SCIENTIFIC REPORT

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Avian influenza overview September–November 2025

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Abstract

Between 6 September and 28 November 2025, 2,896 highly pathogenic avian influenza (HPAI) A(H5) virus detections were reported in domestic (442) and wild (2,454) birds in 29 countries in Europe. The magnitude and geographical extent of these detections were unprecedented for this time of the year, particularly in wild birds. Large numbers of waterfowl were affected by the disease, and mass mortality of common cranes was observed along their migratory routes in Europe. Given the high levels of virus circulation in wild birds and the resulting high environmental contamination, most HPAI outbreaks in domestic birds were primary, with indirect contact with wild birds being the most likely source of infection. Among poultry species, turkeys were proportionally the most affected, and HPAI outbreaks were once again reported in vaccinated ducks. A slight increase in HPAI virus detections in mammals was noted among foxes and domestic cats in Europe, consistent with the increase in detections in wild birds. Between 9 September and 28 November 2025, 19 cases of avian influenza virus infection in humans, including two deaths, were reported in four countries: Cambodia (three A(H5N1) cases, one death), China (14 A(H9N2) cases), Mexico (one A(H5N2) case), and United States of America (USA) (one fatal A(H5N5) case). All of the A(H5) human cases (n = 5/5) reported exposure to poultry or a poultry environment prior to detection or onset of illness. The current high level of avian influenza virus in bird populations increases the risk of human exposure to infected animals. Nevertheless, given the widespread circulation of avian influenza viruses in animal populations, human infections remain rare. No instances of human-to-human transmission were documented during the reporting period. The risk posed by avian A(H5N1) clade 2.3.4.4b influenza viruses currently circulating in Europe remains low for the general public in the European Union/European Economic Area 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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[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 in wild birds, that occurred in and outside Europe between 6 September and 28 November 2025. In addition, HPAI virus detections in mammals up until 28 November 2025 and cases of avian influenza infection in humans between 9 September and 28 November 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 (TOR), 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 six and the current epidemiological year[4] by month of suspicion. For the current epidemiological year 2025–2026, starting on 1 October 2025, data reported are truncated on 28 November 2025.

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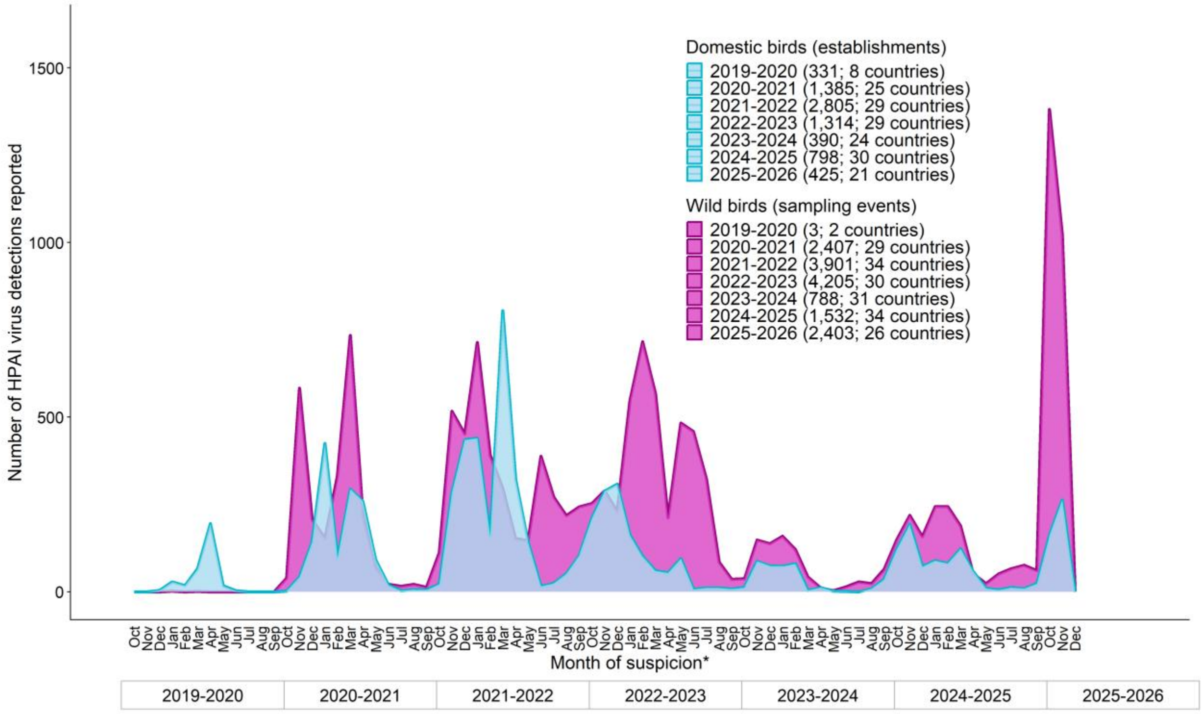
[2] According to Regulation (EU) 2016/429 of the European Parliament and of the Council of 9 March 2016, point (9), 'poultry' means birds that are reared or kept in captivity for: (a) the production of: (i) meat; (ii) eggs for consumption; (iii) other products; (b) restocking supplies of game birds; (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-WAHIS for the United Kingdom (excluding Northern Ireland) and ADNS/ADIS for the United Kingdom (Northern Ireland)[5].
Source: ADNS/ADIS and WOAH-WAHIS (data extraction carried out on 28 November 2025).

Figure 1: Distribution of the number of HPAI virus detections in wild birds (cumulative number n = 15,239) (pink) and establishments keeping domestic birds (cumulative n = 7,448) (blue) reported in Europe during seven epidemiological years by month of suspicion, from 1 October 2019 to 28 November 2025 (total n = 22,687)

Considering the current reporting period from 6 September to 28 November 2025, a total of 2,896 HPAI virus detections were reported, including 368 in poultry, 74 in captive birds, and 2,454 in wild birds, in 29 countries in Europe (Table 1, Figure 2).

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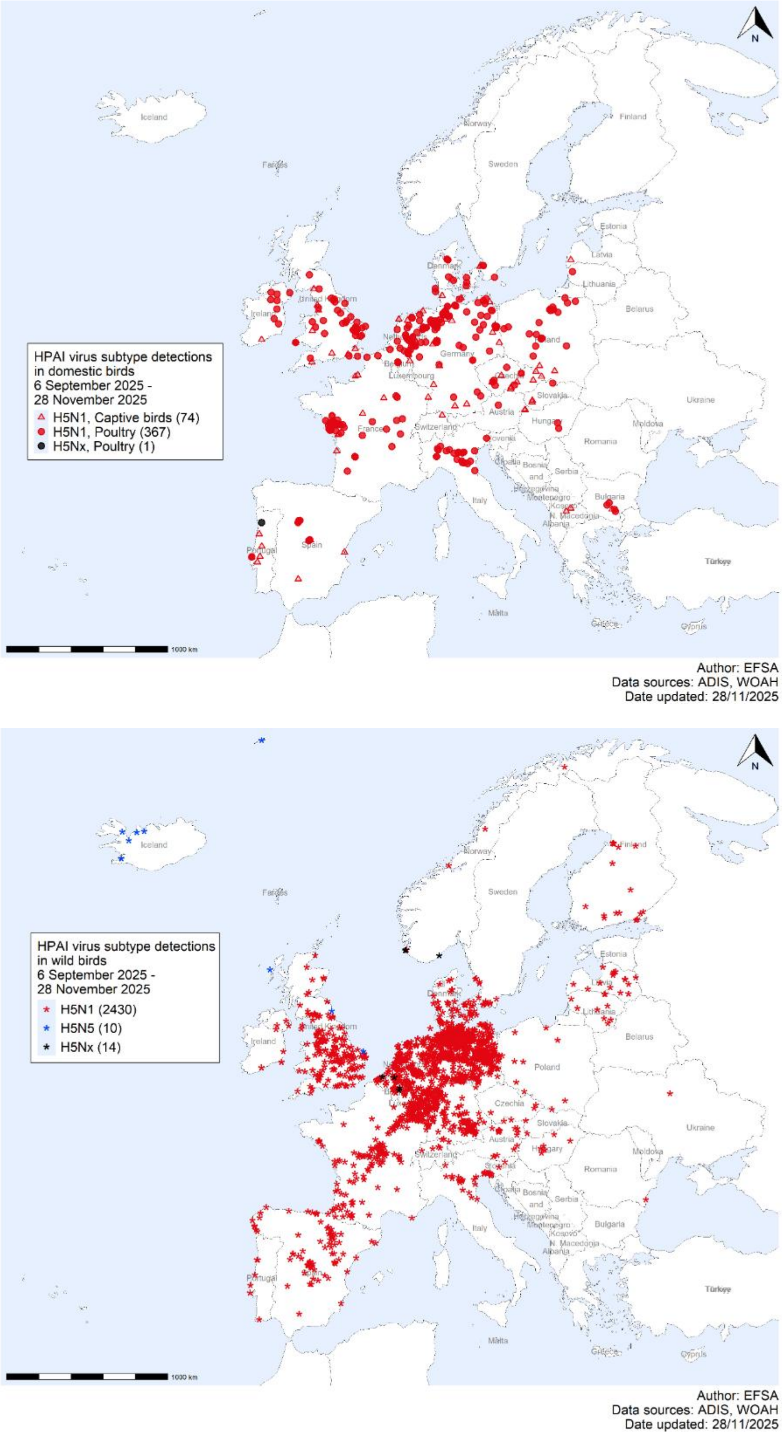
[5] In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Windsor Framework, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).

Table 1: Number of HPAI outbreaks reported in Europe by country, virus subtype and affected sub-population, from 6 September to 28 November 2025. Cumulative numbers since the start of the 2025–2026 epidemiological year are reported in parentheses (1 October to 28 November 2025)

Country	**Captive birds**	**Poultry**		**Wild birds**			**Total**
	A(H5N1)	**A(H5Nx)**	**A(H5N1)**	**A(H5Nx)**	**A(H5N1)**	**A(H5N5)**	
Austria	2 (2)	-	1 (1)	-	33 (28)	-	**36 (31)**
Belgium	1 (1)	-	9 (9)	5 (5)	81 (81)	-	**96 (96)**
Bulgaria	1 (1)	-	4 (4)	-	-	-	**5 (5)**
Czechia	9 (8)	-	9 (9)	-	3 (3)	-	**21 (20)**
Denmark	1 (1)	-	8 (8)	-	48 (47)	-	**57 (56)**
Finland	-	-	-	-	18 (18)	-	**18 (18)**
France	9 (9)	-	68 (68)	-	171 (167)	-	**248 (244)**
Germany	16 (16)	-	138 (134)	-	1,521 (1,516)	-	**1,675 (1,666)**
Hungary	-	-	2 (2)	-	8 (7)	-	**10 (9)**
Iceland	-	-	-	1 (0)	-	6 (1)	**7 (1)**
Ireland	1 (1)	-	4 (4)	-	6 (6)	-	**11 (11)**
Italy	-	-	24 (23)	-	45 (45)	-	**69 (68)**
Latvia	1 (1)	-	-	-	19 (18)	-	**20 (19)**
Lithuania	-	-	1 (1)	-	9 (9)	-	**10 (10)**
Luxembourg	-	-	-	-	19 (19)	-	**19 (19)**
Netherlands	6 (6)	-	19 (19)	-	122 (122)	-	**147 (147)**
North Macedonia	2 (2)	-	-	-	-	-	**2 (2)**
Norway	-	-	-	8 (8)	7 (4)	1 (0)	**16 (12)**
Poland	2 (2)	-	22 (18)	-	9 (8)	-	**33 (28)**
Portugal	5 (4)	1 (1)	2 (2)	-	8 (4)	-	**16 (11)**
Romania	-	-	-	-	2 (2)	-	**2 (2)**
Slovakia	2 (2)	-	1 (1)	-	3 (3)	-	**6 (6)**
Slovenia	-	-	-	-	5 (5)	-	**5 (5)**
Spain	4 (4)	-	9 (5)	-	81 (72)	-	**94 (81)**
Sweden	1 (1)	-	3 (3)	-	13 (11)	-	**17 (15)**
Switzerland	1 (1)	-	-	-	5 (5)	-	**6 (6)**
Ukraine	-	-	-	-	1 (1)	-	**1 (1)**
United Kingdom (excluding Northern Ireland)	10 (10)	-	39 (38)	-	190 (183)	3 (2)	**242 (233)**
United Kingdom (Northern Ireland)[*]	-	-	4 (3)	-	3 (3)	-	**7 (6)**
Total	**74 (72)**	**1 (1)**	**367 (352)**	**14 (13)**	**2,430 (2,387)**	**10 (3)**	**2,896 (2,828)**

[*] 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: 28/11/2025

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Date updated: 28/11/2025

*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-WAHIS, whereas United Kingdom (Northern Ireland)[6] data are from ADIS.
Source: ADIS, EFSA and WOAH-WAHIS (data extraction carried out on 28 November 2025).

Figure 2: Geographic distribution, based on available geocoordinates, of HPAI virus detections in poultry and captive birds (442) (upper panel), and in wild birds (2,454) (lower panel), reported by virus subtype in Europe from 6 September to 28 November 2025

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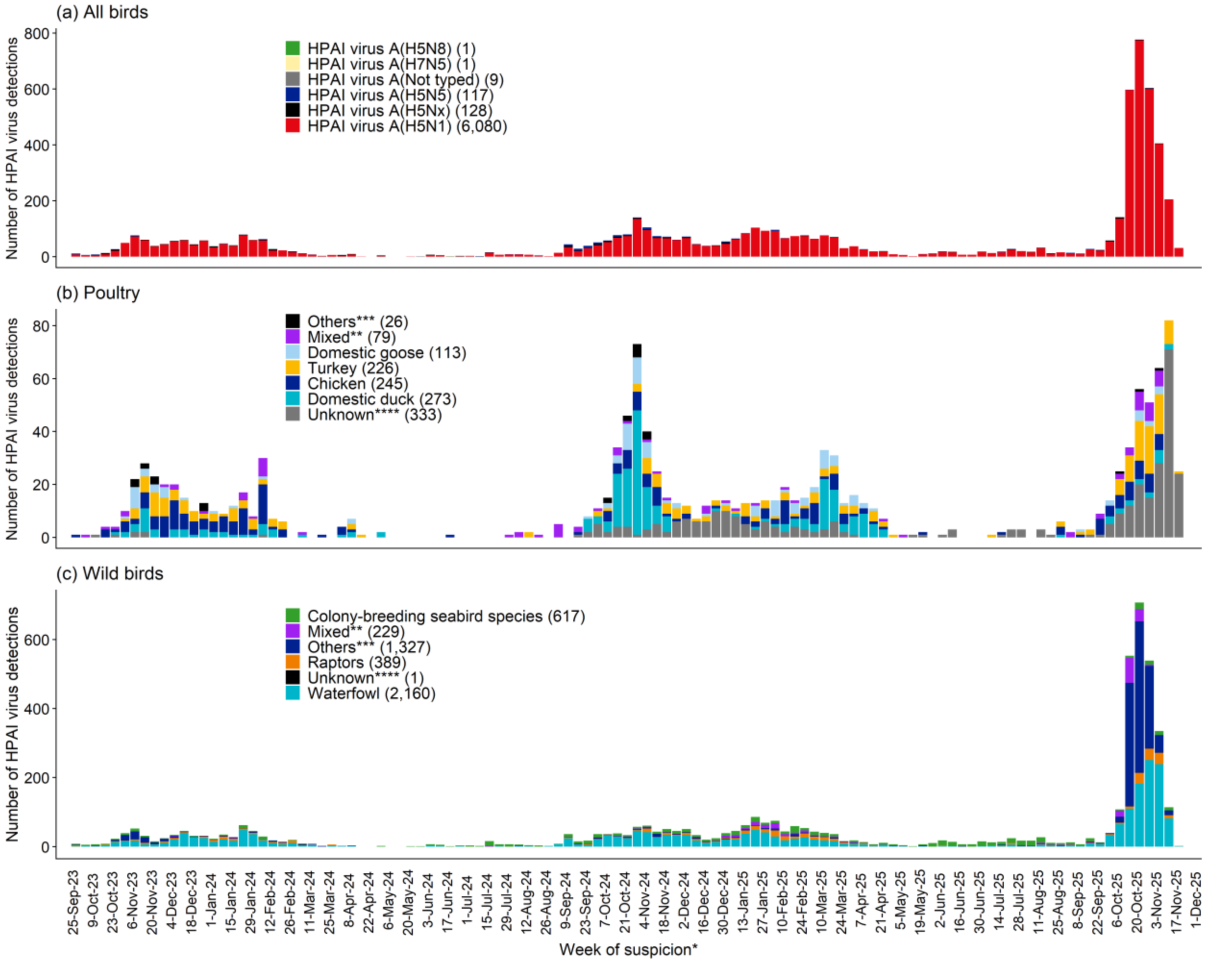
[6] In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Windsor Framework, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).

After a mild increase during the previous reporting period (7 June to 5 September 2025), there was a steep increase in the number HPAI virus detections in both wild and domestic birds during the current reporting period (6 September to 28 November 2025). Compared to the same dates in previous years, for wild birds, this number was six times higher than in 2024, 12 times higher than in 2023, three times higher than in 2022, and four times higher than in 2021 (Figure 1, Table 1). For domestic birds, this number was similar to that in 2024 and 2022, but five times higher than in 2023, and almost twice as high as in 2021. Such a sharp increase and high number of HPAI virus detections, particularly in wild birds, is unprecedented at this time of the year and has not been observed since at least 2016 (EFSA and EURL, 2025). The geographical extent of HPAI outbreaks in domestic birds (Figure 2, upper panel) has likely been a consequence of high levels of virus circulation in wild birds (Figure 2, lower panel) and the resulting high contamination of the environment. Observations from previous epidemiological years indicate a correlation between HPAI virus detections in waterfowl and incursions into domestic birds.

During the current reporting period, HPAI A(H5N1) virus detections in domestic birds were found in large parts of Europe, roughly forming a quadrilateral with corners in the northwest (Northern Ireland), northeast (Latvia), southeast (Bulgaria) and southwest (Portugal) (Figure 2, upper panel). Most HPAI A(H5) virus detections in wild birds were reported in a broad band across Europe, from Lithuania in the northeast to Portugal in the southwest, with rarely any detections in southeast Europe, and only a few in Scandinavia and Iceland. While most HPAI virus detections were due to A(H5N1), there were a few A(H5N5) virus detections in wild birds in Iceland (6), the United Kingdom (excluding Northern Ireland) (3), and Norway (1) (Table 1, Figure 2, Figure 3).



*If the date of suspicion was not available, the date of confirmation was used to assign the week of suspicion.
**'Mixed' refers to outbreaks in which multiple species or categories were involved.
***'Others' groups all other affected categories that are not indicated in the legend.
****'Unknown' refers to affected categories that were not further specified during reporting.
Source: ADNS/ADIS, EFSA and WOAH-WAHIS (data extraction carried out on 28 November 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 28 November 2025

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

Poultry

Between 6 September and 28 November 2025, 368 HPAI outbreaks in poultry were reported in 19 countries in Europe: Germany (138), France (68), United Kingdom (excluding Northern Ireland) (39), Italy (24), Poland (22), Netherlands (19), Belgium (9), Czechia (9), Spain (9), Denmark (8), Bulgaria (4), Ireland (4), United Kingdom (Northern Ireland)[8] (4), Portugal (3), Sweden (3), Hungary (2), Austria (1), Lithuania (1), and Slovakia (1) (Table 1, Figure 2, Figure 4).

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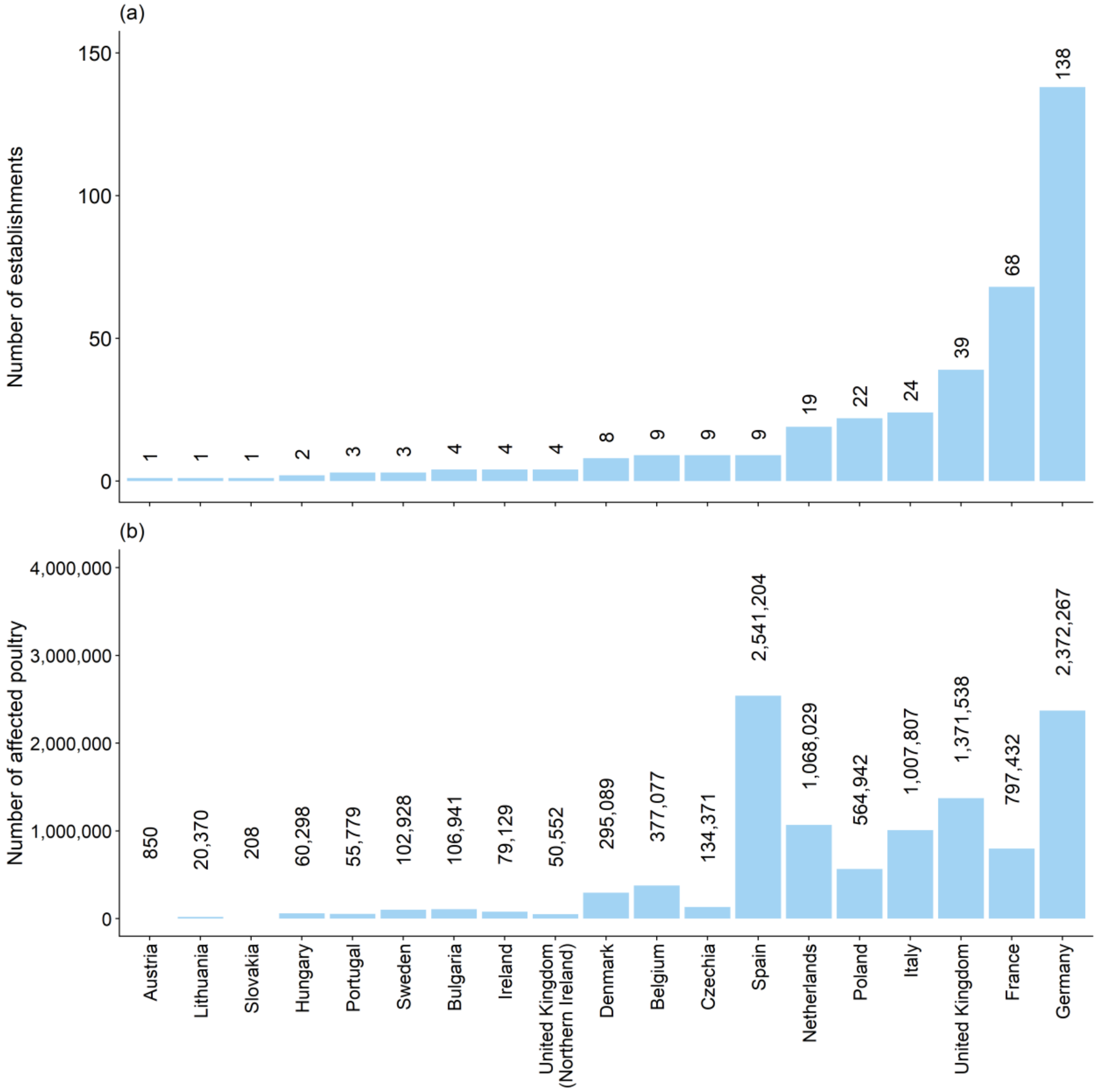
[7] http://hpai.efsa.aus.vet/

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



United Kingdom (excluding Northern Ireland) data are from WOAH-WAHIS, whereas United Kingdom (Northern Ireland)[9] data are from ADIS.

Figure 4: Number of HPAI-affected establishments (368) (a) and number of poultry heads in the HPAI-affected establishments (11,006,811) (b) per country in Europe between 6 September and 28 November 2025 (countries are ranked according to the number of outbreaks)

HPAI A(H5N1) viruses were detected in all but one (99.7%, 367/368) HPAI outbreaks in poultry, whereas the neuraminidase gene was not identified for one A(H5Nx) outbreak in Portugal. This compares to a total of 272 A(H5N1) and one A(H5N5) outbreaks during the same period in 2024, when 57% (155/273) of the HPAI outbreaks in poultry were secondary (i.e. farm-to-farm transmission). In contrast, during the current reporting period, 80.7% (297/368) of the HPAI outbreaks in poultry were classified as primary, 8.7% (32/368) as secondary, and for the remaining 39 outbreaks (10.6%), all from the United

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Kingdom (excluding Northern Ireland), this information was not available. Germany accounted for 37.5% (138/368) of the outbreaks in poultry, with 2,372,267 poultry heads involved, which represent approximately 23.7% of the total number of poultry heads affected. In comparison, Spain accounted for 2.4% (9/368) of the outbreaks in poultry, but a larger number of poultry heads were involved (2,541,204), corresponding to 25.4% of the total number of poultry heads affected during this period (Figure 4).

During the current reporting period, 'turkeys' were the most affected poultry category, accounting for 20.9% of HPAI outbreaks (77/368), followed by chickens (11.7%, 43/368), 'domestic ducks' (4.9%, 18/368), 'domestic geese' (3.3%, 12/368), and other poultry categories (0.8%, 3/368). Mixed-species establishments represented 7.9% of the outbreaks (29/368). For the remaining 186 establishments (50.5%), no information on the poultry species present was reported. These 186 establishments were distributed across several countries, with the highest numbers coming from France (68), the United Kingdom (excluding Northern Ireland) (39), and Italy (24).

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 6 September to 28 November 2025, 368 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 182 outbreaks (49.5%, 182/368), reported from Belgium, Czechia, Denmark, Germany, Hungary, Ireland, Lithuania, Netherlands, Poland, Spain, Sweden, and the United Kingdom (Northern Ireland)[10] (Annex B). Among these, 92.3% (168/182) were reported as primary and 7.7% (14/182) as secondary. Among the primary outbreaks for which additional data were available, in 88.7% of cases (149/168) indirect contact with wild birds was identified as the most likely source of introduction, whereas the source remained unknown for another 10.7% (18/168). In one outbreak (0.6%), direct contact with wild birds was identified as the most likely source of introduction. Among the secondary outbreaks for which additional data were available, indirect contact with poultry was identified as the most likely source of introduction for 50% (7/14) of the outbreaks, according to the information provided by Czechia and Germany, and indirect contact with wild birds was identified as the most likely source of introduction for another 50% (7/14), as reported by Czechia, Poland, and Spain.

For the remaining 186 outbreaks (50.6%) no additional data were provided, either because they occurred in countries from which no additional data are reported, or they occurred too close to the publication of this report. Therefore, only a short summary of these outbreaks will be provided in this report, while additional data will only be collected during the following round and included in Annex B of the following report.

Austria

During the current reporting period from 6 September to 28 November 2025, a single A(H5N1) outbreak in poultry was reported in Austria via ADIS. No additional data were collected from the country to complement the information available in ADIS, as the outbreak occurred too close to the publication of this report. On 19 November, the primary

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outbreak was detected in an establishment for which no information on the poultry species present (n = 850) was available via ADIS. According to the media, the outbreak concerned an establishment keeping domestic geese that had outdoor access (Outbreak News, online-a). Both clinical signs and mortality were observed at the time of detection.

Belgium

During the current reporting period from 6 September to 28 November 2025, nine A(H5N1) outbreaks in poultry were reported in Belgium via ADIS. Additional data were collected and provided by the reporting country for two of these outbreaks (Annex B), while the remaining seven occurred too close to the publication of this report. Among all outbreaks, 89% (8/9) were classified as primary and 11% (1/9) as secondary. Clinical signs were documented in 89% (8/9) of the outbreaks, for which a median mortality of 0.42% (range: 0.05–6.19%) was reported. In total, 377,077 poultry heads were affected across the nine establishments. Information on the poultry species present was only available for two (22%, 2/9) of these outbreaks, affecting one establishment with mixed species (broilers and turkeys for fattening) and one establishment with broilers, both without outdoor access. In both cases, the most likely source of introduction was indirect contact with wild birds, and a total of four people were reported as exposed. No further information was available for the remaining 78% (7/9) of the outbreaks, but according to ADIS, one of these establishments involved mulard ducks.

Bulgaria

During the current reporting period from 6 September to 28 November 2025, four primary A(H5N1) outbreaks in poultry were reported in Bulgaria via ADIS. No additional data to complement the information in ADIS were provided by the country. These four outbreaks affected a total of 106,941 poultry heads and, according to ADIS, two of them involved laying hens (n = 25,007 and n = 32,984), whereas one was detected in an establishment keeping mulard ducks (n = 9,000). No information on the poultry species present was available for the most recent outbreak. Mortality (median: 0.77%, range: 0.33–11.0%) and clinical signs were observed in all four establishments.

Czechia

During the current reporting period from 6 September to 28 November 2025, nine A(H5N1) outbreaks in poultry were reported in Czechia via ADIS. Additional data were collected and provided by the reporting country for seven of these outbreaks (Annex B), while the remaining two occurred too close to the publication of this report. Among all outbreaks, 78% (7/9) were classified as primary and 22% (2/9) as secondary. Most affected establishments kept domestic ducks for fattening (56%, 5/9), followed by domestic ducks (11%, 1/9) and chickens (11%, 1/9) for breeding. None of these seven establishments provided outdoor access, and the total number of exposed people was 228. No information on the poultry species present, outdoor access, or the number of exposed people was available for the remaining two outbreaks (22%, 2/9). Mortality, with a median value of 0.75% (range: 0–34.51%), was observed in all outbreaks, whereas clinical signs were documented in seven (78%, 7/9). These included neurological signs in domestic ducks (European Commission, online). In total, 134,371 poultry heads were affected across the nine establishments. For 67% (6/9) of the outbreaks, indirect contact with wild birds was identified as the most likely source of introduction, one outbreak (11%, 1/9) was linked to indirect contact with poultry, and for the remaining 22% (2/9), no information on the possible source was available. Epidemiological investigations suggest a link between these poultry outbreaks and a major nocturnal wild bird migration detected on 13–14 October by meteorological radar. Poultry outbreaks first appeared three weeks later, supporting this association (European Commission, online).

Denmark

During the current reporting period from 6 September to 28 November 2025, eight primary A(H5N1) outbreaks in poultry were reported in Denmark via ADIS. Additional data were collected and provided by the reporting country for seven of these outbreaks (Annex B), while the eighth occurred too close to the publication of this report. Among the seven outbreaks with additional data available, all occurred in commercial establishments keeping fattening turkeys (43%, 3/7), laying hens (29%, 2/7), pheasants for breeding (14%, 1/7), and mixed species (laying hens and Muscovy ducks) (14%, 1/7). Outdoor access was available for the two latter. Mortality (median: 1.34%, range: 0.11–62.74%) was reported in all outbreaks. Other clinical signs observed included neurological signs (e.g. ataxia and torticollis), respiratory distress and discharge from the airways, cyanosis and oedema of combs/wattles, and diarrhea. In total, 295,089 poultry heads were affected across the eight establishments. Among the seven outbreaks with additional data available, indirect contact with wild birds was identified as the most likely source of introduction for 57% (4/7), while information on the source was not available for the remaining 43% (3/7). The number of exposed people was available for two outbreaks and comprised 126 individuals.

France

During the current reporting period from 6 September to 28 November 2025, 68 A(H5N1) outbreaks in poultry were reported in France via ADIS. No additional data to complement the information in ADIS were provided by the country. Most outbreaks (75%, 51/68) occurred in the Pays-de-la-Loire region, west France, near or in areas with high densities of poultry establishments. Among all outbreaks, 85.3% (58/68) were classified as primary and 14.7% (10/68) as secondary. Preliminary full genome sequence analyses of the detected HPAI viruses also suggest that there is a dual epidemiologic pattern involving several independent virus introductions in poultry establishments (most probably from infected wild bird populations) and some instances of possibly extended transmission events between establishments, when introduction occurred in areas with high densities of poultry establishments. No additional information on the production type or poultry species present was reported, but according to ADIS, these outbreaks involved establishments keeping ducks (36; 31 of which had been vaccinated), turkeys (12), chickens (6), geese (2), pheasants (2), and quails (1). In addition, eight establishments kept mixed species. Clinical signs and mortality were reported in 71% (48/68) and 65% (44/68) of outbreaks, respectively, with mortality ranging from 0.01% to 65.42% (median: 0.06%).

Germany

During the current reporting period from 6 September to 28 November 2025, 138 A(H5N1) outbreaks in poultry were reported in Germany via ADIS. Additional data were collected and provided by the reporting country for 118 of these outbreaks (Annex B), while the remaining 20 occurred too close to the publication of this report. Among all outbreaks, 92% (127/138) were classified as primary and 8% (11/138) as secondary. A total of 72.5% of the outbreaks (100/138) occurred in commercial single-species establishments, including turkeys for fattening (37.7%, 52/138), laying hens (9.4%, 13/138), geese for fattening (4.3%, 6/138), turkeys for breeding (4.4%, 6/138), broilers (3.6%, 5/138), ducks for fattening (2.9%, 4/138), ducks for breeding (2.2%, 3/138), geese for breeding (2.2%, 3/138), and chickens for breeding (1.4%, 2/138). Mixed-species establishments accounted for 17.4% of the outbreaks (24/138), of which 91.7% (22/24) were commercial and 8.3% (2/24) non-commercial. For 14.5% of the outbreaks (20/138), no information on the production type or poultry species present was available. Outdoor access of poultry was reported in 19.6% (27/138) of the establishments, mainly related to laying hens at the beginning of the current reporting period. Many of the affected establishments keeping turkeys for fattening were located in an area with an extremely high density of poultry production. Mortality was observed in almost all outbreaks (98.6%, 136/138), with a median value of 0.19% (range: 0–85.26%). Clinical signs were documented in 44.9% (62/138) of the outbreaks, while in 40.6% (56/138) of the outbreaks no clinical signs were reported, and for the remaining 14.5% (20/138) no information was available. In total, 2,372,267 poultry heads were affected across the 138 establishments. For primary outbreaks, indirect contact with wild birds was identified as the most likely source of introduction for 88.2% (112/127), while no information was available for the remaining 11.8% (15/127). For secondary outbreaks, indirect contact with poultry was reported as the most likely source for 54.5% (6/11), while no information was available for the remaining 45.5% (5/11).

Hungary

During the current reporting period from 6 September to 28 November 2025, two primary A(H5N1) outbreaks in poultry were reported in Hungary via ADIS. Additional data were collected and provided by the reporting country for both outbreaks (Annex B). The first outbreak was confirmed on 28 October in a commercial establishment keeping ducks for fattening (n = 19,700), where mortality (5.1%) was observed and clinical signs were reported. Eighteen people were reported as exposed. The second outbreak was confirmed on 11 November in a commercial establishment keeping turkeys for fattening (n = 40,598), where mortality (2.95%) was observed and clinical signs were reported. Twenty-three people were reported as exposed.

Ireland

During the current reporting period from 6 September to 28 November 2025, four primary A(H5N1) outbreaks in poultry were reported in Ireland via ADIS. Additional data were collected and provided by the reporting country for three of these outbreaks (Annex B), while the fourth occurred too close to the publication of this report. All outbreaks occurred in commercial establishments and, among the three outbreaks with additional data available, two occurred in mixed-species establishments: one keeping domestic geese and turkeys for fattening (n = 3,252), and one keeping laying hens and turkeys for fattening (n = 29,030). In both cases, the different species were not co-mingling. Outdoor access was only provided to some of the birds in the latter. A third outbreak occurred in a single-species establishment keeping turkeys for fattening (n = 7,320). Mortality was reported in all outbreaks, with a median value of 14.92% (range: 0.78–96.24%), and a varied range of clinical signs were documented: neurological signs (ataxia/incoordination, paralysis), respiratory sings (sneezing, gasping, cyanosis), digestive (diarrhoea, decreased feed and water consumption), and others such as depression. In total, 79,129 poultry heads were affected across the four establishments. Information on the number of exposed people was available for three outbreaks, with a total of 52 individuals reported.

Italy

During the current reporting period from 6 September to 28 November 2025, 24 A(H5N1) outbreaks in poultry were reported in Italy via ADIS. No additional data to complement the information in ADIS were provided by the country. Among all outbreaks, 96% (23/24) were classified as primary and 4% (1/24) as secondary. No additional information on the production type or poultry species present was reported, but according to ADIS, these outbreaks involved turkeys for fattening (10), laying hens (3), broilers (3), chickens for breeding (2), Muscovy ducks (1), and pheasants (1). In addition, four mixed-species establishments were reportedly affected. Mortality, with a median value of 0.81% (range: 0.01–100%), and clinical signs were reported in all outbreaks, where birds frequently exhibited sensory depression as well as nervous and enteric signs. In total, 1,007,807 poultry heads were affected across the 24 establishments.

Lithuania

During the current reporting period from 6 September to 28 November 2025, a single A(H5N1) outbreak in poultry was reported in Lithuania via ADIS, for which additional data were collected and provided by the reporting country (Annex B). The primary outbreak was confirmed on 14 October in a commercial establishment keeping fattening turkeys with outdoor access (n = 20,370), where mortality (26.4%) but no clinical signs were observed, and 11 people were reported as exposed.

Netherlands

During the current reporting period from 6 September to 28 November 2025, 19 A(H5N1) outbreaks in poultry were reported in the Netherlands via ADIS. Two of the 19 A(H5N1) outbreaks reported to ADIS on or before 28 November 2025 were later withdrawn, as they referred to outbreaks in captive birds. Additional data were collected and provided by the reporting country for seven of these outbreaks (Annex B), while the remaining ten occurred too close to the publication of this report. Among the seven outbreaks with additional data available, all occurred in commercial establishments keeping chickens for breeding (43%, 3/7), laying hens (43%, 3/7), and pheasants for fattening (14%, 1/7). Apart from the latter, none of these establishments provided outdoor access. According to ADIS, nine other outbreaks occurred in laying hens (5), broilers (4), and in a mixed-species establishment keeping both laying and rearing hens (1). Mortality was reported in 16 outbreaks, with a median value of 0.09% (range: 0.01–11.65%), and clinical signs were documented in all 17 affected establishments.

Poland

During the current reporting period from 6 September to 28 November 2025, 22 A(H5N1) outbreaks in poultry were reported in Poland via ADIS. Additional data were collected and provided by the reporting country for 20 of these outbreaks (Annex B), while the remaining two occurred too close to the publication of this report. Among all outbreaks, 86.4% (19/22) were classified as primary and 13.6% (3/22) as secondary. The outbreaks occurred in commercial establishments keeping single species: turkeys for fattening (36%, 8/22), ducks for fattening (18%, 4/22), geese for fattening (14%, 3/22), turkeys for breeding (14%, 3/22), laying hens (4.5%, 1/22), and broilers (4.5%, 1/22). For two outbreaks (9%, 2/22), no information on the species present was available. Three outbreaks involved outdoor access, two of which occurred in geese fattening establishments, and one in a laying hen establishment. A total of 411 individuals were reported as exposed across the 20 establishments for which additional data were available. Clinical signs and mortality, with a median value of 5.30% (range: 0.01–100%), were documented in all outbreaks. In total, 564,942 poultry heads were affected across the 22 establishments. Indirect contact with wild birds was identified as the most likely source of introduction for 81.8% (18/22) of the outbreaks, while no information was available for the remaining 18.2% (4/22).

Portugal

During the current reporting period from 6 September to 28 November 2025, two A(H5N1) and one A(H5Nx) outbreaks in poultry were reported in Portugal via ADIS. No additional data were collected from the country to complement the information available in ADIS, as the outbreaks occurred too close to the publication of this report. Two of these outbreaks were classified as primary (66.7%, 2/3) and one as secondary (33.3%, 1/3). No additional information on the production type or poultry species present was reported, but according to ADIS, these outbreaks involved turkeys for fattening (1; n = 17,186), chickens for breeding (1; n = 38,209), and mixed species (1; n = 384). The latter establishment kept several species of poultry as well as exotic captive birds, with no clinical signs, and was sampled due to an epidemiological link to an outbreak which occurred at a captive birds exhibition. In the other two outbreaks increased mortality was observed, and the fattening turkeys showed neurological clinical signs.

Slovakia

During the current reporting period from 6 September to 28 November 2025, a single A(H5N1) outbreak in poultry was reported in Slovakia via ADIS. No additional data to complement the information in ADIS were provided by the country. The primary outbreak was confirmed on 21 October in an establishment registered for the direct supply of small quantities of animal products from the farm to the consumer. In total, 208 poultry heads were present: chickens (n = 159), geese (n = 28), and ducks (n = 21). Mortality was recorded at 35% (chickens: 37.7%, geese: 46.4%, ducks: 0%) and clinical signs such as haemorrhages of the inner organs (i.e. intestines, spleen, lungs) were observed.

Spain

During the current reporting period from 6 September to 28 November 2025, nine A(H5N1) outbreaks in poultry were reported in Spain via ADIS. Additional data were collected and provided by the reporting country for all outbreaks (Annex B). Among these, 67% (6/9) were classified as primary and 33% (3/9) as secondary. Most outbreaks (89%, 8/9) occurred in commercial establishments keeping laying hens, while one outbreak (11%, 1/9) affected an establishment keeping broilers. Only one laying hen establishment reported outdoor access. Six laying hen establishments were spatially clustered, of which five were linked by the same farm ownership (European Commission, online). Clinical signs and mortality were reported in all outbreaks, with a median value of 0.23% (range: 0.003–2.68%). In total, 2,541,204 poultry heads were affected across the nine establishments. In four outbreaks (44.5%, 4/9), indirect contact with wild birds was identified as the most likely source of introduction, in two outbreaks (22.2%, 2/9), operational biosecurity issues were identified (i.e. feed manufactured at the same farm, shared veterinarians), whereas no information was available for the remaining three (33.3%, 3/9). The number of exposed people was reported for a single laying hen establishment, involving 37 individuals.

Sweden

During the current reporting period from 6 September to 28 November 2025, three primary A(H5N1) outbreaks in poultry were reported in Sweden via ADIS. Additional data were collected and provided by the reporting country for all outbreaks (Annex B). The first outbreak was confirmed on 25 October in a commercial establishment keeping turkeys for fattening (n = 31,961), where mortality was recorded at 18%, and three people were reported as exposed. The second outbreak, confirmed on 5 November, affected a commercial mixed-species establishment comprising turkeys, broilers and ducks (n = 55,499), where overall mortality was recorded at 17% but was particularly high in turkeys (100%; 80% at the time of suspicion), most of which died suddenly (European Commission, online). A total of 11 people were reported as exposed. The third outbreak, confirmed on 7 November, occurred in a commercial establishment keeping chickens for breeding (n = 15,468), where mortality was recorded at 7%, and six people were reported as exposed. Clinical signs were not reported in any of the outbreaks. Indirect contact with wild birds was identified as the most likely source of introduction in all cases.

United Kingdom (excluding Northern Ireland)

During the current reporting period from 6 September to 28 November 2025, 39 A(H5N1) outbreaks in poultry were reported in the United Kingdom (excluding Northern Ireland) via WOAH-WAHIS. Information on the poultry species present was available for 87% (34/39) of the outbreaks: rearing turkeys (29.4%; 10/34), fattening turkeys (11.8%; 4/34), breeding turkeys (2.9%; 1/34), laying hens (17.6%; 6/34), chicken breeders (17.6%; 6/34), laying ducks (2.9%; 1/34), rearing ducks (5.9%; 2/34), fattening geese (2.9%; 1/34), and pheasants (2.9%; 1/34). In addition, 5.9% (2/34) of the outbreaks were reported in mixed-species establishments including combinations of chickens, ducks, and geese. Mortality was reported in all outbreaks, with a median value of 0.63% (range: 0.02–30.76%), but no clinical signs were observed. In total, 1,371,538 poultry heads were affected across the 39 establishments.

United Kingdom (Northern Ireland)

During the current reporting period from 6 September to 28 November 2025, four primary A(H5N1) outbreaks in poultry were reported in Northern Ireland via ADIS. Additional data were collected and provided by the reporting country for three of these outbreaks (Annex B), while the fourth occurred too close to the publication of this report. All outbreaks occurred in commercial establishments, and information on the poultry species present was available for three of them: one establishment keeping chickens for breeding (n = 23,150), one establishment keeping turkeys for fattening (n = 15,300), and one establishment keeping laying hens with outdoor access (n = 12,000). Clinical signs and mortality were reported in all outbreaks, with a median value of 20.42% (range: 3.24–36.67%). A total of 80 persons were reported as exposed across the three establishments for which additional data were available.

Captive birds

Between 6 September and 28 November 2025, 74 HPAI outbreaks in captive birds were reported in 18 countries in Europe: Germany (16), United Kingdom (excluding Northern Ireland) (10), Czechia (9), France (9), Netherlands (6), Portugal (5), Spain (4), Austria (2), North Macedonia (2), Poland (2), Slovakia (2), Belgium (1), Bulgaria (1), Denmark (1), Ireland (1), Latvia (1), Sweden (1), and Switzerland (1) (Table 1, Figure 2).

Most outbreaks occurred in non-commercial establishments keeping poultry for hobby purposes (e.g. in Austria, Belgium, Czechia, Germany, Latvia, Netherlands, Poland, Portugal, Slovakia, and Sweden), where mass mortality (Czechia; Náš chov, online) and neurological signs were occasionally described (Slovakia). In this type of establishments, different poultry species, such as ducks, geese, and chickens, were often kept together.

In addition, HPAI outbreaks in captive birds during the current reporting period involved birds kept in wildlife parks (e.g. in Ireland) or zoos (e.g. in the Netherlands, Poland, and Spain) (Córdoba, online; Las Provincias, online; Rijksoverheid, online; RTE, online), as well as collection (e.g. peacocks, cranes, and ducks) and exhibition birds (Portugal).

Wild birds

During the current reporting period from 6 September to 28 November 2025, a total of 2,454 HPAI virus detections in wild birds (with one HPAI virus detection potentially representing a mixed-species outbreak) were reported in 27 countries in Europe: Germany (1,521), United Kingdom (excluding Northern Ireland) (193), France (171), Netherlands (122), Belgium (86), Spain (81), Denmark (48), Italy (45), Austria (33), Latvia (19), Luxembourg (19), Finland (18), Norway (16), Sweden (13), Lithuania (9), Poland (9), Hungary (8), Portugal (8), Iceland (7), Ireland (6), Slovenia (5), Switzerland (5), Czechia (3), Slovakia (3), United Kingdom (Northern Ireland)[11] (3), Romania (2), and Ukraine (1) (Table 1, Figure 2).

Overall, 2,430 HPAI virus detections in wild birds were reported as A(H5N1), ten as A(H5N5), and 14 as A(H5Nx) (Table 1, Figure 2). The overall number of HPAI virus detections reported in wild birds during the current reporting period (2,454) was 13 times higher than during the previous reporting period (193) (Figure 3).

Considering that multiple wild bird species can be associated with a single HPAI virus detection, HPAI A(H5) was mostly recorded in 'other' wild bird species (46%, 1,128/2,454), followed by waterfowl (40%, 984/2,454), mixed wild bird species (5%, 130/2,454), raptors (5%, 125/2,454), and colony-breeding seabirds (4%, 87/2,454) (Figure 5).

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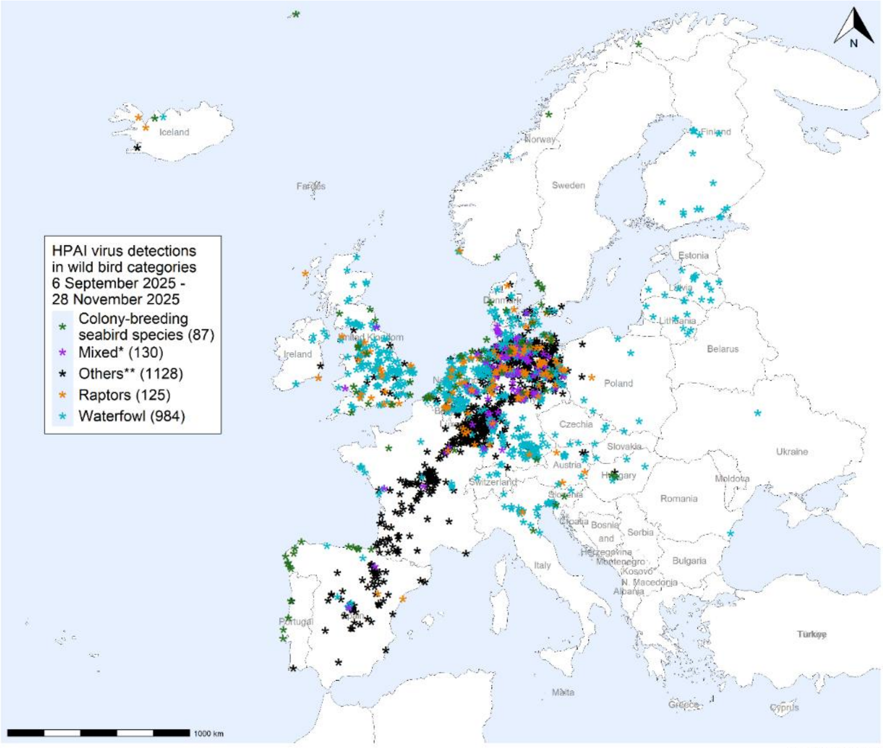
[11] In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Windsor Framework, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 28/11/2025

*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.
United Kingdom (excluding Northern Ireland) data are from WOAH-WAHIS, whereas United Kingdom (Northern Ireland)[12] data are from ADIS.
Source: ADIS, EFSA and WOAH-WAHIS (data extraction carried out on 28 November 2025).

Figure 5: Geographic distribution, based on available geocoordinates, of HPAI virus detections in different categories of wild birds in Europe, by species category, from 6 September to 28 November 2025

This pattern differs from the previous reporting period, when 73% of all HPAI virus detections in wild birds could be attributed to colony-breeding seabirds, whereas they only contributed to 4% of all HPAI virus detections during the current reporting period. At the same time, waterfowl accounted for three times more HPAI virus detections during the current (40%) than during the previous reporting period (14%), while the percentage of HPAI virus detections in raptors remained on a similar level. Of note was the predominance of the category 'Others', comprising any other wild bird species, during the current reporting period (increase from 5% to 46%), mostly due to the involvement of common cranes, as well as the increase in the percentage of the 'mixed' category (from 3% to 5%), most of which also involved common cranes.

Between 6 September and 28 November 2025, colony-breeding seabirds were primarily detected along coastlines, whereas other wild bird species were found both along coastlines

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

and inland. Of note was the band of HPAI virus detections in ‘other’ wild bird species (mostly common cranes) from northeast Germany to southwest Spain, overlapping with one of their major migratory routes across Europe (Figure 5) (EFSA and EURL, 2025).

The wild bird species in which HPAI viruses were detected belonged mainly to two orders: Gruiformes (1,132 birds) and Anseriformes (1,118). The most frequently and only reported Gruiformes identified to species was the common crane (229 during the current vs 0 during the previous reporting period). Another 901 birds of the family Gruidae were not further specified, but these were likely common cranes, as they represent the only crane species commonly found in Europe. The three most frequently reported Anseriformes identified to species were the mute swan (187 vs 7), greylag goose (95 vs 10), and Canada goose (74 vs 2). A large number of Anatidae species (552) remained unidentified. Among the category of raptors, the most frequently reported and identified species was the Eurasian buzzard (33 vs 2). Among the category of colony-breeding seabirds, the two most frequently reported and identified species were the European herring gull (25 vs 59) and yellow-legged gull (17 vs 23). Apart from Gruiformes, there was also a relatively large number of grey herons (46 vs 2) involved in HPAI virus detections among the category ‘Others’. The complete list of wild bird species found as HPAI-affected from 6 September to 28 November 2025 is reported in Figure A.1 in Annex A. The proportion of HPAI-affected wild birds that were not identified to species was 1,599/2,633 (61%), almost five times higher than in the previous reporting period (30/214, 14%) (Figures A.1–A.2 in Annex A).

In addition to the detections in dead birds, HPAI virus was identified in apparently healthy dabbling ducks through active surveillance activities (e.g. prevalence in apparently healthy mallards in the Netherlands was higher than ever before; Tweede Kamer, online), indicating an even higher circulation of HPAI viruses in the wild bird population than the number of HPAI virus detections in wild birds found dead suggests. Moreover, the contemporaneous high prevalence of low pathogenic avian influenza (LPAI) and HPAI A(H5) viruses in wild waterfowl, as demonstrated by the SENTINEL Wild Birds project in recent weeks (Söderquist et al., 2025), increases the chance of mixed infections potentially resulting in new reassortant viruses that play an important role in the rapid evolution of HPAI A(H5) viruses.

Only ten HPAI A(H5N5) virus detections (comprising a total of 11 birds) were reported in wild birds in Europe (Iceland, Norway, and United Kingdom (excluding Northern Ireland)) during the current reporting period in Eurasian buzzard (2), great black-backed gull (2), Anatidae (1), black-headed gull (1), common raven (1), glaucous gull (1), gyrfalcon (1), mew gull (1), and white-tailed eagle (1) (Figure 2, lower panel). HPAI A(H5N5)-associated mortality involving 20 birds each was described for black-headed gulls and mew gulls along the shores of Iceland. Compared to the same dates in 2024, when 53 A(H5N5) virus detections were recorded in wild birds, the current number of detections can be considered low. Although A(H5N5) virus has been reported in a wide range of wild bird species until now, the high proportion of Laridae species involved in the current reporting period (46%, 5/11) and in the previous epidemiological year (29/70, 41%) (Table A.4 in Annex A) suggests that this bird family may be important for the persistence of this subtype.

The highest mortality of wild birds from HPAI during the current reporting period was in common cranes during their autumn migration along the West European flyway. The estimated 300,000 to 350,000 birds using this flyway migrate south from breeding areas in Norway, Sweden and part of Finland, traveling across Germany and Luxembourg to wintering areas in France (important stopover sites: Lac du Der Chantecoq, Arjuzanx) and

Spain (important stopover site: Laguna de Gallocanta) (natuurpunkt, online). Common cranes using the two other flyways in Europe (Baltic-Hungarian and East European) did not appear to be affected.

Initial mortality of common cranes from HPAI was recorded in Germany starting in the first half of October. The highest levels of mortality were seen in Linum (state of Brandenburg), about 40 km northwest of Berlin, where 2,500 cranes were found dead by the end of October (Tagesspiegel, online), and in Kelbra (state of Saxony-Anhalt), about 200 km to the southwest, where 500 cranes were found dead in the second half of October, with 100 additional deaths per day. However, mortality of cranes from HPAI was reported in all states of Germany (FLI, online).

Mortality of common cranes from HPAI was subsequently recorded in France and Luxembourg from the middle of October. Up to 10,000 cranes were found dead in the northeast region of Grand Est, including more than 5,000 cranes at Lac du Der-Chantecoq and 2,000–2,500 at Valleroy, both major stop-over sites (ici, online-a; Metro, online). Crane mortality was also seen starting in the middle of October in La Nièvre, in the southeast region of Auvergne-Rhône-Alpes, with more than 100 cranes found dead from HPAI A(H5) at La Nièvre (L'Yonne Républicaine, online). At the end of October, smaller numbers of cranes dead from HPAI were seen in the southern regions of Occitanie (in Mancioux and Lac du Puydarieux) (ici, online-b) and Nouvelle-Aquitaine (in Lac d'Arjuzanx) (ici, online-c). In Luxembourg, two cases of HPAI were recorded in cranes in Howald and Rumelange, both towns close to Luxembourg City.

Finally, mortality of common cranes from HPAI was seen in Spain at the end of October and beginning of November. In the northern autonomous community of Aragón, 720 cranes were found dead from HPAI (Heraldo, online), including 250 at the nature reserve of Laguna de Gallocanta, an important stopover site for cranes (El País, online). Further south, in the autonomous community of Castilla-La Mancha, small numbers of dead or affected cranes were detected at Parque Nacional de Las Tablas de Daimiel, a wetland in the province of Ciudad Real (EFE:Verde, online), and Campillo de Dueñas y La Yunta, province of Guadalajara (Diario de Teruel, online).

During the reporting period, increased mortality of swans (likely mute swans) suspected or confirmed from HPAI was observed at multiple locations in the United Kingdom (BBC, online-a,b), Ireland (Irish Independent, online), France (Le Parisien, online) and Italy (ANSA, online; Il Goriziano, online; VET33, online). Most reports are of mortality events of around ten swans per location, but in the western French region Brittany more than 60 swans were reported dead from HPAI. However, mortality from HPAI was not only observed in mute swans. In the United Kingdom, 86 whooper swans were reported dead, likely from HPAI, since 1 October 2025 (BBC News, online).

Still, this picture of HPAI-associated mortality of wild birds 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-affected 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 HPAI virus detections in birds from other countries outside Europe that were notified to WOAH from 6 September to 28 November 2025 is presented in Table 2 and Figure 6.

Table 2: Number of HPAI virus detections in non-European countries notified to WOAH, by virus subtype and country, from 6 September to 28 November 2025. Cumulative numbers since the start of the 2025–2026 epidemiological year are reported in parentheses (1 October to 28 November 2025)

Region (total in season)	Country	Domestic birds			Wild birds			Total
		A(H5N1)	A(H5Nx)	A(Not typed)	A(H5N1)	A(H5N9)	A(H5Nx)	
Africa (32)	Nigeria	15 (15)	-	-	-	-	-	15 (15)
	South Africa	6 (3)	-	-	11 (7)	-	-	17 (10)
Americas (196)	Argentina	-	-	1 (1)	-	-	-	1 (1)
	Canada	60 (54)	-	-	-	-	-	60 (54)
	Mexico	2 (0)	-	-	-	-	-	2 (0)
	United States of America	129 (99)	2 (0)	-	2 (0)	-	-	133 (99)
Asia (41)	Cambodia	2 (2)	-	-	-	-	-	2 (2)
	China	-	-	-	-	-	2 (0)	2 (2)
	Iran	1 (0)	-	-	-	-	-	1 (0)
	Iraq	3 (3)	-	-	-	-	-	3 (3)
	Israel	-	-	-	1 (1)	-	-	1 (1)
	Japan	4 (4)	-	1 (1)	20 (20)	-	-	25 (25)
	Mongolia	-	-	-	1 (1)	-	-	1 (1)
	South Korea	2 (1)	-	-	1 (1)	1 (1)	-	4 (3)
	Taiwan	2 (1)	-	-	-	-	-	2 (1)
Total		**226 (182)**	**2 (0)**	**2 (2)**	**36 (30)**	**1 (1)**	**2 (0)**	**269 (217)**

'-' means that no HPAI outbreaks were notified to WOAH.
Source: WOAH-WAHIS (data extraction carried out on 28 November 2025).

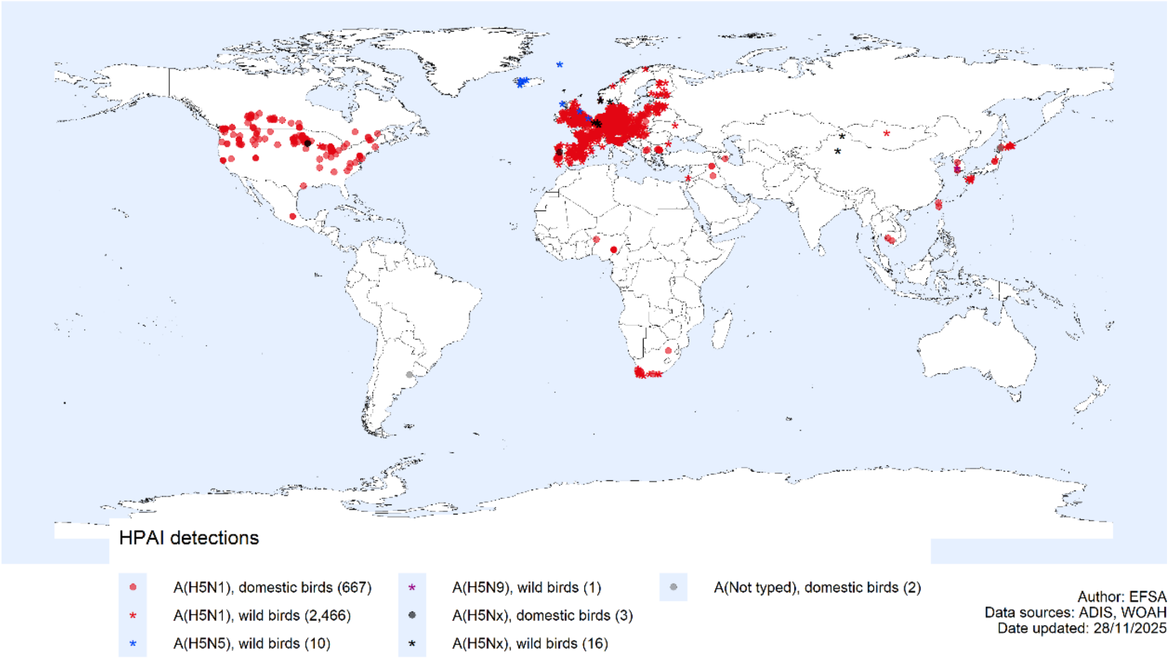

Figure 6: Geographic distribution, based on available geocoordinates, of HPAI virus detections reported worldwide in domestic (672) and wild (2,493) birds by virus type, from 6 September to 28 November 2025

The tables and figures of the present report only include data extracted from WOAH-WAHIS on 28 November 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 7 June to 5 September 2025, during which 107 HPAI virus detections were officially notified to WOAH from outside Europe (Table A.5 in Annex A), the total number of HPAI virus detections in domestic and wild birds during the current reporting period rose to 269, while also the number of reporting countries outside Europe increased from 14 to 15 (Table 2, Table A.5 in Annex A). Of the 672 HPAI virus detections reported in domestic birds worldwide (Figure 6), 230 (34%) were officially notified to WOAH from outside Europe, whereas only 39 (1.6%) of the 2,493 HPAI virus detections reported in wild birds can be attributed to those regions. Compared to the same period in the previous year, the number of official notifications to WOAH from outside Europe during the current reporting period was lower than the number of outbreaks reported between 6 September and 28 November 2024 (269 vs 303 outbreaks).

As during the previous reporting period (Table A.5 in Annex A), HPAI A(H5N1) outbreaks were reported to WOAH in both domestic and wild birds from South Africa. The epidemic in poultry continued, with some very large establishments affected. While the virus had not been detected in the province since 2024, Western Cape encountered mortality of hundreds of Hartlaub's gulls, great white pelicans, grey-headed gulls, kelp gulls, white-breasted cormorants, crowned cormorants, and sacred ibises, but also in domestic chickens and ducks in July–August 2025, as reported in the media (IOL, online). In addition, there were over 1,000 suspected cases in African penguins (IOL, online).

During this reporting period, HPAI A(H5N1) outbreaks in one large poultry establishment and several backyard farms were reported to WOAH also from West Africa (Nigeria). The media reported on an HPAI outbreak in the northeast of the country (Taraba state), associated with a movement ban of poultry and poultry products (The Guardian, online). On 25 October, an HPAI outbreak in broiler chicks was also reported by the Burkina Faso media (n = 4,500 poultry heads; AllAfrica, online).

Compared to the previous reporting period (Table A.5 in Annex A), the total number of HPAI virus detections in domestic and wild birds officially notified to WOAH from the United States of America (USA) and Canada increased substantially from 11 to 133 for the USA and from 8 to 60 for Canada. The United States Department of Agriculture (USDA) reported 188 outbreaks in all types of poultry establishments between 6 September and 28 November, mostly in turkeys and ducks for fattening (USDA, online-a). Poultry production in the states of Indiana, Minnesota, and California has particularly been hit in recent months (USDA, online-a). Furthermore, the USDA reported 1,578 HPAI virus detections in wild bird species between 6 September and 28 November 2025 (USDA, online-b), substantially more than the detections officially notified to WOAH. Close to 60 wild bird species were affected, most of which were mallards (22%, 353/1,578), wood ducks (13%, 206/1,578), blue-winged teals (11%, 170/1,578), Canada geese (11%, 165/1,578), and black vultures (7%, 102/1,578) (USDA, online-b). The media reported on a whooping crane, an endangered wild bird species, in a wildlife refuge in Wisconsin (AP, online). During the current reporting period, no HPAI A(H5N5) virus detections were reported in the USA or elsewhere outside Europe. In contrast to the previous reporting period, Canada only officially reported HPAI virus detections in domestic birds to WOAH. The virus was mainly detected in large and very large poultry establishments, and only a small number of medium-sized or backyard establishments were affected. The latter category also included a petting farm with chickens nearby Calgary (Avian Flu Diary, online-a). In addition, the media reported on an HPAI outbreak in poultry in Québec (M105, online). Mexico officially reported two outbreaks of HPAI A(H5N1) in domestic birds to WOAH. According to the media, these outbreaks involved combat birds, and also genes corresponding to A(H5N2) sequencing were detected through sequencing (WATTPoultry, online). In addition, an A(H5N1) outbreak was reported in gulls on Bagdad beach, in the far northeast of Mexico, with more than 400 dead wild birds found dead according to the media (Excelsior, online). The media also reported on an A(H5N1) outbreak in backyard poultry in Guatemala (Beacon, online-a). In contrast to the previous reporting period, in South America only Argentina reported an HPAI outbreak in captive birds (Argentina.gob.ar, online). In the Caribbean, the Caiman Islands reported an HPAI A(H5N1)-positive bird in an establishment located in Grand Cayman after the discovery of dead turkeys (Cayman Islands Government, online).

Outbreaks of HPAI A(H5) continued to be officially reported to WOAH from Asia and, in comparison to the previous reporting period, more countries were additionally affected by HPAI (H5), namely China, Iran, Iraq, Israel, and Mongolia (Table 2, Table A.5 in Annex A). In Cambodia and Iran, a small number of backyard and medium-sized poultry establishments were affected. In contrast, Taiwan detected HPAI A(H5N1) in a large laying hen establishment (UDN, online) and another medium-sized establishment, while in Iraq three very large establishment were affected. One of these housed broilers that showed high mortality in the northern Nineveh Governorate (Beacon, online-b). In India, two painted storks and two black-necked ibises tested positive for HPAI A(H5N1) in Delhi's zoo (the National Zoological Park) according to the media, with in total six painted storks, two black-necked ibises and four other migratory birds that had died in the waterfowl enclosure (Amar Ujala, online). In Israel and Mongolia, HPAI A(H5N1) virus was detected in a great white pelican and in whooper swans, respectively. The latter were found around Ugiinuur Lake, an important stopover site along the Central Asian flyway (Beacon, online-c). China reported two HPAI outbreaks in wild birds without further specifying the species. Japan officially notified to WOAH five HPAI outbreaks in very large poultry establishments. According to the media, these included three establishments of laying hens that had been reported positive for A(H5N1): a flock of 280,000 and another of 630,000 in Niigata prefecture (Japan Today, online), as well as a flock of 459,000 in Hokkaido province (China News, online). Furthermore, Japan detected HPAI virus in several wild bird species, such as Eurasian wigeon, whooper swan, red-crowned crane, Blakiston's fish owl, peregrine falcon, eastern buzzard, Eurasian goshawk, white-tailed eagle, and large-billed crow. In Kazakhstan, mass mortality was reported in seven villages across Pavlodar Region with chickens, ducks, and geese affected. The source of infection is yet unknown, but HPAI is suspected (Tengri News, online). In South Korea, besides two HPAI outbreaks in medium-sized poultry establishments officially notified to WOAH, an HPAI A(H5N1) outbreak in a small-sized goose establishment in Nam-gu, Gwangju Metropolitan City, was mentioned by the media, as well as outbreaks in a laying hen establishment in Pyeongtaek, and in a native chicken establishment in Paju City, Gyeonggi Province. Furthermore, the country reported the detection of HPAI A(H5N9) virus in a Eurasian teal. In Viet Nam, an outbreak of HPAI A(H5N1) was recorded in ducks, and the media mentioned the detection of the virus in several households keeping chickens and mixed species (chickens and pheasants) (Nông nghiệp và Môi trường, online).

Following several suspicions, on 29 October 2025, gentoo penguins in Little Creek and at Volunteer Lagoon, Falkland Islands (about 1200 km north of the Antarctic Peninsula), were confirmed positive for HPAI A(H5N1) (SCAR, online).

A list of all wild bird species that were reported to WOAH as HPAI-affected from outside Europe between 6 September and 28 November 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, more than 2,080 complete genome sequences of European viruses from 33 countries including Russia and the Republic of Georgia have been characterised. All the viruses belong to clade 2.3.4.4b, which is the only clade detected in Europe since 2016.

Overview of the genetic characteristics of the 2024–2025 HPAI A(H5Nx) viruses

Based on the genetic data available as of 28 November 2025, during the 2024–2025 epidemiological year the vast majority (approximately 80%) of the sequenced viruses belonged 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. EA-2024-DI.1 and EA-2024-DI.2, with DI.2 being the most frequent and widespread variant, identified all over Europe, in the south – from Portugal to the North Caucasus region in south Russia and the Republic of Georgia – and in the north – from the United Kingdom/Ireland to Finland.

During summer 2025 (June–August), a marked change in the frequency of the circulating genotypes was observed: the prevalence of the EA-2024-DI.2 genotype declined, while the gull-adapted genotypes EA-2022-BB and EA-2023-DT accounted for more than half of detections, primarily in gulls, along the Atlantic coasts of Spain, Portugal, and France (EA-2023-DT) and the coasts of Norway, Germany, France, Belgium, the Netherlands, the United Kingdom, and Ireland (EA-2022-BB). This change likely reflects increased virus circulation among colonial-breeding Laridae compared with lower detection rates in solitary-breeding Anseriformes. The A(H5N5) EA-2021-I genotype, which during winter 2024–2025 was reported in six northern European countries, was identified in Norway and Finland during summer 2025. Notably, outside Europe, the EA-2021-I genotype has also been reported in Canada and the USA during the 2024–2025 epidemiological year.

Genetic characteristics of the HPAI A(H5Nx) viruses, September–November 2025

Since September 2025, the complete genome sequences of approximately 400 HPAI A(H5) viruses from 17 European countries have been characterised. The vast majority of the A(H5N1) viruses (about 85%) belong to a new sub-lineage of the EA-2024-DI.2 genotype. This novel sub-lineage, designated EA-2024-DI.2.1, likely represents a new introduction of the virus into Europe. Based on the available data, the progenitors are A(H5N1) EA-2024-DI.2 viruses detected at the beginning of 2025 in Israel and the Republic of Georgia. The long branch that separates this new lineage in the phylogeny from the progenitor viruses is indicative of its circulation for at least seven months in an unknown geographic area.

EA-2024-DI.2.1 was first identified in mid-September in Poland. Since then, it rapidly spread all over Europe and, to date (based on sequences available up until 28 November 2025), it has been detected mainly in wild Anseriformes and domestic birds from 17 countries (Austria, Belgium, Czechia, Denmark, Finland, France, Germany, Ireland, Italy, Latvia, Lithuania, Luxembourg, the Netherlands, Norway, Poland, Sweden, and the United Kingdom). Of note, about 85% of the genetically characterised viruses from poultry (n > 170) reported in Europe in the period September–November 2025 were caused by this new genotype. Preliminary data from Germany, France, Belgium, and Luxembourg indicates that this genotype was also responsible for the mass mortality events reported in common cranes in these countries. Of note, all the characterised viruses from common cranes collected from these countries cluster together, suggesting a single virus introduction in this species followed by intra-species transmission. Outside Europe, this genotype has been identified in October 2025 in wild Anseriformes in Kazakhstan.

Besides EA-2024-DI.2.1, between September and November 2025 some of the genotypes circulating during the summer have still been still detected in some geographical areas. Specifically, EA-2022-BB was detected in Norway and the United Kingdom, EA-2023-DT in Portugal, and EA-2024-DI.2 in Portugal, the United Kingdom, and France.

In early September 2025, Portugal reported the first detection of HPAI A(H5N6) virus of clade 2.3.4.4b in a gull. This new subtype likely originated from a reassortment event in Europe and is not related to other A(H5N6) viruses from Asia.

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) 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 binding site in the neuraminidase protein have been identified in the circulating A(H5Nx) viruses 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, 2023-2024, 2024–2025), some of the mutations in the HA protein which have been shown by in vitro assays to gain human-type receptors recognition (i.e. S133A, S154N, T156A, 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. D94N, G139R, HA1:S123P and HA2:R167KV210I, T188I, E251K, S155N and Q192R) have only been sporadically observed (≤ 15 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 0.8%, 0.9%, and 0.4% of the analysed A(H5Nx) viruses collected in Europe since October 2024, (n > 2,080) respectively. However, for PA inhibitors, it is important to mention that mutations have been studied in seasonal influenza viruses and not specifically in 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 70 European viruses collected from birds, more specifically in i) 48 A(H5N1) viruses collected from wild and domestic birds from ten 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% of the 2023–2024 epidemiological year to about 4% in the 2024–2025 epidemiological year. Viruses containing such mutations have occasionally spread in birds, as suggested by the identification in the phylogenetic tree of clusters of viruses sharing the same substitution.

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.

Based on the data available up until 28 November 2025, none of the characterised EA-2024-DI.2.1 viruses collected from birds in Europe since mid-September 2025 contain markers of mammalian adaptation in the PB2 protein. On the other hand, all the A(H5N1) viruses of genotype EA-2024-DI.2.1 detected in Europe since mid-September 2025 contain a truncated NS1, with a length of 217 amino acids instead of 230, thus resembling that of human influenza A(H1N1) (219 amino acids in length). Such truncation of 13 amino acids has been observed in only 2.7% of the European A(H5N1) viruses of the 2024–2025 epidemiological year. An in vivo and in vitro study (Blaurock et al., 2021) showed that A(H5N8) viruses of clade 2.3.4.4b with a shorter NS1 are more efficient at blocking apoptosis and IFN-β response without a significant impact on virus replication in human cells and are capable to spread more efficiently among human and avian cells. The role of the variation in the NS1 lengths in the virulence of avian influenza viruses in birds and mammals is controversial and highly strain-dependent.

Genetic diversity of HPAI A(H5N1) viruses outside Europe

In Europe, Africa and the Americas, clade 2.3.4.4b is the only circulating clade of the Gs/GD/96 lineage. Differently, in Asia, besides the detection of clade 2.3.4.4b in several countries, clade 2.3.2.1a is present in India and Bangladesh, clade 2.3.2.1e in Cambodia, Viet Nam and Laos, and clade 2.3.2.1g in Indonesia, Cambodia, Viet Nam and Laos (OFFLU, online). Of note, based on the few data available, the HPAI A(H5N1) viruses of clade 2.3.2.1e circulating among birds, humans and non-human mammals in Viet Nam and Cambodia have shown in the last two years (2024–2025) an increase in the frequency of the mammal-adaptive marker E627K in the PB2 protein.

2.2 HPAI virus detections in non-human mammals

From 6 September to 28 November 2025, HPAI A(H5N1) and A(H5N5) viruses were reported in wild, pet 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 3).

In wildlife in Europe, HPAI A(H5N1) virus was once again reported in red foxes found dead in France (4) (Plateforme ESA, online), Germany (4), Italy (1), the Netherlands (1) (FluTrackers.com, online; PoultryMed, online-a), and Spain (1). In addition, HPAI A(H5N5) virus was reported in Arctic foxes found ill and shot in Iceland (4), and in an individual found dead on Svalbard in Norway. France also reported the detection of A(H5N1) virus in a Eurasian otter (Préfet Des Landes, online).

As regards pets, in Germany and the Netherlands domestic cats tested positive for A(H5N1) virus. In the first case, a cat that underwent routine pathological examination after its death was tested and found positive, but no further information was available (personal communication by Christoph Staubach, FLI). In the Netherlands, two kittens from a litter of eight were found with neurological signs on a goat farm, where they died. The mother had reportedly fed a wild bird to her kittens. The rest of the litter was rehomed and found dead later (DutchNews, online; NL Times, online). No link to contaminated (raw) pet food was established, and the most likely source of infection for all of these cats can be considered direct or indirect contact with wild birds.

At the same time, several European countries actively reported the absence of HPAI viruses in mammals during the current reporting period: Denmark, Luxembourg, and Sweden. Austria moreover shared detailed test results of analyses performed in mammals, all of which resulted negative: pig (69), bat (43), fox (15), badger (3), cattle (3), wild boar (3), cat (1), ferret (1), horse (1), and wolf (1) (personal communication by Sandra Revilla-Fernández, AGES). In Belgium, during the current reporting period, 32 foxes and two grey seals were tested, all of which resulted negative (personal communication with Ingeborg Mertens, favv).

Outside Europe, the number of dairy cattle farms reportedly affected by HPAI A(H5N1) in the USA rose by four to 1,083 in 18 states (for the first time in Nebraska) during the current reporting period, but the rate of new infections has gradually been decreasing (USDA, online-c). Three additional domestic cats tested positive for HPAI A(H5N1) in California after showing severe illness and dying following the consumption of raw pet food (Beacon, online-d). In one case in San Francisco, the B3.13 genotype was identified in both the cat and two lots of the frozen raw pet food consumed by the cat (PoultryMed, online-b). As regards wildlife, HPAI A(H5) virus was identified in house mouse (13), unidentified skunks (2), Virginia opossum (2), American black bear (1), raccoon (1), striped skunk (1), and thirteen-lined ground squirrel (1) (USDA, online-d). Moreover, one HPAI virus detection was retrospectively reported in a polar bear from Alaska back in August 2025 (USDA, online-d).

During the current reporting period, more information became available on mortality events affecting various seal species around the world. Additional HPAI virus detections in harbour seals (June 2025) and southern elephant seals (February 2025) were officially reported from the South Georgia and the South Sandwich Islands via WOAH-WAHIS. The impact on the population of the HPAI-induced mass mortality of southern elephant seals in the world's largest breeding colony of this species at South Georgia in 2023 has recently been assessed. Based on population counts at the three main breeding beaches in 2022 and 2024, there was a 47% decline in the number of breeding females, which was attributed to the direct impact of HPAI. The scale of this mortality event may impact the ongoing recruitment (number of new births), and therefore the recovery of this world's largest breeding population of southern elephant seals (Bamford et al., 2025). In addition, an unusual mortality event of southern elephant seals at Heard Island, an Australian external territory in the Southern Ocean, in November was confirmed to be caused by HPAI A(H5N1) (Australian Government, online; Minister for Agriculture, Fisheries and Forestry, online). This represents the first report of HPAI A(H5N1) in animals in Australia and in the continental region of Oceania.

The wild mammal species involved are mainly those that hunt wild birds, feed on dead wild birds, or both. The species in which A(H5N1) virus was most frequently reported is the red fox, likely a consequence of its wide distribution, which largely overlaps with the geographic spread of the HPAI A(H5N1) outbreaks, and its diet, which partly includes both hunted and scavenged wild birds.

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	Fosse et al. (2025), GovUK (online-a,b)
		Camelidae	Alpaca (*Lama pacos*)	United States of America	USDA (online-c)
		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, Spain, 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**, Germany, Hungary**, Italy*, Netherlands**, Poland, South Korea, United States of America	WOAH USDA DutchNews (online), TF1 Info (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)

Virus	Animal (order, family, species)			Country	Reference
			Leopard (*Panthera pardus*)	India, United States of America, Viet Nam	USDA The Times of India (online-a)
			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, France, Sweden, United Kingdom	WOAH Préfet des Landes (online)
			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 Banyard et al. (2024), Bennison et al. (2024)
			Northern fur seal (*Callorhinus ursinus*)	Russia	WOAH
			South American fur seal (*Arctocephalus australis*)	Argentina, Brazil, Peru, Uruguay	WOAH

Virus	Animal (order, family, species)			Country	Reference
			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)
			Grey seal (*Halichoerus grypus*)	Canada, Germany, Netherlands, Poland, Sweden**, United Kingdom, United States of America	WOAH
			Harbour seal (*Phoca vitulina*)	Canada, Denmark, Germany, Japan, South Georgia and the South Sandwich Islands, 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 Banyard et al. (2024), Bennison et al. (2024), PASTAAF (online-a, b)
		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 USDA
	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

Virus	Animal (order, family, species)			Country	Reference
	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
			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
			Thirteen-lined ground squirrel (*Ictidomys tridecemlineatus*)	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 Ingeborg Slettebø Wathne (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)

Virus	Animal (order, family, species)			Country	Reference
			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, 2025)
		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-b), Outbreak News (online-b)

[*] 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).

Overview of the genetic characteristics of the 2024–2025 HPAI A(H5Nx) viruses in non-human mammals

During the 2024–2025 epidemiological year, the complete or partial genome sequences of 39 HPAI A(H5) viruses of clade 2.3.4.4b collected from nine distinct mammalian species (i.e. Arctic fox, domestic cat, Eurasian badger, Eurasian lynx, Eurasian otter, grey seal, harbour seal, red fox, and sheep) in ten different European countries have been analysed. The majority of the characterised viruses belong to the A(H5N1) genotype EA-2024-DI (53.8%) and the A(H5N5) EA-2021-I (41%). The viruses from wild mammals show the highest identity with the A(H5Nx) viruses collected from wild birds in the same area. Differently, the majority of viruses collected from 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 highly related to the viruses collected from poultry.

Among the characterised viruses from mammals in Europe during the 2024–2025 epidemiological year, 26% of the A(H5N1) and 93.7% of the A(H5N5) viruses possess the amino acid lysine (K) or valine (V) instead of glutamic acid (PB2-E627K/V substitution), a mutation that facilitates a more efficient virus replication in mammals (Aggarwal et al., 2011).

Genetic characteristics of the HPAI A(H5Nx) viruses in non-human mammals, September–November 2025

As of 28 November 2025, one virus collected from a domestic cat in the Netherlands and viruses from four red foxes and a Eurasian otter in France were genetically characterised. All belong to the EA-2024-DI.2.1 genotype. Specifically, the A(H5N1) viruses collected from wild mammals in France cluster together with viruses associated with the mass mortality events in common cranes in the country. Of note, all six viruses contain molecular markers of mammalian adaptation, which have not been identified in the phylogenetically related viruses collected from avian species. Specifically, five out of six viruses collected from mammals contain the substitution PB2 E627K, while one virus acquired the PB2 substitutions E192K and Q591K (Yamada et al., 2010; Taft et al., 2015).

2.3 Avian influenza virus infections in humans

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

Since 9 September and as of 28 November 2025, 19 new human cases of infection with avian influenza viruses have been reported from four countries: Cambodia (n = 3), China (n = 14), Mexico (n =1), and United States of America (USA) (n = 1). These infections were caused by four different subtypes, including one type that was reported for the first time in humans: A(H5N1), A(H5N2), A(H5N5), and A(H9N2) (Table 4). Most of the cases had exposure to poultry or live animal markets (Table 5).

Table 4: Globally reported cases or detections of avian influenza virus in humans, including virus subtypes reported in the last 12 months

Subtype	Cases reported 2025-09-09–2025-11-28			Cases reported since first report			
	Cases reported	Deaths	Reporting countries	First report	Cases reported	Deaths	Reporting countries
A(H5N1)	3	1	1 (Cambodia)	1997	1,013*	476**	25
A(H5N2)	1	0	1 (Mexico)	2024	2	1	1
A(H5N5)	1	1	1 (USA)	2025	1	1	1
A(H9N2)	14	0	1 (China)	1998	187	2	10
A(H10N3)	0	0	0	2021	6	0	1

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

**Deaths reported since 2003 out of a total of 993 cases reported 2003–28 November 2025. Mortality data are not available for cases reported prior to 2003.

Table 5: Identified exposure associated with human cases of avian influenza, reported globally 9 September–28 November 2025 by zoonotic influenza subtype

Subtype	Reported exposure*	Cases
A(H5N1)	Poultry	3
A(H5N2)	Avian (all species)	1
	Dog	1
	Poultry	1
A(H5N5)	Poultry	1
A(H9N2)	Poultry	13
	Not reported**	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 (Shu and McCauley, 2017) submitted since the previous report was retrieved for two A(H5N1) strains representing cases in Cambodia and Mexico, two A(H5N2) cases in Mexico, and one A(H5N5) strain from the USA. The strains were analysed phylogenetically in the context of strains described in the December 2024–September 2025 reports (EFSA, ECDC and EURL, 2025a,b,c) and for mutation markers (Table 6, Figure 7). In addition, approximately five of the most closely related non-human strains are displayed.

Table 7: Human strains included in phylogenetic and mutation analysis. Sequences include those deposited in GISAID’s EpiFlu™ database (Shu and McCauley, 2017) from 9 September 2025 to 27 November 2025

Isolate name	Subtype	Clade	Collection date	Continent	Country	Markers
A/Cambodia/j09083708/2025	A(H5N1)	2.3.2.1e	2025-09-07	Asia	Cambodia	PB1:N66S,H115Q(PB2:E627K);PA:A37S,K142N;PB2:E627K
A/Mexico City/INER INF1427/2025	A(H5N2)	2.3.4.4b	2025-09-29	North America	Mexico	Minor variants of PB2: K526R, E627K reported (Vázquez-Pérez et al., 2025)
A/Mexico/Dur Indre 2292/2025	A(H5N1)	2.3.4.4b	2025-03-18	North America	Mexico	PB1:N66S
A/Mexico/Mex Indre F3546/2024	A(H5N2)	Am_nonGsGD	2024-04-24	North America	Mexico	MP:L26F,S31N;NP:Y52N;HA:A156V,E186V,K189R
A/Washington/2148/2025	A(H5N5)	2.3.4.4b	2025-11-10	North America	United States of America	PB1:N66S;NA:K432E

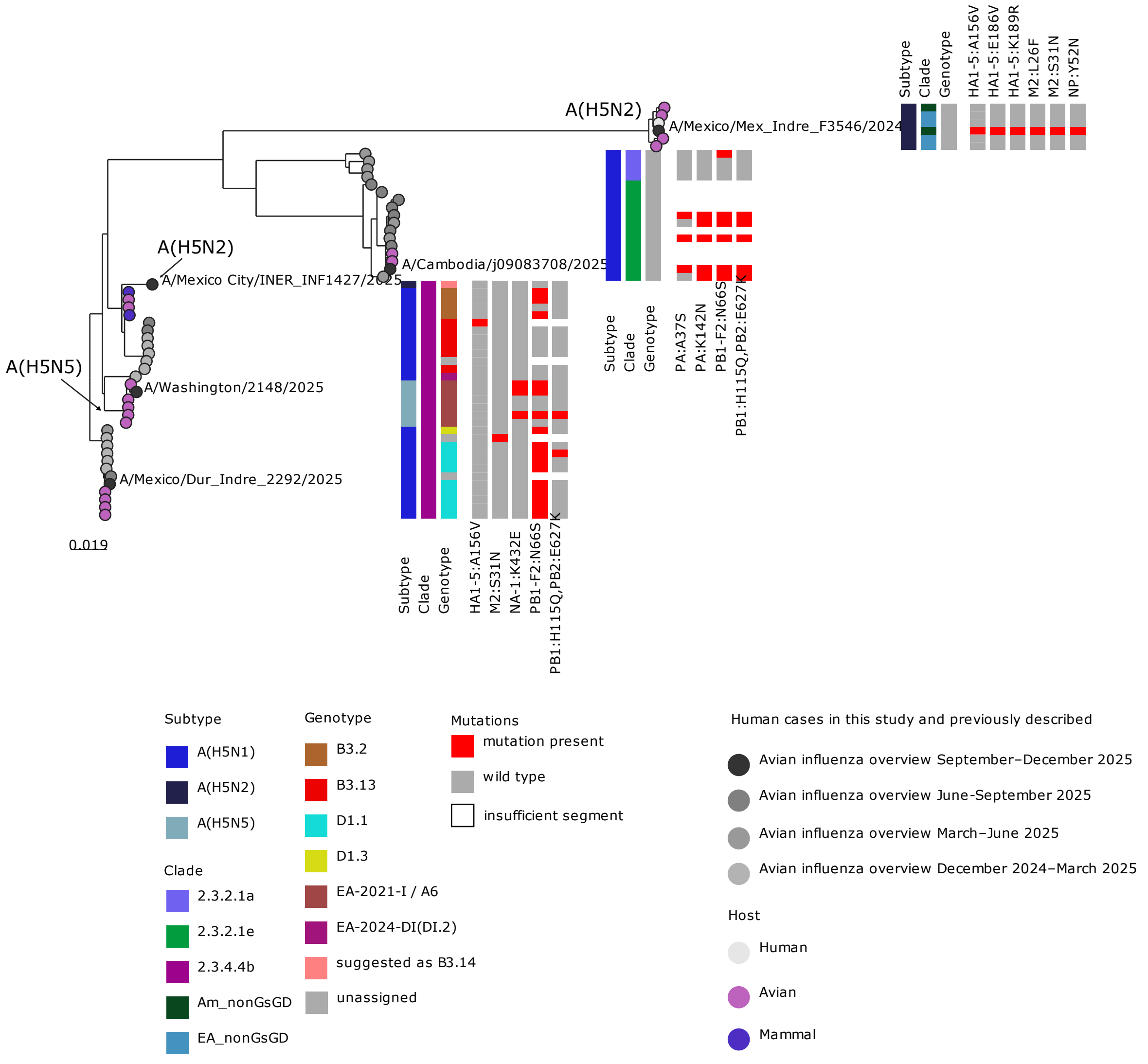

Figure 7: Phylogenetic tree from nucleotide alignment of the HA segment annotated with significant mutation marker findings from all segments. Strains from the December 2024–September 2025 report (EFSA, ECDC and EURL, 2025a,b,c) are included and annotated accordingly. Closely related non-human strains are annotated according to their host. The phylogenetic tree can be viewed interactively on Microreact (https://microreact.org/project/s6VQEZpckU8nrh8bekVcbs-avian-influenza-overview-9-september-28-november-2025) (Argimón et al., 2016).

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 1,013 cases have been reported to the World Health Organization (WHO) from 25 countries (Figure 8). Since 2003, there have been 476 deaths out of a total of 993 cases reported.

Between 9 September and 28 November 2025, three new human cases of influenza A(H5N1) virus infection were reported, all from Cambodia. Among these cases, one death was reported.

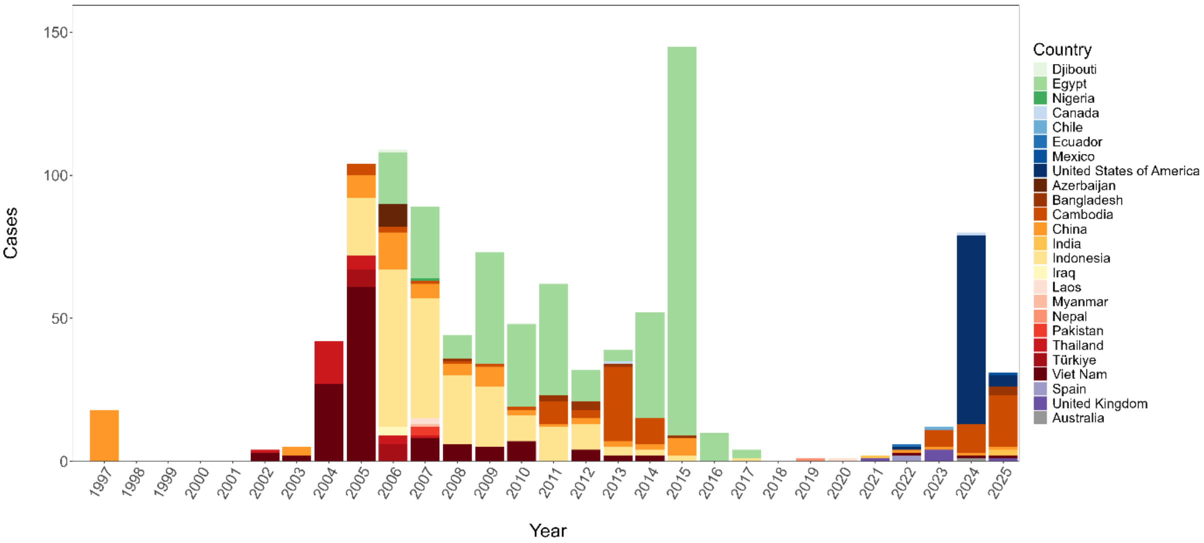

Figure 8: Distribution of reported human cases of A(H5N1) virus infection by year of onset or detection and reporting country from 1997 to 28 November 2025. The figure includes detections of A(H5N1) due to suspected environmental contamination reported in 2022 by Spain (2) and the USA (1), and in 2023 by the United Kingdom (three detections, one inconclusive). Human cases of A(H5) epidemiologically linked to A(H5N1) outbreaks in poultry and dairy cattle farms in the USA are included in the number of A(H5N1) cases.

Cambodia

Three human cases were reported from multiple provinces in Cambodia, including Kampong Speu, and Takeo provinces, and Phnom Penh autonomous municipality (Ministry of Health of Cambodia, online; WHO, online-b,c). Two of the cases were children (aged three and 14 years, respectively) and one was a young adult. No underlying conditions were reported in these patients. The reported symptoms included fever, cough, and difficulty breathing. One patient had gastrointestinal symptoms (diarrhoea and abdominal pain). Two patients developed pneumonia. All three had exposure to poultry, with reported mortality either in backyard poultry of the household or in the affected village. One death was reported in a young man from Phnom Penh who, prior to onset of symptoms in November 2025, visited his family in another province (Kampong Cham). The patient died within a week (five days) of symptom onset, despite being treated at a hospital. No additional cases have been reported among close contacts.

The isolate of the case from Takeo belongs to clade 2.3.2.1e and has a mutation profile identical to similar viruses from Cambodia previously described – e.g. A/Cambodia/25030237/2025 (EFSA, ECDC and EURL, 2025b). The HA segment of the strain is genetically similar to two recently collected bird isolates from the same country. A/Cambodia/25030237/2025 carries markers for mammalian adaptation – e.g. in PA, PB1 and PB2. However, the bird isolates lack these segments, which means a comparison cannot be made (Figure 7).

Mexico

In a previous report covering March–June 2025 (EFSA, ECDC and EURL, 2025b), an A(H5) human case was announced on 8 April 2025 by the Mexican Ministry of Health. No sequence was available at that time. On 28 October 2025, an updated genome of the sequenced isolate A/Mexico/Dur Indre 2292/2025 was made available and is included in this report. The virus is assigned to genotype D1.1 and has a mutation profile similar to that of other human strains of genotype D1.1.

2.3.3 Human A(H5N2) cases

During the reporting period, one new human case with avian influenza A(H5N2) was reported in Mexico, making it the second case in Mexico and globally. The first human infection with A(H5N2) was reported in April 2024, in a resident of the State of Mexico, who subsequently died due to a worsening of underlying conditions. During the investigation it was not possible to establish exposure to birds, although laboratory analysis indicated that the virus showed similarity to strains circulating among birds in the nearby area (WHO, online-c). The second case is a young woman with an underlying condition (obesity) from Mexico City, who developed respiratory symptoms in mid-September 2025 and was hospitalised two weeks later due to her condition worsening (Vázquez-Pérez et al., 2025; WHO, online-c). The patient had exposure to poultry, pigeons and a dog in her residential area that tested positive for avian influenza A(H5). No new cases have been detected among contacts of this case. A bronchoalveolar lavage sample collected from the patient on 29 September 2025 tested positive for un-subtypeable influenza A. Influenza A(H5) was confirmed on 30 September by RT-PCR test, later confirmed as A(H5) through molecular diagnostics. The neuraminidase was identified as N2. The sample was also sent to a WHO Collaborating Centre for influenza.

The sequenced strain of the second case, A/Mexico City/INER INF1427/2025, belongs to clade 2.3.4.4b and, unlike the strain from the first case, has a highly pathogenic avian influenza signature in the HA segment. The HA segment is highly divergent from the LPAI A(H5N2) strains collected from the human case and birds in Mexico in 2024. The HA gene of the recent case clusters with A(H5N1) viruses of clade 2.3.4.4b genotype B3.2 (Figure 7). In a recent pre-print (Vázquez-Pérez et al., 2025), the authors suggest that the strain is a result of a reassortment event between an enzootic LPAI A(H5N2) virus ancestor from 2024, detected in Central Mexico, and A(H5N1) clade 2.3.4.4b genotype B3.2 viruses. A new genotype designation, B3.14, is also proposed. No mutations known to increase its zoonotic potential were found in the consensus sequence deposited on GISAID, however, minor variants of K526R and E627K in PB2 are reported from deeper analysis of sequencing reads. Isolates carrying both 526R and 627K replicate more efficiently in mammalian cells (Song et al., 2014).

The sequence from an LPAI A(H5N2) virus, A/Mexico/Mex Indre F3546/2024, from the first human infection with A(H5N2) in Mexico (WHO, online-d) collected on 24 April 2024, was also available and included in the analysis. Interestingly, the virus contained HA mutations A156V and E186V, associated with increased attachment to human-type receptors, and Y52N in NP, associated with evasion of innate immunity and counteraction of mammalian restriction factors (EFSA AHAW Panel and ECDC, 2025). As mentioned in the section regarding mutations identified in HPAI viruses from avian species in Europe, Y52N is common in European HPAI A(H5N1) avian strains of genotypes EA-2022-BB and EA-2023-DT.

2.3.4 Human A(H5N5) cases

On 13 November 2025, the first human infection with avian influenza A(H5N5) virus globally was reported in the USA (CDC, online; Washington State Department of Health, online). An adult individual, resident of Grays Harbor County, Washington State, USA, with underlying conditions, had onset of symptoms at the end of October 2025 (week 43, 2025), was hospitalised at the beginning of November 2025 (Week 45, 2025), and died on 21 November 2025. The person had a backyard flock of mixed domestic birds. The environmental samples tested positive for avian influenza. According to public health officials, the most likely source of exposure for this patient was poultry, their environment, or wild birds. No new cases have been reported among contacts of this case. The authorities are continuing to monitor other people who may have had contact with the backyard poultry and environment for symptoms, as well the identified contacts of the patient. So far, no human-to-human transmission has been detected, and the US public health authorities assess the risk to the public as low. The Washington State Department of Health is collaborating with local health authorities and the State Department of Agriculture to assess human and animal health risks.

The sequenced isolate, A/Washington/2148/2025, belongs to clade 2.3.4.4b. The genotype is EA-2021-I / A6, which has commonly been reported for recent A(H5N5) viruses from birds and mammals in North America. The HA segment clusters closely with clade 2.3.4.4b avian strains of the same genotype but is distinct from A(H5N1) genotypes B3.13 and D1.1, which include strains from human infections in the USA. A/Washington/2148/2025 carries the mutations PB1-F2:N66S and NA:K432E, which are listed as markers associated with increased risk of adaptation to mammals (EFSA AHAW Panel and ECDC, 2025). However their significance is unclear, since they also occur in isolates from birds included in the analysis in proportions of > 50% and > 10%, respectively.

As of 14 November 2025, the US Centers for Disease Control and Prevention (CDC) have reported 71 human cases with avian influenza A(H5), including the recent case with A(H5N5) infection (note: other reported cases involved avian influenza A(H5N1) virus infection), and two deaths – which includes the recent death (CDC, online).

2.3.5 Human A(H9N2) cases

Since the first report of human infection with avian influenza A(H9N2) virus in 1998, a total of 187 cases, including two deaths, have been reported to WHO (Figure 9).

Between 9 September and 28 November 2025, 14 new human cases of influenza A(H9N2) virus infection were reported from China. The cases were reported from Anhui, Chongqing Municipality, Guangdong, Guangxi Zhuang Autonomous Region, Henan, Hubei, Hunan, Jiangxi, Sichuan, and Tianjin provinces. The cases were children (age range 0−12 years) and two adults. Four of the cases were hospitalised. Thirteen of the cases had exposure to poultry, while for one patient no exposure was identified. All cases recovered. No epidemiological links were identified between the cases (CHP, online; F.I.C., online). No sequences were where obtained for the A(H9N2) cases.

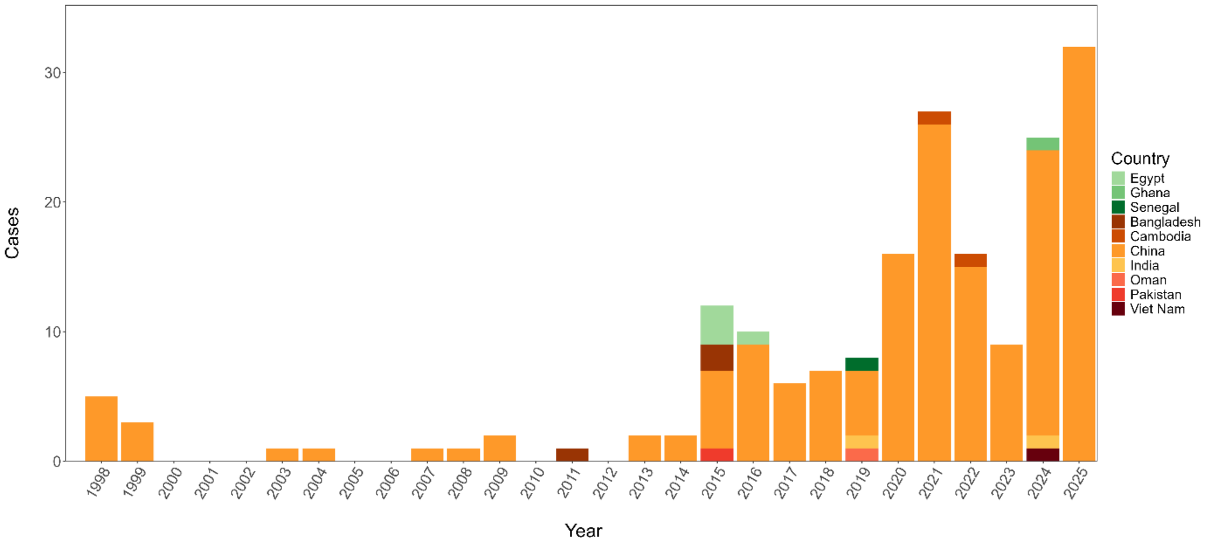

Figure 9: Distribution of reported human cases of A(H9N2) virus infection by year of onset, or detection and reporting country, from 1998 to 28 November 2025

2.3.6 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 9 September and 28 November 2025, no new cases of influenza A(H10N3) were reported in humans.

2.3.7 Additional information relevant for public health and international risk assessments

A scoping review of asymptomatic cases of A(H5N1) reported in humans found that the majority of asymptomatic cases were identified through enhanced surveillance of individuals exposed to A(H5N1)-infected animals or contact tracing of household members. Most of the asymptomatic cases reported had been identified through molecular testing alone, and some of them were likely environmental contaminations. To estimate the occurrence of asymptomatic A(H5N1) infections with or without seroconversion, the review concluded that enhanced surveillance of individuals with high-risk exposure to animals or humans infected with A(H5N1) would be required, including serial sampling for molecular and serological testing (Dawood et al., 2025).

The Strategic Advisory Group of Experts (SAGE) on immunisation advised that countries should consider developing recommendations on the use of licensed influenza A(H5) vaccines for the interpandemic period, depending on national priorities and based on evidence synthesis. The main objective of influenza A(H5) vaccination should be prevention of severe disease in those at higher risk of infection. Groups to be considered for vaccination, based on their exposure risk, included laboratory workers, responders to influenza A(H5) outbreaks in animals, healthcare workers, and individuals having continuous contact with animals or contaminated environments in geographical areas with reported detections or outbreaks (WHO, online-e).

Candidate vaccine viruses for zoonotic influenza viruses were reviewed at the WHO vaccine composition meeting in September 2025, based on recently characterised zoonotic influenza viruses, to enhance pandemic preparedness. Based on the currently available epidemiological, genetic, and antigenic data for avian A(H5), A(H9N2) and A(H10N3) viruses detected in animals and humans, no new candidate vaccine viruses were proposed (WHO, online-f).

ECDC has published a framework to guide a scalable public health response to zoonotic influenza across evolving pre-pandemic scenarios, based on the epidemiological situation, genetic characteristics, and severity of infection. In the current epidemiological context in the EU/EEA, recommended public health actions include preventive measures to reduce human exposures to zoonotic influenza viruses, surveillance, and laboratory preparedness, integrated into a One Health approach. In the event of an evolving situation, the framework outlines escalating actions for each scenario, covering preparedness, surveillance, diagnostics, case investigation and management, One Health coordination and communication, and additional research needs. The document provides a detailed guide and a downloadable tool for defining and scoring the different scenarios based on early triggers, promoting transparency and consistency across countries (ECDC, 2025).

The Food and Agriculture Organisation of the United Nations (FAO), WHO and WOAH tripartite assessment of the public health risk posed by influenza A(H5N1) viruses remains unchanged. In the assessment published on 28 July 2025, the risk of infection was considered low for the general public and low-to-moderate for occupationally exposed individuals (FAO, WHO and WOAH, online). In the latest summary and risk assessment of 'Influenza at the human-animal interface' (WHO, online-c), 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 public health risk posed by avian influenza A(H5) viruses has not changed and is currently considered low in the USA (CDC, online).

Similarly, during the reporting period, the UK Health Security Agency (UK HSA) risk assessment of HPAI A(H5) to the general public has remained unchanged and is still considered to be very low (GovUK, online-d).

2.3.8 ECDC risk assessment

ECDC's assessment of the risk of human infection with HPAI A(H5N1) clade 2.3.4.4b viruses remains unchanged. Overall, ECDC assesses the risk posed by HPAI A(H5N1) 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 ECDC's 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(H5N1) clade 2.3.4.4b viruses in the EU/EEA:

- This autumn, there has been an unprecedented surge in detections of HPAI A(H5N1) virus in wild birds in Europe, accompanied by many outbreaks in poultry in affected areas. The high circulation of avian influenza virus in bird populations raises the risk of human exposure to infected animals.
- Despite the extensive circulation of avian influenza A(H5N1) virus in animal populations in Europe this autumn and 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 capable of infecting humans, or having the ability to transmit between humans.
- Sporadic cases of infection with avian influenza A(H5N1) virus have been reported in humans globally, most of whom have had a history of unprotected exposure to poultry, cattle or contaminated environments. For the human cases of A(H5N1) reported globally between 9 September and 28 November 2025, all cases (n = 3) had documented exposure to poultry.
- To date, there has been no evidence of human-to-human transmission of influenza A(H5N1) clade 2.3.4.4b viruses.

The impact of human infection with HPAI A(H5N1) clade 2.3.4.4b viruses:

- Historically, clinical presentations of individuals infected with A(H5N1), also including clades other 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 9 September and 28 November 2025, no new cases of human infection with an A(H5N1) clade 2.3.4.4b virus were reported globally.
- 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). Targeted surveillance of individuals exposed to infected animals is therefore 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 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 wild 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 is regularly reviewing the risk assessment, taking into consideration any new developments or information that becomes available.

The high level of HPAI A(H5N1) virus in birds in Europe during the autumn migration in 2025 (EFSA and EURL, 2025) coincides with an unusually early start to the influenza season in humans, where an increase in seasonal influenza A was observed three to four weeks earlier than in the past two years (https://erviss.org/) (ECDC, online). This could increase the likelihood of individuals infected with seasonal influenza being exposed to animals infected with avian influenza, particularly among those who are in contact with domestic and wild animals on a routine basis. Such exposures may lead to an increased risk of co-infection with seasonal and avian influenza viruses, reassortment and emergence of novel influenza viruses.

3. Conclusions

3.1 Birds

- Compared to previous years, there was an unprecedented sharp increase in detections and high circulation of HPAI viruses in the wild bird population in Europe during the current reporting period, based on detections in both apparently healthy wild birds and wild birds found dead. These HPAI virus detections in wild birds involved increasing numbers of waterfowl species (ducks, geese and swans) and common cranes found positive in large parts of Europe. It is too early to know the underlying mechanisms for this high virus circulation; possible explanations include a relatively high proportion of immunologically naïve individuals in the wild bird population and the higher transmissibility of a newly introduced sub-lineage of HPAI virus from outside Europe.

- It is expected that the level of virus circulation in wild birds in Europe will remain high in the coming weeks, followed by a decline towards the end of winter.

- There was high mortality of common cranes from HPAI across a wide band stretching from northeast to southwest Europe. The pattern of mortality corresponded to the autumn migration of this species along the West European flyway, where cranes have not been affected by HPAI before. Based on the media reports examined, at least 13,000 cranes died. However, there is no coordinated international monitoring of HPAI-associated wild bird mortality, and this is undoubtedly a substantial underestimate of the actual mortality level.

- Compared to previous years, HPAI outbreaks in domestic birds during the current reporting period were mainly attributed to primary introductions from wild birds, while secondary spread was reported only rarely. This is likely a reflection of the high concentration of HPAI virus in the environment surrounding poultry establishments and the inadequacy of biosecurity measures in the current epidemiological situation.

- During the current reporting period, proportionally more turkeys were affected than other poultry species.

- In France, more than 30 HPAI outbreaks were recorded in establishments where vaccinated ducks were kept. The factors involved in these events have yet to be assessed before reaching any conclusions.

- The ten HPAI A(H5N5) virus detections in wild birds during the current reporting period suggest that this subtype is persisting in wild birds in Europe, although it is confined to certain areas of northern Europe, and there were fewer detections than in the same period in the previous year.
- An HPAI A(H5N6) virus was detected in a gull in Portugal in September, which has however not been submitted to ADIS yet.
- Most clade 2.3.4.4b HPAI A(H5N1) viruses identified in Europe since mid-September 2025 belong to a new sub-lineage, namely EA-2024.DI.2.1, which evolved from the previously circulating EA-2024-DI.2 genotype. This sub-lineage was likely introduced into Europe during the autumn migration of wild birds and has since spread quickly westward.
- Since September 2025, markers of mammalian adaptation in the PB2 protein have been rarely detected in viruses collected from birds. As of 28 November, none of the viruses of the EA-2024.DI.2.1 genotype isolated from avian species carry these mammalian adaptive markers or other mutations linked to increased zoonotic potential, compared to the previously circulating European A(H5) of clade 2.3.4.4b.
- Outside Europe, HPAI virus detections were increasingly reported from North America, particularly in large establishments keeping turkeys and ducks for fattening.
- HPAI A(H5N9) was reported in a Eurasian teal in South Korea.
- 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.

3.2 Mammals

- During the current reporting period, there was a slight increase in the number of both HPAI A(H5N1) and A(H5N5) virus detections in mammals in Europe, predominantly in wild carnivores.
- The number of HPAI virus detections in ill and dead mammals can still be considered low given the high circulation of HPAI virus in the wild bird population and the resulting high contamination of the environment. However, this number might increase in the coming weeks due to the continued high circulation of HPAI virus in the wild bird population.
- In Germany and the Netherlands, domestic cats tested positive for HPAI virus, most likely due to direct or indirect contact with wild birds, without any link to contaminated (raw) pet food, as it has been the case for other countries outside Europe.
- In the USA, the number of new HPAI virus detections in dairy cattle declined, while additional domestic cats were affected after exposure to contaminated raw pet food.
- One new mammal species, a thirteen-lined ground squirrel, was detected positive for HPAI virus for the first time in the USA.
- HPAI A(H5N1) virus was confirmed in southern elephant seals on Heard Island, an Australian territory. This is the first case of HPAI A(H5N1) virus in an animal in the continental region of Oceania.

- Genetic data available for six A(H5N1) viruses collected from wild and domestic mammals in Europe indicate that they belong to clade 2.3.4.4b, genotype EA-2024-DI.2.1. All the six viruses are distinguishable from genetically related viruses identified in avian species by the presence of molecular markers of adaptation to mammals in the PB2 protein.

3.3 Humans

- Sporadic cases of zoonotic avian influenza A(H5N1), A(H5N2), A(H5N5), and A(H9N2) were reported outside of the EU/EEA during the period September–November 2025. The A(H5N5) case represents the first human infection with avian influenza A(H5N5) reported globally.
- 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(H5) 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 9 September to 28 November 2025, there were three human cases of avian influenza A(H5N1) infection reported globally, all which had documented exposure to sick and dead poultry.
- 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

- Biosecurity measures in domestic bird establishments and compliance thereof should be optimised and maintained at high level both during the production cycle and culling operations. This is particularly the case for establishments under the same ownership and located in high-density poultry areas.
- Housing orders for domestic birds are highly recommended in areas where HPAI virus is circulating in wild birds or mass mortality events in wild birds are reported.
- While vaccination of poultry can substantially reduce the risk of outbreaks taking place in vaccinated compared to unvaccinated flocks, it does not provide complete protection on its own. Therefore, as it would be the case for unvaccinated flocks, vaccination should be accompanied by strict biosecurity measures and adequate surveillance.
- Surveillance in domestic birds should be enhanced to ensure early detection of infected poultry establishments.
- Surveillance activities in wild birds should be enhanced, particularly in wetland areas and migratory stopover sites in and outside Europe. Given the low level of HPAI-associated mortality in wild waterfowl, particularly wild ducks, relative to the high level of virus circulation in apparently healthy individuals, there is a greater need to sample

apparently healthy waterfowl (‘active surveillance’) in addition to waterfowl found dead (‘passive surveillance’) in order for avian influenza surveillance in wild birds to act as a more sensitive early warning system for the presence of HPAI in a geographical region. This ‘active surveillance’ is particularly relevant in autumn at key sites along the migratory flyways of migratory waterfowl.

- Wildlife rescue/rehabilitation centers and bird shelters should be part of surveillance activities and implement adequate biosecurity to protect both animal and public health.
- Given the low mortality observed in some wild bird species, environmental surveillance can be a cost-effective way to better understand the extent of virus circulation in specific geographical areas and to enable early detection. Environmental surveillance in wetlands based on the use of passive samplers (Panzarin et al., 2025) allowed HPAI (H5) virus detection in northeast Italy in September 2025 before any HPAI outbreaks in birds were identified in the country (Fornasiero et al., submitted). Such detections should promptly trigger strengthened ‘active surveillance’ efforts and the implementation of increased biosecurity measures in domestic bird establishments within the affected area.
- EFSA’s Bird Flu Radar may be consulted to monitor the probability of HPAI virus introduction in wild bird populations over space and time: https://app.bto.org/hpai
- For wild birds, options for response include accurate and comprehensive recording of HPAI-associated mortality events (to estimate the impact on wild bird populations), preventing disturbance of areas undergoing HPAI outbreaks to reduce virus spread (e.g. hunting activities, tourism, leisure activities, use of drones), 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.
- Artificial feeding of wild birds, particularly of cranes and swans, should be avoided during high-risk periods to reduce the level of crowding of these species.
- 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.
- Strengthening the genetic characterisation of viruses is recommended to quickly identify molecular markers of adaptation to mammals, which could indicate potential virus circulation in mammals and subsequent mammal-to-avian transmission. Viruses carrying such mutations may have an increased zoonotic potential and their biological characteristics should be further evaluated to assess the actual impact of the acquired mutations. To serve as an effective early warning system, sequences should be generated and shared in public databases as promptly as possible. 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.

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 compatible 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 raw 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.

- At times of high HPAI virus circulation in an area, it is recommended to keep pets indoors or on a leash.

- 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 can be reduced by implementing some of the prevention measures suggested below.

- Use of appropriate personal protective equipment 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 ensure safe handling of potentially contaminated biological materials.

- Provision of information and guidance to raise awareness among people at risk of exposure and indicate how the risk can be mitigated. Guidance should be tailored to specific occupational groups, or individuals engaged in recreational activities where additional measures may be beneficial. Recommendations for personal protective measures should consider the working environment, tasks performed, 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. If they find dead animals, they should inform the relevant authorities in order to ensure safe removal and further investigation.

- Detections of HPAI in apparently healthy wild ducks (EFSA and EURL, 2025) highlight the importance of precautionary measures when handling wild birds, even in the absence of clinical signs. Information to increase awareness of the risk of infection from animals and set out the appropriate preventive measures should also be made available to those in contact with wild birds, such as hunters and wildlife workers.

- People 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 '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, including primary care providers, in affected areas should be made aware of the epidemiological situation in animal populations and the range of symptoms associated with avian influenza infection in humans.

- In areas with ongoing avian influenza outbreaks in animals, healthcare workers should ask patients with symptoms compatible with zoonotic avian influenza infection (e.g. symptoms of upper or lower respiratory tract infection, but also non-respiratory symptoms, such as conjunctivitis, gastrointestinal, or neurological symptoms) about their history of exposure to animals (ECDC, 2024).

- Detections of human cases of zoonotic avian influenza through surveillance systems for seasonal influenza (EFSA, ECDC and EURL, 2024) 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 in EU/EEA countries), 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 individuals with known exposure to potentially infected animals, or cases 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 or 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 should be offered to individuals who are occupationally exposed to avian influenza viruses to prevent infection with seasonal influenza in humans and reduce the risk of co-infection with human and avian subtypes of influenza (EFSA AHAW Panel and ECDC, 2025).

- 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 protection against severe clinical disease (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[13] 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[14] and Commission Delegated Regulation (EU) 2020/687[15]).

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[13] 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.

[14] 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.

[15] 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[16] and Articles 29 and 31 of Regulation (EC) No 178/2002[17], 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 6 September and 28 November 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 June to September 2025 (EFSA, ECDC and EURL, 2025c) and that might affect the interpretation of risks related to avian influenza introduction and/or spread in Europe.

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[16] 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.

[17] 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 6 September and 28 November 2025 and submitted by Member States and other European countries via ADIS, were taken into account. Data extraction was carried on 28 November 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 4, respectively.

The annexes to this Scientific Report are available here: https://doi.org/10.5281/zenodo.17898702

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 28 November 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, 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 27 November 2025 to retrieve sequences from human cases of avian influenza reported since 6 September 2025. In cases where the same strain had multiple submissions, the ones with the most complete segment data were chosen. Sequences placed under an embargo were excluded from any analysis. 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 information was retrieved from GISAID or assigned according to specified literature. Genin2 (https://github.com/izsvenezie-virology/genin2) and GenoFLU (Youk et al., 2023) was used to assign genotypes.

Annex A – Data on HPAI virus detections in wild birds

Annex A is available on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.17898702

Annex B – Data on poultry outbreaks

Annex B includes the HPAI outbreaks in poultry for which additional data on the characteristics of the affected poultry establishments was collected and provided by reporting countries during the current reporting period. It also includes data on outbreaks that occurred too close to the publication of the previous report and are therefore included here. The Annex is available on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.17898702

Annex C – Acknowledgements

All genome sequences and associated metadata linked in the below dataset are published in GISAID's EpiFlu™ database. To view the contributors of each individual sequence with details such as accession number, virus name, collection date, originating lab and submitting lab, and the list of authors, visit: https://doi.org/10.55876/gis8.251209fo and https://doi.org/10.55876/gis8.251118xd.