SCIENTIFIC REPORT

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Avian influenza overview June–September 2025

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Abstract

Between 7 June and 5 September 2025, 183 highly pathogenic avian influenza (HPAI) A(H5) virus detections were reported in domestic (27) and wild (156) birds across 15 countries in Europe. Although HPAI A(H5N1) virus detections were predominant in western and southwestern Europe, they also occurred on the northernmost coast of Norway. More than 75% of the detections in wild birds related to colony-breeding seabirds, particularly European herring gulls, while the number of detections in waterfowl decreased compared to the previous months. Less poultry establishments were affected during the current reporting period, with no secondary spread occurring. Regarding mammals in Europe, HPAI A(H5N5) virus detections were reported in four Arctic foxes in Norway. In the United States of America (USA), the number of HPAI A(H5N1) virus detections in dairy cattle stagnated, while the muskrat and round-tailed ground squirrel were reportedly affected for the first time. Between 7 June and 8 September 2025, 19 cases of avian influenza virus infection in humans, including three deaths, were reported in four countries: Bangladesh (one A(H5N1) case), Cambodia (11 A(H5N1) cases), China (one A(H10N3), five A(H9N2) cases) and India (one A(H5N1) case). Most of the A(H5N1) human cases (n = 12/13) reported exposure to poultry prior to detection or onset of illness. Given the widespread circulation of avian influenza viruses in animal populations, human infections remain rare. No human-to-human transmission was documented during the reporting period. The risk of infection with the avian A(H5) clade 2.3.4.4b influenza viruses currently circulating in Europe remains low for the general public in the European Union/European Economic Area (EU/EEA) and 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] and captive birds[3] (domestic birds), as well as wild birds, that occurred in and outside Europe between 7 June and 5 September 2025. In addition, HPAI virus detections in mammals up until 5 September 2025 and cases of avian influenza infection in humans between 7 June and 8 September 2025 are reported. 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 5 September 2025.

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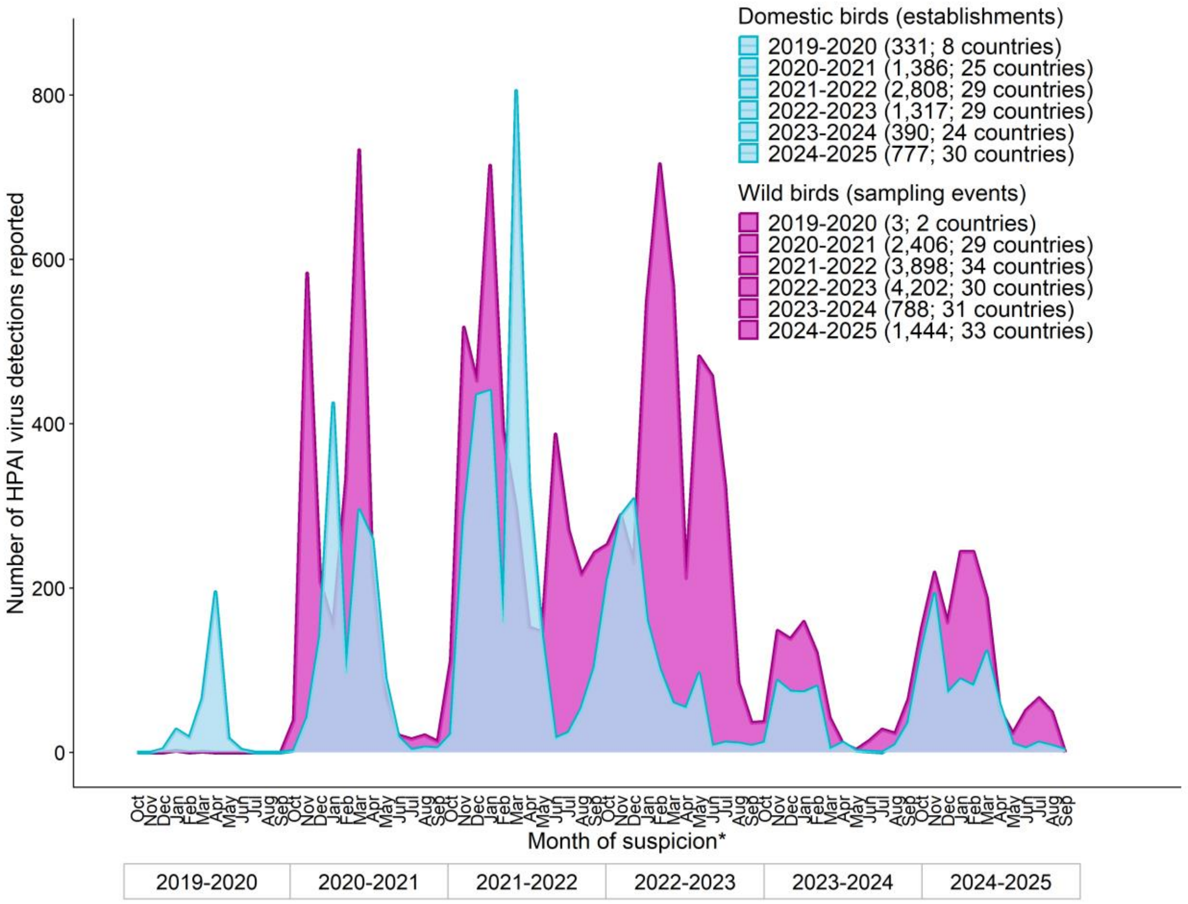
[2] According to Regulation (EU) 2016/429 of the European Parliament and of the Council of 9 March 2016, point (9), 'poultry' means birds that are reared or kept in captivity for: (a) the production of: (i) meat; (ii) eggs for consumption; (iii) other products; (b) restocking supplies of game birds; (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 on 1 October and ending on 30 September of the following year, based on the dates on which the first HPAI virus detections were observed in wild birds in Europe in 2016–2017, 2020–2021 and 2021–2022.



*If the date of suspicion was not available, the date of confirmation was used to assign the week of suspicion. United Kingdom data are from the Animal Disease Notification System (ADNS, former ADIS) up until 31 December 2020. From 1 January 2021 onwards, the data source was 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 5 September 2025).

Figure 1: Distribution of the number of HPAI virus detections in wild birds (cumulative number n = 12,741) (pink) and establishments keeping domestic birds (cumulative n = 7,009) (blue) reported in Europe during six epidemiological years by month of suspicion, from 1 October 2019 to 5 September 2025 (total n = 19,750)

Considering the current reporting period from 7 June to 5 September 2025, 183 HPAI virus detections were reported in poultry (20), captive (7) and wild (156) birds across 15 countries in Europe (Table 1, Figure 2).

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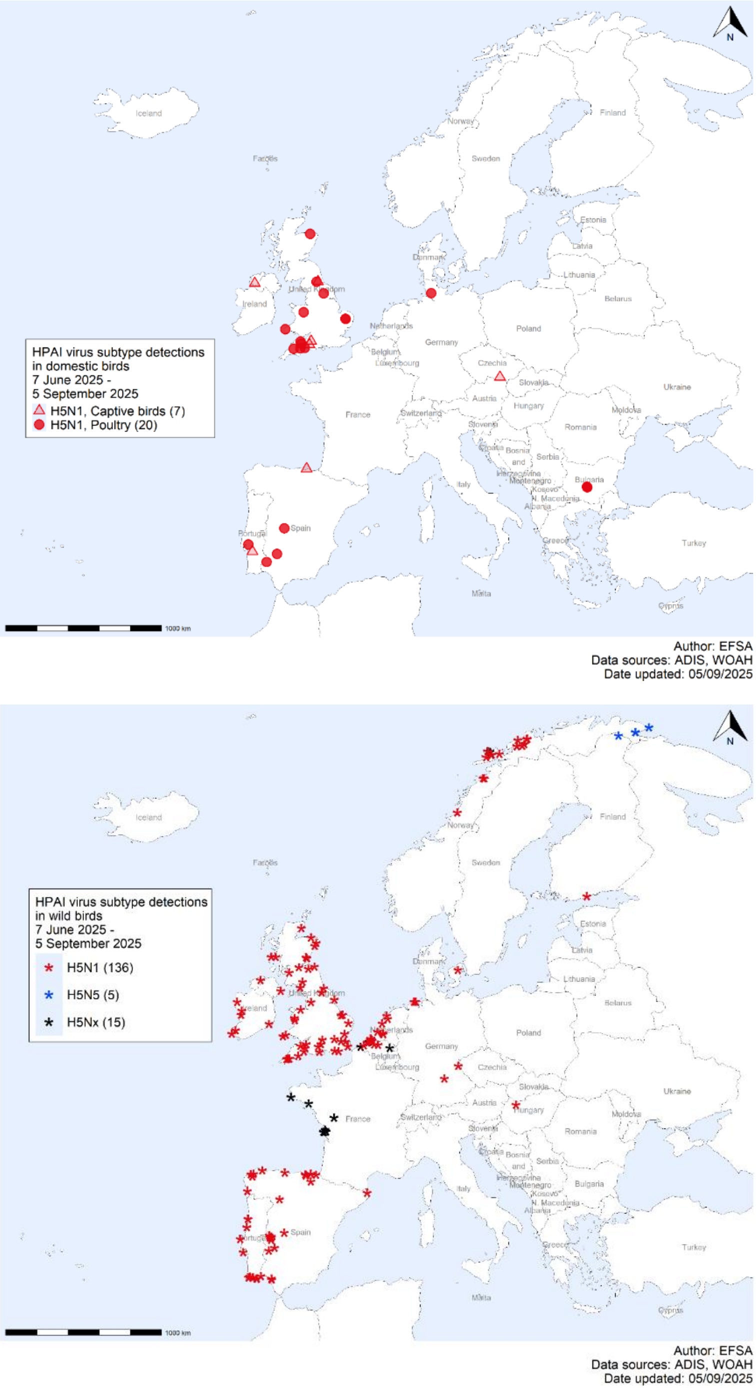
[5] In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Windsor Framework, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).

Table 1: Number of HPAI outbreaks reported in Europe by country, virus subtype and affected sub-population, from 7 June to 5 September 2025. Cumulative numbers since the start of the 2024–2025 epidemiological year are reported in parentheses (1 October 2024 to 5 September 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	-	-	-	-	0 (5)	-	-	0 (2)	-	-	**0 (7)**
Austria	-	0 (2)	-	-	0 (6)	-	0 (5)	0 (57)	-	-	**0 (70)**
Belgium	-	0 (5)	-	-	0 (3)	-	2 (6)	5 (40)	0 (1)	-	**7 (55)**
Bosnia and Herzegovina	-	-	-	-	0 (1)	-	-	0 (1)	-	-	**0 (2)**
Bulgaria	-	-	-	-	3 (12)	-	-	0 (1)	-	-	**3 (13)**
Croatia	-	0 (1)	-	-	0 (2)	-	-	0 (10)	-	-	**0 (13)**
Czechia	-	1 (29)	-	-	0 (4)	-	-	0 (11)	-	-	**1 (44)**
Denmark	-	-	-	-	0 (2)	-	-	1 (17)	-	-	**1 (19)**
Estonia	-	-	-	-	-	-	-	0 (1)	-	-	**0 (1)**
Faeroe Islands	-	-	-	-	-	-	-	-	0 (1)	-	**0 (1)**
Finland	-	-	-	-	-	-	-	1 (6)	1 (1)	-	**2 (7)**
France	0 (3)	-	-	-	0 (11)	-	8 (11)	0 (24)	-	-	**8 (49)**
Germany	-	0 (24)	-	-	1 (23)	-	0 (13)	4 (210)	0 (1)	-	**5 (271)**
Greece	-	-	-	-	-	-	-	0 (3)	-	-	**0 (3)**
Hungary	-	0 (2)	-	-	0 (292)	-	-	1 (46)	-	-	**1 (340)**
Iceland	-	-	-	-	-	0 (1)	0 (2)	-	0 (25)	-	**0 (28)**
Ireland	-	1 (1)	-	-	-	-	-	7 (22)	-	-	**8 (23)**
Italy	-	-	-	0 (6)	0 (50)	-	0 (5)	0 (90)	-	-	**0 (151)**
Latvia	-	-	-	-	0 (1)	-	-	-	-	-	**0 (1)**
Lithuania	-	0 (1)	-	-	0 (1)	-	-	0 (3)	-	-	**0 (5)**
Moldova	-	0 (19)	-	-	-	-	-	0 (3)	-	-	**0 (22)**
Netherlands	-	0 (2)	-	-	0 (5)	-	-	16 (227)	-	-	**16 (234)**
North Macedonia	-	0 (1)	-	-	0 (1)	-	-	-	-	-	**0 (2)**
Norway	-	-	0 (1)	-	-	-	5 (5)	17 (20)	4 (13)	-	**26 (39)**
Poland	-	0 (30)	-	-	0 (109)	-	-	0 (69)	-	-	**0 (208)**
Portugal	-	1 (4)	-	-	1 (3)	-	-	13 (17)	-	-	**15 (24)**
Romania	-	0 (2)	-	-	0 (2)	-	-	0 (8)	-	-	**0 (12)**
Serbia	-	-	-	-	-	-	-	0 (4)	-	-	**0 (4)**
Slovakia	-	0 (6)	-	-	0 (2)	-	-	0 (15)	-	0 (1)	**0 (24)**
Slovenia	-	0 (1)	-	-	-	-	-	0 (47)	-	-	**0 (48)**
Spain	-	1 (1)	-	-	3 (3)	-	-	25 (35)	-	-	**29 (39)**
Sweden	-	-	-	-	0 (1)	-	-	0 (13)	0 (1)	-	**0 (15)**
Switzerland	-	-	-	-	-	-	-	0 (9)	-	-	**0 (9)**
Türkiye	-	0 (3)	-	-	0 (7)	-	-	-	-	-	**0 (10)**
Ukraine	-	0 (7)	-	-	-	-	-	0 (1)	-	-	**0 (8)**
United Kingdom (excluding Northern Ireland)	-	3 (12)	-	-	12 (62)	0 (1)	-	45 (309)	0 (23)	-	**60 (407)**
United Kingdom (Northern Ireland)	-	0 (1)	-	-	0 (3)	-	-	1 (9)	-	-	**1 (13)**
Total	**0 (3)**	**7 (154)**	**0 (1)**	**0 (6)**	**20 (611)**	**0 (2)**	**15 (47)**	**136 (1330)**	**5 (66)**	**0 (1)**	**183 (2221)**

*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: 05/09/2025

Author: EFSA
Data sources: ADIS, WOAH
Date updated: 05/09/2025

*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.
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 5 September 2025).

Figure 2: Geographic distribution, based on available geocoordinates, of HPAI virus detections in poultry and captive birds (27) (upper panel), and in wild birds (156) (lower panel), reported by virus subtype in Europe from 7 June to 5 September 2025

After constantly declining during the previous reporting period (8 March to 6 June 2025), there was a mild increase in HPAI virus detections, peaking in July, in both domestic

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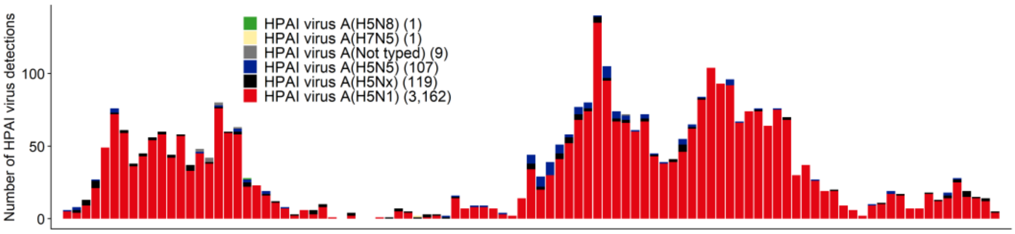
[6] In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Windsor Framework, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).

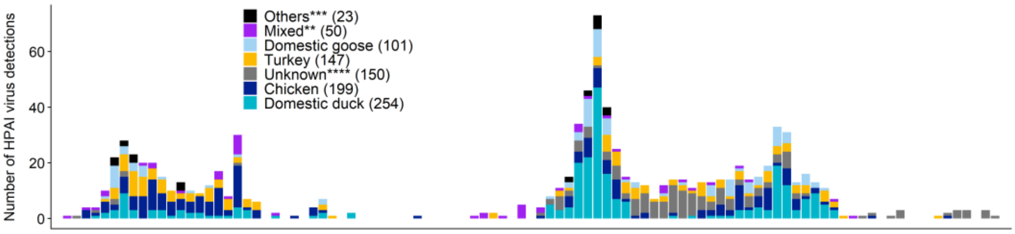
and wild birds during the current reporting period (7 June to 5 September 2025). The overall number of detections during the current reporting period was higher than during the same period in the previous epidemiological year in both domestic and wild birds. The number of HPAI virus detections in the whole epidemiological year 2024–2025 so far (n = 2,221; data from 6 to 30 September 2025 still missing) was about twice as high as in 2023–2024 (n = 1,178), but about two to three times lower than in 2022–2023 (n = 5,519) and 2021–2022 (n = 6,706) in both domestic and wild birds (Figure 1).

During the current reporting period, HPAI A(H5N1) virus detections in domestic and wild birds largely overlapped and were concentrated in the United Kingdom, while an increasing number of detections were reported from the Iberian Peninsula (Figure 2). In contrast, there were only five HPAI A(H5N5) virus detections, and all of them occurred in wild birds: four in northern Norway and one in northern Finland (Figure 2, lower panel). Overall, the majority of HPAI virus detections in wild birds during the current reporting period concerned colony-breeding seabirds (Figure 3, Figure 4).

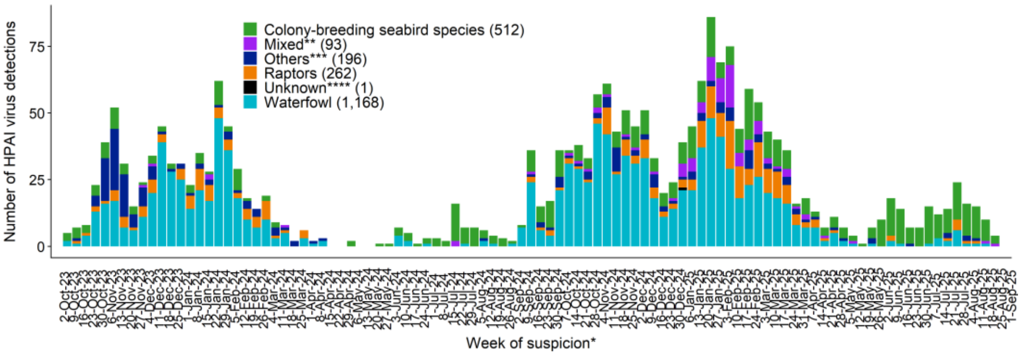
(a) All birds



(b) Poultry



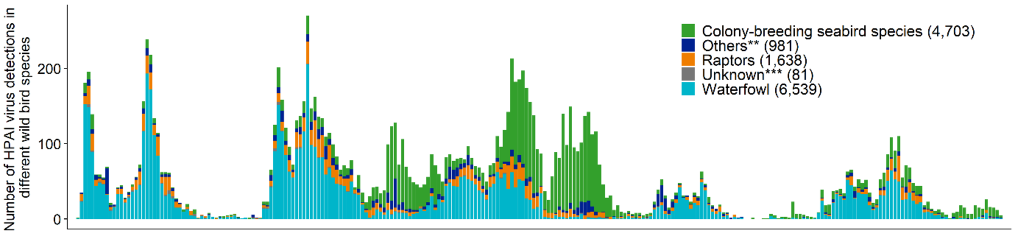
(c) Wild birds



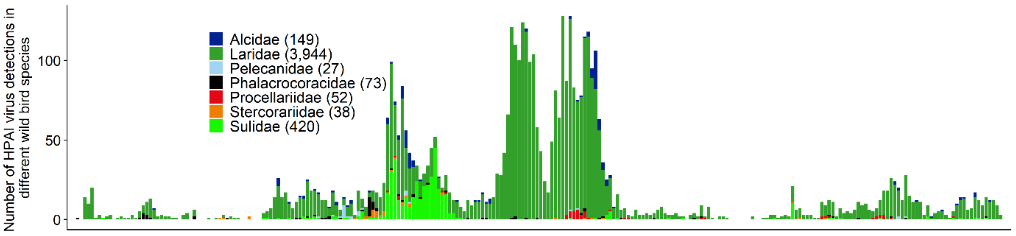
*If the date of suspicion was not available, the date of confirmation was used to assign the week of suspicion.
**'Mixed' refers to outbreaks in which multiple species or categories were involved.
***'Others' groups all other affected categories that are not indicated in the legend.
****'Unknown' refers to affected categories that were not further specified during reporting.
Source: ADNS/ADIS, EFSA and WOAH (data extraction carried out on 5 September 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 5 September 2025

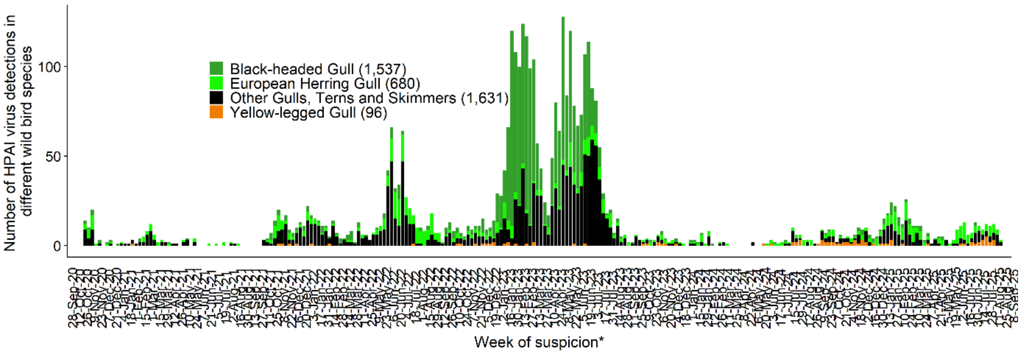
(a) Wild birds



(b) Colony-breeding seabird species



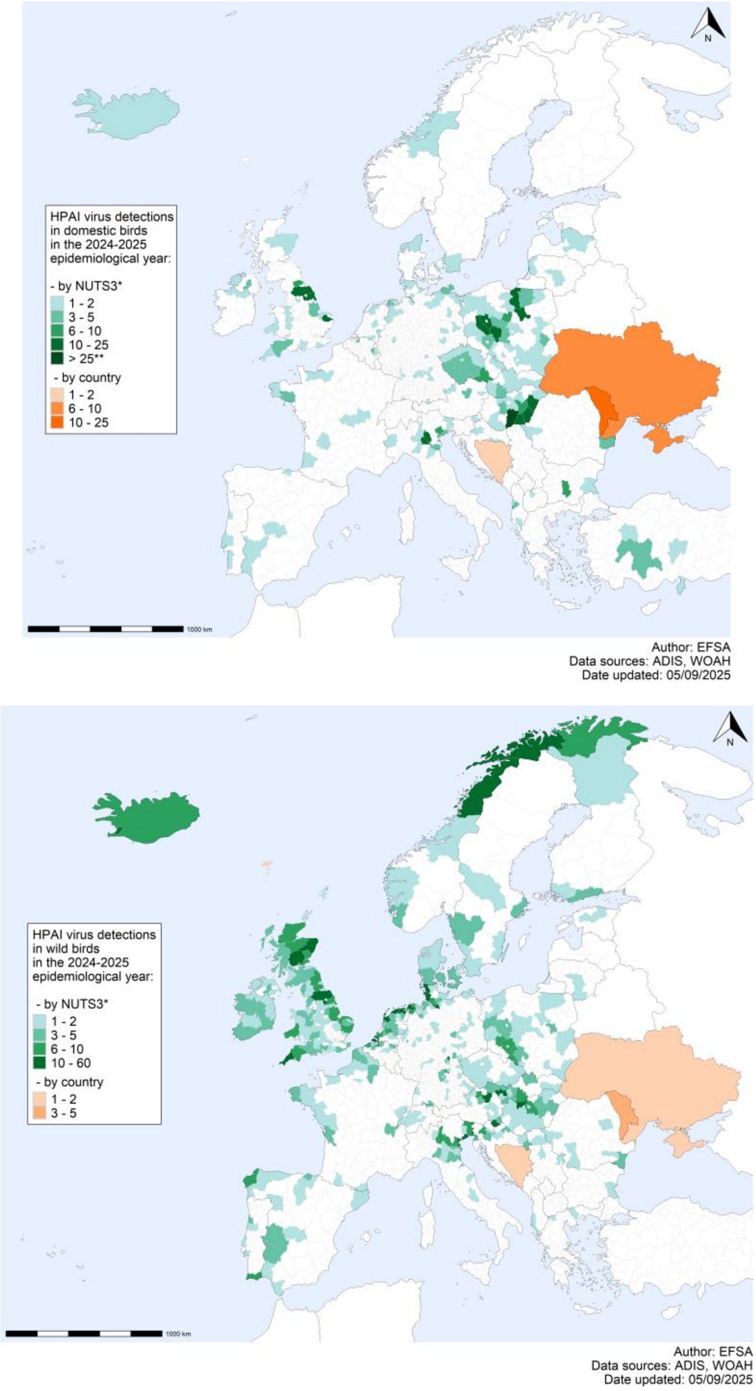
(c) Laridae species



*If the date of suspicion was not available, the date of confirmation was used to assign the week of suspicion.
**'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 5 September 2025).

Figure 4: 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 affected wild bird categories (a), affected colony-breeding seabird species (b) and affected Laridae species (c), from 1 October 2020 to 5 September 2025

An overview of the geographical distribution of all reported HPAI virus detections in domestic and wild birds in the 2024–2025 epidemiological year (up until 5 September 2025) is shown in Figure 5. In general, regions with HPAI virus detections in domestic birds geographically overlap with regions where HPAI virus detections in wild birds were reported. In some regions, particularly in Poland and Hungary, high numbers of affected establishments keeping domestic birds were observed as a result of extensive secondary farm-to-farm spread in certain poultry production systems.



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 05/09/2025

Author: EFSA
Data sources: ADIS, WOAH
Date updated: 05/09/2025

*NUTS2024 for all countries except the United Kingdom for which a similar but different system applies.
**228 HPAI virus detections were observed in one specific NUTS3 in Hungary.
Source: ADIS, EFSA and WOAH (data extraction carried out on 5 September 2025).

Figure 5: Overview of the geographical distribution of all reported HPAI virus detections in affected establishments keeping domestic birds (upper panel), and in wild birds (lower panel), by NUTS 3 in Europe for the 2024–2025 epidemiological year (up until 5 September 2025)

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

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

Poultry

Between 7 June and 5 September 2025, 20 HPAI outbreaks in poultry were reported in five countries in Europe: United Kingdom (12), Bulgaria (3), Spain (3), Germany (1) and Portugal (1) (Table 1, Figure 2, Figure 6). The outbreaks in Spain where the first outbreaks reported during the current epidemiological year.

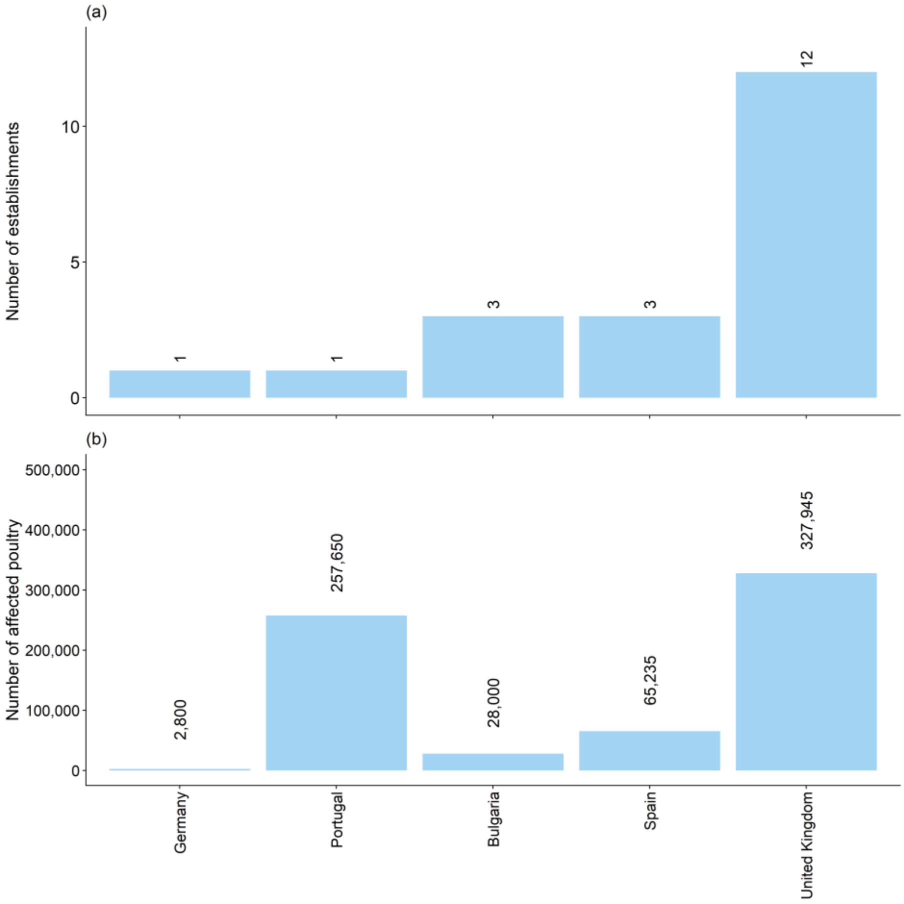
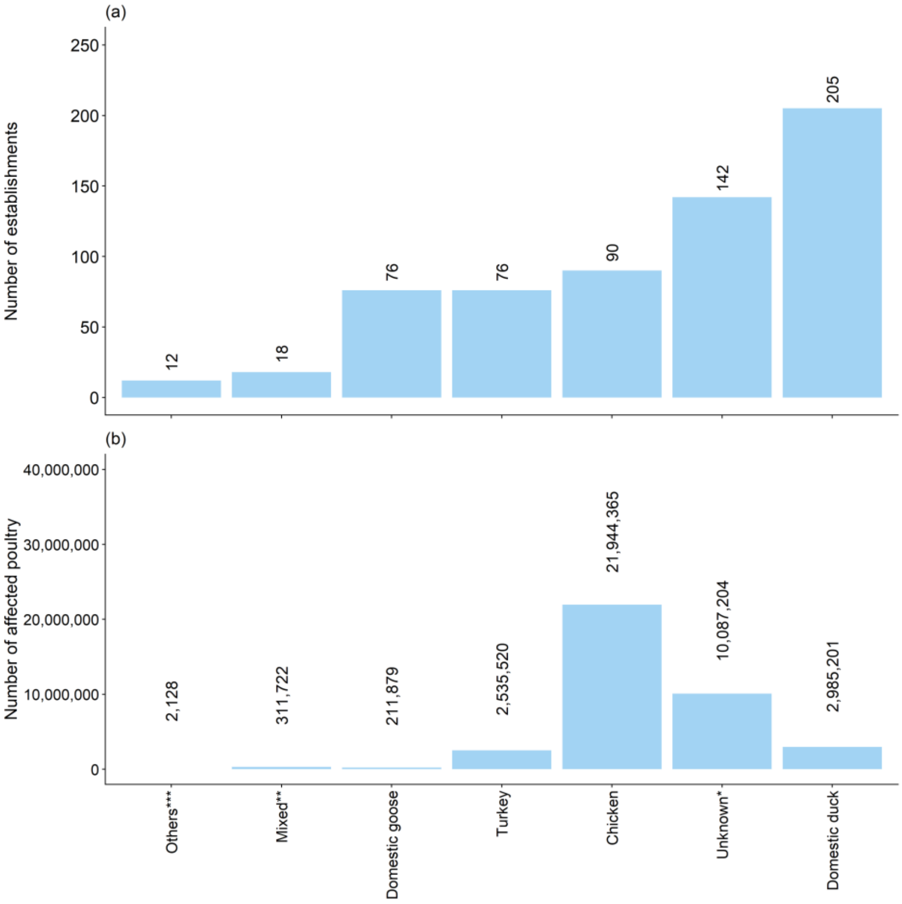


Figure 6: Number of HPAI-affected establishments (20) (a) and number of poultry in the HPAI-affected establishments (681,630) (b) per country in Europe between 7 June and 5 September 2025 (countries are ranked according to the number of outbreaks)

All 20 HPAI outbreaks in poultry were due to HPAI A(H5N1) viruses. This compares to a total of six A(H5N1) and one A(H7N5) outbreaks during the same period in the 2023–2024 epidemiological year, but the current number was lower or at similar levels compared to the years before. During the current reporting period, the United Kingdom accounted for 60% (12/20) of the HPAI outbreaks in poultry and 48% of the number of affected birds (Figure 6). In total, 681,630 birds died or were culled in the HPAI-affected establishments (Figure 6), about 91% less compared to the previous reporting period. Overall, 40% (8/20) of the HPAI outbreaks in poultry were classified as primary, and for the remaining 12 outbreaks (60%), all from the United Kingdom, this information was not available. In contrast to the previous reporting period, when 81 secondary outbreaks were reported between two countries (Hungary and Poland) (Figure 7), no secondary outbreaks were reported between 7 June and 5 September 2025.

Overall, in the current epidemiological year 2024–2025 (up until 5 September 2025), a total of 619 HPAI outbreaks in poultry were reported in Europe (Figure 7, Table 1). The most affected poultry category during this time was the ‘domestic duck’ category (33%, 205/619 outbreaks), followed by the 'chicken' (15%, 90/619), 'domestic goose' (12%, 76/619), 'turkey' (12%, 76/619) and 'other' (2%, 12/619) categories. Multiple species were kept in 18 (3%) establishments, and no information on the species kept was available for 142 (23%) establishments (Figure 7). A substantial proportion of these 142 establishments without further information were concentrated in the United Kingdom, from which no additional data are collected, and two other countries in Europe that did not provide this information to EFSA.



*'Unknown' refers to affected categories that were not further specified during reporting.
**'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.

Figure 7: Overview of the number of HPAI-affected establishments (619) (a) and number of birds in the HPAI-affected establishments (38,078,019) (b) per poultry category in Europe for the 2024–2025 epidemiological year (up until 5 September 2025)

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 June to 5 September 2025, 20 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 two of these 20 (10%) outbreaks reported to ADIS before 29 August 2025 from Spain (Annex B). For the other 18 (90%) outbreaks in poultry, no additional data were provided, either because they occurred in the United Kingdom, from which no additional data are collected, or because they were reported to ADIS after 29

August 2025 and therefore occurred too shortly before the publication of this report. In this report, a short summary of these outbreaks will be provided, but additional data will only be collected in the next round and included in Annex B of the following report.

In the whole epidemiological year 2024–2025 (up until 5 September 2025), additional data were collected for 477 of the 619 (77%) HPAI outbreaks in poultry. Among these, 46% (219/477) were reported as primary and 54% (258/477) as secondary. In 78% (170/219) of primary outbreaks, indirect contact with wild birds was considered the most likely source of introduction, followed by direct contact with wild birds (3%, 7/219). For one of the outbreaks reported as primary, indirect contact with poultry was considered the most likely source of introduction, suggesting it was a secondary rather than a primary outbreak. For the remaining 19% (41/219), the source was reported as unknown. For 93% (241/258) of the secondary outbreaks, indirect contact with poultry was considered the most likely source of introduction, followed by indirect contact (5%, 12/258) among affected establishments through wild birds. For one of the outbreaks reported as secondary, direct contact with wild birds was considered the most likely source of infection, suggesting it was a primary rather than a secondary outbreak. For the remaining 2% (4/258), the source was reported as unknown.

Bulgaria

During the current reporting period from 7 June to 5 September 2025, three 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 23 August, three A(H5N1) outbreaks were detected in three different establishments keeping mulard ducks (n = 9,000, n = 5,500 and n = 13,500; production type not reported), with no known epidemiological link between these establishments (European Commission, online). Clinical signs were described, but no mortality was observed in any of the outbreaks.

Germany

During the current reporting period from 7 June to 5 September 2025, one primary outbreak in poultry was reported in Germany via ADIS. No additional data to complement the information in ADIS were provided by the country, as the outbreak occurred too shortly before the publication of this report. On 1 September, an A(H5N1) outbreak was detected in a establishment keeping laying hens (n = 2,800), where mortality but no clinical signs were observed.

Portugal

During the current reporting period from 7 June to 5 September 2025, one primary outbreak in poultry was reported in Portugal via ADIS. No additional data to complement the information in ADIS were provided by the country, as the outbreak occurred too shortly before the publication of this report. On 2 September, an A(H5N1) outbreak was detected in a commercial establishment keeping ducks for fattening (n = 257,650), where mortality and clinical signs were observed.

Spain

During the current reporting period from 7 June to 5 September 2025, three primary outbreaks in poultry were reported in Spain via ADIS. Additional data were collected and provided by the reporting country for two of the outbreaks (Annex B), while the third occurred too shortly before the publication of this report. On 18 July, an A(H5N1) outbreak was confirmed in a commercial establishment keeping turkeys for fattening (n = 12,035).

At the time of culling[8], high mortality (65.5%) was reported, and clinical signs were observed. The birds were kept indoor. Two people were reported as exposed. On 28 July, an A(H5N1) outbreak was confirmed in a commercial establishment keeping breeding hens (n = 45,000). At the time of culling, high mortality (91.1%) was reported, and clinical signs were observed. The birds were kept indoor. Twelve people were reported as exposed. After 29 August, one additional A(H5N1) outbreak was reported via ADIS in an establishment keeping fattening turkeys (n = 8,200), where mortality and clinical signs were observed. The most probable source of introduction in all outbreaks was indirect contact with wild animals.

United Kingdom (excluding Northern Ireland)

During the current reporting period from 7 June to 5 September 2025, 12 outbreaks in poultry were reported in the United Kingdom via WOAH-WAHIS. All 12 outbreaks were confirmed as A(H5N1) and occurred in commercial establishments. Information regarding the poultry species kept was reported for all establishments but one, i.e. pheasants for game purposes (n = 4), laying hens (n = 2), ducks (n = 1; production type not reported), turkeys (n = 1; production type not reported) and broilers (n = 1). Two establishments kept multiple species: pheasants and partridges for game purposes (n = 1), and chickens, ducks and geese (n = 1; production type not reported). Overall, 327,945 birds were culled in the 12 HPAI-affected establishments.

Captive birds

Between 7 June and 5 September 2025, seven HPAI outbreaks in captive birds, predominantly in establishments keeping chickens, were reported from five countries in Europe: United Kingdom (excluding Northern Ireland) (3), Czechia (1), Ireland (1), Portugal (1) and Spain (1) (Table 1, Figure 2). The HPAI outbreak in Spain concerned a yellow-legged gull in a wildlife recovery centre, where 17 other birds sharing the same aviary were culled (Diario Veterinario, online).

Wild birds

During the current reporting period from 7 June to 5 September 2025, a total of 156 HPAI virus detections in wild birds (with one HPAI virus detection potentially including more than one wild bird species) were reported from the United Kingdom (excluding Northern Ireland) (45), Norway (26), Spain (25), Netherlands (16), Portugal (13), France (8), Belgium (7), Ireland (7), Germany (4), Finland (2), Denmark (1), Hungary (1) and the United Kingdom (Northern Ireland)[9] (1).

Overall, 136 HPAI virus detections in wild birds were reported as A(H5N1), five as A(H5N5) and 15 as A(H5Nx) (Table 1, Figure 2). The overall number of HPAI virus detections reported in wild birds (156) during the current reporting period was about one third lower than during the previous reporting period (217) (Figure 3) but more than twice as high compared to the same period in the previous epidemiological year (66).

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 mostly recorded in colony-breeding seabirds (78%, 121/156), followed by waterfowl (11%,

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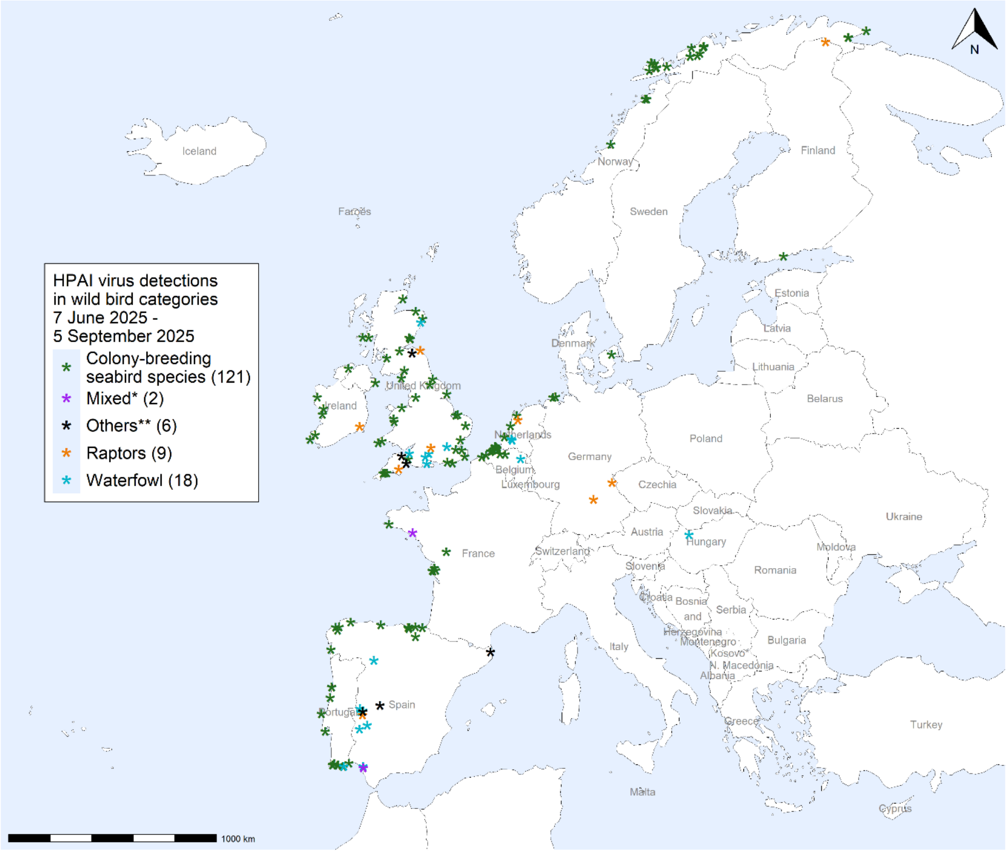
[8] For these two outbreaks in Spain, the mortality was calculated based on the number of dead birds at the time of culling instead of the number of dead birds at the time of detection of the outbreak.

[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).

18/156), raptors (6%, 9/156), other (4%, 6/156) and mixed wild bird species (1%, 2/156) (Figure 8).



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 05/09/2025

[*] 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.
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 5 September 2025).

Figure 8: Geographic distribution, based on available geocoordinates, of HPAI virus detections in different categories of wild birds in Europe, by species category, from 7 June to 5 September 2025

This pattern differs from the previous reporting period, when A(H5) was recorded in one third more waterfowl than colony-breeding seabirds. Relative to the total number of HPAI virus detections in wild birds, the percentage of HPAI virus detections in raptors during the current reporting period (6%, 9/156) was about two thirds lower than during the previous reporting period (18%, 38/217). In the whole epidemiological year 2024–2025 (up until 5 September 2025), HPAI A(H5) was mostly recorded in waterfowl (51%, 732/1444), followed by colony-breeding seabirds (25%, 363/1444), raptors (12%, 177/1444), other (6%, 86/1444) and mixed wild bird species (6%, 85/1444).

Between 7 June and 5 September 2025, colony-breeding seabirds were primarily detected along coastlines, whereas other wild bird species were found both in coastal and inland locations. The wild bird species in which HPAI viruses were detected belonged mainly to three orders: Charadriiformes (124 HPAI virus detections), Anseriformes (22) and

Accipitriformes (8). The three most frequently reported gulls identified to species were the European herring gull (54 in the current vs 38 in the previous reporting period), yellow-legged gull (20 vs 1) and mew gull (6 vs 1) (Figures A.1–A.2 in Annex A). However, HPAI virus detections were reported in at least eight different Laridae species. A comparison of the number of HPAI virus detections in European herring gulls, yellow-legged gulls and black-headed gulls over the last five epidemiological years (Figure 4, bottom panel) shows that HPAI virus detections in European herring gulls were reported regularly in small numbers throughout the whole period; HPAI virus detections in yellow-legged gulls were reported in small numbers, mainly in the past year; and HPAI virus detections in black-headed gulls were reported in small numbers until spring and summer of 2023, when HPAI outbreaks in this species occurred across Europe and the numbers of HPAI virus detections were very high, but only in very small numbers in the years thereafter, possibly due to flock immunity. During the current epidemiological year, the observed increase in HPAI virus detections in colony-breeding seabirds occurred slightly later than in previous years (Figure 4), possibly due to a certain level of immunity developed by adult birds. In the order Anseriformes, most HPAI virus detections were still reported in mute swan (7 vs 37) and greylag goose (6 vs 24), followed by gadwall (3 vs 0). The Accipitriformes detected positive for HPAI viruses during the current reporting period were distributed among many different species, with the common buzzard at the top of the list (2 vs 17). The complete list of wild bird species found as HPAI virus-infected from 7 June to 5 September 2025 is reported in Figure A.1 in Annex A. The proportion of HPAI virus-affected wild birds that were not identified to species was 21/168 (12.5%), similar to the previous reporting period (30/256, 12%) (Figures A.1–A.2 in Annex A). In the whole epidemiological year 2024–2025 (up until 5 September 2025), the wild bird species in which HPAI viruses were most frequently detected were mute swan (18%, 299/1690), European herring gull (10%, 173/1690) and greylag goose (8%, 140/1690).

Only five HPAI A(H5N5) virus detections were reported in wild birds in Europe during the current reporting period, in mew gull (2), European herring gull (1), golden eagle (1) and great black-backed gull (1) (Table 2). All positive gulls were reported from Norway, while the golden eagle was reported from Finland. Although A(H5N5) virus has been reported in a wide range of wild bird species in the current epidemiological year, the high proportion of Laridae species involved (40%, 28/70) (Table 2) suggests that this bird family may be important for persistence of this subtype.

Table 2: 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 (31)	European herring gull	10
	Unidentified Laridae species	4
	Great black-backed gull	4
	Mew gull	3
	Black-headed gull	3
	Pallas's gull	2
	Black-legged kittiwake	1
	Grey gull	1
	Iceland 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
Raptors (14)	Red kite	4
	White-tailed eagle	4
	Common buzzard	2
	Common barn owl	2
	Golden eagle	1
	Gyrfalcon	1
Others* (11)	Common raven	6
	Hooded crow	3
	Ring-necked pheasant	2
Total		**70**

*'Others' groups all other affected wild bird categories.

During the current reporting period, several HPAI A(H5N1) virus detections in wild birds were reported in public urban parks in Spain (e.g. Sevilla and Málaga), where mortality in ducks, geese, coots and gulls was observed (Diario de Sevilla, online; El Correo de Andalucía, online-a, b). Other than that, no reports of unusual mortality in wild birds were reported in Europe. 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 actually dying 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.

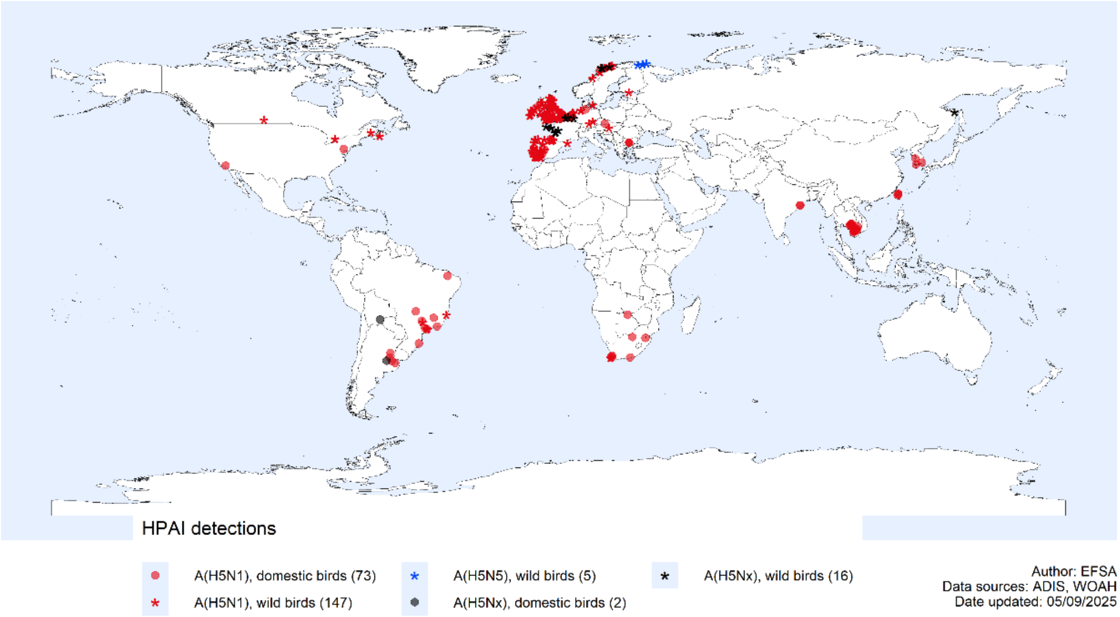
2.1.2 HPAI virus detections in birds outside Europe

An overview of the HPAI virus detections in birds from other countries outside Europe that were notified to WOAH from 7 June to 5 September 2025 is presented in Table 3 and Figure 9.

Table 3: Number of HPAI virus detections in non-European countries notified to WOAH, by virus subtype and country, from 7 June to 5 September 2025. Cumulative numbers since the start of the 2024–2025 epidemiological year are reported in parentheses (1 October 2024 to 5 September 2025)

Region (total in season)	Country	Domestic birds									Wild birds						Total
		A(H5N1)	A(H5N2)	A(H5N5)	A(H5N9)	A(H5Nx)	A(H7N3)	A(H7N6)	A(H7N8)	A(H7N9)	A(H5N1)	A(H5N2)	A(H5N3)	A(H5N5)	A(H5N8)	A(H5Nx)	
Africa (35)	Botswana	1 (1)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**1 (1)**
	Liberia	0 (1)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**0 (1)**
	Niger	0 (1)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**0 (1)**
	Nigeria	0 (19)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**0 (19)**
	South Africa	6 (6)	-	-	-	-	-	-	-	-	2 (3)	-	-	-	-	-	**8 (9)**
	Togo	0 (3)	-	-	-	0 (1)	-	-	-	-	-	-	-	-	-	-	**0 (4)**
Americas (774)	Argentina	4 (4)	-	-	-	1 (2)	-	-	-	-	-	-	-	-	-	-	**5 (6)**
	Bolivia	-	-	-	-	1 (1)	-	-	-	-	-	-	-	-	-	-	**1 (1)**
	Brazil	8 (13)	-	-	-	-	-	-	-	-	5 (6)	-	-	-	-	-	**13 (19)**
	Canada	0 (109)	0 (2)	0 (1)	-	-	-	-	-	-	4 (14)	-	-	0 (8)	-	-	**4 (134)**
	Colombia	0 (8)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**0 (8)**
	Greenland	-	-	-	-	-	-	-	-	-	-	-	-	0 (1)	-	-	**0 (1)**
	Mexico	0 (5)	-	-	-	-	0 (16)	-	-	-	0 (12)	-	-	-	-	-	**0 (33)**
	Panama	0 (1)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**0 (1)**
	Peru	-	-	-	-	0 (14)	-	-	-	-	-	-	-	-	-	0 (10)	**0 (24)**
	Puerto Rico	0 (1)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**0 (1)**
	United States of America	2 (520)	-	-	-	0 (8)	-	-	-	0 (1)	0 (5)	-	-	-	-	0 (12)	**2 (546)**
Antarctica (1)	Falkland Islands	-	-	-	-	-	-	-	-	-	0 (1)	-	-	-	-	-	**0 (1)**
Asia (503)	Bangladesh	-	-	-	-	0 (1)	-	-	-	-	-	-	-	-	-	-	**0 (1)**
	Cambodia	17 (25)	-	-	-	-	-	-	-	-	0 (2)	-	-	-	-	-	**17 (27)**
	Hong Kong	-	-	-	-	-	-	-	-	-	0 (1)	-	-	-	-	-	**0 (1)**
	India	2 (36)	-	-	-	-	-	-	-	-	0 (5)	-	-	-	-	-	**2 (41)**
	Israel	0 (13)	-	-	-	-	-	-	-	-	0 (3)	-	-	-	0 (1)	-	**0 (17)**
	Japan	0 (51)	-	-	-	-	-	-	-	-	0 (205)	-	-	-	-	0 (6)	**0 (263)**
	Mongolia	-	-	-	-	-	-	-	-	-	0 (1)	-	-	-	-	-	**0 (1)**
	Nepal	0 (1)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**0 (1)**
	Philippines	0 (4)	0 (1)	-	0 (1)	-	-	-	-	-	0 (1)	-	-	-	-	-	**0 (7)**
	Russia	-	-	-	-	-	-	-	-	-	0 (3)	-	-	-	-	1 (1)	**1 (4)**
	South Korea	3 (50)	-	-	-	-	-	-	-	-	0 (42)	0 (1)	0 (1)	-	-	-	**3 (93)**
	Taiwan	3 (28)	-	-	-	-	-	-	-	-	0 (9)	-	-	-	-	-	**3 (37)**
	Viet Nam	0 (10)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**0 (10)**
Oceania (5)	Australia	-	-	-	-	-	-	-	0 (4)	-	-	-	-	-	-	-	**0 (4)**
	New Zealand	-	-	-	-	-	-	0 (1)	-	-	-	-	-	-	-	-	**0 (1)**
Total		**46 (910)**	**0 (3)**	**0 (1)**	**0 (1)**	**2 (27)**	**0 (16)**	**0 (1)**	**0 (4)**	**0 (1)**	**11 (313)**	**0 (1)**	**0 (1)**	**0 (9)**	**0 (1)**	**1 (29)**	**60 (1318)**

'-' means that no HPAI outbreaks were notified to WOAH.
Source: WOAH (data extraction carried out on 5 September 2025).



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 05/09/2025

Figure 9: Geographic distribution, based on available geocoordinates, of HPAI virus detections reported worldwide in domestic (75) and wild (168) birds by virus type, from 7 June to 5 September 2025

The tables and figures of the present report only include data extracted from WOAH on 5 September 2025. 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.

Compared to the previous reporting period from 8 March to 6 June 2025, the total number of HPAI virus detections in domestic and wild birds officially notified to WOAH from outside Europe decreased again, this time by almost 75% from 224 to 60 (by 84% in the last report (EFSA, ECDC and EURL, 2025a), and also the number of reporting countries outside Europe dropped from 17 during the previous to 12 during the current reporting period (Table 3, Figure 9). Of the 75 HPAI virus detections reported in domestic birds worldwide (Figure 9), 48 (64%) were officially reported to WOAH from outside Europe, whereas only 12 (7%) of the 168 HPAI virus detections reported in wild birds can be attributed to those regions. Compared to the same period in the previous epidemiological year (EFSA, ECDC and EURL, 2024), the number of official notifications to WOAH during the current reporting period was about half th(e number of outbreaks reported between 7 June and 5 September 2024 (60 vs 115 outbreaks).

In contrast to the previous reporting periods, HPAI A(H5N1) outbreaks were reported to WOAH not from West Africa but instead from Botswana, with one outbreak in a backyard farm in the northern part of the country (WOAH; Sunday Standard, online), and South Africa, with three outbreaks in chicken and duck in one very large and two medium-sized establishments (WOAH; Sunstar, online). Furthermore, the virus was detected in a black sparrowhawk and a Hartlaub’s gull in South Africa. The media also reported about the occurrence of HPAI in great white pelicans in the Western Cape area (Sunstar, online), and in a poultry establishment in the Volta region, Ghana (CediRates, online).

Compared to the previous reporting period (EFSA, ECDC and EURL, 2025a), the total number of HPAI virus detections in domestic and wild birds officially notified to WOAH from the USA and Canada decreased significantly from 59 to 2 for the USA (one in a large game bird and another one in a medium-sized poultry establishment) and from 12 to 4 for Canada. In addition to the outbreaks already reported to WOAH, the United States Department of Agriculture (USDA) also reported outbreaks in backyard farms, several large turkey establishments (fattening and breeding) and a live bird market between the end of August and beginning of September (USDA, online-a). Furthermore, the detections reported by the USDA in wild bird species have also declined from 90 to 79, although still much higher than the detections officially notified to WOAH. A total of 21 wild bird species were affected, most of which were common eiders (41%, 32/79), mallards (13%, 10/79) and black vultures (9%, 7/79) (USDA, online-b). In contrast to the previous reporting period, Canada only reported HPAI virus detections in wild birds to WOAH. The species affected at the four outbreak sites were Arctic tern, bald eagle, Canada goose, double-crested cormorant, European herring gull, great horned owl, ring-billed gull and snow goose (WOAH; CFIA, online). Furthermore, only media reported about an outbreak in a raven and a ring-billed gull in the North-West Territories (NNSL Media, online). In South America, the HPAI A(5) virus detections continued in Brazil and newly occurred in Argentina and Bolivia, accounting for most of the cases in the Americas. In Argentina, HPAI A(H5N1) and A(H5Nx) were detected in a large laying hen establishment and three backyard farms with chickens, turkeys and pheasants (WOAH; Primera Edicion, online; El Litoral, online). Brazil officially notified to WOAH eight new outbreaks in backyard farms, mainly in chickens, with increased mortality (WOAH; Diário do Comércio, online-a; AviSite, online). Several additional outbreaks in backyard farms in different regions of the country (Capital News, online; Diário do Comércio, online-b), as well as a zoo in Brasília (emu with neurological signs; R7 Brasília, online) and the BioParque nearby Rio de Janeiro (ducks, guineafowls, parakeets and peafowls; Extra Globo, online), were mentioned by the media. Brazil reported several cases in waterfowl species from different regions, e.g. black-bellied whistling duck and white-faced whistling duck, as well as one suspicion in a raptor species, a crested caracara (WOAH; Noticias UOL, online; Globo Rural, online; Itatiaia, online; Capital News, online-b). In Bolivia, the HPAI A(H5) outbreak officially notified to WOAH concerned a backyard farm.

In Antarctica, no new HPAI virus detections in birds were reported through the monitored communication channels (PASTAAF, online-a; SCAR, online) during the current reporting period. This may suggest a decrease in HPAI virus circulation in the region. However, it could also reflect reduced surveillance efforts during the winter season in the southern hemisphere.

Outbreaks of HPAI A(H5) continued to be officially reported to WOAH from Asia, but less establishments were affected in Japan (0 vs 85) and South Korea (3 vs 15), while an increased number of poultry establishments was affected in Cambodia (17 vs 3). In both South Korea and Cambodia, HPAI virus was detected in backyard farms and medium-sized poultry establishments. Taiwan reported an outbreak of HPAI A(H5N1) in an establishment keeping breeding and fattening geese (WOAH; CNA, online). In contrast to the previous reporting period, India officially reported to WOAH two outbreaks in large poultry establishments, while the media reported again about the infection of captive birds (black-necked ibis and painted stork) in a zoo (Amar Ujala, online). Altogether, 41 outbreaks in ten states occurred in 2025 according to media reports (United News of India, online; Hans India, online). Russia notified to WOAH the detection of A(H5N1) in a carrion crow on the far eastern Pacific coast opposite Sakhalin Island. Only the media reported about an HPAI outbreak in a medium-sized poultry establishment in Viet Nam selling chickens via a vehicle transporting also ducks (Voice of Vietnam, online).

A list of all wild bird species that were reported to WOAH as HPAI virus-infected from outside Europe between 7 June and 5 September 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 HPAI A(H5N1) viruses have been performed using FluMut (Giussani et al., 2025) 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 more than 1,500 clade 2.3.4.4b HPAI A(H5) viruses from 32 European countries including Russia and the Republic of Georgia have been characterised. Based on the genetic data available as of 11 September 2025, the vast majority (about 82%) of the sequenced viruses during the 2024–2025 epidemiological year belong to a single genotype, EA-2024-DI, which has been detected in wild (mainly Anseriformes) and domestic birds from 31 European countries, including Russia and the Republic of Georgia, representing the most widespread genotype in Europe. 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 (> 94% of the EA-2024-DI viruses) and widespread variant, identified all over Europe, in southern Europe – from Portugal to the North Caucasus region in Southern Russia and the Republic of Georgia – and in the north – from the United Kingdom/Ireland to Finland. Based on the data available so far (N < 40 from nine countries), during the current reporting period (June–August) a change in the frequency of the circulating genotypes was observed, with a decrease of EA-2024-DI.2 and an increase of detection of the gull-adapted genotypes EA-2022-BB and EA-2023-DT. EA-2024-DI.2 continues to circulate in Europe, mainly in domestic birds and wild Anseriformes in southwestern countries (France, Spain and Portugal), suggesting a southward spread of this genotype. In contrast, the majority of the viruses collected from different gull species in Belgium, France, Norway, Portugal, Spain and the United Kingdom belong to the gull-adapted genotypes EA-2022-BB and EA-2023-DT, which represented about 50% of the characterised viruses from the June–August period. In particular, genotype EA-2023-DT has been mainly circulating in gulls along the Atlantic coasts of the Iberian Peninsula, where it has completely replaced genotype EA-2022-BB, and France. Differently, genotype EA-2022-BB has been mainly detected in northwestern Europe, although the recent detection (August 2025) in gulls in Norway may indicate its northeastward spread. The decrease during the summer months of the genotype EA-2024-DI in favour of the genotypes EA-2022-BB and EA-2023-DT may be associated with the increase of the virus circulation in Laridae, which generally breed in colonies, and a decrease of virus detection in Anseriformes, most of which are solitary breeders. However, bias due to the limited number of available sequences for this time period cannot be excluded. Additionally, since June 2025, two distinct viruses, both emerging from reassortment between the EA-2022-BB genotype and LPAI viruses have been identified in the United Kingdom.

During the 2024-2025 epidemiological year, the A(H5N5) EA-2021-I genotype has been reported in Norway, the United Kingdom and Iceland, and sporadically in Belgium, the Netherlands, Finland and probably in Germany (partial genome). During the summer, this genotype persistently circulated in Norway and Finland. Of note, all the 2025 European A(H5N5) viruses belonging to this genotype contain a molecular marker of virus adaptation to mammals. Specifically, they fall within two distinct clusters, characterised by the PB2-E627K (Aggarwal et al., 2011) or by the PB2-E627V (Taft et al., 2015; Guo et al., 2025) substitution, circulating since November 2024 in Norway, the United Kingdom, Finland and Iceland. Of note, viruses of both clusters were identified at the end of 2024 also in Canada.

In poultry, the vast majority (about 90%) of the outbreaks reported in the 2024–2025 epidemiological year in Europe have been associated with genotype EA-2024-DI, with DI.2 being the most frequent (about 90% of the EA-2024-DI viruses). Few other outbreaks were caused by other genotypes, with the genotype EA-2022-BB associated with outbreaks reported in France and the United Kingdom. Of note is the identification of old genotypes (EA-2023-DA and EA-2020-AF) exclusively in poultry in Bulgaria (October 2024–May 2025) and Czechia (November 2024–May 2025), which were not detected in wild birds during the current epidemiological year in or outside other regions of Europe, suggesting undetected persistent circulation of these genotypes in an unknown ecological or domestic niche.

Outside Europe, genotype EA-2024-DI was detected in wild and domestic birds also in Israel (September 2024–January 2025). Besides EA-2024-DI, new genotypes originating from reassortment events between European genotypes and LPAI viruses were identified in this country. Of note, one of these novel genotypes identified in a wild bird in Israel has been detected in West Africa since summer 2024 (FAO, online).

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 (Du et al., 2018, 2021; Suttie et al., 2019; Pinto et al., 2023) have been identified as being associated with i) enhanced polymerase activity and replication in mammals or mammalian cells, ii) increased virulence, iii) increased/conferred resistance towards antiviral drugs, iv) increased in vitro binding to human-type receptors α2,6-SA, v) decreased antiviral response in ferrets, vi) evasion of human butyrophilin subfamily 3 member A3 (BTN3A3), and vii) disruption of the second sialic acid (SIA) binding site in the neuraminidase protein, with a frequency varying by 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 and 2023-2024), some of the mutations in the HA protein that have been shown by in vitro assays to gain human-type receptors recognition (i.e. S133A, S154N, T156A and H5 numbering), have been identified in the majority of the A(H5N1) viruses that have been circulating in Europe since October 2024, whereas others (i.e. V210I, T188I, E251K, S155N and Q192R) have only been sporadically observed (≤ 8 viruses). The impact of all these HA mutations on the biological characteristics of the circulating viruses is still unknown; however, in the vast majority of circulating A(H5Nx) strains none of the mutations 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, which indicates 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 due to the evasion of innate immunity and mammalian restriction factors or disruption of the second sialic acid binding site (2SBS).

All the currently circulating A(H5N5) viruses (genotype EA-2021-I) contain a deletion in the NA stalk region, which is a virulence determinant in chickens (Stech et al., 2015).

Mutations associated with 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 and rimantadine, NA and PA inhibitors (WHO, online-a) have been detected in approximately 0.5%, 1% and 0.4% of the analysed A(H5N1) viruses collected in Europe since October 2024, 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, K526R or 271A) (Suttie et al., 2019) have been detected in 65 European viruses collected from birds, more specifically in i) 43 A(H5N1) viruses collected from wild and domestic birds from nine different countries and ii) 22 A(H5N5) viruses (genotype EA-2021-I) collected from wild and domestic birds in the United Kingdom, Norway, Iceland and Finland. Based on the available data, in the 2024–2025 epidemiological year, a slightly increased frequency of detection of such mutations has been observed in birds, from about 2.5% in the 2023–2024 epidemiological year to about 4% in the current epidemiological year (up until August 2025). This may be explained by the spread in birds of viruses containing such mutations, as suggested by the identification in the phylogenetic tree of clusters of viruses sharing the same substitution. Some of these clusters include viruses collected from the same geographic area, the same species and time period, while others contain viruses collected from multiple countries and species, such as seven A(H5N1) viruses with PB2-701N collected from wild and domestic birds in Italy and Croatia between October and November 2024, and two clusters, composed of nine and 24 A(H5N5) viruses, with PB2-627V and PB2-627K, respectively, collected from birds and mammals in Northern Europe.

Of note, overall more than 20% of the European A(H5N5) viruses of the genotype EA-2021-I collected from birds in Europe since the 2020-2021 epidemiological year contain one of the PB2 mammalian adaptive markers, while this frequency drops to about 1% considering all the other viruses belonging to different genotypes.

2.2 HPAI virus detections in non-human mammals

From 7 June to 5 September 2025, HPAI A(H5N1) and A(H5N5) viruses were reported in wild, captive and domestic mammals both in and outside Europe. The data described in this report 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 4).

In Europe, no new HPAI A(H5N1) virus detections were reported in mammals during the current reporting period. However, Norway reported four HPAI A(H5N5) virus detections in Arctic fox pups on Svalbard (personal communication by Lars-Erik Rondestveit, Norwegian Food Safety Authority). In addition, the detection of anti-H5 antibodies in an ewe in Norway, as anticipated in the last report (EFSA, ECDC and EURL, 2025a), has now been fully described in a pre-print, highlighting the risk for spillover given the proximity between the sheep and a northern kittiwake colony in which an HPAI A(H5N1) outbreak had been reported 11 months earlier (Fosse et al., 2025). Lastly, several European countries actively reported the absence of HPAI viruses in mammals during the current reporting period: Denmark, Finland, Germany, Luxembourg, Slovakia, Spain, and Switzerland. Austria moreover shared detailed test results of analyses performed on mammals, all of which resulted negative: bat (27), fox (16), pig (11), wolf (5), badger (3), marten (3), horse (2) and cat (1) (personal communication by Sandra Revilla-Fernández, AGES).

Outside Europe, the number of dairy cattle farms reportedly affected by HPAI A(H5N1) virus in the USA rose by six to 1,079 in 17 states during the current reporting period, but the rate of new infections has gradually been stagnating (USDA, online-c). In terms of surveillance, the USDA Food Safety and Inspection Service (FSIS) extended its program for testing of dairy cow carcasses (started in September 2024) until 30 September 2025 (FSIS, online). New pieces of evidence have recently been published to better understand HPAI A(H5N1) virus shedding and transmission in dairy cattle. A first study showed that 10 TCID50 was sufficient to experimentally infect dairy cows via the intramammary route with manifestation of clinical signs (mastitis) as well as shedding of high viral titers in the milk, but the authors, after exposing two sentinels to two infected donor cows, were not successful in reproducing transmission from contaminated milking equipment and direct contact with infected cows in this experimental setting (Lee et al., 2025). Flies have also been suspected to mechanically transport HPAI A(H5N1) virus, as a full B3.13 genome could be retrieved from a fly (GISAID). Finally, a study reported the detection of HPAI A(H5N1) virus in dairy cattle farms in California, highlighting the presence of virus not only in bulk tank milk but also in milk parlour air, and to a lesser extent in wastewater and exhaled breath, suggesting spread may be possible via indirect exposure to air/water and not just milk (Campbell et al., 2025). The efficient cow-to-cow transmission in infected dairy farms contrasts with the difficulty of reproducing transmission events under experimental conditions (Lee et al., 2025).

In the USA, during the current reporting period, three additional domestic cats tested positive to HPAI A(H5N1) virus in New Jersey, Oregon and California, with the latter having consumed raw chicken-based cat food prior to illness (FDA, online). In addition, more information became available on an HPAI A(H5N1) outbreak in three cats from California between November and December 2024. These cats had consumed raw milk that was later recalled by the California Department of Public Health. Two of the cats succumbed to infection, while the third cat developed hind limb paresis and blindness but recovered after hospitalisation. Apart from representing the first proof of infectious virus being present in commercially sold raw milk, virus could also be isolated from the latter cat’s urine (CDC, online-a).

As regards wildlife, a black rat and a round-tailed ground squirrel were reported from Arizona, and a harbour seal from Maine. The USDA (USDA, online-d) retrospectively reported the detection of A(H5N1) virus in two raccoons (June/March 2025), two domestic cats and multiple unidentified skunks (February/March 2025) in Texas, a desert cottontail in Arizona (May 2025), a red fox in Colorado (May 2025), a red fox in New York (May 2025), a red fox in Virginia (March 2025), a striped skunk in Nevada (March 2025), a harbour seal in Massachusetts (February 2025), a muskrat and a raccoon in New York (January 2025), a domestic cat in California (December 2024), and a raccoon in Washington (November 2024). Canada retrospectively (from the beginning of 2025) reported the detection of A(H5N1) virus in red fox (3) and striped skunk (3), and of A(H5N5) virus in raccoon (1) and red fox (1). The muskrat and round-tailed ground squirrel represent new species that had not been reported positive before.

Table 4: 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
			Sheep (*Ovis aries*)	Norway, United Kingdom	GovUK (online-a,b) Fosse et al. (2025)
		Camelidae	Alpaca (*Lama pacos*)	United States of America	USDA (online-d)
		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)
			Gray fox (*Urocyon cinereoargenteus*)	United States of America	USDA
			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 Aleksandra Hari (AFSVSPP) Personal communication by Sandra Revilla-Fernández (AGES)
			South American bush dog (*Speothos venaticus venaticus*)	United Kingdom	WOAH
		Felidae	Bobcat (*Lynx rufus*)	United States of America	WOAH USDA
			Canadian 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*, Poland, South Korea, United States of America	WOAH USDA TF1 Info (online), Rijksoverheid (online) Personal communication by Ingeborg Mertens (FAVV)
			Cheetah (*Acinonyx jubatus*)	United States of America	USDA
			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	USDA The Times of India (online-a)

Virus	Animal (order, family, species)			Country	Reference
			Leopard cat (*Prionailurus bengalensis*)	South Korea	WOAH
			Lion (*Panthera leo*)	India, Peru, United States of America, Viet Nam	WOAH USDA Hindustan Times (online), The Times of India (online-b)
			Mountain lion (*Puma concolor*)	United States of America	WOAH USDA
			Serval (*Leptailurus serval*)	Bangladesh, United States of America	WOAH USDA
			Tiger (*Panthera tigris*)	India, United States of America, Viet Nam	WOAH USDA Hindustan Times (online), The Times of India (online-a,b)
		Mephitidae	Striped skunk (*Mephitis mephitis*)	Canada, United States of America	WOAH USDA
		Mustelidae	American marten (*Martes americana*)	United States of America	WOAH USDA
			American mink (*Neovison vison*)	Canada, Finland, Spain, United States of America	WOAH USDA
			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 USDA
			Long-tailed weasel (*Neogale frenata*)	United States of America	USDA
			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, Japan, United Kingdom, United States of America	WOAH USDA The Mainichi (online)
			Southern elephant seal (*Mirounga leonina*)	Argentina, South Georgia and the South Sandwich Islands, Possession Island	WOAH Bennison et al. (2024), Banyard et al. (2024), PASTAAF (online-b, c)
		Procyonidae	Raccoon (*Procyon lotor*)	Canada, Germany, United States of America	WOAH USDA
			South American coati (*Nasua nasua*)	Germany, Uruguay	WOAH
		Ursidae	American black bear (*Ursus americanus*)	Canada, United States of America	WOAH USDA
			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
			Muskrat (*Ondatra zibethicus*)	United States of America	USDA
			Prairie vole (*Microtus ochrogaster*)	United States of America	USDA
		Muridae	Black rat (*Rattus rattus*)	United States of America	USDA

Virus	Animal (order, family, species)			Country	Reference
			Brown rat (*Rattus norvegicus*)	Egypt, United States of America	USDA Kutkat et al. (2024)
			House mouse (*Mus musculus*)	United States of America	WOAH USDA
			House rat (*Rattus rattus*)	Egypt	Kutkat et al. (2024)
		Sciuridae	Abert's squirrel (*Sciurus aberti*)	United States of America	WOAH
			Eastern gray squirrel (*Sciurus carolinensis*)	United States of America	WOAH USDA
			Round-tailed ground squirrel (*Xerospermophilus tereticaudus*)	United States of America	USDA
A(H5N1) clade 2.3.2.1a	Carnivora	Felidae	Cat (*Felis catus*)	India	Raut et al. (2025) The Times of India (online-c)
A(H5N5) clade 2.3.4.4b	Carnivora	Canidae	Arctic fox (*Vulpes lagopus*)	Iceland, Norway	WOAH Personal communication by Brigitte Brugger (MAST, 2025) Personal communication by Lars-Erik Lund Rondestveit (Norwegian Food Safety Authority, 2025)
			Red fox (*Vulpes vulpes*)	Canada, Norway	WOAH
		Felidae	Bobcat (*Lynx rufus*)	Canada	WOAH
			Cat (*Felis catus*)	Canada, Iceland	WOAH Personal communication by Brigitte Brugger (MAST, 2025)
			Eurasian lynx (*Lynx lynx*)	Norway	Personal communication by Silje Granstad (Norwegian Veterinary Institute, 2025) and Lars-Erik Lund Rondestveit (Norwegian Food Safety Authority, 2025)
		Mephitidae	Striped skunk (*Mephitis mephitis*)	Canada	WOAH CFIA (online)
		Mustelidae	American mink (*Neovison vision*)	Iceland	Personal communication by Brigitte Brugger (MAST, 2025)
			Eurasian otter (*Lutra lutra*)	Norway	Personal communication by Silje Granstad (Norwegian Veterinary Institute, 2025) and Lars-Erik Lund Rondestveit (Norwegian Food Safety Authority, 2025)
			European pine marten (*Martes martes*)	Netherlands	Personal communication by Dennis Bol (NVWA, 2024)

Virus	Animal (order, family, species)			Country	Reference
		Phocidae	Grey seal (*Halichoerus grypus*)	United Kingdom	WOAH FarmingUK (online), GovUK (online-c)
			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)
	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, 2024)
			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).

2.2.1 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 (Giussani et al., 2025) with FluMutDB v6.4 mutation database (https://github.com/izsvenezie-virology/FluMutDB).

Since October 2024, the complete or partial genome sequences of 35 HPAI A(H5) viruses of clade 2.3.4.4b collected from seven distinct mammalian species (i.e. domestic cat, Eurasian badger, Eurasian lynx, Eurasian otter, grey seal, red fox and sheep) in ten different European countries have been characterised. As expected, the viruses collected from domestic (four cats and one sheep) and wild mammals (13 red foxes, two Eurasian otters) in Italy, Belgium, Poland, Slovenia, Germany, the Netherlands, the United Kingdom and Finland belong to the A(H5N1) genotype EA-2024-DI, which has been the most prevalent genotype circulating in birds in these geographic areas. The 15 A(H5N1) viruses from the wild mammals show the highest identity with the A(H5N1) viruses collected from wild birds in the same area, and two of them (one red fox from Italy and another one from Germany) differ from the most closely related viruses circulating in wild birds in the position 627 of the PB2, having the amino acid lysine (K) instead of glutamic acid (PB2-E627K substitution), a mutation that facilitates a more efficient virus replication in mammals

(Aggarwal et al., 2011). On the other hand, genetic data indicate that the domestic mammals – a sheep from England and domestic cats from Italy, Belgium and Poland – living on or near infected backyard (Poland, Italy and England) or commercial (Belgium) establishments where A(H5N1) had been confirmed were likely infected following exposure to poultry or virus-contaminated fomites. The virus sampled from the cat in Italy differs from the virus collected from the chicken from the same establishment in the mammalian-adaptive substitution PB2-E627K.

The viruses characterised from a domestic cat with outdoor access in Iceland as well as from a Eurasian lynx, a Eurasian otter, two red foxes in Norway and grey seals from a pinniped colony in Norfolk, England, belong to the A(H5N5) EA-2021-I genotype. Of note, the A(H5N5) viruses collected from the cat in Iceland and from the red foxes in Norway cluster within a group of viruses sampled from wild birds and mammals from different countries all sharing the PB2-E627V mammalian adaptive marker (Suttie et al., 2019; Guo et al., 2025). Similarly, the viruses collected from the grey seals in England and the Eurasian lynx in Norway cluster together within a group of viruses previously collected from wild birds in multiple European countries, all sharing the substitution PB2-E627K. Whether these mutations may have favoured the mammalian infection is still unknown.

At the end of March 2025, the novel genotype EA-2024-EE was identified for the first time in two mammals, a red fox and a Eurasian badger sampled in northern Germany. Both viruses possess the substitution PB2-E627K.

Overall, since October 2024 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).

Of note, about 88% of the European A(H5N5) viruses of the genotype EA-2021-I collected from mammals in Europe since the 2020–2021 epidemiological year contain one of the PB2 mammalian adaptive markers, while this frequency drops to about 42% considering all the European viruses collected from mammals of other genotypes.

Beside the clade 2.3.4.4b A(H5) viruses, a low pathogenic A(H7N1) virus was identified in a grey seal in England. The virus possesses the mammalian adaptive mutation E627K in the PB2 protein (GovUK, online-d).

2.3 Avian influenza virus infections in humans

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

Since 7 June and as of 8 September 2025, 19 new human cases of infection with avian influenza viruses have been reported from four countries: Bangladesh (n = 1), Cambodia (n = 11), China (n = 6) and India (n = 1). These infections were caused by three different subtypes: A(H5N1), A(H9N2) and A(H10N3) (Table 5). Most of the cases had exposure to poultry or live animal markets (Table 6).

Table 5: Globally reported cases or detections of avian influenza virus in humans, including virus subtypes reported in the last 12 months

	Cases reported 07.06.2025–08.09.2025			**Cases reported since first report**			
Subtype	**Cases reported**	**Deaths**	**Reporting countries**	**First report**	**Cases reported**	**Deaths**	**Reporting countries**
A(H5N1)	13	3	3	1997	1010*	474**	25
A(H9N2)	5	0	1	1998	173	2	10
A(H10N3)	1	0	1	2021	6	0	1

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

**Deaths reported since 2003 out of a total of 990 cases reported between 2003 and 8 September 2025. Mortality data are not available for cases reported prior to 2003.

Table 6: Identified exposure associated with human cases of avian influenza, reported globally 7 June–8 September 2025 by zoonotic influenza subtype

Subtype	**Reported exposure***	**Cases**
A(H5N1)	Poultry	12
	Not reported**	1
A(H9N2)	Poultry	5
A(H10N3)	Poultry	1

*Exposure to more than one animal species can be reported for cases.
**Not reported or publicly available.

Sequence data from GISAID's EpiFlu™ database submitted since the previous report was retrieved for eleven A(H5N1) strains representing cases in Bangladesh, Cambodia, India and Mexico. The strains were analysed phylogenetically in the context of strains described in the December 2024–March 2025 report (EFSA, ECDC and EURL, 2025b) and for mutation markers (Figure 10; Table 7). The cases were reported either during the current reporting period (7 June to 8 September 2025) or before. The virus from a case in Mexico (A/Mexico/DUR_InDRE_2292/2025) was described in the previous report (EFSA, ECDC and EURL, 2025a). The sequence was now accessible, and the results did not reveal any substitutions of significance. In addition, two strains collected on 16 December 2024 and 10 January 2025 from the same patient, a child in the USA without known exposure (Tobolowsky et al., 2025), clustered with previously described strains having a similar mutation profile. Interestingly, although no critical markers of mammalian adaptation were found, the strain from the second specimen had acquired several changes, such as E34G, A156V, K325R in HA (mature H5 numbering). Two strains of A(H9N2) from China were also retrieved and analysed (Figure 10; Table 7). The genotype of the A(H9N2) strains was assigned according to Fusaro et al. (2024).

Table 7: Strains included in phylogenetic and mutation analysis. Sequences include those deposited in GISAID's EpiFlu^{TM} database from 7 June 2025 to 8 September 2025

Isolate name	Subtype	Clade	Collection_date	Continent	Country	Markers
A/California/227/2024	A / H5N1	2.3.4.4b	2024-12-16	North America	United States of America	PB2:M631L,HA1-5:T195I, PA:K497R
A/California/227-1/2024	A / H5N1	2.3.4.4b	2025-01-10	North America	United States of America	PA:K497R,HA1-5:T195I,PB2:-, HA1-5:A156V,PB2:M631L
A/Bangladesh/Khulna/IEDCR-icddr,b-IC2/2025	A / H5N1	2.3.2.1a	2025-02-01	Asia	Bangladesh	PB2:L339T,M2:A30S, HA1-5:T195I,HA1-5:V210I, PB2:D9N
A/Mexico/DUR_InDRE_2292/2025	A / H5N1	2.3.4.4b	2025-02-18	North America	Mexico	PA:-,PB2:-
A/India/Udupi NIV/ 876 /2025	A / H5N1	2.3.2.1a	2025-05-03	Asia	India	
A/Cambodia/j05273701/2025	A / H5N1	2.3.2.1e	2025-05-26	Asia	Cambodia	NA-1:I396M,HA1-5:N154D, PA:-,PB2:-
A/Cambodia/NPH250408/2025	A / H5N1	2.3.2.1e	2025-06-12	Asia	Cambodia	PA:-,HA1-5:N154D,PB2:-
A/Cambodia/SVH250298/2025	A / H5N1	2.3.2.1e	2025-06-19	Asia	Cambodia	PA:-,HA1-5:N154D,NA-1:-,PB2:-
A/Cambodia/RL250003/2025	A / H5N1	2.3.2.1e	2025-06-29	Asia	Cambodia	M2:-,PB2:-,HA1-5:N154D, PA:-,NA-1:-
A/Cambodia/j07213708/2025	A / H5N1	2.3.2.1e	2025-07-21	Asia	Cambodia	PA:-,HA1-5:N154D,PB2:-
A/Cambodia/NIPH-25070671/2025	A / H5N1	2.3.2.1e	2025-07-21	Asia	Cambodia	HA1-5:-,PA:-,PB2:-
A/Cambodia/NIPH-RL250008/2025	A / H5N1	2.3.2.1e	2025-07-25	Asia	Cambodia	PA:-,HA1-5:N154D,PB2:-
A/Cambodia/NIPH-25080754/2025	A / H5N1	2.3.2.1e	2025-08-04	Asia	Cambodia	PA:-,HA1-5:N154D,PB2:-
A/Changsha/SR353/2025	A / H9N2	B4.7.2	2025-04-07	Asia	China	M2:I27A,NA-1:S369C,PB2:E627V
A/Changsha/992/2025	A / H9N2	B4.7.2	2025-04-21	Asia	China	M2:I27A,PA:-,PB2:-

-: insufficient segment

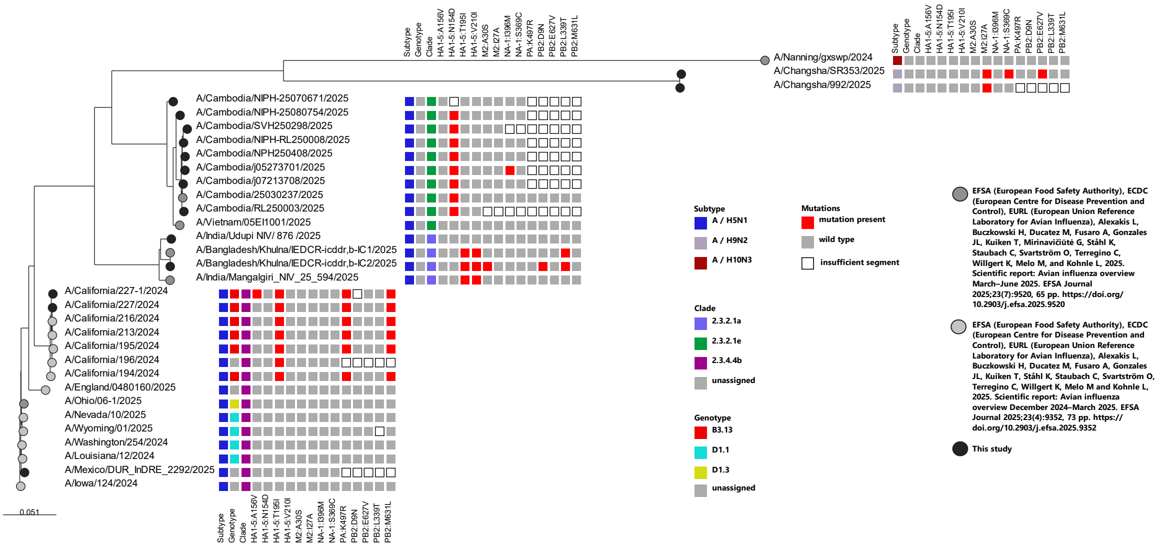


Figure 10: Phylogenetic tree from nucleotide alignment of the HA segment annotated with significant mutation marker findings from all segments (Microreact, online). Strains from the December 2024–March 2025 report (EFSA, ECDC and EURL, 2025b) are included and annotated accordingly

2.3.2 Human A(H5N1) cases

Since the first report of human infection with avian influenza A(H5N1) virus in 1997, a total of 1,010 cases, including 474 deaths, have been reported to the World Health Organization (WHO) from 24 countries (Figure 11).

Between 7 June and 8 September 2025, 13 new human cases of influenza A(H5N1) virus infection were reported from Cambodia (n = 11), India (n = 1) and Bangladesh (n = 1). Among these cases, three deaths were reported: two in Cambodia and one in India.

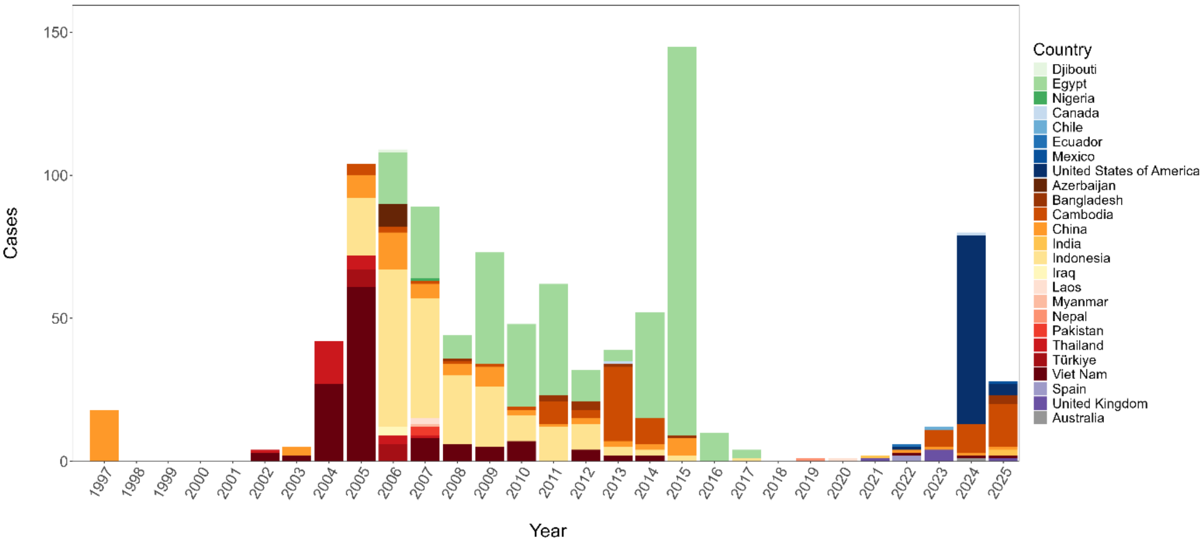


Figure 11: Distribution of reported human cases of A(H5N1) virus infection by year of onset or detection and reporting country from 1997 to 8 September 2025. The figure includes detections of A(H5N1) due to suspected environmental contamination reported in 2022 by Spain (2) and the USA (1), and in 2023 by the United Kingdom (three detections, one inconclusive). Human cases of A(H5) epidemiologically linked to A(H5N1) outbreaks at poultry and dairy cattle farms in the USA are included in the number of A(H5N1) cases.

Cambodia

Eleven human cases were reported from multiple provinces in Cambodia, including Siem Reap, Takeo, Svay Rieng, Kampot and Tbong Khmum (CHP, online-a, b, c, d, e, f, g; WHO, online-a, b, c, d). Five reported cases were children (age ranging from 19 months to 16 years), and the remaining cases were adults (age ranging from 26 to 65 years). When reported, symptoms included fever, cough and shortness of breath, but two cases were reported as asymptomatic. All cases had a history of contact with sick or dead backyard poultry. Two deaths were reported: a 19-month-old child from Siem Reap Province who developed severe respiratory illness, was hospitalised and died seven days after symptom onset, and a 52-year-old male from Takeo Province with a history of poultry exposure who died after developing acute respiratory symptoms.

The virus sequences from eight of these cases were available. All belonged to clade 2.3.2.1e and clustered closely on the same branch together with sequences from Cambodia and Viet Nam described in a previous report (EFSA, ECDC and EURL, 2025a). Several segments were not available, leaving the genotype unassigned and the presence of mammalian adaptations unclear, for example in PB2 (Table 7). All seven strains with sufficient HA segment had the mutation N154D, a substitution occurring in A(H7N9) strains propagated in the presence of monoclonal antibodies (Chang et al., 2023). Interestingly, this substitution is not present in the vast majority of closely-related non-human A(H5N1) isolates, but it was observed in previously analysed strains from Cambodia (EFSA, ECDC and EURL, 2025a) (Figure 10). It should be noted that this substitution has not been associated with phenotypic changes in A(H5N1) viruses to make it a relevant marker of mammalian adaptation in this subtype (Suttie et al., 2019). In addition, A/Cambodia/j05273701/2025 had the I396M substitution in the neuraminidase, which was observed in farmed minks, was associated with disruption of the second sialic acid binding site (2SBS) and may be a marker of mammalian adaptation (de Vries and de Haan, 2023).

India

One fatal infection was reported in a 41-year-old male from Karnataka state in India. The case was detected in May 2025. (CHP, online-h; WHO, online-a).

The sequenced virus A/India/Udupi NIV/876/2025 belonged to clade 2.3.2.1a, clustered with a virus from India described in a previous report (EFSA, ECDC and EURL, 2025a) (Figure 10) and did not contain any mutations of significance.

Bangladesh

One non-fatal human case was reported in Bangladesh (CHP, online-i; WHO, online-a). The patient, who had exposure to backyard poultry before onset of symptoms, has recovered following hospitalisation with influenza-like illness.

The sequence of the virus for this case was not available, but the virus 'A/Bangladesh/Khulna/IEDCR-icddr,b-IC2/2025' from a case with collection date 1 February 2025 was recently deposited in GISAID, belonging to clade 2.3.2.1a (EFSA, ECDC and EURL, 2025a). The virus carried the A30S substitution in M2, suggesting a reduced antiviral susceptibility (Suttie et al., 2019). Furthermore, the HA contained T195I, which was found in strains from dairy cattle outbreaks in USA and was phenotypically associated with increased receptor binding breadth (Good et al., 2024). The HA also contained the V210I, linked to increased virus binding to α2-6 and previously observed in bird sequences in Egypt when A(H5N1) human cases were detected (Watanabe et al., 2011). In PB2, the virus had acquired the L339T substitution which, although phenotypically associated with decreased polymerase activity in mice, is argued to increase viral fitness in hosts other than birds (Liu et al., 2013), as well as the D9N substitution that was associated with increased virulence in mice (Suttie et al., 2019).

2.3.3 Human A(H9N2) cases

Since the first report of human infection with avian influenza A(H9N2) virus in 1998, a total of 171 cases have been reported to WHO (Figure 12).

Between 7 June and 8 September 2025, five new human cases of influenza A(H9N2) virus infection were reported from China (CHP, online-b, h; WHO, online-e, f), including two adults (WHO, online-a). The cases were reported from Henan, Sichuan, Hunan, Guangdong and Hubei provinces. All cases had a history of exposure to poultry and all recovered. No epidemiological links were identified between the cases.

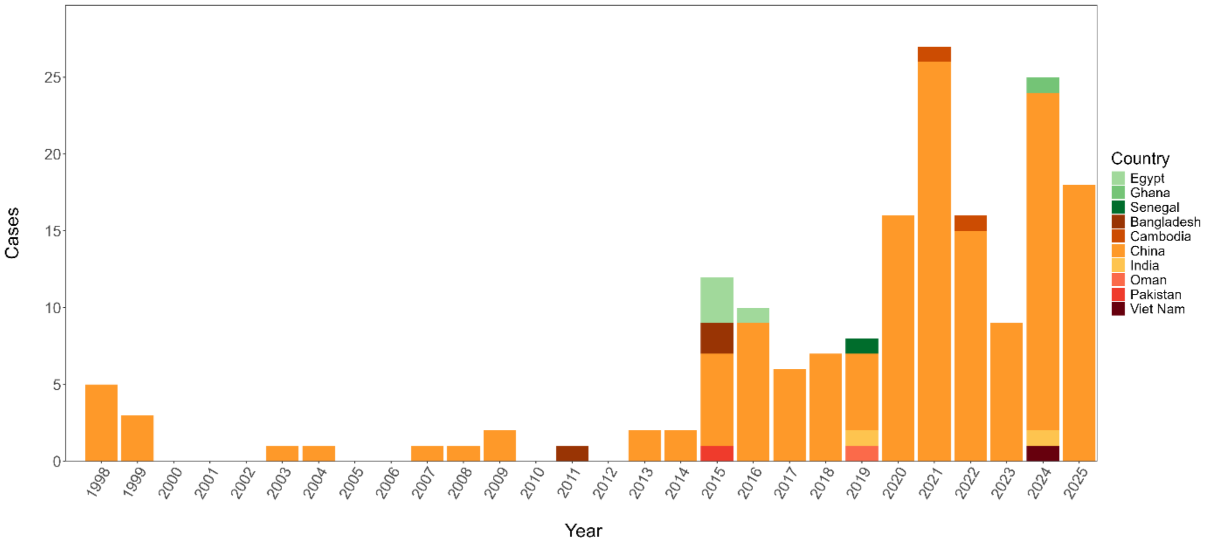


Figure 12: Distribution of reported human cases of A(H9N2) virus infection by year of onset, or detection and reporting country, from 1998 to 8 September 2025

No sequence was available for the cases reported between 7 June and 8 September. However, the data of two sequenced strains from cases detected in April 2025 displayed the presence of I27A in the M2 protein, which has been related to reduced M2-blocker antiviral susceptibility (Suttie et al., 2019). A/Changsha/SR353/2025 had also acquired S369C in the neuraminidase, which is associated with disruption of the second sialic acid binding site (2SBS) (Du et al., 2018), as well as E627V in the PB2 polymerase subunit, which is highlighted as a substitution that may increase virus zoonotic potential (EFSA AHAW Panel and ECDC, 2025). This mutation is very uncommon in birds but, as described earlier for H5 viruses, more common in mammals. The PB2 sequence length for the other strain, A/Changsha/992/2025, was insufficient.

2.3.4 Human A(H10N3) cases

Since the first report of human infection with avian influenza A(H10N3) virus in 2021, a total of six cases have been reported to WHO.

Between 7 June and 8 September 2025, one new human case of influenza A(H10N3) virus infection was reported from Shaanxi Province, China (CHP, online-b; WHO, online-e) (ref). The case was hospitalised with pneumonia and was reported to be improving at the time of notification. The patient had a history of exposure to backyard poultry. All identified contacts tested negative and are no longer being monitored.

No sequence was available for the virus responsible for this case.

2.3.5 Additional information relevant for public health and international risk assessments

The detection of human cases of A(H5N1) clade 2.3.4.4b linked to dairy cattle in the USA since April 2024 (Rolfes et al., 2025) has triggered numerous studies of relevance to public health. During the reporting period (7 June–8 September 2025), the results of several studies have been published.

The high proportion of mild or asymptomatic human cases reported in the USA in 2024−2025 prompted researchers to investigate the possibility of using new tools − i.e. artificial-intelligence-based large language models to review electronic health records − to support clinicians and improve identification of suspicious cases (Goodman et al., 2025).

Two independent studies looked at the capacity for antibodies raised against seasonal human influenza viruses to neutralise A(H5N1) viruses (Arroyave et al., 2025) (Zhang et al., 2025). Both studies used sera from vaccinated individuals, but different methodologies, and showed little to no virus neutralisation capacity, in agreement with the study by Stevenson-Legget et al. (2025) mentioned in the previous report.

Numerous studies used an animal model, including experiments in ferrets, to assess A(H5N1) clade 2.3.4.4b viruses in terms of pathogenicity and susceptibility to antivirals. Current results showed that these viruses have the potential to cause severe forms of the diseases in mammals (Andersen et al., 2025) (Bordes et al., 2025) (Guilfoyle et al., 2025), highlighting the need for continuous surveillance. Comparison of bovine and human A(H5N1) clade 2.3.4.4b viruses from the USA enabled the identification of specific substitutions in the PB2 polymerase subunit that were sufficient to explain the differences observed in replication capacity in human cells in vitro and in pathogenicity in mice in vivo (Bayoumi et al., 2025). On the other hand, two studies demonstrated that so far the A(H5N1) clade 2.3.4.4b viruses remain susceptible in vivo to the antivirals available in human medicine against influenza viruses (Kiso et al., 2025) (Fabrizio et al., 2025).

In early 2025, the European Food Safety Authority (EFSA) and the European Centre for Disease Prevention and Control (ECDC) provided recommendations to improve preparedness, prevention and control of zoonotic avian influenza viruses in the European Union (EFSA AHAW Panel and ECDC, 2025; ECDC and EFSA, 2025), including the need to increase awareness among healthcare professionals. A survey conducted in the USA in August 2024, when detection in dairy cattle and associated human cases were increasing, confirmed this need by showing that general practitioners were considered to be the most trusted source of information on avian influenza by the population (Piltch-Loeb et al., 2025).

Based on information currently available, the Food and Agriculture Organisation of the United Nations (FAO), WHO and WOAH released an update of their tripartite assessment of the public health risk posed by influenza A(H5N1) viruses on 28 July 2025 (FAO, WHO and WOAH, online). No changes were noted, and the risk of infection remains low for the general public and low-to-moderate for occupationally exposed individuals. In the latest 'Summary of influenza at the human-animal interface' (WHO, online-g) and the latest 'Avian influenza weekly update' (WHO, online-h), WHO has not changed its assessment of the risk to public health for the currently known avian influenza viruses, which is still considered to be low.

During the reporting period, the US Centers for Disease Control and Prevention (CDC) assessment of the risk to people from HPAI A(H5N1) viruses has not been updated and the risk remains low for the general population in the USA, but is considered moderate-to-high for populations in contact with potentially infected animals, contaminated surfaces or fluids (CDC, online-b). The assessment is still mainly driven by the likelihood of infection, with the impact of infection being generally ranked as moderate.

Similarly, during the reporting period, there has been no update of the UK Health Security Agency (UK HSA) risk assessment of HPAI A(H5) to the general public (still considered to be very low) (GovUK, online-e) or the guidance for the management of individuals exposed to influenza A(H5) infected animals (GovUK, online-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 animals in Europe to be 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 related to the transmission, prevalence, and characteristics of A(H5N1) viruses currently circulating in animals in Europe, as well as knowledge acquired from human cases of influenza A(H5N1) 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 the epidemiological year 2023−2024. Nevertheless, detections are still lower than those reported in 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) clade 2.3.4.4b 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) clade 2.3.4.4b viruses from mammals and 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 the human cases of A(H5N1) reported globally between 7 June and 8 September 2025, almost all cases (n = 12/13) had documented exposure to poultry.
- To date, there has been no evidence of sustained human-to-human transmission of influenza A(H5N1) viruses.

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 a case fatality estimated at 48% since 2003. However, this figure can only be based on reported cases and may be overestimated.
- The majority of human cases of infection with influenza A(H5N1) clade 2.3.4.4b reported in the USA since March 2024, and the human case reported in the United Kingdom in January 2025, experienced mild symptoms, such as conjunctivitis or mild respiratory illness. Between 7 June and 8 September 2025, no new cases of human infection with an A(H5N1) clade 2.3.4.4b virus were reported.

- During the same period, 13 cases of A(H5N1) of clade 2.3.2.1a and 2.3.2.1e were reported in Asia, with three of them being fatal.

- The reasons for the variation in outcome of infection with influenza A(H5N1) virus are 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). 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 for A(H5N1), and targeted surveillance of individuals exposed to infected animals is recommended (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 environments. 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

- As expected, HPAI continued to circulate in wild bird populations during the summer months despite the decreasing number of detections in the previous reporting period. Since 2020, there has been a consistent and persistent circulation of HPAI A(H5) viruses in wild bird populations in Europe. This situation is expected to continue in the coming years, with variations in outbreak numbers, geographic 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(H5) 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.

- After a marked decline in the size of the epidemic peak in both wild and domestic birds between 2022–2023 and 2023–2024, the 2024–2025 epidemic peak again increased in size. The persisting circulation during the current epidemiological year of some of the predominant genotypes emerging and circulating in Europe during the previous epidemiological years supports the conclusion that HPAI A(H5) virus is persisting in wild birds in Europe.

- High mortality rates in poultry observed at the time of detection or culling may suggest late detection and/or delayed culling. Late detection and/or delayed culling is considered a risk factor for secondary spread as well as for exposure to people in contact with affected poultry, in particular in larger poultry establishments where high morbidity and mortality rates are associated with very high viral contamination of the environment.

- HPAI virus detections in wild birds during the current reporting period involved mainly gull species in coastal locations from Portugal to Norway, predominantly infected with one of three genotypes: EA-2023-DT, EA-2022-BB or EA-2021-I. HPAI virus detections in gulls peaked in July, coinciding with their gathering at breeding colonies.
- Over the years, the pattern of HPAI infection in gulls and other Charadriiformes has changed. While gulls and other colony-breeding seabird species were among the species most affected by the circulation of HPAI A(H5Nx) viruses during spring and summer of previous epidemiological years, there have been few cases of infection and mass mortality events during this reporting period, potentially due to acquired flock immunity.
- Although the number of HPAI virus detections in wild waterfowl (swans, geese and ducks) during the current reporting period was very low, it is likely to increase in the coming reporting period as waterfowl start their autumn migration and aggregate in large numbers at wintering locations in Europe, with concomitant increased chance for spillover to establishments with captive birds and poultry.
- The five HPAI A(H5N5) virus detections in wild birds during the current reporting period suggest that this subtype is still persisting in wild birds in Europe, albeit it is confined to certain areas of northern Europe and associated with fewer detections than in the autumn and winter season of 2024.
- During the current reporting period, less outbreaks in domestic and wild birds were reported in North America compared to previous months, while most of the outbreaks outside Europe were reported in South America. These outbreaks were mainly located in the central and western part of the continent, most of them in Brazil. In Asia, Japan and South Korea officially notified less outbreaks to WOAH, while Cambodia recorded more than 15 outbreaks in poultry within a short period of time.
- In general, low numbers of wild birds infected with HPAI viruses have been reported from outside Europe via official notifications to WOAH, which may represent an underestimation of the actual numbers of infections.
- Currently available genetic data indicate that, starting from October 2024, EA-2024-DI has been the most frequent and widespread genotype in wild and domestic birds in Europe, detected in almost all the affected European countries and associated with about 90% of the poultry outbreaks. However, during the summer months, a rapid shift in the frequency of the circulating genotypes was observed, with an increased detection in wild birds of the gull-adapted genotypes EA-2022-BB and EA-2023-DT. This change may be associated to the increase of the virus circulation in Laridae species.
- Since October 2024, 65 HPAI A(H5) viruses containing markers of mammalian adaptation in the PB2 protein (E627K/V, K526R or D701N) were identified in wild and domestic birds collected from 11 European countries, suggesting that viruses with an enhanced capacity to replicate in mammalian cells can infect birds. Phylogenetic clustering indicates that wild birds can also occasionally spread such viruses across countries.

3.2 Mammals

- During the current reporting period, no new HPAI A(H5N1) virus detections were reported in mammals in Europe, which contrasts with previous reporting periods but is similar to the situation observed in spring/summer 2024. However, Norway reported the detection of HPAI A(H5N5) virus in four Arctic fox pups on Svalbard in late July.

- Two new mammal species, the muskrat and round-tailed ground squirrel, were detected positive for HPAI A(H5N1) virus in the USA in early 2025 (reported retrospectively during the current reporting period). A retrospective clinical case also highlighted the risk of raw milk consumption, with the description of HPAI A(H5N1) infection in cats in California in late 2024 due to the consumption of commercially sold raw milk with milk lot numbers that were tested positive for HPAI A(H5N1) virus and subsequently recalled by the California Department of Public Health (CDC, online-a).

- A recent pre-print investigated HPAI virus in environmental samples on an affected dairy farm in California and highlighted the presence of virus not only in bulk tank milk but also in milk parlour air, and to a lesser extent also in wastewater and exhaled breath, suggesting spread may also be possible via indirect exposure to air/water (Campbell et al., 2025). Flies were also recently suspected of being able to mechanically carry HPAI A(H5N1) virus (GISAID).

- Further research demonstrated that a very low dose of HPAI A(H5N1) virus (10 TCID50) was sufficient to efficiently infect dairy cows in an experimental setting (Lee et al., 2025).

- The vast majority of the characterised HPAI viruses collected from mammals 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 mammalian cells.

3.3 Humans

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

- In the reporting period from 7 June to 8 September 2025, of the 13 human cases of avian influenza A(H5N1) infection reported globally for which exposure data were available, 12 had documented exposure to poultry, with dead birds identified on the premises in some instances.

- 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

- The ongoing circulation of HPAI viruses in various species of migratory wild birds increases the risk of introduction of these viruses into European countries during winter migration. Consequently, adequate preparedness measures, such as strengthened biosecurity and housing orders, will be necessary to protect poultry and captive birds during the autumn and winter seasons.

- The low number of wild birds identified as infected with HPAI viruses, primarily detected due to the observation of sporadic mortality, highlights the need for implementation of effective surveillance systems in wild birds in order to ascertain the true extent to which these viruses are circulating in these species.

- 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 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. Specific training activities should be provided to poultry workers to raise their awareness of the risks associated with HPAI to improve early warning of suspect cases and their knowledge of biosecurity measures. To this end, EFSA has recently launched a comprehensive communication toolkit: https://www.efsa.europa.eu/en/no-bird-flu

- 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.

- 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 again reported – albeit in small numbers – in the current reporting period, should continue to be closely monitored in 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 (e.g. fur animals, ruminants, pigs and camelids), 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.

- In pigs, swine influenza viruses are widely circulating (Mena-Vasquez et al., 2025). Moreover, multiple spillover events of seasonal influenza viruses from human to swine and vice-versa have been frequently demonstrated. Pigs may play an important role in the emergence of new reassortant viruses with unknown biological properties and possible increased pandemic potential. The role of pigs as mixing vessel is well known; therefore, surveillance of avian influenza viruses in pigs in close contact with HPAI virus-infected poultry or wildlife is recommended.

- 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.
    - In some cases, the diagnostic performance of commercial ELISA kits have changed due to updates in the protocols recommended by the manufacturers. Comparison and assessment of the performance of protocols for different mammalian species is in progress. For this reason, it is advisable to rely on the EURL indications for serological surveillance of HPAI virus infections in mammals (contact details are available on the EURL website:

https://www.izsvenezie.com/reference-laboratories/avian-influenza-newcastle-disease/)

- 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 been reported in several countries in the world, including in the EU, stresses the importance of highly sensitive surveillance systems for early detection, and of the removal and destruction of infected poultry flocks as well as of contaminated animal 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 the prevention measures set out below:
    - 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 this 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 the working environment and tasks involved, routes of exposure and environmental factors.
    - Recommendations to the general public and those keeping backyard or commercial poultry 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. Where appropriate protective measures have not been taken, asymptomatic individuals exposed to animals with suspected or confirmed avian influenza virus infection 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 '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. 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 be performed using a risk-based approach, depending on the epidemiological situation in animal populations and 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 could be considered as a complementary preventive measure depending on context-specific considerations and based on national recommendations. While data on immune response induction are available, there is limited information on reduction in infection or onward transmission and on protection against severe clinical disease. At this stage, there is insufficient evidence to recommend zoonotic influenza vaccination in the whole of the EU/EEA (EFSA AHAW Panel and ECDC, 2025).
- The options for response are based on current available evidence, the epidemiological situation and the 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[10] 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[11] and Commission Delegated Regulation (EU) 2020/687[12]).

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[10] 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.

[11] 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.

[12] 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[13] and Articles 29 and 31 of Regulation (EC) No 178/2002[14], 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 June and 5 September 2025, 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 March to June 2025 (EFSA, ECDC and EURL, 2025a) and that might affect the interpretation of risks related to avian influenza introduction and/or spread in Europe.

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[13] 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.

[14] Regulation (EC) No 178/2002 of the European Parliament and of the Council of 28 January 2002 laying down the general principles and requirements of food law, establishing the European Food Safety Authority and laying down procedures in matters of food safety. OJ L 31, 1.2.2002, 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 June and 5 September 2025 and submitted by Member States and other European countries via ADIS, were taken into account. Data extraction was carried on 5 September 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.17199120

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 5 September 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 9 September 2025 to retrieve sequences from human cases of avian influenza reported since 7 June 2025. 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 approximately 1,700 gap-free nucleotides. A neighbour joining tree was produced by Jukes-Cantor nucleotide distance measurement with 100 bootstrap replicates. Blast searches were made directly on GISAID to retrieve approximately 100 non-human isolates for each distinct branch in the phylogenetic tree. Mutations were retrieved using FluMut (Github izsvenezie-virology, online-a, b) with the FluMutDB v6.4 mutation database (https://github.com/izsvenezie-virology/FluMutDB). Mutations found in less than 10% of the background sequences were considered significant. Clade and genotype information was retrieved from GISAID or assigned according to specified literature.

Annex A – Data on HPAI detections in wild birds

Annex A is available on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.17199120

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.17199120

Annex C – Acknowledgements

All genome sequences and associated metadata in this dataset are published in GISAID's EpiFlu^{TM} 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/gis8.250916cp, https://doi.org/10.55876/gis8.250916zn and https://doi.org/10.55876/gis8.250912eg.