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# Avian influenza overview December 2023–March 2024

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## Abstract

Between 2 December 2023 and 15 March 2024, highly pathogenic avian influenza (HPAI) A(H5) outbreaks were reported in domestic (227) and wild (414) birds across 26 countries in Europe. Compared to previous years, although still widespread, the overall number of HPAI virus detections in birds was significantly lower, among other reasons, possibly due to some level of flock immunity in previously affected wild bird species, resulting in reduced contamination of the environment, and a different composition of circulating A(H5N1) genotypes. Most HPAI outbreaks reported in poultry were primary outbreaks following the introduction of the virus by wild birds. Outside Europe, the majority of outbreaks in poultry were still clustered in North America, while the spread of A(H5) to more naïve wild bird populations on mainland Antarctica is of particular concern. For mammals, A(H5N5) was reported for the first time in Europe, while goat kids in the United States of America represented the first natural A(H5N1) infection in ruminants. Since the last report and as of 12 March 2024, five human avian influenza A(H5N1) infections, including one death, three of which were clade 2.3.2.1c viruses, have been reported by Cambodia. China has reported two human infections, including one fatal case, with avian influenza A(H5N6), four human infections with avian influenza A(H9N2) and one fatal case with co-infection of seasonal influenza A(H3N2) and avian influenza A(H10N5). The latter case was the first documented human infection with avian influenza A(H10N5). Human infections with avian influenza remain rare and no sustained human-to-human infection has been observed. 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 those occupationally or otherwise exposed to infected animals.

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## 1. Introduction

This Scientific Report provides an overview of highly pathogenic avian influenza (HPAI) virus detections in poultry<sup>1</sup>, captive birds<sup>2</sup>, wild birds and mammals that occurred in and outside Europe between 2 December 2023 and 15 March 2024, as well as human cases due to avian influenza viruses up until 12 March 2024.

The background, Terms of Reference (TOR) 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

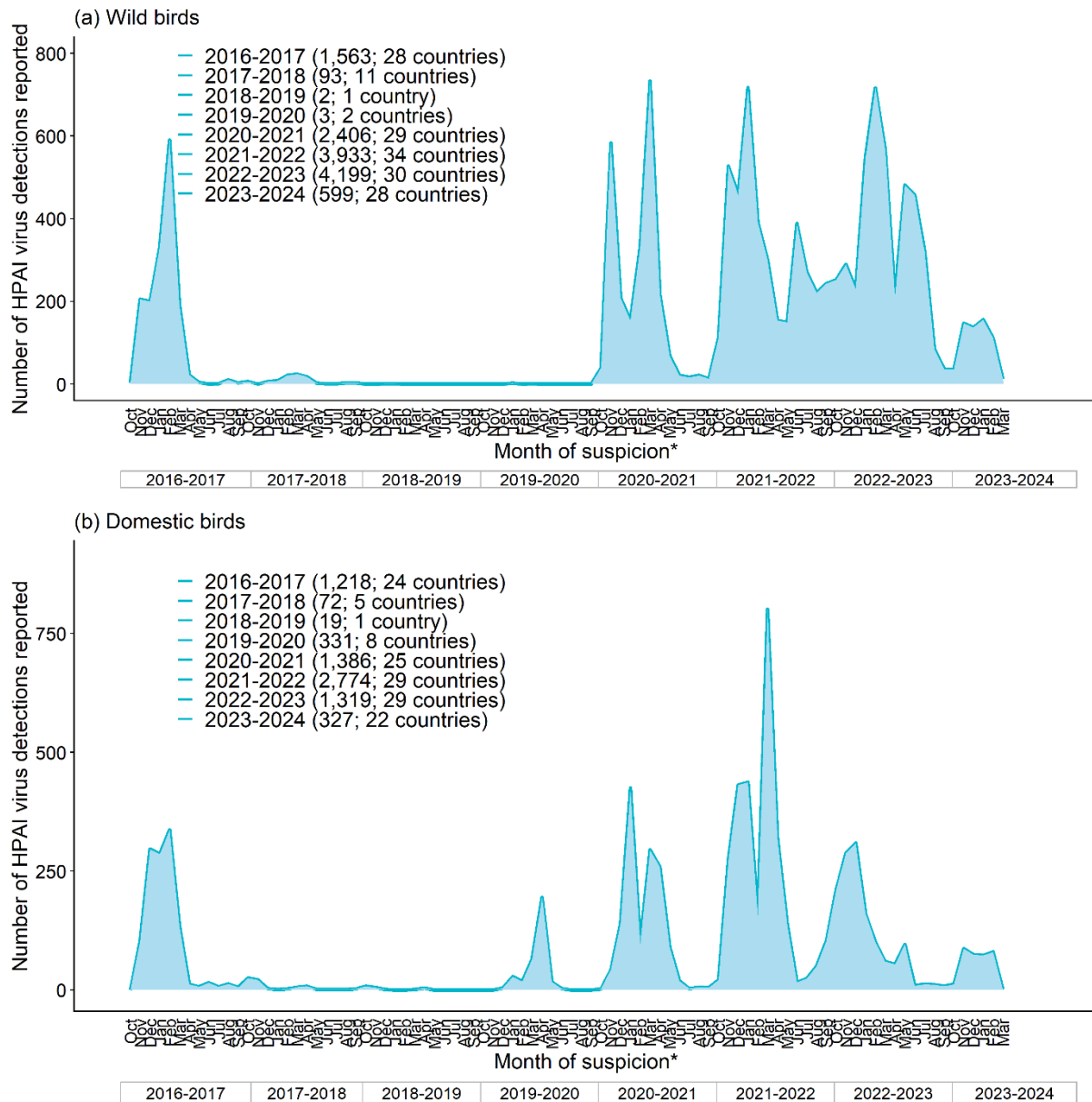
Figure 1 shows all HPAI virus detections in birds that were reported via the European Union (EU) Animal Disease Information System (ADIS) or the World Animal Health Information System (WOAH-WAHIS) of the World Organisation for Animal Health (WOAH) in Europe for the last seven and the current epidemiological years<sup>3</sup> by month of suspicion. For the current epidemiological year 2023–2024, starting on 1 October 2023, data reported are truncated on 15 March 2024.

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<sup>1</sup> 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).

<sup>2</sup> 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.

<sup>3</sup> 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.



\*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 WOAHP for the United Kingdom (excluding Northern Ireland) and ADNS/ADIS for the United Kingdom (Northern Ireland)<sup>4</sup>. Source: ADNS/ADIS and WOAHP (data extraction carried out on 15 March 2024).

**Figure 1:** Distribution of the number of HPAI virus detections in wild (12,798) (a) and domestic (7,446) (b) birds reported in Europe during eight epidemiological years by month of suspicion, from 1 October 2016 to 15 March 2024 (20,244)

The increase in reported HPAI virus detections from October 2023 onward, expected to continue also after December 2023, did not manifest itself in a surge, but remained at a similar level throughout the following months and reached smaller peaks for wild and domestic birds in January and February 2024, respectively (Figure 1).

During this reporting period, the overall number of HPAI virus detections in birds was much lower than during the same time period in previous years. At the same time, less

<sup>4</sup> In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Windsor Framework, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).

mortality events have been described in wild birds in Europe since the beginning of the epidemiological year 2023–2024.

Considering the current reporting period, from 2 December 2023 to 15 March 2024, 640 HPAI virus detections were reported in poultry (179), captive (48) and wild birds (414), respectively (Table 1, Figure 2).

**Table 1:** Number of HPAI outbreaks reported in Europe, by country, virus subtype and affected sub-population, from 2 December 2023 to 15 March 2024. Cumulative numbers since the start of the 2023–2024 epidemiological year are reported in parentheses (1 October 2023 to 15 March 2024)

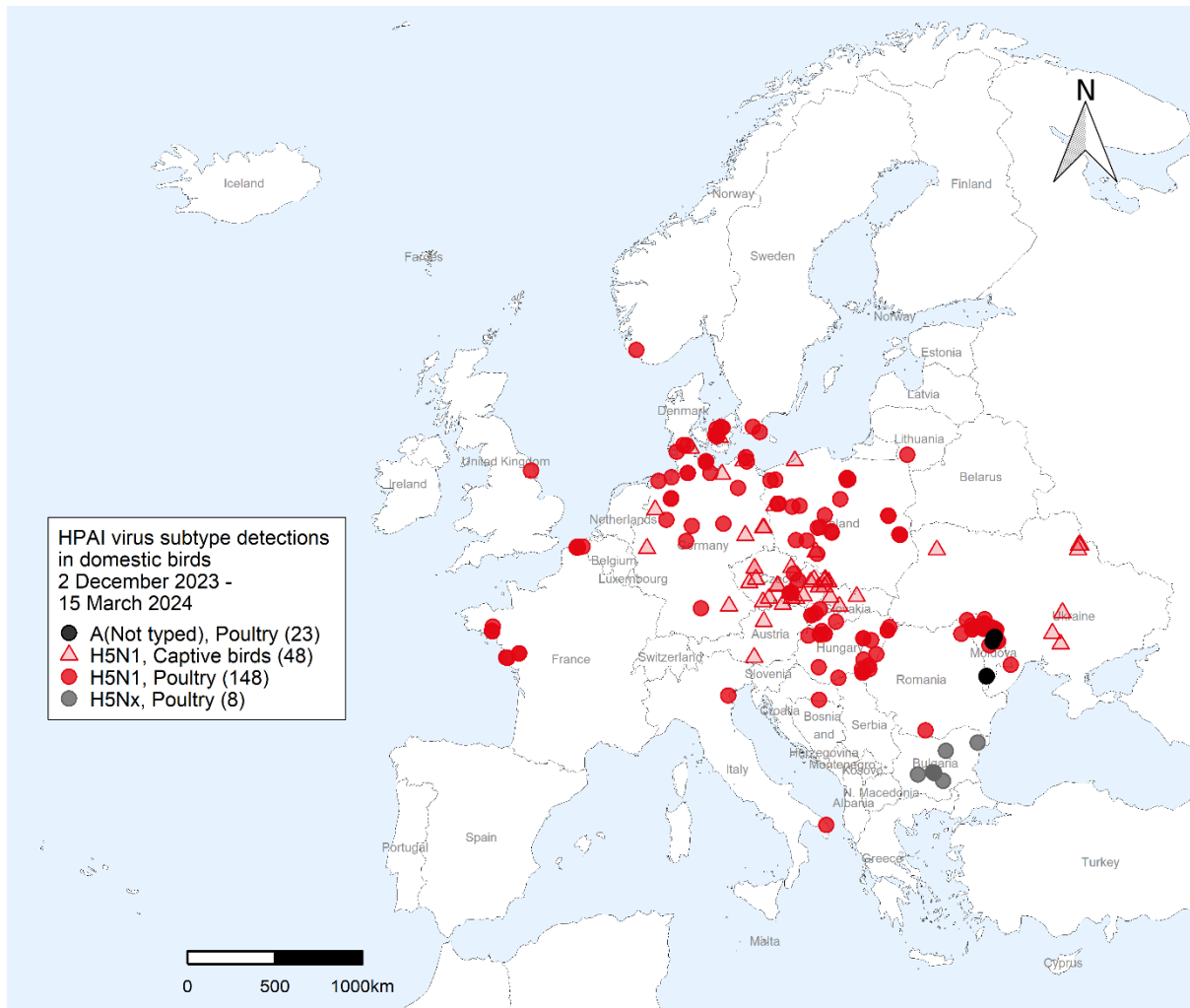
Reporting country	Captive birds		Poultry			Wild birds				Total
	A(H5N1)	A(H5N5)	A(H5N1)	A(H5Nx)	A(Not typed)	A(H5N1)	A(H5N5)	A(H5Nx)	A(Not typed)	
Austria	3 (4)	-	-	-	-	13 (23)	-	1 (2)	-	17 (29)
Belgium	-	-	3 (4)	-	-	5 (5)	-	1 (1)	-	9 (10)
Bosnia and Herzegovina	-	-	-	-	-	1 (1)	-	-	-	1 (1)
Bulgaria	-	-	0 (5)	8 (12)	-	-	-	-	-	8 (17)
Croatia	-	-	1 (2)	-	-	6 (7)	-	-	-	7 (9)
Cyprus	-	-	-	-	-	1 (1)	-	-	-	1 (1)
Czechia	22 (22)	-	5 (5)	-	-	7 (7)	-	-	-	34 (34)
Denmark	1 (1)	-	8 (11)	-	-	65 (71)	-	-	-	74 (83)
Faroe Islands	-	0 (1)	-	-	-	-	-	-	-	0 (1)
Finland	-	-	-	-	-	0 (3)	-	-	-	0 (3)
France	-	-	8 (10)	-	-	-	-	7 (13)**	-	15 (23)
Germany	9 (11)	-	20 (26)	-	-	117 (148)	2 (2)	1 (2)	-	149 (189)
Hungary	-	-	22 (76)	-	-	14 (49)	-	-	-	36 (125)
Iceland	-	-	-	-	-	-	0 (4)	-	-	0 (4)
Italy	-	-	2 (6)	-	-	8 (19)	-	-	-	10 (25)
Kosovo*	-	-	0 (1)	-	-	-	-	-	-	0 (1)
Lithuania	-	-	1 (1)	-	-	1 (1)	-	-	-	2 (2)
Moldova	-	-	35 (35)	-	23 (23)	30 (30)	-	-	-	88 (88)
Netherlands	0 (2)	-	0 (3)	-	-	18 (39)	-	1 (1)	-	19 (45)
Norway	0 (1)	-	1 (1)	-	-	1 (1)	1 (4)	0 (3)	-	3 (10)
Poland	3 (3)	-	31 (33)	-	-	18 (18)	-	-	-	52 (54)
Portugal	-	-	-	-	-	1 (6)	-	-	-	1 (6)
Romania	-	-	2 (4)	-	-	25 (32)	-	-	-	27 (36)
Serbia	-	-	-	-	-	0 (9)	-	-	-	0 (9)
Slovakia	3 (3)	-	6 (6)	-	-	9 (9)	-	-	-	18 (18)
Slovenia	-	-	-	-	-	12 (13)	-	-	-	12 (13)
Spain	-	-	-	-	-	3 (13)	-	-	-	3 (13)
Sweden	-	-	2 (2)	-	-	24 (29)	-	3 (4)	-	29 (35)



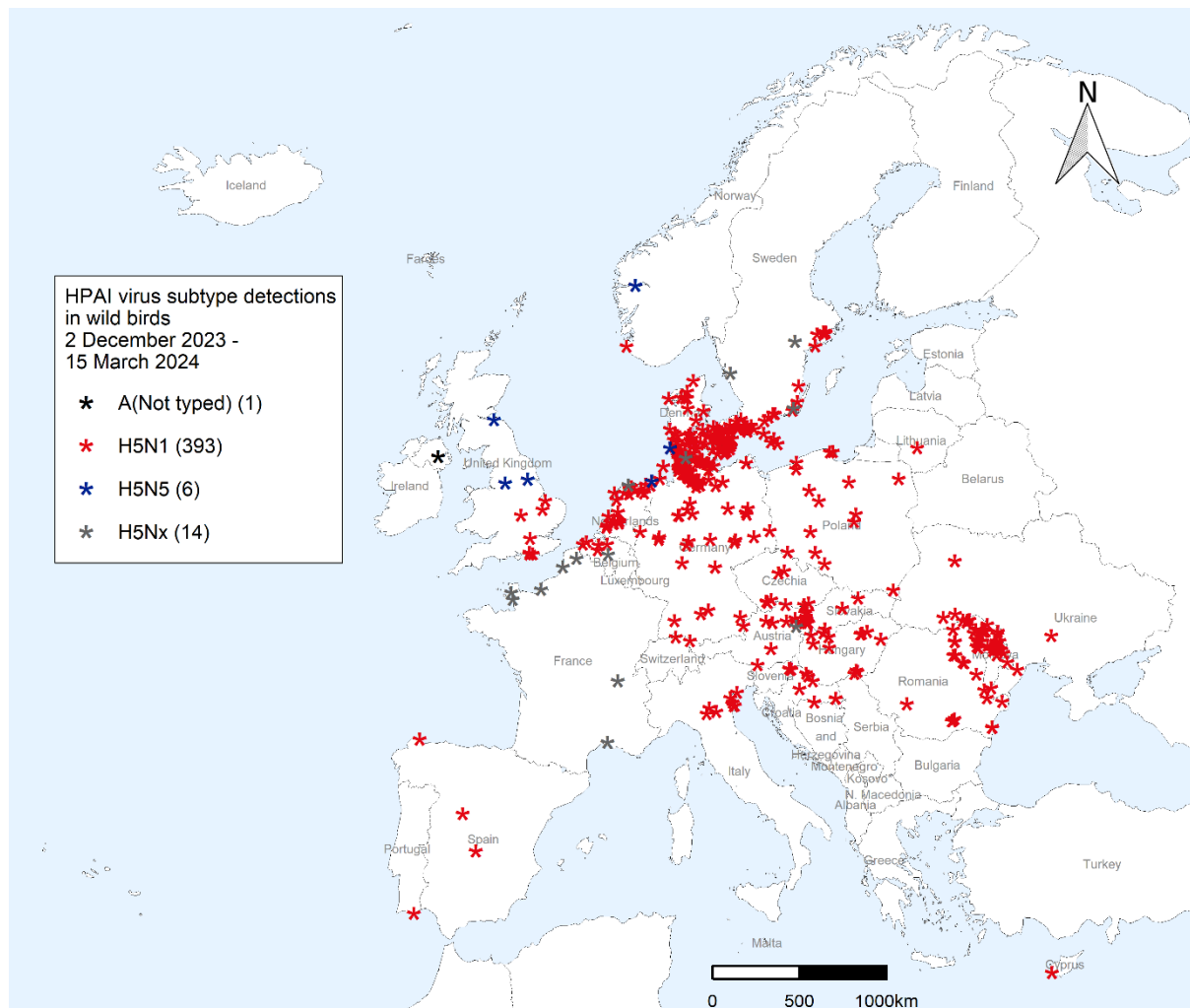
Switzerland	-	-	-	-	-	1 (1)	-	-	-	1 (1)
Ukraine	7 (7)	-	-	-	-	6 (6)	-	-	-	13 (13)
United Kingdom	-	-	1 (6)	-	-	7 (17)	3 (4)	-	1 (1)	12 (28)
<b>Total</b>	<b>48 (54)</b>	<b>0 (1)</b>	<b>148 (237)</b>	<b>8 (12)</b>	<b>23 (23)</b>	<b>393 (558)</b>	<b>6 (14)</b>	<b>14 (26)</b>	<b>1 (1)</b>	<b>641 (926)</b>

\*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.

\*\*In France, during this reporting period, 6 A(H5N1) and 1 A(H5Nx) virus detections were reported in wild birds. Since the beginning of the epidemiological year 2023–2024 10 A(H5N1) and 3 A(H5Nx) virus detections were reported in wild birds. Not all those data have been updated in ADIS yet.



Author: EFSA  
 Data sources: ADIS, WOAH  
 Date updated: 15/03/2024



Author: EFSA  
Data sources: ADIS, WOAH  
Date updated: 15/03/2024

\*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)<sup>5</sup>.  
Source: ADIS, EFSA and WOAH (data extraction carried out on 15 March 2024).

**Figure 2:** Geographic distribution, based on available geocoordinates, of HPAI virus detections in poultry and captive birds (227) (upper panel), and in wild birds (414) (lower panel) reported by virus subtype in Europe from 2 December 2023 to 15 March 2024

In the current epidemiological year 2023–2024 up until now, except for a few countries (e.g. Hungary), HPAI outbreaks in poultry can largely be attributed to the current reporting period (Table 1). The number of outbreaks in poultry were generally lower compared to previous epidemiological years, which may be due to a reduction in the level of contamination in the environment around poultry establishments, and thus possibly associated with the lower number of HPAI virus detections in wild birds compared to the previous epidemiological years.

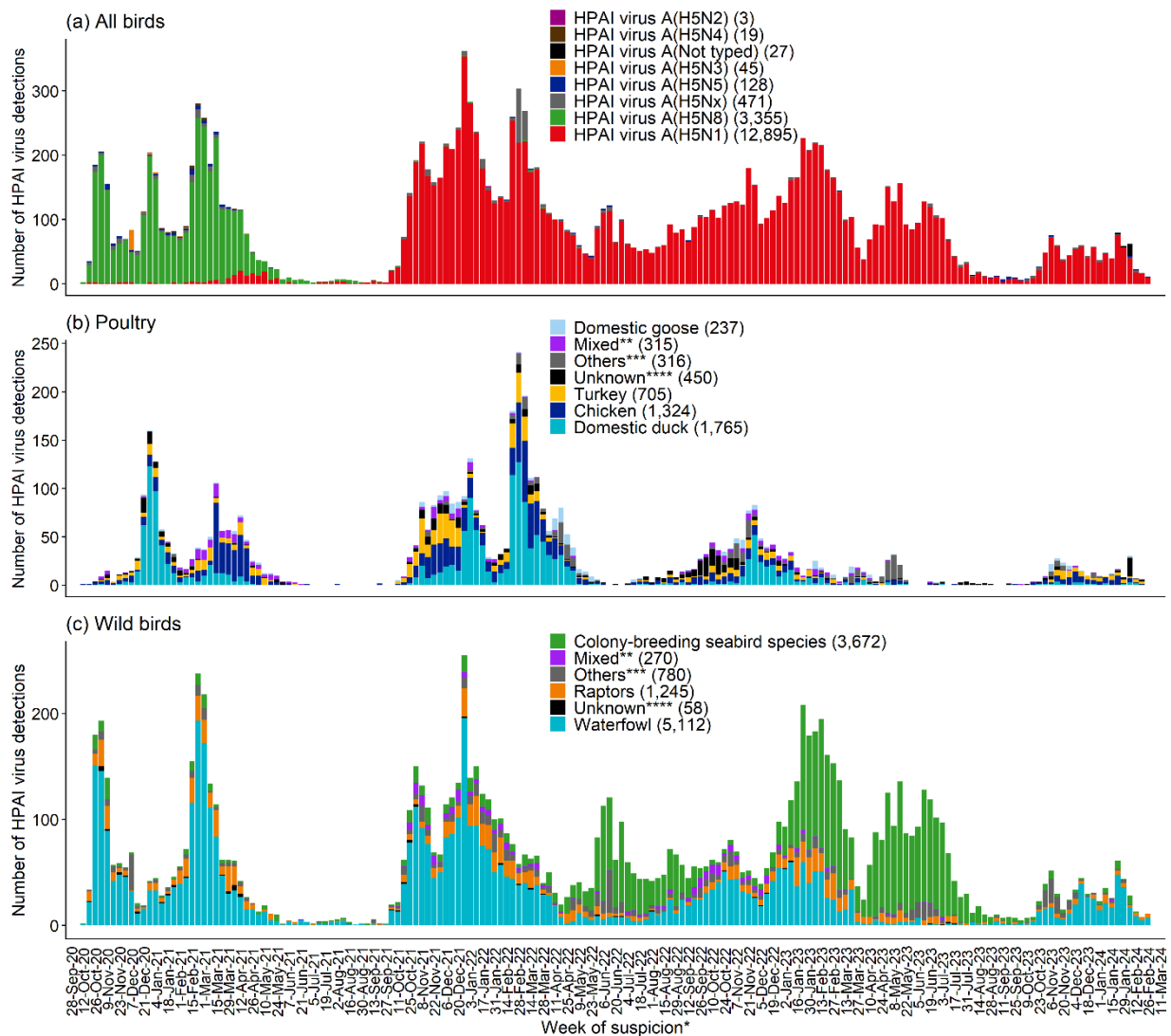
HPAI virus detections in domestic birds were reported from large parts of Europe, especially from the north and east, with two major clusters along the North Sea and the

<sup>5</sup> In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Windsor Framework, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).

Baltic Sea coasts, and west of the Black Sea (Figure 2). In other parts of Europe, such as in large parts of Scandinavia and on the Iberian Peninsula, HPAI virus was almost absent. The spatial pattern of HPAI virus detections during this reporting period was similar in wild and domestic birds, with some exceptions: Bosnia and Herzegovina, Cyprus, the Netherlands, Portugal, Slovenia, Spain and Switzerland only reported HPAI virus detections in wild birds, whereas Bulgaria only reported HPAI virus detections in domestic birds.

Changes in the overall incidence and distribution of HPAI virus detections in Europe are also influenced by the changing composition of A(H5N1) genotypes, with a significant reduction in the EA-2022-BB genotype and the emergence of new genotypes in the epidemiological year 2023–2024. A(H5N1) virus continued to be predominant (589 out of 641 HPAI virus detections), while A(H5N5) virus was still sporadically detected in wild birds in Germany (2), Norway (1) and the United Kingdom (3). A(H5Nx) or untyped influenza A viruses were involved in another 46 outbreaks (Figure 2).

The majority of HPAI virus detections in wild birds during this reporting period were attributed to waterfowl, while the low number of HPAI virus detections reported in colony-breeding seabirds between September and December 2023 also continued in the current reporting period (Figure 3). This was to be expected, as those seabird species only start to form colonies again from April. Compared to waterfowl, lower numbers of HPAI virus detections in raptors and other wild bird species, mostly common cranes, were reported between 2 December 2023 and 15 March 2024.



United Kingdom data are from ADNS up until 31 December 2020. From 1 January 2021 onwards, the data source was WOA for the United Kingdom (excluding Northern Ireland) and ADNS/ADIS for the United Kingdom (Northern Ireland)<sup>6</sup>.

\*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 WOA (data extraction carried out on 15 March 2024).

**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 (16,943) (a), affected poultry categories (5,112) (b) and affected wild bird categories (11,137) (c), from 1 October 2020 to 15 March 2024

Spatio-temporal information on all HPAI virus detections reported in Europe since October 2016 is available via EFSA’s interactive dashboard<sup>7</sup>.

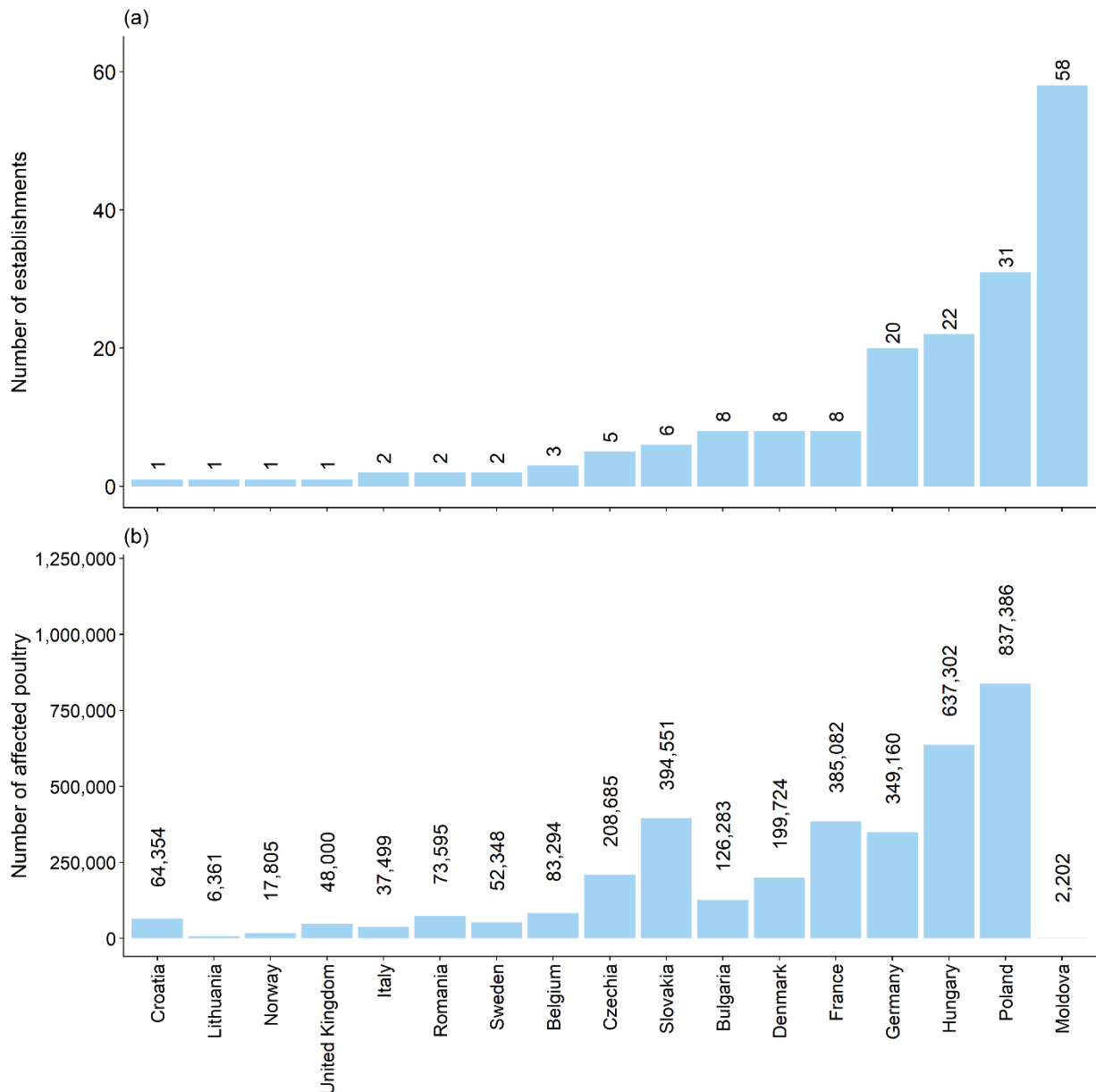
### Domestic birds

HPAI outbreaks in poultry during this reporting period were all identified as A(H5), most of them as A(H5N1), with the exception of 23 outbreaks reported from Moldova due to

<sup>6</sup> In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Windsor Framework, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).

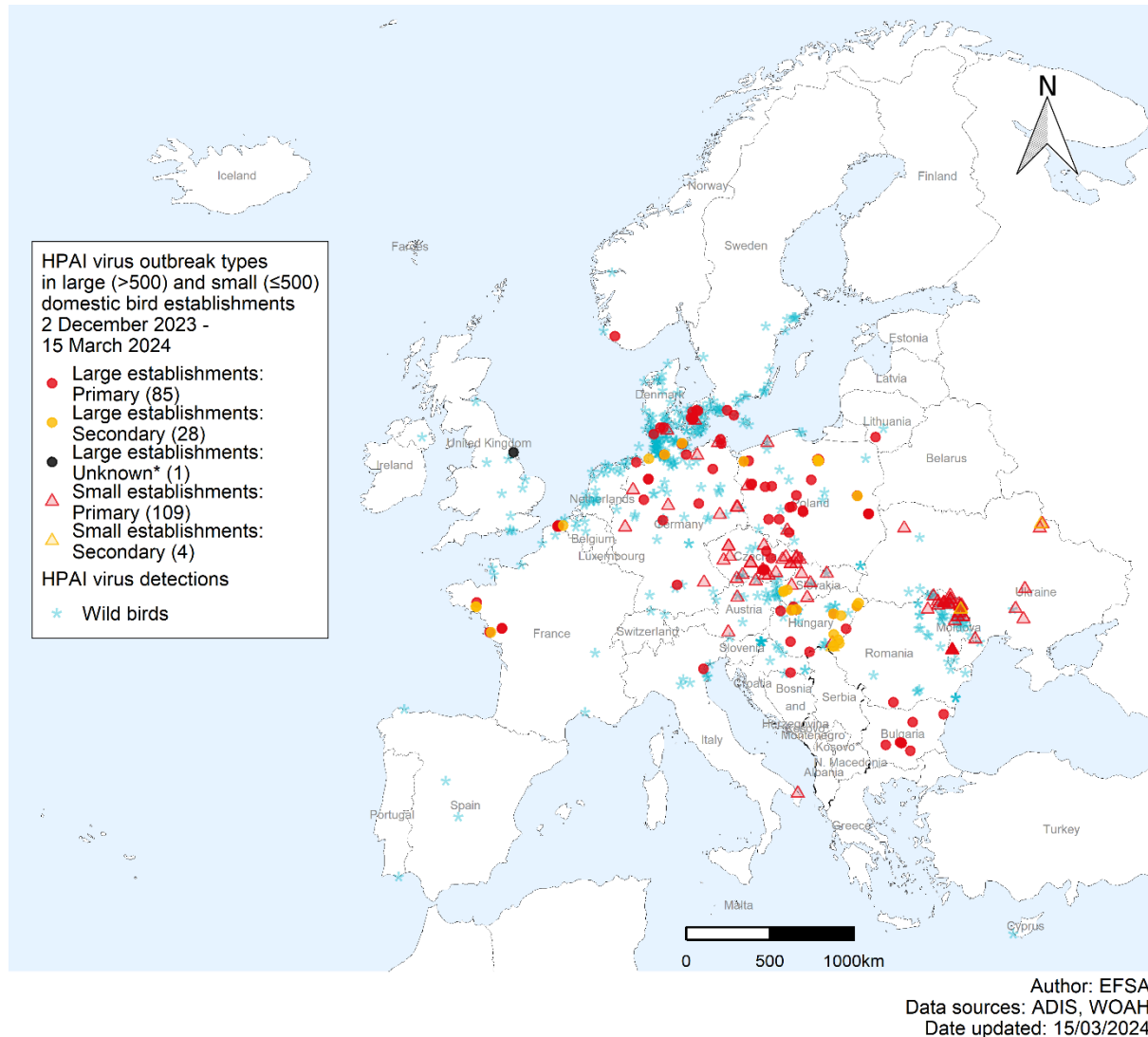
<sup>7</sup> <http://hpaiefsa.eu>

untyped influenza A viruses. A total of 179 HPAI outbreaks in poultry were reported from Moldova (58), Poland (31), Hungary (22), Germany (20), France (8), Denmark (8), Bulgaria (8), Slovakia (6), Czechia (5), Belgium (3), Italy (2), Romania (2), Sweden (2), Croatia (1), Lithuania (1), Norway (1) and the United Kingdom (1) (Table 1, Figure 4). Overall, more than 3.5 million birds died or were culled in the HPAI-affected poultry establishments, with large differences in the size of affected poultry establishments between countries. The highest losses (24% of the birds that died or were culled) were reported from Poland (17% of the affected establishments), whereas Moldova, despite reporting the highest number of affected establishments (32%), accounted for less than 0.1% of the birds that died or were culled (Figure 4).



**Figure 4:** Number of HPAI-affected establishments (179) (a) and number of poultry in the HPAI-affected establishments (3,521,429) (b) in Europe between 2 December 2023 and 15 March 2024

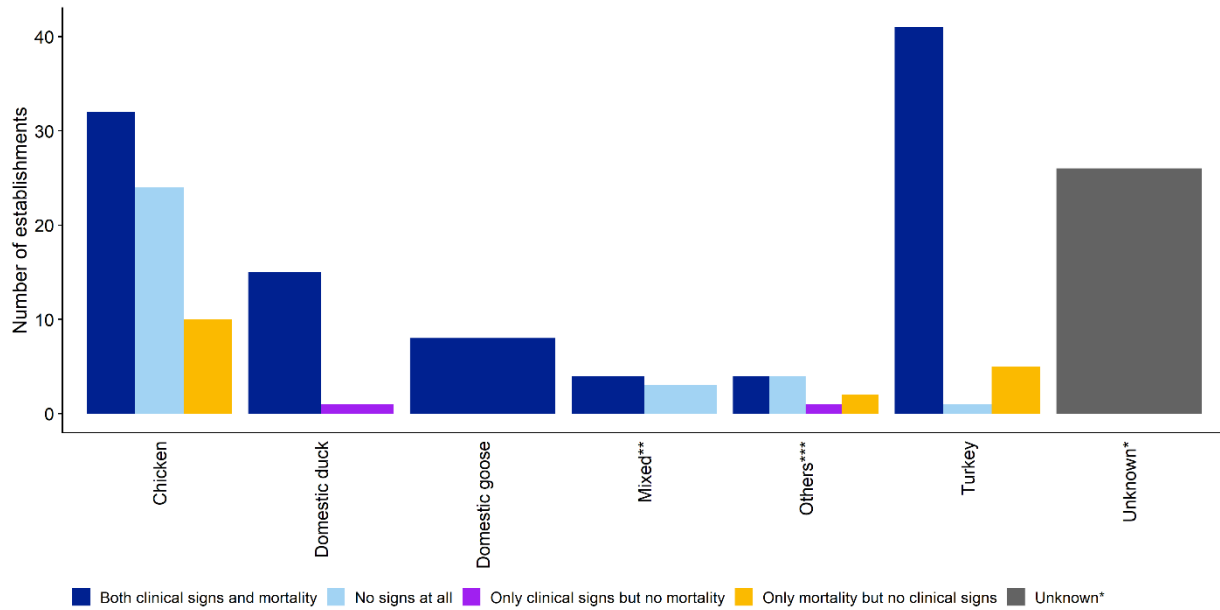
Most of the HPAI outbreaks reported in poultry were primary outbreaks (147 out of 179 outbreaks) and many of the smaller poultry establishments (less than 500 birds) that were affected were located in Czechia and Moldova (Figure 5).



\*It was not known whether the affected establishment experienced a primary or secondary outbreak.

**Figure 5:** Number of primary and secondary HPAI outbreaks in small (113) and large (114) domestic bird establishments in Europe between 2 December 2023 and 15 March 2024

HPAI outbreaks in poultry affected a wide range of species and production systems. In almost all affected poultry establishments keeping turkeys, the birds showed both clinical signs and mortality (41 out of 47), whereas in more than a third (24 out of 66) of the poultry establishments keeping chickens, birds did not show any signs at all (Figure 6). Those 24 A(H5N1)-affected poultry establishments keeping chickens without reported clinical signs or mortality were all located in Moldova and detected through active serological surveillance in poultry establishments around HPAI virus detections in swans. This absence of reported clinical signs or mortality combined with the serological response in chickens (with outdoor access) might indicate previous or ongoing infection with low pathogenic avian influenza (LPAI) viruses. Serological detection of these flocks is therefore not a confirmation of recent or ongoing infection with HPAI virus.



\*Either the poultry species or presence of signs (or both) was unknown.

\*\*'Mixed' refers to outbreaks in which multiple species were involved.

\*\*\*'Others' groups all other affected species that are not indicated in the legend.

**Figure 6:** Number of HPAI-affected poultry establishments by species and presence of signs of HPAI virus infection in Europe between 2 December 2023 and 15 March 2024. Note that information was available for 153 HPAI-affected poultry establishments.

In the following paragraphs, a brief description of HPAI outbreaks in poultry is given by country. This description is based on information collected by EFSA from ADIS, WOH-WAHIS, reporting countries (in form of additional data submitted and personal communications) and media reports. In the time period from 2 December 2023 to 15 March 2024, 178 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 153 of those 178 outbreaks from Belgium, Bulgaria, Croatia, Czechia, Denmark, France, Germany, Hungary, Italy, Lithuania, Moldova, Norway, Poland, Romania, Slovakia and Sweden. Those data on the characteristics of the affected poultry establishments and poultry species reared are presented in [Annex B](#). The remaining 25 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.

### Belgium

During the current reporting period from 2 December 2023 to 15 March 2024, three outbreaks in poultry were reported in Belgium via ADIS. A poultry housing order was in place when these outbreaks occurred (Nouvelles du monde, online). At the beginning of December, an A(H5N1) outbreak was confirmed in a commercial establishment housing laying hens (n = 24,644) which had no outdoor access. Indirect contact with poultry during the culling of infected animals in an outbreak located 400 meters upwind the establishment was the most likely source of introduction. The virus was detected through outbreak-related surveillance. An increase in mortality but the absence of clinical signs were observed. Two other outbreaks were detected through active surveillance in commercial establishments keeping chickens for breeding (n = 33,441) and turkeys for fattening (n = 25,209) at the end of December. These establishments did not provide outdoor access and the most likely source of introduction was indirect contact with wild birds. Increased mortality was observed in both



establishments, but clinical signs were only observed in the establishment keeping chickens (neurological signs such as tremor). No decrease in feed or water intake, or in egg production, were reported in these three outbreaks occurred in the country. No information on the number of exposed people was available at the time of production of this report.

### *Bulgaria*

During the current reporting period from 2 December 2023 to 15 March 2024, eight outbreaks in poultry were reported in Bulgaria via ADIS. A poultry housing order was in place when these outbreaks occurred. In mid-January, two A(H5N1) outbreaks were confirmed in commercial establishments rearing mulard ducks for foie gras production ( $n = 4,850$  and  $n = 3,900$ ). No increase in mortality was detected in either of the establishments, but clinical signs were observed in one of the two establishments (neurological signs such as trembling, running in circles and loss of balance). The presence of the virus was detected in the establishments through intensified active surveillance. As part of risk-based selection, several poultry establishments underwent increased official animal health visits, including clinical examinations, sampling and checks for biosecurity measures. Two other outbreaks were detected in commercial establishments keeping mulard ducks for foie gras production ( $n = 9,000$  and  $n = 8,725$ ) some weeks after. No increase in mortality or clinical signs were reported in these establishments. These outbreaks were detected through outbreak-related surveillance. In February, three other outbreaks were detected in commercial establishments rearing Muscovy ducks for fattening ( $n = 37,850$ ), laying hens ( $n = 40,000$ ) and mulard ducks for foie gras production ( $n = 9,510$ ). Increased mortality was observed in all establishments (115 and 103 birds in the case of mulard ducks and laying hens, respectively), but clinical signs were only observed in mulard ducks. The virus was detected in these establishments through passive surveillance. Outdoor access for birds was not provided by any of those seven establishments. On 12 March 2024, another establishment keeping mulard ducks ( $n = 12,636$ ) was found affected by A(H5). Additional information was not available for this outbreak, as it occurred too close to the time of production of this report. For all seven outbreaks, the results from the epidemiological investigation are inconclusive concerning the most likely source of introduction. Information on the number of exposed people was only available for four of the seven outbreaks. Twenty people were reported as exposed.

### *Croatia*

During the current reporting period from 2 December 2023 to 15 March 2024, one primary outbreak in poultry was reported in Croatia via ADIS. The outbreak was confirmed in a commercial establishment keeping turkeys for fattening ( $n = 64,354$ ) without outdoor access at the end of January. A poultry housing order was in place when the outbreak occurred. The high number of wild birds residing around ponds in the vicinity of the establishment were indicated as the most likely source of introduction. Increased mortality (140 birds in one house), clinical signs and decreased food and water intake were observed. Twenty people were reported as exposed.

### *Czechia*

During the current reporting period from 2 December 2023 to 15 March 2024, five outbreaks in poultry were reported in Czechia via ADIS. During this time period, no national poultry housing order was in place in the country. However, commercial poultry establishments, based on the provisions of the national Veterinary Act, were required to follow guidelines to protect their flocks against dangerous animal diseases. Some



recommendations were also issued for backyard flocks regarding the housing of poultry. At the end of January 2024, an A(H5N1) outbreak was confirmed in a commercial establishment housing chickens for breeding ( $n = 69,082$ ). The establishment was kept by the same owner who had experienced an outbreak in another establishment in Slovakia the week before. Sudden death of poultry and clinical signs were observed. One week later, another outbreak was detected in a commercial establishment owned by the same individual, which also housed chickens for breeding ( $n = 20,098$ ). Sudden death of poultry and clinical signs were observed in the establishment. Another outbreak was detected some days later in an establishment keeping ducks for fattening ( $n = 49,380$ ). A large increase in mortality ( $n = 10,250$ ) and clinical signs were reported. Indirect contact with wild birds frequenting the two ponds near the establishment was reported as the most likely source of introduction. In mid-February, two A(H5N1) outbreaks were detected through outbreak-related surveillance in commercial establishments keeping chickens, one of them for breeding. Increased mortality and clinical signs were observed in both establishments. The most likely source of introduction was indirect contact with poultry, with the virus suspected of having penetrated in the establishment through the ventilation system. Outdoor access for birds was not provided by any of the five establishments. Two hundred and sixty people were reported as exposed.

### *Denmark*

During the current reporting period from 2 December 2023 to 15 March 2024, eight outbreaks in poultry were reported in Denmark via ADIS. Due to the high risk level, a national order on biosecurity has been in force, which includes, among others, a ban on outdoor keeping. On 13 December 2023, an A(H5N1) outbreak was confirmed in a multi-species commercial establishment housing ducks for fattening ( $n = 1,967$ ) and chickens for breeding ( $n = 161$ ). This establishment provided outdoor access and the most likely source of introduction was from indirect contact with wild birds. No clinical signs or increase in mortality were reported. The virus was detected through active sampling as part of the national avian influenza surveillance in ducks and geese. Following this initial detection, a national poultry housing order was implemented in Denmark. Seven outbreaks were reported in January and February 2024, in establishments housing turkeys for fattening (4), laying hens (2) and chickens for breeding (1). Outdoor access for birds was not provided by any of the seven establishments and the most likely source of introduction was unknown. Increased mortality was reported in all of these establishments, with clinical signs observed in six of them, and a drop in feed and water intake in four of them. No information on the number of exposed people for the eight reported outbreaks was available at the time of publication of the report.

### *France*

During the current reporting period from 2 December 2023 to 15 March 2024, eight outbreaks in poultry were reported in France via ADIS. On 2 and 4 December 2023, two A(H5N1) outbreaks were detected in commercial establishments keeping turkeys for fattening ( $n = 4,000$  and  $n = 13,770$ ) in Morbihan, Brittany. The first detection occurred through outbreak-related surveillance and was a secondary outbreak close to the initial outbreak detected in Brittany at the very end of the previous reporting period, 26 November 2023. The second detection was a primary outbreak identified by passive surveillance, further away from the previous outbreaks. The affected establishments did not provide outdoor access. Increased mortality and a decreased food and water intake were observed. At that time, the housing order for poultry establishments was in force in higher-risk areas: those with a risk of introduction (mostly wetlands) or a higher risk of diffusion (some areas

with high density of poultry establishments). These outbreaks occurred within 10 km of a higher-risk area. After the detection of A(H5N1) in these two establishments, the risk level was raised to high for mainland France and Corsica. A poultry housing order was implemented nationwide. Two other outbreaks were reported in December in establishments keeping turkeys (secondary outbreak in Brittany;  $n = 9,660$ ) and laying hens (primary outbreak;  $n = 303,700$ ). No outdoor access was available in these establishments and the most likely source of introduction was unknown at the time of publication of the report. Increased mortality associated with clinical signs and decreased food and water intake were reported in the establishments. At the beginning of January 2024, an A(H5N1) outbreak was confirmed in a vaccinated establishment housing Muscovy ducks for fattening ( $n = 8,700$ ). At the time of the outbreak, only 74-day-old male Muscovy ducks were still present in the establishment and they had already received two vaccine injections: a H5-subunit vaccine (Volvac B.E.S.T. AI + ND, derived from virus strain A/duck/China/E319-2/2003 (H5N1), clade 2.3.2) was used and the second injection took place 41 days before the HPAI virus infection was detected. Available data on the humoral immune response and virological protection induced by the same vaccine in mule ducks indicated that the levels of detected H5 post-vaccination antibodies and the proportion of seropositive ducks tended to decrease between 7–11 weeks of age and that the corresponding reduction of excretion after challenge at 11 weeks of age was lower than that observed at seven weeks of age (GovFR, online). A similar pattern of reduced vaccine protection, with increasing age after their second vaccine injection, may also have occurred in Muscovy ducks. The outbreak was detected during event-based surveillance of vaccinated establishments (40 ducks were found dead). Clinical signs, including neurological disorders and decreased food and water intake, were also reported. A few days later, a secondary outbreak, close to the previous one, was reported in a vaccinated establishment housing Muscovy ducks for fattening ( $n = 17,206$ ) during outbreak-related surveillance. At the time of the outbreak, the 25-day-old ducks had accordingly received only one vaccine injection. Increased mortality, but no other reported clinical signs, were observed. Still in the Vendée region, two primary outbreaks were reported in establishments keeping turkeys ( $n = 21,648$ ) and unvaccinated ducks for breeding ( $n = 6,397$ ) in the following week. Increased mortality and clinical signs were observed in both establishments, along with a significant decrease in food and water intake. Additionally, a drop in egg production was observed in the establishment keeping ducks. No outdoor access was available in any of the establishments. During this reporting period, no outbreaks in poultry were reported in the southwest of France. No information was available at the time of producing this report regarding the most likely source of introduction, as well as the number of people exposed.

### *Germany*

During the current reporting period from 2 December 2023 to 15 March 2024, 20 outbreaks in poultry were reported in Germany via ADIS. The majority of the 20 outbreaks were primary ( $n = 17$ ) and all of them occurred in commercial establishments. One establishment was a multi-species establishment keeping goose for fattening, ducks and chickens. The other establishments were mono-species establishments keeping laying hens (6), broilers (1), turkeys for fattening (7), ducks for fattening (3) and chickens for breeding (2). An increase in mortality was observed in all establishments, whereas clinical signs were observed in 14 establishments. Outdoor access for poultry was available in three establishments. The most likely source of introduction for these three establishments, as well as for another establishment keeping laying hens without outdoor access, was indirect contact with wild birds. For two establishments, the most likely source of introduction was from indirect contact with poultry. For the other 14 outbreaks, it was unknown. Information

on the 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 December 2023 to 15 March 2024, 22 outbreaks in poultry were reported in Hungary via ADIS. A poultry housing order was in place when these outbreaks occurred. Half of the 22 outbreaks were considered primary and almost all of them ( $n = 20$ ) occurred in commercial establishments. All those commercial establishments were mono-species establishments keeping turkeys (7), ducks (3) or geese (1) for fattening, geese (3), ducks (1) or turkeys (1) for breeding, hens (1) for egg production, geese (1) for foie gras production, and mallards (1) or pheasants (1) for game. Outdoor access was available in two of the commercial establishments, and for ten of them the most likely source of introduction was indirect contact with wild birds. For the other ten establishments located close to an outbreak (8) or owned by an individual who also owned an establishment where an outbreak had recently been reported (2), the most likely source of introduction was indirect contact with poultry. The 2 non-commercial establishments were keeping chickens ( $n = 27$ ) and another unspecified species for mixed production ( $n = 254$ ). Outdoor access was available in both establishments, and the most likely source of introduction was indirect contact with poultry for the establishment housing chickens, while for the establishment keeping unspecified species for mixed production, it was indirect contact with wild birds. Increased mortality and clinical signs were observed in both non-commercial establishments. The virus was detected through passive surveillance in the two establishments. Increased mortality was observed in all the outbreaks reported in commercial establishments, except for the one keeping mallards for game. In 17 of those 19, clinical signs were observed, with a decrease in feed and water intake reported in 14 establishments. No drop in egg production was reported in any of the establishments. No information on the number of exposed people was available at the time of production of this report.

### *Italy*

During the current reporting period from 2 December 2023 to 15 March 2024, two outbreaks in poultry were reported in Italy via ADIS. As of the date they were confirmed, no poultry housing order was in place in the regions where they were detected. On 16 December 2023, an A(H5N1) outbreak was confirmed in a non-commercial multi-species establishment keeping geese, ducks, ostriches, pigeons and chickens ( $n = 100$ ) in the Puglia region. On 19 February 2024, the virus was detected in a commercial establishment keeping turkeys for fattening ( $n = 37,905$ ) in the Veneto region. The outbreak in Puglia was the first outbreak reported in poultry in this region, although HPAI virus had already been detected in wild birds in the region since 2005. Wintering grounds for several wild bird species (mainly ducks, gulls and waders) are present in this region. Increased mortality and clinical signs (neurological signs and reduced food and water intake) were observed in the establishment keeping turkeys. An increase in mortality was also the signal that triggered the suspicion of HPAI in the Puglia outbreak. The viruses identified belonged to two different genotypes and showed a high similarity to A(H5N1) viruses detected in wintering wild birds. The findings of the epidemiological investigations also suggest that the most likely source of introduction into the two poultry establishments was indirect contact with wild birds. No information on the number of exposed people was available at the time of production of this report.

### *Lithuania*

During the current reporting period from 2 December 2023 to 15 March 2024, one outbreak in poultry was reported in Lithuania via ADIS. The outbreak occurred in a commercial establishment housing turkeys for fattening ( $n = 6,361$ ) in mid-December 2023. The establishment did not provide outdoor access for birds and the most likely source of introduction was unknown. A significant increase in mortality ( $n = 2,300$ ) and clinical signs (diarrhea, weakness, neurological signs) were observed. Eight people were reported as exposed.

### *Moldova*

During the current reporting period from 2 December 2023 to 15 March 2024, 58 outbreaks in poultry were reported in Moldova via ADIS. Following detections of the virus in the country with 21 swans found positive for A(H5N1) viruses in mid-December 2023, surveillance activities in domestic birds from non-commercial and commercial establishments were initiated in Moldova. Additionally, to prevent the occurrence of avian influenza, a poultry housing order was implemented in the country for breeders and non-commercial bird owners (Expresul, online). All outbreaks were detected through serological testing. The majority of the 58 outbreaks were primary ( $n = 56$ ) and all outbreaks were reported in non-commercial establishments. For 56 of those 58 outbreaks, the establishments housed fewer than 100 susceptible birds. In the two most populated establishments, 594 and 118 susceptible birds were kept, respectively. Non-compliance with the housing order and lack of biosecurity in non-commercial establishments may explain the high number of this type of establishments affected in Moldova. Information on the poultry species present was available for 35 establishments. Out of these, 33 were reported to raise chickens, one establishment was a multi-species establishment keeping geese and ducks for fattening, and one establishment was a mono-species establishment housing geese for fattening. All of these 25 establishments provided outdoor access and the most likely source of infection was direct contact with wild birds. In only 11 of the 35 outbreaks for which additional information was available, an increase in mortality was reported, and in 8 of those 11, also clinical signs were observed, including a decrease in food or water intake, and in egg production. In 24 out of the 35 outbreaks for which additional information was available, presence of the virus was detected through active surveillance. Information on the number of exposed people was only available for 35 of the 58 outbreaks. Sixty-three people were reported as exposed.

### *Norway*

During the current reporting period from 2 December 2023 to 15 March 2024, one outbreak in poultry was detected in Norway via ADIS. No national poultry housing order was in place in the country when it was reported. In February 2024, an A(H5N1) outbreak was confirmed in an establishment rearing breeding poultry ( $n = 17,805$ ). The establishment comprised two distinct buildings, each housing pullets and cockerels held in separate areas. Increased mortality and clinical signs were only reported among the cockerels in one of the two buildings. No outdoor access was available. The most likely source of introduction was from indirect contact with wild birds present in wetlands and a lake near the establishment. Genetic analysis of the virus showed a 99% similarity to three HPAI virus-positive wild birds from Sweden that were reported in November and December 2023. Five people were reported as exposed.

## *Poland*

During the current reporting period from 2 December 2023 to 15 March 2024, 31 outbreaks in poultry were reported in Poland via ADIS. National regulations require on all establishments keeping poultry: feeding and watering poultry and birds kept by humans in a closed room or sheltered place in a way that protects feed and water against access by wild birds and their excrements, locating nests for poultry inside buildings, keeping poultry isolated from wild birds. These restrictions do not apply to establishments housing ducks or geese. The majority of the 31 outbreaks were primary ( $n = 25$ ) and all of them were reported in commercial establishments. Almost all of them (30) were mono-species establishments keeping turkeys (19) or ducks (5) for fattening, geese (2) or ducks (2) for breeding, and broilers (2). The one multi-species establishment was housing fattening ducks ( $n = 7,915$ ), breeding ducks ( $n = 3,808$ ) and hens ( $n = 25$ ). No outdoor access was available and the most likely source of introduction was from indirect contact with wild birds. For 24 out of the 30 outbreaks reported in mono-species establishments, the most likely source of introduction was indirect contact with wild birds. These establishments were reported to be in the vicinity of wild bird habitats, such as water reservoirs or migration routes. Five of those 30 outbreaks were situated at close distance to another outbreak or had contact with another HPAI virus-positive establishment. For these outbreaks, the most likely source of introduction was from indirect contact with poultry. For one of the reported outbreaks, the most likely source of introduction was unknown. In 29 of all 31 outbreaks, an increase in mortality was reported, and in 28 of those 29, clinical signs were observed, including a decrease in food or water intake. A drop in egg production was reported in three establishments keeping geese (1) and ducks (2). Information on the number of exposed people was only available for 28 outbreaks at the time of production of this report. One hundred and eighty people were reported as exposed.

## *Romania*

During the current reporting period from 2 December 2023 to 15 March 2024, two primary outbreaks in poultry were reported in Romania via ADIS. During this time period, no national poultry housing order was in place in the country. The first outbreak occurred at the end of December 2023 in a commercial establishment keeping laying hens ( $n = 73,583$ ), in which no outdoor access was available for poultry. The most likely source of introduction was indirect contact with wild birds, reportedly due to a failure in biosecurity protocols. Increased mortality and clinical signs were observed, including a decrease in feed and water intake and egg production. Twenty-one people were reported as exposed to the virus in the establishment. At the beginning of March 2024, another outbreak was confirmed in a non-commercial establishment keeping chickens ( $n = 12$ ). No additional information was available for this outbreak.

## *Slovakia*

During the current reporting period from 2 December 2023 to 15 March 2024, six outbreaks in poultry were reported in Slovakia via ADIS. During this time period, official recommendations were issued for breeders to house poultry, but no national poultry order was in place in the country. At the end of December 2023 and during the first week of January 2024, two primary outbreaks occurred in non-commercial establishments keeping chickens ( $n = 27$  and  $n = 40$ ), in which outdoor access was available. The most likely source of introduction was from indirect contact with wild birds. Increased mortality and clinical signs were reported in both establishments. On 25 January 2024, a primary outbreak was reported in a commercial establishment keeping chickens for breeding ( $n = 191,325$ ) in



which no outdoor access was available for poultry. The most likely source of introduction was from indirect contact with wild birds. Increased mortality and clinical signs were observed, including a decrease in feed or water intake, and in egg production. On 2 February, two secondary A(H5N1) outbreaks were confirmed in commercial establishments keeping chickens for breeding ( $n = 131,934$  and  $n = 23,228$ ) in which no outdoor access was available. These outbreaks were considered secondary, due to an epidemiological link to the first reported affected commercial establishment. The most probable route of virus introduction into these establishments was through fomites (vehicles, people) via the owner's shared hatching eggs warehouse. In both establishments, increased mortality and clinical signs were observed, including a decrease in feed or water intake, and in egg production. On 28 February, an establishment keeping chickens ( $n = 48,027$ ) was confirmed to be affected by A(H5N1). No outdoor access was available in the establishment. The virus was suspected to have been introduced through indirect contact with poultry from an infected establishment. Increased mortality and clinical signs were observed, including a decrease in feed or water intake, and in egg production. No information on the number of exposed people was available at the time of production of this report.

### *Sweden*

During the current reporting period from 2 December 2023 to 15 March 2024, two primary outbreaks in poultry were reported in Sweden via ADIS. When these outbreaks were declared, a national poultry housing order was in place in the affected part of the country. On 5 January 2024, A(H5N1) was confirmed in a commercial establishment keeping a broiler parent flock ( $n = 47,938$ ). On 16 January, a second outbreak was reported in an establishment keeping turkeys for fattening ( $n = 4,410$ ). No outdoor access was available in these two establishments. HPAI virus-positive wild birds were found in areas near the different establishments. Phylogenetic analysis showed that both poultry isolates had high genetic similarity with virus detected in different wild birds. The two isolates from poultry did not have high genetic similarity. Therefore, the most likely source of introduction in both cases was from indirect contact with wild birds. Increased mortality was observed in both establishments. Clinical signs were only observed in the establishment keeping turkeys. For these two outbreaks, a total of 34 people were reported as exposed.

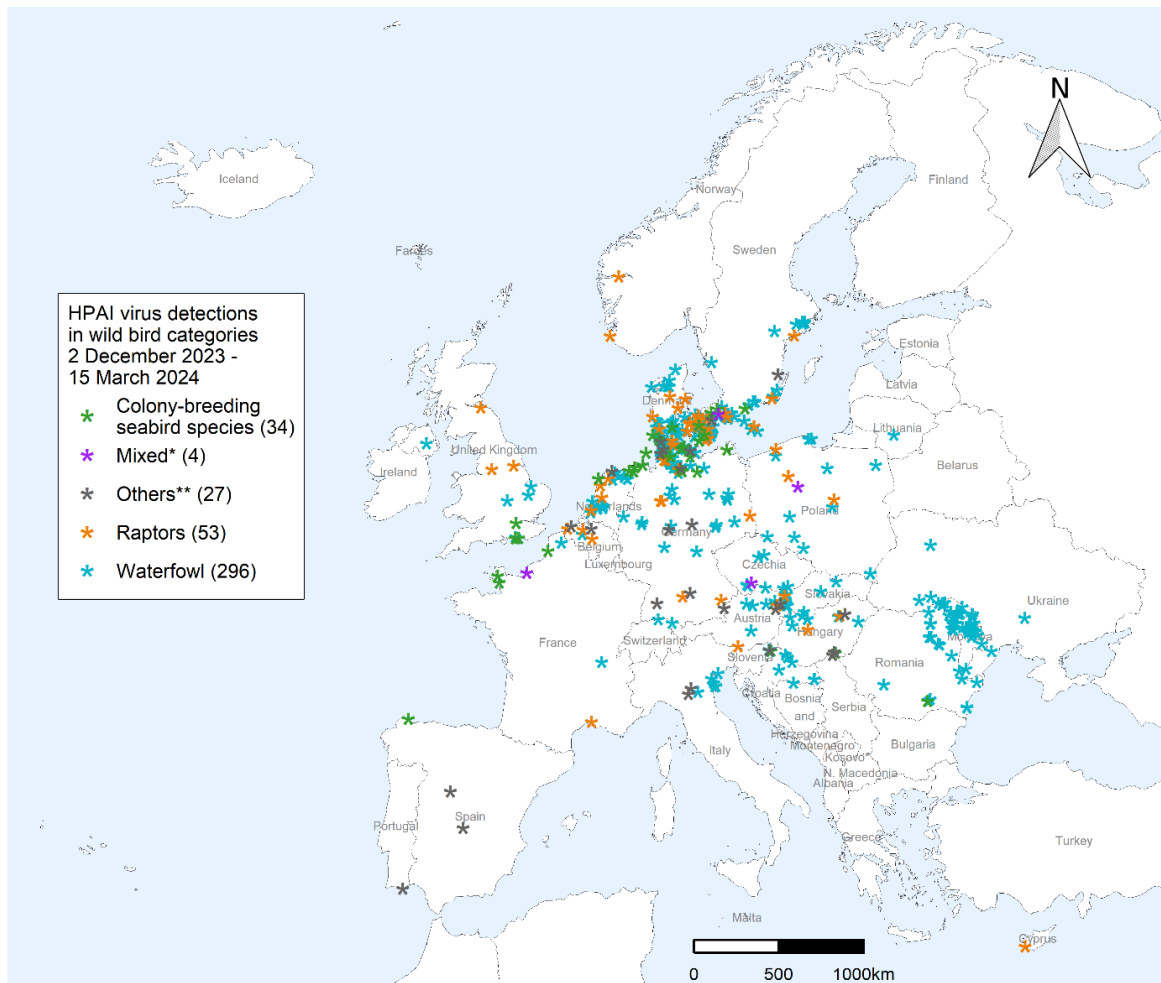
### *United Kingdom*

During the current reporting period from 2 December 2023 to 15 March 2023, one outbreak in poultry was reported in the United Kingdom via WOH-WAHIS. On 14 February 2024, the outbreak was confirmed in England, near Hutton Cranswick (Yorkshire), in an establishment keeping laying hens ( $n = 48,000$ ) (GovUK, online-a).

Forty-eight HPAI virus detections in captive birds, all due to A(H5N1) viruses, were reported from Czechia (22), Germany (9), Ukraine (7), Austria (3), Poland (3), Slovakia (3) and Denmark (1) (Figure 2, Table 1). In Czechia, those HPAI virus detections were reported in several small establishments with up to 50 captive birds for own consumption (laying hens, geese and ducks). In Denmark, the HPAI outbreak in Næstved concerned a small establishment with 5 captive birds, which showed increased mortality. In Germany, one HPAI outbreak in captive birds concerned several wild bird species around a pond in a zoo, for which introduction from wild birds was suspected. In Poland, two of the HPAI outbreaks in captive birds concerned 80 hens and 23 mixed birds (19 hens and 4 geese) for own consumption. In Slovakia, all three HPAI outbreaks concerned establishments with up to 20 raptors/owls and/or waterbirds that had contact with wild birds through their exterior aviaries.

## Wild birds

During the time period 2 December 2023 to 15 March 2024, a total of 393 A(H5N1), 6 A(H5N5), 14 A(H5Nx) and 1 untyped influenza A virus detections were reported from Germany (120), Denmark (65), Moldova (30), Sweden (27), Romania (25), the Netherlands (19), Poland (18), Austria (14), Hungary (14), Slovenia (12), the United Kingdom (11), Slovakia (9), Italy (8), Czechia (7), France (7), Czechia (7), Belgium (6), Croatia (6), Ukraine (6), Spain (3), Norway (2), Bosnia and Herzegovina (1), Cyprus (1), Lithuania (1), Portugal (1) and Switzerland (1) (Figure 2, Figure 7, Table 1).



Author: EFSA  
Data sources: ADIS, WOAH  
Date updated: 15/03/2024

\*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 15 March 2024).

**Figure 7:** Geographic distribution, based on available geocoordinates, of HPAI virus detections in different categories of wild birds in Europe, by species category, from 2 December 2023 to 15 March 2024

The overall number of HPAI virus detections in wild birds (including detections in mixed species) (414) was almost twice as high as the one of the previous reporting period (219 from 2 September to 1 December 2023), mainly due to a higher number of HPAI virus

detections affecting the wild bird categories of waterfowl (296 in the current vs 75 in the previous reporting period) and raptors (53 vs 21). Also the number of HPAI virus detections involving mixed wild bird species was higher (4 vs 1). On the other hand, the number of HPAI virus detections in the categories of colony-breeding seabirds (34 vs 54) and other wild bird species (27 vs 68) were lower (Figure 7).

HPAI virus detections in wild birds still occurred widely across Europe, although not as numerous as in the same periods in previous years (Figure 3). Reasons may be acquired flock immunity after previous infections, depletion of certain wild bird populations and underreporting due to decreased efforts in some countries. Different patterns in the distribution of HPAI virus detections in different wild bird categories were evident during this reporting period. Cases in waterfowl extended from the western Black Sea coast to southern Scandinavia and the United Kingdom, and as far as northern Italy, whereas cases in seabirds were mainly limited to the North and Baltic Sea coasts. Cases in raptors were located mainly where cases in waterfowl and seabirds were concentrated, along the North Sea and Baltic Sea coasts of the Netherlands, Germany and Denmark, whereas cases in other wild bird species were mostly limited to the southern parts of Europe. More HPAI virus detections in colony-breeding seabirds, in particular in black-headed gulls, cannot be excluded in the following reporting period, as they will start forming colonies from April onwards.

During this reporting period, no new wild bird species were reported as infected with HPAI viruses in Europe.

The top three waterfowl species identified to species in which HPAI virus detections were reported were the mute swan (103 in the current vs 17 in the previous reporting period), barnacle goose (52 vs 7) and whooper swan (26 vs 2) (Figure A.1 in [Annex A](#)). The high number of HPAI virus detections in mute swans and whooper swans is partly attributable to the die-off centred in Moldova and the adjacent part of Romania. The top three waterfowl species identified in the previous reporting period were the mute swan, greylag goose (12 in the previous vs 19 in the current reporting period) and mallards (12 vs 12). A large number of Anatidae (65) remained unidentified. The reasons thereof need to be examined, but may be related to the similarity among species, especially first-year birds and adults in eclipse plumage. Larger numbers of HPAI virus detections in swans were reported during the same period in previous years (Figure A.3 in [Annex A](#)). The migratory patterns of mute swans differ per region of Europe. For example, mute swans in the United Kingdom, Northwest France, Belgium, the Netherlands and West Germany are mainly sedentary, but can perform short-distance movements: some mute swans breeding in central Europe migrate west and south in winter, while mute swans breeding in Ukraine move to the coast of the Black Sea (including Moldova), the Danube Delta, or continue to the Balkans and Italy in winter (Atkinson et al., 2006).

The top two raptors identified to species in which HPAI virus detections were reported were the common buzzard (29 in the current vs 2 in the previous reporting period) and peregrine falcon (4 vs 7). The latter was the most reported raptor species in the previous reporting period, whereas the white-tailed eagle was the second most reported raptor species (4 in the previous vs 1 in the current reporting period). Between 2 December 2023 and 15 March 2024, 2 cases each were reported for the common kestrel (2 in the current vs 0 in the previous reporting period), Eurasian sparrowhawk (2 vs 1) and northern goshawk (2 vs 1). A number of Accipitridae (9) remained unidentified.

The top two colony-breeding seabirds identified to species in which HPAI virus detections were reported were the European herring gull (14 in the current vs 16 in the previous



reporting period) and black-headed gull (5 vs 5) (Figure A.1 in [Annex A](#)). Two cases each were reported for the mew gull (2 vs 0) and great cormorant (2 vs 0). A number of Laridae (7) remained unidentified.

The main species in the 'other' wild bird category was the common crane (9 in the current vs 55 in the previous reporting period) (Figure A.1 in [Annex A](#)). Being the wild bird species most frequently found infected with HPAI viruses between September and December 2023, it continued to be reported in lower numbers from Austria (2), Hungary (2), Italy (2), Spain (2) and Germany (1) during this reporting period. Additionally, in February 2024, a large number of cranes (130) were found dead and tested positive to A(H5N1) in Israel (JPost, online; The Time of Israel, online).

The wild bird species most frequently found infected with HPAI viruses during this reporting period was the mute swan, with cases reported from Moldova (18), Romania (13), Poland (12), Slovenia (9), Austria (7), Slovakia (7), Croatia (6), Denmark (6), Sweden (6), Ukraine (6), Czechia (4), Hungary (4), Bosnia and Herzegovina (1), France (1), Lithuania (1), Switzerland (1) and the United Kingdom (1). HPAI virus-infected whooper swans were reported from Romania (12), Moldova (11) and the United Kingdom (2). The cases in Moldova were associated with the reported mortality of 261 mute swans in December 2023 and January 2024 (WOAH, online-a). In Romania, the prohibition of sports, other recreational activities and commercial fishing was implemented in the area where infected swans were found (Adevarul.ro, online). In the same time period, but about 1,800 km east, HPAI H5 virus was reported in mute swans in association with mortality of 227 mute swans at Lake Karakol, Kazakhstan, part of the Karagiye-Karakolsky reserve on the east coast of the Caspian Sea (WOAH, online-b). As of 21 December 2023, it was reported that 601 swan carcasses were found around Lake Karakol, with 90% of the birds being juvenile (Orda, online). The nature reserve hosts rare and endangered species (Le Journal de Montréal, online).

HPAI virus-infected barnacle geese were reported from Denmark (28), Sweden (11), Germany (8) and the Netherlands (5). They had reportedly been seen grazing near poultry establishments.

During this reporting period, A(H5N5) virus was identified in common buzzards (2), European herring gull (1), Eurasian sparrowhawk (1), an unidentified Laridae species (1) and white-tailed eagle (1) in Germany, Norway and the United Kingdom. This subtype has been expanding slowly since 2021 (see Section 2.1.3).

The complete list of wild bird species found as HPAI virus-infected from 2 December 2023 to 15 March 2024 is reported in Figure A.1 in [Annex A](#). The number of HPAI virus-affected wild birds that were not identified to species was 89/425 (20.9%), a small increase compared to the previous reporting period (35/221, 15.8%) (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 7 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

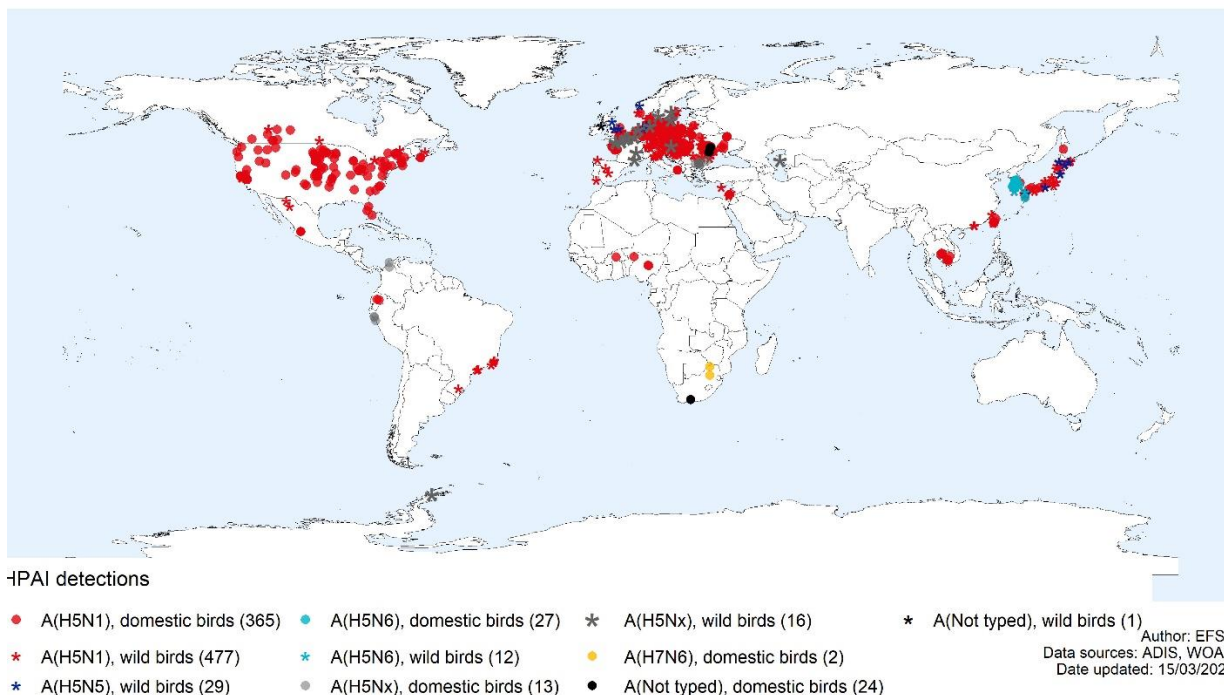
An overview of the HPAI virus detections in birds that were notified from other countries not reporting via ADIS but via WOAAH from 2 December 2023 to 15 March 2024 is presented in Table 2 and Figure 8.

**Table 2:** Number of HPAI virus detections in non-European countries, by virus subtype and country, from 2 December 2023 to 15 March 2024

Region	Country	Domestic birds					Wild birds				Total
		A(H5N1)	A(H5N6)	A(H5Nx)	A(H7N6)	A(Not typed)	A(H5N1)	A(H5N5)	A(H5N6)	A(H5Nx)	
Africa (7)	Burkina Faso	1	-	-	-	-	-	-	-	-	1
	Nigeria	3	-	-	-	-	-	-	-	-	3
	South Africa	-	-	-	2	1	-	-	-	-	3
Americas (158)	Brazil	-	-	-	-	-	9	-	-	-	9
	Canada	13	-	-	-	-	5	-	-	-	18
	Colombia	-	-	2	-	-	-	-	-	-	2
	Ecuador	2	-	-	-	-	-	-	-	-	2
	Mexico	4	-	-	-	-	2	-	-	-	6
	Peru	-	-	3	-	-	-	-	-	-	3
	United States of America	115	-	-	-	-	3	-	-	-	118
Antarctica (1)	Antarctica	-	-	-	-	-	-	-	-	1	1
Asia (158)	Cambodia	8	-	-	-	-	-	-	-	-	8
	China	-	-	-	-	-	1	-	-	-	1
	Hong Kong	-	-	-	-	-	6	-	-	-	6
	Israel	1	-	-	-	-	7	-	-	-	8
	Japan	7	1	-	-	-	45	23	1	-	77
	Kazakhstan	-	-	-	-	-	-	-	-	1	1
	South Korea	6	26	-	-	-	4	-	11	-	47
	Taiwan	8	-	-	-	-	2	-	-	-	10
Europe (1)	Russia	1	-	-	-	-	-	-	-	-	1
<b>Total</b>		<b>169</b>	<b>27</b>	<b>5</b>	<b>2</b>	<b>1</b>	<b>84</b>	<b>23</b>	<b>12</b>	<b>2</b>	<b>325</b>

'-' means that no HPAI outbreaks were notified to WOAAH.

Source: WOAAH (data extraction carried out on 15 March 2024).



**Figure 8:** Geographic distribution, based on available geocoordinates, of HPAI virus detections reported worldwide in domestic (552) and wild (535) birds by virus type, from 2 December 2023 to 15 March 2024

In the tables and figures of the present report, only data extracted from WOA on 15 March 2024 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 WOA-WAHIS has been integrated in the text below.

In comparison to the previous reporting period (EFSA, ECDC and EURL, 2023a) and in particular compared to the report from the previous year during the same period (EFSA, ECDC and EURL, 2023b), a decreasing number of HPAI outbreaks in poultry and wild birds were notified from a lower number of countries outside Europe. The total number of outbreaks in domestic and wild birds reported to WOA from outside Europe dropped from 513 to 325 and the number of countries from 22 to 20, compared to the period 2 September to 1 December 2023. The decrease in the number of outbreaks and countries is also evident compared to the report for the period from December 2022 to March 2023 (471 vs 325 outbreaks and 29 vs 20 countries). In Africa, the number of affected countries has risen (3 in the current vs 2 in the previous reporting period), and in contrast to the previous report, western and southern Africa were affected. In the Americas, A(H5) virus continued to be detected in poultry and wild birds, but only in countries that were already affected in the previous reporting period, and the number of reporting countries halved overall. In Asia, the number of affected countries increased with reports from China, Hong Kong, Japan, Kazakhstan and South Korea, which notified outbreaks to WOA after a period of absence, in addition to the previously affected countries (Cambodia, Israel and Taiwan), which continued to report outbreaks. Overall, HPAI outbreaks in domestic birds decreased (375 vs 204) and also the number of cases in wild birds reported to WOA (138 vs 121) declined in the current vs the previous reporting period.

The major epidemic of A(H7N6) in South Africa now appears to be under control and the cases in January 2024 involved two ostrich farms, according to media reports (WATTpoultry, online). The full genome sequences of three A(H7N6) viruses, collected from a single poultry outbreak affecting layers in Mozambique on 16 October 2023, were obtained (Monjane et al., 2024). Increased mortality was observed in the infected poultry establishment, and the birds showed unspecified respiratory and enteric signs. All three sequences clustered together and, for their H7 and N6 segments, were highly related to an A(H7N6) virus collected from layers in South Africa in May 2023. No other sequences were available for this last virus, making comparisons impossible for the other segments. All previously mentioned viruses shared the same polybasic cleavage site on their hemagglutinin and identical patterns of glycosylation in their H7 and N6 proteins. Although mutations associated with mammalian adaptations (namely, increased virus replication or polymerase activity in mammals or mammalian cells, increased virulence and decreased interferon response) were present in the PB2, PB1, PA, M and NS proteins, their effects on the genotype of these viruses are still to be documented. Burkina Faso reported to WOAHA the first outbreak of A(H5N1) in a very large poultry establishment in this epidemiological year. Furthermore, A(H5N1) was detected again after a period of four months in two backyard flocks and a small poultry establishment in Nigeria. Only the media reported on an outbreak of HPAI in a medium-to-large poultry establishment in western Ghana in January 2024 (Adom online, online). As in the previous reporting period, no outbreaks of A(H5N1) or cases of A(H5) in wild birds from Africa were reported to WOAHA.

The large epidemic of A(H5N1) in the United States of America and Canada continued in poultry establishments of all sizes on a high level and accounted now for almost 80% of the reported outbreaks in domestic birds worldwide. This may be partly due to the continued high circulation of A(H5N1) in wild bird populations in Canada and the United States of America, where the virus was detected in several wild bird species, including Canada goose, snow goose, trumpeter swan, American goshawk, great horned owl, American crow, double-crested cormorant, cattle egret, grey plover and western sandpiper. The poultry outbreaks in Canada and the United States of America correlate with the migration pathway of migrating wild birds from South America to their breeding areas in North America during this time of the year. Spring migration may also play a role in increasing the number of HPAI virus detections in the following months as migratory waterbirds return to their breeding areas in the prairies in the Midwest and south-central Canada. In contrast to the previous reporting period, Brazil did not confirm any HPAI outbreaks in poultry, but reported A(H5N1) virus detections in several wild bird species (e.g. common tern, royal tern, Cabot's tern, Manx shearwater and white-faced ibis) at previously affected locations on the Brazilian Atlantic coast. Other affected South American countries (Colombia, Ecuador and Peru) only reported poultry outbreaks of A(H5N1) and A(H5Nx) in backyard holdings with the exception of Peru, where also a large poultry establishment was affected. Furthermore, media reported about an outbreak of A(H7N3) in several large poultry establishments on the western Mexican coast and in central states (Echemi, online). The lower outbreak numbers in domestic birds might be partially explained by the start of vaccination campaigns against avian influenza in several countries. 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.

In Asia, Cambodia was the only country reporting outbreaks of A(H5N1) exclusively in poultry to WOAHA again from regions where human cases of A(H5N1) belonging to clade 2.3.2.1c have occurred (Khmer Times, 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. China, Hong Kong and Kazakhstan detected A(H5N1) and A(H5Nx) exclusively in waterfowl and waders, as e.g. in Eurasian wigeon, Eurasian teal, falcated duck, pin-tailed snipe and swans in Kazakhstan, based on media reports (Le Journal de Montréal, online). The outbreaks of A(H5N1) and A(H5N6) of clade 2.3.4.4b in poultry establishments of all sizes and wild birds in Israel, Japan and Taiwan continued and several wild bird species were recorded, such as Eurasian wigeon, Eurasian teal, tufted duck, common pochard, whooper swan, black-headed gull, European herring gull, yellow-legged gull, common crane, hooded crane, white-naped crane, grey heron, dunlin, black-faced spoonbill, white-tailed eagle, peregrine falcon, Ural owl and large-billed crow. New outbreaks of A(H5N1) and H(H5N6) in mainly large to very large poultry establishments were detected in South Korea this season, which had been accompanied by cases in wild birds, such as in northern pintail, Eurasian wigeon, mallard, gadwall, mandarin duck, northern shoveler, whooper swan, golden eagle and great cormorant. A large number of A(H5N5) virus detections (23) were also reported in wild birds from Japan, mainly in large-billed crows, but also in a peregrine falcon and common pochard. Furthermore, only the media reported outbreaks of A(H5N1) in domestic birds in India (The New Indian Express, online) and Laos (Vietnam plus, online), countries that have been affected in previous epidemiological years. Russia detected A(H5N1) virus in a very large poultry establishment in the Amur republic in far eastern Russia. Furthermore, media reported about a further outbreak in a very large poultry establishment in Southwest Russia for the second time (Arbuz today, online).

The first HPAI outbreaks on mainland Antarctica, in which A(H5N1) virus was confirmed, were reported in two dead skuas in February 2024, and Adélie penguins and Antarctic cormorants in March 2024 (CIDRAP, online; Inach, online; The Guardian, online-a). This represents the first time that A(H5N1) was found in penguins in the Antarctic region (León et al., 2024). On the Falkland Islands, outside the Antarctic convergence, the marine belt encircling the Antarctic region, about 30 black-browed albatrosses were found dead, six brown skuas and one variable hawk were symptomatic or found dead, and approximately 70 gentoo penguins (two positive for A(H5N1) virus) were found dead, likely due to avian influenza, between late November 2023 and March 2024 (GOVFK, online; Reuters, online; SCAR, online). Further mortalities of around 200 juvenile and adult gentoo penguins under the same circumstances were reported (Reuters, online). On the South Georgia and the South Sandwich Islands, inside of the Antarctic convergence, following the first detection of HPAI in brown skuas in October 2023, A(H5N1) virus was detected in wandering albatrosses, brown skuas, kelp gulls and Antarctic terns (BAS, online-a). Furthermore, the first HPAI virus detections in king penguins (five birds, Will point) and gentoo penguins (five birds, nearby Bird Island) in South Georgia were reported in March 2024 (BAS, online-b). It was reported that those cases were relatively isolated and no rapid spread within penguin colonies was seen.

The incursion of A(H5N1) into South Georgia Island increases the likelihood that the subtype will become established in Southern Ocean seabirds that move circumpolar through the sub-Antarctic and Antarctic colonies potentially spreading to New Zealand (Gartrell et al., 2024). To date, no HPAI virus detection have been reported in Oceania (Australia and New Zealand) since 2020 (SCAR, online).

The list of wild bird species that have been reported to WOA as HPAI virus-infected from 2 December 2023 to 15 March 2024 is presented in Table A.1 in [Annex A](#).



### 2.1.3 Genetic characteristics of HPAI viruses of the A(H5Nx) 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. Genotypes are assigned using the criteria described in (Fusaro et al., in press).

#### **Genetic diversity of HPAI A(H5Nx) viruses in avian species**

Since October 2023, complete genome sequences of more than 400 European clade 2.3.4.4b HPAI A(H5) viruses have been characterised. The vast majority (> 90%) belong to A(H5N1) (n = 7) and A(H5N5) (n = 1) genotypes, namely:

- EA-2021-AB (H5N1 A/duck/Saratov/29-02/2021-like),
- EA-2022-BB (H5N1-A/Herring\_gull/France/22P015977/2022-like),
- EA-2023-DA (H5N1-A/mute\_swan/Slovenia/PER1486-23TA\_23VIR10323-22/2023-like),
- EA-2023-DB (H5N1-A/herring\_gull/Germany-NI/2023AI08764/2023-like),
- EA-2023-DG (H5N1- H5N1-A/Gallus\_gallus/Belgium/11307\_0002/2023-like),
- EA-2024-DI (H5N1 A/mute\_swan/Poland/MB008-1/2024-like),
- EA-2023-DJ (H5N1-A/barnacle\_goose/Denmark/09302-1.02/2023-like),
- EA-2021-I (H5N5 A/whooper\_swan/Romania/10123\_21VIR849-1/2021-like).

Three out of eight genotypes (EA-2021-AB, EA-2022-BB and EA-2021-I) have persistently been circulating in Europe from previous epidemiological years, while five have newly emerged from reassortment events of the internal gene segments with LPAI viruses. 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.

Based on the available data, in the 2023–2024 epidemiological year, genotypes EA-2021-AB, EA-2022-BB, EA-2023-DB, EA-2023-DG, EA-2023-DJ and EA-2021-I have mainly or exclusively been detected in wild and domestic birds in northern Europe, while genotypes EA-2023-DA and EA-2024-DI have mostly been circulating in wild and domestic birds in eastern and southern Europe. Of note, all the cases characterised to date in common cranes in Europe in the current epidemiological year belong to genotype EA-2023-DA.

Interestingly, genotype EA-2022-BB, which had extensively circulated among Laridae in Europe in summer 2023, has been persistently circulating at low level also in the current epidemiological year.

Subtype A(H5N5), genotype EA-2021-I, which had emerged in Russia at the end of 2020, has been 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, the United Kingdom and Greenland, and subsequently, in February 2024, in Germany, which suggests a geographic expansion of this variant. A(H5N5) subtype has also been detected in Faroe Islands and Japan during the current epidemiological year.

## Mutations identified in HPAI A(H5Nx) viruses from avian species

Molecular analyses of the A(H5N1) viruses circulating in birds in Europe during the 2023–2024 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 (Du et al., 2018; Suttie et al., 2019; Pinto et al., 2023) have been identified as being associated with i) enhanced polymerase activity and replication in mammals or mammalian cells, ii) increased virulence in Galliformes or mammals, 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. Since October 2023, mutations in the PB2 protein associated with virus adaptation in mammals (E627K or D701N) have been detected in seven European viruses collected from birds, more specifically in i) three genetically related A(H5N5) viruses (genotype EA-2021-I) collected in Norway and Germany from wild birds in January–February 2024 and ii) four A(H5N1) viruses collected between October 2023 and February 2024 from separate outbreaks in domestic birds in Poland (genotypes EA-2022-CH and EA-2022-AB) and Denmark (genotype EA-2023-DB). Whether these mutations emerged in mammals or birds cannot be assessed from the available data. The Polish virus, belonging to genotype EA-2022-CH with PB2-E627K, collected in October 2023, was related to the virus responsible of the 2023 outbreaks in cats in the country. A recent study demonstrated that clade 2.3.3.4b A(H5N1) viruses containing the PB2-E627K mutation were able to replicate in the nose of inoculated pigs and to be transmitted to contact pigs (Arruda et al., 2024). Circulation in domestic birds of viruses with such mammalian adaptive markers may increase the risk for virus transmission to pigs and for reassortment of the A(H5N1) with endemic swine influenza viruses.

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 which have been circulating in Europe since October 2023, while others (i.e. E251K, E75K-S123P, P235S and S155N) 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 has 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 EA-2022-BB genotype contain mutations NP-Y52N and NA-S369I, which may increase their zoonotic potential, and all the currently circulating A(H5N5) viruses (genotype EA-2021-I) contain a deletion in the NA stalk region, which is a virulence determinant in chickens (Stech et al., 2015). Mutations associated with antiviral resistance have been rarely identified in the circulating strains (< 3%).

## 2.2 HPAI virus detections in non-human mammals

### 2.2.1 HPAI virus detections in non-human mammals worldwide

From 2 December 2023 to 15 March 2024, A(H5N1) and A(H5N5) viruses were reported in farmed, feral and wild mammals in Europe and North America. Data were collected from WOAH-WAHIS and supplemented with additional information provided by Member States and retrieved from media reports (Table 3).

Surveillance for avian influenza viruses was carried out in all fur animal farms in Finland (n = 346) between September 2023 and January 2024. Specifically, surveillance was carried

out in 70 establishments keeping only American minks, 230 establishments keeping only red or Arctic foxes/raccoon dogs, and 46 establishments keeping both American mink and red or Arctic foxes/raccoon dogs. A(H5) antibodies were found in animals from a total of 44 establishments (12.7%). Virological accompanied serological tests only at the beginning of the survey in September 2023 and were then discontinued. Of those 44 antibody-positive farms, 42 were mainly asymptomatic (sometimes clinical signs were present, but their cause could not be fully determined). Since July 2023, a total of 71 fur animal farms were found virologically or serologically positive for A(H5) viruses. All animals on infected farms were culled and disposed of. The suspected source of introduction was from wild birds, particularly black-headed gulls.

A(H5N1) was reported in four cats in Alberta, Canada, as well as in 10 neonatal goat kids displaying neurological signs and mortality from a backyard poultry establishment in Minnesota, United States of America (WOAH, online-c). The A(H5N1) cases in goats represent the first natural infection of A(H5N1) virus in any ruminant species (suborder Ruminantia) worldwide (Veldhuis Kroeze and Kuiken, 2016; FAO, online).

In wild mammals, in Europe, A(H5N1) virus was detected in red foxes in Germany and Sweden. The latter had already been shot in August 2023, but was only confirmed at the end of December 2023. A(H5N5) virus was identified in two red foxes displaying neurological signs in Norway. Outside Europe, A(H5N1) virus was reported in a raccoon, a mountain lion and three striped skunks in the United States of America. A polar bear and an Abert's squirrel were found infected with A(H5N1) in Alaska and Arizona, United States of America, but these detections had already occurred prior to the current reporting period, in August 2023. Detections in southern elephant seals and South American fur seals continued on the South Georgia and South Sandwich Islands (BAS, online-a). Respiratory signs in elephant seals have been observed (The Guardian, online-b). South Georgia is reported to be the habitat of 98% of the world's population of Antarctic fur seals, which are at constant threat (Forcada et al., 2023; The Guardian, online-b).

It can be assumed that the low number of HPAI virus detections in wild carnivores during the current reporting period is associated with the low number of HPAI virus detections in wild birds and thus with a lower level of contamination of the environment.



**Table 3:** Avian influenza A(H5Nx) virus detections in mammal species other than humans related to circulating viruses worldwide, 2016–2024

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

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

Virus	Animal (order, family, species)		Country	Reference	
	Cetacea	Delphinidae	Bottlenose dolphin ( <i>Tursiops truncatus</i> )	Peru, United States of America	WOAH UFHealth (online)
			Chilean dolphin ( <i>Cephalorhynchus eutropia</i> )	Chile	FAO Sernapesca (online)
			Common dolphin ( <i>Delphinus delphis</i> )	Peru, United Kingdom	WOAH Leguia et al. (2023)
			White-sided dolphin ( <i>Lagenorhynchus acutus</i> )	Canada	Avian Flu Diary (online-a)
		Phocoenidae	Burmeister's porpoise ( <i>Phocoena spinipinnis</i> )	Chile	FAO
			Harbour porpoise ( <i>Phocoena phocoena</i> )	Sweden, United Kingdom	SVA
Didelphimorphia	Didelphidae	Virginia opossum ( <i>Didelphis virginiana</i> )	United States of America	USDA, WOH	
A(H5N5) clade 2.3.4.4b	Carnivora	Canidae	Red fox ( <i>Vulpes vulpes</i> )	Canada, Norway	WOAH
		Procyonidae	Raccoon ( <i>Procyon lotor</i> )	Canada	WOAH
A(H5N6) clade 2.3.4.4b	Carnivora	Canidae	Dog ( <i>Canis lupus familiaris</i> )	China	Yao et al. (2023)
A(H5N8) clade 2.3.4.4b	Artiodactyla	Suidae	Domestic pig ( <i>Sus scrofa</i> )*	France	Herve et al. (2021)
			Wild boar ( <i>Sus scrofa</i> )*	Germany	Schülein et al. (2021)
	Carnivora	Canidae	Red fox ( <i>Vulpes vulpes</i> )	United Kingdom	Floyd et al. (2021)
		Phocidae	Grey seal ( <i>Halichoerus grypus</i> )	Poland, Sweden, United Kingdom	SVA Shin et al. (2019), Floyd et al. (2021) Personal communication by Siamak Zohari (Sweden)
			Harbour seal ( <i>Phoca vitulina</i> )	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(H5Nx) 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. Genotypes are assigned using the criteria described in Fusaro et al. (in press).

### Genetic diversity of HPAI A(H5Nx) 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 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, harbour porpoise, harbour seal, red fox and South American coati) have been generated. The characterised viruses belonged to 9 different A(H5N1) and A(H5N8) genotypes, most of which previously identified in birds. All the A(H5N1) viruses associated with infection in fur animal farms in Spain (October 2022) and in Finland (July–October 2023) belonged to the EA-2022-BB genotype. In mid-February 2024, two red foxes were found positive for the A(H5N5) subtype in Norway. The genetic characterisation of one of the two A(H5N5) viruses indicates that it belonged to the EA-2021-I genotype. This represents the first identification of this genotype in a mammalian species.

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 starting from October 2020. This observation suggests that these mutations with potential public health implications have likely emerged upon transmission to mammals.

Outside Europe, it is worth mentioning the mass mortality events caused by HPAI A(H5N1) of clade 2.3.4.4b reported in marine mammals in Argentina in 2023 (Rimondi et al., 2024). Genetic analyses reveal that the viruses collected from mammals cluster separately from the viruses identified in birds in the country, while they are closely related to A(H5N1) viruses detected in South American sea lions in Chile and Peru in the period 2022–2023. Similarly to these viruses, the A(H5N1) viruses collected in marine mammals in Argentina possess the mammalian adaptive mutations in the PB2 protein Q591K and D701N. Based on these observations, the authors suggest that mammal-to-mammal transmission may have occurred in South America.

## 2.3 Avian influenza virus infections in humans

### 2.3.1 Most recent human infections with avian influenza A(H3N8), A(H5N1), A(H5N6), A(H9N2) and A(H10N5) viruses

Since the last report and as of 12 March 2024, 12 new human cases with avian influenza infection have been reported from Cambodia (five cases of A(H5N1)) and China (two A(H5N6), four A(H9N2) and one coinfection of seasonal A(H3N2) and avian influenza A(H10N5)) (Table 4). All except one of the cases 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 1 Dec 2023–12 Mar 2024	Number of reports with disease onset or detection in 2023 and 2024	Total cases (deaths)	Countries reporting human cases
A(H3N8)	-	One case in 2023	3 (1) since 2022	China
A(H5N1)	Five cases in Cambodia, including one death	A total of 12 cases/detections in 2023  Five cases in 2024	887 (462) since 2004	A total of 23 countries reported cases. EU/EEA: Spain, with virus fragment detections in two poultry workers considered contamination and no productive infections.
A(H5N6)	Two cases in China, including one death	Six cases in 2023	90 (35) since 2014	China (89), Laos (1)
A(H9N2)	Four cases in China	Nine cases in 2023  Two cases in 2024	132 (2) since 1998	No EU/EEA country. China (119), Egypt (4), Bangladesh (3), Cambodia (2), Oman (1), Pakistan (1), India (1), Senegal (1)
A(H10N5)	One fatal case in China	One case with onset in 2023	1 (1) first reported in 2024	China (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 as of 12 March 2024. During 2022 and 2023, a total of three infections were reported from China, with two in children (four and five 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). 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

Since the previous report and as of 12 March 2024, Cambodia has reported five new human infections with A(H5N1), including one death. The clade has been confirmed in three of the cases, all of which were infected with virus of clade 2.3.2.1c (GISAID, online; WHO, online-a). All five individuals had contact with sick or dead backyard poultry in their villages, some of which were handled and consumed, before onset of symptoms (WHO, online-a).

The first case was reported in January 2024 in a three-year-old child from Prey Veng province who developed symptoms on 13 January and was hospitalised three days later.

A second case, a 69-year-old man from Siem Reap province, developed symptoms on 21 January and was admitted to hospital on 24 January. No avian influenza infection was detected among contacts of these two cases and close contacts received prophylactic treatment with oseltamivir. Genome sequencing and phylogenetic analysis revealed that in both cases the virus belonged to H5 clade 2.3.2.1c. (Ministry of Health of the Kingdom of Cambodia, 2024a; WHO, online-a).

Two more cases were reported in February 2024 in siblings from Kratie province, a nine-year-old boy, who developed symptoms on 31 January, was admitted to hospital on 5 February due to a worsening condition and died on 8 February 2024. Phylogenetic analysis showed the virus belonged to H5 clade 2.3.2.1c (GISAID: EPI\_ISL\_18879683). His 16-year-old sibling tested positive for A(H5N1) on 11 February as part of the contact tracing. He reportedly did not have symptoms (Ministry of Health of the Kingdom of Cambodia, 2024b, c).

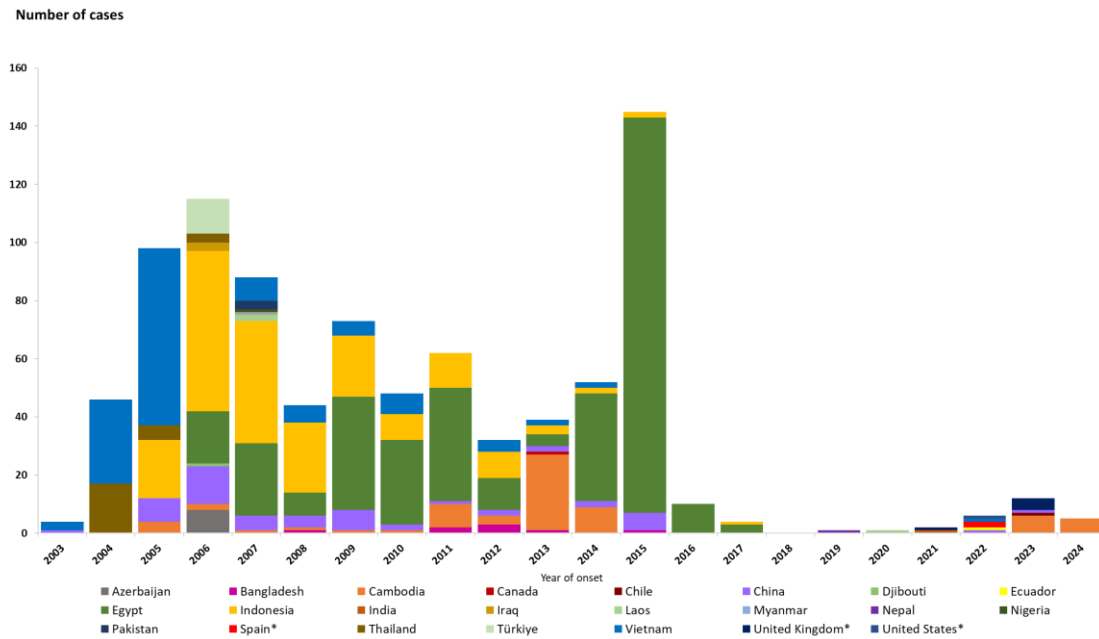
The fifth case was a 17-year-old from Kampot province who developed symptoms (cough, fever, difficulty breathing and fatigue) on 15 February. She had received unspecific treatment for her cough on the same day. Her lung condition worsened, and she was referred to a hospital where she received antiviral treatment (oseltamivir). The girl was from the same district as two earlier cases reported in November 2023. Close contacts of the fifth case tested negative and were asymptomatic (Ministry of Health of the Kingdom of Cambodia, 2024d).

Overall, in 2023, four countries reported 12 cases/detections of A(H5N1): Cambodia (6, clade 2.3.2.1c), Chile (1), China (1) and the United Kingdom (4). So far in 2024, five cases have been reported by one country – Cambodia (5).

As of 12 March 2024, there have been 887 human cases including 462 deaths (case fatality rate: 52%), 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<sup>8</sup>, Thailand, Türkiye, Vietnam, United Kingdom, United States of America; Figure 9).

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<sup>8</sup> A(H5N1) virus detections in two Spanish poultry workers involved in culling activities are considered contaminations and not productive infections.



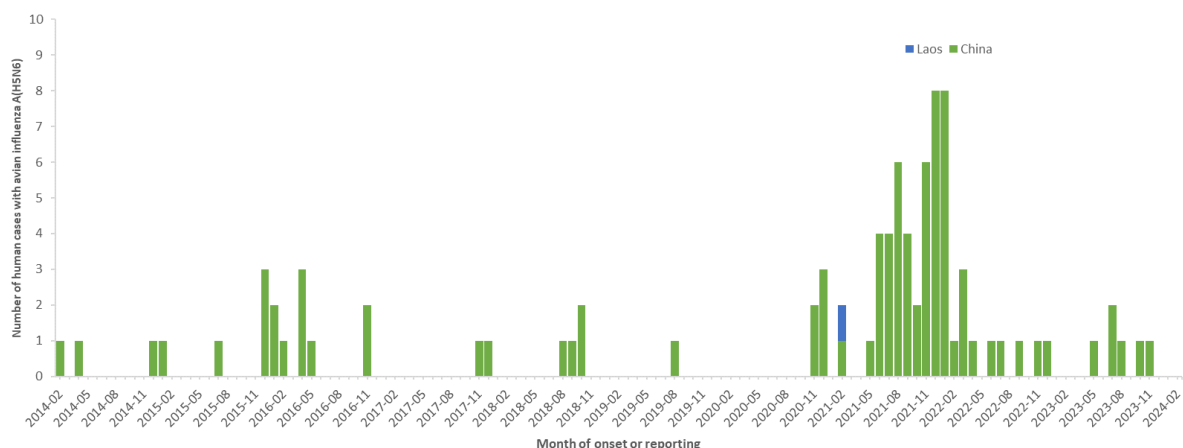
\*Includes detections due to suspected environmental contamination and no evidence of infection reported in 2022 from Spain (2) and the United States (1), and in 2023 from the United Kingdom (3, 1 inconclusive).

**Figure 9:** Distribution of confirmed human cases of A(H5N1) virus infection by year of onset and country, 2003–2024 (data as of 12 March 2024, n = 887)

### 2.3.4 Human A(H5N6) cases, summary

Since the last report, two additional cases have been reported in a 33- and a 59-year-old woman, respectively. According to WHO reports, both cases were from Sichuan province in China and developed severe symptoms with dates of onset in October and November 2023. Both women had previous exposure to live birds at live poultry markets. The 33-year-old woman, who had an underlying condition, died 26 days after developing symptoms. No new cases have been detected among the contacts of these two cases (ECDC, 2024a, b).

As of 12 March 2024, and since 2014, China (89) and Laos (1) have reported a total of 90 human infections with A(H5N6) (Figure 10), including 35 (38.9%) with fatal outcome according to notifications to WHO. Since 2021, the majority of A(H5N6) viruses identified in humans have belonged 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).



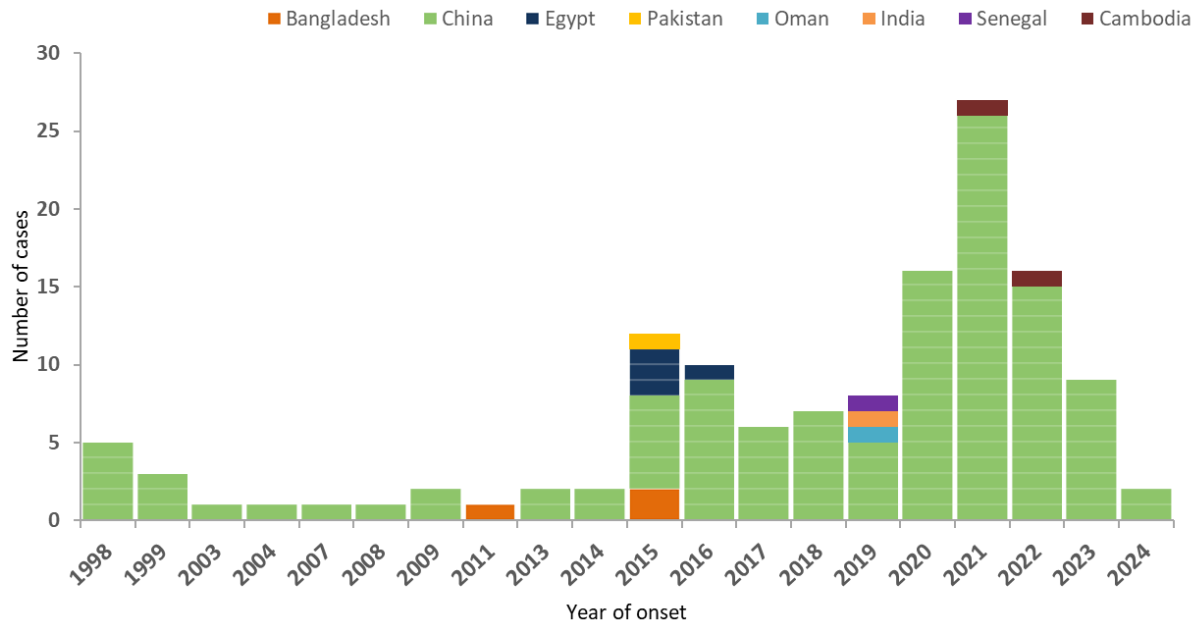
**Figure 10:** Distribution of confirmed human cases of A(H5N6) virus infection by month and year of onset and country, 2014–2024 (data as of 12 March 2024, n = 90)

### 2.3.5 Human A(H9N2) cases, summary

Since the last report and as of 12 March 2024, four new human cases with A(H9N2) infection have been reported by China. Two A(H9N2) cases, in a 74-year-old woman and an one-year-old child, were from Sichuan province. Both cases had a mild symptom onset, on 5 and 14 November 2023 (ECDC, 2024a), and both had previous exposure to sick poultry. Another case occurred in a one-year-old child from the Hong Kong Special Administrative Region who developed symptoms on 15 February 2024. The child did not have direct exposure to poultry or uncooked meat, but had travelled to Guangdong province in China prior to symptom onset. The virus showed no re-assortment with genes of human influenza origin and was sensitive to the antiviral medicine oseltamivir (ECDC, 2024c; GovHK, online). The fourth case was in a six-year-old boy from Anhui province with symptom onset on 3 January 2024 (CHP, 2024).

As of 12 March 2024 and since 1998, a total of 132 human infections with A(H9N2), including two fatalities, have been reported from eight countries, all outside the EU (Figure 11): Bangladesh (3), China (119), Cambodia (2), Egypt (4), Pakistan (1), Oman (1), India (1) and Senegal (1). The majority of infections were identified in children up to nine years of age (98; 74%) and women were more affected than men (76 versus 54; 2 of unknown sex).





**Figure 11:** Distribution of confirmed human cases of A(H9N2) virus infection by month and year of onset and country, 1998–2024 (as of 12 March 2024, n = 132)

### 2.3.6 Human A(H10N5) cases, summary

In February 2024, the Chinese National Disease Control and Prevention Administration reported a human co-infection with seasonal influenza A(H3N2) and avian influenza A(H10N5) in a 63-year-old woman from Anhui province, China. The woman had multiple underlying conditions and developed symptoms (cough, sore throat and fever) on 30 November 2023. She was admitted to the local healthcare facility on 2 December, and was moved to a hospital in Zhejiang Province on 7 December where she subsequently died on 16 December 2023. The coinfection was confirmed from subsequent diagnostic tests in January 2024 by the China CDC (ECDC, 2024d). According to a WHO report (WHO, online-b), the woman had contact with a live duck, which she purchased in a market on 26 November 2023 and later consumed. Laboratory investigation of the remaining duck meat stored in the fridge confirmed the presence of A(H10N5). No new cases have been detected among contacts of this case. The sequences are available on GISAID (Isolate ID: EPI\_ISL\_18846022).

This is the first human case of avian influenza A(H10N5) reported. No human-to-human transmission has been observed for this influenza subtype so far and the investigation of the current event has been finalised. Despite coinfection with A(H3N2) seasonal influenza virus in this patient, genomic analysis revealed that the A(H10N5) influenza virus genes were all of avian influenza origin, showing no signs of reassortment (ECDC, 2024d).

### 2.3.7 Genetic characteristics of avian influenza viruses from humans A(H5N1)

Based on the data available from the GISAID’s EpiFlu™ Database (Shu and McCauley, 2017) accessed on 4 March 2024, two A(H5N1) sequences from human cases have been reported since 1 December 2023 (EPI\_ISL\_18823967, EPI\_ISL\_18879683), both from Cambodia. The available segments for both were HA and NA and additionally NP, MP and NS for EPI\_ISL\_18879683. All the available gene segments were of avian origin.

Both A(H5N1) sequences were assigned to clade 2.3.2.1c and carried the previously detected HA amino acid substitutions T108I (H5 numbering, the combination S107R-T108I has been associated with increased virulence in chickens and mice and increased pH of fusion) (Wessels et al., 2018), S133A (increased pseudovirus binding to  $\alpha$ 2–6 human-type receptors) (Yang et al., 2007) and S155N (associated with increased virus binding to  $\alpha$ 2–6 human-type receptors) (Wang et al., 2010), of which the latter is present in most viruses of this clade. Furthermore, they also carried D94N (associated with increased virus binding to  $\alpha$ 2–6) (Su et al., 2008), and one (A/Cambodia/i0125001G/2024, EPI\_ISL\_18823967) had N154D (associated with decreased virulence in mice) (Jin et al., 2019). These mutations have also been described in four sequences of clade 2.3.2.1c (EPI\_ISL\_18373263, EPI\_ISL\_18540514, EPI\_ISL\_18366401, EPI\_ISL\_18543643) previously detected in human cases in Cambodia in 2023 (EFSA, ECDC and EURL, 2023a).

Further comparison confirmed the presence of HA single deletion at position 328 (a polybasic cleavage motif) which is seen in the vast majority of clade 2.3.2.1.c, compared to A/Goose/Guangdong/1/96, in A/Cambodia/i0125001G/2024 (EPI\_ISL\_18823967) and all four sequences of A(H5N1) from human cases (Cambodia, 2023) in the specific group of 2.3.2.1c. A deletion of this type may lead to increased pathogenicity of avian influenza viruses (Bosch et al., 1981; Webster and Rott, 1987; Subbarao et al., 1993; Horimoto and Kawaoka, 1994; Perdue et al., 1997; Schrauwen et al., 2012; Sugitan et al., 2012; Zhang et al., 2012). However, A/Cambodia/NIPH-2402155/2024 was an exception and did not have such a deletion. In addition, an NA deletion at approximately position 46–75 (stalk region) was detected in all six sequences, as well as in all the closely related A(H5N1) viruses collected in Southeast Asia from birds. NA deletion at this position is associated with enhanced virulence in mice (Matsuoka et al., 2009; Zhou et al., 2009).

### *A(H9N2)*

There were two avian influenza A(H9N2) sequences (EPI\_ISL\_18926219 from Hong Kong, China; EPI\_ISL\_18853922 from Sichuan province, China) available for cases reported between 1 December 2023 and 4 March 2024. HA analysis revealed the presence of Q226L (H3 numbering) associated with increased virus binding to  $\alpha$ 2–6, enhanced replication in mammalian cells and ferrets, and enhanced contact transmission in ferrets (Wan and Perez, 2007; Wan et al., 2008). Furthermore, R164Q (H9 numbering) was detected in A/Hong Kong/VM24002346/2024 (EPI\_ISL\_18926219), which leads to increased thermostability and faster elution from chicken RBCs. In addition, there was a valine (V) at position 220 which is different from wild type but of unknown phenotype. A recent paper for H9N2 (Zhang et al., 2023) revealed that various combinations of the HA amino acid substitutions T150A, R164Q, N166D, and I220T (H9 numbering) are involved in antibody escape, increased viral replication in avian and mammalian cells and enhanced viral replication in mice.

Neither T150A, R164Q, N166D nor I220T were present in the other sequence A/Yaan/001/2023 (EPI\_ISL\_18853922).

### *A(H10N5)*

For the recent human case of co-infection with seasonal influenza A(H3N2) and avian influenza A(H10N5) in China in December 2023, genetic analysis of the A(H10N5) sequences (EPI\_ISL\_18846022) suggested all segments were of avian influenza origin, with no indication of reassortment having occurred. No information regarding mutations of

importance could be found for A(H10N5) and, as a result, the A(H10N5) sequence could not be analysed further.

### 2.3.8 Additional information and international risk assessments

#### **Additional information from recent publications relevant for public health**

The Health Security Committee of the European Commission published an opinion on zoonotic avian influenza, calling for a One Health Approach with integrated surveillance, joint assessments and response, and communication across sectors for avian influenza. They encouraged the evaluation of capacity, strategies and needs for medical countermeasures in countries to inform provision of support, research and development on avian influenza in the European Union (European Commission, 2023).

ECDC recently published an investigation protocol for human exposures and cases of avian influenza, with guidance for follow-up of individuals exposed to animals infected with avian influenza and management of human cases (ECDC, 2023b). A survey of protection measures applied during HPAI outbreaks and follow-up of people exposed to HPAI in the EU/EEA suggested most countries responding had guidelines for occupational groups, such as farmers and veterinarians, when managing avian influenza outbreaks in poultry. Furthermore, most countries had similar recommendations for personal protective equipment in poultry outbreaks and the testing of symptomatic individuals following avian influenza exposure (ECDC, 2023a). Laboratory capacities for detection and characterisation of zoonotic influenza viruses, including avian influenza, in the EU/EEA and the Western Balkans was summarised in a recent ECDC report (ECDC, 2023c). There was a high capacity to identify avian influenza in human specimens, with 97% of laboratories being able to test for avian influenza viruses and 69% of laboratories also being able to sequence A(H5) and unsubtypable influenza A viruses.

#### *A(H3N8)*

In 2022, a novel reassortant avian influenza A(H3N8) virus was first documented in humans and has been reported in three people to date, all in China (Cheng et al., 2022; Tan et al., 2022; Zhuang et al., 2023). A(H3N8) virus generated from one of the human isolates was able to replicate in both mice and ferrets and weight loss was observed. There was limited transmission via respiratory droplets in ferrets. Neutralising antibodies against the A(H3N8) virus were present in 69% of human sera tested and more prevalent in older age groups where people may have had previous exposure to earlier A(H3N2) viruses (Gu et al., 2024).

#### *A(H5N1)*

A study assessing the zoonotic potential of an A(H5N1) clade 2.3.2.1c isolate (A/Cambodia/NPH230032/2023) from a lethal case of A(H5N1) in an 11-year-old girl in Cambodia in 2023 found that antigenicity and receptor binding were similar to an earlier virus of A(H5N1) clade 2.3.2.1c from 2012. No preference for binding human-like receptors was observed (Chang et al., 2023).

A case report described co-infection with A(H5N1) and SARS-CoV-2 in a 52-year old woman in China in 2023. The patient presented with history of a temperature and continued to develop severe pneumonia and low blood pressure. Metagenome next-generation sequencing identified A(H5N1), after which co-infection with A(H5N1) and

SARS-CoV-2 was confirmed by PCR. The patient improved following treatment with the antivirals peramivir and nirmatrelvir-ritonavir (Jin et al., 2024).

In serum samples from healthy adults in Hong Kong, cross-reactive neuraminidase inhibition (NAI) antibodies to A(H5N1) virus clade 2.3.4.4b were observed in 96.8% (n = 61/63) of assessed individuals with previous exposure to seasonal influenza viruses. However, additional research would be required to assess if the presence of cross-reactive NAI antibodies translates into protection against A(H5N1) infection or altered disease severity (Daulagala et al., 2024).

In two surveys of the knowledge and perspectives of backyard poultry keepers and veterinarians on avian influenza in the United Kingdom, most poultry keepers (99%) and all veterinarians (100%) were aware of the ongoing A(H5N1) outbreak in 2021/2022. For poultry owners, social media was the main source of information regarding the avian influenza outbreak. The majority of veterinarians would advise clients to contact the appropriate authority if they suspected avian influenza (Jewitt et al., 2024; McCloughlin et al., 2024).

### *A(H5N6)*

Five patients infected with A(H5N6) in China in 2021–2022 with acute respiratory distress syndrome (ARDS) and viral sepsis were either treated with the antivirals oseltamivir and baloxavir sequentially or given both antivirals combined. Median time from developing disease to receiving oseltamivir was five days (range 4–18 days) and baloxavir 11 days (range 7–28 days). The viral load decreased substantially in four out of five patients after receiving baloxavir and the authors concluded that baloxavir administration may contribute towards reduced viral load, even when administered during the advanced stages of disease (Guan et al., 2024).

### *A(H9N2)*

In 2021, 80% of human cases with A(H9N2) in China were in children under 12 years of age, the majority presenting with influenza-like illness. All sequenced A(H9N2) viruses from humans had mutations associated with increased viral binding to human-type  $\alpha$ 2-6 receptors and mammalian adaptation (Tan et al., 2023).

Isolates of A(H9N2) were assessed from two people, a cat and dead chicken from a backyard farm in China in 2018. Clinical symptoms in the affected individuals included mild abdominal discomfort, diarrhoea and joint pain. The A(H9N2) viruses showed an exclusive preference for binding human-type  $\alpha$ 2-6 receptors, consistent with many other A(H9N2) viruses isolated in China. Furthermore, isolated A(H9N2) viruses from the human and cat were able to replicate in mice and weight loss was observed. The authors highlighted the fact that the absence of influenza-like symptoms in infected people may complicate identification of human cases (Yang et al., 2023).

## **International risk assessments**

The recent human case of avian influenza A(H10N5) infection in China was the first reported human case with this subtype. Since A(H10N5) is an LPAI virus, it is not notifiable in animals and, as a result, its prevalence in animal populations is unknown. Further research is required to evaluate the occurrence in animal populations and the risk of human infection. There is currently no indication of human-to-human transmission of avian

influenza A(H10N5) virus and the risk of spread among humans is considered low by WHO (WHO, online-b).

Risk assessments by WHO, the United States Centers for Disease Control and Prevention (US CDC), and the UK Health Security Agency (UKHSA) evaluating the risk of infection for humans with the recently reported A(H5N1) viruses have been summarised previously (EFSA, ECDC and EURL, 2023a). The WHO assessment of the risk posed by currently known zoonotic influenza viruses to public health remains unchanged (WHO, 2023a). WHO assessed the risk associated with the recently reported HPAI A(H5N1) viruses infecting humans as low for the general population and low-to-moderate for occupationally exposed individuals (WHO, 2022a, b, 2023). The risk posed by A(H5N1) in wild birds and poultry to human health continues to be considered low by the US CDC, but may be higher in individuals with occupational or recreational exposure to infected birds (CDC, online). There has been no update to the UKHSA's most recent risk assessment of A(H5N1) clade 2.3.4.4b to human health, which was assessed as level 3 (limited mammalian transmission, excluding humans) of 6 with low confidence (GovUK, online-b).

### 2.3.9 ECDC risk assessment

Overall, ECDC assesses the risk of human infection with avian influenza A(H5) clade 2.3.4.4b viruses currently circulating in Europe as low for the general public in the EU/EEA. The risk is considered low-to-moderate for people who are occupationally or otherwise exposed to birds or mammals infected with avian influenza (ECDC, EFSA and EURL, 2023a). Further information on the methodology of the risk assessment can be found in ECDC's operational tool on rapid risk assessment methodology (ECDC, 2019).

Since 2020, A(H5N1) has emerged in new geographical areas globally, and several of these areas have animal husbandry systems where close contact with poultry is common. Although fewer virus detections were reported in poultry and wild birds compared to the same time period last year, widespread occurrence of A(H5N1) was observed in European bird populations between December 2023 and March 2024. Considering the extensive circulation of avian influenza in animal populations with frequent human exposures in recent years, human infection with avian influenza viruses remains rare. To date, there have been no symptomatic infections with A(H5N1) in humans documented in EU/EEA.

Globally, sporadic cases of A(H5N1) infection have been reported in humans, most of which have had a history of direct contact with infected poultry or exposure to a contaminated environment. However, no sustained transmission between humans has been observed. Clinical presentations have ranged from asymptomatic and mild to severe, including death, with an estimated case fatality rate of 52%. Sporadic infections with avian influenza in humans are likely to continue occurring in areas where the virus is prevalent and individuals have unprotected contact with avian influenza infected animals or their environment.

A(H5N1) viruses circulating in Europe remain adapted to birds with a binding preference for  $\alpha$ 2-3 avian-type receptors. However, mutations associated with mammalian adaptation of A(H5N1) that may affect virulence and replication in mammals have been observed. Further understanding of the implication of such mutations for mammalian adaptation, infection and transmission is required to assess any change in the associated risk to humans.

Outbreaks of A(H5N1) clade 2.3.4.4b in animals on fur farms (Aguero et al., 2023; Lindh et al., 2023) suggest mammal-to-mammal transmission of the virus may occur in certain settings. Nevertheless, no mammal-to-human transmission has been documented.

Detection of antibodies against HPAI A(H5) in fur farm animals, such as American mink, without a history of clinical disease, is a concern as workers may be exposed to infected animals unknowingly and without the use of appropriate personal protective equipment. Furthermore, given that transmission of A(H5N1) virus may be undetected in fur farm animals without active surveillance, contact with fur animal species susceptible to human seasonal influenza should, where possible, be avoided when experiencing symptoms of acute respiratory illness to reduce the risk of co-infection with human and avian subtypes of influenza, which could lead to reassortment and emergence of viruses better adapted for human-to-human transmission.

## 3. Conclusions

### 3.1 Birds

- Compared to the December–March periods in previous epidemiological years, there has been a lower number of HPAI virus detections in wild birds. This may be partly due to some level of flock immunity in previously affected wild bird species, the changing composition of HPAI virus genotypes or other reasons that need to be further investigated.
- Compared to previous epidemiological years, an overall low number of HPAI outbreaks in poultry has been observed, which may be associated with the lower number of reported HPAI virus detections in wild birds and thus a lower level of environmental contamination. In contrast, clusters of HPAI outbreaks in poultry establishments were reported from the North Sea and the Baltic Sea coastal areas, associated with larger numbers of HPAI virus detections in wild birds and consequently a higher level of environmental contamination.
- Primary introduction via indirect contact with wild birds was reported to be the main route of infection for most of the reported HPAI outbreaks in poultry. However, secondary spread of HPAI virus between farms, although in fewer numbers than reported primary introductions, have been observed. Between-farm transmission events were often associated with indirect contact via shared equipment or close proximity between farms. Of note was the association with same farm ownership, as reported in three Member States. Same farm ownership appears to have been also a factor for between-farm transmission between two Member States. These indirect contact transmission events highlight the need to keep high levels of biosecurity and controls to minimise the risk of farm-to-farm transmission.
- Some HPAI outbreaks in smaller non-commercial establishments keeping chickens were only detected as a result of active serological surveillance around mortality events in swans. Chickens in most of these establishments had outdoor access and did not show mortality or clinical signs. These observations combined with a positive serological response might indicate previous or ongoing infection with LPAI viruses. Hence, serological detection of these flocks cannot be confirmed with certainty as HPAI virus infections.



- In France, where preventive vaccination against A(H5) viruses has been implemented since October 2023, targeting the duck production sector with compulsory vaccination (with the exception of duck breeders), most of the outbreaks reported in poultry (8 out of 10, since the beginning of the current epidemiological year) occurred in unvaccinated poultry establishments. In addition, no outbreaks were detected in Southwest France, where there were recurring epizootics in areas of high-density duck establishments in previous epidemiological years (since 2020–2021). In the two infected establishments holding vaccinated Muscovy ducks, increased mortality was observed, which provides an indication that increased mortality can still be an indicator of HPAI virus suspicions in vaccinated flocks where vaccination was not fully effective.
- During this reporting period, more long-distance migrating waterfowl species were affected. The spatial pattern of HPAI virus detections in those species differs considerably from HPAI virus detections in colony-breeding seabirds, which were the main wild bird category affected in the previous epidemiological year.
- There was a die-off of mute swans and whooper swans due to A(H5N1) virus infection in Moldova and the adjacent part of Romania in December 2023 and January 2024, involving at least 261 mute swans and an undetermined number of whooper swans. This was temporally linked to a die-off of mute swans due to A(H5) virus infection in Kazakhstan.
- It is expected that the number of HPAI virus detections in wild birds will decrease in the coming weeks as wintering waterbirds migrate to their breeding areas, with the end of the cold season. It cannot be excluded that colony-breeding seabirds form an exception as they congregate at their breeding colony sites during the coming weeks.
- The rate of HPAI virus detections in which the wild bird was not identified to species increased. This makes it more difficult to understand the epidemiology of HPAI viruses in wild birds, and to recommend options for response.
- A similar reduction in reported HPAI outbreaks in domestic and wild birds as in Europe can be observed worldwide. Compared to the previous reporting period (EFSA, ECDC and EURL, 2023a), HPAI outbreaks in domestic and wild birds decreased both and a lower number of countries reported to WOAHA overall, especially from the Americas.
- The severe HPAI outbreak in poultry in the United States of America and Canada continued on a high level and accounted now for almost 80% of the reported outbreaks in domestic birds worldwide. This is most likely related to the return of migrating wild birds from South America to the breeding areas in North America. The HPAI virus detections in both domestic and wild birds in South America even on a lower level may indicate continuous circulation of HPAI viruses among migratory wild bird species on the continent. In contrast to the Americas, the number of HPAI virus detections notified in domestic poultry and wild birds from Asia increased during this reporting period. Furthermore, in addition to the widespread subtype A(H5N1), subtypes A(H5N6) and A(H5N5) have also been detected in Japan and South Korea as well as in wild birds in Japan, respectively.

- Subtype A(H5N1) continues to affect naïve wild bird population in the sub-Antarctic and Antarctic regions, in the current reporting period for the first time in wild birds on mainland Antarctica. There is concern for the virus spreading from Antarctica to Australia and New Zealand in the future.
- Subtype A(H5N5), genotype EA-2021-I, which has persistently been detected in Norway since the 2021–2022 epidemiological year, has since September 2023 spread to Iceland, the United Kingdom, Greenland and Germany, and – besides infecting wild birds – infected red foxes in Norway. A(H5N5) was also detected in Faroe Islands and Japan during the current epidemiological year.
- Since October 2023, there has been an increase in the number of circulating genotypes originating from multiple reassortment events, likely due to the increased prevalence of HPAI virus circulation in wild Anseriformes. Most of these genotypes had never been detected in Europe before. It is not possible to assess whether these new genotypes originated from Europe or if they represent new introductions of the virus, given the limited data available from other countries outside Europe.
- The identified A(H5Nx) virus genotypes circulating in northern Europe mostly differ from those circulating in eastern and southern Europe, where a lower genetic diversity is observed. This geographical difference in circulating virus genotypes might be partly due to different wild bird populations arriving following separate migratory routes. Assuming that these genotypes originated in Europe, the higher genetic diversity observed in Northern Europe might be associated with the higher prevalence of LPAI virus in wild birds in this region than in southern Europe (Pérez-Ramírez et al., 2010). This higher LPAI virus prevalence may increase the probability of reassortment events with A(H5Nx) viruses.
- In the 2023–2024 epidemiological year, the detection of seven A(H5) viruses in wild and domestic birds containing markers of mammalian adaptation in the PB2 protein (E627K or D701N) indicates that viruses with an enhanced capacity to infect mammals can replicate and spread in birds. This is of concern for host jumps and reassortments with influenza A viruses circulating in mammals.
- 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.

### 3.2 Mammals

- The serological survey conducted in all 346 fur animal farms in Finland following the introduction of A(H5N1) viruses from black-headed gulls in July 2023 resulted in an overall A(H5) seroprevalence of 12.7%.
- The low number of HPAI virus detections in wild carnivores during the current period can be assumed to be associated with the low number of HPAI virus detections in wild birds and thus with a lower level of contact between carnivores and infected birds through feeding or scavenging.



- Unlike the mammalian infections reported in Europe during the summer months in 2023, mainly caused by the EA-2022-BB genotype, the recent A(H5) viruses identified in wild mammals belonged to different A(H5N1) and A(H5N5) genotypes. The detection of A(H5N5) virus in two red foxes from Norway represents the first detection of this subtype in mammals in Europe.
- In North America, feral cats in Canada and goat kids in the United States of America were found infected with A(H5N1) virus. The A(H5N1) cases in goats represent the first natural infection of A(H5N1) virus in any ruminant species (suborder Ruminantia) worldwide.
- 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

- Sporadic cases of zoonotic avian influenza A(H5N1), A(H5N6) and A(H9N2) continued to be reported in Asia during the period December 2023 to March 2024. In addition, there was a case of co-infection with seasonal influenza A(H3N2) and avian influenza (H10N5) virus, which was the first documented human infection with A(H10N5) virus.
- The majority of human infections with avian influenza viruses have been associated with unprotected exposure to sick or dead poultry, live poultry markets or a contaminated environment. To date, there has been no sustained human-to-human transmission observed.
- Despite the widespread occurrence of A(H5N1) in wild birds, poultry and some mammals, with many possible human exposures since 2020, there have been no symptomatic human cases detected in the EU/EEA.
- With the extensive circulation of avian influenza viruses in bird populations globally, sporadic transmission to humans is likely to continue occurring in settings where people are exposed to infected animals or their environment without appropriate protective equipment.

## 4. Options for response

### 4.1 Birds

- Primary introduction, particularly in chicken breeder farms, which are expected to have higher levels of biosecurity than other production systems, are a continuous reminder of the importance of keeping high biosecurity measures to minimise the risk of virus introduction from a contaminated environment.

- Early detection and reporting of outbreaks in poultry as well as keeping strict biosecurity measures will contribute to minimise the risk of farm-to-farm transmission. Sharing farm equipment and personnel, particularly when farms have the same ownership, should be, if possible avoided, or at least kept to a minimum. In case of shared equipment or personnel, strict disinfection and biosecurity protocols should be strictly followed.
- For wild birds, general options for response include accurate and comprehensive recording of HPAI-associated mortality events to guide HPAI policy, preventing disturbance of areas undergoing HPAI outbreaks to reduce virus spread, and, if on time, removal of HPAI-affected carcasses from areas where wild birds congregate to reduce environmental contamination and further virus spread.
- The geographic expansion of HPAI A(H5N5) viruses in wild birds in northern parts of Europe and worldwide should continue to 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, as well as to estimate viral prevalence and seroprevalence among different species to improve our understanding of the epidemiology of those viruses. Serological studies, combined with mortality data, may also help infer whether some level of flock immunity has been reached in different species.
- 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 animal farms, measures taken should account for the risk of HPAI for both animal and human health. Options for response include: improving biosecurity in fur animal 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 to early detect HPAI viruses (through virological testing or timely follow-up of positive serological tests with virological tests) (Sun et al., 2021) to prevent the emergence of mutations and to avoid risk of virus transmission to humans (Kibenge, 2023); prompt culling (destroying) of all animals present in

HPAI-affected fur farms; 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. Surveillance efforts should also prioritise domestic mammals present in or around HPAI-affected poultry establishments (including ruminants) and those in possible contact with infected poultry, wild birds or other mammals. Research activities to investigate the role of 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

- Measures should be taken to reduce human risk of exposure to avian influenza:
  - The general public should avoid contact with sick or dead birds and other animals susceptible to avian influenza and, if they find dead animals, inform relevant authorities to ensure safe removal and further investigation, if required.
  - Appropriate personal protective equipment should be used to reduce the risk of infection when in contact with potentially infected animals or highly contaminated environments.
  - Information should be provided to raise awareness among people at potential risk of exposure on how it can be mitigated. Guidance tailored to specific occupational groups, or people engaged in recreational activities where additional measures may be beneficial, should be provided.
- Countries should remain vigilant for potential human cases of avian influenza, especially in geographical areas where the virus is known to occur in poultry, wild birds or other animals.
- People who have been exposed to animals infected with avian influenza while not wearing appropriate personal protective equipment should be monitored for symptoms for 10–14 days after the last exposure and tested if symptoms develop. Testing can also be considered in individuals without symptoms following exposure to infected animals. Given the uncertainty of potential mammal-to-mammal transmission, individuals with unprotected exposure to infected mammals, such as household pets or fur animals, should get tested as soon as possible as a precaution.

Further information on follow-up and management of individuals with exposure and confirmed infection can be found in the ECDC investigation protocol for human exposures and cases of avian influenza (ECDC, 2023b).

- Avian influenza viruses from humans should be sequenced and shared in public databases in a timely manner. Genetic changes in avian influenza viruses that may alter zoonotic potential or susceptibility to available antivirals should be monitored.
- Although there is no indication of an increased risk of avian influenza transmission to humans at present based on available epidemiological and sequencing data, the risk assessment should be reviewed regularly, taking into consideration any new developments and information becoming available.
- Humans experiencing acute respiratory illness should, where possible, avoid contact with fur animal species susceptible to human seasonal influenza to reduce the risk of co-infection and potential reassortment between human and avian subtypes of influenza. Where contact is unavoidable, appropriate protective measures should be taken to reduce the risk of transmission.
- Vaccination against seasonal influenza can be offered to individuals who are occupationally exposed to avian influenza to reduce the risk of reassortment between avian and human influenza viruses. Furthermore, vaccination against A(H5) virus can be considered for protection of those at higher risk of exposure to A(H5N1) as a component of a wider, comprehensive approach to prevent human infections. Specific vaccination recommendations are under the remit of national authorities (EFSA, ECDC and EURL, in press).

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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<sup>9</sup>, 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 December 2023 to 15 March 2024 and reported by Member States and neighbouring countries to ADIS or WOA. 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 WOA. 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 December 2023 to 15 March 2024. Possible actions for preparedness in the EU are discussed.

<sup>9</sup> 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 September to December 2023 (EFSA, ECDC and EURL, 2023a) 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 December 2023 and 15 March 2024 and submitted by Member States or other European countries to ADIS were taken into account for this report. Data extraction was carried on 15 March 2024. WOA-H-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.10876048>

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

Data from WOA-H-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 15 March 2024 and extracted by EFSA. They were used and reproduced with permission. WOA-H 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, 2023b).

## B.2 Data on humans

The number of human cases caused by infection with avian influenza viruses was 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 on human infections, risk factors, and the results from studies on infection and transmission in mammals with relevance for human health are included. Literature is searched using different search terms for the respective virus subtypes and assessed for relevance before being included.

## **Annex A – Data on Birds**

Annex A is available on the EFSA Knowledge Junction community on Zenodo at:  
<https://doi.org/10.5281/zenodo.10876048>

## **Annex B – Data on poultry outbreaks**

Annex B is available on the EFSA Knowledge Junction community on Zenodo at:  
<https://doi.org/10.5281/zenodo.10876048>

## **Annex C – Acknowledgements**

Annex C is available on the EFSA Knowledge Junction community on Zenodo at:  
<https://doi.org/10.5281/zenodo.10876048>