SCIENTIFIC REPORT

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Avian influenza overview

December 2024–March 2025

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Abstract

Between 7 December 2024 and 7 March 2025, 743 highly pathogenic avian influenza (HPAI) A(H5) virus detections were reported in domestic (239) and wild (504) birds across 31 countries in Europe. HPAI A(H5N1) virus detections were predominant and mainly located in central, western and south-eastern Europe. Most HPAI A(H5) virus detections in wild birds concerned waterfowl, particularly mute swans, barnacle geese and greylag geese. Limited secondary spread was observed among the poultry outbreaks, and outdoor poultry access remained an important risk factor at the interface between wild and domestic birds. HPAI A(H5N5) outbreaks occurred only in wild birds and were increasingly reported in waterfowl. For the first time since spring 2024, several HPAI virus detections were reported in domestic cats and wild carnivores in Europe. In the United States of America (USA), the number of dairy cattle farms reportedly affected rose to almost 1,000 in 17 States, and a different HPAI A(H5N1) virus genotype (D1.1) was reported in this species. Between 12 December 2024 and 7 March 2025, 22 new cases of avian influenza virus infection in humans were reported in the USA (12 A(H5) cases), Cambodia (two A(H5N1) cases), United Kingdom (one A(H5N1) case), and China (six A(H9N2) cases and one A(H10N3) case). Most of the A(H5) human cases (93%, n = 14/15) had reported exposure to poultry or dairy cattle prior to avian influenza virus detection or onset of illness. Considering the widespread circulation of avian influenza viruses in animal populations, human infections with avian influenza viruses remain infrequent. No evidence of human-to-human transmission has been documented during the reporting period. The risk of infection with the avian A(H5) influenza viruses of clade 2.3.4.4b currently circulating in Europe remains low for the general public in the European Union/European Economic Area (EU/EEA). The risk of infection remains low-to-moderate for those occupationally or otherwise exposed to infected animals or contaminated environments.

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

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Declarations of interest: If you wish to access the declaration of interests of any expert contributing to an EFSA scientific assessment, please contact interestmanagement@efsa.europa.eu

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[1] 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).

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1. Introduction

This Scientific Report provides an overview of highly pathogenic avian influenza (HPAI) virus detections in poultry[2], captive[3] and wild birds that occurred in and outside Europe between 7 December 2024 and 7 March 2025, as well as HPAI virus detections in mammals up until 12 March 2025, and cases of avian influenza infection in humans between 12 December 2024 and 7 March 2025. Detections of low pathogenic avian influenza (LPAI) virus in birds are discussed whenever they are of zoonotic concern, or otherwise relevant.

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

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 in Europe 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) for the last five and the current epidemiological year[4] by month of suspicion. For the current epidemiological year 2024–2025, starting on 1 October 2024, data reported are truncated on 7 March 2025.

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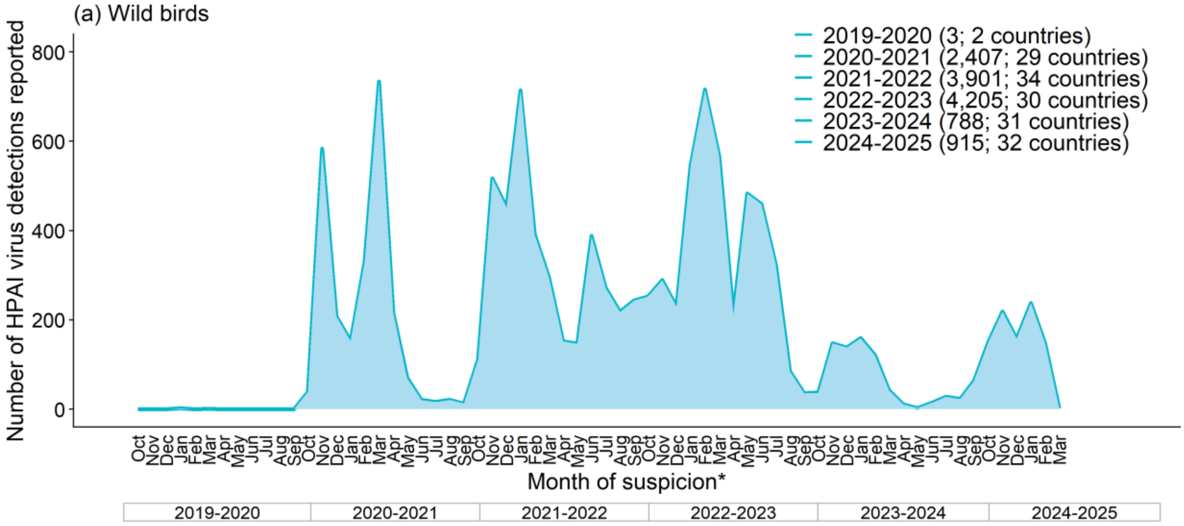
[2] According to Regulation (EU) 2016/429 of the European Parliament and of the Council of 9 March 2016, point (9), 'poultry' means birds that are reared or kept in captivity for: (a) the production of: (i) meat; (ii) eggs for consumption; (iii) other products; (b) restocking supplies of game birds;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

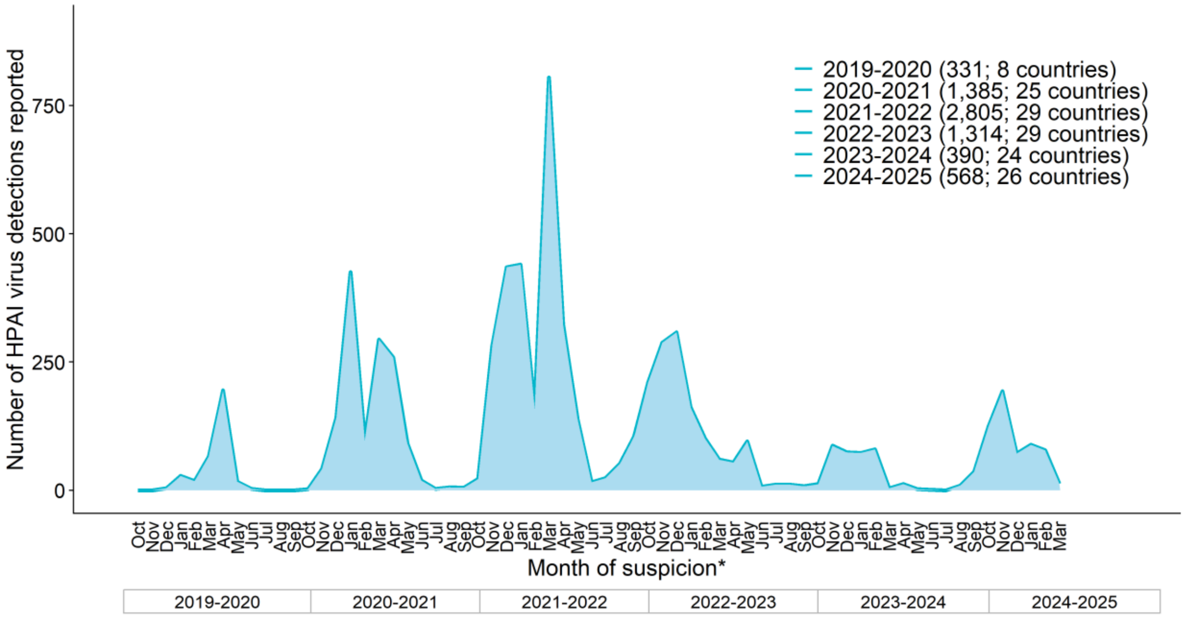
[3] According to Regulation (EU) 2016/429 of the European Parliament and of the Council of 9 March 2016, point (10), 'captive birds' means any birds other than poultry that are kept in captivity for any reason other than those referred to in point (9), including those that are kept for shows, races,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

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

(a) Wild birds



(b) Domestic birds



*If the date of suspicion was not available, the date of confirmation was used to assign the week of suspicion. United Kingdom data are from the Animal Disease Notification System (ADNS, former ADIS) up until 31 December 2020. From 1 January 2021 onwards, the data source was WOAH for the United Kingdom (excluding Northern Ireland) and ADNS/ADIS for the United Kingdom (Northern Ireland)[5].
Source: ADNS/ADIS and WOAH (data extraction carried out on 7 March 2025).

Figure 1: Distribution of the number of HPAI virus detections in wild (cumulative number n = 12,219) (a) and domestic (n = 6,793) (b) birds reported in Europe during six epidemiological years by month of suspicion, from 1 October 2019 to 7 March 2025 (total n = 19,012)

Considering the current reporting period from 7 December 2024 to 7 March 2025, 743 HPAI virus detections were reported in poultry (167), captive (72) and wild birds (504) in 31 countries in Europe (Table 1, Figure 2).

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

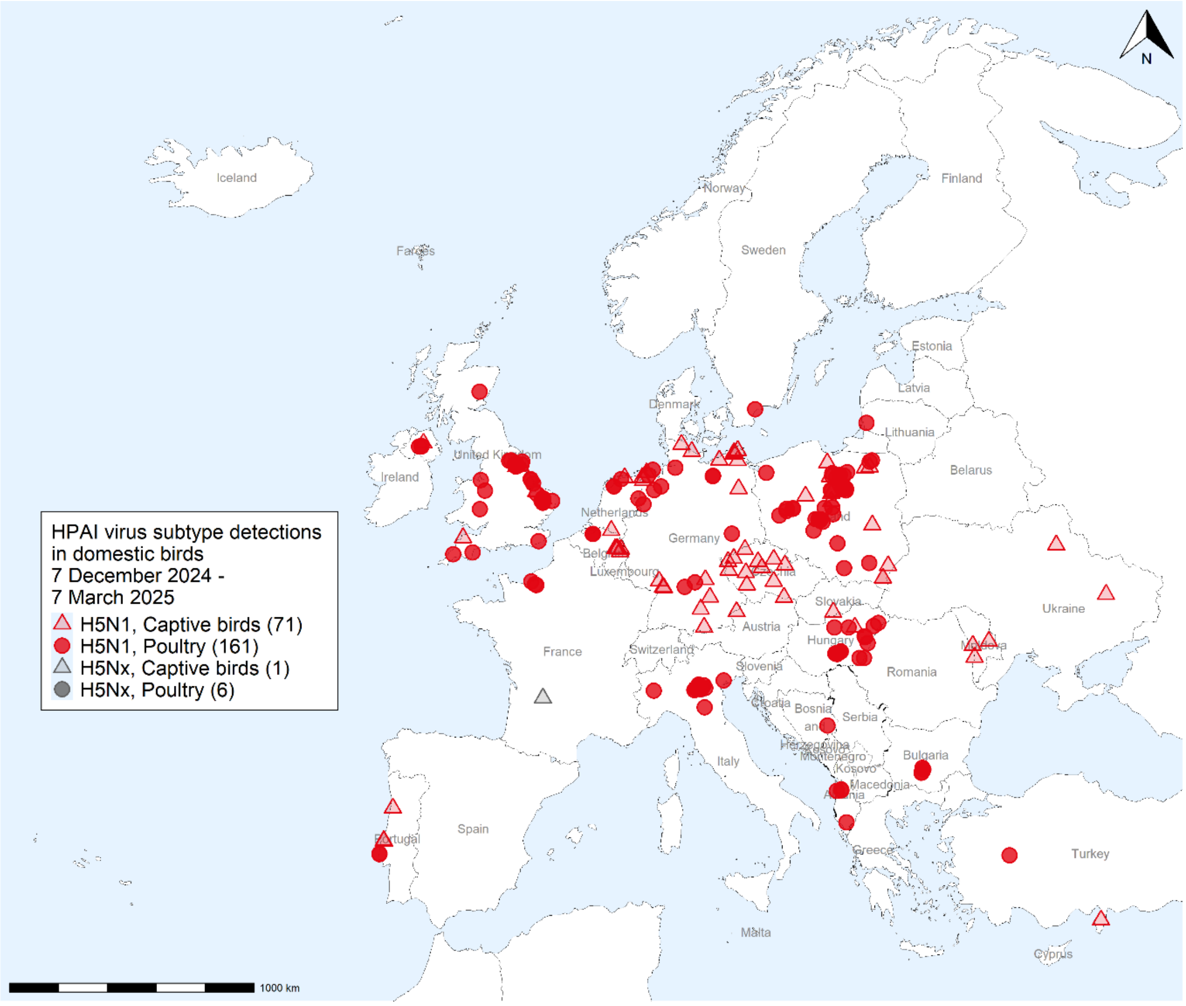
Table 1: Number of HPAI outbreaks reported in Europe by country, virus subtype and affected sub-population, from 7 December 2024 to 7 March 2025. Cumulative numbers since the start of the 2024–2025 epidemiological year are reported in parentheses (1 October 2024 to 7 March 2025)

Reporting country	Captive birds			Poultry			Wild birds				Total
	A(H5Nx)	A(H5N1)	A(H5N5)	A(H5Nx)	A(H5N1)	A(H5N5)	A(H5Nx)	A(H5N1)	A(H5N5)	A(Not typed)	
Albania	-	-	-	-	4 (5)	-	-	2 (2)	-	-	**6 (7)**
Austria	-	1 (2)	-	-	0 (6)	-	1 (5)	4 (56)	-	-	**6 (69)**
Belgium	-	5 (5)	-	-	3 (3)	-	-	14 (14)	0 (1)	-	**22 (23)**
Bosnia and Herzegovina	-	-	-	-	1 (1)	-	-	1 (1)	-	-	**2 (2)**
Bulgaria	-	-	-	-	5 (7)	-	-	1 (1)	-	-	**6 (8)**
Croatia	-	0 (1)	-	-	0 (2)	-	-	1 (8)	-	-	**1 (11)**
Czechia	-	13 (25)	-	-	0 (3)	-	-	3 (7)	-	-	**16 (35)**
Denmark	-	-	-	-	-	-	-	5 (9)	-	-	**5 (9)**
Faroes	-	-	-	-	-	-	-	-	0 (1)	-	**0 (1)**
Finland	-	-	-	-	-	-	-	2 (2)	-	-	**2 (2)**
France	1 (3)	-	-	-	3 (11)	-	7 (8)	6 (14)	-	-	**17 (36)**
Germany	-	19 (21)	-	-	12 (20)	-	0 (13)	103 (156)	1 (1)	-	**135 (211)**
Greece	-	-	-	-	-	-	-	3 (3)	-	-	**3 (3)**
Hungary	-	1 (2)	-	-	25 (211)	-	-	19 (41)	-	-	**45 (254)**
Iceland	-	-	-	-	-	0 (1)	1 (2)	-	15 (24)	-	**16 (27)**
Ireland	-	-	-	-	-	-	-	6 (7)	-	-	**6 (7)**
Italy	-	-	-	6 (6)	26 (50)	-	2 (5)	23 (90)	-	-	**57 (151)**
Lithuania	-	-	-	-	1 (1)	-	-	1 (1)	-	-	**2 (2)**
Moldova	-	3 (19)	-	-	-	-	-	2 (3)	-	-	**5 (22)**
Netherlands	-	2 (2)	-	-	3 (4)	-	-	135 (155)	-	-	**140 (161)**
North Macedonia	-	0 (1)	-	-	0 (1)	-	-	-	-	-	**0 (2)**
Norway	-	-	0 (1)	-	-	-	-	2 (2)	0 (8)	-	**2 (11)**
Poland	-	14 (18)	-	-	42 (61)	-	-	22 (52)	-	-	**78 (131)**
Portugal	-	3 (3)	-	-	2 (2)	-	-	1 (4)	-	-	**6 (9)**
Romania	-	-	-	-	0 (2)	-	-	3 (5)	-	-	**3 (7)**
Serbia	-	-	-	-	-	-	-	0 (3)	-	-	**0 (3)**
Slovakia	-	1 (6)	-	-	0 (2)	-	-	5 (13)	-	0 (1)	**6 (22)**
Slovenia	-	0 (1)	-	-	-	-	-	4 (47)	-	-	**4 (48)**
Spain	-	-	-	-	-	-	-	0 (8)	-	-	**0 (8)**
Sweden	-	-	-	-	1 (1)	-	-	1 (1)	-	-	**2 (2)**
Switzerland	-	-	-	-	-	-	-	7 (9)	-	-	**7 (9)**
Türkiye	-	1 (3)	-	-	1 (6)	-	-	-	-	-	**2 (9)**
Ukraine	-	2 (6)	-	-	-	-	-	1 (1)	-	-	**3 (7)**

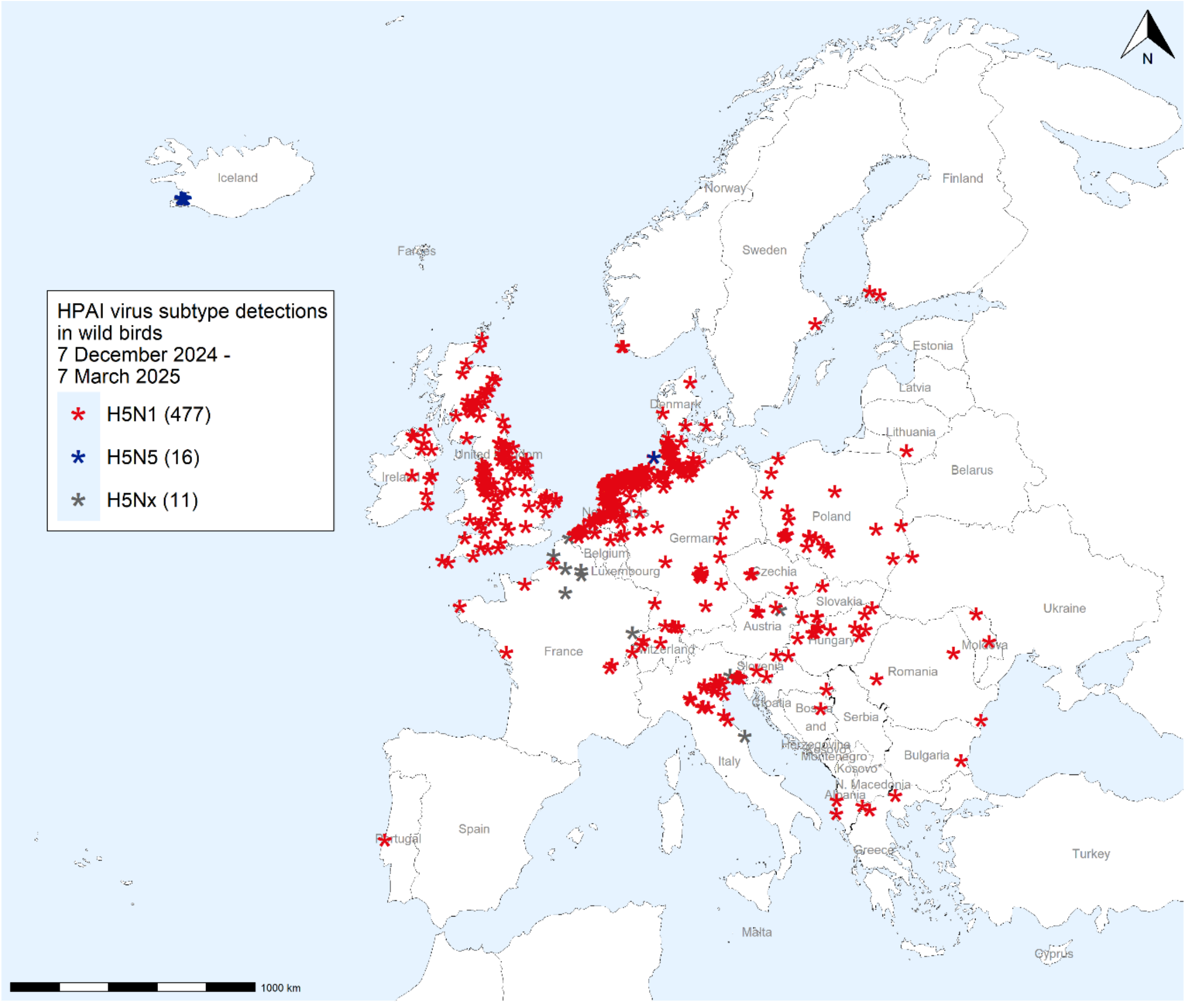
Reporting country	Captive birds			Poultry			Wild birds				Total
	A(H5Nx)	A(H5N1)	A(H5N5)	A(H5Nx)	A(H5N1)	A(H5N5)	A(H5Nx)	A(H5N1)	A(H5N5)	A(Not typed)	
United Kingdom (excluding Northern Ireland)	-	5 (5)	-	-	29 (33)	0 (1)	-	95 (105)	0 (21)	-	**129 (165)**
United Kingdom (Northern Ireland)*	-	1 (1)	-	-	3 (3)	-	-	5 (5)	-	-	**9 (9)**
Total	**1 (3)**	**71 (121)**	**0 (1)**	**6 (6)**	**161 (435)**	**0 (2)**	**11 (33)**	**477 (825)**	**16 (56)**	**0 (1)**	**743 (1483)**

* 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).

'-' means that no HPAI outbreaks were notified via ADIS.



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 07/03/2025



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 07/03/2025

*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.
A(H5Nx) virus detections in poultry are located in Italy and overlap with A(H5N1) virus detections.
United Kingdom (excluding Northern Ireland) data are from WOAH and ADIS for the United Kingdom (Northern Ireland)[6].
Source: ADIS, EFSA and WOAH (data extraction carried out on 7 March 2025).

Figure 2: Geographic distribution, based on available geocoordinates, of HPAI virus detections in poultry and captive birds (239) (upper panel), and in wild birds (504) (lower panel) reported by virus subtype in Europe from 7 December 2024 to 7 March 2025

After a short decline in HPAI virus detections in both domestic and wild birds following a peak in November 2024 of the previous reporting period (21 September to 6 December 2024), reports started to increase again in January 2025 and reached a second peak in the current 2024–2025 epidemiological year (Figure 1). The occurrence of this second peak mirrors patterns observed in previous years, although the underlying reasons are unclear. The overall number of HPAI virus detections in birds in the current epidemiological year has already surpassed that of the 2023–2024 epidemiological year, though it remains lower than in earlier years.

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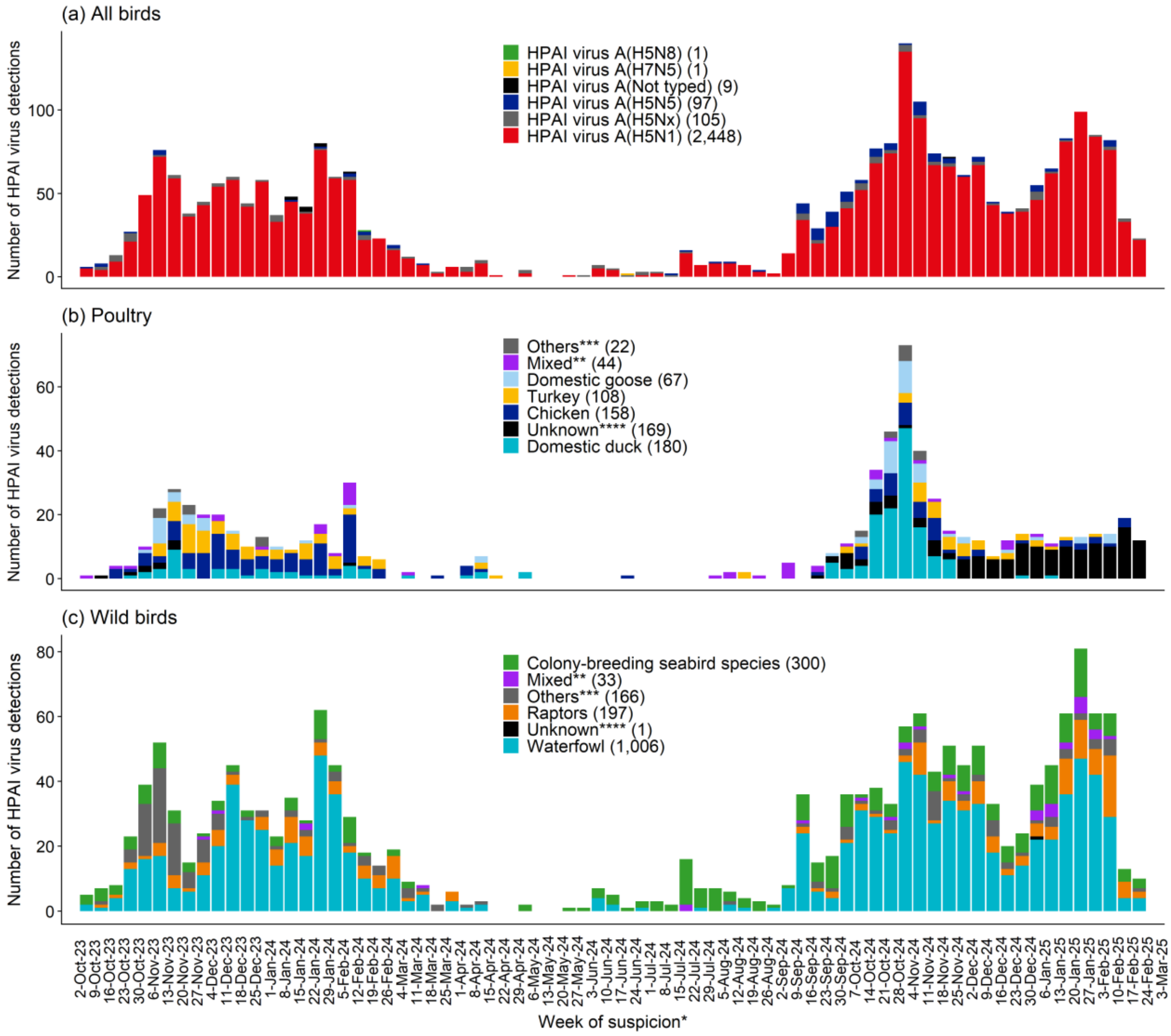
[6] In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Windsor Framework, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).

During the current reporting period, HPAI A(H5N1) outbreaks in poultry and captive birds appeared in clusters and were mostly located in the western (United Kingdom, northern France), central (northern Germany, central Poland, Czechia) and south-eastern (northern Italy, Hungary) parts of Europe, while they were almost absent from the north (one outbreak in Sweden) and south-west (five outbreaks in Portugal) (Figure 2, upper panel). HPAI A(H5N1) outbreaks in wild birds followed a similar geographical pattern (Figure 2, lower panel) with the exceptions of Czechia and the Netherlands. In Czechia, 13 outbreaks in captive birds were geographically spread over the country, while only one detection in wild birds was reported in the south-east. The Netherlands had the highest number of HPAI virus detections in wild birds (135), yet only three outbreaks in poultry and two outbreaks in captive birds were reported. The limited spillover from wild birds to poultry observed in the Netherlands is likely related to the housing order for poultry in place since 20 November 2024, although other factors may also have contributed. HPAI A(H5N5) virus detections in wild birds were markedly lower than in the previous reporting period (Figure 3) and were limited to Iceland, except for one detection in Germany. There were no HPAI A(H5N5) outbreaks in poultry or captive birds in contrast to the previous reporting period, when there were three, one each in Iceland, Norway and the United Kingdom. In addition, there was a noteworthy decrease in the number of HPAI A(H5N1) outbreaks in poultry in Hungary compared to the period from 21 September to 6 December 2024. Overall, the majority of HPAI virus detections in wild birds during the current reporting period were in waterfowl, but an increasing number of HPAI-infected raptors were reported (Figure 3).



*If the date of suspicion was not available, the date of confirmation was used to assign the week of suspicion.
**'Mixed' refers to outbreaks in which multiple species or categories were involved.
***'Others' groups all other affected categories that are not indicated in the legend.
****'Unknown' refers to affected categories that were not further specified during reporting.
Source: ADNS/ADIS, EFSA and WOAH (data extraction carried out on 7 March 2025).

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 (a), affected poultry categories (b) and affected wild bird categories (c), from 1 October 2023 to 7 March 2025

Spatio-temporal information on all HPAI virus detections reported in Europe since October 2016 is available via EFSA's interactive dashboard[7].

Poultry

Between 7 December 2024 and 7 March 2025, 167 HPAI outbreaks in poultry were reported from 16 countries in Europe: Poland (42), Italy (32), United Kingdom (excluding Northern Ireland) (29), Hungary (25), Germany (12), Bulgaria (5), Albania (4), Belgium (3), France (3), Netherlands (3), United Kingdom (Northern Ireland)[8] (3), Portugal (2),

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

[8] 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).

Bosnia and Herzegovina (1), Lithuania (1), Sweden (1), and Türkiye (1) (Table 1, Figure 2, Figure 4).

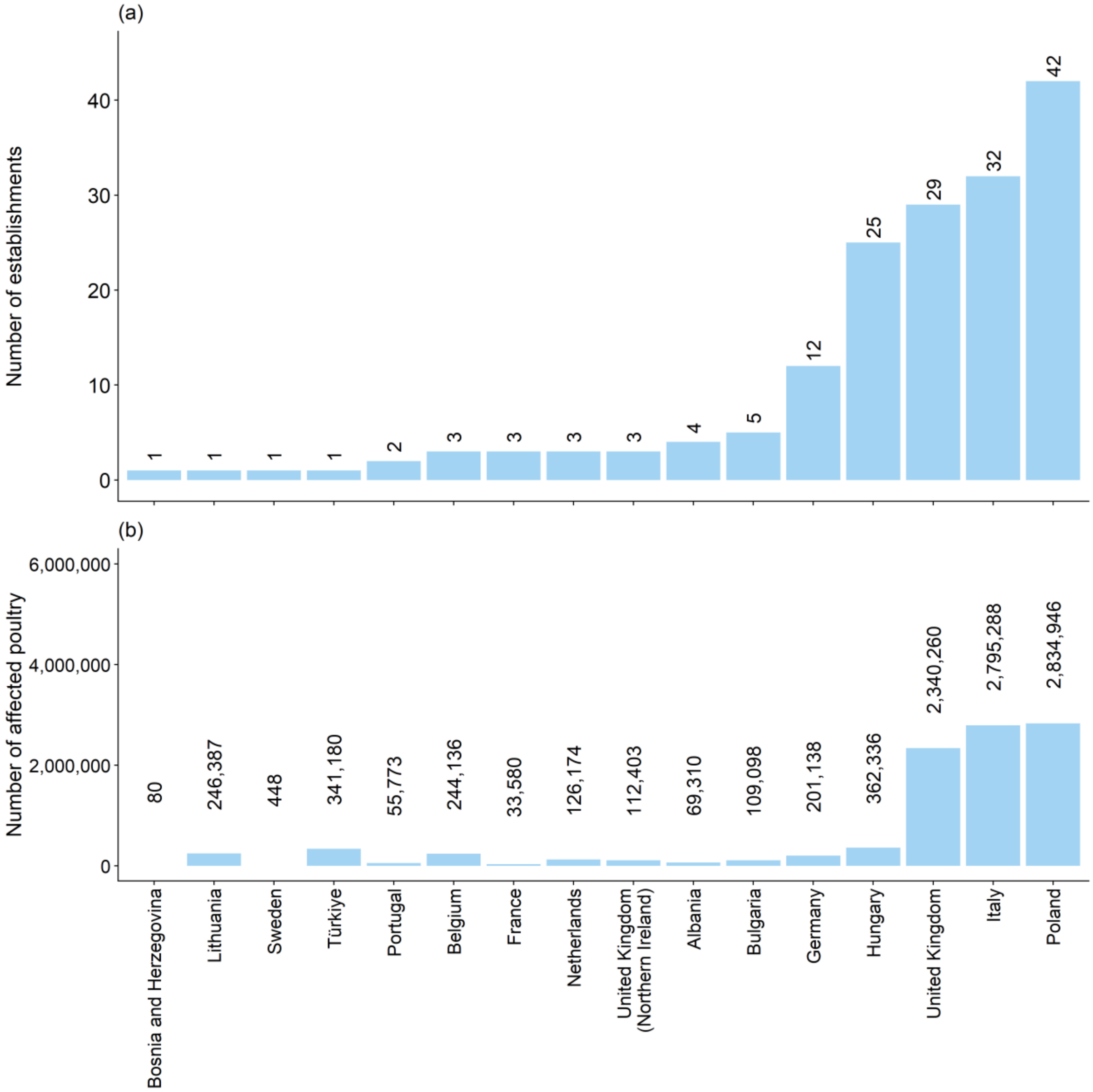

Figure 4: Number of HPAI-affected establishments (167) (a) and number of poultry in the HPAI-affected establishments (9,872,537) (b) in Europe between 7 December 2024 and 7 March 2025 (countries are ranked according to the number of outbreaks)

The vast majority of these outbreaks (96%, 161/167) were due to HPAI A(H5N1) viruses, while in the remaining six outbreaks (4%) the virus was not fully typed. This compares to a total of 161 A(H5) outbreaks during the same period in the previous epidemiological year, when Moldova reported the highest number of outbreaks (32%, 52/161). During the current reporting period, Italy, Poland and the United Kingdom (excluding Northern Ireland) accounted for 62% (103/167) of the HPAI outbreaks in poultry and 81% of the number of poultry culled (Figure 4). In total, almost 10 million birds died or were culled in the HPAI-affected establishments (Figure 4), about 25% less than in the previous reporting period. Overall, 70% (117/167) of the HPAI outbreaks in poultry were classified as primary, 13% (21/167) as secondary, and for 29 outbreaks

(17%) this information was not available. Unlike the previous reporting period, when 99% (153/154) of the secondary outbreaks were reported by a single country (Hungary), the 21 secondary outbreaks between 7 December 2024 and 7 March 2025 occurred across seven different countries: Hungary (14), France (2), Albania (1), Belgium (1), Germany (1), Poland (1), and Portugal (1). During the current reporting period, information on the poultry species kept was not available for most (75%, 125/167) affected establishments. Among the outbreaks for which this information was reported (25%, 42/167), 14 establishments kept turkeys (33.3%), another 14 kept chickens (33.3%), seven kept domestic geese (16.7%), and two kept domestic ducks (4.7%). Multiple species were kept by five (12%) establishments (Figure 3).

In the following paragraphs, a brief description of the HPAI outbreaks in poultry is given by country. This description is based on information collected by EFSA from ADIS and WOAH-WAHIS, reporting countries (in form of additional data submitted and personal communications) and media reports. In the period from 7 December 2024 to 7 March 2025, 167 HPAI outbreaks in poultry were reported in Europe via ADIS or WOAH-WAHIS. Additional data on the characteristics of the affected poultry establishments (e.g. poultry species, production type, source of introduction, number of exposed people, clinical signs and mortality) were collected for 42 of these 167 (25%) outbreaks, reported to ADIS on or before 21 February 2025, from Belgium, France, Germany, Hungary, Lithuania, Netherlands, Poland, Portugal, Türkiye, and United Kingdom (Northern Ireland)[9] (Annex B). Among these, 35 were reported as primary and seven as secondary. In 80% (28/35) of primary outbreaks, indirect contact with wild birds was considered the most likely source of introduction, followed by direct contact with wild birds (3%, 1/35), and for the remaining 17% (6/35) the source was unknown. For 43% (3/7) of these secondary outbreaks, indirect contact with poultry was considered the most likely source of introduction, followed by direct (14%, 1/7) and indirect (14%, 1/7) contact with wild birds, while the source was unknown for the remaining 29% (2/7). For the other 125 (75%) outbreaks in poultry, no additional data were provided or they were reported to ADIS after 21 February 2025 and therefore occurred too shortly before the publication of this report. In this report, a short summary on these outbreaks will be given, but additional data will only be collected in the next round and included in Annex B of the following report.

Albania

During the current reporting period from 7 December 2024 to 7 March 2025, four outbreaks in poultry were reported in Albania via ADIS. No additional data to complement the information in ADIS were provided by the country. On 27 December 2024, a primary A(H5N1) outbreak was detected in an establishment keeping turkeys (n = 400; production type not reported), where mortality and clinical signs were observed. On 6 January 2025, a secondary A(H5N1) outbreak occurred in a small non-commercial establishment keeping chickens (n = 10; production type not reported), where mortality and clinical signs were described. On 10 January, another primary A(H5N1) outbreak was detected in a small non-commercial establishment (n = 14; species and production type not reported), where clinical signs and mortality were observed. On 2 March, the last primary A(H5N1) outbreak was detected in a large establishment (n = 68,886; species and production type not reported), where only mortality was reported.

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[9] 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).

Belgium

During the current reporting period from 7 December 2024 to 7 March 2025, three outbreaks in poultry were reported in Belgium via ADIS. Additional data were collected and provided by the reporting country for two of the three outbreaks, occurred up until 21 February 2025 (Annex B). On 17 February 2025, a primary A(H5N1) outbreak was detected in a commercial laying hen establishment (n = 90,000) through outbreak-related surveillance. At the time of detection, mortality (0.7%) and clinical signs were observed. The birds had no outdoor access and indirect contact with wild birds was the suspected source of introduction. Sixty-one people were reported as exposed. On the same day, a secondary A(H5N1) outbreak was detected through the same type of surveillance in another commercial laying hen establishment (n = 59,690) belonging to the same owner. At the time of detection, mortality was still low (0.01%) but clinical signs were already apparent. The birds had no outdoor access and the suspected source of introduction was indirect contact with poultry, likely due to sharing of equipment between the two establishments. Sixty-one people were reported as exposed. After 21 February, one additional outbreak was reported via ADIS. On 5 March, a primary A(H5N1) outbreak was detected in an establishment keeping broilers (n = 94,446), where mortality and clinical signs were observed.

Bosnia and Herzegovina

During the current reporting period from 7 December 2024 to 7 March 2025, one primary outbreak in poultry was reported in Bosnia and Herzegovina via ADIS. No additional data to complement the information in ADIS were provided by the country. On 7 February 2025, an A(H5N1) outbreak was detected in a small establishment (n = 80; species and production type not reported), where mortality and clinical signs were observed.

Bulgaria

During the current reporting period from 7 December 2024 to 7 March 2025, five primary outbreaks in poultry were reported in Bulgaria via ADIS. No additional data to complement the information in ADIS were provided by the country. On 31 January 2025, an A(H5N1) outbreak was detected in a commercial establishment keeping laying hens (n = 83,600), where mortality and clinical signs were observed. On 13 February, a second A(H5N1) outbreak occurred in a commercial establishment keeping mulard ducks for fattening (n = 6,045), where no mortality or clinical signs were described. On the same day, a third A(H5N1) outbreak was detected in a commercial establishment keeping mulard ducks (n = 7,073; production type not reported), where no mortality was observed but some birds presented clinical signs. On 21 and 25 February, the fourth and fifth A(H5N1) outbreaks occurred in two commercial establishments keeping mulard ducks (n = 4,240 and n = 8,140, respectively; production type not reported), where both mortality and clinical signs were observed.

France

During the current reporting period from 7 December 2024 to 7 March 2025, three outbreaks in poultry were reported in France via ADIS. Additional data were collected and provided by the reporting country for all three outbreaks (Annex B). On 23 December 2024, a primary A(H5N1) outbreak was detected through passive surveillance in a commercial multi-species establishment (n = 25,000) keeping domestic guineafowl for fattening and broilers. Mortality and clinical signs (weakness as well as subglossal and facial edema) were reported. The birds were kept indoors and the most likely source of introduction remained unknown at the time of publication of this report. On 26 December, a secondary A(H5N1) outbreak was detected in another commercial multi-species establishment (n = 8,024) keeping broilers and vaccinated ducks for fattening. No mortality or clinical signs were observed before infection was confirmed. The birds were kept indoors and the most likely source of introduction remained unknown at the time of publication of this report. The outbreak was detected through outbreak-related surveillance. On 27 December, another secondary A(H5N1) outbreak was detected through outbreak-related surveillance in a commercial multi-species establishment (n = 556) keeping broilers as well as domestic guineafowl and geese for fattening. Mortality was reported but no clinical signs were observed. The birds had no outdoor access and the most likely source of introduction remained unknown at the time of publication of this report. No information was available on the number of exposed people for all affected establishments at the time of publication of this report. Since 31 October 2024, the national risk level of introduction of HPAI from wild birds increased from moderate to high, prompting the implementation of a nationwide housing order for all poultry and captive birds across France.

Germany

During the current reporting period from 7 December 2024 to 7 March 2025, 12 outbreaks in poultry were reported in Germany via ADIS. Additional data were collected and provided by the reporting country for ten of the 12 outbreaks, occurred up until 21 February 2025 (Annex B). These ten outbreaks were all confirmed as A(H5N1) and occurred in commercial establishments. Nine outbreaks were reported as primary and one as secondary. All affected establishments housed only single species, with the majority keeping turkeys (60%, 6/10) for fattening, followed by laying hens (30%, 3/10) and broilers (10%, 1/10). For nine of the ten outbreaks, birds with clinical signs were described and mortality (between 0.09% and 17.1%) was observed at the time of detection. The broiler and fattening turkey establishments (n = 7) kept birds indoors, while the laying hen establishments provided outdoor access. For all ten outbreaks, the suspected source of introduction was indirect contact with wild birds, although most outbreaks occurred in a high-density area of turkey establishments (municipalities of Garrel, Bösel and Friesoythe) (European Commission, online). No information was available on the number of exposed people for any of the affected establishments at the time of publication of this report. After 21 February, two additional outbreaks were reported via ADIS. On 22 February, a primary A(H5N1) outbreak was detected in an establishment keeping laying hens (n = 10,000), where clinical signs but no mortality were reported. On 28 February, a primary A(H5N1) outbreak was detected in a small multi-species establishment keeping chickens (n = 33), turkeys (n = 25), ducks (n = 14) and geese (n = 2), where no clinical signs were observed but mortality was reported. Overall, 201,138 birds were culled in the 12 affected establishments.

Hungary

During the current reporting period from 7 December 2024 to 7 March 2025, 25 outbreaks in poultry were reported in Hungary via ADIS. Additional data were collected and provided by the reporting country for 11 of the 25 outbreaks, occurred up until 21

February 2025 (Annex B). These 11 outbreaks were all confirmed as A(H5N1), with the majority (82%, 9/11) being reported as primary and two (18%) representing secondary outbreaks. All 11 outbreaks occurred in commercial establishments keeping single species: geese (46%, 5/11) for foie gras production, ducks (18%, 2/11) for fattening, turkeys (18%, 2/11) and geese (9%, 1/11) for breeding, and laying hens (9%, 1/11). In all eleven outbreaks birds with clinical signs were described and mortality at the time of detection ranged between 1.1% and 75.5% for Anseriformes, and between 2.1% and 24.7% for Galliformes. Only two of the 11 (18%) establishments provided outdoor access, while in the remaining nine (82%) the birds were kept indoors. The most common suspected source of introduction was indirect contact with wild birds, reported for nine (82%) outbreaks, followed by indirect contact with poultry for two (18%). No information was available on the number of exposed people for any of the affected establishments at the time of publication of this report. After 21 February, 14 additional outbreaks were reported via ADIS. These 14 outbreaks were all confirmed as A(H5N1), 12 of them as secondary and two as primary. Most affected establishments housed geese (n = 7) and ducks (n = 6) for foie gras production, while one housed ducks for breeding. Overall, 362,336 birds were culled across the 25 affected establishments.

Italy

During the current reporting period from 7 December 2024 to 7 March 2025, 32 outbreaks in poultry were reported in Italy via ADIS. No additional data to complement the information in ADIS were provided by the country. All outbreaks were confirmed as A(H5N1). The species involved were laying hens (50%, 16/32), turkeys for fattening (28%, 9/32), broilers (16%, 5/32), ducks (3%, 1/32), and a mixture in a multi-species establishment (3%, 1/32). The total number of susceptible birds was about 2,800,000. The disease was characterised by a sudden and exponential increase in mortality, often in only one sector of the flock, and a clinical picture consistent with HPAI. Contrary to the first part of the current epidemic (September–October 2024), when several primary introductions were observed, the geographical clustering in poultry between the provinces of Mantua and Verona (in the Lombardy and Veneto regions) and the high genetic similarity of the viruses may indicate virus spread between the affected establishments during the second phase of the epidemic (November 2024–January 2025). However, for the vast majority of these outbreaks, epidemiological investigations have not clarified the route of virus transmission. It is a possibility that some outbreaks reported as primary may in fact be secondary outbreaks, since epidemiological investigations often fail to determine the exact route of virus transmission and therefore the number of secondary outbreaks may be underestimated. The introduction of viruses into poultry in these areas may have also been facilitated by large numbers of invasive wild birds (African sacred ibis), which are increasingly approaching poultry establishments and in which two viruses with high genetic similarity to those found in poultry have been detected. The numbers of African sacred ibises in Italy have increased in recent decades. For example, 10,880 individuals were counted at winter roots in north-western Italy in 2019 (Cucco et al., 2021). Finally, the latest outbreak, classified as primary, was confirmed in a broiler establishment in the Piedmont region on 1 February. A housing order has been in place in high-risk areas of north-eastern Italy since September 2024.

Lithuania

During the current reporting period from 7 December 2024 to 7 March 2025, one primary outbreak in poultry was reported in Lithuania via ADIS. Additional data were collected and provided by the reporting country for this outbreak (Annex B). On 27 January 2025, an A(H5N1) outbreak was detected in a commercial establishment keeping laying hens (n = 246,387). At the time of detection, mortality (8.1%) and clinical signs were observed. The birds had no outdoor access and the most likely source of introduction remained unknown at the time of publication of this report. Nine people were reported as exposed. A housing order has been in place since the beginning of the autumn migration period (11 October 2024) and will be maintained until the end of the spring migration period.

Netherlands

During the current reporting period from 7 December 2024 to 7 March 2025, three primary outbreaks in poultry were reported in the Netherlands via ADIS. Additional data were collected and provided by the reporting country for all three outbreaks (Annex B). On 7 December 2024, an A(H5N1) outbreak was detected in a commercial establishment keeping broilers (n = 62,925). At the time of detection, mortality (0.01%) and clinical signs were observed. The birds were kept indoors and the most likely source of introduction remained unknown at the time of publication of this report. No people were reported as exposed. On 30 January 2025, a second A(H5N1) outbreak was detected in a commercial establishment keeping laying hens (n = 25,508). At the time of detection, mortality (0.1%) and clinical signs were observed. The birds were kept indoors and the most likely source of introduction remained unknown at the time of publication of this report. No people were reported as exposed. On 17 February, a third A(H5N1) outbreak was detected in a commercial establishment keeping laying hens (n = 37,741). At the time of detection, mortality (0.05%) and clinical signs were observed. While the birds had no outdoor access, the most likely source of introduction and the number of exposed people remained unknown at the time of publication of this report. All three outbreaks occurred in an area where most HPAI virus detections in wild birds were reported.

Poland

During the current reporting period from 7 December 2024 to 7 March 2025, 42 outbreaks in poultry were reported in Poland via ADIS. Additional data were collected from the reporting country for eight of the 42 outbreaks, occurred up until 21 January 2025 (Annex B). All eight outbreaks were reported as primary, confirmed as A(H5N1) and occurred in commercial establishments. One establishment kept multiple species (ducks and geese for breeding) (12.5%, 1/8), while the seven other establishments housed only single species: turkeys (75%, 6/8) for fattening and ducks (12.5%, 1/8) for breeding. Birds with clinical signs and mortality at the time of detection (between 0.6% and 20.4% for Anseriformes, and between 0.9% and 10.4% for Galliformes) were observed in all eight outbreaks. Two of the eight (25%) establishments provided outdoor access, while in the remaining six (75%) the birds were kept indoors. In all eight outbreaks, indirect contact with wild birds was the suspected source of introduction. The number of exposed people (total n = 89) had been reported for six of the eight outbreaks at the time of publication of this report. After 21 February, 34 more outbreaks were reported via ADIS. The 34 outbreaks were all confirmed as A(H5N1), 33 of them as primary and one as secondary. Most of these establishments housed turkeys (14) and ducks (3) for fattening; followed by laying hens (6); geese (5), chickens (3) and ducks (2) for breeding; and a mixture in a multi-species establishment (geese for fattening and breeding as well as broilers). Overall, 2,834,946 poultry were culled in the 42 affected establishments.

Portugal

During the current reporting period from 7 December 2024 to 7 March 2025, two outbreaks in poultry were reported in Portugal via ADIS. Additional data outbreaks were collected and provided by the reporting country for both outbreaks (Annex B). On 3 January 2025, a primary A(H5N1) outbreak occurred in a commercial establishment keeping laying hens (n = 55,427). At the time of detection, mortality (0.5%) and clinical signs were observed. The birds had no outdoor access and breaches in the implementation of biosecurity were identified. Direct contact with wild birds was the suspected source of introduction. The epidemiological investigation identified inadequately protected sections of the ventilation system and found evidence of common starlings entering the establishment. Thirty-three people were reported as exposed. On 17 January, a secondary A(H5N1) outbreak was detected through outbreak-related surveillance in a non-commercial multi-species establishment keeping ducks (n = 336; production type not reported), chickens (n = 6; production type not reported) and geese (n = 4; production type not reported). At the time of detection, mortality (8.9%) and clinical signs were observed, but only in the ducks. The birds had outdoor access and breaches in the implementation of biosecurity were identified. Direct contact with wild birds was the suspected source of introduction. Seven people were reported as exposed. A housing order for domestic birds has been in place in Portugal since 4 January.

Sweden

During the current reporting period from 7 December 2024 to 7 March 2025, one primary outbreak in poultry was reported in Sweden via ADIS. No additional data to complement the information in ADIS were collected, as the outbreak was reported too close to the time of publication of this report. On 26 February 2025, an A(H5N1) outbreak was confirmed in an establishment keeping pheasants for game purposes (n = 448). The pheasants were kept in an establishment covered with nets on all sides to prevent wild bird contact. A mild increase in mortality was reported to authorities on 24 February. The severity progressed with rising mortality and clinical signs consistent with HPAI leading to culling of the flock on 27 February. Domestic mammals present in the affected establishment (dogs, cattle, horses) have been tested and found negative for the virus in the initial sampling. A housing order was only implemented in parts of southern Sweden after the outbreak was confirmed (since 27 February)[10].

Türkiye

During the current reporting period from 7 December 2024 to 7 March 2025, one primary outbreak in poultry was reported in Türkiye via ADIS. Additional data were collected and provided by the reporting country for this outbreak (Annex B). On 11 December 2024, the A(H5N1) outbreak was detected in a commercial establishment keeping laying hens (n = 341,180) through outbreak-related surveillance. At the time of detection, mortality (0.2%) and clinical signs were observed. The birds had no outdoor

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[10] Prior to the outbreak in kept pheasants, Sweden had not confirmed any cases of HPAI in wild or domestic birds in the current season, and a housing order had not been implemented. At the same time as the confirmation of the outbreak, a case was confirmed in wild birds in Stockholm and there were also for the first time this season and increase in reports of sick or dead wild birds to the Swedish Veterinary Agency. The national disease situation in combination with the EU situation, and wild bird spring migrations was the basis for a decision on establishment of a HPAI high risk area and housing order in parts of southern Sweden on 27 February

access and the most likely source of introduction remained unknown at the time of publication of this report. No people were reported as exposed.

United Kingdom (excluding Northern Ireland)

During the current reporting period from 7 December 2024 to 7 March 2025, 29 outbreaks in poultry were reported in the United Kingdom via WOAH-WAHIS. All 29 outbreaks were confirmed as A(H5N1). Almost all outbreaks (93%, 27/29) occurred in commercial establishments and the total number of susceptible birds was 2,340,260. All affected establishments housed only single species, with the majority keeping laying hens (9); followed by turkeys (8) and ducks (2) for fattening; broilers (2); turkeys (2), ducks (2) and chickens (1) for breeding; and a mixture of laying hens and broilers (1). The poultry species involved were not reported for two outbreaks. The presence of clinical signs remained unknown for all 29 outbreaks at the time of publication of this report. However, mortality was observed in 26 of the 29 outbreaks. Seven establishments provided outdoor access, while for the remaining 22 this information was not available.

United Kingdom (Northern Ireland)

During the current reporting period from 7 December 2024 to 7 March 2025, three primary outbreaks in poultry were reported in the United Kingdom (Northern Ireland)[11] via ADIS. Additional data were collected and provided by the reporting country for one of the three outbreaks, occurred up until 21 February 2025 (Annex B). On 14 February 2025, an A(H5N1) outbreak was detected in a commercial establishment keeping laying hens (n = 63,127). At the time of detection, mortality (14.7%) and clinical signs were observed. The birds had no outdoor access and the most likely source of introduction was indirect contact with wild birds. Thirty-one people were reported as exposed. After 21 February, two more outbreaks were reported via ADIS. On 21 and 22 February, the second and third A(H5N1) outbreaks occurred in two establishments (n = 15,868 and n = 33,408, respectively), where mortality and clinical signs were observed. No housing order for domestic birds has been put in place.

Captive birds

Between 7 December 2024 and 7 March 2025, 72 HPAI outbreaks in captive birds were reported from 14 countries in Europe: Germany (19), Poland (14), Czechia (13), Belgium (5), United Kingdom (excluding Northern Ireland) (5), Moldova (3), Portugal (3), Netherlands (2), Ukraine (2), Austria (1), France (1), Hungary (1), Slovakia (1), and Türkiye (1) (Table 1, Figure 2).

Several zoos were affected by HPAI viruses once again, six of which were located in Germany (Table 2).

Table 2: List of zoos affected by HPAI viruses in Germany from 7 December 2024 to 7 March 2025 and respective bird types involved

Place (district)	Date of suspicion	Bird types involved (tested positive)

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[11] 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).

Vorpommern-Rügen	2 December 2024	97 chickens, 10 ducks, 10 pigeons, 6 turkeys, 4 geese, 3 guineafowls, 3 ibis; 9 unspecified captive birds
Karlsruhe	9 December 2024	1 swan
Nürnberger Land	14 December 2024	10 white storks, 4 pelicans
Karlsruhe	16 December 2024	2 chickens
Augsburg, Stadt	27 December 2024	2 (wild) ducks (1 wood duck, 1 mandarin duck), 1 goose (BR24, online)
Rostock, Stadt	27 December 2024	2 geese

In Dordogne, France, three dead geese were sampled for analysis on 20 January 2025 in a theme park and found positive: consequently, around 80 birds (swans, peacocks, quails, chickens, guineafowl, turkeys) were euthanised (Ici, online). All birds were kept in aviaries and protected from direct contact with wild birds by nets. However, wild mallards and herons were observed in the surroundings of the park.

The high number of HPAI A(H5) outbreaks in zoo birds raises the question of whether vaccination should be more widely implemented in this population within the EU. The European Association of Zoos and Aquaria (EAZA) and the European Association of Zoo and Wildlife Veterinarians (EAZWV) have summarised the existing legislation on vaccination against HPAI in zoo birds (Table A.4 in Annex A). In brief, as of February 2022 (date of the report), only Denmark and France had vaccination plans in place in zoos, HPAI vaccines (H5N2 MSD or GALLIMUNE Flu H5N9) were only available in these two countries as well as in Hungary. In practice, the majority of zoos in France implement vaccination, which is however not the case in other EU countries. A recent study tested 977 French vaccinated zoo birds (sera collected in 2008–2022) for anti-H5 antibodies and revealed a high vaccine seroprevalence (88%) (Bosseur, 2024). Older studies on A(H5) seroprevalence in vaccinated zoo birds conducted in the 2000s reported lower to similar percentages, ranging from 51 to 85% (Bertelsen et al., 2007; Furger et al., 2008; Lécu et al., 2009; Oh et al., 2005; Philippa et al., 2007; Vergara-Alert et al., 2011). The difference in seroconversion rates between studies may be explained by the species studied, Anseriformes having been shown to respond best to vaccination, with 97% seropositive (Bosseur, 2024), while Sphenisciformes show much lower immune response (Bertelsen et al., 2007; Bosseur, 2024; Furger et al., 2008; Lécu et al., 2009; Philippa et al., 2007; Roberts et al., 2024).

Wild birds

During the current reporting period from 7 December 2024 to 7 March 2025, a total of 504 HPAI virus detections in wild birds (with one HPAI virus detection potentially including more than one wild bird species) were reported from Netherlands (135), Germany (104), United Kingdom (excluding Northern Ireland) (95), Italy (25), Poland (22), Hungary (19), Iceland (16), Belgium (14), France (13), Switzerland (7), Ireland (6), Austria (5), Denmark (5), Slovakia (5), United Kingdom (Northern Ireland)[12] (5), Slovenia (4), Czechia (3), Greece (3), Romania (3), Albania (2), Finland (2), Moldova (2), Norway (2), Bosnia and

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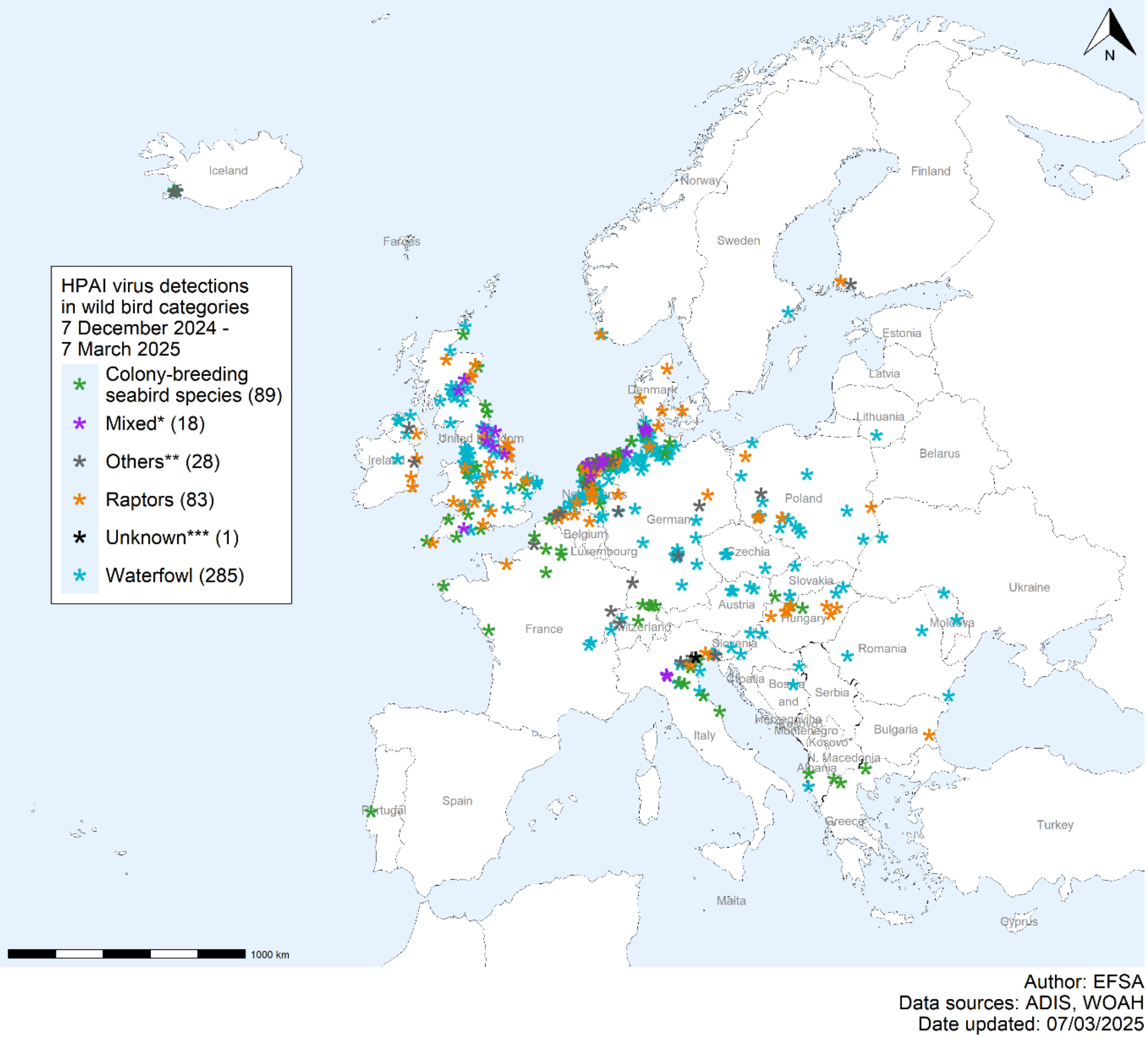
[12] In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Windsor Framework, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).

Herzegovina (1), Bulgaria (1), Croatia (1), Lithuania (1), Portugal (1), Sweden (1), and Ukraine (1). Overall, 477 HPAI virus detections in wild birds were reported as A(H5N1), 16 as A(H5N5), and 11 as A(H5Nx) (Table 1, Figure 2). The overall number of HPAI virus detections reported in wild birds (504) during this reporting period was 17% higher than in the previous reporting period (432) (Figure 3) and 19% higher compared to the same period in the previous epidemiological year (424).

Regarding the wild bird categories involved and considering that more than one wild bird species can be included in a single HPAI virus detection, HPAI A(H5) was recorded in three times more waterfowl (285) than in colony-breeding seabirds (89) (Figure 5).



*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 total 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.
***'Unknown' refers to outbreaks for which no information on the wild bird species involved is available.
Source: ADIS, EFSA and WOAH (data extraction carried out on 7 March 2025).

Figure 5: Geographic distribution, based on available geocoordinates, of HPAI virus detections in different categories of wild birds in Europe, by species category, from 7 December 2024 to 7 March 2025

This pattern is similar to the previous reporting period, when A(H5) was recorded in four times more waterfowl than colony-breeding seabirds. However, almost three times more raptors were found positive for HPAI viruses during the current (83) compared to the previous reporting period (32), and two times more mixed outbreaks (18 vs 7) occurred. HPAI virus detections in raptors were often co-localised with detections in other wild bird categories, suggesting that predation or scavenging on infected birds was the likely route of transmission. Colony-breeding seabirds were primarily detected along the coast, although they were also found further inland during the current reporting period (e.g. around Lake of Constance), and waterfowl were more frequently detected along major rivers.

The wild bird species in which HPAI viruses were detected belonged mainly to three orders: Anseriformes (323 HPAI virus detections), Charadriiformes (101), and Accipitriformes (71). The main waterfowl identified to species were the mute swan (74 in the current vs 155 in the previous reporting period; almost half of them in the United Kingdom), greylag goose (57 vs 35; mostly in the United Kingdom, the Netherlands and Iceland), and barnacle goose (47 vs 4; almost all in the Netherlands) (Figures A.1–A.2 in Annex A). Another 77 HPAI virus detections were described in unidentified Anatidae (77 vs 34, all except one from Germany – mainly barnacle geese according to Member State information (TSN, 2025). In the order Charadriiformes at least seven different gull species were affected during the current reporting period: the main ones identified to species were the European herring gull (33 vs 18), black-headed gull (21 vs 9), and yellow-legged gull (10 vs 20). The Accipitriformes detected positive for HPAI viruses during the current reporting period were mostly Eurasian buzzards (54 vs 8). Apart from these, the category of raptors was also represented by several Falconiformes (10 vs 9) and barn owls (5 vs 2). The complete list of wild bird species found as HPAI virus-infected from 7 December 2024 to 7 March 2025 is reported in Figure A.1 in Annex A. The number of HPAI virus-affected wild birds that were not identified to species was 107/551 (19%), 72% higher than in the previous reporting period (51/455, 11%), and almost all of them were reported from Germany (Figures A.1–A.2 in Annex A).

After no major mortality events had been reported in wild birds in Europe since spring 2024, the number of wild birds found dead in association with HPAI A(H5) in the northern and western parts of the Netherlands increased rapidly since November 2024. In particular, barnacle geese were greatly affected: large numbers of dead birds were reported, with up to several dozen per location, as well as sick birds with clinical signs characteristic for HPAI (DWHC, online-a). The total number of dead barnacle geese reported in the Netherlands in the period 7 December 2024 to 28 February 2025 was 3,446 (personal communication by Valentina Caliendo, AI-Impact). The comparison between this figure and the number of HPAI A(H5) detections in barnacle geese in this reporting period (47) illustrates the potential lack of association between the number of HPAI virus detections in a species and the number of HPAI-associated deaths in a species. In addition, increased numbers of dead greylag geese and European herring gulls, as well as a localised mortality event involving more than 70 Eurasian curlews, were found in association with HPAI A(H5) in the Netherlands (DWHC, online-a; personal communication by Valentina Caliendo, AI-Impact). In the United Kingdom, swans were found dead in several locations, including public parks, and clinical signs such as swimming in circles were reported (BBC, online; Worcester News, online). In Iceland, around 150 carcasses of greylag geese were found in Reykjavík in the first three weeks of 2025 in association with an outbreak of HPAI A(H5N5) (RÚV, online-a). Finally, mortality in various wild bird categories such as waterfowl, gulls and pelicans was reported in Albania (Albanian Daily News, online; Vizion Plus, online).

During the current reporting period, less HPAI A(H5N5) virus detections were reported in wild birds in Europe. Given the wide range of wild bird species in which A(H5N5) has been reported in the current epidemiological year (Table 3), it is not possible to point to a single species in which this subtype is persisting.

Table 3: Number of HPAI A(H5N5)-affected birds per wild bird category and species in the 2024–2025 epidemiological year

Wild bird category	Species	Number of affected birds
Colony-breeding seabirds (25)	European herring gull	8
	Unidentified Laridae species	4
	Great black-backed gull	3
	Black-headed gull	3
	Pallas’s gull	2
	Black-legged kittiwake	1
	Grey gull	1
	Mew gull	1
	Unidentified Phalacrocoracidae species	1
	Unidentified Sulidae	1
Waterfowl (14)	Greylag goose	9
	Whooper swan	2
	Eurasian wigeon	1
	Mallard	1
	Mute swan	1
Others* (10)	Common raven	5
	Hooded crow	3
	Ring-necked pheasant	2
Raptors (10)	Red kite	3
	White-tailed eagle	3
	Common buzzard	2
	Barn owl	1
	Gyrfalcon	1

*‘Others’ groups all other affected wild bird categories.

However, it is noteworthy that waterfowl have increasingly been affected by HPAI A(H5N5), especially greylag geese in Iceland, which may be related to the detection of more than 150 dead birds in the Reykjavík area since the beginning of 2025 (Morgunblaðið, online; RÚV, online-a).

Compared to the previous reporting period when sporadic mass mortality events were recorded in mute swans, gulls and crows, the current reporting period shows continued high mortality in a few species, particularly mute swans, barnacle geese, greylag geese, and European herring gulls. However, this picture is incomplete, as reporting counts of dead wild birds in association with HPAI is not part of the current avian influenza surveillance system in Europe. Available data largely rely on voluntary efforts in some countries and media reports. Additionally, only a small proportion of wild birds found dead are submitted for HPAI testing. Therefore, HPAI virus detections in wild birds generally underestimate the number of wild birds that actually died from A(H5) virus infection.

Note that 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 outside Europe to WOAH from 7 December 2024 to 7 March 2025 is presented in Table 4 and Figure 6.

Table 4: Number of HPAI virus detections in non-European countries notified to WOAH, by virus subtype and country, from 7 December 2024 to 7 March 2025. Cumulative numbers since the start of the 2024–2025 epidemiological year are reported in parentheses (1 October 2024 to 7 March 2025)

Region (total in season)	**Country**	**Domestic birds**					**Wild birds**				**Total**
		A(H5N1)	**A(H5N2)**	**A(H5Nx)**	**A(H7N6)**	**A(H7N8)**	**A(H5N1)**	**A(H5N3)**	**A(H5N5)**	**A(H5Nx)**	
Africa (15)	Niger	1 (1)	-	-	-	-	-	-	-	-	**1 (1)**
	Nigeria	14 (14)	-	-	-	-	-	-	-	-	**14 (14)**
Americas (567)	Argentina	-	-	1 (1)	-	-	-	-	-	-	**1 (1)**
	Canada	25 (96)	0 (2)	-	-	-	-	-	0 (4)	-	**25 (102)**
	Colombia	3 (8)	-	-	-	-	-	-	-	-	**3 (8)**
	Greenland	-	-	-	-	-	-	-	0 (1)	-	**0 (1)**
	Mexico	-	-	-	-	-	9 (13)	-	-	-	**9 (13)**
	Panama	1 (1)	-	-	-	-	-	-	-	-	**1 (1)**
	Peru	-	-	7 (8)	-	-	-	-	-	7 (7)	**14 (15)**
	Puerto Rico	1 (1)	-	-	-	-	-	-	-	-	**1 (1)**
	United States of America	292 (419)	-	2 (4)	-	-	0 (2)	-	-	-	**294 (425)**
Antarctica (1)	Falkland Islands	-	-	-	-	-	0 (1)	-	-	-	**0 (1)**
Asia (301)	Cambodia	3 (3)	-	-	-	-	2 (2)	-	-	-	**5 (5)**
	Taiwan	17 (20)	-	-	-	-	1 (7)	-	-	-	**18 (27)**
	Hong Kong	-	-	-	-	-	0 (1)	-	-	-	**0 (1)**
	India	7 (7)	-	-	-	-	3 (3)	-	-	-	**10 (10)**
	Israel	11 (12)	-	-	-	-	1 (3)	-	-	-	**12 (15)**
	Japan	39 (51)	-	-	-	-	37 (109)	-	-	1 (3)	**77 (163)**
	Mongolia	-	-	-	-	-	0 (1)	-	-	-	**0 (1)**
	Nepal	1 (1)	-	-	-	-	-	-	-	-	**1 (1)**

Region (total in season)	Country	Domestic birds					Wild birds				Total
		A(H5N1)	A(H5N2)	A(H5Nx)	A(H7N6)	A(H7N8)	A(H5N1)	A(H5N3)	A(H5N5)	A(H5Nx)	
	Philippines	0 (1)	0 (1)	-	-	-	-	-	-	-	**0 (2)**
	Russia	-	-	-	-	-	1 (1)	-	-	-	**1 (1)**
	South Korea	27 (35)	-	-	-	-	22 (36)	0 (1)	-	-	**49 (72)**
	Viet Nam	0 (3)	-	-	-	-	-	-	-	-	**0 (3)**
Oceania (5)	Australia	-	-	-	-	4 (4)	-	-	-	-	**4 (4)**
	New Zealand	-	-	-	0 (1)	-	-	-	-	-	**0 (1)**
Total		**442 (673)**	**0 (3)**	**10 (13)**	**0 (1)**	**4 (4)**	**76 (179)**	**0 (1)**	**0 (5)**	**8 (10)**	**540 (889)**

'-' means that no HPAI outbreaks were notified to WOAH.
Source: WOAH (data extraction carried out on 7 March 2025).

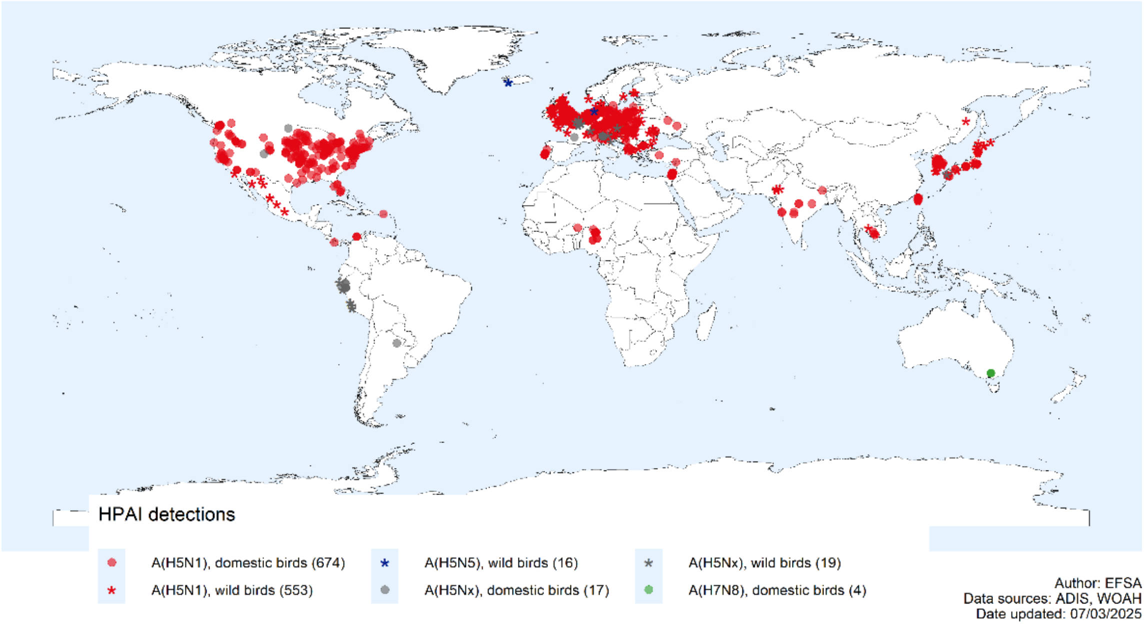


Figure 6: Geographic distribution, based on available geocoordinates, of HPAI virus detections reported worldwide in domestic (695) and wild (588) birds by virus type, from 7 December 2024 to 7 March 2025

In the tables and figures of the present report, only data extracted from WOAH on 7 March 2025 are presented. However, HPAI virus detections in domestic and wild birds are also reported to the public via different means. This additional information on HPAI virus detections available from sources other than WOAH-WAHIS has been integrated in the text below.

In comparison to the previous reporting period from 21 September to 6 December 2024 (EFSA, ECDC and EURL, 2025), the total number of HPAI virus detections in domestic and wild birds officially notified to WOAH from outside Europe increased from 357 to 540 and the number of reporting countries outside Europe from 16 to 19 (Table 4, Figure 6). The number of official notifications to WOAH was about 58% higher than the number of outbreaks reported between 7 December 2023 and 7 March 2024 (540 vs 341 outbreaks).

Overall, HPAI virus detections in domestic birds officially reported to WOAH from outside Europe increased notably from the previous to the current reporting period (242 vs 456), but the number of outbreaks in wild birds decreased by a small amount (115 vs 84). In contrast to the previous reporting period, two African countries officially notified outbreaks to WOAH.

In the current reporting period from 7 December 2024 to 7 March 2025, the USA and Canada accounted for 70% of the reported HPAI A(H5) outbreaks in domestic birds outside Europe, but no HPAI virus detections in wild birds were notified by these countries to WOAH. Based on data retrieved from the United States Department of Agriculture (USDA), the large epidemic of A(H5N1) in the USA remained at a high level in domestic bird establishments of all sizes (USDA, online-a). Poultry farms with more than 50,000 birds accounted for 42% of the outbreaks, and 15 affected establishments with more than one million chickens each were reported to WOAH. In addition, several medium- and some small-sized farms, as well as captive bird establishments were affected by the epidemic. Between 2 February and 11 March 2025, infections were confirmed in 63 commercial establishments and 69 backyard flocks nationwide, collectively affecting 12.89 million birds (USDA, online-a). Furthermore, a co-infection of A(H5N1) and A(H5N9) was reported for the first time in a commercial duck establishment in California (ENCA News, online). Lastly, following the identification of a genetic link between turkeys infected with A(H5N1) and virus detection in raw pet food, the USDA announced the implementation of a pilot enhanced pre-slaughter surveillance in establishments keeping more than 500 turkeys in the States of Minnesota and South Dakota. Specifically, measures such as isolation with clinical monitoring and pre-movement testing 72 hours prior to sending to slaughter were described (USDA, online-b). The USDA reported the detection of A(H5) in 12 captive and 1,011 wild birds (almost four times higher than in the previous reporting period). These detections involved 53 different wild bird species in the period from 7 December 2024 to 7 March 2025 (USDA, online-c). Moreover, based on data available in the GISAID EpiFlu™ database, in 2025 the HPAI A(H5N5) subtype of Eurasian origin, similar to the A(H5N5) from Canada, was detected in two wild birds in the USA (EPI_ISL_19712970 and EPI_ISL_19755851). As in Europe, several zoos in the USA were affected by the A(H5N1) epidemic. The infection was detected in waterfowl in zoos of the States of New York, West Virginia, Illinois and Connecticut (12 On Your Side, online; Independent, online-a; Lincoln Park Zoo, online; NBC New York, online). Mass morbidity and mortality were observed in multiple waterfowl species (e.g. Canada geese, ducks, swans and red-breasted mergansers) and also high numbers of dead raptors were observed in Florida, Massachusetts, Michigan, Minnesota, New Jersey, Texas and Wisconsin (Abc Action News, online; CBS News, online-a; Chicago News, online; NJ News, online; Wbur, online). Mortality in sandhill cranes was reported from Indiana (Smithsonian Magazine, online). In contrast to the previous reporting period, Canada officially reported only outbreaks of A(H5N1) to WOAH. No new A(H5N2) outbreaks and no cases in wild birds were notified. These A(H5N1) outbreaks were mainly detected in medium-sized establishments in western Canada in the border region with the USA (province British Columbia, Fraser valley). Furthermore, inspection Canada reported the detection of A(H5N5) virus in poultry and ostriches in eastern Canada (Labrador and Newfoundland; Inspection Canada, online). Media reported about mortality events in wild birds (e.g. Canada geese and cackling geese, snow owls) related to A(H5Nx) infections in British Colombia and Ontario (CBC News, online; Cowichan Valley Citizen, online). In South America, sporadic HPAI virus detections were officially reported to WOAH in poultry in Argentina, Colombia, Panama, Peru and Puerto Rico, and in wild birds in Mexico and Peru (e.g. black vulture, Canada goose, Eurasian coot, Humboldt penguin, Peruvian booby, Peruvian pelican, snow goose, wild turkey). Furthermore, the media reported an outbreak in backyard poultry in Paraguay in the border region with Argentina (Noticias Argentina, online).

In Antarctica, HPAI A(H5N1) was confirmed in Adélie penguins, Antarctic sheathbills, gentoo penguins (resulting in high mortality), kelp gulls, and skuas (resulting in high mortality (Science, online) on six islands located in the Weddell Sea. This suggests that the virus has expanded its host range and is still circulating or has reemerged during the current breeding season (elDiario.es, online; Phys.org, online). Air sampling helped identify the virus in apparently healthy penguin colonies (Phys.org, online; Science, online). Research expeditions and studies exploring the impact of A(H5N1) on birdlife of the Antarctic region are still ongoing (FLI, online; IAATO, online). In the sub-Antarctic region several thousand kilometres east of South Georgia and the Antarctic Peninsula, HPAI A(H5) has been detected in several dozen king penguins, as well as wandering albatrosses, skuas, Kerguelen shags, kelp gulls, gentoo penguins and Cape petrels on Possession Island (Crozet archipelago) and the Courbet Peninsula (Kerguelen archipelago), and has been linked to an increase in mortality in these species (PASTAAF, online-a; PASTAAF, online-b).

In contrast to the previous reporting period, outbreaks of HPAI A(H5N1) were reported to WOAH from Niger and Nigeria in Africa. The virus was detected in a backyard farm in Niger and poultry on several medium-sized establishments and backyard farms in Nigeria were affected (WOAH).

The reported outbreaks of HPAI A(H5N1) in Japan and South Korea represented two thirds of all outbreaks in poultry in Asia and concerned mainly chickens, quails and ducks. In Japan, more than 2 million birds were culled due to HPAI (WOAH; Japan Times, online). Both countries detected A(H5N1) virus in several wild bird species, such as bean goose, carrion crow, cinereous vulture, common pochard, eastern buzzard, Eurasian goshawk, Eurasian wigeon, European herring gull, great egret, hooded crane, large-billed crow, mandarin duck, peregrine falcon, tufted duck, whooper swan, and white-naped crane (WOAH). The outbreaks of HPAI A(H5N1) of clade 2.3.4.4b in commercial layer and other chicken farms in Taiwan continued (WOAH; China Taiwan Network, online; CNA News, online; UDN News, online). Furthermore, Taiwan detected the virus also in several wild bird species, such as black-faced spoonbill, eastern grass owl and waterfowl (WOAH; TW News, online). Israel and Nepal reported outbreaks of A(H5N1) in medium-sized poultry establishments and Israel detected the virus also in a common buzzard. In contrast to the previous reporting period, India and Cambodia notified numerous outbreaks of A(H5N1) in poultry, particularly in chicken, duck and quail establishments (WOAH; NDTV online; Zeenews India, online), but also detected HPAI viruses in several wild bird species, such as crows and demoiselle cranes, resulting in high mortality (WOAH; Devdiscourse, online; Tripura Times, online). The detection of HPAI A(H5Nx) virus in poultry in Russia’s Rostov region, near the Black Sea, was only reported by the media (Rostov Gazeta, online); however, one A(H5N1) virus detection in a hooded crow in the easternmost part of the country was officially notified to WOAH.

Australia notified to WOAH four outbreaks of A(H7N8) on four medium- to large-sized poultry establishments in the province Victoria. The strain is different from those that affected poultry establishments in the previous epidemiological year in the same province (News Australia, online).

A list of wild bird species that were reported to WOAH as HPAI virus-infected from outside Europe between 7 December 2024 and 7 March 2025 is presented in Table A.1 in Annex A.

2.1.3 Genetic characteristics of HPAI viruses of the A(H5Nx) subtype 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. (2024) and the tool GenIn2 (https://github.com/izsvenezie-virology/genin2). Mutation analyses of the A(H5N1) viruses have been performed using FluMut (Github izsvenezie-virology, online-a, b) with the FluMutDB v6.4 mutation database (https://github.com/izsvenezie-virology/FluMutDB).

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

Since October 2024, complete genome sequences of > 600 European clade 2.3.4.4b HPAI A(H5) viruses from 27 countries have been characterised. The vast majority of these viruses (about 85%) belong to genotype EA-2024-DI, which represents the most widespread genotype in Europe. Based on the data available, during the 2024–2025 epidemiological year this genotype has been detected in 25 European countries, mainly among Anseriformes and domestic birds. Phylogenetic analyses indicate that the viruses belonging to this genotype form two genetic groups, i.e. DI.1 and DI.2, with DI.2 being the most frequent (> 90% of the EA-2024-DI viruses) and widespread variant, identified all over Europe, in the south from Portugal to Bulgaria and in the north from the United Kingdom/Ireland to Lithuania, with the northernmost detection in Norway.

New genotypes, all originating from reassortment events between EA-2024-DI and LPAI viruses, have been sporadically detected, and only three of them have been characterised in multiple countries: EA-2024-EA was identified in Italy, Croatia and Poland; EA-2024-EE was identified in Austria, Switzerland and Germany; and EA-2024-EF in Germany and Denmark.

During the current epidemiological year, detection of the gull-adapted genotypes EA-2022-BB and EA-2023-DT has been reported mainly in seabirds (Laridae), with the EA-2022-BB circulating along the northern European coasts of France, Belgium, the Netherlands and the United Kingdom, and the EA-2023-DT genotype along the Atlantic coast of Spain. A persistent circulation of the A(H5N5) EA-2021-I genotype has been reported in northern Europe. Based on the available data, the extensive circulation of this genotype among wild birds (mainly colony-breeding seabirds and raptors) has been reported in Norway, the United Kingdom and Iceland; however, it has also been sporadically identified in Belgium, the Netherlands and, probably, in Germany (partial genome). Based on the available data from the GISAID-EpiFlu^{TM} database, outside Europe this genotype has been characterised also in Japan, Canada and in the USA.

In poultry, the vast majority (> 90%) of the outbreaks reported in the 2024–2025 epidemiological year in Europe have been associated with genotype EA-2024-DI. Few other outbreaks were caused by genotypes EA-2022-BB (France, Kingdom and in Stavropol in Russia), A(H5N5) EA-2021-I (Iceland and Norway), EA-2023-DA (Bulgaria and Czechia), and EA-2023-EA in Poland.

Overall, compared to the period October 2023–February 2024 of the previous epidemiological year, when 25 different genotypes were identified in Europe, the genetic diversity seems much lower in the current epidemiological year, with a single genotype dominating over the others.

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

Molecular analyses of the HPAI A(H5N1) viruses circulating in birds in Europe since October 2024 indicate that these viruses do not contain critical mutations detected in previous pandemic strains in the receptor binding site of the HA protein, meaning that they continue to be well-adapted to avian species. However, several mutations previously described in literature (Suttie et al., 2019; Pinto et al., 2023; Du et al., 2018, 2021) as being associated with i) enhanced polymerase activity and replication in mammals or mammalian cells, ii) increased virulence, iii) increased/conferred resistance towards antiviral drugs, iv) increased in vitro binding to human-type receptors alpha2,6-SA, v) decreased antiviral response in ferrets, vi) evasion of human butyrophilin subfamily 3 member A3 (BTN3A3), and vii) disruption of the second sialic acid (SIA) binding site in the neuraminidase protein, have been identified 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 research is needed to improve existing knowledge.

Similarly to the viruses collected during the previous epidemiological years (2020–2021, 2021–2022, 2022–2023), some of the mutations in the HA protein that have proved to increase in vitro binding to human-type receptors (i.e. S133A, S154N, T156A, H5 numbering) have been identified in the majority of the A(H5N1) viruses which have been circulating in Europe since October 2024, whereas others (i.e. E251K and Q192R) have only been sporadically observed (≤ six viruses). The impact of all these HA mutations on the biological characteristics of the circulating viruses is still unknown; however, none of the mutations present in the vast majority of circulating A(H5Nx) strains has been shown to cause a shift from avian-like to human-like receptor binding preference or changes in the pH of membrane fusion or virus thermostability, indicating that the currently circulating viruses have limited potential for human-to-human transmission (Yang et al., 2025). Besides the mutations in the HA protein, it is important to mention that most of the A(H5N1) viruses belonging to the EA-2022-BB and EA-2023-DT genotypes contain mutations NP-Y52N and NA-S369I, which may increase their zoonotic potential. All of 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 a reduced susceptibility of A(H5N1) viruses to the available antiviral drugs authorised for use in humans have rarely been identified in the circulating strains. Specifically, mutations associated with resistance to amantadine, NA and PA inhibitors (WHO, online-a) have been detected in approximately 0.6%, 1% and 0.3% of the analysed A(H5N1) viruses, respectively. However, for PA inhibitors, it is important to mention that mutations have been studied in seasonal influenza viruses and not specifically for A(H5N1) viruses; the threshold of ≥ 3 IC50 fold-change was used for the assignment of viruses with a reduced susceptibility to PA inhibitors.

Since October 2024, mutations in the PB2 protein associated with virus adaptation in mammals (E627K/V, D701N or K526R) (Suttie et al., 2019) have been detected in 35 European viruses collected from birds, more specifically in i) 27 A(H5N1) viruses collected from wild and domestic birds from seven different countries and ii) eight A(H5N5) viruses (genotype EA-2021-I) collected from wild and domestic birds in the United Kingdom, Norway and Iceland. Of note, based on the available data, in the 2024–2025 epidemiological year an increase in the relative frequency of detection of such mutations in birds was observed, from about 2.5% of the 2023–2024 epidemiological year to about 5.6% of the current epidemiological year (up to February 2025). Phylogenetic analyses indicate some genetic clustering of viruses containing such mutations. Some of these clusters include viruses collected from the same geographic area, the same species and time period, such as three H5N1 viruses collected from mute swans in October 2024 in Italy with PB2-627V, or nine H5N1 viruses collected from mute swans in November 2024 in Austria with PB2-526R. In contrast, other clusters contain viruses collected from multiple countries and species, such as seven A(H5N1) viruses containing the mutation PB2-701N collected from wild and domestic birds in Italy and Croatia between October and November 2024, and two clusters, composed of three and five A(H5N5) viruses, with the mutation PB2-627V and PB2-627K, respectively, collected from birds and mammals in Norway and Iceland. These data suggest that viruses containing mutations associated to mammalian adaptation can circulate in birds and spread between different countries.

2.2 HPAI virus detections in non-human mammals

2.2.1 HPAI virus detections in non-human mammals worldwide

From 7 December 2024 to 12 March 2025, HPAI A(H5N1) and A(H5N5) viruses were reported in pet, farmed and wild mammals both within and outside Europe. After a period of absence since spring 2024, HPAI viruses were reported again in mammals in Europe, with the first retrospective reports dating back to October 2024. The data described were actively collected from Member States and other European countries, retrieved through WOAH-WAHIS and from the USDA websites (for cases that occurred in the USA), and supplemented with information from media reports (Table 5).

In Europe, HPAI viruses were detected in several domestic cats during the current reporting period. One of these cats was positive for A(H5N1) virus and associated with a small rural farm in Italy where poultry had already been affected by HPAI (La Stampa, online). The free-roaming cat developed respiratory signs and later died on 13 January 2025. The virus collected from the cat was genetically closely related to the virus found in poultry (EA-2024-DI.2 genotype), but the zoonotic PB2 627K mutation was found in the PB2 sequence of the virus from the infected cat. In addition to this virological finding, another cat from the same farm and with similar clinical signs recovered within a few days and tested serologically positive for A(H5N1) infection. No virological data are available for this second cat, as it was not possible to sample the animal during the early phase of infection. In Belgium, two feral cats associated with an affected laying hen establishment were found positive for A(H5N1) virus in East Flanders in February (personal communication by Ingeborg Mertens, FAVV). The suspected source of infection was ingestion of contaminated eggs and/or water from the affected establishment. Both cats showed fever, neurological signs (ataxia, paralysis) and diarrhea, based on which they were euthanised. In Iceland, a total of five domestic cats were found positive for A(H5N5) virus between the end of December 2024 and the beginning of February 2025 (personal communication by Brigitte Brugger, MAST). The littermate and two 10-week-old kittens in a household in Ísafjörður first showed a decrease in feed and water intake, lethargy and neurological signs (stiffness, tremors, seizures) for several days before they died (RÚV, online-b). As the cats had outdoor access and the virus involved showed genetic similarity to those found in wild birds in Iceland at the same time (and in Norway in November 2024), the suspected source of infection was direct contact with wild birds. Other kittens from the same litter that were rehomed shortly before remained unaffected. A fourth case of A(H5N5) was detected in Reykjavík, where a cat in a household of three developed fever and neurological signs (epileptic seizures) and was later euthanised. As this cat had outdoor access, mortality in greylag geese in the same area was observed, and the virus involved showed genetic similarity to those found in wild birds in Iceland at the same time, the suspected route of transmission was direct contact with wild birds. A fifth cat was positive for the same subtype in the north-east of the country and, as the cat had outdoor access, direct contact with wild birds was the suspected route of transmission. All these cats had only been fed with heat-treated commercial cat food and none of them received raw meat or milk. Serological studies involving cats in France (TF1 Info, online) and the Netherlands (Rijksoverheid, online) indicated that 2.2 to 2.8% of domestic cats (with in most cases outdoor access) and 5.8 to 11.8% of feral cats had H5-specific antibodies, respectively (Bessiere et al., manuscript in preparation; DWHC, online-b).

In wildlife, HPAI A(H5N1) viruses were again detected in several red foxes across Europe. Two of these foxes were reported from Italy, one of which was found dead, while the other was apparently healthy and only identified after killing as part of the regional red fox control plan. In the Netherlands, two red foxes were found positive (personal communication by Dennis Bol, NVWA), one of which showed neurological signs and was euthanised (DWHC, online-b). Similarly, Slovenia reported the detection of A(H5N1) virus in a red fox in an area where also wild birds were found dead (personal communication by Aleksandra Hari, AFSVSPP) and one red fox carcass was found positive in Scotland (GovUK, online-a). In Belgium, A(H5) virus was detected in a red fox found dead in East Flanders, which was likely infected through direct contact with wild birds (personal communication with Ingeborg Mertens, FAVV). In Iceland, A(H5N5) virus was found in an American mink in the same area where mortality in greylag geese was reported and an Arctic fox that was shot due to lameness and ataxia (personal communication by Brigitte Brugger, MAST). In Norway, a young Eurasian lynx tested positive for A(H5N5) virus in the north of the country, where several detections of the same subtype in wild birds had been reported in the past. The animal was found apathic back in November 2024 and was later euthanised due to a poor prognosis. The necropsy showed that the animal was in good condition but suffered from acute illness. The virus was only detected in brain samples (personal communication by Silje Granstad, Norwegian Veterinary Institute, and Lars-Erik Lund Rondestveit, Norwegian Food Safety Authority). Two grey seals on the east coast of England were found dead and positive for A(H5N5) virus (FarmingUK, online; GovUK, online-a). In addition, Norway retrospectively reported the detection of the same subtype in a Eurasian otter found weak and with little movement back in October 2024. The animal was euthanised (personal communication by Silje Granstad, Norwegian Veterinary Institute, and Lars-Erik Lund Rondestveit, Norwegian Food Safety Authority).

During the current reporting period, several EU countries actively reported the absence of HPAI viruses in mammals: Austria, Czechia, Cyprus, Denmark, Finland, Germany, Greece, Luxembourg, Moldova, Slovakia, Spain, Sweden, Switzerland, United Kingdom (Northern Ireland)[13]. At the same time, testing of mammals continued during the current reporting period. In Austria, 119 samples from mammals were analysed, all of which resulted negative for A(H5N1) virus (55 pigs, 30 foxes, 8 wild boar, 7 bats, 3 cattle, 2

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[13] 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).

rabbits, 2 wolves, 1 cat, 1 rat) (personal communication by Sandra Revilla-Fernández, AGES). In Belgium, 41 foxes, four cats, two porpoises, two seals and one stone marten were tested, of which one fox and two cats were found positive for HPAI viruses (described above). Moreover, testing of raw milk in Belgium has so far turned out negative (personal communication by Ingeborg Mertens, FAVV).

Outside Europe, the United States of America (USA) continued to report HPAI A(H5N1) virus detections in farmed mammals, most of them in dairy cattle. As of 12 March 2025, 985 establishments in 17 States have been reported positive, predominantly in California, with most of the disease burden expected to be concentrated along the US West Coast (Rawson et al., 2025). Apart from the prevailing B3.13 genotype, to which pigs have recently been shown to be susceptible under experimental conditions (Kwon et al., 2025), a different genotype that has extensively been circulating in birds since autumn 2024 (D1.1) has now been detected in dairy cattle in different States following country-wide milk testing (CBS News, online-b; The New York Times, online). This evidence indicates that at least two other spillover events from wild birds to dairy cattle have happened (FluTrackers, online; USDA, online-d). Similar clinical signs as manifested by the B3.13 genotype have been described for the D1.1 genotype: fever, reduced feed and water intake, drop in milk production, and mild respiratory signs. A recently published case report from Ohio dating back to spring 2024 indicates that A(H5N1) seroprevalence in dairy cattle can reach 89.4% in a herd, with a large number of seropositive animals (76.1%) being subclinically infected (Peña-Mosca et al., 2025). Given the vast economic impact, vaccination of dairy cows is currently being discussed (Abousenna et al., 2025). During the current reporting period, the USA also reported the detection of A(H5N1) virus in 60 domestic cats in various States (California-17, Oregon-12, New Jersey-7, Colorado-5, South Dakota-5, Kansas-3, Washington-3, Louisiana-2, Idaho-1, Iowa-1, Michigan-1, Minnesota-1, Montana-1, New Mexico-1) (USDA) and an exotic cat kept as a pet, for most of which no direct exposure to infected birds or contaminated environments could be identified (CDC, online-a). However, in several instances, infection could be linked to the ingestion of raw milk (LatestLY, online; SBCPHD, online) or raw pet food of different brands (based on turkey or chicken) produced and sold in different States (AP News, online; CBS News, online-c; Independent, online-b; NBC News, online; The Guardian, online; PoultryMed, online-a, b), suggesting that the virus may have entered the pet food chain undetected. As previously described, many of these cats showed neurological (Chothe et al., 2025) or respiratory signs leading to death or euthanasia.

In addition to domestic cats, an increasing number of large felines have been found dead and reported positive for HPAI viruses in zoos and other types of animal sanctuaries across the country (Fox News, online). In Washington State, 20 of 37 large felines (African servals-5, mountain lions-4, lynxes-4, Canadian lynxes-2, caracal-1, hybrid Amur-Bengal tiger-1, Geoffroy's cat-1) were affected by the virus in an animal sanctuary (Baja News, online). In Arizona, a cheetah and a mountain lion were found positive in addition to several bird species in a zoo (The Arizona Republic, online). Also these cases were supposedly linked to ingestion of raw contaminated poultry meat. Finally, the USDA reported the detection of A(H5N1) virus in several bobcats, mountain lions, servals and tigers as well as an African lion, a Canada lynx, and a savannah cat. Other captive mammals affected by A(H5N1) virus in the USA included a harbour seal in a zoo in Illinois (Lincoln Park Zoo, online).

In other wildlife species, the USA reported additional A(H5N1) virus detections in several black rats, bottlenose dolphins, house mice, foxes and Norway rats as well as in an eastern gray squirrel, a deer mouse and a harbour seal.

Apart from Europe and the USA, HPAI A(H5N1) virus of the 2.3.2.1a clade was also identified in domestic cats in India (Raut et al., 2025; The Times of India, online-a). In addition, three tigers and one leopard (of 12 and 26, respectively) were found positive in a rescue centre in Nagpur (The Times of India, online-b).

In Antarctica, in the Weddell Sea (mainly on Joinville Island), crabeater seals were found positive for A(H5N1) virus for the first time (Phys.org, online). Additionally, further mortality events in southern elephant seals were reported from Possession Island (Crozet archipelago) (PASTAAF, online-a; PASTAAF, online-b).

Table 5: Avian influenza A(H5Nx) virus detections in mammalian species other than humans related to circulating viruses worldwide, 2016–2025

Virus	Animal (order, family, species)			Country	Reference
A(H5N1) or A(H5Nx) clade 2.3.4.4b	Artiodactyla	Bovidae	Cattle (*Bos taurus*)	United States of America	WOAH USDA
			Goat (*Capra hircus*)	United States of America	WOAH USDA
		Camelidae	Alpaca (*Lama pacos*)	United States of America	USDA (online-e)
		Suidae	Pig (*Sus scrofa*)	Italy*, United States of America	WOAH Rosone et al. (2023)
	Carnivora	Canidae	Arctic fox (*Vulpes lagopus*)	Finland	WOAH
			Common raccoon dog (*Nyctereutes procyonoides*)	Finland, Japan, Sweden*	WOAH Personal communication by Malin Grant (SVA)
			Coyote (*Canis latrans*)	United States of America	WOAH USDA
			Dog (*Canis lupus familiaris*)	Canada, Italy*, Poland	WOAH Szaluś-Jordanow et al. (2024)
			Japanese raccoon dog (*Nyctereutes viverrinus*)	Japan	WOAH
			Red fox (*Vulpes vulpes*)	Austria, Belgium, Canada, Denmark, Estonia, Finland, France, Germany, Ireland, Italy, Japan, Latvia, Netherlands, Norway, Slovenia, Sweden**, United Kingdom (Northern Ireland)***, United Kingdom, United States of America	WOAH Personal communication by Sandra Revilla-Fernandéz (AGES) Personal communication by Aleksandra Hari (AFSVSPP)
			South American bush dog (*Speothos venaticus venaticus*)	United Kingdom	WOAH
		Felidae	Bobcat (*Lynx rufus*)	United States of America	WOAH
			Canada lynx (*Lynx canadensis*)	United States of America	WOAH USDA
			Caracal (*Caracal caracal*)	Poland, United States of America	WOAH USDA
			Cat (*Felis catus*)	Canada, Belgium, France**, Hungary**, Italy*, Netherlands*,	WOAH TF1 Info, online Rijksoverheid, online

Virus	Animal (order, family, species)			Country	Reference
				Poland, South Korea, United States of America	Personal communication by Ingeborg Mertens (FAVV)
			Eurasian lynx (*Lynx lynx*)	Finland, Sweden*, United States of America	WOAH USDA Personal communication by Malin Grant (SVA)
			Leopard (*Panthera pardus*)	India, United States of America, Viet Nam	The Times of India, online-b
			Lion (*Panthera leo*)	Peru, Viet Nam, United States of America	WOAH USDA
			Mountain lion (*Puma concolor*)	United States of America	WOAH
			Serval (*Leptailurus serval*)	United States of America	WOAH USDA
			Tiger (*Panthera tigris*)	India, United States of America, Viet Nam	WOAH USDA The Times of India, online-b
		Mephitidae	Striped skunk (*Mephitis mephitis*)	Canada, United States of America	WOAH
		Mustelidae	American marten	United States of America	WOAH
			American mink (*Neovison vison*)	Canada, Finland, Spain	WOAH
			Beech marten (*Martes foina*)	Netherlands	GISAID (online)
			Eurasian otter (*Lutra lutra*)	Netherlands, Finland, Sweden, United Kingdom	WOAH
			European badger (*Meles meles)*	Netherlands	WOAH
			European pine marten (*Martes martes*)	Germany	WOAH
			European polecat (*Mustela putorius*)	Belgium, Netherlands	WOAH
			Ferret (*Mustela furo*)	Belgium, Poland, Slovenia	WOAH Golke et al. (2024)
			Fisher (*Pekania pennanti*)	United States of America	WOAH
			Marine otter (*Lontra felina*)	Chile	WOAH
			North American river otter (*Lontra canadensis*)	United States of America	WOAH
			Southern river otter (*Lontra provocax*)	Chile	WOAH
			Stoat (*Mustela erminea*)	United States of America	WOAH USDA
		Odobenidae	Walrus (*Odobenus rosmarus*)	Norway	WOAH
		Otariidae	Antarctic fur seal (*Arctocephalus gazella*)	South Georgia and the South Sandwich Islands, Uruguay	WOAH Bennison et al. (2024), Banyard et al. (2024)
			Northern fur seal (*Callorhinus ursinus*)	Russia	WOAH
			South American fur seal (*Arctocephalus australis*)	Argentina, Brazil, Peru, Uruguay	WOAH
			South American sea lion (*Otaria flavescens*)	Argentina, Brazil, Chile, Peru, Uruguay	WOAH
		Phocidae	Caspian seal (*Pusa caspica*)	Russia	WOAH
			Crabeater seal (*Lobodon carcinophaga*)	Joinville Island	Phys.org, online

Virus	Animal (order, family, species)			Country	Reference
			Grey seal (*Halichoerus grypus*)	Canada, Germany, Netherlands, Poland, Sweden**, United Kingdom, United States of America	WOAH
			Harbour seal (*Phoca vitulina*)	Canada, Denmark, Germany, United Kingdom, United States of America	WOAH
			Southern elephant seal (*Mirounga leonina*)	Argentina, South Georgia and the South Sandwich Islands, Possession Island	WOAH PASTAAF, online-a PASTAAF, online-b Bennison et al. (2024), Banyard et al. (2024)
		Procyonidae	Raccoon (*Procyon lotor*)	Canada, Germany, United States of America	WOAH
			South American coati (*Nasua nasua*)	Germany, Uruguay	WOAH
		Ursidae	American black bear (*Ursus americanus*)	Canada, United States of America	WOAH
			Asian black bear (*Ursus thibetanus*)	France	WOAH
			Brown bear (*Ursus arctos*)	United States of America	WOAH
			Kodiak grizzly bear (*Ursus arctos horribilis*)	United States of America	WOAH
			Polar bear (*Ursus maritimus*)	United States of America	WOAH
	Cetacea	Delphinidae	Bottlenose dolphin (*Tursiops truncatus*)	Peru, United States of America	WOAH USDA
			Chilean dolphin (*Cephalorhynchus eutropia*)	Chile	WOAH
			Common dolphin (*Delphinus delphis*)	Peru, United Kingdom	WOAH Leguia et al. (2023)
			White-sided dolphin (*Lagenorhynchus acutus*)	Canada	WOAH
		Phocoenidae	Burmeister's porpoise (*Phocoena spinipinnis*)	Chile	WOAH
			Harbour porpoise (*Phocoena phocoena*)	Sweden, United Kingdom	WOAH
	Didelphimorphia	Didelphidae	Virginia opossum (*Didelphis virginiana*)	United States of America	WOAH USDA
	Lagomorpha	Leporidae	Desert cottontail (*Sylvilagus audubonii*)	United States of America	USDA
	Rodentia	Cricetidae	Deer mouse (*Peromyscus* spp.)	United States of America	USDA
			Prairie vole (*Microtus ochrogaster*)	United States of America	USDA
		Muridae	Brown rat (*Rattus norvegicus*)	Egypt	Kutkat et al. (2024)
			House rat (*Rattus rattus*)	Egypt	Kutkat et al. (2024)
			House mouse (*Mus musculus*)	United States of America	WOAH USDA

Virus	Animal (order, family, species)			Country	Reference
		Sciuridae	Abert's squirrel (*Sciurus aberti*)	United States of America	WOAH
			Eastern gray squirrel (*Sciurus carolinensis*)	United States of America	WOAH USDA
A(H5N1) clade 2.3.2.1a	Carnivora	Felidae	Cat (*Felis catus*)	India	Raut et al., 2025 The Times of India, online-a
A(H5N5) clade 2.3.4.4b	Carnivora	Canidae	Arctic fox (*Vulpes lagopus*)	Iceland	WOAH Personal communication by Brigitte Brugger, MAST
			Red fox (*Vulpes vulpes*)	Canada, Norway	WOAH
		Felidae	Cat (*Felis catus*)	Iceland	WOAH Personal communication by Brigitte Brugger, MAST
			Eurasian lynx (*Lynx lynx*)	Norway	Personal communication by Silje Granstad, Norwegian Veterinary Institute and Lars-Erik Lund Rondestveit, Norwegian Food Safety Authority
		Mephitidae	Striped skunk (*Mephitis mephitis*)	Canada	CFIA, online
		Mustelidae	American mink (*Neovison vision*)	Iceland	Personal communication by Brigitte Brugger, MAST
			Eurasian otter (*Lutra lutra*)	Norway	Personal communication by Silje Granstad, Norwegian Veterinary Institute and Lars-Erik Lund Rondestveit, Norwegian Food Safety Authority
			European pine marten (*Martes martes*)	Netherlands	Personal communication by Dennis Bol (NVWA, 2024)
		Phocidae	Grey seal (*Halichoerus grypus*)	United Kingdom	WOAH FarmingUK, online GovUK, online-a
			Ringed seal (*Pusa hispida*)	Canada	WOAH CFIA, online
		Procyonidae	Raccoon (*Procyon lotor*)	Canada	WOAH
A(H5N6) clade 2.3.4.4b	Carnivora	Canidae	Dog (*Canis lupus familiaris*)	China	Yao et al. (2023)
		Mustelidae	American mink (*Neovison vison*)	China	Zhao et al. (2024)
A(H5N8) clade 2.3.4.4b	Artiodactyla	Suidae	Pig (domestic) (*Sus scrofa*)*	France	Herve et al. (2021)
			Pig (wild boar) (*Sus scrofa*)*	Germany	Schülein et al. (2021)

Virus	Animal (order, family, species)			Country	Reference
	Carnivora	Canidae	Red fox (*Vulpes vulpes*)	United Kingdom	WOAH
		Phocidae	Grey seal (*Halichoerus grypus*)	Poland, Sweden, United Kingdom	SVA Shin et al. (2019), Floyd et al. (2021) Personal communication by Siamak Zohari (SVA)
			Harbour seal (*Phoca vitulina*)	Denmark, Germany, United Kingdom	WOAH Floyd et al. (2021), Ärzteblatt (online), Avian Flu Diary (online), Outbreak News (online)

[*] Serological detection.

[**] Both virological and serological detection.

[***] 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).

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. (2024) and the tool GenIn2 (https://github.com/izsvenezie-virology/genin2). Mutation analyses of the A(H5N1) viruses have been performed using FluMut (Github izsvenezie-virology, online-a, b) with FluMutDB v6.4 mutation database (https://github.com/izsvenezie-virology/FluMutDB).

Since October 2024, the complete genome sequences of eight HPAI A(H5) viruses of clade 2.3.4.4b collected from four distinct mammalian species (i.e. domestic cat, Eurasian lynx, Eurasian otter, grey seal and red fox) in six different European countries have been characterised. As expected, the viruses collected from three cats in Italy and Belgium, and from four red foxes in Italy, Slovenia and the Netherlands belong to genotype EA-2024-DI, which is the most prevalent circulating in birds in these geographic areas. The virus collected from a domestic cat with outdoor access found dead at a backyard poultry farm in Italy is highly related to the A(H5N1) virus collected from chickens of the same farm. Similarly, the viruses collected from two domestic cats with outdoor access living on a commercial laying hen establishment where an A(H5N1) outbreak was detected some days before are highly related to the A(H5N1) viruses collected from chickens of the same farm. These two findings suggest that in both episodes the cats were infected following exposure to infected poultry or virus-contaminated fomites on the same farm where they were found ill or dead. Further, viruses from the red foxes show the highest identity with the A(H5N1) viruses collected from wild birds in the same area.

The viruses characterised from a domestic cat in Iceland as well as from a Eurasian otter and a Eurasian lynx in Norway belong to the A(H5N5) EA-2021-I genotype, which is currently the prevalent or unique genotype identified in birds in these countries. Interestingly, the EA-2021-I genotype has also recently been detected in grey seals off the east coast of England. This virus contains the E627K mutation in PB2 and the impact of infection on seals is currently being investigated.

More than 50% of the characterised viruses from mammals in Europe contain at least one of the adaptive markers associated with an increased virulence and replication in mammals in the PB2 protein (E627K or E627V) (Suttie et al., 2019). These mutations have been identified in nine HPAI A(H5) viruses of clade 2.3.4.4b collected in birds in the same countries (Italy, Norway, United Kingdom and Iceland) over the current epidemiological year. Of note, the A(H5N5) viruses collected from the domestic cat in Iceland with PB2-E627V and from the Eurasian lynx in Norway with PB2-E627K cluster with viruses previously collected from wild birds containing the same mutation. Whether these mutations may have favoured the mammalian infection is still unknown.

2.3 Avian influenza virus infections in humans

2.3.1 Overview of the most recent human infections with avian influenza viruses

Since 12 December 2024 and as of 7 March 2025, a total of 22 cases of avian influenza virus infection in humans have been reported worldwide. This includes 12 A(H5N1) cases in the USA, two in Cambodia, and one in the UK. In addition, China reported six human cases of avian influenza A(H9N2) and one case of avian influenza A(H10N3) (Table 6). Of 18 cases in humans for which information on animal exposure was publicly available, nine reported exposure to poultry, two to poultry and wild birds, and six to cattle. For one case no known animal exposure was established from the epidemiological investigation (Table 7). Sequence data from GISAID's EpiFlu^{TM} database was retrieved and analysed for 12 strains from the USA, one from United Kingdom, and two from Cambodia (Table 8).

Table 6: Globally reported cases or detections of avian influenza virus in humans, including virus subtypes reported in the last 12 months

	Cases reported 2024-12-12 - 2025-03-07			**Cases reported since first report**			
Subtype	Cases reported	Deaths	Reporting countries	First report	Cases reported	Deaths	Reporting countries
A(H5N1)	15*	3	3	1997	989*	467**	24
A(H5N2)	0	0	0	2024	1	1	1
A(H5N6)	0	0	0	2014	93	36	2
A(H9N2)	6	0	1	1998	157	2	10
A(H10N3)	1	0	1	2021	4	0	1

*Human cases of A(H5) epidemiologically linked to A(H5N1) outbreaks at poultry and dairy cattle farms in the USA are included in the reported number of A(H5N1) cases.

**Deaths reported since 2003 from a total of 969 cases reported between 2003 and 7 March 2025. Mortality data are not available for cases reported prior to 2003.

Table 7: Identified exposures associated with human cases of avian influenza, reported globally 12 December 2024 – 7 March 2025 by zoonotic influenza subtype

Subtype	**Reported exposure****	**Cases**
A(H5N1)*	Poultry	8
	Wild birds	2

	Cattle	6
	Exposure source unknown[†]	1
A(H9N2)	Poultry	2
	Not reported[‡]	4
A(H10N3)	Poultry	1

[*]Human cases of A(H5) epidemiologically linked to A(H5N1) outbreaks at poultry and dairy cattle farms in the United States are included in the reported number of cases of A(H5N1).

[**]Exposure to more than one animal species can be reported for cases.

[†]No epidemiological exposure was identified after investigation

[‡]Not reported or publicly available

Table 8: Strains included in phylogenetic and mutation analysis. Sequences include those deposited in GISAID's EpiFluTM database from 11 December 2024 to 7 March 2025

Isolate Name	Subtype	Genotype	Clade	Location	Collection Date	Mutations
A/California/194/2024	A(H5N1)	B3.13	2.3.4.4b	USA, California	2024-11-22	HA, PA and PB2[a]
A/California/195/2024	A(H5N1)	B3.13	2.3.4.4b	USA, California	2024-11-23	HA, PA and PB2[a]
A/California/196/2024	A(H5N1)	-	2.3.4.4b	USA, California	2024-11-27	-
A/California/213/2024	A(H5N1)	B3.13	2.3.4.4b	USA, California	2024-12-06	HA, PA and PB2[a]
A/California/214/2024	A(H5N1)	-	-	USA, California	2024-12-06	-
A/California/216/2024	A(H5N1)	B3.13	2.3.4.4b	USA, California	2024-12-10	HA, PA and PB2[a]
A/Washington/254/2024	A(H5N1)	D1.1	2.3.4.4b	USA, Washington	2024-10-23	HA[b]
A/Iowa/124/2024	A(H5N1)		2.3.4.4b	USA, Iowa	2024-12-17	HA[b], M2:S31N
A/Louisiana/12/2024	A(H5N1)	D1.1	2.3.4.4b	USA, Louisiana	2024-12-11	HA[b]
A/Nevada/10/2025	A(H5N1)	D1.1	2.3.4.4b	USA, Nevada	2025-02-04	HA[b], PA:S421I,PB2:D701N
A/Wisconsin/179/2024	A(H5N1)	-	2.3.4.4b	USA, Wisconsin	2024-12-13	-
A/Wyoming/01/2025	A(H5N1)	D1.1	2.3.4.4b	USA, Wyoming	2025-02-11	HA[b], PB2:E627K
A/England/0480160/2025	A(H5N1)	DI.2	2.3.4.4b	United Kingdom	2025-01	HA[b], PB2:I292V
A/Cambodia/KSH250004/2025	A(H5N1)		2.3.2.1c	Cambodia	2025-01-08	HA[c], PB2:E627K
A/Cambodia/NPH250131/2025	A(H5N1)		2.3.2.1c	Cambodia	2025-02-24	HA[c], PB2:-

- : insufficient segments

a : HA T108I, S123P, S133A, K218Q, S223R, 327-328del; PA K497R; PB2 M631L (e.g. A/California/147/2024) (EFSA, ECDC and EURL, 2025)

b : HA T108I, S123P, S133A, K218Q, S223R, 328del, e.g. A/Washington/240/2024 (EFSA, ECDC and EURL, 2025)

c : HA D94N, T108I, S133A, N154D, S155N, 328del, e.g. similar to A/Cambodia/24070331/2024 (EFSA, ECDC and EURL, 2024a)

2.3.2 Human A(H5N1) cases

Since 1997, a total of 989 confirmed cases of influenza A(H5N1) have been reported globally (Figure 7). During the current reporting period (12 December 2024 – 7 March 2025), 15 human influenza A(H5N1) cases were reported, the majority in the USA. Six individuals required hospitalisation, including one who was hospitalised for isolation purposes only and not due to the severity of the disease. Three cases, one in the USA and two in Cambodia, resulted in death of the patients.

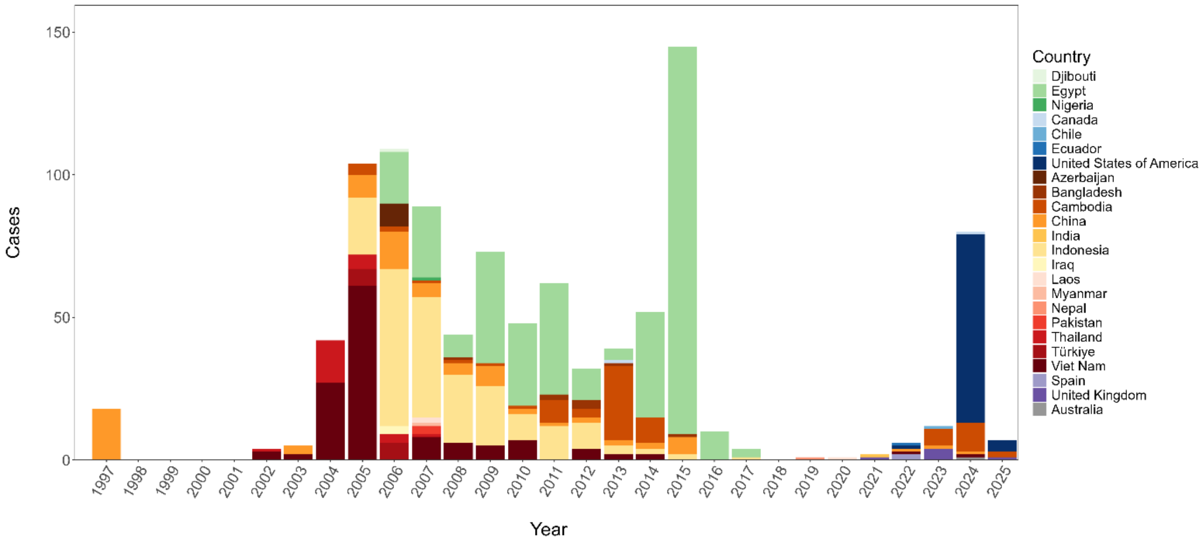

Figure 7: Distribution of reported human cases of A(H5N1) virus infection by year of onset or detection and reporting country from 1997 to 7 March 2025. The figure includes detections of A(H5N1) due to suspected environmental contamination reported by Spain (2) and the USA (1) in 2022, and the United Kingdom (three, one inconclusive) in 2023. Human cases of A(H5) cases epidemiologically linked to A(H5N1) outbreaks at poultry and dairy cattle farms in the USA are included in the number of A(H5N1) cases.

United States of America

Of the 12 cases reported in the USA, six occurred in California, and one case each in Iowa, Louisiana, Nevada, Ohio, Wisconsin, and Wyoming. Most cases reported in the USA have been mild, presenting with symptoms such as conjunctivitis and respiratory symptoms. However, three individuals experienced severe illness requiring hospitalisation, with one resulting in death.

The first severe case was reported in Louisiana on 14 December 2024 (WHO, online-b). The individual, who was over 65 years old and had underlying medical conditions, developed symptoms in early December and initially sought medical care. When the condition worsened, the patient returned to the emergency department a few days later, was hospitalised in a critical condition with pneumonia, and given antiviral treatment. Despite medical intervention, the patient passed away. None of the patient's household contacts tested positive for influenza viruses. The individual owned backyard poultry and had observed deaths among domestic and wild birds on the property before developing symptoms. Testing confirmed the presence of avian influenza A(H5N1) virus in poultry on the property.

The second and third hospitalised cases were in individuals from Wyoming and Ohio, reported on 19 and 21 February 2025, respectively (CDC, online-b). The case in Wyoming was an adult woman, with pre-existing medical conditions, who had exposure to backyard poultry around her house. The case in Ohio was an adult person, who had exposure to poultry while carrying out depopulation activities at a commercial poultry farm where avian influenza A(H5N1) virus was detected in birds. The individual developed respiratory and non-respiratory symptoms and was subsequently hospitalised. The person has since been discharged and, at the time of reporting, was recovering at home.

Of the 12 cases reported from the USA during this period, five cases in California and one in Nevada were linked to occupational exposure to A(H5N1)-infected dairy cattle (Central Nevada Health District, online). Five cases reported exposure to poultry: the three cases in Iowa, Ohio and Wisconsin followed occupational exposure, while the case in Wyoming reported backyard poultry exposure (CDC, online-b). The fatal case in Louisiana was associated with exposure to infected backyard poultry and wild birds on the individual's property (WHO, online-b). One case in California, a child under 18 years, had no known exposure to infected animals or humans.

Strains from cases in California (genotype B3.13) and Louisiana (genotype D1.1), as well as an additional strain from Washington (genotype D1.1) described in the previous avian influenza overview report (EFSA, ECDC and EURL, 2025) displayed mutation profiles previously reported for these genotypes (Table 8). The virus strain from Iowa contained the antiviral-drug-related mutation S31N in M2, with a phenotype of increased resistance to amantadine and rimantadine (Suttie et al., 2019). The PB2 mutation D701N was present in the virus sequence A/Nevada/10/2025 from the case in Nevada, which was the first observation of PB2:D701N in genotype D1.1 from a human infection. The PB2:D701N mutation is associated with mammalian adaptation, increased virulence and contact transmission in guinea pigs and increased virulence in mice (Suttie et al., 2019). The change has not been observed in any of the genotype D1.1 strains from birds, however it was seen in sequenced viruses of genotype D1.1 from dairy cattle in Nevada (USDA, online-f). Furthermore, the PA segment of A/Nevada/10/2025 has the S421I substitution which, although associated with increased virulence in mice (Kim et al., 2010), is common in isolates from birds. Mutation analysis of the strain from the Wyoming case revealed the presence of mutation E627K in the PB2 segment which is associated with several mammalian adaptations for A(H5N1), such as increased virulence in mice (Suttie et al., 2019). No sequence data was available for the Ohio case (CDC, online-b).

Cambodia

On 10 January 2025, the Cambodian Ministry of Health reported a fatal case of human A(H5N1) infection in an adult male from Kampong Cham province (WHO, online-b). The case was laboratory-confirmed by the National Institute of Public Health on 9 January 2025. The patient developed severe illness, including fever, cough, fatigue, and difficulty breathing, and passed away on 10 January. Investigations revealed that the individual raised backyard poultry and had prepared and consumed meat from a sick chicken.

On 25 February 2025, the second fatal case of human infection with avian influenza A(H5N1) virus was reported from Cambodia (Cambodia Ministry of Health, online). The case was in a two-year-old child from Prey Veng province. The child, who was in a critical condition and exhibited symptoms such as fever, cough, fatigue, and difficulty breathing, passed away shortly after being admitted to the hospital on 25 February 2025. The case was confirmed by the National Institute of Public Health on the same day. Investigations revealed that the child’s family raised poultry, and some of the birds had recently fallen ill and died. The child reportedly played and slept near or in the chicken coop.

Phylogenetic analysis of the strains from the first case (A/Cambodia/KSH250004/2025) and the second (A/Cambodia/NPH250131/2025) places the viruses among other strains of the emerging reassortant of clade 2.3.2.1c, with internal segments of clade 2.3.4.4b associated with human cases in Cambodia (Siegers et al., 2024). The PB2 segment of the strain A/Cambodia/KSH250004/2025 had mutation E627K, detected in many strains of this reassortant isolated both from humans and birds. This segment was not available for A/Cambodia/NPH250131/2025 (Table 8).

United Kingdom

On 27 January 2025, the UK Health Security Agency (UKHSA) confirmed a human case of A(H5N1) in the West Midlands region (GovUK, online-b). The case was identified at the national reference laboratory on 24 January 2025 and was linked to close and prolonged occupational exposure to a large number of infected birds on a farm. The individual experienced mild respiratory symptoms and eye irritation. One symptomatic household contact was identified during the investigation, but tested negative for avian influenza virus infection.

The sequenced strain, A/England/0480160/2025, was of the genotype EA-2024-DI.2, currently common in Europe, and had change I292V in the PB2 segment. This change is associated with increased polymerase activity in mammalian cell line and increased virulence in mice (tested on subtypes H10N8 and H9N2) (Suttie et al., 2019). The HA segment of the strain is nearly identical to that of a strain collected on 18 January 2025 from a chicken in the United Kingdom.

2.3.3 Human A(H9N2) cases

Since 1998 and as of 7 March 2025, 155 human influenza A(H9N2) cases have been reported globally (Figure 8). During the current reporting period (12 December 2024 – 7 March 2025), six human cases of influenza A(H9N2) were reported from China.

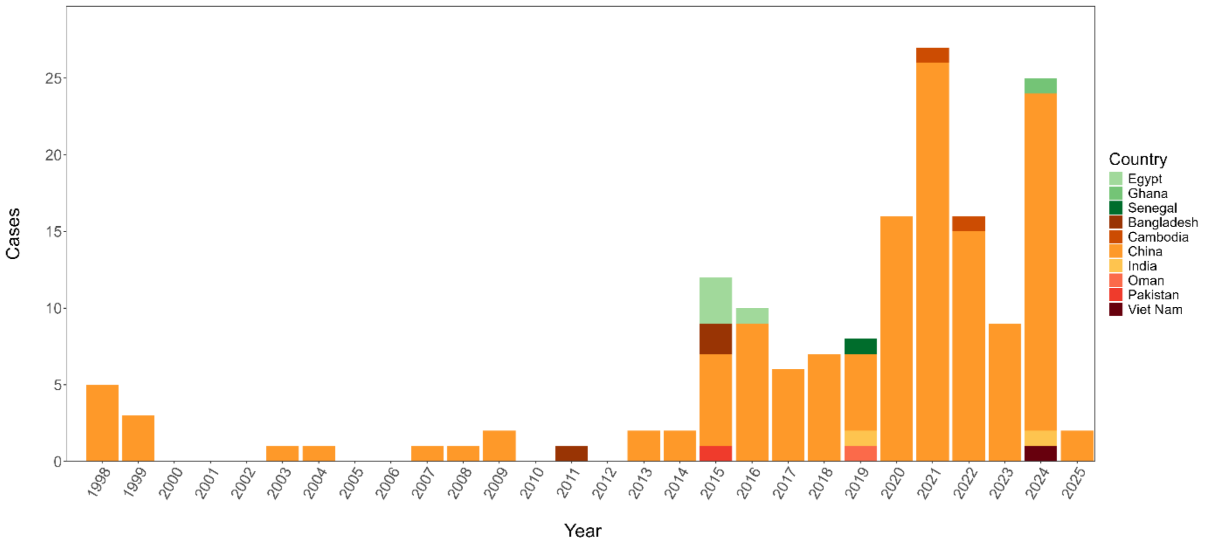

Figure 8: Distribution of reported human cases of A(H9N2) virus infection by year of onset, or detection and reporting country, from 1998 to 7 March 2025

On 14 January 2025, Hong Kong's Centre for Health Protection reported two human cases of avian influenza A(H9N2), detected through influenza-like illness (ILI) surveillance (CHP, online-a). The first was a one-year-old girl from Chongqing Municipality who developed symptoms on 13 December 2024. The second was an eight-year-old girl from Hubei Province, with symptom onset on 27 November 2024. Both had prior exposure to live poultry markets, experienced mild illness, and have since recovered. Environmental samples collected from wet markets tested positive for avian influenza A(H9) virus. No additional cases were detected among their contacts.

On 11 February 2025, two more human cases of A(H9N2) were reported from Hunan Province, China (CHP, online-b). These two involved a two-year-old boy with symptom onset on 27 December 2024 and a 15-year-old boy who developed symptoms on 8 January 2025. Both were alive at the time of reporting.

Finally, on 18 February 2025, Hong Kong's Centre for Health Protection reported two additional cases of A(H9N2) from Guangdong Province (CHP, online-c). The cases were in a 72-year-old woman and a 56-year-old woman, who developed symptoms on 26 December 2024 and 20 January 2025, respectively. Both were alive at the time of reporting.

No public information on exposure or symptoms was available for the cases reported on 11 and 18 February 2025.

2.3.4 Human A(H10N3) cases

Since 2021, four cases of human infection with avian influenza A(H10N3) have been reported worldwide. All cases were reported from China.

The most recent case was reported to the World Health Organization (WHO) on 3 January 2025 (WHO, online-b). The case was a 23-year-old female from Guangxi Zhuang Autonomous Region with an underlying medical condition. She developed symptoms on 12 December 2024 and was hospitalised on 19 December with severe pneumonia. The patient, who was treated with oseltamivir, was initially in a critical condition but has since improved.

A clinical sample collected on 22 December tested positive for influenza A, and on 26 December, the infection was confirmed as influenza A(H10N3). Before symptom onset, the patient worked at a supermarket and had been exposed to freshly slaughtered poultry. At the time of reporting, no family members had developed symptoms, and all close contacts tested negative for influenza A(H10N3). In addition, all environmental samples collected from various locations tested negative for the virus.

2.3.5 Additional information relevant for public health and international risk assessments

The risk of zoonotic avian influenza viruses and measures for preparedness, prevention and control are outlined in a new Scientific Opinion published jointly by the European Food Safety Authority (EFSA) and the European Centre for Disease Prevention and Control (ECDC). The Scientific Opinion includes a comprehensive list of mutations which might increase the zoonotic potential of avian influenza viruses. The list of mutations can be used as a reference to monitor the emergence of viruses that could be associated with an increased zoonotic risk (EFSA AHAW Panel and ECDC, 2025). Furthermore, ECDC and EFSA have published a practical guidance for the investigation and management of zoonotic avian influenza outbreaks affecting both humans and animals, using a coordinated One Health approach. The guidance outlines response actions for five outbreak scenarios at the human-animal-environment interface, emphasising the need for an interdisciplinary approach among all stakeholders (ECDC and EFSA, 2025).

A recent summary of serological studies in different exposure settings suggested undetected asymptomatic or mild infections with zoonotic avian influenza viruses may occur at low levels in individuals occupationally or otherwise exposed to poultry or infected animals (EFSA AHAW Panel and ECDC, 2025). Furthermore, a serosurvey carried out in September 2024 by veterinarians working with cattle in the USA and Canada found that three of the 150 participants surveyed had antibodies to HPAI A(H5), suggestive of recent infection with HPAI A(H5) virus. The veterinarians with positive serology tests worked with multiple animals and one of them had worked with poultry infected with HPAI A(H5) virus. All three wore gloves or protective clothing when working with cattle but none of them wore respiratory or eye protection. None of the three practitioners reported recent influenza-like symptoms or conjunctivitis. Detection of A(H5) antibodies in individuals without apparent symptoms suggests that surveillance strategies focusing on the testing of exposed, symptomatic individuals may result in unidentified infections in humans (CDC, online-c).

In the context of emerging infections, diagnostic testing is often limited to individuals meeting pre-defined clinical or epidemiological criteria, such as symptoms of illness and exposure risk to known sources of infection. However, such target testing may limit detection of cases to known transmission routes and cases from alternative sources of infection may be undetected or their identification may be delayed. When there is high transmission in multiple species and potential for novel transmission routes, it may be necessary to expand diagnostic testing to individuals beyond current case definitions and exposure histories, depending on the evolving epidemiological situation. In California, USA, a recent human case of A(H5N1) in a child with no known exposure source was identified by expanding A(H5) subtyping to all samples positive for influenza A, including samples positive for A(H1) and A(H3), to facilitate detection of potential co-infections with multiple subtypes (Karan et al., 2025).

In June 2024, Finland initiated voluntary vaccination of individuals at risk of occupational exposure to HPAI A(H5N1), such as workers at poultry and fur farms, veterinarians, and laboratory workers, with an inactivated vaccine based on influenza A(H5N8) clade 2.3.4.4b. A recent pre-print, describing the immune response in vaccinated individuals, suggests that vaccination with two doses resulted in seroconversion above the threshold considered to infer protection for seasonal influenza viruses (EMA, online) in 97% (based on haemagglutination inhibition assay) and 83% (based on microneutralisation assay) of previously unvaccinated individuals. Among target groups for whom the zoonotic influenza A(H5) vaccine was recommended in Finland, the vaccine uptake has so far been reported as low (Liedes et al., 2025), highlighting the need for strategies to overcome potential barriers in order to improve coverage in future vaccination campaigns.

Based on information currently available, the WHO assessment of the risk to public health from the avian influenza viruses that are currently known remains unchanged, and this risk is still considered to be low (WHO, online-b).

The US CDC assessment of the risk to people from HPAI A(H5N1) viruses remains low for the general population in the United States but is considered moderate-to-high for populations in contact with potentially infected animals, contaminated surfaces or fluids (CDC, online-d). The US CDC listed four areas that are closely monitored to inform the risk assessment of avian influenza A(H5N1) to public health: virus transmission and any evidence of sustained human-to-human transmission, disease severity; case distribution and known exposure to animals, and possible effects of genetic changes in the virus on transmission in humans; performance of diagnostic tests, and effectiveness of antivirals and vaccines. Any changes in these factors may result in the assessed risk for the general public being reconsidered and additional public health actions being implemented. These additional actions may include updating guidance for protection of individuals exposed to avian influenza A(H5), procuring treatments and vaccines, and initiating voluntary vaccination programmes for exposed individuals or broader groups if transmission risk or severity of disease increases (CDC, online-e).

According to the UK Health Security Agency (UKHSA), the risk of HPAI A(H5) to the general public is still considered very low (GovUK, online-c). UKHSA outlined management of individuals exposed to influenza A(H5) in animals if the assessed risk associated with circulating viruses remains unchanged. This management included reducing the number of individuals exposed to infected animals, providing advice on the appropriate use of personal protective equipment, passive or active follow-up of individuals exposed to infected animals depending on the exposure risk, and offering post-exposure prophylaxis based on the level of exposure. If future assessments identify an increase in the risk posed by circulating viruses, a strict approach should be taken to managing exposure to avian influenza. This includes limiting the number of individuals exposed to an absolute minimum, offering pre- and post-exposure antiviral prophylaxis to individuals exposed to infected animals, and actively following up on exposed individuals (GovUK, online-d, e).

2.3.6 ECDC risk assessment

ECDC's assessment of the risk of human infection with HPAI A(H5) clade 2.3.4.4b viruses remains unchanged. Overall, ECDC assesses the risk of human infection with the HPAI A(H5) clade 2.3.4.4b viruses currently circulating in Europe as low for the general public in the EU/EEA, and low-to-moderate for those occupationally or otherwise exposed to infected animals or contaminated environments. The assessment considers the risk of infection at population level in the EU/EEA, taking into account the probability of human infection and transmission, as well as the potential impact of infection, based on the ECDC framework for risk assessments (ECDC, 2019).

The risk assessment was informed by available evidence relating to the transmission, prevalence, and characteristics of A(H5N1) viruses currently circulating in animals in Europe, as well as knowledge from human cases of influenza A(H5N1) clade 2.3.4.4b that have been reported globally. This evidence is set out below:

The likelihood of human infection with HPAI A(H5) clade 2.3.4.4b viruses in the EU/EEA:

- In the current epidemiological year (1 October 2024 – 30 September 2025), there has already been a higher number of detections of HPAI viruses in wild and domestic birds in Europe compared to 2023−2024. Nevertheless, detections are still lower than those reported in the previous epidemiological years (2020−2023).
- Despite the extensive circulation of avian influenza viruses in animal populations in Europe over the past few years, with frequent opportunities for human exposure, there have been no confirmed cases of A(H5N1) infection in humans in the EU/EEA, and transmission from infected animals to humans remains a rare event globally.
- In Europe, mutations associated with viral adaptation to mammalian hosts have been identified in sequences of A(H5N1) viruses from mammals as well as birds. Further understanding of the implications of such mutations for mammalian adaptation, infection and transmission is required to assess any change in the

associated risk to humans. However, circulating viruses retain a binding preference for α2–3 sialic acid (avian-type) receptors and are still considered to be avian-like. There is currently no evidence of the viruses being more adapted to infection of humans or having the ability to transmit between humans.

- Sporadic cases of infection with avian influenza A(H5N1) virus have been reported in humans on a global basis, most of which have had a history of unprotected exposure to poultry, cattle or contaminated environments. For human cases of A(H5) reported globally between 12 December 2024 – 7 March 2024, 93% (n=14/15) cases had known exposure to dairy cattle or poultry. Of the 14 cases of influenza A(H5) with known animal exposure, 10 cases were exposed to infected animals in an occupational setting. The remaining four cases had reported exposure to backyard poultry.
- To date, there has been no evidence of sustained human-to-human transmission of influenza A(H5N1).

The impact of human infection with HPAI A(H5) clade 2.3.4.4b viruses:

- Historically, clinical presentations of individuals infected with A(H5N1), also including other clades than 2.3.4.4b, have ranged from asymptomatic or mild, such as conjunctivitis and upper respiratory tract symptoms, to severe illness resulting in death, with an estimated case fatality of 48% among reported cases since 2003.
- The majority of human cases of infection with influenza A(H5N1) clade 2.3.4.4b reported since March 2024 in the USA experienced mild symptoms, such as conjunctivitis or mild respiratory illness. Between 12 December 2024 and 7 March 2025, three of 12 A(H5) cases reported in the USA, including two with underlying medical conditions, experienced severe illness requiring hospitalisation, with one being fatal.
- The A(H5N1) case of clade 2.3.4.4b in the United Kingdom experienced conjunctivitis and mild respiratory symptoms.
- In Cambodia, there were two cases of A(H5N1) of clade 2.3.2.1c reported during the same period which were both severe and resulted in death.
- The reasons for the variation in outcome of infection with influenza A(H5N1) virus is likely to be multi-factorial and may be attributed to the virus genotype, duration of exposure, viral load, transmission route, individual health status, personal protective measures taken, and medical treatment provided (FAO, WHO and WOAH, online-a). The detection of several mild cases of A(H5N1) virus infection and seropositive individuals without a history of clinical symptoms in the USA suggests that mild and asymptomatic cases may be more common than previously reported, although targeted surveillance of individuals exposed to infected animals is required for identification (EFSA AHAW Panel and ECDC, 2025).
- Most of the circulating A(H5N1) clade 2.3.4.4b viruses detected in Europe remain susceptible to the antiviral medicines available to treat humans, including adamantanes, neuraminidase inhibitors (e.g. oseltamivir) and polymerase acidic inhibitors (e.g. baloxavir marboxil).

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 animals infected with avian influenza viruses, or their environment. Events or conditions that increase mammalian or human exposure to avian influenza viruses may lead to spillover events and further transmission, increasing the probability of avian influenza viruses adapting to mammals (EFSA AHAW Panel and ECDC, 2025). Given the extensive transmission of A(H5N1) in birds and poultry, and in some mammals in certain settings, viral evolution through mutations or reassortment may occur, which could change the current assessment. As a result, ECDC will continue to review the risk assessment, taking into consideration any new developments or information that becomes available.

3. Conclusions

3.1 Birds

- After exceptionally low numbers of HPAI virus detections in wild birds during the 2023–2024 epidemiological year, there has been a notable increase in recent months, including clusters of high mortality in certain parts of Europe. This increase in HPAI virus detections in wild birds has also been accompanied by an increased number of HPAI outbreaks in poultry, which together increase the exposure risk for mammals and people.

- Since 2020, there has been a consistent and persistent circulation of HPAI A(H5Nx) viruses in wild bird populations in Europe. This situation is expected to continue for many years, with variations in outbreak numbers, geographical distribution, and affected species, influenced by multiple factors, both intrinsic and extrinsic to these populations, some of which are not yet fully known. This epidemiological situation is fundamentally different from the period before 2020, when HPAI A(H5Nx) viruses in wild birds in Europe occurred as irregular epidemics, restricted to the autumn and winter periods of certain years, rather than persisting year-round.

- The high numbers of HPAI A(H5) virus detections in wintering geese (barnacle, greylag) in a few countries (mainly in the United Kingdom, the Netherlands and Germany) are temporally close to their spring migration, with the risk of virus spread along their migratory routes to breeding areas at higher latitudes (e.g. Iceland, Norway, Sweden, Estonia, Finland, and Russia). The high numbers of HPAI virus detections in wintering gulls (mainly European herring gull and black-headed gull) are temporally close to their return to breeding colony sites, with the risk of virus spread there.

- HPAI virus subtype A(H5N5), genotype EA-2021-I, continued to be detected in wild birds at higher northern latitudes in the current reporting period. The outbreak of this genotype in greylag geese in Iceland suggests that it can transmit efficiently not only among colony-breeding seabirds but also among waterfowl.

- The identification of HPAI A(H5N1) viruses in new species that feed habitually in agricultural fields, some of which are considered invasive and alien to some countries, such as the African sacred ibis in Italy, and the increasing number of these birds in densely populated poultry areas, raises additional concerns for poultry.

- There was a geographic overlap between HPAI virus detections in wild birds and poultry, which, together with the genetic similarity (see below) among viruses circulating in wild birds and poultry, support reports that primary introductions in poultry are likely due to direct or indirect contact with wild birds.

- In several HPAI outbreaks in poultry during the current reporting period birds had outdoor access. This, combined with the high risk of HPAI virus circulation in wild birds during the winter period, suggests that outdoor access increases the risk of introduction of infection in poultry establishments. Implementation of housing orders can help to reduce this risk. The latter may have contributed to the low number of outbreaks observed in the Netherlands, despite the detection of high numbers of wild birds affected.

- During the current reporting period, some clusters of farm-to-farm transmission have been linked to establishments of the same ownership, where personnel and/or equipment were shared among establishments. Same ownership has been a risk factor for virus transmission over many years, highlighting the need for improved biosecurity practices in this type of establishments.

- Investigations at molecular level (using whole genome sequencing) performed in Italy have helped to identify clusters of farm-to-farm transmission, which could not be identified using field data only. The experience reported in Italy may indicate that some of the outbreaks in poultry reported as ’primary’ outbreaks may in fact be secondary outbreaks, as epidemiological investigations often fail to provide conclusive evidence on the route of virus spread. Therefore the number of secondary outbreaks may be underestimated.

- In the HPAI outbreaks in poultry in which mortality at detection was reported, levels in gallinaceous poultry ranged from 0.01% to 24.7%, and for duck and geese from 0.6% to 75.5%. Outbreaks in commercial establishments in which mortality at detection was higher than 5% may indicate delayed detection, with these outbreaks being detected a few weeks following introduction of infection in the affected flock (longer high-risk period), increasing thereby the risk of transmission to other establishments.

- Another HPAI outbreak in an establishment keeping vaccinated ducks was reported in France. Disease in vaccinated flocks is often mild, with clinical signs difficult to be noticed by farmers, thereby reducing the probability of detecting infections via passive surveillance. The active surveillance component following vaccination that has been put in place by France in accordance with Delegated Regulation (EU) 2023/361[14] addresses this limitation of passive surveillance.

- During the current reporting period, a relatively high number of zoos and other animal/theme parks keeping captive birds were affected by HPAI viruses. This raises the question of whether vaccination against HPAI should be implemented at a wider scale in zoo birds.

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

- Currently available genetic data indicate that, starting from October 2024, EA-2023-DI has been the most frequent and widespread genotype in Europe, detected in almost all the affected European countries and associated with about 90% of the poultry outbreaks. Although at a lower level, EA-2022-BB and EA-2021-I (A(H5N5)) genotypes are persistently circulating in Europe, mostly among seabirds, with occasional spillover to domestic birds, along the Arctic Ocean, Atlantic Ocean and North Sea coasts.

- Since October 2024, the detection of 35 HPAI A(H5) viruses in wild and domestic birds collected from nine different European countries containing markers of mammalian adaptation in the PB2 protein (E627K/V, K526R or D701N) indicates that viruses with an enhanced capacity to infect mammals can replicate and spread in birds. Of particular concern is the increased frequency of viruses collected from birds containing such mutations, which has risen from about 2.5% of the 2023–2024 epidemiological year to about 5.6% of the current epidemiological year (up to February 2025).

- The majority of HPAI A(H5N1) viruses circulating in birds in Europe since October 2024 have at least some amino acid substitutions in the HA protein that have been proven to increase in vitro binding to human-type receptors. However, a recent study (Yang et al., 2025) demonstrated that viruses with the amino acid composition typical of the vast majority of circulating A(H5Nx) strains bind exclusively to avian-like receptors and retain a pH fusion and thermostability typical of avian influenza viruses.

- Outside Europe, there has been an increase in the number of HPAI virus detections in both domestic and wild birds reported to WOAH compared to the previous reporting period (EFSA, ECDC and EURL, 2025). There are few official reports to WOAH from many countries, particularly in Africa and Asia, but also no HPAI virus detections in wild birds have been reported from North America during the current reporting period. This makes the global extent of HPAI A(H5Nx) viruses in the world unclear.

- Several examples, in many cases detected through genomic analysis, have shown that Europe has become a source of HPAI viruses for other parts of the world (i.e. Africa, North America, East Asia).

- Most of the HPAI outbreaks reported in poultry worldwide continued to be concentrated in the Americas, particularly in the USA. Besides the USA, Canada, Japan and South Korea experienced most of the poultry outbreaks outside Europe. HPAI virus subtypes other than H5N1 reported outside Europe were the H5N5 subtype once again detected in Canada, the H5N9 subtype detected in the USA, and the H7N8 subtype detected in Australia. Although reported at a lower level, the HPAI situation in domestic and wild birds also continues on other continents, particularly in Asia, where multiple avian influenza viruses are endemic.

- The pattern of HPAI A(H5) virus detections in the Antarctic and subantarctic regions in this reporting period indicate an increased number of infected species, a southward spread to within the Antarctic Circle, and an eastward spread of several thousand kilometres to the Crozet and Kerguelen Islands. These results show that the virus is not only present again in the 2024–2025 austral summer but also has expanded substantially its host and geographical range in the Antarctic and subantarctic regions, with a higher risk of incursion into Oceania.

3.2 Mammals

- After a short period of absence since spring 2024, HPAI A(H5N1) and A(H5N5) virus detections in mammals have been reported again in Europe since October 2024.

- During the current reporting period, several domestic cats have been found infected by HPAI A(H5N1) and A(H5N5) viruses in different European countries, with the suspected source of infection being contact with either affected poultry or wild birds. No mammal-to-mammal transmission has been observed.

- Outside Europe, large numbers of domestic cats and captive felines infected by HPAI A(H5N1) viruses have been found in the USA. In many of these cases, exposure was linked to ingestion of contaminated raw poultry meat, raw pet food (based on poultry) or raw milk. A(H5N1) virus of the 2.3.4.4.a clade was also detected in domestic cats in India.

- The number of dairy cattle farms in the USA reportedly affected by HPAI A(H5N1) virus (clade 2.3.4.4.b) continued to increase, reaching nearly 1,000 across 17 States during the current reporting period. Two new spillover events to dairy cattle were detected in the USA, leading to circulation of a new virus genotype (D1.1.) in this species. These events highlight the importance of identifying risk factors that facilitate spillover events to guide surveillance and early detection in other regions in the world, where there is geographical overlap of high wild bird population densities and dairy farming.

- Wildlife, especially carnivores, continued to be affected by HPAI viruses in and outside Europe. Mortality events in southern elephant seals in the Antarctica continued to be reported.

- New mammal species affected by HPAI A(H5N1) viruses reported during the current reporting period include the crabeater seal (Antarctica) and ringed seal (Canada) as well as the black rat, Canadian lynx, cheetah, eastern gray squirrel, Norway rat, savannah cat, serval, and stoat (all USA). Several additional carnivore species were affected by A(H5N5) viruses in Europe and Canada for the first time.

- All the characterised HPAI viruses collected from mammalian species in Europe since October 2024 belong to the A(H5N1) EA-2024-DI and A(H5N5) EA-2021-I genotypes. To date, no key mutations associated with the switch in the virus binding preference from avian- to human-type receptors have been identified in these viruses. However, more than 50% of the characterised viruses from mammals in Europe during the current epidemiological year contain the PB2-E627K/V mutation, which confers a more efficient replication in mammals.

3.3 Humans

- Sporadic cases of zoonotic avian influenza A(H5N1), A(H9N2) and A(H10N3) were reported outside of the EU/EEA during the period December 2024 – March 2025.

- Despite the widespread occurrence of HPAI A(H5N1) in wild birds, poultry and some mammals in recent years, with many potential exposures of humans to infected animals, there have been no confirmed human cases of influenza A(H5N1) in the EU/EEA.

- The majority of human infections with avian influenza viruses reported since 1997 have been associated with unprotected exposure to poultry, live poultry markets, or contaminated environments. In addition, since March 2024, there have been 41 human cases of influenza A(H5N1) reported following exposure to dairy cattle infected with A(H5N1) virus. To date, there has been no evidence of sustained human-to-human transmission observed.
- In the reporting period from 12 December 2024 to 7 March 2025, of the 18 human cases of avian influenza reported globally for which exposure data were available, only one had no known exposure identified following epidemiological investigation. The other 17 cases had exposure to infected animals in an occupational setting or exposure to backyard poultry and wild birds.
- 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 have unprotected exposure to infected animals or their environment.

4. Options for response

4.1 Birds

- Given the persistent circulation of HPAI in wild birds in Europe, which is likely to continue for many years, it is necessary to consider medium- and long-term risk reduction strategies in the poultry sector, such as not locating poultry establishments near wetlands (areas with high risk for introduction of HPAI from wild birds to poultry), reducing farm densities in these areas, keeping high biosecurity standards and compliance, preventive vaccination, risk based implementation of housing orders or implementing housing systems that keep poultry indoors (or completely restrict access of wild birds to free range) whilst keeping high levels of welfare.
- Improved biosecurity requires in some production systems improved infrastructure. Besides infrastructure, high level of compliance is necessary. This would require increasing awareness and training of farm workers. Such high levels of compliance are particularly needed in establishments of the same ownership. Here farm workers need to follow strict biosecurity procedures when moving themselves or equipment between establishments to minimise between-farm transmission.
- Vaccination is considered a valuable tool for the prevention of HPAI infection of zoo birds (Globig et al., 2017; Philippa et al., 2005). The question of whether vaccination should be more frequently implemented in zoo birds was raised because of the high number of HPAI A(H5) virus detections in zoo birds during the reporting period. The European Association of Zoos and Aquaria (EAZA) and the European Association of Zoo and Wildlife Veterinarians (EAZWV) have developed a joined Position Statement on vaccination against HPAI A(H5N1) in zoo birds in the EU (EAZA and EAZWV, 2023). This statement encourages zoos to vaccinate their birds against HPAI A(H5) with the best commercially available product approved by the relevant competent authority.

- For wild birds, general options for response include accurate and comprehensive recording of HPAI-associated mortality events (e.g. estimating the impact on wild bird populations), preventing disturbance of areas undergoing HPAI outbreaks to reduce virus spread, and, depending on the circumstances, removal of HPAI virus-affected carcasses from areas where wild birds congregate to reduce environmental contamination and further virus spread.

- Studies are recommended to better understand the role of the African sacred ibis, or other potentially relevant new invasive species, as a potential bridge for the transmission of HPAI between wild birds and poultry, especially in countries such as Italy where thousands of them spend the winter.

- It is important to continuously monitor LPAI viruses of the A(H5) and A(H7) subtypes in wild and domestic birds, and introductions of these subtypes into poultry establishments, as these subtypes can mutate into their highly pathogenic forms once circulating in poultry.

- The geographic expansion of HPAI A(H5N5) viruses in wild birds, which were found in increased numbers in greylag geese in the current reporting period, should continue to be closely monitored in northern parts of Europe and worldwide.

- The 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 amino acid changes associated with increased zoonotic potential, resistance toward antiviral drugs or different antigenic properties. The biological characteristics of these variants should be further evaluated to assess the actual impact of the acquired mutations. Genetic data are also instrumental to track the virus spread, to support epidemiological investigations in the distinction between primary and secondary outbreaks and to identify novel incursions of viruses that may represent a threat for human or animal health.

- Reinforcing the genetic characterisation of viruses collected from birds in areas where a high number of infections in mammalian species have been 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

- Increased virological and serological surveillance of HPAI viruses in wild (e.g. red foxes) and free-roaming domestic carnivores (e.g. cats and dogs) in areas with high HPAI virus circulation continues to be recommended to monitor both the level of virus infection in these species and the risk of emergence and transmission of mammalian-adapted viruses. Surveillance should also focus on domestic and farmed mammals exposed to highly contaminated environments, in close contact with HPAI virus-infected poultry or wildlife, or present in mixed-species farms. Research to investigate the role of mammals in maintaining HPAI viruses and driving their evolutionary dynamics is recommended.

- In light of the ongoing outbreak in dairy cattle in the USA, testing of/surveillance in ruminants is recommended when a combination of factors is observed, such as the manifestation of overt and unresolved clinical signs typically associated with HPAI virus infection in ruminants (e.g. undiagnosed severe decrease in milk production and presence of darker, thickened milk), but also the occurrence of HPAI virus infection in other domestic, peridomestic and wild animals in/around cattle farms. In addition, HPAI should be considered as a differential diagnosis in cases of undiagnosed or unresolved clinical signs during periods of HPAI virus circulation in the area where ruminants are kept.

- National reference laboratories should consider the procurement of tests and reagents to be prepared for carrying out virological and serological diagnostic activities targeting mammals, including ruminants, to allow for rapid escalation of testing capacity. Liaison with the EURL is recommended to ensure that appropriate virological and serological tests are used. Such activities should serve the purpose of increasing knowledge on HPAI and LPAI viruses posing a potential zoonotic risk.

- Pets and other captive mammals should not be fed with raw meat, raw pet food or other animal products (e.g. raw milk) from sources that have not been adequately controlled for possible HPAI contamination. The risk associated with feeding contaminated raw pet food (based on poultry) to domestic cats, a practice that has also been reported in other countries in the world, including in the EU, stresses the importance of highly sensitive surveillance systems for early detection, and the removal and destruction of infected poultry flocks as well as contaminated poultry products.

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

4.3 Humans

- The risk of human exposure to avian influenza viruses could be limited by implementing prevention measures such as:

    - Use of appropriate personal protective equipment to reduce the risk of infection when in contact with potentially infected animals or highly contaminated environments.

    - Implementation of adequate biosecurity and biosafety measures at occupational sites where there is increased risk of exposure in order to reduce the zoonotic risk and assure safe handling of potentially contaminated biological materials.

    - Provision of information to raise awareness among people at potential risk of exposure and to indicate how it can be mitigated. Guidance should be tailored to specific occupational groups, or people engaged in recreational activities where additional measures may be beneficial. Recommendations for personal protective measures and equipment should take into consideration and be adapted to the working environment and tasks involved, routes of exposure and environmental factors.

    - Recommendations to the general public, including backyard poultry keepers, to avoid contact with sick or dead birds and wild animals and, if they find dead animals, to inform the relevant authorities in order to ensure safe removal and further investigation.

- People who have been exposed to animals with suspected or confirmed avian influenza virus infection 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. Asymptomatic individuals exposed to animals with suspected or confirmed avian influenza virus infection where appropriate protective measures have not been taken should be assessed on a case-by-case basis and tested depending on the level of exposure. Further information on testing, follow-up and management of individuals with exposure and confirmed infection can be found in ECDC's 'Guidance on testing and detection of zoonotic influenza virus infections in humans' (ECDC, 2022), 'Investigation protocol for human exposures and cases of avian influenza' (ECDC, 2023), and the ECDC/EFSA guidance for 'Coordinated One Health investigation and management of outbreaks in humans and animals caused by zoonotic avian influenza viruses' (ECDC and EFSA, 2025).

- Countries should remain vigilant for potential human cases of avian influenza, especially in geographical areas where the virus is known to circulate in poultry, wild birds, or other animals. Healthcare workers in these areas should be made aware of the epidemiological situation and the range of symptoms that can be associated with avian influenza infection in humans.

- The recent detections of human cases of zoonotic avian influenza through surveillance systems for seasonal influenza highlight the importance of typing and subtyping samples. Samples collected through seasonal influenza surveillance that are positive for influenza type A virus but cannot be assigned to seasonal influenza subtypes A(H1) or A(H3), which are circulating widely in the human population, should be further analysed for novel influenza viruses, such as avian influenza viruses. Ideally, all sentinel influenza-positive specimens from both primary and secondary care sources should be typed and subtyped.

- During periods of high seasonal influenza virus circulation (typically during the winter months in EU/EEA countries), exhaustive subtyping of influenza type A-positive samples might not be possible. Testing and subtyping for avian influenza virus could then be performed using a risk-based approach, based on the epidemiological situation in the animal populations as well as focusing on cases from outbreaks, or with severe respiratory signs or neurological symptoms of unknown aetiology. Further guidance is available in ECDC's technical report on targeted surveillance to identify human infections with avian influenza virus during the influenza season (ECDC, 2024).

- Genetic changes in avian influenza viruses that may alter their zoonotic potential (increase capacity to infect humans, increase transmissibility) or their susceptibility to antivirals available to treat humans should be monitored (EFSA AHAW Panel and ECDC, 2025). Avian influenza viruses detected in humans should be sequenced and the sequence shared in public databases in a timely manner.

- 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, zoonotic avian influenza A(H5) vaccination in individuals occupationally or otherwise routinely exposed to infected animals or contaminated environments can also be considered as an optional, complementary preventive measure, based on national recommendations. While data on immune response induction are available, currently no real-world evidence of vaccine effectiveness (e.g. reduction in infection or onward transmission, protection against severe clinical disease) is available to support public health recommendations for the implementation of zoonotic avian influenza vaccination (EFSA AHAW Panel and ECDC, 2025).

- The options for response are based on the current available evidence, epidemiological situation and risk assessment for the EU/EEA. Recommended measures may need to be adapted if the epidemiological situation changes or new evidence becomes available.

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Appendix A – Terms of Reference of the joint EFSA-ECDC mandate (M-2024-00009) accepted in March 2024

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.

The evolution of the HPAI epidemiological situation with high number of birds and new mammalian species affected is prompting response by both animal health and public health authorities in EU Member States and indicates the need for enhanced preparedness and prevention. Given the mammalian adaptation mutations detected in certain circulating viruses, the infection of mammals in fur farms, as well as an outbreak amongst cats extending the animal/human interface along with the suspicion of events of mammal-to-mammal transmission, animal health and public health authorities are currently working on addressing these challenges. In that context, they are developing or adapting their tools for epidemiological investigations, strengthening their collaboration issuing new emergency national legislations as well as adapting their surveillance guidance and programmes in the light of the upcoming seasonal flu season. The situation and actions above have been taken in reaction to:

- ECDC's current risk assessment (ECDC, online) that focuses on the immediate risk of avian influenza for human health fulfilling ECDC's new mandate and the Regulation (EU) 2022/2371[15] aiming to prevent and prepare for cross-border health threats, including epidemics; and
- EFSA's latest scientific opinions and reports (EFSA, online) coupled by measures taken (i.e., surveillance, prevention and control measures) under the Animal Health Law (i.e., Commission Delegated Regulation (EU) 2020/689[16] and Commission Delegated Regulation (EU) 2020/687[17]).

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[15] Regulation (EU) 2022/2371 of the European Parliament and of the Council of 23 November 2022 on serious cross-border threats to health and repealing Decision No 1082/2013/EU. OJ L 314, 6.12.2022, p. 26–63.

[16] Commission Delegated Regulation (EU) 2020/689 of 17 December 2019 supplementing Regulation (EU) 2016/429 of the European Parliament and of the Council as regards rules for surveillance, eradication programmes, and disease-free status for certain listed and emerging diseases. OJ L 174, 3.6.2020, p. 211–340.

[17] Commission Delegated Regulation (EU) 2020/687 of 17 December 2019 supplementing Regulation (EU) 2016/429 of the European Parliament and the Council, as regards rules for the prevention and control of certain listed diseases. OJ L 174, 3.6.2020, p. 64–139.

In view of the One Health nature of this subject, and pursuant to Article 3 of Regulation (EU) 2022/2370[18] and Articles 29 and 31 of Regulation (EC) No 178/2002[19], the European Centre for Disease Prevention and Control (ECDC) and the European Food Safety Authority (EFSA) are requested to carry out the following task:

To provide regular quarterly scientific reports, updating on the avian influenza situation within the Union and worldwide, to the Commission by:

1) Analysing the epidemiological data on HPAI and LPAI from Member States and describe the evolution of virus spread from certain regions towards the EU and in case of significant changes in the epidemiology of avian influenza;
2) Analysing the temporal and spatial pattern of HPAI and LPAI, as appropriate, in poultry, captive and wild birds, kept and wild mammals, as well the risk factors involved in the occurrence, spread and persistence in the EU of the avian influenza virus in and at the interface of these animal populations with specific attention to zoonotic risks;
3) Describing the options for adapting preparedness, prevention, and control measures, based on the finding from point 1) and 2).

A.2 Interpretation of the Terms of Reference

In reply to the TORs above, this Scientific Report gives an overview of the HPAI virus detections in poultry, captive and wild birds, as well as in mammals, in Europe and worldwide between 7 December 2024 and 7 March 2025 (12 March for mammals) 2024, as reported by Member States and third countries via ADIS or WOAH-WAHIS. In addition, LPAI virus detections of specific relevance are included, and possible actions for preparedness in the EU are discussed based on the situation worldwide. 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.

However, it was not possible to collect data for a comprehensive risk factor analysis on the occurrence and persistence of HPAI viruses within the EU. Risk factor analysis requires not only case-related information but also data on the susceptible population (e.g. location of establishments and 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).

This report mainly describes information that has become available since the publication of the EFSA report for the period June to September 2024 (EFSA, ECDC and EURL, 2024a) and that might affect the interpretation of risks related to avian influenza introduction and/or spread in Europe.

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[18] Regulation (EU) 2022/2370 of the European Parliament and of the Council of 23 November 2022 amending Regulation (EC) No 851/2004 establishing a European centre for disease prevention and control. OJ L 314, 6.12.2022, p. 1–25.

[19] 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, p. 1–24.

Appendix B – Data and Methodologies

B.1 Data on animals

B.1.1 Overview of avian influenza outbreaks in Europe

For this report, data on HPAI outbreaks reported in Europe between 7 December 2024 and 7 March 2025, and submitted by Member States and other European countries via ADIS, were taken into account. Data extraction was carried on 7 March 2025. WOAH-WAHIS was consulted to complement the information for European countries not reporting HPAI notifications via 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 information is provided in Annex B. In addition, the information European 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 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, and the common and scientific names of wild bird species described in this report for Europe are reported in Table A.3 (both in Annex A). The public GISAID's EpiFlu™ database was accessed to download newly released avian influenza virus sequences.

Scientific species names of wild birds and mammals mentioned in this report are listed in Table A.3 (Annex A) and Table 5, respectively.

The annexes to this Scientific Report are available here: https://doi.org/10.5281/zenodo.15063214

B.1.2 Overview of avian influenza outbreaks in other countries not reporting via ADIS

Data from WOAH-WAHIS on HPAI A(H5) and A(H7) 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 all regions of the world based on the observation dates. Data were retrieved on 7 March 2025 and extracted by EFSA. They were used and reproduced with permission. WOAH bears no responsibility for the integrity or accuracy of the data contained herein, but not limited to, any deletion, manipulation, or reformatting of data that may have occurred beyond its control.

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

The HA gene of clade 2.3.4.4 A(H5) viruses has rapidly evolved since the most recent official update of the nomenclature of the A/goose/Guangdong/1/1996-lineage H5Nx virus (Smith et al., 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, 2023).

B.2 Data on humans

Data on the number of human cases caused by infection with avian influenza viruses was collected by ECDC. As part of epidemic intelligence activities at ECDC, multiple sources are scanned regularly 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 since the first human case was reported. Therefore, data on human cases refer to different time periods. Relevant information on human infections, risk factors, and the results from studies on infection and transmission with relevance for human health are included.

B.2.1 Method for phylogenetic and mutation analysis

The GISAID's EpiFlu™ Database (Shu and McCauley, 2017) was accessed on 7 March 2025 to retrieve sequences from human cases of avian influenza reported since 11 December 2024. In cases where the same strain had multiple submissions, the ones with the most complete segment data were chosen. The phylogenetic analysis was performed at nucleotide on HA segments in CLC Genomics Workbench 24.0.2 (Qiagen). An alignment was produced in very accurate mode with default parameters and subsequently trimmed into 1 694 gap-free nucleotides. A neighbour joining tree was produced by Jukes-Cantor nucleotide distance measurement with 100 bootstrap replicates. The protein sequences were analysed using a script developed in-house, with A/Goose/Guangdong/1/96 (EPI_ISL_1254) as reference to determine mutations of interest (H5 numbering, unless otherwise stated). Clade and genotype information was retrieved from GISAID.

Annex A – Data on HPAI detections in wild and captive birds

Annex A is available on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.15063214

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.15063214

Annex C – Acknowledgements

All genome sequences and associated metadata in this dataset are published in GISAID's EpiFlu database. To view the contributors of each individual sequence with details such as accession number, Virus name, Collection date, Originating Lab and Submitting Lab and the list of Authors, visit: https://doi.org/10.55876/gis8.250318aq (GISAID Identifier: EPI_SET_250318aq), https://doi.org/10.55876/gis8.250319tp (EPI_SET_250319tp).