farms since the beginning of September 2023. Those farms were keeping American mink, red and Arctic foxes, common raccoon dogs and sables. Only a few of those farms reported mortality (3) and clinical signs (2), which indicates possible asymptomatic infection that could go undetected by passive surveillance in those species.

- Unlike the mammalian infections reported in Europe during the summer months, mainly caused by the BB genotype, the recent A(H5N1) viruses identified in wild mammals (Eurasian lynx, Eurasian otter and harbor seals) in Finland and Denmark belonged to the AB genotype.

- In South America, HPAI continued to spread along the east coast and resulted in high mortality of major breeding colonies of South American sea lions and southern elephant seals in Argentina, Brazil and Uruguay. The virus has also been detected in southern elephant seals in the Antarctic region, home to half of their global population. There is also concern for high mortality in other wild mammal populations such as Antarctic fur seals on those islands.

- The high percentage (about 43%) of European viruses collected from mammalian species containing molecular markers of mammalian adaptation in the PB2 protein indicates that these mutations can be rapidly acquired by the virus during infection in mammalian species. Viruses containing such mutations may have a greater zoonotic potential.

- To date, no key mutations associated with the switch in the virus binding preference from avian- to human-type receptors were identified in the A(H5) virus collected from mammalian species in Europe.

3.3 Humans

- Continued sporadic human avian influenza A(H3N8), A(H5N1), A(H5N6) and A(H9N2) virus detections or (severe) infections have been reported from different countries globally during 2023.

- Severe and fatal infections in humans have so far been mainly related to unprotected exposure to sick and dead poultry, particularly in backyard settings, as well as to contaminated environment or to live bird markets.

- No symptomatic human cases have been detected in the EU despite the likely large number of exposure events over the last years.

- With the continued circulation of avian influenza viruses, sporadic transmission events to humans will likely occur related to settings where people are exposed to sick and dead birds without wearing protective equipment.

4. Options for response

4.1 Birds

- For wild birds, general options for response include accurate and comprehensive recording of HPAI-associated mortality events to guide future policy changes regarding HPAI; preventing disturbance of areas undergoing HPAI outbreaks to reduce virus spread; if on time, removal of HPAI-affected carcasses from areas where wild birds are congregated to reduce virus spread. Options for response specific to the current situation include increased monitoring of common cranes along the rest of the Baltic-Hungarian migration route, as well as along other migration routes (Western European, Eastern European), both at stopover and wintering sites in Europe, the Middle East, and northern and eastern Africa.

- Predictions of the probability of HPAI virus introduction into wild birds in Europe for the coming weeks can be consulted via EFSA's Bird Flu Radar: https://app.bto.org/hpai/

- For poultry, the expected increase in HPAI virus detections in waterfowl, and subsequent increased chance of incursion into poultry farms, need to be accounted for. Both short-term preparedness and medium- to long-term prevention strategies have been described in detail in previous EFSA reports.

- The geographic expansion of HPAI A(H5N5) viruses in wild birds in northern parts of Europe should be closely monitored.

- Active surveillance in wild birds, especially in those that silently maintain HPAI viruses in the wild (e.g. waterfowl), is indicated to improve knowledge on HPAI viruses circulating in wild bird populations.

- Timely generation and sharing of genome sequence data from avian influenza viruses is of utmost importance to promptly detect the possible emergence of viruses with mutations associated with increased zoonotic potential, resistance toward antiviral drugs or different antigenic properties, whose biological characteristics should be further evaluated. Genetic data are also instrumental to track the virus spread and identify novel incursions of viruses which may represent a threat for human or animal health.

- Reinforcement of genetic characterisation of viruses collected from birds in areas where a high number of infections in mammalian species was identified is recommended to promptly detect possible mammal-to-avian transmission of viruses containing markers of virus adaptation to mammalian species, which may have a higher zoonotic potential.

4.2 Mammals

- For fur farms, measures taken should account for the risk of HPAI for both animal and human health. Options for response include: improving biosecurity in fur farms, which currently allow access of wild birds and mammals (Sikkema et al., 2022); prohibition to feed raw poultry or pig by-products, which may be infected with influenza A viruses, including HPAI viruses (Veldhuis Kroeze and Kuiken T, 2016); inclusion of fur farms in the national surveillance programmes for avian influenza (early detection through virological testing, timely follow-up of positive serological tests with virological tests) (Sun et al., 2021); prompt culling (destroying) of all animals present in HPAI-affected fur farms; exploration of the options for vaccination of fur animals to prevent the emergence of mutations and to avoid risk of virus transmission to humans (Kibenge, 2023); and avoidance of locating fur farms in areas with dense populations of waterfowl and/or seabirds.

- Increased surveillance of HPAI viruses in wild (e.g. red foxes) and free-roaming domestic carnivores (e.g. cats and dogs) continues to be recommended, for evaluating both the level of virus infections in those species and the risk of emergence and transmission of mammal-adapted viruses. Such surveillance efforts should prioritise domestic mammals present in or around HPAI-affected poultry establishments and those in possible contact with infected poultry, wild birds or other mammals. Research activities to investigate the role of asymptomatic mammals in maintaining HPAI viruses and driving their evolutionary dynamics are recommended.

- Disease dynamics associated with HPAI virus infection during mass mortality events in mammal species should be thoroughly investigated. Testing a sufficient number of animals and assuring a prompt generation and sharing of viral sequences are of utmost importance to shed light on the virus origin, evolution and possible transmission between individuals. The latter is also indicated to timely assess the pandemic risk.

- More accurate and timely reporting of HPAI virus detections in mammals is recommended in a way that reliable numbers of infected animals could be used as quantitative information for risk assessment.

4.3 Humans

- The general public should avoid contact with sick or dead animals and inform authorities or veterinarians if they see dead birds or other animals to coordinate safe removal and control measures.

- Appropriate personal protective equipment should be used when in contact with potentially infected animals.

- People in unprotected direct contact with sick or dead birds, infected mammals and contaminated environment should be followed up for 10–14 days after last exposure and tested immediately following the onset of respiratory or any other symptoms to identify transmission events early. Following exposure to infected mammals, testing can also be considered without indications of onset of symptoms in the exposed people.

- During winter months, when seasonal influenza viruses are circulating in the population, testing and subtyping approaches for avian influenza virus need to be proportionate to the epidemiological situation and the capacities of reference laboratories. Therefore, in areas with ongoing avian influenza outbreaks in poultry and detections in wild birds and other animals, a risk-based targeted approach, focusing on outbreaks and severe respiratory or unexplained neurological disease, is proposed (https://www.ecdc.europa.eu/en/publications-data/avian-influenza-infections-surveillance-eu-eea).

- Options for response including vaccination of occupationally exposed people and additional information are available on ECDC webpages: Avian influenza

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Appendix A – Terms of Reference

A.1. Background and Terms of Reference as provided by the requestor

Avian influenza is an infectious viral disease in birds, including domestic poultry. Infections with avian influenza viruses in poultry cause two main forms of that disease that are distinguished by their virulence. The low pathogenic (LPAI) form generally only causes mild symptoms, while the highly pathogenic (HPAI) form results in very high mortality rates in most poultry species. That disease may have a severe impact on the profitability of poultry farming.

Avian influenza is mainly found in birds, but under certain circumstances infections can also occur in humans even though the risk is generally very low.

More than a decade ago, it was discovered that virus acquired the capability to be carried by wild birds over long distances. This occurred for the HPAI of the subtype A(H5N1) from South East and Far East Asia to other parts of Asia, Europe and Africa as well as to North America. In the current epidemic the extent of the wild bird involvement in the epidemiology of the disease is exceptional.

Since late October 2016 up until early February 2017, highly pathogenic avian influenza (HPAI) of the subtype A(H5N8) has been detected in wild migratory birds or captive birds on the territory of 21 Member States, namely Austria, Belgium, Bulgaria, Croatia, Czechia, Denmark, Finland, France, Germany, Greece, Hungary, Ireland, Italy, the Netherlands, Poland, Portugal, Slovakia, Slovenia, Spain, Sweden and the United Kingdom. In 17 Member States the virus has spilled over to poultry holdings leading also to lateral spread between holdings in a few Member States, in particular in those with a high density of duck and geese holdings where the poultry cannot sufficiently be protected against contacts with wild birds. A second HPAI subtype A(H5N5) has been detected in wild birds and recently also in poultry holdings in Germany.

The number of infected migratory wild birds found dead and the geographic extent of these findings are posing an immense threat for virus introduction into poultry or captive birds holdings as demonstrated by the high number of outbreaks (~700 as of 08/02/2017).

In the event of an outbreak of avian influenza, there is a risk that the disease agent might spread to other holdings where poultry or other captive birds are kept. As a result, it may spread from one Member State to other Member States or to third countries through trade in live birds or their products.

There is knowledge, legislation, technical and financial tools in the EU to effectively deal with outbreaks of avian influenza in poultry and captive birds. However, the very wide virus spread by wild birds and the increased risk of direct or indirect virus introduction into poultry or captive bird holdings has led to the largest HPAI epidemic in the EU so far. This situation calls for a reflection and evaluation how preparedness, risk assessment, early detection and control measures could be improved.

The Commission and Member States are therefore in need of an epidemiological analysis based on the data collected from the disease affected Member States. The use of the EFSA Data Collection Framework is encouraged given it promotes the harmonisation of data collection. Any data that is available from neighbouring third countries should be used as well, if relevant.

Therefore, in the context of Article 31 of Regulation (EC) No. 178/2002[14], EFSA should provide the technical and scientific assistance to the Commission based on the following Terms of Reference (TOR):

1) Analyse the epidemiological data on highly pathogenic avian influenza (HPAI) and low pathogenic avian influenza (LPAI), where co-circulating or linked within the same epidemic, from HPAI disease affected Member States.

2) Analyse the temporal and spatial pattern of HPAI and LPAI as appropriate in poultry, captive birds and wild birds, as well the risk factors involved in the occurrence, spread and persistence of the HPAI virus in and at the interface of these avian populations.

3) Based on the findings from the points above, describe the effect of prevention and control measures.

4) Provide for regular quarterly reports updating on the avian influenza situation within the Union and worldwide, in particular with a view to describe the evolution of virus spread from certain regions towards the EU. In case of significant changes in the epidemiology of avian influenza, these reports could be needed more frequently. These reports should in particular closely follow the developments of zoonotic avian influenza viruses (such as HPAI A(H5N6) and LPAI A(H7N9)) in collaboration with the European Centre for Disease Prevention and Control (ECDC).

A.2 Interpretation of the Terms of Reference

In reply to ToR 1 and ToR 2, this Scientific Report gives an overview of the HPAI outbreaks in poultry, captive and wild birds detected in Europe from 2 September to 1 December 2023 and reported by Member States and neighbouring countries to ADIS or WOAH. Member States and other European countries where HPAI outbreaks have occurred in poultry submitted additional epidemiological data to EFSA, which have been used to analyse the characteristics of the affected poultry establishments.

It was not possible to collect data for a risk factor analysis on the occurrence and persistence of HPAI virus within the EU. Risk factor analysis requires not only case-related information but also data on the susceptible population (e.g. location of establishments, population structure), which should be collected in a harmonised manner across the EU. Limitations in data collection, reporting and analysis were explained in the first avian influenza overview report (EFSA, ECDC and EURL, 2017).

Monitoring of the avian influenza situation in other countries (ToR 4) is based on data reported to WOAH. The description focuses only on findings of avian influenza viruses occurring in countries that are considered to be of epidemiological interest for the EU/EEA and the United Kingdom, or of public health relevance, specifically on HPAI A(H5N1), A(H5N2), A(H5N5), A(H5N6), A(H5N8), A(H7N6), HPAI/LPAI A(H7N9) and LPAI A(H9N2). The background and epidemiology, detections, phenotypic and genetic characterisations are described based on information from confirmed human, poultry and wild bird cases that occurred from 2 September to 1 December 2023. Possible actions for preparedness in the EU are discussed.

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[14] Regulation (EC) No 178/2002 of the European Parliament and of the Council of 28 January 2002 laying down the general principles and requirements of food law, establishing the European Food Safety Authority and laying down procedures in matters of food safety. OJ L 31, 1.2.2002, pp. 1–24.

This report mainly describes information that has become available since the publication of the EFSA report for the period June to September 2023 (EFSA, ECDC and EURL, 2023) and that might affect the interpretation of risks related to avian influenza introduction and/or spread in Europe.

Appendix B – Data and Methodologies

B.1 Data on animals

B.1.1 Overview of avian influenza outbreaks in Europe (ToR 1 and ToR 2)

Data on HPAI outbreaks occurred in Europe between 2 September and 1 December 2023 and submitted by Member States or other European countries to ADIS were taken into account for this report. Data extraction was carried out on 1 December 2023. WOAH-WAHIS was consulted to complement the information for European countries not reporting HPAI notifications to ADIS. In addition, HPAI-affected countries were asked to provide more detailed epidemiological information on HPAI outbreaks occurred in poultry directly to EFSA. This information included details on the poultry species and production systems affected by HPAI, which were supplied in form of additional variables to complement the data reported via ADIS. All details are provided in Annex B. The information EU countries affected by HPAI and LPAI presented to the Standing Committee on Plants, Animals, Food and Feed (SCOPAFF), and the evidence on HPAI and LPAI outbreaks provided in the info notes from the affected countries to EC were consulted to extract relevant information that is reported in Section 2.1.1. The presentations delivered at the SCOPAFF meetings are available on the EC website (European Commission, online).

Wild bird species have been categorised according to Table A.2 in Annex A, and the common and scientific names of wild bird species described in this report for Europe are reported in Table A.3 in Annex A. The public GISAID’s EpiFlu™ database was accessed to download newly released avian influenza virus sequences.

The annexes to this Scientific Report are available on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.10371651

B.1.2 Overview of avian influenza outbreaks in other countries not reporting via ADIS (ToR 4)

Data from WOAH-WAHIS on HPAI A(H5N1), A(H5N2), A(H5N5), A(H5N6), A(H5N8) and A(H7N6) in domestic and wild birds were used to describe and map the geographic distribution of avian influenza virus detections in domestic and wild birds in Africa, the Americas, Asia and Europe based on the observation dates. Data were retrieved on 1 December 2023 and extracted by EFSA. They were used and reproduced with permission. WOAH bears no responsibility for the integrity or accuracy of the data contained herein, but not limited to, any deletion, manipulation, or reformatting of data that may have occurred beyond its control.

B.1.3 Genetic characterisation of avian influenza viruses: description of the nomenclature of the HPAI A(H5) viruses used in the document

The HA gene of clade 2.3.4.4 A(H5) viruses has rapidly evolved since the most recent official update of the nomenclature of the A/goose/Guangdong/1/1996-lineage H5Nx virus (Smith and Donis, 2015). This clade emerged in China in 2008 and since then it has acquired various neuraminidase subtypes, including N1, N2, N3, N4, N5, N6 and N8, by reassortments with other avian influenza viruses from different regions, and has evolved into several subgroups. While a revised nomenclature of clade 2.3.4.4 viruses is pending, in previous reports we used the genetic clustering described in 2018 by Lee and co-authors, who recognised four groups (a–d) within clade 2.3.4.4 (Lee et al., 2018). Recently, an update to the unified nomenclature for clade 2.3.4.4 A(H5) viruses has been proposed by the WHO and eight genetic groups (a–h) have been recognised. To align the nomenclature system between international organisations this classification has been adopted for this report. Based on this proposed clustering, A(H5) viruses of clades 2.3.4.4a and d–h have mainly been circulating in poultry in Asia, while clades 2.3.4.4b and 2.3.4.4c have spread globally through wild bird migrations during 2014–2015 (2.3.4.4c) and from 2016 to the present day (2.3.4.4b). A list with the distribution of the different genetic clades reported by countries globally from birds, humans and the environment has been published by WHO in February 2023 (WHO, 2023c).

B.2 Data on humans

The numbers of human cases caused by infection with avian influenza viruses were collected by ECDC. Multiple sources are scanned regularly as part of Epidemic Intelligence activities at ECDC to collect information on laboratory-confirmed human cases. Data were extracted and line lists developed to collect case-based information on virus type, date of disease onset, country of reporting, country of exposure, sex, age, exposure, clinical information (hospitalisation, severity) and outcome. All cases included in the line list and mentioned in the document have been laboratory-confirmed. Data are continuously checked for double entries and validity. The data on human cases cover the full period of time since the first human case was reported. Therefore, data on human cases refer to different time periods and are included irrespective of whether there have been any new human cases during the reporting period. Relevant information about human infections, risk factors as well as data from studies on virus transmission to and between mammals are included. Literature is searched using different search terms for the respective virus subtypes and assessed of their relevance for inclusion by two independent experts.

Annex A – Data on Birds

Annex A is available under the Supporting Information section in the online version of the scientific output.

Annex B – Data on poultry outbreaks

Annex B is available under the Supporting Information section in the online version of the scientific output.

Annex C – Acknowledgements

Annex C is available under the Supporting Information section in the online version of the scientific output.