SCIENTIFIC REPORT

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# Avian influenza overview March–June 2025

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## Abstract

Between 8 March and 6 June 2025, 365 highly pathogenic avian influenza (HPAI) A(H5) virus detections were reported in domestic (167) and wild (198) birds across 24 countries in Europe. HPAI A(H5N1) virus detections were predominant and mainly located in western, central and south-eastern Europe. Most detections in wild birds concerned waterfowl, particularly swans and geese, but also gulls were involved. Poultry establishments, particularly domestic ducks and chickens, continued to be affected in large numbers in Hungary and Poland. In mammals, HPAI A(H5N1) and A(H5N5) virus detections were reported in a domestic cat, red foxes, Eurasian otters and grey seals. For the first time ever, HPAI A(H5N1) viral infection was detected in a sheep in the United Kingdom. Outside Europe, the United States of America (USA) continued to report A(H5N1) virus detections in dairy cattle, while the virus was found for the first time in a gray fox (USA), a leopard cat (South Korea) and a long-tailed weasel (USA). Between 8 March and 6 June 2025, 20 cases of avian influenza virus infection in humans, including four deaths, were reported in six countries: Bangladesh (two A(H5N1) cases), Cambodia (two A(H5N1) cases), China (one A(H10N3), one A(H5N1), and 11 A(H9N2) cases), India (one A(H5N1) case), Mexico (one A(H5N1) case), and Viet Nam (one A(H5N1) case). Most of the A(H5N1) human cases (n = 5/8) reported exposure to poultry prior to detection or onset of illness. Given the widespread circulation of avian influenza viruses in animal populations, human infections remain rare. No human-to-human transmission has been documented during the reporting period. The risk of infection with the avian A(H5) clade 2.3.4.4b influenza viruses currently circulating in Europe remains low for the general public in the European Union/European Economic Area (EU/EEA) and low-to-moderate for those occupationally or otherwise exposed to infected animals or contaminated environments.

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

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[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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# Table of Contents

# 1. Introduction

This Scientific Report provides an overview of highly pathogenic avian influenza (HPAI) virus detections in poultry[2] and captive birds[3] (domestic birds), as well as wild birds, that occurred in and outside Europe between 8 March and 6 June 2025. In addition, HPAI virus detections in mammals up until 11 June 2025 and cases of avian influenza infection in humans between 8 March and 6 June 2025 are reported. Detections of low pathogenic avian influenza (LPAI) virus in birds are discussed whenever they are of zoonotic concern, or otherwise relevant.

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

# 2. Assessment

## 2.1 HPAI virus detections in birds

### 2.1.1 HPAI virus detections in birds in Europe

Figure 1 shows all HPAI virus detections in birds in Europe that were reported via the European Union (EU) Animal Disease Information System (ADIS) or the World Animal Health Information System (WOAH-WAHIS) of the World Organisation for Animal Health (WOAH) for the last five and the current epidemiological year[4] by month of suspicion. For the current epidemiological year 2024–2025, starting on 1 October 2024, data reported are truncated on 6 June 2025.

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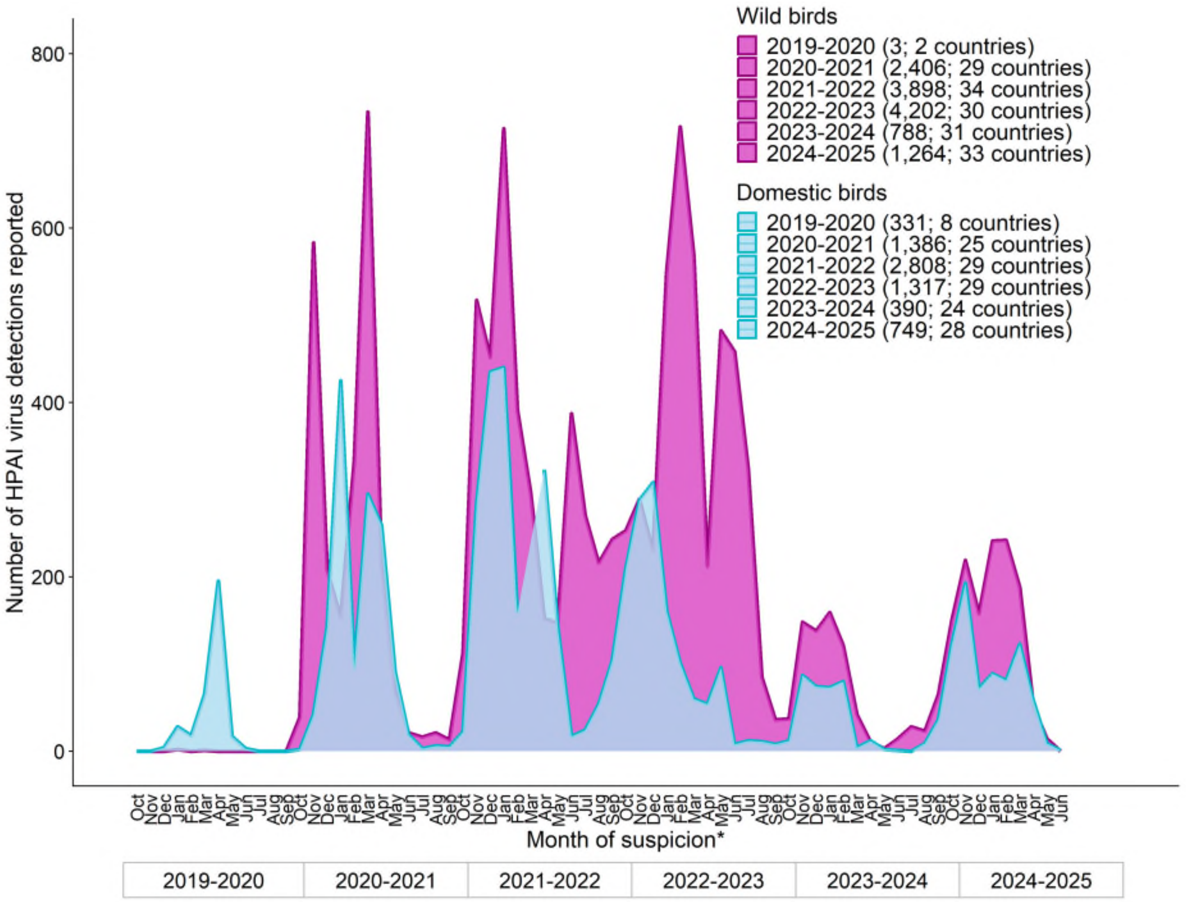
[2] According to Regulation (EU) 2016/429 of the European Parliament and of the Council of 9 March 2016, point (9), 'poultry' means birds that are reared or kept in captivity for: (a) the production of: (i) meat; (ii) eggs for consumption; (iii) other products; (b) restocking supplies of game birds;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

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

[4] In this document an 'epidemiological year' refers to the period starting on 1 October and ending on 30 September of the following year, based on the dates on which the first HPAI virus detections were observed in wild birds in Europe in 2016–2017, 2020–2021 and 2021–2022.



*If the date of suspicion was not available, the date of confirmation was used to assign the week of suspicion. United Kingdom data are from the Animal Disease Notification System (ADNS, former ADIS) up until 31 December 2020. From 1 January 2021 onwards, the data source was WOAH for the United Kingdom (excluding Northern Ireland) and ADNS/ADIS for the United Kingdom (Northern Ireland)[5].
Source: ADNS/ADIS and WOAH (data extraction carried out on 6 June 2025).

**Figure 1:** Distribution of the number of HPAI virus detections in wild birds (cumulative number n = 12,561) (pink) and in establishments keeping domestic birds (n = 6,981) (blue) reported in Europe during six epidemiological years by month of suspicion, from 1 October 2019 to 6 June 2025 (total n = 19,542)

Considering the current reporting period from 8 March to 6 June 2025, 365 HPAI virus detections were reported in poultry (147), captive (20) and wild birds (198) in 24 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 8 March to 6 June 2025. Cumulative numbers since the start of the 2024–2025 epidemiological year are reported in parentheses (1 October 2024 to 6 June 2025)

| Reporting country | Captive birds | | | Poultry | | | Wild birds | | | | Total |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | A(H5Nx) | A(H5N1) | A(H5N5) | A(H5Nx) | A(H5N1) | A(H5N5) | A(H5Nx) | A(H5N1) | A(H5N5) | A(Not typed)* | |
| Albania | - | - | - | - | 0 (5) | - | - | 0 (2) | - | - | **0 (7)** |
| Austria | - | 0 (2) | - | - | 0 (6) | - | 0 (5) | 1 (57) | - | - | **1 (70)** |
| Belgium | - | 0 (5) | - | - | 0 (3) | - | 3 (3) | 9 (33) | 0 (1) | - | **12 (45)** |
| Bosnia and Herzegovina | - | - | - | - | 0 (1) | - | - | 0 (1) | - | - | **0 (2)** |
| Bulgaria | - | - | - | - | 2 (9) | - | - | 0 (1) | - | - | **2 (10)** |
| Croatia | - | 0 (1) | - | - | 0 (2) | - | - | 2 (10) | - | - | **2 (13)** |
| Czechia | - | 3 (28) | - | - | 1 (4) | - | - | 4 (11) | - | - | **8 (43)** |
| Denmark | - | - | - | - | 2 (2) | - | - | 4 (16) | - | - | **6 (18)** |
| Estonia | - | - | - | - | - | - | - | 1 (1) | - | - | **1 (1)** |
| Faeroe Islands | - | - | - | - | - | - | - | - | 0 (1) | - | **0 (1)** |
| Finland | - | - | - | - | - | - | - | 2 (5) | - | - | **2 (5)** |
| France | 0 (3) | - | - | - | 0 (11) | - | 0 (3) | 3 (24) | - | - | **3 (41)** |
| Germany | - | 3 (24) | - | - | 2 (22) | - | 0 (13) | 22 (200) | 0 (1) | - | **27 (260)** |
| Greece | - | - | - | - | - | - | - | 0 (3) | - | - | **0 (3)** |
| Hungary | - | 0 (2) | - | - | 79 (292) | - | - | 2 (45) | - | - | **81 (339)** |
| Iceland | - | - | - | - | - | 0 (1) | 0 (2) | - | 0 (25) | - | **0 (28)** |
| Ireland | - | - | - | - | - | - | - | 7 (15) | - | - | **7 (15)** |
| Italy | - | - | - | 0 (6) | 0 (50) | - | 0 (5) | 0 (90) | - | - | **0 (151)** |
| Latvia | - | - | - | - | 1 (1) | - | - | - | - | - | **1 (1)** |
| Lithuania | - | 1 (1) | - | - | 0 (1) | - | - | 2 (3) | - | - | **3 (5)** |
| Moldova | - | 0 (19) | - | - | - | - | - | 0 (3) | - | - | **0 (22)** |
| Netherlands | - | 0 (2) | - | - | 1 (5) | - | - | 34 (206) | - | - | **35 (213)** |
| North Macedonia | - | 0 (1) | - | - | 0 (1) | - | - | - | - | - | **0 (2)** |
| Norway | - | - | 0 (1) | - | - | - | - | 1 (3) | 0 (8) | - | **1 (12)** |
| Poland | - | 10 (30) | - | - | 46 (109) | - | - | 14 (69) | - | - | **70 (208)** |
| Portugal | - | 0 (3) | - | - | 0 (2) | - | - | 0 (4) | - | - | **0 (9)** |

| Reporting country | Captive birds |  |  | Poultry |  |  | Wild birds |  |  |  | Total |
|---|---|---|---|---|---|---|---|---|---|---|---|
|  | A(H5Nx) | A(H5N1) | A(H5N5) | A(H5Nx) | A(H5N1) | A(H5N5) | A(H5Nx) | A(H5N1) | A(H5N5) | A(Not typed)* |  |
| Romania | - | 0 (2) | - | - | 0 (2) | - | - | 3 (8) | - | - | **3 (12)** |
| Serbia | - | - | - | - | - | - | - | 0 (4) | - | - | **0 (4)** |
| Slovakia | - | 0 (6) | - | - | 0 (2) | - | - | 2 (15) | - | 0 (1) | **2 (24)** |
| Slovenia | - | 0 (1) | - | - | - | - | - | 0 (47) | - | - | **0 (48)** |
| Spain | - | - | - | - | - | - | - | 1 (10) | - | - | **1 (10)** |
| Sweden | - | - | - | - | 0 (1) | - | - | 7 (13) | 1 (1) | - | **8 (15)** |
| Switzerland | - | - | - | - | - | - | - | 0 (9) | - | - | **0 (9)** |
| Türkiye | - | 0 (3) | - | - | 1 (7) | - | - | - | - | - | **1 (10)** |
| Ukraine | - | 0 (7) | - | - | - | - | - | 0 (1) | - | - | **0 (8)** |
| United Kingdom (excluding Northern Ireland) | - | 3 (9) | - | - | 12 (49) | 0 (1) | - | 70 (255) | 1 (23) | - | **86 (337)** |
| United Kingdom (Northern Ireland)[6] | - | 0 (1) | - | - | 0 (3) | - | - | 2 (8) | - | - | **2 (12)** |
| **Total** | **0 (3)** | **20 (147)** | **0 (1)** | **0 (6)** | **147 (590)** | **0 (2)** | **3 (31)** | **193 (1172)** | **2 (60)** | **0 (1)** | **365 (2013)** |

*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.

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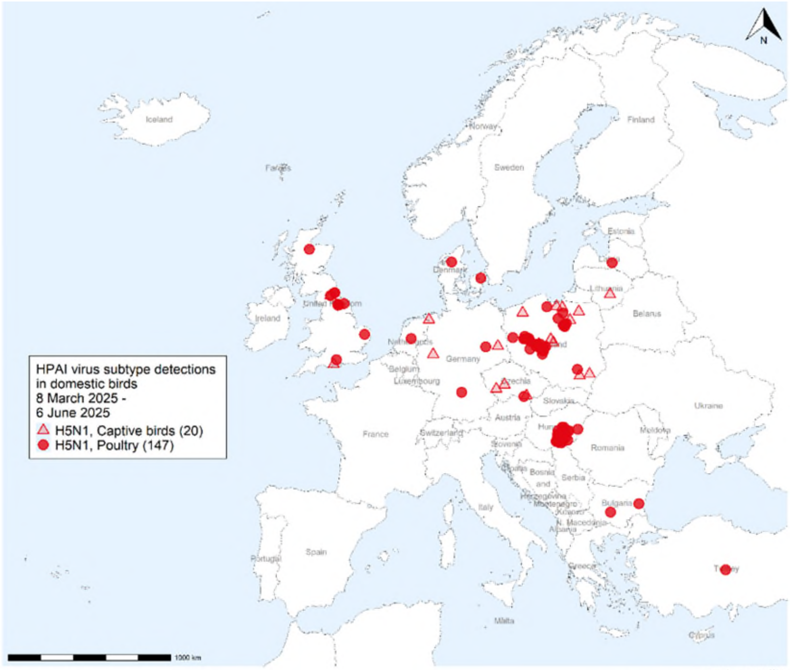
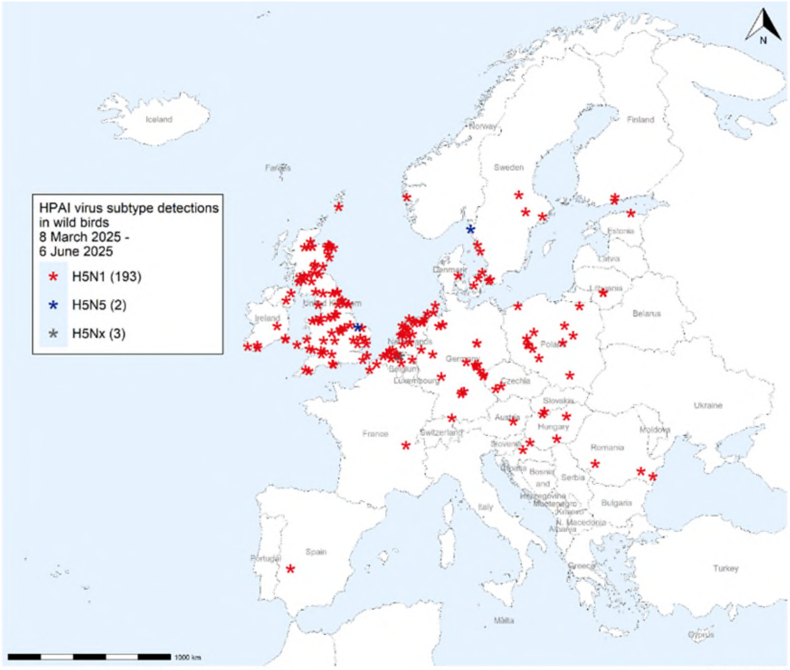
[6] In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Windsor Framework, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 06/06/2025



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 06/06/2025

*This designation is without prejudice to positions on status and is in line with United Nations Security Council Resolution 1244 and the International Court of Justice Opinion on the Kosovo Declaration of Independence.
United Kingdom (excluding Northern Ireland) data are from WOAH and ADIS for the United Kingdom (Northern Ireland)[7].
Source: ADIS, EFSA and WOAH (data extraction carried out on 6 June 2025).

**Figure 2:** Geographic distribution, based on available geocoordinates, of HPAI virus detections in poultry and captive birds (167) (upper panel), and in wild birds (198) (lower panel) reported by virus subtype in Europe from 8 March to 6 June 2025

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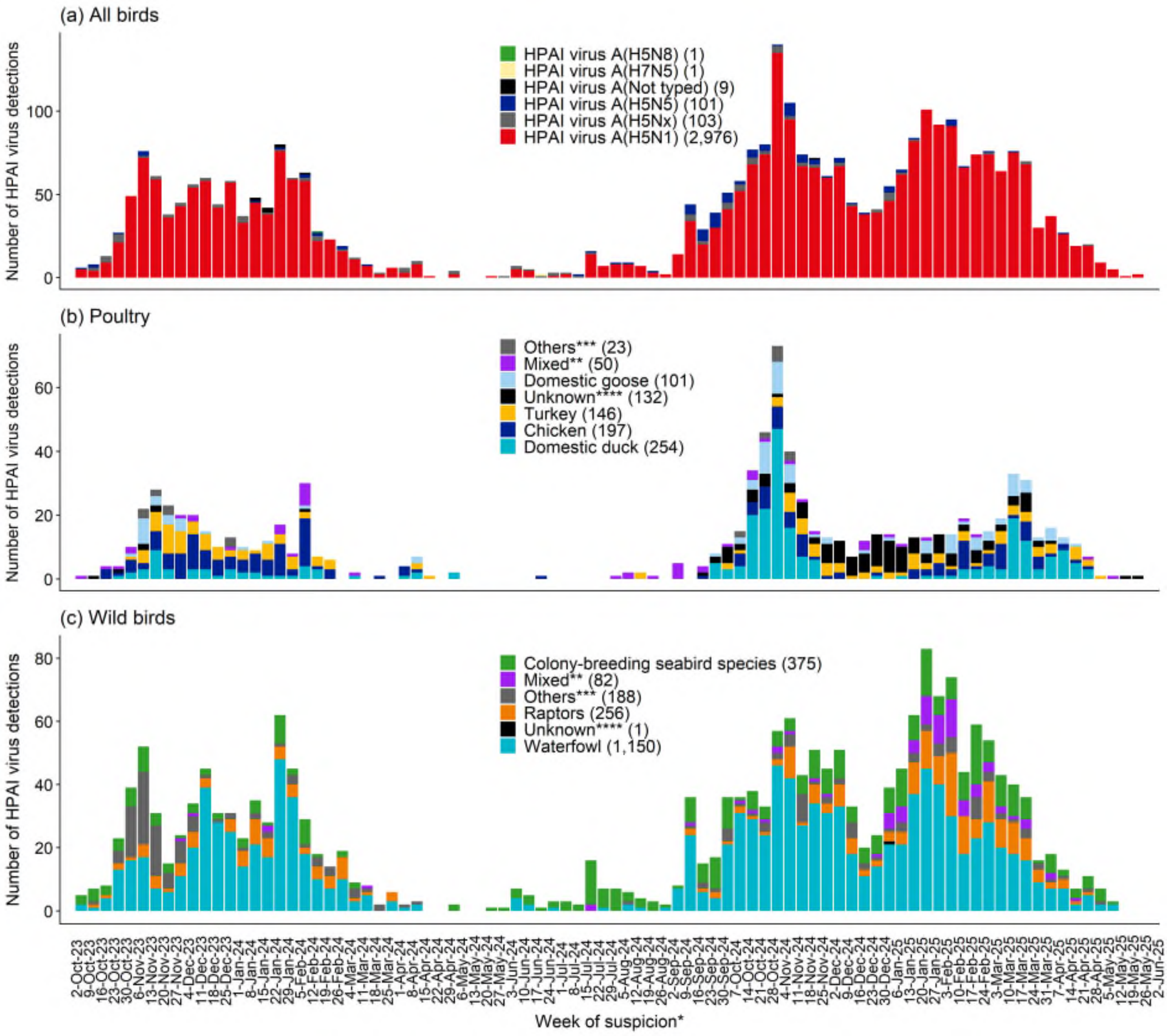
[7] In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Windsor Framework, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).

After reaching a peak at the end of the previous reporting period (7 December 2024 to 7 March 2025), there was a constant decline in HPAI virus detections in both domestic and wild birds during the current period (8 March to 6 June 2025). This decline coincides with the reduction in the number of wild waterfowl in wintering areas of Europe. The overall number of HPAI virus detections during this period was higher than during the same period in the previous epidemiological year but similar or lower to the years before. The 2024–2025 epidemic peak was both longer (from about September 2024 to April 2025) and higher (up to about 250 reported detections per week, both in wild and domestic birds) than the 2023–2024 epidemic peak (from about October 2023 to February 2024; up to about 125–150 reported detections per week, both in wild and domestic birds) (Figure 1).

During the current reporting period, HPAI A(H5N1) outbreaks in poultry and captive birds occurred in a broad band across the western (United Kingdom, Netherlands, Denmark), central (Germany, Poland, Czechia) and south-eastern (Hungary, Bulgaria, Türkiye) parts of Europe, while they were absent in the north-east, central south and south-west (Figure 2, upper panel). There were two large clusters of outbreaks in poultry in Hungary (79 establishments) and Poland (46 establishments). HPAI A(H5N1) virus detections in wild birds followed more or less the same geographical pattern, although there were a few reported detections in the north-east (Norway, Sweden, Finland, Estonia) and south-west (France, Spain) (Figure 2, lower panel). There were only two HPAI A(H5N5) virus detections in the current reporting period in wild birds (Sweden, United Kingdom), and none in poultry or captive birds (Figure 2, lower panel). Overall, the majority of HPAI virus detections in wild birds during the current reporting period were in waterfowl (Figure 3).



*If the date of suspicion was not available, the date of confirmation was used to assign the week of suspicion.
**'Mixed' refers to outbreaks in which multiple species or categories were involved.
***'Others' groups all other affected categories that are not indicated in the legend.
****'Unknown' refers to affected categories that were not further specified during reporting.
Source: ADNS/ADIS, EFSA and WOAH (data extraction carried out on 6 June 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 6 June 2025

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

## Poultry

Between 8 March and 6 June 2025, 147 HPAI outbreaks in poultry were reported from 10 countries in Europe: Hungary (79), Poland (46), United Kingdom (excluding Northern Ireland) (12), Bulgaria (2), Denmark (2), Germany (2), Czechia (1), Latvia (1), Netherlands (1), and Türkiye (1) (Table 1, Figure 2, Figure 4).

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

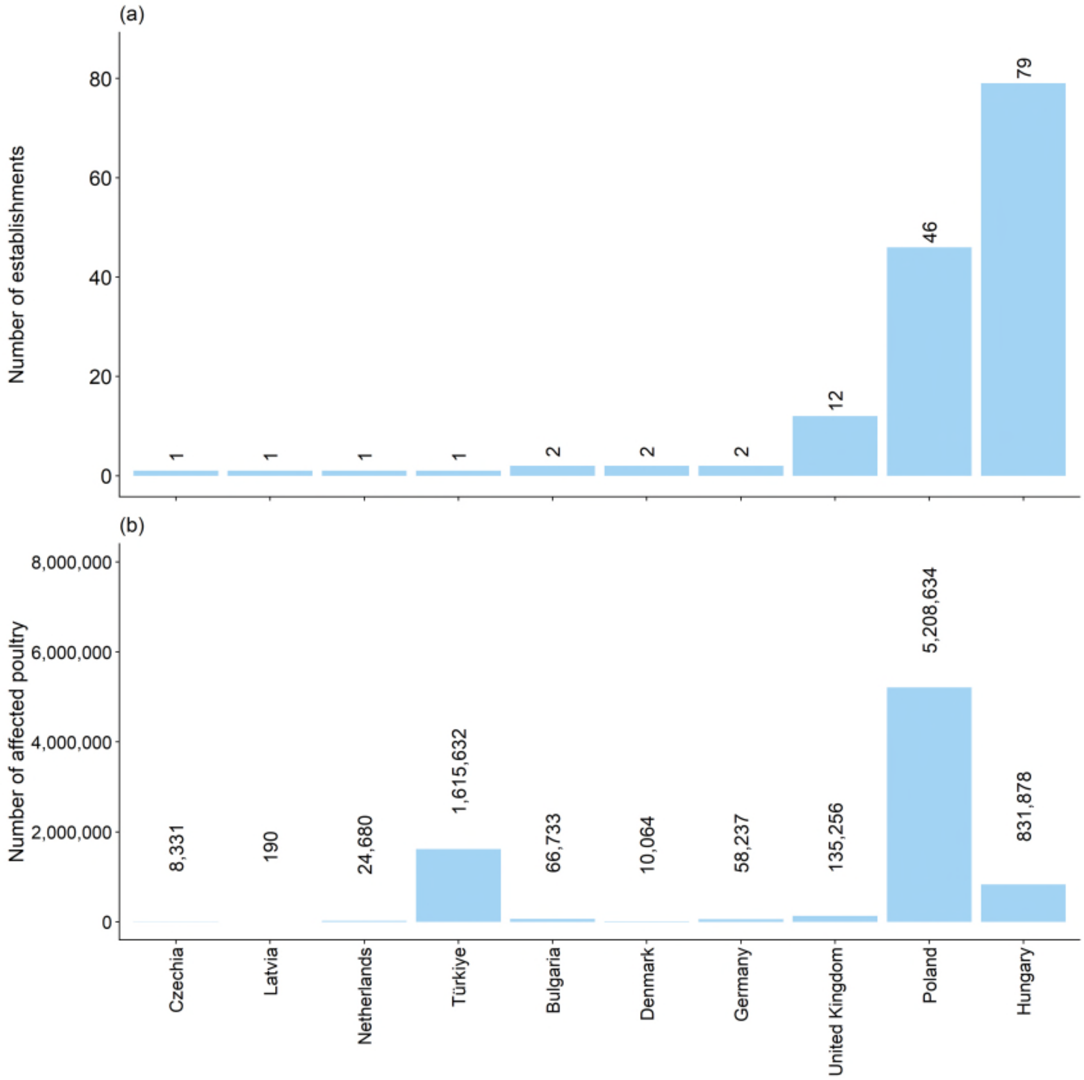

**Figure 4:** Number of HPAI-affected establishments (147) (a) and number of poultry in the HPAI-affected establishments (7,959,635) (b) in Europe between 8 March and 6 June 2025 (countries are ranked according to the number of outbreaks)

All 147 outbreaks in poultry were due to HPAI A(H5N1) viruses. This compares to a total of only 15 A(H5) outbreaks during the same period in the previous epidemiological year, which was however exceptionally low compared to the years before. During the current reporting period, Hungary and Poland accounted for 85% (125/147) of the HPAI outbreaks in poultry and 76% of the number of poultry culled (Figure 4). In total, almost 8 million birds died or were culled in the HPAI-affected establishments (Figure 4), about 19% less than in the previous reporting period. Overall, 37% (54/147) of the HPAI outbreaks in poultry were classified as primary, 55% (81/147) as secondary, and for 12 outbreaks (8%) this information was not available. In contrast to the previous reporting period, when the 21 secondary outbreaks occurred across seven different countries, the 81 secondary outbreaks between 8 March and 6 June 2025 occurred within only two countries: Hungary (55) and Poland (26). During the current reporting period, the most affected poultry category in Europe was the 'domestic duck' category (42%, 61/147 outbreaks), followed by the 'chicken' (16%, 24/147), 'turkey' (16%, 23/147), and 'domestic goose' (14%, 21/147) categories. Multiple species were kept by two (1%) establishments and no information was available on the species kept for another 16 (11%) establishments (Figure 3). Hungary accounted for 84% (51/61) of the outbreaks in the 'domestic duck' category, while Poland accounted for 83% (20/24) of the affected establishments keeping chickens.

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 8 March to 6 June 2025, 147 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 131 of these 147 (89%) outbreaks, reported to ADIS before 23 May 2025, from Czechia, Denmark, Germany, Hungary, Netherlands, and Poland (Annex B). Among those, 50 were reported as primary and 81 as secondary. In 88% (44/50) of primary outbreaks, indirect contact with wild birds was considered the most likely source of introduction, followed by direct contact with wild birds (2%, 1/50). For the remaining 10% (5/50) the source was reported as unknown. For 86% (70/81) of the secondary outbreaks, indirect contact with poultry was considered the most likely source of introduction, followed by indirect contact (10%, 8/81) among infected establishments through wild birds, and for the remaining 4% (3/81) the source was reported as unknown. For the other 16 (11%) outbreaks in poultry, no additional data were provided or they were reported to ADIS after 23 May 2025 and therefore occurred too shortly before the publication of this report. In this report, a short summary on these outbreaks will be given, but additional data will only be collected in the next round and included in Annex B of the following report.

*Bulgaria*

During the current reporting period from 8 March to 6 June 2025, two primary outbreaks in poultry were reported in Bulgaria via ADIS. No additional data to complement the information in ADIS were provided by the country. On 16 March and 19 May, two A(H5N1) outbreaks were detected in two commercial establishments keeping laying hens (n = 39,188 and n = 27,545, respectively), where mortality and clinical signs were observed.

*Czechia*

During the current reporting period from 8 March to 6 June 2025, one primary outbreak in poultry was reported in Czechia via ADIS, for which additional data were collected and provided by the reporting country (Annex B). On 17 May, an A(H5N1) outbreak was detected in a commercial multi-species establishment keeping pheasants (n = 6,887; production type not reported), chickens (n = 1,350; production type not reported), ducks (n = 50; production type not reported), peafowls (n = 30; production type not reported), geese (n = 11; production type not reported), and turkeys (n = 3; production type not reported). At the time of detection, high mortality (52.6%) and clinical signs were observed, but only in the pheasants. The birds had outdoor access, and the most likely source of introduction was direct contact with wild birds. Twenty-five people were reported as exposed.

*Denmark*

During the current reporting period from 8 March to 6 June 2025, two primary outbreaks in poultry were reported in Denmark via ADIS. Additional data were collected and provided by the reporting country for both outbreaks (Annex B). On 1 April, an A(H5N1) outbreak was detected in a non-commercial establishment keeping laying hens (n = 24). At the time of detection, increased mortality (45.8%) was reported as well as clinical signs of depression and lethargy immediately before death were observed. The birds had outdoor access, and the most likely source of introduction was indirect contact with wild birds. Two people were reported as exposed. Both were professionals in disease control measures and performed the culling, destruction and cleaning with protective equipment. On 10 April 2025, a second A(H5N1) outbreak was confirmed in a commercial establishment keeping turkeys for fattening (n = 10,040). At the time of detection, mortality (0.6%) was reported and clinical signs of depression and respiratory distress were observed. The birds were kept indoor, and the most likely source of introduction was indirect contact with wild birds. Forty-five people were reported as exposed. All forty-five exposed persons were professionals in disease control measures and performed the culling, destruction and cleaning with protective equipment.

*Germany*

During the current reporting period from 8 March to 6 June 2025, two primary outbreaks in poultry were reported in Germany via ADIS. Additional data were collected and provided by the reporting country for both outbreaks (Annex B). On 9 March, an A(H5N1) outbreak was detected in a commercial establishment keeping turkeys for fattening (n = 30,000). At the time of detection, increased mortality (25.0%) was reported but no clinical signs were observed. The birds were kept indoor, and the most likely source of introduction was indirect contact with wild birds. The number of exposed people was reported as unknown. On 28 March, a second A(H5N1) outbreak was detected in a commercial establishment keeping chickens for breeding (n = 28,237). At the time of detection, mortality (0.3%) was reported but no clinical signs were observed. The birds were kept indoor, and the most likely source of introduction was indirect contact with wild birds. The number of exposed people was reported as unknown.

*Hungary*

During the current reporting period from 8 March to 6 June 2025, 79 outbreaks in poultry were reported in Hungary via ADIS. Additional data were collected and provided by the reporting country for all these outbreaks (Annex B). The 79 outbreaks were all confirmed as A(H5N1), with the majority (70%, 55/79) being reported as secondary and 30% (24/79) as primary outbreaks. All 79 outbreaks occurred in commercial establishments keeping single species: ducks (47%, 37/79) and geese (23%, 18/79) for foie gras production, ducks (17%, 13/79), turkeys (9%, 7/79) and geese (1%, 1/79) for fattening, broilers (2%, 2/79), and ducks for breeding (1%, 1/79). Birds with clinical signs were described in all 79 outbreaks. Mortality at the time of detection was observed in 97% (77/79) of the outbreaks and ranged between 0.05% and 96.9% (median = 4.1%) for Anseriformes, and between 0.5% and 72.3% (median = 7.0%) for Galliformes. Only two of the 79 (3%) establishments provided outdoor access, while in the remaining 77 (97%) the birds were kept indoor. Indirect contact with poultry was reported as the most likely source of introduction for 55 (70%) outbreaks, followed by indirect contact with wild birds for 24 (30%). No information was available on the number of exposed people for any of the affected establishments at the time of publication of this report. Overall, 831,702 birds were culled across the 79 affected establishments.

*Latvia*

During the current reporting period from 8 March to 6 June 2025, one primary outbreak in poultry was reported in Latvia via ADIS. No additional data to complement the information in ADIS were provided by the country, as the outbreak occurred shortly before the publication of this report. On 27 May, an A(H5N1) outbreak was detected in a non-commercial establishment keeping laying hens (n = 98), where mortality and clinical signs were observed. This outbreak represents the first HPAI outbreak in poultry in the country.

*Netherlands*

During the current reporting period from 8 March to 6 June 2025, one primary outbreak in poultry was reported in the Netherlands via ADIS, for which additional data were collected and provided by the reporting country (Annex B). On 18 March, an A(H5N1) outbreak was detected in a commercial establishment keeping turkeys for fattening (n = 24,680). At the time of detection, mortality (0.1%) and clinical signs were observed. The birds were kept indoor. The source of introduction as well as the number of exposed people were reported as unknown.

*Poland*

During the current reporting period from 8 March to 6 June 2025, 46 outbreaks in poultry were reported in Poland via ADIS. Additional data were collected from the reporting country for all these outbreaks (Annex B). The 46 outbreaks were all confirmed as A(H5N1), with over half of them (57%, 26/46) being reported as secondary and 43% (20/46) as primary outbreaks. All 46 outbreaks occurred in commercial establishments. One of these establishments kept multiple species (chickens and geese for fattening) (2%, 1/46), while the remaining 45 housed only single species: turkeys (28%, 13/46), ducks (9%, 4/46) and geese (2%, 1/46) for fattening, followed by laying hens (18%, 8/46), chickens (15%, 7/46), ducks (13%, 6/46) and geese (2%, 1/46) for breeding, and broilers (11%, 5/46). In all 46 outbreaks birds with clinical signs were described. Mortality at the time of detection was observed in 96% (44/46) of the outbreaks and ranged between 0.05% and 2.1% (median = 0.2%) for Anseriformes, and between 0.01% and 40.4% (median = 0.4%) for Galliformes. Only two of the 46 (4%) establishments provided outdoor access, while in the remaining 44 (96%) the birds were kept indoor. Indirect contact with wild birds was reported as the most likely source of introduction for 24 (52%) outbreaks, followed by indirect contact with poultry for 15 (33%). For the seven (15%) remaining outbreaks, the source of introduction remained unknown at the time of publication of this report. The total number of exposed people in all 46 outbreaks was 874. Overall, 5,208,634 birds were culled across the 46 affected establishments.

*Türkiye*

During the current reporting period from 8 March to 6 June 2025, one primary outbreak in poultry was reported in Türkiye via ADIS. No additional data to complement the information in ADIS were provided by the country. On 5 April, an A(H5N1) outbreak was detected in a commercial establishment housing 1,615,632 birds (poultry species not reported), where mortality and clinical signs were observed.

*United Kingdom (excluding Northern Ireland)*

During the current reporting period from 8 March to 6 June 2025, 12 outbreaks in poultry were reported in the United Kingdom via WOAH-WAHIS. All 12 outbreaks were confirmed as A(H5N1). Seven outbreaks (58%) occurred in commercial establishments and five (42%) in non-commercial establishments. Most of them housed chickens (n = 7; n = 3 in combination with ducks, geese and pigeons in non-commercial establishments, respectively), turkeys (n = 3; housing between 9,300 and 36,000 birds), pheasants (n = 1) and pheasant breeders (n =1). Overall, 135,256 birds were culled across the 12 affected establishments.

### Captive birds

Between 8 March and 6 June 2025, 20 HPAI outbreaks in captive birds, predominantly in establishments keeping chickens and ducks for own consumption, were reported from five countries in Europe: Poland (10), Czechia (3), Germany (3), United Kingdom (excluding Northern Ireland) (3), and Lithuania (1) (Table 1, Figure 2).

### Wild birds

During the current reporting period from 8 March to 6 June 2025, a total of 198 HPAI virus detections in wild birds (with one HPAI virus detection potentially including more than one wild bird species) were reported from United Kingdom (excluding Northern Ireland) (71), Netherlands (34), Germany (22), Poland (14), Belgium (12), Sweden (8), Ireland (7), Czechia (4), Denmark (4), France (3), Romania (3), Croatia (2), Finland (2), Hungary (2), Lithuania (2), Slovakia (2), United Kingdom (Northern Ireland)[9] (2), Austria (1), Estonia (1), Norway (1), and Spain (1).

Overall, 193 HPAI virus detections in wild birds were reported as A(H5N1), two as A(H5N5), and three as A(H5Nx) (Table 1, Figure 2). The overall number of HPAI virus detections reported in wild birds (198) during this reporting period was three times lower than in the previous reporting period (655) (Figure 3) and six times higher compared to the same period in the previous epidemiological year (35), which was however exceptionally quiet compared to the years before.

Regarding the wild bird categories involved and considering that more than one wild bird species can be included in a single HPAI virus detection, HPAI A(H5) was mostly recorded in waterfowl (45%, 89/198), followed by colony-breeding seabirds (25%, 49/198) and raptors (19%, 38/198) (Figure 5).

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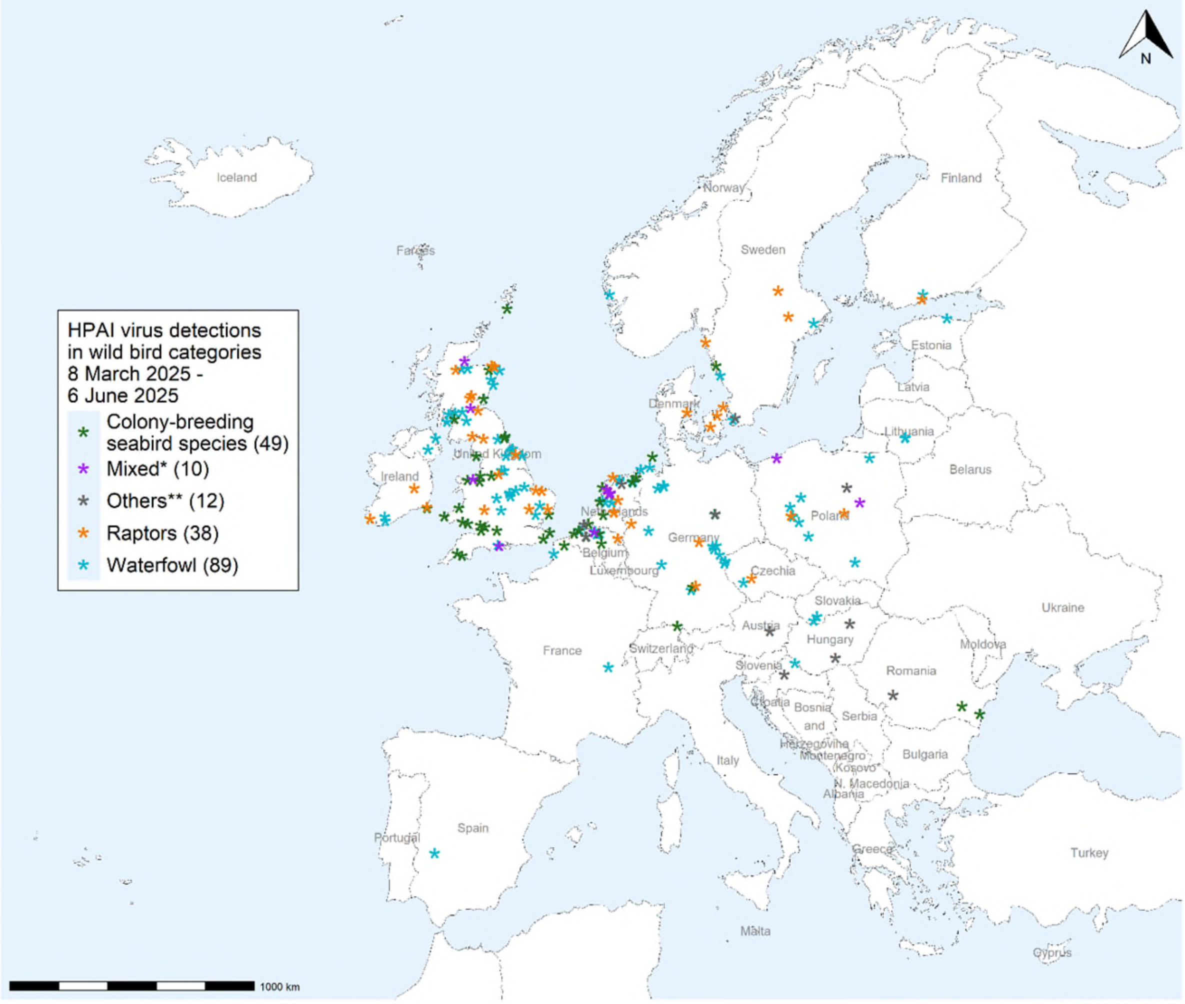
[9] In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Windsor Framework, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 06/06/2025

*This designation is without prejudice to positions on status and is in line with United Nations Security Council Resolution 1244 and the International Court of Justice Opinion on the Kosovo Declaration of Independence.
Note that the unit reported is the number of HPAI virus detections in different wild bird categories and not the total number of HPAI virus detections in wild birds (as more than one species can be involved in one single HPAI virus detection reported).
*'Mixed' refers to outbreaks in which multiple categories were involved.
**'Others' groups all other affected categories that are not indicated in the legend.
***'Unknown' refers to outbreaks for which no information on the wild bird species involved is available.
Source: ADIS, EFSA and WOAH (data extraction carried out on 6 June 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 9 March to 6 June 2025

This pattern is similar to the previous reporting period, when A(H5) was recorded in three times more waterfowl than colony-breeding seabirds. Relative to the total number of HPAI virus detections in wild birds, the percentage of HPAI virus detections in raptors in the current reporting period (18%, 35/196) was similar to the previous reporting period (16%, 83/504). Colony-breeding seabirds were primarily detected along the coast, while other wild bird species were found both in coastal and inland locations. The wild bird species in which HPAI viruses were detected belonged mainly to three orders: Anseriformes (108 HPAI virus detections), Charadriiformes (58), and Accipitriformes (36). The main waterfowl identified to species were the mute swan (36 in the current vs 101 in the previous reporting period), greylag goose (23 vs 78), and Canada goose (14 vs 15) (Figures A.1–A.2 in Annex A). In the order Charadriiformes at least seven different gull species were affected during the current reporting period: the main ones identified to species were the European herring gull (24 vs 59), great black-backed gull (10 vs 10), and black-headed gull (9 vs 31). The Accipitriformes detected positive for HPAI viruses during the current reporting period were mostly Eurasian buzzards (17 vs 71), followed by peregrine falcons (5 vs 10) and white-tailed eagles (4 vs 4). The complete list of wild bird species found as HPAI virus-infected from 8 March to 6 June 2025 is reported in Figure A.1 in Annex A. The number of HPAI virus-affected wild birds that were not identified to species was 26/198 (13%), 32% lower than in the previous reporting period (151/799, 19%) (Figures A.1–A.2 in Annex A).

Only two HPAI A(H5N5) virus detections were reported in wild birds in Europe during the current reporting period, in a white-tailed eagle from Sweden and a red kite from the United Kingdom (Table 3). Given the wide range of wild bird species in which A(H5N5) has been reported in the current epidemiological year, it is not possible to point to a single species in which this subtype is persisting.

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

| Wild bird category | Species | Number of affected birds |
|---|---|---|
| Colony-breeding seabirds (27) | European herring gull | 9 |
| | Unidentified Laridae species | 4 |
| | Great black-backed gull | 3 |
| | Black-headed gull | 3 |
| | Pallas's gull | 2 |
| | Black-legged kittiwake | 1 |
| | Grey gull | 1 |
| | Mew gull | 1 |
| | Unidentified Phalacrocoracidae species | 1 |
| | Unidentified Sulidae | 1 |
| Waterfowl (14) | Greylag goose | 9 |
| | Whooper swan | 2 |
| | Eurasian wigeon | 1 |
| | Mallard | 1 |
| | Mute swan | 1 |
| Raptors (13) | Red kite | 4 |
| | White-tailed eagle | 4 |
| | Common buzzard | 2 |
| | Common barn owl | 2 |
| | Gyrfalcon | 1 |
| Others* (10) | Common raven | 5 |
| | Hooded crow | 3 |
| | Ring-necked pheasant | 2 |
| **Total** | | **64** |

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

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

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

### 2.1.2 HPAI virus detections in birds outside Europe

An overview of the HPAI virus detections in birds from other countries outside Europe that were notified to WOAH from 8 March to 6 June 2025 is presented in Table 4 and Figure 6.

**Table 4:** Number of HPAI virus detections in non-European countries notified to WOAH, by virus subtype and country, from 8 March to 6 June 2025. Cumulative numbers since the start of the 2024–2025 epidemiological year are reported in parentheses (1 October 2024 to 6 June 2025)

| **Region (total in season)** | **Country** | **Domestic birds** | | | | | | | | **Wild birds** | | | | | **Total** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | **A(H5N1)** | **A(H5N2)** | **A(H5N5)** | **A(H5N9)** | **A(H5Nx)** | **A(H7N6)** | **A(H7N8)** | **A(H7N9)** | **A(H5N1)** | **A(H5N3)** | **A(H5N5)** | **A(H5N8)** | **A(H5Nx)** | |
| Africa (25) | Liberia | 0 (1) | - | - | - | - | - | - | - | - | - | - | - | - | **0 (1)** |
| | Niger | 0 (1) | - | - | - | - | - | - | - | - | - | - | - | - | **0 (1)** |
| | Nigeria | 5 (19) | - | - | - | - | - | - | - | - | - | - | - | - | **5 (19)** |
| | Togo | 3 (3) | - | - | - | 0 (1) | - | - | - | - | - | - | - | - | **3 (4)** |
| Americas (698) | Argentina | - | - | - | - | 0 (1) | - | - | - | - | - | - | - | - | **0 (1)** |
| | Brazil | 3 (3) | - | - | - | - | - | - | - | 1 (1) | - | - | - | - | **4 (4)** |
| | Canada | 11 (109) | 0 (2) | 0 (1) | - | - | - | - | - | 0 (9) | - | 0 (7) | - | - | **11 (128)** |
| | Colombia | 0 (8) | - | - | - | - | - | - | - | - | - | - | - | - | **0 (8)** |
| | Greenland | - | - | - | - | - | - | - | - | - | - | 0 (1) | - | - | **0 (1)** |
| | Mexico | 0 (4) | - | - | - | - | - | - | - | 0 (9) | - | - | - | - | **0 (13)** |
| | Panama | 0 (1) | - | - | - | - | - | - | - | - | - | - | - | - | **0 (1)** |
| | Peru | - | - | - | - | 0 (9) | - | - | - | - | - | - | - | 0 (7) | **0 (16)** |
| | Puerto Rico | 0 (1) | - | - | - | - | - | - | - | - | - | - | - | - | **0 (1)** |

| **Region (total in season)** | **Country** | **Domestic birds** | | | | | | | | **Wild birds** | | | | | **Total** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | **A(H5N1)** | **A(H5N2)** | **A(H5N5)** | **A(H5N9)** | **A(H5Nx)** | **A(H7N6)** | **A(H7N8)** | **A(H7N9)** | **A(H5N1)** | **A(H5N3)** | **A(H5N5)** | **A(H5N8)** | **A(H5Nx)** | |
| | United States of America | 51 (514) | - | - | - | 1 (8) | - | - | 1 (1) | 0 (2) | - | - | - | - | **53 (525)** |
| Antarctica (1) | Falkland Islands | - | - | - | - | - | - | - | - | 0 (1) | - | - | - | - | **0 (1)** |
| Asia (373) | Bangladesh | - | - | - | - | 1 (1) | - | - | - | - | - | - | - | - | **1 (1)** |
| | Cambodia | 3 (8) | - | - | - | - | - | - | - | 0 (2) | - | - | - | - | **3 (10)** |
| | Hong Kong | - | - | - | - | - | - | - | - | 0 (1) | - | - | - | - | **0 (1)** |
| | India | 0 (30) | - | - | - | - | - | - | - | 0 (5) | - | - | - | - | **0 (35)** |
| | Israel | 0 (13) | - | - | - | - | - | - | - | 0 (3) | - | - | 1 (1) | - | **1 (17)** |
| | Japan | 0 (51) | - | - | - | - | - | - | - | 0 (109) | - | - | - | 0 (6) | **0 (166)** |
| | Mongolia | - | - | - | - | - | - | - | - | 0 (1) | - | - | - | - | **0 (1)** |
| | Nepal | 0 (1) | - | - | - | - | - | - | - | - | - | - | - | - | **0 (1)** |
| | Philippines | 3 (4) | 0 (1) | - | 1 (1) | - | - | - | - | 1 (1) | - | - | - | - | **5 (7)** |
| | Russia | - | - | - | - | - | - | - | - | 0 (3) | - | - | - | - | **0 (3)** |
| | South Korea | 11 (47) | - | - | - | - | - | - | - | 4 (42) | 0 (1) | - | - | - | **15 (90)** |
| | Taiwan | 0 (25) | - | - | - | - | - | - | - | 1 (9) | - | - | - | - | **1 (34)** |
| | Viet Nam | 1 (10) | - | - | - | - | - | - | - | - | - | - | - | - | **1 (10)** |
| Oceania (5) | Australia | - | - | - | - | - | - | 0 (4) | - | - | - | - | - | - | **0 (4)** |
| | New Zealand | - | - | - | - | - | 0 (1) | - | - | - | - | - | - | - | **0 (1)** |
| **Total** | | **91 (853)** | **0 (3)** | **0 (1)** | **1 (1)** | **2 (20)** | **0 (1)** | **0 (4)** | **1 (1)** | **7 (198)** | **0 (1)** | **0 (8)** | **1 (1)** | **0 (13)** | **103 (1105)** |

'-' means that no HPAI outbreaks were notified to WOAH.
Source: WOAH (data extraction carried out on 6 June 2025).

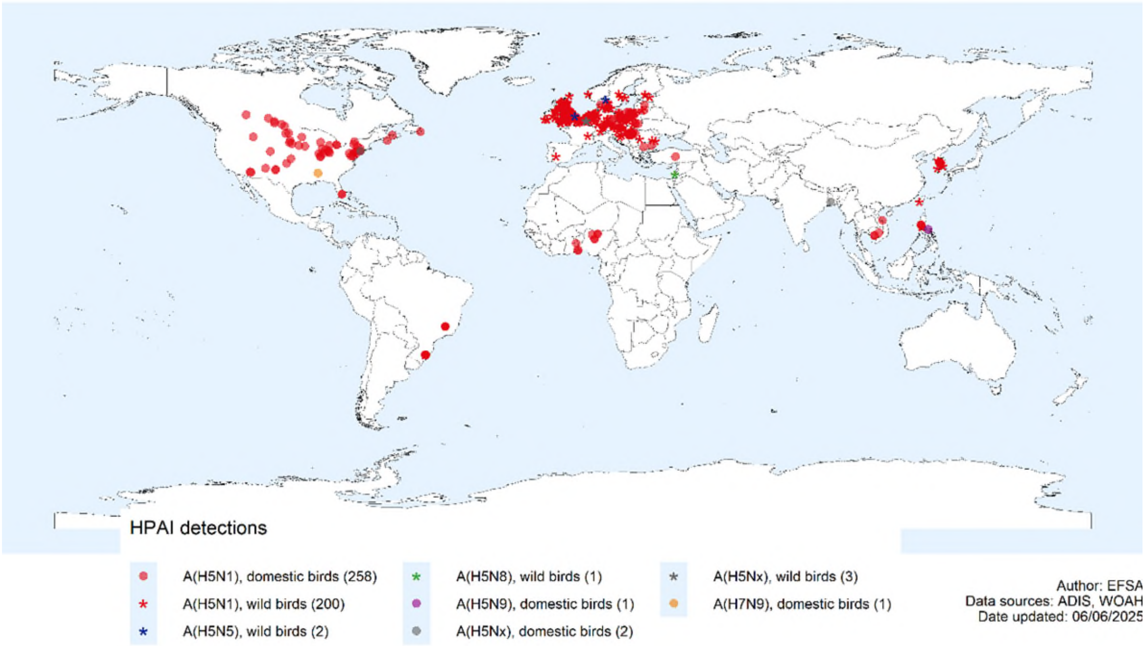


**Figure 6:** Geographic distribution, based on available geocoordinates, of HPAI virus detections reported worldwide in domestic (262) and wild (206) birds by virus type, from 8 March to 6 June 2025

In the tables and figures of the present report, only data extracted from WOAH on 6 June 2025 are presented. However, HPAI virus detections in domestic and wild birds are also reported to the public via different means. This additional information on HPAI virus detections available from sources other than WOAH-WAHIS has been integrated in the text below.

In comparison to the previous reporting period from 7 December 2024 to 7 March 2025 (EFSA, ECDC and EURL, 2025a), the total number of HPAI virus detections in domestic and wild birds officially notified to WOAH from outside Europe decreased from 655 to 103 and the number of reporting countries outside Europe from 22 to 12 (Table 4, Figure 6). Overall, HPAI virus detections in domestic birds officially reported to WOAH from outside Europe decreased notably from the previous to the current reporting period (548 vs 95), and the number of outbreaks in wild birds almost vanished (105 vs 8). Compared to the same period in the previous epidemiological year, the number of official notifications to WOAH during the current reporting period was about 40% lower than the number of outbreaks reported between 8 March and 6 June 2024 (103 vs 171 outbreaks).

In the current reporting period from 8 March to 6 June 2025, Africa continued to officially report HPAI A(H5N1) virus detections to WOAH with 5 and 3 outbreaks reported in domestic poultry from Nigeria and Togo, respectively.

In the Americas, the USA and Canada accounted for 67% of the reported HPAI A(H5) outbreaks in domestic birds outside Europe (n = 53 and n = 11, respectively), but no HPAI virus detections in wild birds were notified by these countries to WOAH. Based on data retrieved from the United States Department of Agriculture (USDA), the large epidemic of HPAI A(H5N1) in the USA remained at a high level in domestic bird establishments of all sizes with 23 states affected (USDA, online-a). Affected commercial establishments comprised turkeys for meat production (n = 5; housing between 13,400 and 33,400 birds), laying hens and pullets for egg production (n = 5 and n = 4, respectively; housing between

293,000 and 2.25 million birds), and duck (n = 1; housing 3,400 birds) and broiler (n = 1, housing 47,700 birds) breeders. In addition, 20 live bird markets were affected in the USA, specifically in the states of Florida, New Jersey, New York, and Pennsylvania. An outbreak of A(H7N9) was reported in broiler breeders in Mississippi (n = 1; housing 46,000 birds). As regards wild birds, the USDA reported 90 A(H5) virus detections, mainly in mallards (n = 33), black vultures (n = 15) and bald eagles (n = 7) (USDA, online-b). Other affected species included the bufflehead, Canada goose, common grackle, European starling, great blue heron, great horned owl, hooded merganser, house sparrow, osprey, peregrine falcon, red-tailed hawk, sanderling, sandhill crane, snow goose, and turkey vulture. As in the previous reporting period, Canada officially reported outbreaks of HPAI A(H5N1) to WOAH in 11 domestic bird establishments with a total of 94,499 birds affected (CFIA, online-a). As regards wild birds, the Canadian Food Inspection Agency National Centre for Foreign Animal Disease reported 45 A(H5N1) virus detections, namely in waterfowl (n = 23), raptors (n = 18), seabirds (n = 3) and corvids (n = 1). Furthermore, A(H5N5) was detected in 7 wild birds: American crow (n = 5), bald eagle (n = 1) and herring gull (n = 1) (CFIA, online-b). In South America, only Brazil officially reported HPAI A(H5N1) virus detections in domestic (n = 3) and wild birds (n = 1) to WOAH, which marks the first HPAI virus detection in poultry in the country ever. According to the Brazilian Ministry of Agriculture, Livestock and Food Supply (MAPA, online), during the current reporting period two poultry outbreaks were confirmed in a commercial and a backyard establishment, both housing chickens. As regards captive birds, 14 HPAI virus detections were confirmed in the following species: anhinga, black swan, black-necked swan, coscoroba swan, greylag goose, Indian peafowl, Muscovy duck, mute swan, ringed teal, and wood duck. Among those were a zoo in Rio Grande do Sul, where around 100 waterfowl were affected (Asiaone, online), and another zoo in Brasilia, where a duck and a pigeon were found dead (Poder360, online). Finally, three HPAI virus detections in wild birds (emu, rufous hornero and white-faced whistling) were reported (MAPA, online). In Mexico, HPAI A(H7N3) virus was detected in a commercial poultry establishment in Nuevo León (Intolerancia diario, online).

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

HPAI A(H5) virus detections continued to be officially reported to WOAH in large numbers from Asia, particularly from South Korea (n = 15), the Philippines (n = 5) (Manila Standard, online), Cambodia (n = 3), Israel (n = 1), Taiwan (n = 1), and Viet Nam (n = 1). This includes the first detection of the HPAI A(H5N9) subtype in domestic ducks in the Philippines (Daily Tribune, online) and a report of HPAI A(H5N8) in a booted eagle in Israel. In addition, Bangladesh officially reported the first detection of A(H5) virus in domestic birds in 7 years. Only the media reported about further detections in India, where small- to medium-sized domestic bird establishments (chickens, quails) continued to be affected (The Times of India, online-a; News Meter, online). Vaccination has been discussed as a potential control option given the current situation (Devdiscourse, online). In addition, a peacock and a ruddy shelduck were found dead in a zoo in Kanpur (The Times of India, online-b). The media also reported the detection of HPAI A(H5) virus in a bean goose and a peregrine falcon in Japan (The Pinnacle Gazette, online).

A list of all wild bird species that were reported to WOAH as HPAI virus-infected from outside Europe between 8 March and 6 June 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 (Github izsvenezie-virology, online-a, b) with the FluMutDB v6.4 mutation database (https://github.com/izsvenezie-virology/FluMutDB).

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

Since October 2024, complete genome sequences of more than 1,400 clade 2.3.4.4b HPAI A(H5) viruses from 29 European countries including Russia and the Republic of Georgia have been characterised. Based on the genetic data available as of 1 June 2025, the vast majority (about 85%) of the sequenced viruses during the 2024–2025 epidemiological year belong to a single genotype, EA-2024-DI, which has been detected in wild (mainly Anseriformes) and domestic birds from 27 European countries, including Russia and the Republic of Georgia, representing the most widespread genotype in Europe. Phylogenetic analyses indicate that the viruses belonging to this genotype form two genetic groups, i.e. DI.1 and DI.2, with DI.2 being the most frequent (> 90% of the EA-2024-DI viruses) and widespread variant, identified all over Europe, in southern Europe – from Portugal to the North Caucasus region in Southern Russia and the Republic of Georgia – and in the north from the United Kingdom/Ireland to Finland. Based on the data available so far, during the current reporting period (March–May) EA-2024-DI.2 continues to be the most prevalent genotype in Europe. Of note, this same genotype was detected in different wild bird species and domestic birds also in Israel (October 2024–January 2025).

New genotypes, all originating from reassortment events between EA-2024-DI and LPAI viruses, have been sporadically detected, and only three of them have been characterised in multiple countries: EA-2024-EA identified in Italy, Croatia and Poland; EA-2024-EE identified in Austria, Denmark, Switzerland, Sweden and Germany; and EA-2024-EF in Germany, Denmark, the Netherlands, Norway and Sweden. Based on the data available so far, during this reporting period genotypes EA-2024-EE and EA-2024-EF continue to be sporadically detected in different northern and central European countries.

Since October 2024, the detection of the gull-adapted genotypes EA-2022-BB and EA-2023-DT has been reported mainly (EA-2022-BB) or exclusively (EA-2023-DT) in seabirds (Laridae), with the EA-2022-BB circulating along the northern European coasts of France, Belgium, the Netherlands, the United Kingdom and in the mainland of Germany, and the EA-2023-DT genotype (last characterisation in November 2024) along the Atlantic coast of Spain. Since March 2025, the EA-2022-BB genotype has been found in domestic birds and different gull species in the United Kingdom, in a common tern in Ireland, in a common moorhen and European herring-gull in Belgium, and also in a black-headed gull at Lake Constance in Germany.

A persistent circulation of the A(H5N5) EA-2021-I genotype has been reported in Norway, the United Kingdom and Iceland, and sporadically in Belgium, the Netherlands and probably in Germany (partial genome). Based on the available data from the GISAID-EpiFlu database, outside Europe this genotype has been detected also in Japan, Canada and the USA.

In poultry, the vast majority (about 90%) of the outbreaks reported in the 2024–2025 epidemiological year in Europe have been associated with genotype EA-2024-DI, with DI.2 being the most frequent (about 90% of the EA-2024-DI viruses). Few other outbreaks were caused by genotypes EA-2022-BB (France, the United Kingdom and in Stavropol in Russia), A(H5N5) EA-2021-I (Iceland and Norway), EA-2024-EA in Poland, EA-2024-EF in Germany, as well as few minor genotypes detected in single or few outbreaks. Of note is the identification of old genotypes (EA-2023-DA and EA-2020-AF) in poultry in Bulgaria (October 2024) and Czechia (November 2024, February and May 2025), which were not detected in wild birds during the current epidemiological year in or outside other regions of Europe, suggesting undetected persistent circulation of these genotypes in an unknown ecological or domestic niche.

During the current reporting period, Poland and Hungary are the countries that have registered the highest number of poultry outbreaks. In Poland, the viruses collected since October 2024 from more than 130 outbreaks belong to three genotypes, with the vast majority (94%) belonging to the genotype EA-2024-DI. Genetic analysis indicates the occurrence of multiple introductions into the domestic bird population, followed by some possible secondary spread among the affected farms. In particular, a cluster of > 50 EA-2024-DI.2 viruses collected between January and April 2025 from commercial and backyard establishments from different geographic areas, mainly within the Voivodeship of Masovian and of Greater Poland, may indicate sustained between-farm transmission events, although multiple introductions of genetically similar viruses circulating in wild birds into the domestic population cannot be excluded. In Hungary, the genetic data obtained from 15 A(H5N1) viruses collected from October 2024 to April 2025 from wild and domestic birds showed that they all belonged to a single genotype (EA-2024-DI.2). The characterised viruses cluster with viruses collected from domestic birds in Czechia, Slovakia and Germany, indicating the circulation of a genetically highly related strain in this geographic area.

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

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

Similarly to the viruses collected during the previous epidemiological years (2020–2021, 2021–2022, 2022–2023), some of the mutations in the HA protein, 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 which have been circulating in Europe since October 2024, whereas others (i.e. V210I, T188I, E251K, S155N and Q192R) have only been sporadically observed (≤ 8 viruses). The impact of all these HA mutations on the biological characteristics of the circulating viruses is still unknown; however, in the vast majority of circulating A(H5Nx) strains none of the mutations has been shown to cause a shift from avian-like to human-like receptor binding preference or changes in the pH of membrane fusion or virus thermostability, which indicates that the currently circulating viruses have limited potential for human-to-human transmission (Yang et al., 2025). Besides the mutations in the HA protein, it is important to mention that most of the A(H5N1) viruses belonging to the EA-2022-BB and EA-2023-DT genotypes contain mutations NP-Y52N and NA-S369I, which may increase their zoonotic potential due to the evasion of innate immunity and mammalian restriction factors or disruption of the second sialic acid binding site (2SBS). All the currently circulating A(H5N5) viruses (genotype EA-2021-I) contain a deletion in the NA stalk region, which is a virulence determinant in chickens (Stech et al., 2015).

Mutations associated with a reduced susceptibility of A(H5N1) viruses to the available antiviral drugs authorised for use in humans have rarely been identified in the circulating strains. Specifically, mutations associated with resistance to amantadine and rimantadine, NA and PA inhibitors (WHO, online-a) have been detected in approximately 0.5%, 1% and 0.5% of the analysed A(H5N1) viruses, respectively. However, for PA inhibitors, it is important to mention that mutations have been studied in seasonal influenza viruses and not specifically for A(H5N1) viruses; the threshold of ≥ 3 $IC_{50}$ fold-change was used for the assignment of viruses with a reduced susceptibility to PA inhibitors.

Since October 2024, mutations in the PB2 protein associated with virus adaptation in mammals (E627K/V, D701N or K526R) (Suttie et al., 2019) have been detected in 49 European viruses collected from birds, more specifically in i) 33 A(H5N1) viruses collected from wild and domestic birds from eight different countries and ii) 16 A(H5N5) viruses (genotype EA-2021-I) collected from wild and domestic birds in the United Kingdom, Norway and Iceland. 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 3.2% in the current epidemiological year (up to May 2025). This may be explained by the spread in birds of viruses containing such mutations, as suggested by the identification in the phylogenetic tree of clusters of viruses sharing the same substitution. Some of these clusters include viruses collected from the same geographic area, the same species and time period, while others contain viruses collected from multiple countries and species, such as seven A(H5N1) viruses with PB2-701N collected from wild and domestic birds in Italy and Croatia between October and November 2024, and two clusters, composed of three and five A(H5N5) viruses, with PB2-627V and PB2-627K, respectively, collected from birds and mammals in Norway and Iceland.

## 2.2 HPAI virus detections in non-human mammals

From 8 March to 11 June 2025, HPAI A(H5N1) and A(H5N5) viruses were reported in wild and captive mammals both in and outside Europe. The data described were actively collected from Member States and other European countries, retrieved through WOAH-WAHIS and from the USDA websites (for cases that occurred in the USA), and supplemented with information from media reports (Table 5).

In wildlife in Europe, HPAI A(H5N1) virus was once again detected in red foxes in the Netherlands (n = 2), Germany (n = 1) and Finland (n = 1), and in a Eurasian otter in Finland (n = 1). For another Eurasian otter in Finland, the exact H5 subtype could not be determined (n = 1). Of note were the HPAI A(H5N5) virus detections in a red fox in Norway (n = 1) and in grey seals in the United Kingdom. Among a total of 40 carcasses sampled in Norfolk on the east coast of England, 15 (37.5%) tested positive (BBC, online).

In Poland, a domestic cat associated with an affected backyard poultry establishment tested positive for HPAI A(H5N1) virus after presumably hunting infected wild birds. In addition, in March 2025, HPAI A(H5N1) virus was found for the first time ever in a sheep in the United Kingdom. The case was identified following routine surveillance of farmed livestock in an establishment in Yorkshire where HPAI A(H5N1) had been confirmed in captive birds. The single animal was an ewe with signs of mastitis but no other clinical signs. It was kept in the same stable as the ducks in the establishment (GovUK, online-a). The milk was positive by polymerase chain reaction (PCR) and the blood tested positive for H5 antibodies (GovUK, online-b). Later there was a report of the detection of antibodies in a sheep in Norway. The sheep had grazed among dead and sick seabirds during the major outbreak of HPAI A(H5N1) in Finnmark, Norway, in 2023 and has recently tested positive for the presence of antibodies specific for type A influenza and H5 subtype avian influenza. In June 2024, retrospective blood samples were obtained from 220 sheep that grazed in the region during the outbreak 11 months earlier. Initial screening was conducted using a commercial ELISA targeting type A influenza following the manufacturer's recommendations for bovine samples available at that time, and all samples tested negative. When samples were reanalysed in May 2025 according to current recommendations for bovine samples, two ewes (born 2022 and 2023) tested positive for antibodies to type A influenza virus. Only one of these (born 2022) tested positive for the presence of antibodies specific for H5 subtype avian influenza by a commercial ELISA. The same sample tested weakly positive (titer 1:20) by haemagglutination inhibition (HI) test using a 2.3.4.4 clade H5N1 antigen and was later confirmed positive by both HI and microneutralisation assays by the EURL. No clinical disease was noted among sheep in association with the 2023 avian outbreak, and there is no indication of sheep-to-sheep transmission (personal communication by Johanna Hol Fosse, NVI).

During the current reporting period, several European countries actively reported the absence of HPAI viruses in mammals: Belgium, Denmark, Ireland, Luxembourg, Slovakia, Sweden, Switzerland, and the United Kingdom (Northern Ireland)[10].

Outside Europe, the number of dairy cattle farms reportedly affected by HPAI A(H5N1) virus in the USA rose to 1,073 in 17 states during the current reporting period, but the rate of new infections has been gradually slowing. An experimental infection study assessed the risk of infecting 7 to 11-week-old calves (n = 5) by feeding them with milk from HPAI A(H5N1) experimentally inoculated lactating cows for 4 days. Calves showed mild clinical signs and shed virus in their upper respiratory tracts (nasal swabs) for 2–4 days post infection and seroconverted, confirming the risk of transmission of A(H5N1) to calves if fed with unpasteurised milk from A(H5N1)-positive dairy cows diverted from the human food supply (Davila et al., 2025).

In addition, the virus was detected in more cats, including cats exposed to raw pet feed (FDA, online; NJ Health, online; The Mercury, online). According to the USDA (USDA, online-c), HPAI A(H5N1) virus was once again found in a wide range of wildlife species, including American mink, black bear, bobcat, bottlenose dolphin, fisher, gray fox, harbour seal, house mouse, long-tailed weasel (first time ever), mountain lion, raccoon, red fox and striped skunk. In Canada, in the first quarter of 2025, before the current reporting period, additional detections of the HPAI A(H5N5) subtype were reported in cats, a bobcat, a red fox and a striped skunk. In addition, HPAI A(H5N1) virus was found in striped skunks and an American mink. For the first time ever, HPAI A(H5N1) virus was detected in harbour seals in Japan, two of which tested positive (The Mainichi, online). As previously described, HPAI viruses continued to affect large felines worldwide, among which were several captive (serval in Bangladesh, Asiatic lion and tiger in India) (Hindustan Times, online; The Times of India, online-c) and wild animals (leopard cat (first time ever) in South Korea, several species in the USA).

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[10] 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 5:** Avian influenza A(H5Nx) virus detections in mammalian species other than humans related to circulating viruses worldwide, 2016–2025

| Virus | Animal (order, family, species) | | | Country | Reference |
|---|---|---|---|---|---|
| A(H5N1) or A(H5Nx) clade 2.3.4.4b | Artiodactyla | Bovidae | Cattle (*Bos taurus*) | United States of America | WOAH<br>USDA |
| | | | Goat (*Capra hircus*) | United States of America | WOAH<br>USDA |
| | | | Sheep (*Ovis aries*) | Norway, United Kingdom | GovUK (online-a,b)<br>Personal communication by Johanna Hol Fosse (NVI) |
| | | Camelidae | Alpaca (*Lama pacos*) | United States of America | USDA (online-d) |
| | | Suidae | Pig (*Sus scrofa*) | Italy*, United States of America | WOAH<br>Rosone et al. (2023) |
| | Carnivora | Canidae | Arctic fox (*Vulpes lagopus*) | Finland | WOAH |
| | | | Common raccoon dog (*Nyctereutes procyonoides*) | Finland, Japan, Sweden* | WOAH<br>Personal communication by Malin Grant (SVA) |
| | | | Coyote (*Canis latrans*) | United States of America | WOAH<br>USDA |
| | | | Dog (*Canis lupus familiaris*) | Canada, Italy*, Poland | WOAH<br>Szaluś-Jordanow et al. (2024) |
| | | | Gray fox (*Urocyon cinereoargenteus*) | United States of America | USDA |
| | | | Japanese raccoon dog (*Nyctereutes viverrinus*) | Japan | WOAH |
| | | | Red fox (*Vulpes vulpes*) | Austria, Belgium, Canada, Denmark, Estonia, Finland, France, Germany, Ireland, Italy, Japan, Latvia, Netherlands, Norway, Slovenia, Sweden**, United Kingdom (Northern Ireland)***, United Kingdom, United States of America | WOAH<br>Personal communication by Aleksandra Hari (AFSVSPP)<br>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<br>USDA |
| | | | Canadian lynx (*Lynx canadensis*) | United States of America | WOAH<br>USDA |
| | | | Caracal (*Caracal caracal*) | Poland, United States of America | WOAH<br>USDA |
| | | | Cat (*Felis catus*) | Canada, Belgium, France**, Hungary**, Italy*, Netherlands*, Poland, South Korea, United States of America | WOAH<br>USDA<br>TF1 Info (online), Rijksoverheid (online)<br>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<br>USDA<br>Personal communication by Malin Grant (SVA) |

| Virus | Animal (order, family, species) | | | Country | Reference |
|---|---|---|---|---|---|
| | | | Leopard (*Panthera pardus*) | India, United States of America, Viet Nam | USDA<br>The Times of India (online-d) |
| | | | Leopard cat (*Prionailurus bengalensis*) | South Korea | WOAH |
| | | | Lion (*Panthera leo*) | India, Peru, United States of America, Viet Nam | WOAH<br>USDA<br>Hindustan Times (online), The Times of India (online-c) |
| | | | Mountain lion (*Puma concolor*) | United States of America | WOAH<br>USDA |
| | | | Serval (*Leptailurus serval*) | Bangladesh, United States of America | WOAH<br>USDA |
| | | | Tiger (*Panthera tigris*) | India, United States of America, Viet Nam | WOAH<br>USDA<br>Hindustan Times (online), The Times of India (online-c,d) |
| | | Mephitidae | Striped skunk (*Mephitis mephitis*) | Canada, United States of America | WOAH<br>USDA |
| | | Mustelidae | American marten (*Martes americana*) | United States of America | WOAH<br>USDA |
| | | | American mink (*Neovison vison*) | Canada, Finland, Spain, United States of America | WOAH<br>USDA |
| | | | Beech marten (*Martes foina*) | Netherlands | GISAID (online) |
| | | | Eurasian otter (*Lutra lutra*) | Netherlands, Finland, Sweden, United Kingdom | WOAH |
| | | | European badger (*Meles meles)* | Netherlands | WOAH |
| | | | European pine marten (*Martes martes*) | Germany | WOAH |
| | | | European polecat (*Mustela putorius*) | Belgium, Netherlands | WOAH |
| | | | Ferret (*Mustela furo*) | Belgium, Poland, Slovenia | WOAH<br>Golke et al. (2024) |
| | | | Fisher (*Pekania pennanti*) | United States of America | WOAH<br>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<br>USDA |
| | | Odobenidae | Walrus (*Odobenus rosmarus*) | Norway | WOAH |
| | | Otariidae | Antarctic fur seal (*Arctocephalus gazella*) | South Georgia and the South Sandwich Islands, Uruguay | WOAH<br>Bennison et al. (2024), Banyard et al. (2024) |
| | | | Northern fur seal (*Callorhinus ursinus*) | Russia | WOAH |
| | | | South American fur seal (*Arctocephalus australis*) | Argentina, Brazil, Peru, Uruguay | WOAH |
| | | | South American sea lion (*Otaria flavescens*) | Argentina, Brazil, Chile, Peru, Uruguay | WOAH |
| | | Phocidae | Caspian seal (*Pusa caspica*) | Russia | WOAH |

| Virus | Animal (order, family, species) | | | Country | Reference |
|---|---|---|---|---|---|
| | | | 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, United Kingdom, United States of America | WOAH<br>USDA<br>The Mainichi (online) |
| | | | Southern elephant seal (*Mirounga leonina*) | Argentina, South Georgia and the South Sandwich Islands, Possession Island | WOAH<br>Bennison et al. (2024), Banyard et al. (2024), PASTAAF (online-b, c) |
| | | Procyonidae | Raccoon (*Procyon lotor*) | Canada, Germany, United States of America | WOAH<br>USDA |
| | | | South American coati (*Nasua nasua*) | Germany, Uruguay | WOAH |
| | | Ursidae | American black bear (*Ursus americanus*) | Canada, United States of America | WOAH<br>USDA |
| | | | Asian black bear (*Ursus thibetanus*) | France | WOAH |
| | | | Brown bear (*Ursus arctos*) | United States of America | WOAH |
| | | | Kodiak grizzly bear (*Ursus arctos horribilis*) | United States of America | WOAH |
| | | | Polar bear (*Ursus maritimus*) | United States of America | WOAH |
| | Cetacea | Delphinidae | Bottlenose dolphin (*Tursiops truncatus*) | Peru, United States of America | WOAH<br>USDA |
| | | | Chilean dolphin (*Cephalorhynchus eutropia*) | Chile | WOAH |
| | | | Common dolphin (*Delphinus delphis*) | Peru, United Kingdom | WOAH<br>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<br>USDA |
| | Lagomorpha | Leporidae | Desert cottontail (*Sylvilagus audubonii*) | United States of America | USDA |
| | Rodentia | Cricetidae | Deer mouse (*Peromyscus* spp.) | United States of America | USDA |
| | | | Prairie vole (*Microtus ochrogaster*) | United States of America | USDA |
| | | Muridae | Black rat (*Rattus rattus*) | United States of America | USDA |

| Virus | Animal (order, family, species) | | | Country | Reference |
|---|---|---|---|---|---|
| | | | Brown rat (*Rattus norvegicus*) | Egypt, United States of America | USDA<br>Kutkat et al. (2024) |
| | | | House mouse (*Mus musculus*) | United States of America | WOAH<br>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<br>USDA |
| A(H5N1) clade 2.3.2.1a | Carnivora | Felidae | Cat (*Felis catus*) | India | Raut et al. (2025)<br>The Times of India (online-e) |
| A(H5N5) clade 2.3.4.4b | Carnivora | Canidae | Arctic fox (*Vulpes lagopus*) | Iceland | WOAH<br>Personal communication by Brigitte Brugger (MAST, 2025) |
| | | | Red fox (*Vulpes vulpes*) | Canada, Norway | WOAH |
| | | Felidae | Bobcat (*Lynx rufus*) | Canada | WOAH |
| | | | Cat (*Felis catus*) | Canada, Iceland | WOAH<br>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<br>CFIA (online-b) |
| | | Mustelidae | American mink (*Neovison vision*) | Iceland | Personal communication by Brigitte Brugger (MAST, 2025) |
| | | | Eurasian otter (*Lutra lutra*) | Norway | Personal communication by Silje Granstad (Norwegian Veterinary Institute, 2025) and Lars-Erik Lund Rondestveit (Norwegian Food Safety Authority, 2025) |
| | | | European pine marten (*Martes martes*) | Netherlands | Personal communication by Dennis Bol (NVWA, 2024) |
| | | Phocidae | Grey seal (*Halichoerus grypus*) | United Kingdom | WOAH<br>FarmingUK (online),<br>GovUK (online-c) |
| | | | Ringed seal (*Pusa hispida*) | Canada | WOAH<br>CFIA (online-b) |
| | | 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) |

| Virus | Animal (order, family, species) | | | Country | Reference |
|---|---|---|---|---|---|
| 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<br>Shin et al. (2019), Floyd et al. (2021)<br>Personal communication by Siamak Zohari (SVA, 2024) |
| | | | Harbour seal (*Phoca vitulina*) | Denmark, Germany, United Kingdom | WOAH<br>Floyd et al. (2021), Ärzteblatt (online), Avian Flu Diary (online-a), Outbreak News (online) |

*Serological detection.
**Both virological and serological detection.
***In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Windsor Framework, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).

### 2.2.1 Genetic characteristics of HPAI viruses of the A(H5Nx) subtype circulating in Europe in non-human mammals

Details on the nomenclature of the HPAI A(H5) viruses used in this section are reported in Appendix B. Genotypes are assigned using the criteria described in Fusaro et al. (2024) and the tool GenIn2 (https://github.com/izsvenezie-virology/genin2). Mutation analyses of the A(H5N1) viruses have been performed using FluMut (Github izsvenezie-virology, online-a, b) with FluMutDB v6.4 mutation database (https://github.com/izsvenezie-virology/FluMutDB).

Since October 2024, the complete or partial genome sequences of 28 HPAI A(H5) viruses of clade 2.3.4.4b collected from seven distinct mammalian species (i.e. domestic cat, Eurasian badger, Eurasian lynx, Eurasian otter, grey seal, red fox, and sheep) in ten different European countries have been characterised. As expected, the viruses collected from four domestic cats in Italy, Belgium and Poland, ten red foxes in Italy, Slovenia, Germany, the Netherlands and England, a Eurasian otter in Finland and a sheep in England belong to the A(H5N1) genotype EA-2024-DI, which is the most prevalent in birds in these geographic areas. The eight A(H5N1) viruses from the wild mammals (red foxes and a Eurasian otter) show highest identity with the A(H5N1) viruses collected from wild birds in the same area, and two of them (one red fox from Italy and one from Germany) differ from the most closely related viruses circulating in wild birds in the PB2-E627K substitution, a mutation that facilitates a more efficient virus replication in mammals (Aggarwal et al., 2011). On the other hand, genetic data indicate that the domestic mammals – a sheep from England and domestic cats with outdoor access from Italy, Belgium and Poland – living on or near backyard (Poland, Italy, England) or commercial (Belgium) establishments where A(H5N1) had been confirmed were likely infected following exposure to poultry or virus-contaminated fomites. The virus sampled from the cat in Italy differs from the virus collected from the chicken from the same establishment in the mammalian-adaptive substitution PB2-E627K. Although the partial nature of the genome sequences retrieved prevents assessing the presence of PB2 mutations in the virus sampled from the cat in Poland, the PB2-E627K substitution was identified in the backyard chickens from which the cat likely got the infection, thus suggesting a potential bird-to-mammal-to-bird transmission.

The viruses characterised from a domestic cat with outdoor access in Iceland as well as from a Eurasian lynx, a Eurasian otter, and a red fox in Norway belong to the A(H5N5) EA-2021-I genotype, which represents the prevalent or unique genotype identified in birds in these countries. Interestingly, the EA-2021-I genotype has also been detected in grey seals off the east coast of England. Of note, the A(H5N5) viruses collected from the cat in Iceland and from the red fox in Norway cluster within a group of viruses sampled from wild birds and mammals from different countries all sharing the PB2-E627V mammalian adaptive marker (Suttie et al., 2019). Similarly, the viruses collected from a seal in England and the Eurasian lynx in Norway cluster together within a group of viruses previously collected from wild birds in multiple European countries and all sharing the substitution PB2-E627K. Whether these mutations may have favoured the mammalian infection is still unknown.

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

Overall, since October 2024, more than 55% of the characterised viruses from mammals in Europe contain at least one of the adaptive markers associated with an increased virulence and replication in mammals in the PB2 protein (E627K or E627V) (Suttie et al., 2019).

## 2.3 Avian influenza virus infections in humans

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

Since 8 March and as of 6 June 2025, a total of 20 cases of avian influenza virus infection in humans, including four deaths, have been reported in six countries worldwide, involving both children and adults. Eight cases were A(H5N1) reported in Bangladesh (n= 2), Cambodia (n=2, two deaths), China ex Viet Nam (n=1), India (n=1, one death), Mexico (n=1, one death) and Viet Nam (n=1). In addition, China reported one case of human infection with A(H10N3) and 11 cases with A(H9N2) infection (Table 6).

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

| | **Cases reported 2025-03-08 - 2025-06-06** | | | **Cases reported since first report** | | | |
|---|---|---|---|---|---|---|---|
| **Subtype** | **Cases reported** | **Deaths** | **Reporting countries** | **First report** | **Cases reported** | **Deaths** | **Reporting countries** |
| A(H5N1) | 8* | 4 | 6 | 1997 | 997* | 471** | 25 |
| A(H5N6) | 0 | 0 | 0 | 2014 | 93 | 36 | 2 |
| A(H9N2) | 11 | 0 | 1 | 1998 | 168 | 2 | 10 |
| A(H10N3) | 1 | 0 | 1 | 2021 | 5 | 0 | 1 |

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

**Deaths reported since 2003 out of a total of 977 cases reported from 2003 until 6 June 2025. Mortality data are not available for cases reported prior to 2003.

Seventeen human cases had publicly available information on animal exposure: 16 reported exposure to poultry and, despite being investigated, the epidemiological exposure for the remaining case could not be established (Table 7).

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

| **Subtype** | **Reported exposure**** | **Cases** |
|---|---|---|
| A(H5N1)* | Poultry | 5 |
| | Exposure source unknown† | 1 |
| | Not reported‡ | 2 |
| A(H9N2) | Poultry | 10 |
| | Not reported‡ | 1 |
| A(H10N3) | Poultry | 1 |

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

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

†No epidemiological exposure was identified after investigation.

‡Not reported or publicly available.

Sequence data from GISAID's EpiFlu™ database submitted since the previous report was retrieved for ten A(H5N1) strains representing cases in Bangladesh, Cambodia, India and Viet Nam, reported during this reporting period (8 March – 6 June), and an additional A(H5N1) strain from the United States for a human infection reported in the previous report (EFSA, ECDC and EURL, 2025a). The strains were analysed phylogenetically and for mutation markers (Figure 8; Table 8). In addition, one A(H10N3) strain, representing a case in China from 2024, was recently deposited in GISAID and was also included in the mutation analysis (Table 8).

**Table 8:** Strains included in phylogenetic and mutation analysis. Sequences include those deposited in GISAID's EpiFlu™ database from 8 March 2025 to 28 May 2025

| Isolate Name | Subtype | Clade | Country | Collection Date | Markers |
|---|---|---|---|---|---|
| A/Bangladesh/Khulna/IEDCR-icddr_b-IC2/2025 | H5N1 | 2.3.2.1a | Bangladesh | 2025-02-01 | [a];M2:A30S;PB2:D9N;PB2:I292V |
| A/Bangladesh/Khulna/IEDCR-icddr_b-IC1/2025 | H5N1 | 2.3.2.1a | Bangladesh | 2025-04-24 | [a];PB2:I292V |
| A/India/Mangalgiri_NIV_25_594/2025 | H5N1 | 2.3.2.1a | India | 2025-03-07 | [a];PB2:I292V |
| A/Cambodia/24070331/2024 | H5N1 | 2.3.2.1e[c] | Cambodia | 2024-07-30 | NA:-;PA:-;PB1:-;PB2:- |
| A/Cambodia/SVH240441/2024 | H5N1 | 2.3.2.1e[c] | Cambodia | 2024-08-02 | PA:K142N;PB1:H115Q,PB2:E627K |
| A/Cambodia/KSH240409/2024 | H5N1 | 2.3.2.1e[c] | Cambodia | 2024-08-17 | NA:-;PA:-;PB1:-;PB2:- |
| A/Cambodia/KSH250004/2025 | H5N1 | 2.3.2.1e[c] | Cambodia | 2025-01-08 | PA:-;PB1:H115Q,PB2:E627K |
| A/Cambodia/NPH250131/2025 | H5N1 | 2.3.2.1e[c] | Cambodia | 2025-02-24 | PA:-;PB1:-;PB2:- |
| A/Cambodia/25030237/2025 | H5N1 | 2.3.2.1e[c] | Cambodia | 2025-03-22 | PA:K142N;PB1:H115Q,PB2:E627K |
| A/Cambodia/j05273701/2025 | H5N1 | 2.3.2.1e[c] | Cambodia | 2025-05-26 | NA:I396M;PA:-;PB1:-;PB2:- |
| A/Vietnam/05EI1001/2025 | H5N1 | 2.3.2.1e[c] | Viet Nam | 2025-04-17 | [b];PA:K142N;PB1:H115Q,PB2:E627K |
| A/Ohio/06-1/2025 (genotype D1.3) | H5N1 | 2.3.4.4b | United States | 2025-02-12 | PB2:I292V |
| A/Nanning/gxswp/2024 | H10N3 |  | China | 2024-01-23 | PB2:A588V;PB2:I292V |

[a] HA1:S154N;HA1-5:T195I;HA1-5:V210I

[b] HA1:S123P,HA2-5:R167K

[c] Previously classified as clade 2.3.2.1c (WHO, online-b)

\- No segment

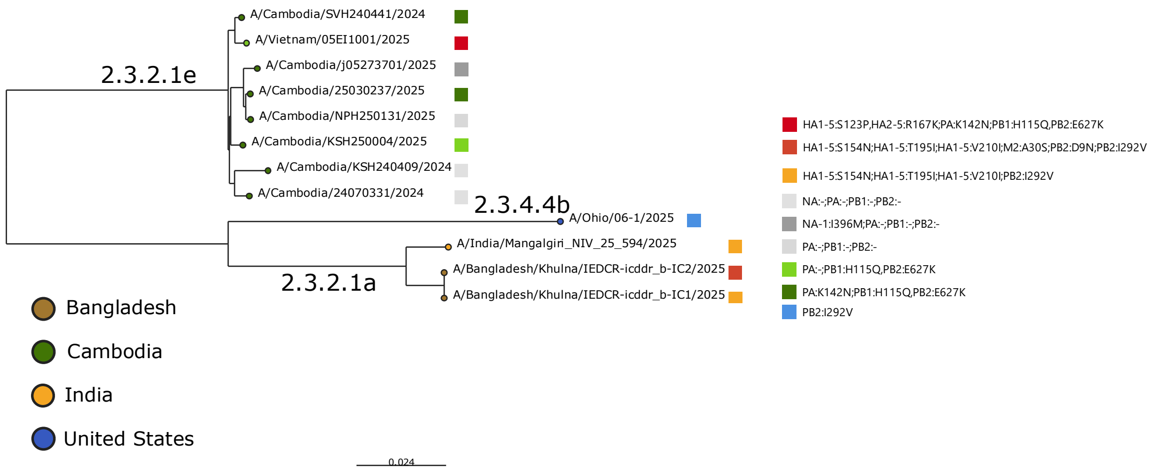

**Figure 8:** Phylogenetic tree from nucleotide alignment of the HA segment annotated with significant mutation marker findings from all segments

### 2.3.2 Human A(H5N1) cases

Since 1997, a total of 997 confirmed cases of influenza A(H5N1) have been reported globally (Figure 7), including 471 deaths (data available from 2003).

During the current reporting period (8 March – 6 June 2025), eight human influenza A(H5N1) cases, including four deaths, were reported in six countries: Bangladesh, Cambodia, China (travelling from Viet Nam), India, Mexico and Viet Nam. Three clades of the A(H5N1) virus were detected, including 2.3.4.4b in Mexico, 2.3.2.1a in Bangladesh and India, and 2.3.2.1e (formerly classified as 2.3.2.1c) in Cambodia and Viet Nam.

All the cases, except one for which information is pending, were hospitalised, with one (a child) having an underlying condition. Seven cases were in children aged from two to 11 years (for one child, the exact age was not reported) and one was in an adult. Information on symptoms was available for six cases: all cases had fever and all but one had respiratory symptoms (cough, shortness of breath). In addition, several children had gastrointestinal symptoms. The child who had an underlying cardiac condition was diagnosed with encephalitis, but did not have any respiratory symptoms, and subsequently recovered.

All four deaths were reported in children. Two deaths were reported in Cambodia (in a three-year-old and an 11-year-old) from different provinces (Kratie and Kampong Speu), one in India (in a two-year-old) and one in Mexico (in a three-year-old). Exposure to backyard poultry was reported for the deceased cases in Cambodia and India. For the case in Mexico, the investigation could not establish epidemiological exposure.

Detailed information on the cases by country is provided below.

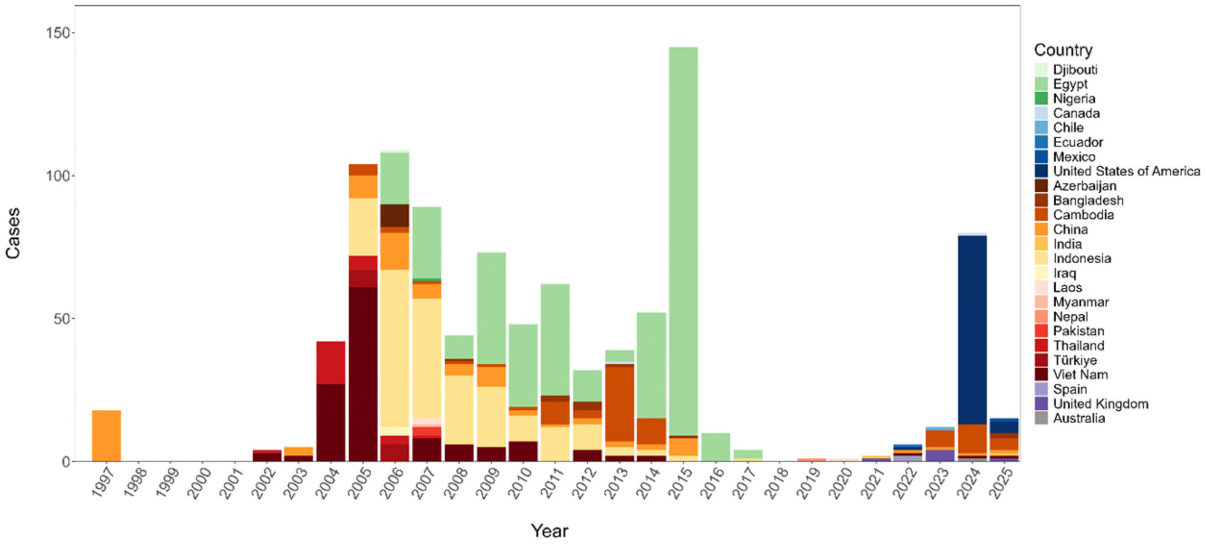

**Figure 7:** Distribution of reported human cases of A(H5N1) virus infection by year of onset or detection and reporting country from 1997 to 6 June 2025. The figure includes detections of A(H5N1) due to suspected environmental contamination reported in 2022 by Spain (2) and the USA (1), and in 2023 by the United Kingdom (three cases, including one inconclusive). Human cases of A(H5) cases epidemiologically linked to A(H5N1) outbreaks at poultry and dairy cattle farms in the USA are included in the number of A(H5N1) cases

### *A(H5N1) clade 2.3.4.4b virus infections*

#### United States of America

No new human cases of avian influenza A(H5N1) or A(H5) infection were reported by the United States of America during the reporting period (8 March – 6 June 2025). The last case in the USA was reported in February 2025 in Ohio state and involved exposure to infected poultry (CDC, online-a; The Colombus Dispatch, online). As of information updated by the USA authorities on 2 June 2025, 70 confirmed human cases with avian influenza A(H5N1), including one death, had been reported (CDC, online-b). The exposure source was known for 67 of the reported cases, with 41 having had exposure to dairy herds (cattle), 24 linked to poultry farms and culling operations, and two categorised as 'exposure related to other animals such as backyard flocks, wild birds, or other mammals' (CDC, online-b).

The A(H5N1) virus responsible for the Ohio case reported in the previous report has since been characterised as clade 2.3.4.4b genotype D1.3, without any substitutions that would indicate adaptation to mammals or lower effectiveness of existing antivirals and candidate vaccines (CDC, online-c).

### Mexico

On 8 April 2025, the Mexican Ministry of Health reported the country's first human case of avian influenza A(H5N1) virus infection, corresponding to the second confirmed A(H5) human case. The infection was confirmed by RT-PCR test on 1 April 2025 by Mexico's Institute of Epidemiological Diagnosis and Reference (InDRE). The case involved a three-year-old child from the state of Durango who had no underlying medical conditions, had not previously received influenza vaccine, and did not have a travel history. The child developed symptoms on 7 March 2025 with fever, malaise and vomiting. On 13 March, the child was hospitalised in a serious condition and was treated with the antiviral medication oseltamivir. On 8 April 2025, the patient died from respiratory complications related to the infection (WHO, online-b, c).

Overall, 91 close contacts have been identified (21 household contacts, 60 healthcare workers, and 10 people from a childcare centre). Nasopharyngeal and pharyngeal swabs were collected from 49 contacts and all tested negative for A(H5N1) virus. The source of infection remains unknown and is still under investigation. A(H5N1) virus infection has been confirmed in several birds in the state of Durango, including a sick vulture at the zoo and a Canada goose at the Peña del Aguila dam in Durango. According to the National Service for Agrifood Health, Safety and Quality, 75 outbreaks of A(H5N1) were reported between January 2022 and August 2024 in poultry from 15 regions across Mexico.

The A(H5N1) virus detected was characterised as clade 2.3.4.4b genotype D1.1, however no sequence was publicly available for analysis at the time when this report was being prepared.

### *A(H5N1) clade 2.3.2.1a virus infections*

### India

On 4 April 2025, a fatal case of avian influenza A(H5N1) infection was reported from India in a two-year-old girl from Palnadu district, Andhra Pradesh, marking the country's second confirmed human case, and death, from A(H5N1) since 2003 (ECDC, online-a). The diagnosis was confirmed by the National Institute of Virology (NIV) in Pune on 31 March 2025. Despite nearly two weeks of clinical care, including respiratory support and antimicrobial treatment, the child died on 15 March while receiving treatment at the All India Institute of Medical Sciences (AIIMS) in Mangalagiri, south-east India. The likely exposure occurred on 27 February, when the child reportedly chewed on a piece of raw chicken. Within two days, the child developed high fever and diarrhoea and was taken to a local hospital on 28 February. As the symptoms progressed, including respiratory distress, the patient was admitted to the Paediatric Intensive Care Unit at AIIMS Mangalagiri on 4 March. Clinical investigations revealed a diagnosis of leptospirosis, alongside a positive influenza A result from a nasopharyngeal swab collected on 7 March. The sample was sent to NIV Pune for subtyping, which subsequently confirmed the presence of avian influenza A(H5N1). Local health authorities noted that the child’s parents and other household members, all of whom consumed only cooked meat, remained asymptomatic. While test results for close contacts were pending at the time of preparing this report, no secondary cases have been identified.

The genetic sequence analysis showed that the virus belongs to clade 2.3.2.1a and had a similar mutation profile to those from Bangladesh (Figure 8).

### Bangladesh

On 27 May 2025, WHO reported two cases in Bangladesh, both in children from Khulna division (WHO, online-d). At the time when this report is being prepared, it is not known whether the cases in the two children were epidemiologically related, other than the fact that they resided in the same district.

The first report described an eight-year-old boy from Jessore district, Khulna division, who was treated at the hospital on 24 April 2025 due to fever and breathing difficulties and recovered. The child could possibly have had exposure to backyard poultry (BSS News, online).

The second case was retrospectively detected in a sample collected in February 2025 from a child in Khulna division, who subsequently recovered (WHO, online-d). Additional epidemiological information was not available at the time when this report was being prepared.

The sequences of both viruses from Bangladesh were available for analysis. Both belonged to clade 2.3.2.1a among A(H5N1) viruses and had identical HA sequences that shared the substitutions S154N, T195I and V210I in the glycoprotein HA1 protein and I292V in the polymerase PB2 protein. Substitutions S154N and T195I in HA1 have both been associated with increased virus binding to α2-6 sialic acids (Suttie et al., 2019). The V210I substitution has been found in all 2.3.4.4b viruses from the dairy cow outbreak in USA and has been associated with increased binding breadth to glycans bearing terminal α2-3 sialic acids (Good et al., 2024). The PB2 I292V has been associated with increased virulence in mice for A(H9N2) (Gao et al., 2019).

### *A(H5N1) clade 2.3.2.1e (previously classified as 2.3.2.1c) virus infections*

### Cambodia

During the reporting period (8 March – 6 June 2025), two fatal human cases of avian influenza A(H5N1) infection were reported by the Cambodian Ministry of Health, bringing the total number of cases in 2025 to four, and the overall number of cases in the country to 76 since 2003.

On 23 March 2025, the Cambodian Ministry of Health reported the third fatal case of human A(H5N1) infection in 2025 in a three-year-old child from Kratie province (Cambodia Ministry of Health, online-a, b; WHO, online-b). The child developed symptoms on 18 March 2025, was hospitalised on 21 March, and died on 23 March. The case was laboratory-confirmed by the National Institute of Public Health on 22 March 2025. The individual developed severe illness, including fever, cough and difficulty breathing. Investigations revealed that the child's family had a chicken farm where several birds had recently died, and that the meat from these dead chickens had been prepared and consumed prior to the child's illness.

On 28 May 2025, a fourth case for 2025, which was fatal, was reported by the Cambodian Ministry of Health. The 11-year-old boy from Kampong Speu province died on 27 May 2025. He presented to the hospital in a severe condition (Avian Flu Diary, online-b). Exposure to backyard poultry was indicated prior to the onset of illness.

Phylogenetic analysis places the virus sequence from the third case (A/Cambodia/25030237/2025) among other strains from Asia belonging to the emerging reassortant clade 2.3.2.1e. This clade was previously classified as clade 2.3.2.1c (WHO, online-b) and contains the internal segments of clade 2.3.4.4b viruses (Siegers et al., 2024). The H5 classification was recently updated to match the evolution observed in the circulating viruses; clade 2.3.2.1e regroups viruses that have emerged from clade 2.3.2.1c. Most A(H5N1) virus strains from Cambodia carry the combination of substitutions H115Q and E627K in the polymerase PB1 and PB2 proteins, respectively, that have been linked to increased virulence and aerosol transmissibility (Zhang et al., 2021), as well as substitution K142N in the polymerase PA protein that has been associated with increased virulence in mice (Kim et al., 2010).

**Viet Nam**

On 18 April 2025, the Ho Chi Minh City Health Department in Vietnam reported a case of A(H5N1) virus infection in an eight-year-old child from Tai Ninh province (Ho Chi Minh City Department of Health, online). Exposure to backyard poultry at the grandmother's house, where many birds were dying, was reported two weeks prior to symptom onset on 11 April 2025. On the day of symptom onset, the child, who had an underlying cardiac disease, was hospitalised with fever, headache and vomiting, but no respiratory symptoms. On 13 April, the child was transferred to another hospital with encephalitis, and nasopharyngeal swab and cerebrospinal fluid samples were taken there for PCR analysis at the Laboratory Department of the Tropical Diseases Hospital. On 17 April 2025, the PCR was returned positive for A(H5) in the cerebrospinal fluid, but negative for influenza in the respiratory sample. Additional analysis of the samples by the Pasteur Institute in Ho Chi Minh City the next day confirmed the presence of A(H5N1) in the cerebrospinal fluid sample and the negative PCR result for the nasopharyngeal sample. The patient was isolated and has remained in a stable condition. The latest update indicated that the child's condition was slowly improving (WHO, online-b).

The HA sequence of the A/Vietnam/05EI1001/2025 virus clusters the virus from the human cases in Cambodia (Figure 8). Specific substitutions in the HA glycoprotein were identified: S123P in HA1 and R167K in HA2. This substitution association has been linked with increased virus binding to α2-6 sialic acids, potentially facilitating recognition of human-type host cell receptors (Yamada et al., 2006). In addition, other segments, for example the PB2 segment, showed a strong similarity with the 2.3.2.1e viruses from Cambodia.

**China**

On 27 May 2025, WHO reported one new confirmed human case of avian influenza A(H5N1) in China in an adult travelling from Viet Nam (WHO, online-d). The patient was admitted to hospital on 7 April 2025 after being detected through routine screening at the port of entry to China. The patient has since recovered. Poultry at the patient's home in Viet Nam was indicated as a likely source of exposure. No virus sequence was available for analysis at the time when this report was being prepared.

### 2.3.3 Human A(H9N2) cases

Since 1998 and as of 6 June 2025, 166 human influenza A(H9N2) cases have been reported globally (Figure 8). During the current reporting period (8 March – 6 June 2025), 11 human cases of influenza A(H9N2) virus infection were reported, all from China. All except two cases had reported exposure to poultry.

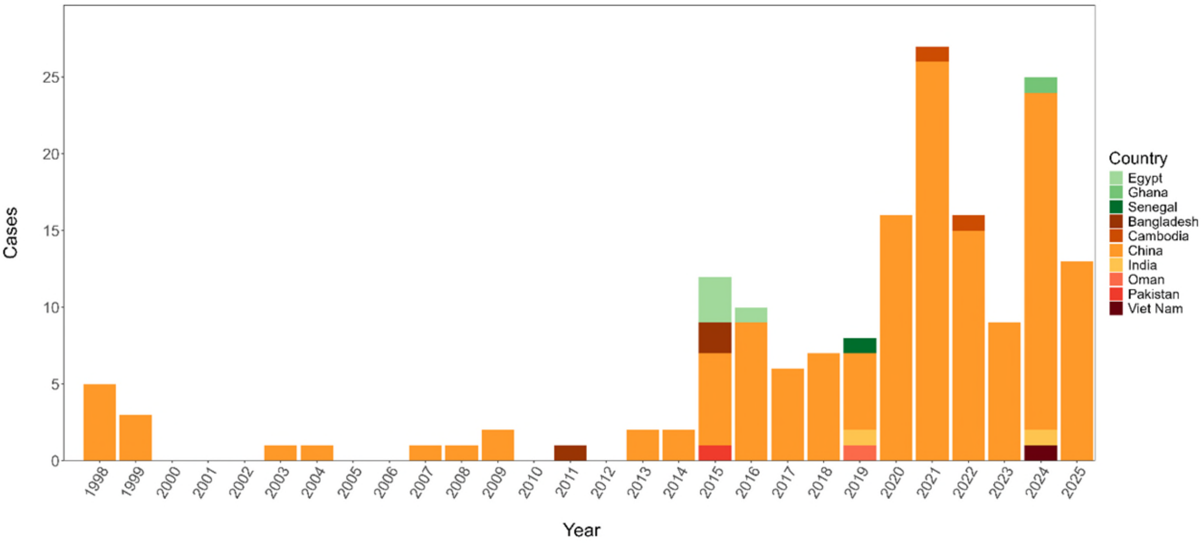

**Figure 8:** Distribution of reported human cases of A(H9N2) virus infection by year of onset, or detection and reporting country, from 1998 to 6 June 2025

On 15 April 2025, Hong Kong's Centre for Health Protection reported three human cases of avian influenza A(H9N2) virus infection in China. The first case was in a child from the Henan Province, with symptom onset on 11 February 2025. The second case was in a child from the Guangxi Autonomous Region, with symptom onset on 3 March 2025. The last case was in a 35-year-old from the Guizhou Province, with symptom onset on 10 March 2025 (ECDC, online-b; CHP, online-a). Both cases in children, detected through the Influenza-Like Illness (ILI) surveillance, had mild illness and recovered. The adult patient had underlying conditions and was hospitalised with pneumonia. Environmental samples tested positive for A(H9) influenza virus for two patients. No epidemiological link was found or any new cases detected among contacts (WHO, online-b).

On 13 May 2025, Hong Kong's Centre for Health Protection reported eight new human cases of avian influenza A(H9N2) virus infection in China, including seven in children under 10 years (CHP, online-b). The first case was a male adult in his sixties from Chongqing municipality, with symptom onset on 18 April 2025. The second and third cases were both one-year-old children from Guizhou with symptom onset on 7 and 15 April 2025. Four other cases were from the Hunan Province: one boy and one girl with symptom onset on 1 April 2025; one girl with symptom onset on 3 April 2025; and one boy with symptom onset on 19 April 2025. The eighth case was a one-year-old girl from the Yunnan province, with symptom onset on 2 April 2025. Seven cases had mild illnesses and were detected through ILI surveillance (WHO, online-d). One child was admitted to hospital with pneumonia: in addition to influenza, respiratory syncytial virus infection was also detected. All patients recovered. Exposure to poultry was reported for all but one case. A(H9) positive samples were detected from environment samples for all but one case. There were no new infections detected among contacts of the reported cases and there was no epidemiological link between the reported cases.

No virus sequence was available for analysis at the time when this report was being prepared.

### 2.3.4 Human A(H10N3) cases

Since 2021, five cases of human infection with avian influenza A(H10N3) have been reported worldwide. All cases were reported from China in adult individuals. All had severe illness, one having underlying conditions, and all five eventually recovered. Exposure to birds was reported for four cases, but the exposure remains unknown for one case.

In the reporting period, one human case with avian influenza A(H10N3) virus infection was reported in China on 13 May 2025 by Hong Kong's Centre for Health Protection. A woman in her sixties from the Shaanxi province developed symptoms on 13 April 2025 (CHP, online-b). The patient, who had exposure to backyard poultry, was hospitalised on 18 April 2025 with pneumonia (WHO, online-d).

No sequence was available for the virus responsible for this case, but a sequence from a 2024 case was released during the reporting period and was used for analysis (Table 8). As with many A(H5N1) viruses responsible for human infections, in addition to the A588V substitution, the I292V substitution was present in the polymerase PB2 protein of the A(H10N3) virus. This substitution combination has been associated with increased polymerase activity of A(H10N8) viruses in mammalian cells (Xiao et al., 2016).

### 2.3.5 Additional information relevant for public health and international risk assessments

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

During the vaccine composition meeting for the Northern Hemisphere season 2025-2026 in February 2025, WHO updated the list of A(H5N1) candidate vaccine viruses (WHO, online-e). There are now candidate vaccine viruses already available or in preparation, based on recent A(H5N1) viruses corresponding to the three clades reported during this reporting period (8 March – 6 June 2025): 2.3.4.4b, 2.3.2.1a and 2.3.2.1e (formerly classified as 2.3.2.1c).

A recent study (Stevenson-Leggett et al., 2025) has evaluated the capacity of the humoral response raised after vaccination with seasonal influenza vaccines to neutralise recent A(H5N1) viruses belonging to the clades 2.3.4.4b and 2.3.2.1e (formerly classified as 2.3.2.1c) that have been responsible for human infections. The high throughput assay used in this study did not detect any neutralising antibody against these two A(H5N1) viruses, when a specific response against a seasonal A(H1N1)pdm09 virus homologous to one of the vaccine components could be detected. The authors concluded that it is unlikely that existing immunity following seasonal influenza vaccination or natural infection would protect the population against A(H5N1). However, they stated that their study looked only at neutralising antibodies, often considered as a correlate of protection against seasonal influenza viruses. However, other types of immunity exist, and it cannot be ruled out that these could contribute to providing some cross-protection against A(H5N1) viruses.

Based on information currently available, the Food and Agriculture Organisation of the United Nations (FAO), WHO and WOAH released an update of their tripartite assessment of the public health risk posed by influenza A(H5N1) viruses on 17 April 2025 (WHO, online-f). The risk of infection remains low for the general public and low-to-moderate for occupationally exposed individuals. In the latest summary of influenza at the human-animal interface, the WHO assessment of the risk to public health from the avian influenza viruses that are currently known remains unchanged, and this risk is still considered to be low (WHO, online-d). In addition, WHO published specific guidance 'Surveillance for human infections with avian influenza A(H5) viruses' that focuses on the objectives, case definitions, and recommendations for testing and reporting under the International Health Regulations (WHO, online-g). ECDC's reporting protocol (ECDC, 2025) is currently being revised to take into account the evolution of the epidemiological situation over the past few months and to align it with the WHO update.

The US CDC assessment of the risk to people from HPAI A(H5N1) viruses remains low for the general population in the United States but is considered moderate-to-high for populations in contact with potentially infected animals, contaminated surfaces or fluids (CDC, online-c). In early May 2025, the US CDC published a risk assessment of two recent A(H5N1) viruses belonging to clade 2.3.4.4b: A/California/147/2024 genotype B3.13 and A/Washington/239/2024 genotype D1.1 (CDC, 2025). Using the IRAT methodology based on ten risk elements (CDC, online-d), the risk of potential emergence for both viruses was estimated to be moderate (mid-low range of the category), while the potential impact on public health was considered to be moderate (mid-range of the category). The scores obtained for both viruses were slightly lower than those estimated for A(H5N1) virus A/Texas/37/2024 in June 2024 (CDC, 2024).

According to the UK Health Security Agency (UK HSA), the risk of HPAI A(H5) to the general public is still considered to be very low (GovUK, online-d). UK HSA's guidance for the management of individuals exposed to influenza A(H5) in animals remains unchanged (GovUK, online-e).

### 2.3.6 ECDC risk assessment

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

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

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

- In the current epidemiological year (1 October 2024 – 30 September 2025), there has already been a higher number of detections of HPAI viruses in wild and domestic birds in Europe compared to the epidemiological year 2023−2024. Nevertheless, detections are still lower than those reported in the previous epidemiological years (2020−2023).
- Despite the extensive circulation of avian influenza viruses in animal populations in Europe over the past few years, with frequent opportunities for human exposure, there have been no confirmed cases of A(H5N1) clade 2.3.4.4b infection in humans in the EU/EEA, and transmission from infected animals to humans remains a rare event globally.

- In Europe, mutations associated with viral adaptation to mammalian hosts have been identified in sequences of A(H5N1) clade 2.3.4.4b viruses from mammals and birds. Further understanding of the implications of such mutations for mammalian adaptation, infection and transmission is required to assess any change in the associated risk to humans. However, circulating viruses retain a binding preference for α2–3 sialic acid (avian-type) receptors and are still considered to be avian-like. There is currently no evidence of the viruses being more adapted to infection of humans or having the ability to transmit between humans.

- Sporadic cases of infection with avian influenza A(H5N1) virus have been reported in humans on a global basis, most of which have had a history of unprotected exposure to poultry, cattle or contaminated environments. For the human cases of A(H5N1) reported globally between 8 March and 6 June 2025, 63% (n = 5/8) cases had documented exposure to poultry.

- To date, there has been no evidence of sustained human-to-human transmission of influenza A(H5N1) viruses.

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

- Historically, clinical presentations of individuals infected with A(H5N1), also including other clades than 2.3.4.4b, have ranged from asymptomatic or mild, such as conjunctivitis and upper respiratory tract symptoms, to severe illness resulting in death, with a case fatality estimated at 48% since 2003. However, this figure can only be based on the reported cases and might 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 8 March and 6 June 2025, the only reported case of infection with an A(H5N1) clade 2.3.4.4b virus was in a three-year-old child in Mexico and was fatal.

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

- The reasons for the variation in outcome of infection with influenza A(H5N1) virus is likely to be multi-factorial and may be attributed to the virus genotype, duration of exposure, viral load, transmission route, individual health status, personal protective measures taken, and medical treatment provided (FAO, WHO and WOAH, online). The detection of several mild cases of A(H5N1) virus infection and seropositive individuals without a history of clinical symptoms in the USA suggests that mild and asymptomatic cases may be more common than previously reported for A(H5N1), and targeted surveillance of individuals exposed to infected animals is recommended (EFSA AHAW Panel and ECDC, 2025).

- Most of the circulating A(H5N1) clade 2.3.4.4b viruses detected in Europe remain susceptible to the antiviral medicines available to treat humans, including adamantanes, neuraminidase inhibitors (e.g. oseltamivir) and polymerase acidic inhibitors (e.g. baloxavir marboxil).

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

# 3. Conclusions

## 3.1 Birds

- During the current reporting period, there was a steady decline in the number of HPAI virus detections in wild birds, accompanied by a lower number of HPAI outbreaks in poultry. Together, these trends decrease the exposure risk for humans and other mammals.

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

- Despite the decreasing number of HPAI virus detections in wild and domestic birds, HPAI virus is expected to continue to circulate in wild bird populations in the coming months. Since 2020, there has been a consistent and persistent circulation of HPAI A(H5) viruses in wild bird populations in Europe. This situation is expected to continue in the coming years, with variations in outbreak numbers, geographic distribution, and affected species, influenced by multiple factors, both intrinsic and extrinsic to these populations, some of which are not yet fully known. This epidemiological situation is fundamentally different from the period before 2020, when HPAI A(H5) viruses in wild birds in Europe occurred as irregular epidemics, restricted to the autumn and winter periods of certain years, rather than persisting year-round.

- The current reporting period was once again characterised by extensive secondary spread between poultry establishments in countries with high poultry population density areas, such as Hungary and Poland, particularly in domestic ducks and chickens, while Latvia reported the first HPAI outbreak in poultry in the country ever.

- HPAI virus detections in wild birds during the current reporting period were predominantly in waterfowl, followed by colony-breeding seabirds and raptors.

- There has been no evidence so far that HPAI A(H5) viruses have spread along the spring migration routes to cause unusual mortality events in breeding areas of barnacle or greylag geese at higher latitudes, or that they have spread to breeding colony sites of gulls or terns (e.g. black-headed gull, European herring gull, sandwich tern) and caused unusual mortality there. No unusual mortality events were reported in wild birds during the current reporting period. However, as the breeding season continues in the coming months, the risk of such events remains, in particular in colony-breeding seabirds.

- The detection of HPAI A(H5N5) virus in two wild birds during the current reporting period suggests that this virus still is persisting in wild birds in Europe, albeit with fewer detections than in the previous reporting period.

- Currently available genetic data indicate that, starting from October 2024, EA-2024-DI has been the most frequent and widespread genotype in wild and domestic birds Europe, detected in almost all the affected European countries and associated with about 90% of the poultry outbreaks. All the new genotypes identified in Europe during the current epidemiological year derive from reassortment events between EA-2024-DI and Eurasian LPAI viruses.

- Available genetic data indicates that during this reporting period genotype EA-2022-BB continued to circulate in Europe, mostly among colony-breeding seabirds along the English Channel coasts.

- Since October 2024, 49 HPAI A(H5) viruses containing markers of mammalian adaptation in the PB2 protein (E627K/V, K526R or D701N) were identified in wild and domestic birds collected from ten European countries, suggesting that viruses with an enhanced capacity to replicate in mammalian cells can infect birds. Phylogenetic clustering indicates that wild birds can also occasionally spread such viruses among countries.

- Outside Europe, the number of HPAI virus detections in domestic and more so in wild birds reported to WOAH has decreased as in Europe compared to the previous reporting period (EFSA, ECDC and EURL, 2025a). There are few official reports to WOAH from many countries, particularly from Asia, but also no HPAI virus detections in wild birds were reported from North America during the current reporting period. This makes the global extent of HPAI A(H5) viruses unclear.

- Most of the HPAI outbreaks reported in poultry worldwide continued to be concentrated in the Americas, particularly in the USA and Canada. Besides the Americas, South Korea experienced most of the poultry outbreaks outside Europe. Brazil at the same time reported the first HPAI A(H5N1) outbreak in poultry in the country ever. HPAI virus subtypes other than H5N1 reported outside Europe were H5N8 in Israel, H5N9 in the Philippines, H7N3 in Mexico, and H7N9 in the USA.

- Although reported at a lower level, HPAI circulation in domestic and wild birds also continues on other continents, particularly in Asia, where multiple avian influenza viruses are endemic. The detection of HPAI A(H5N1) virus in Togo and Nigeria suggests that the actual circulation of HPAI viruses in Africa remains unclear.

- HPAI virus detections continue to be underreported to WOAH, particularly detections in wild birds.

- During the austral winter now in the Antarctic and subantarctic regions, migratory colony-breeding seabirds have left, resulting in a lower risk of HPAI A(H5) virus spread until they return in a few months.

## 3.2 Mammals

- During the current reporting period, further HPAI A(H5N1) and A(H5N5) virus detections were reported in mammals in Europe. These detections concerned both wild (red fox, Eurasian otter, harbour seal) and domestic mammals (cat, sheep). The detection of HPAI A(H5N1) virus in a sheep in the United Kingdom represents the first detection in this species, once again demonstrating the ability of strains belonging to the 2.3.4.4b clade to infect new species.

- The number of dairy cattle farms reportedly affected by HPAI A(H5N1) virus in the USA rose to 1,073 in 17 states during the current reporting period, but the rate of new infections has been gradually slowing.

- Outside Europe, HPAI A(H5N1) virus detections were reported in three new species: gray fox (USA), leopard cat (South Korea), long-tailed weasel (USA).
- Domestic cats and captive felines were confirmed to be highly susceptible to HPAI A(H5N1) virus and continued to be affected outside Europe, where raw pet food remained a concern.
- Canada retrospectively reported detections of HPAI A(H5N5) virus in cats, a bobcat, a red fox and a striped skunk in the first quarter of 2025.
- All the characterised HPAI viruses collected from mammal species in Europe since October 2024 belong to the A(H5N1) EA-2024-DI, EA-2024-EE and A(H5N5) EA-2021-I genotypes. To date, no key mutations associated with the switch in the virus binding preference from avian- to human-type receptors have been identified in these viruses. However, more than 50% of the characterised viruses from mammals in Europe during the current epidemiological year contain the PB2-E627K/V mutation, which confers a more efficient replication in mammals.

## 3.3 Humans

- Sporadic cases of zoonotic avian influenza A(H5N1), A(H9N2) and A(H10N3) were reported outside the EU/EEA during the period March–June 2025.
- Despite the widespread occurrence of HPAI A(H5N1) in wild birds, poultry and some mammals in recent years, with many potential exposures of humans to infected animals, there have been no confirmed human cases of influenza A(H5N1) in the EU/EEA.
- The majority of human infections with avian influenza viruses reported since 1997 have been associated with unprotected exposure to poultry, live poultry markets, or contaminated environments. In addition, since March 2024, there have been 41 human cases of influenza A(H5N1) reported following exposure to dairy cattle infected with A(H5N1) virus. To date, there has been no evidence of sustained human-to-human transmission observed.
- In the reporting period from 8 March to 6 June 2025, of the six human cases of avian influenza A(H5N1) infection reported globally for which exposure data were available, there was only one where epidemiological investigation did not identify the source of exposure. The other five cases had documented exposure to poultry, some with dead birds identified on the premises.
- With the extensive circulation of avian influenza viruses in bird populations globally, sporadic transmission to humans is likely to continue occurring in settings where people have unprotected exposure to infected animals or their environment.

# 4. Options for response

## 4.1 Birds

- Given the persistent circulation of HPAI in wild birds in Europe, which is likely to continue for many years, it is necessary to consider medium- and long-term risk reduction strategies in the poultry sector, such as not locating poultry establishments near areas with high risk for introduction of HPAI from wild birds to poultry, reducing farm densities in these areas, keeping high biosecurity standards and compliance, preventive vaccination, risk-based implementation of housing orders or implementing housing systems that keep poultry indoors (or completely restrict access of wild birds to free range) whilst keeping high levels of welfare.

- Improved biosecurity requires in some production systems improved infrastructure. Besides infrastructure, high level of compliance is necessary. Specific training activities should be provided for poultry workers to raise their awareness of the risks associated with HPAI and to improve their knowledge of biosecurity measures.
- For wild birds, general options for response include accurate and comprehensive recording of HPAI-associated mortality events (e.g. estimating the impact on wild bird populations), preventing disturbance of areas undergoing HPAI outbreaks to reduce virus spread, and, depending on the circumstances, removal of HPAI virus-affected carcasses from areas where wild birds congregate to reduce environmental contamination and further virus spread.
- It is important to continuously monitor LPAI viruses of the A(H5) and A(H7) subtypes in wild and domestic birds, and introductions of these subtypes into poultry establishments, as these subtypes can mutate into their highly pathogenic forms once circulating in poultry.
- The geographic expansion of HPAI A(H5N5) viruses in wild birds, which were again reported —albeit in small numbers— in the current reporting period, should continue to be closely monitored in northern parts of Europe and worldwide.
- The timely generation and sharing of genome sequence data from avian influenza viruses is of utmost importance to promptly detect the possible emergence of viruses with amino acid changes associated with increased zoonotic potential, resistance toward antiviral drugs or different antigenic properties. The biological characteristics of these variants should be further evaluated to assess the actual impact of the acquired mutations. Genetic data are also instrumental to track the virus spread, to support epidemiological investigations in the distinction between primary and secondary outbreaks and to identify novel incursions of viruses that may represent a threat for human or animal health.
- Reinforcing the genetic characterisation of viruses collected from birds in areas where a high number of infections in mammalian species have been identified is recommended to promptly detect possible mammal-to-avian transmission of viruses containing markers of virus adaptation to mammalian species, which may have a higher zoonotic potential.

## 4.2 Mammals

- Increased virological and serological surveillance of HPAI viruses in wild (e.g. red foxes) and free-roaming domestic carnivores (e.g. cats and dogs) in areas with high HPAI virus circulation continues to be recommended to monitor both the level of virus infection in these species and the risk of emergence and transmission of mammalian-adapted viruses. Surveillance should also focus on domestic and farmed mammals exposed to highly contaminated environments (e.g. ruminants, pigs, camelids and fur animals), in close contact with HPAI virus-infected poultry or wildlife, or present in mixed-species farms. Research to investigate the role of mammals in maintaining HPAI viruses and driving their evolutionary dynamics is recommended.
- In light of the ongoing outbreak in dairy cattle in the USA, testing of/surveillance in ruminants is recommended when a combination of factors is observed, such as the manifestation of overt and unresolved clinical signs typically associated with HPAI virus infection in ruminants (e.g. undiagnosed severe decrease in milk production and presence of darker, thickened milk), but also the occurrence of HPAI virus infection in other domestic, peridomestic and wild animals in/around cattle farms.

In addition, HPAI should be considered as a differential diagnosis in cases of undiagnosed or unresolved clinical signs during periods of HPAI virus circulation in the area where ruminants are kept.

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

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

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

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

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

## 4.3 Humans

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

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

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

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

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

- People who have been exposed to animals with suspected or confirmed avian influenza virus infection while not wearing appropriate personal protective equipment should be monitored for symptoms for 10–14 days after the last exposure, and tested if symptoms develop. Where appropriate protective measures have not been taken, asymptomatic individuals exposed to animals with suspected or confirmed avian influenza virus infection should be assessed on a case-by-case basis and tested, depending on the level of exposure. Further information on testing, follow-up and management of individuals with exposure and confirmed infection can be found in ECDC's 'Guidance on testing and detection of zoonotic influenza virus infections in humans' (ECDC, 2022), 'Investigation protocol for human exposures and cases of avian influenza' (ECDC, 2023), and the ECDC/EFSA guidance for 'Coordinated One Health investigation and management of outbreaks in humans and animals caused by zoonotic avian influenza viruses' (ECDC and EFSA, 2025).

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

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

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

- Genetic changes in avian influenza viruses that may alter their zoonotic potential (increase capacity to infect humans, increase transmissibility) or their susceptibility to antivirals available to treat humans should be monitored (EFSA AHAW Panel and

ECDC, 2025). Avian influenza viruses detected in humans should be sequenced and the sequence shared in public databases in a timely manner.

- Vaccination against seasonal influenza can be offered to individuals who are occupationally exposed to avian influenza to reduce the risk of reassortment between avian and human influenza viruses. Furthermore, zoonotic avian influenza A(H5) vaccination in individuals occupationally or otherwise routinely exposed to infected animals or contaminated environments can also be considered as an optional, complementary preventive measure, based on national recommendations. While data on immune response induction are available, there is limited information on reduction in infection or onward transmission and on protection against severe clinical disease. At this stage, there is insufficient evidence to recommend zoonotic influenza vaccination in all EU/EEA countries (EFSA AHAW Panel and ECDC, 2025).
- The options for response are based on the current available evidence, epidemiological situation and risk assessment for the EU/EEA. Recommended measures may need to be adapted if the epidemiological situation changes or new evidence becomes available.

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

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

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

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

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

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

- ECDC's current risk assessment (ECDC, online-c) that focuses on the immediate risk of avian influenza for human health fulfilling ECDC's new mandate and the Regulation (EU) 2022/2371[11] 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[12] and Commission Delegated Regulation (EU) 2020/687[13]).

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[11] 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.

[12] 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.

[13] 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[14] and Articles 29 and 31 of Regulation (EC) No 178/2002[15], 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 8 March and 6 June 2025 (11 June for mammals), 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 December 2024 to March 2025 (EFSA, ECDC and EURL, 2025a) and that might affect the interpretation of risks related to avian influenza introduction and/or spread in Europe.

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[14] 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.

[15] 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 8 March and 6 June 2025and submitted by Member States and other European countries via ADIS, were taken into account. Data extraction was carried on 6 June 2025. WOAH-WAHIS was consulted to complement the information for European countries not reporting HPAI notifications via ADIS. In addition, HPAI-affected countries were asked to provide more detailed epidemiological information on HPAI outbreaks occurred in poultry directly to EFSA. This information included details on the poultry species and production systems affected by HPAI, which were supplied in form of additional variables to complement the data reported via ADIS. All information is provided in Annex B. In addition, the information European countries affected by HPAI and LPAI presented to the Standing Committee on Plants, Animals, Food and Feed (SCOPAFF), and the evidence on HPAI and LPAI outbreaks provided in the info notes from the affected countries to EC, were consulted to extract relevant information reported in Section 2.1.1. The presentations delivered at the SCOPAFF meetings are available on the EC website (European Commission, online).

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

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

The annexes to this Scientific Report are available here: https://doi.org/10.5281/zenodo.15728574

### 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 6 June 2025 and extracted by EFSA. They were used and reproduced with permission. WOAH bears no responsibility for the integrity or accuracy of the data contained herein, but not limited to, any deletion, manipulation, or reformatting of data that may have occurred beyond its control.

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

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

## B.2 Data on humans

Data on the number of human cases caused by infection with avian influenza viruses was collected by ECDC. As part of epidemic intelligence activities at ECDC, multiple sources are scanned regularly to collect information on laboratory-confirmed human cases. Data were extracted and line lists developed to collect case-based information on virus type, date of disease onset, country of reporting, country of exposure, sex, age, exposure, clinical information (hospitalisation, severity) and outcome. All cases included in the line list and mentioned in the document have been laboratory-confirmed. Data are continuously checked for double entries and validity. The data on human cases cover the full period since the first human case was reported. Therefore, data on human cases refer to different time periods. Relevant information on human infections, risk factors, and the results from studies on infection and transmission with relevance for human health are included.

### B.2.1 Method for phylogenetic and mutation analysis

The GISAID's EpiFlu™ Database (Shu and McCauley, 2017) was accessed on 28 May 2025 to retrieve sequences from human cases of avian influenza reported since 8 March 2025. In cases where the same strain had multiple submissions, the ones with the most complete segment data were chosen. The phylogenetic analysis was performed at nucleotide on HA segments in CLC Genomics Workbench 24.0.2 (Qiagen). An alignment was produced in very accurate mode with default parameters and subsequently trimmed into 1,707 gap-free nucleotides. A neighbour joining tree was produced by Jukes-Cantor nucleotide distance measurement with 100 bootstrap replicates. Additional blast searches were made directly on GISAID. 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 present in more than 30% of at least ten non-human strains within the same clade and those with an irrelevant effect were excluded. Clade and genotype information was retrieved from GISAID or assigned according to specified literature.

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

Annex A is available on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.15728574

# Annex B – Data on poultry outbreaks

Annex B is available on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.15728574

# Annex C – Acknowledgements

All genome sequences and associated metadata in this dataset are published in GISAID's EpiFlu$^{TM}$ database. To view the contributors of each individual sequence with details such as accession number, virus name, collection date, originating lab and submitting lab, and the list of authors, visit: https://doi.org/10.55876/gis8.250624hw and https://doi.org/10.55876/gis8.250623kc.