SCIENTIFIC REPORT

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# Avian influenza overview September–December 2024

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## Abstract

Between 21 September and 6 December 2024, 657 highly pathogenic avian influenza (HPAI) A(H5N1) and A(H5N5) virus detections were reported in domestic (341) and wild (316) birds across 27 countries in Europe. Many HPAI outbreaks in domestic birds were clustered in areas with high poultry density and characterised by secondary farm-to-farm spread. Waterfowl, particularly the mute swan, were primarily affected during this reporting period, with HPAI virus detections focused on south-eastern Europe. Notably, A(H5N5) viruses expanded their geographic and host range, resulting in a surge in detections and mortality events described in gulls and crows. No new HPAI virus detections in mammals were reported in Europe during this reporting period, but the number of dairy cattle farms reportedly affected in the United States of America (USA) rose to > 800 in 16 States, and HPAI virus was identified in two pigs in a mixed-species farm. Between 21 September and 11 December 2024, 56 new human cases with avian influenza virus infection were reported from North America (45 A(H5N1) cases), Viet Nam (one A(H5)) and China (ten A(H9N2) cases). Most of the A(H5) human cases in North America (95.6%, n = 43/45) had reported exposure to poultry, live poultry markets, or dairy cattle prior to avian influenza virus detection or onset of illness. Human infections with avian influenza viruses remain rare and no evidence of human-to-human transmission has been documented in the reporting period. The risk of infection with currently circulating avian A(H5) influenza viruses of clade 2.3.4.4b in Europe remains low for the general public in the European Union/European Economic Area (EU/EEA). The risk of infection remains low-to-moderate for those occupationally or otherwise exposed to infected animals or contaminated environments.

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

**Requestor:** European Commission

**Question number:** EFSA-Q-2024-00176 and Commission request 280 to ECDC (SANTE.B.2/IK/mo (2023)2182203)

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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[1], captive[2] and wild birds that occurred in and outside Europe between 21 September and 6 December 2024, as well as HPAI virus detections in mammals up until 10 December 2024, and human cases due to avian influenza infection between 21 September and 11 December 2024. Detections of low pathogenic avian influenza (LPAI) virus in birds are discussed whenever they are of concern and 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[3] by month of suspicion. For the current epidemiological year 2024–2025, starting on 1 October 2024, data reported are truncated on 6 December 2024.

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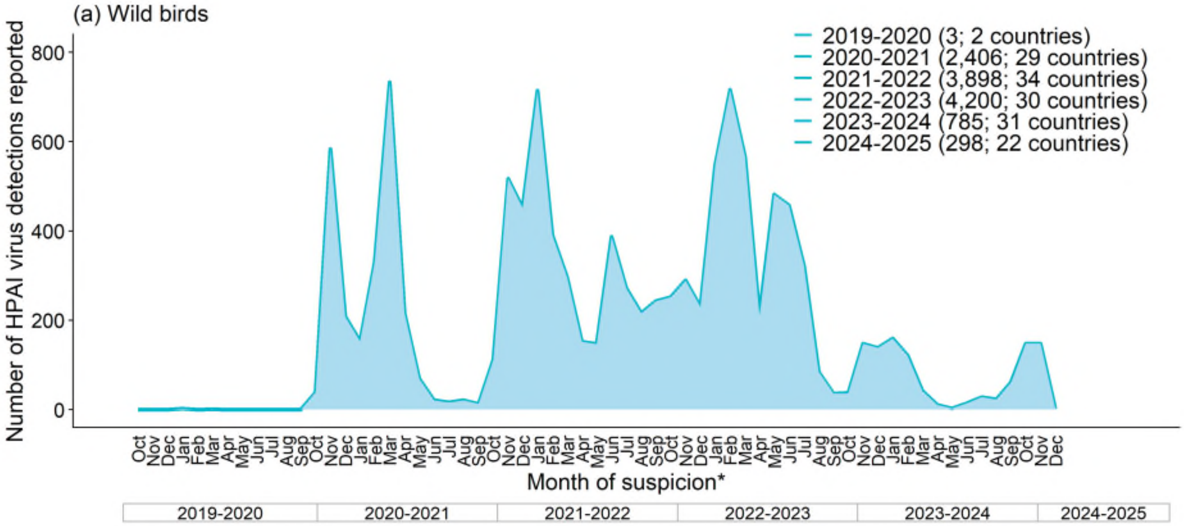
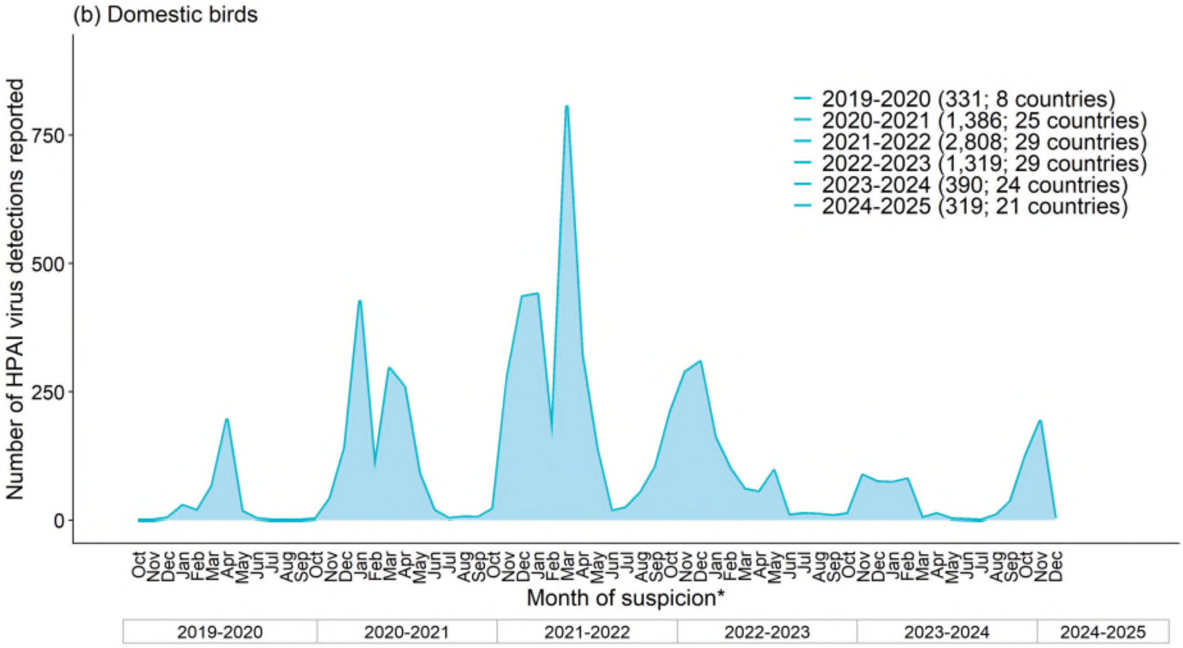
[1] According to Regulation (EU) 2016/429 of the European Parliament and of the Council of 9 March 2016, point (9), 'poultry' means birds that are reared or kept in captivity for: (a) the production of: (i) meat; (ii) eggs for consumption; (iii) other products; (b) restocking supplies of game birds;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

[2] 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.

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





*If the date of suspicion was not available, the date of confirmation was used to assign the week of suspicion. United Kingdom data are from the Animal Disease Notification System (ADNS, former ADIS) up until 31 December 2020. From 1 January 2021 onwards, the data source was WOAH for the United Kingdom (excluding Northern Ireland) and ADNS/ADIS for the United Kingdom (Northern Ireland)[4].
Source: ADNS/ADIS and WOAH (data extraction carried out on 6 December 2024).

**Figure 1:** Distribution of the number of HPAI virus detections in wild (cumulative number n = 11,590) (a) and domestic (n = 6,553) (b) birds reported in Europe during six epidemiological years by month of suspicion, from 1 October 2019 to 6 December 2024 (total n = 18,143)

Considering the current reporting period from 21 September to 6 December 2024, 657 HPAI virus detections were reported in poultry (274), captive (67) and wild birds (316) in Europe (Table 1, Figure 2).

**Table 1:** Number of HPAI outbreaks reported in Europe by country, virus subtype and affected sub-population, from 21 September to 6 December 2024. Cumulative numbers

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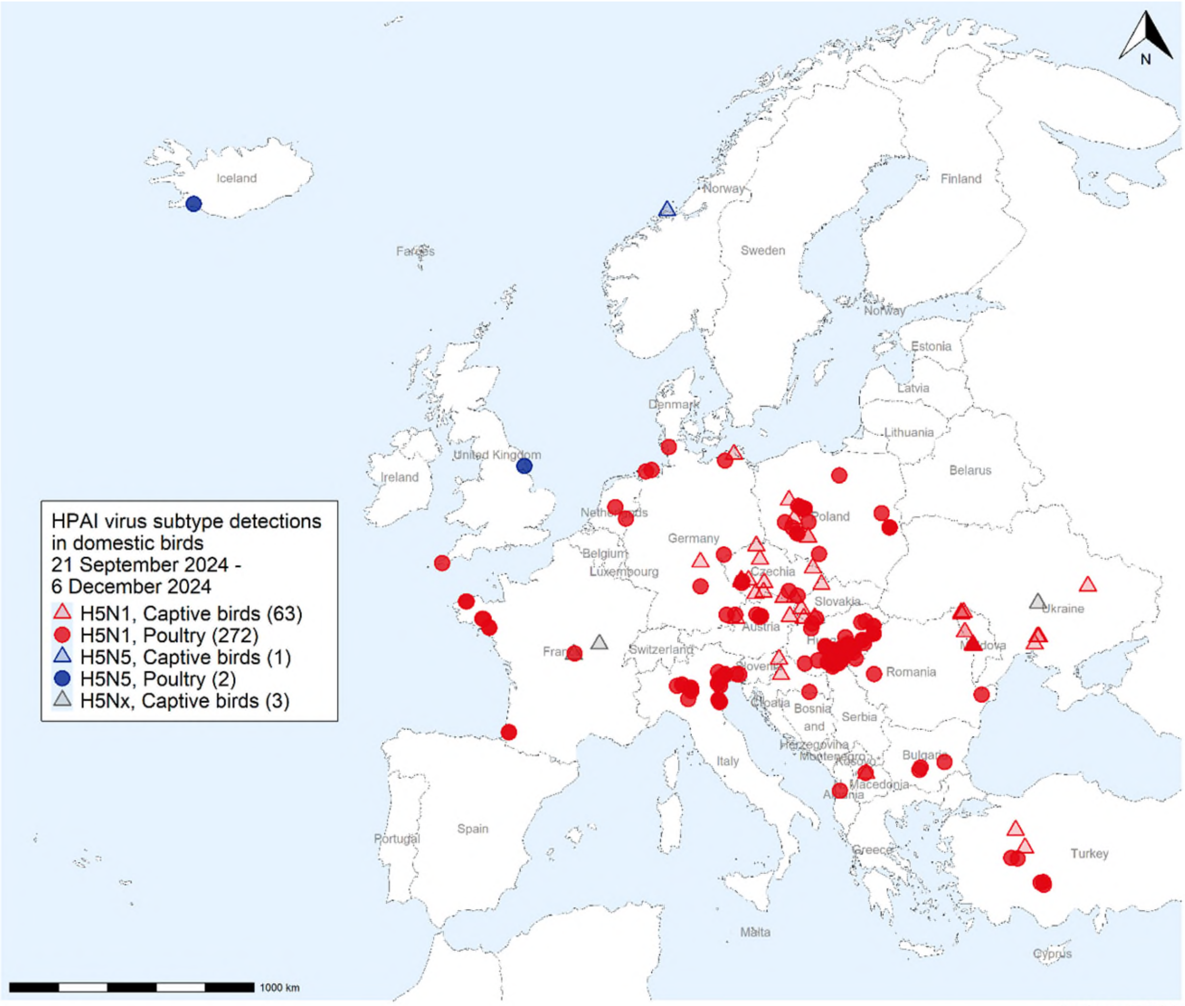
[4] In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Windsor Framework, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).

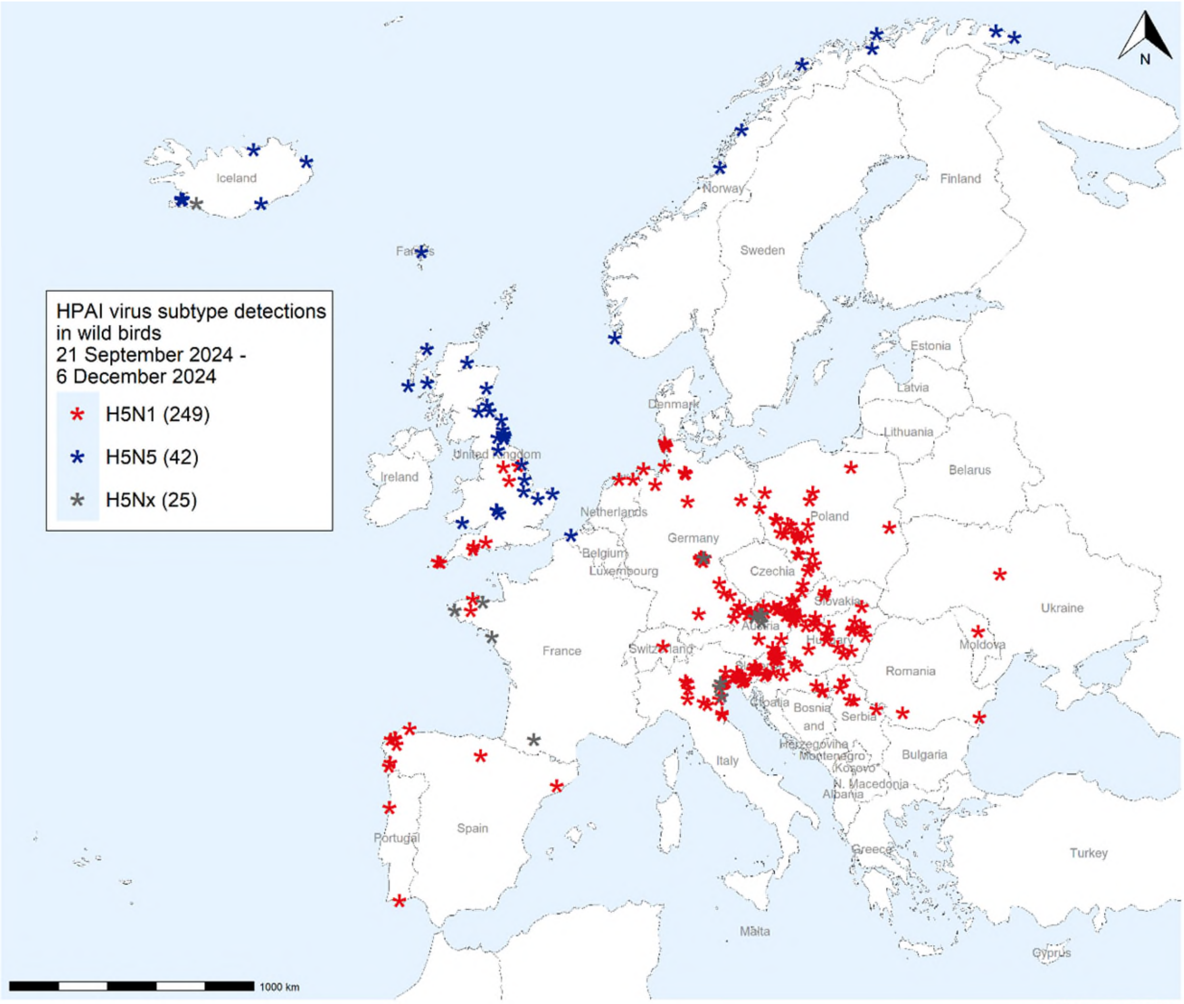
since the start of the 2024–2025 epidemiological year are reported in parentheses (1 October 2024 to 20 September 2025)

| Reporting country | Captive birds | | | Poultry | | Wild birds | | | Total |
|---|---|---|---|---|---|---|---|---|---|
| | A(H5Nx) | A(H5N1) | A(H5N5) | A(H5N1) | A(H5N5) | A(H5Nx) | A(H5N1) | A(H5N5) | |
| Albania | - | - | - | 1 (1) | - | - | - | - | **1 (1)** |
| Austria | - | 2 (1) | - | 6 (6) | - | 4 (4) | 50 (49) | - | **62 (56)** |
| Belgium | - | - | - | - | - | - | - | 1 (1) | **1 (1)** |
| Bulgaria | - | - | - | 3 (2) | - | - | - | - | **3 (2)** |
| Croatia | - | 1 (1) | - | 1 (1) | - | - | 6 (6) | - | **8 (8)** |
| Czechia | - | 12 (10) | - | 4 (3) | - | - | 4 (4) | - | **20 (17)** |
| Faeroe Islands (Denmark) | - | - | - | - | - | - | - | 1 (1) | **1 (1)** |
| France | 2 (2) | - | - | 9 (8) | - | 4 (4) | 2 (2) | - | **17 (14)** |
| Germany | - | 2 (2) | - | 8 (7) | - | 13 (13) | 41 (41) | - | **64 (50)** |
| Hungary | - | 1 (1) | - | 186 (185) | - | - | 18 (15) | - | **205 (201)** |
| Iceland | - | - | - | - | 1 (1) | 1 (1) | - | 7 (5) | **9 (5)** |
| Italy | - | - | - | 23 (23) | - | 3 (2) | 38 (37) | - | **64 (60)** |
| Moldova | - | 29 (16) | - | - | - | - | 1 (1) | - | **30 (17)** |
| Netherlands | - | - | - | 1 (1) | - | - | 2 (2) | - | **3 (3)** |
| North Macedonia | - | 1 (1) | - | 1 (1) | - | - | - | - | **2 (2)** |
| Norway | - | - | 1 (1) | - | - | - | - | 8 (8) | **9 (10)** |
| Poland | - | 4 (4) | - | 19 (19) | - | - | 24 (24) | - | **47 (47)** |
| Portugal | - | - | - | - | - | - | 2 (2) | - | **2 (2)** |
| Romania | - | - | - | 2 (2) | - | - | 2 (2) | - | **4 (4)** |
| Serbia | - | - | - | - | - | - | 5 (3) | - | **5 (3)** |
| Slovakia | - | 4 (4) | - | 2 (2) | - | - | 5 (5) | - | **11 (11)** |
| Slovenia | - | 1 (1) | - | - | - | - | 29 (29) | - | **30 (30)** |
| Spain | - | - | - | - | - | - | 10 (8) | - | **10 (8)** |
| Switzerland | - | - | - | - | - | - | 1 (1) | - | **1 (1)** |
| Türkiye | - | 2 (2) | - | 5 (5) | - | - | - | - | **7 (7)** |
| Ukraine | 1 (0) | 4 (4) | - | - | - | - | 1 (0) | - | **6 (4)** |
| United Kingdom | - | - | - | 1 (1) | 1 (1) | - | 8 (8) | 25 (20) | **35 (29)** |
| **Total** | **3 (2)** | **63 (47)** | **1 (1)** | **272 (267)** | **2 (2)** | **25 (24)** | **249 (239)** | **42 (35)** | **657 (594)** |

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



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 06/12/2024



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 06/12/2024

*This designation is without prejudice to positions on status and is in line with United Nations Security Council Resolution 1244 and the International Court of Justice Opinion on the Kosovo Declaration of Independence.
United Kingdom (excluding Northern Ireland) data are from WOAH and ADIS for the United Kingdom (Northern Ireland)[5].
Source: ADIS, EFSA and WOAH (data extraction carried out on 6 December 2024).

**Figure 2:** Geographic distribution, based on available geocoordinates, of HPAI virus detections in poultry and captive birds (341) (upper panel), and in wild birds (316) (lower panel) reported by virus subtype in Europe from 21 September to 6 December 2024

This represents an increase compared to the low numbers reported in the previous reporting period (15 June to 20 September 2024) (Figure 1). Although this increase is expected and similar to the years before 2023, in 2024 it occurred earlier (already in September) than in the previous year, when it only started in October. This variation may be related to differences in the arrival dates of migratory waterfowl at their wintering sites in Europe.

During the current reporting period, HPAI A(H5N1) outbreaks in poultry and captive birds were mostly located in the central and south-eastern parts of Europe (South Germany, Poland, Czechia, Slovakia, Austria, North Italy, Slovenia, Hungary, Croatia,

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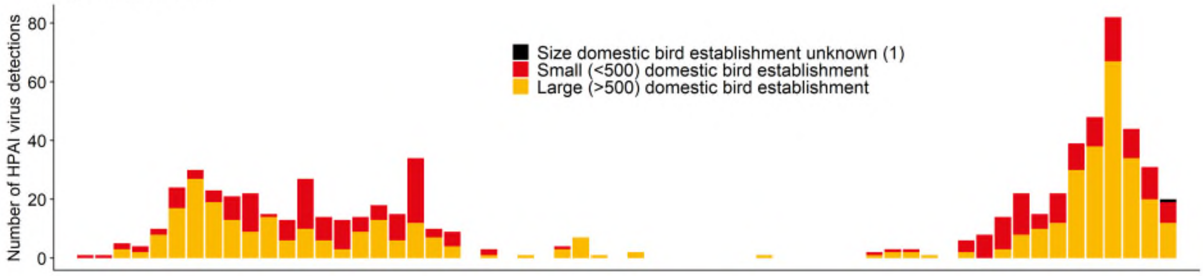
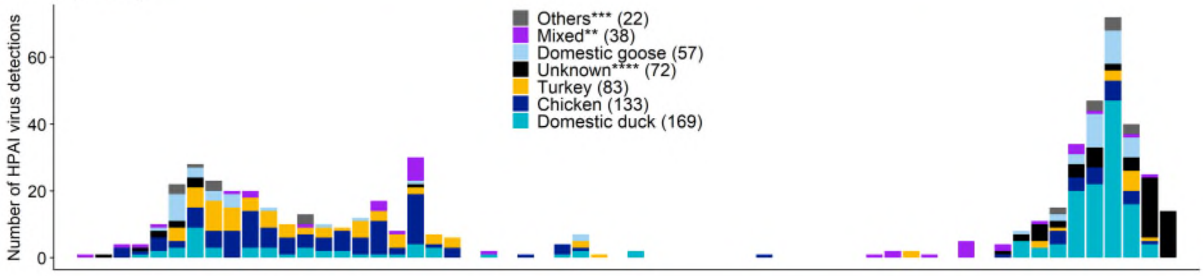
[5] In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Windsor Framework, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).

Romania, Moldova, Ukraine, Albania, North Macedonia, and Bulgaria), except for a few outbreaks on the French Atlantic coast, as well as on the German North and Baltic Sea coasts (Figure 2, upper panel). These outbreaks even reached as far south as Türkiye. HPAI A(H5N1) virus detections in wild birds were more widespread than in domestic birds (Figure 2, lower panel), but they largely overlapped with each other. There was a spatial separation in the distribution of outbreaks in wild birds, with some of them detected on the Atlantic and North Sea coasts on a line from North-West to South-West Europe (Germany, United Kingdom, France, Spain, and Portugal), another group of outbreaks concentrated in South-Central Europe (Italy, Slovenia, Austria, Hungary, Slovakia, and Serbia), and individual reports from northern and eastern parts of Europe (Poland, Ukraine, and Romania). The majority of these HPAI virus detections concerned waterfowl, in contrast to the previous reporting period, when colony-breeding seabirds were in the majority (Figure 3; Figures A.1–A.2 in Annex A).

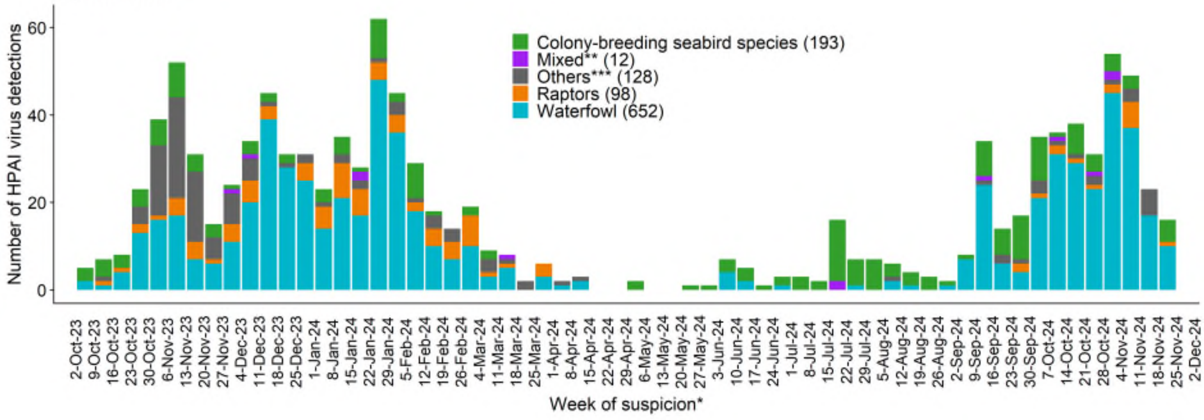
(a) Domestic birds



(b) Poultry



(c) Wild birds



*If the date of suspicion was not available, the date of confirmation was used to assign the week of suspicion.

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

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

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

Source: ADNS/ADIS, EFSA and WOAH (data extraction carried out on 6 December 2024).

**Figure 3:** Distribution of the total number of HPAI virus detections reported in Europe by week of suspicion (dates indicate the first day of the week) and establishment size (a),

affected poultry categories (b) and affected wild bird categories (c), from 1 October 2023 to 6 December 2024

HPAI A(H5N5) outbreaks were again reported from northern parts of Europe, and in greater numbers than before, when they had only been observed sporadically (Figure 1, Figure 2). During the current reporting period, HPAI A(H5N5) outbreaks were reported in poultry in Iceland and the United Kingdom, as well as in captive birds in Norway. These represent the first detections of this subtype in these categories and countries. The last time A(H5N5) viruses were described in poultry was in March 2021, with a total of 15 outbreaks (all HPAI except France) reported in seven countries so far: Germany (5), Croatia (4), Sweden (2), and Belgium, France, Romania, and Slovakia (each 1). In wild birds, a large number of HPAI A(H5N5) virus detections were reported in the United Kingdom (25), Norway (8), Iceland (7), and Belgium and Faroe Islands (Denmark) (each 1).

Spatio-temporal information on all HPAI virus detections reported in Europe since October 2016 is available via EFSA's interactive dashboard[6].

## Poultry

Between 21 September and 6 December 2024, 274 HPAI outbreaks in poultry were reported from 17 countries in Europe: Hungary (186), Italy (23), Poland (19), France (9), Germany (8), Austria (6), Türkiye (5), Czechia (4), Bulgaria (3), Romania (2), Slovakia (2), United Kingdom (2), and Albania, Croatia, Iceland, Netherlands, and North Macedonia (each 1) (Table 1, Figure 2, Figure 4).

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

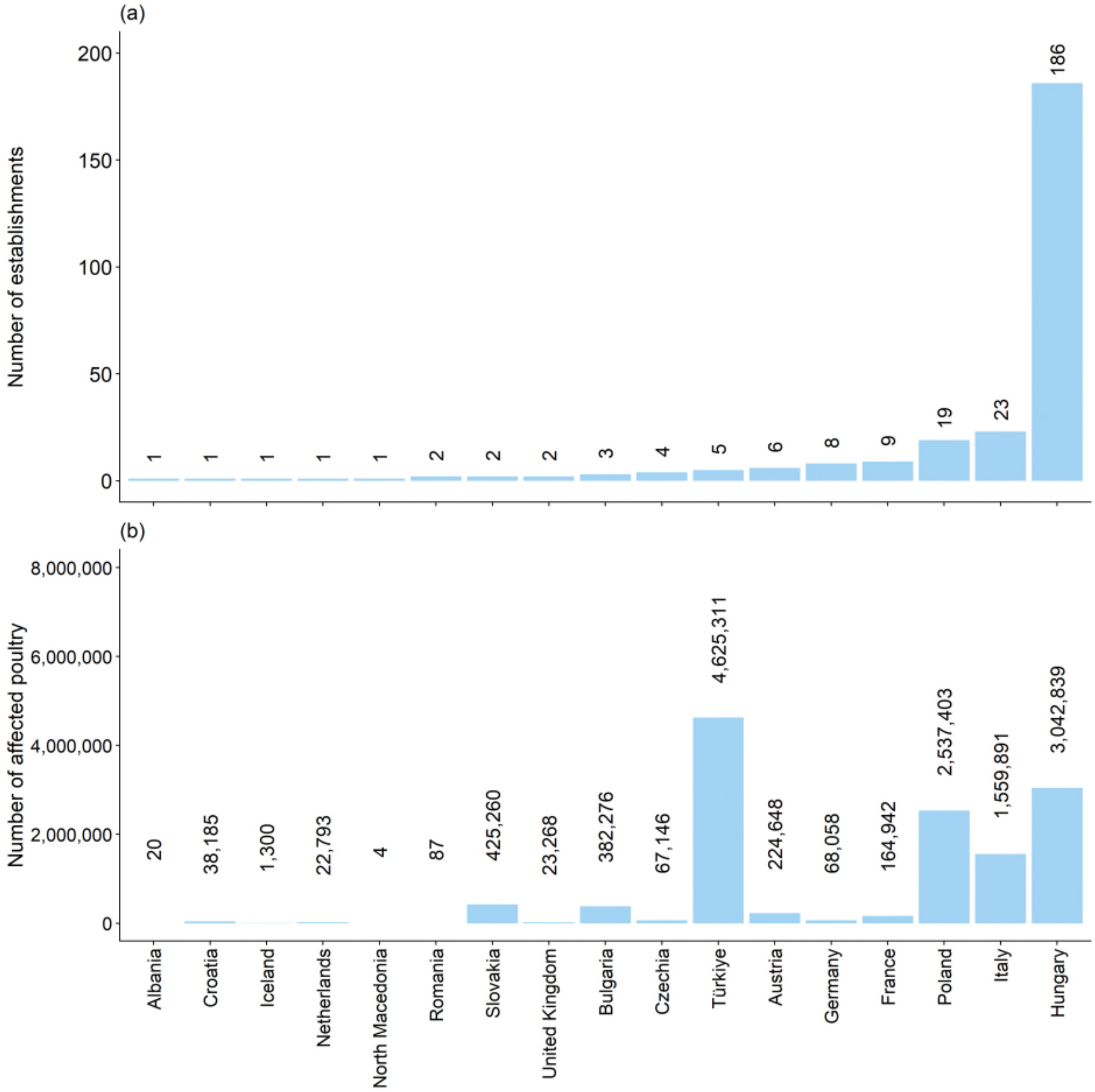


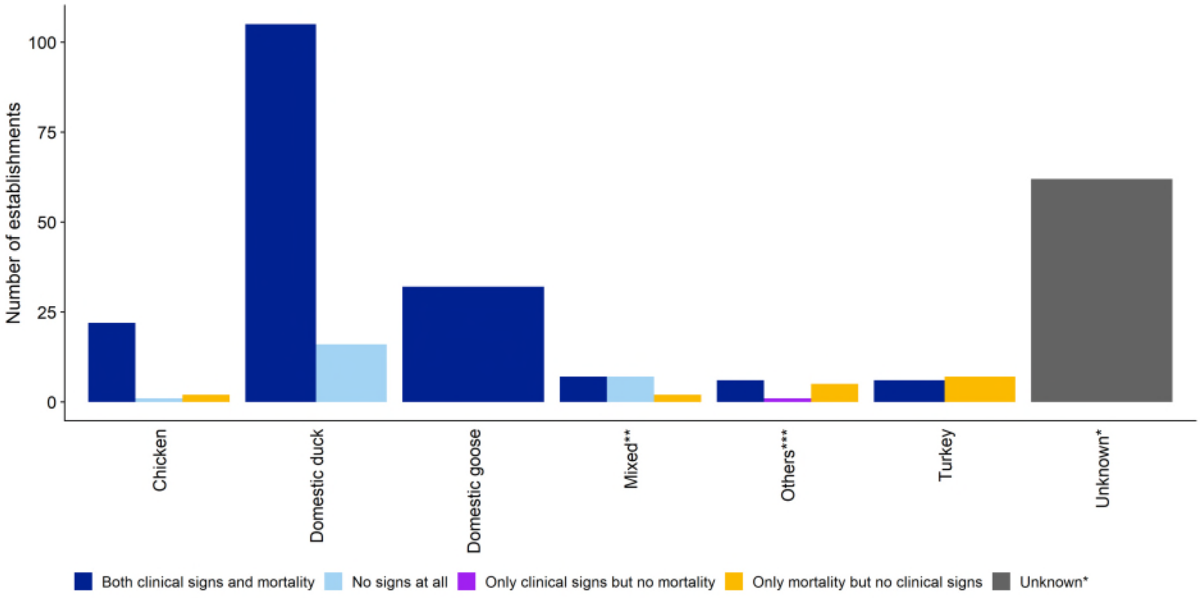
**Figure 4:** Number of HPAI-affected establishments (274) (a) and number of poultry in the HPAI-affected establishments (13,183,431) (b) in Europe between 21 September and 6 December 2024

Almost all of these outbreaks were due to HPAI A(H5N1) viruses. This compares to a total of 112 A(H5) outbreaks during the same period in the previous epidemiological year, when also half of the outbreaks were reported in Hungary (57). The 2023 figures seem particularly low considering that similar numbers to 2024 were reported in the same period in 2022 (445) and 2021 (346). During the current reporting period, Hungary accounted for more than 65% (186/274) of the HPAI outbreaks in poultry, with many smaller establishments involved, while the few outbreaks in Türkiye, Poland and Italy involved larger establishments with higher numbers of susceptible birds (Figure 4). In total, more than 13 million birds died or were culled in the HPAI-affected poultry establishments (Figure 4), 100 times more than in the previous reporting period. Overall, 43% (118/274) of the HPAI outbreaks in poultry were reported as primary, 56% (154/274) as secondary, and for two outbreaks this information was not available. Almost all (99%, 153/154) secondary outbreaks were reported in Hungary, reflecting extensive farm-to-farm spread in a high-density poultry area. For 92% (142/154) of all secondary outbreaks, indirect contact with poultry was considered the most likely source of introduction, and no information was available for the remaining 8% (12/154). For 43% (51/118) of all primary outbreaks, indirect contact with wild birds was considered the most likely source of introduction, followed by direct contact with wild birds (4%, 5/118), and no information was available for the remaining 53% (62/118). During the current reporting period, the most affected poultry category in Europe was the 'domestic duck' category (44%, 121/274 outbreaks), followed by the 'domestic goose' (12%, 32/274), 'chicken' (9%, 25/274), 'turkey' (5%, 13/274), and 'others' (4%, 12/274) categories. Multiple species were kept by 9 (3%) establishments and no information was available on the species kept for another 62 (23%) establishments. Hungary accounted for 91% (110/121) of the outbreaks in the 'domestic duck' category, which included mulard, Muscovy and other ducks (Table 2).

**Table 2:** Characterisation of HPAI-affected establishments housing domestic ducks (121) by species, production type and country, in Europe between 21 September and 6 December 2024

| Domestic duck type | Production type | Number of affected establishments per country |
|---|---|---|
| Mulard ducks | Foie gras | Hungary (76), France (3) |
| Muscovy ducks | Fattening | France (1) |
| Other ducks | Fattening | Hungary (28), Poland (4) |
| | Breeding | Hungary (6), Poland (3) |

Clinical signs and mortality were observed across all poultry categories in Europe, with the 'domestic goose' category persistently displaying both, and the 'domestic duck' category being the category most often associated with the absence of signs of the disease (Figure 5). The latter comprised four establishments in France that involved vaccinated birds.



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

**'Mixed' refers to outbreaks in which multiple species were involved.
***'Others' groups all other affected species that are not indicated in the legend.

**Figure 5:** Number of HPAI-affected poultry establishments by species and presence of signs of HPAI virus infection in Europe between 21 September and 6 December 2024. Note that information was only available for 212 out of 274 HPAI-affected poultry establishments.

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, reporting countries (in form of additional data submitted and personal communications) and media reports. In the period from 21 September to 6 December 2024, 274 HPAI outbreaks in poultry were reported in Europe via ADIS. Additional data on the characteristics of the affected poultry establishments and poultry species reared were collected for 212 out of these 274 outbreaks, reported to ADIS on or before 22 November 2024, from Austria, Croatia, Czechia, France, Germany, Hungary, Netherlands, Poland, Romania, and Slovakia (Annex B). For the remaining 62 outbreaks in poultry, no additional data were provided or they were reported to ADIS after 22 November 2024 and therefore occurred too shortly before the publication of this report. These data will therefore only be collected from the reporting countries for the next report.

*Albania*

During the current reporting period from 21 September to 6 December 2024, one primary outbreak in poultry was reported in Albania via ADIS. No additional data to complement this information in ADIS were provided by the country. On 28 October, an A(H5N1) outbreak was suspected in a small non-commercial establishment keeping laying hens (n = 20). Mortality and clinical signs were observed.

*Austria*

During the current reporting period from 21 September to 6 December 2024, six primary outbreaks in poultry were reported in Austria via ADIS. Additional data were collected and provided by the reporting country for all six outbreaks. On 9 October, an A(H5N1) outbreak was confirmed in a multi-species commercial establishment keeping chickens for breeding (n = 75), turkeys for fattening (n = 22), ducks for fattening (n = 16), and domestic guineafowl for fattening (n = 12). Only one species, the chickens, showed high mortality (100.0%) and clinical signs (including drop in egg production), while the other birds showed no clinical signs or changes in mortality rates. Outdoor access for birds was provided and there were previous reports of wild birds sharing this space. According to the data provided, the most likely source of introduction was direct contact with wild birds. Seven people were reported as exposed. A geographic cluster of five affected poultry establishments was identified in a region with one of the highest poultry densities in Austria, including one of the largest laying hen establishments (European Commission, online). On 29 October, the first A(H5N1) outbreak of this cluster was detected in a commercial laying hen establishment (n = 46,297). The outbreak resulted in increased mortality (37.9%) and clinical signs. Twenty-five people were reported as exposed. On 5 and 6 November, the second and third A(H5N1) outbreaks were reported. The second outbreak occurred in a commercial laying hen establishment (n = 125,573), resulting in mortality (8.0%) and clinical signs. Forty people were reported as exposed. The third outbreak occurred in a commercial turkey fattening establishment (n = 8,923), resulting in high mortality (78.0%) and clinical signs. No outdoor access was provided and the most likely source of introduction was indirect contact with wild birds. Forty people were reported as exposed. On 7 November, the fourth A(H5N1) outbreak was detected in a commercial turkey fattening establishment (n = 11,580). The outbreak resulted in increased mortality (43.4%) and clinical signs. Forty people were reported as exposed. Finally, on 12 November, the fifth A(H5N1) outbreak of the cluster occurred in a commercial laying hen establishment (n = 32,150). The outbreak resulted in high mortality (73.2%). Twenty-five people were reported as exposed. Concerning all outbreaks of the geographic cluster, the birds had no access to the outdoor and the most likely source of introduction was indirect contact with wild birds. Further epidemiological investigations are ongoing.

### *Bulgaria*

During the current reporting period from 21 September to 6 December 2024, three primary outbreaks in poultry were reported in Bulgaria via ADIS. No additional data to complement this information in ADIS were provided by the country. On 27 September, an A(H5N1) outbreak was suspected in a multi-species game bird establishment keeping pheasants (n = 4,342) and other species (partridges and wild American turkeys) for game purposes (n = 3,327), with mortality and clinical signs observed. Another A(H5N1) outbreak was suspected on 14 October in a non-commercial establishment housing two flocks of laying hens (total n = 700), where clinical signs and mortality were observed in one of the flocks (n = 300), and a limited number of waterfowl were kept separately on the premises. On 21 October, the last A(H5N1) outbreak was suspected in a large commercial establishment keeping chickens for various purposes, including laying hens (n = 54,000) and broilers/chicken breeders (n = 320,000), with clinical signs and mortality described.

### *Croatia*

During the current reporting period from 21 September to 6 December 2024, one primary outbreak in poultry was reported in Croatia via ADIS. Additional data on this outbreak were collected and provided by the reporting country. On 14 October, the A(H5N1) outbreak was detected in a commercial establishment keeping turkeys for fattening (n = 38,185). Clinical signs (including drop in feed and water intake) and mortality (0.4%) were observed. The birds had no outdoor access and the most likely source of introduction was indirect contact with wild birds. It was reported that a large number of wild birds resided on nearby ponds. Twenty people were reported as exposed. A housing order for all domestic birds has been in place since 11 May 2024.

### *Czechia*

During the current reporting period from 21 September to 6 December 2024, four primary outbreaks in poultry were reported in Czechia via ADIS. Additional data were collected and provided by the reporting country for all four outbreaks. On 27 September, an A(H5N1) outbreak was detected in a commercial multi-species establishment keeping domestic ducks for fattening (n = 18,000), pheasants for game purposes (n = 2,809), and other game birds (mallards and partridges, n = 8,004). Mortality (1.3%) and clinical signs were observed in the domestic duck population, while the other species showed no clinical signs. All birds were kept indoor and the most likely source of introduction was indirect contact with wild birds. The proximity of the farm to nearby ponds was highlighted. Fifty people were reported as exposed. On 21 October, a second A(H5N1) outbreak occurred in a commercial establishment where domestic geese were kept for fattening (n = 2,746) and breeding (n = 2,389), alongside domestic ducks for fattening (n = 1,042) and other game birds (n = 1,032). Only the domestic geese kept for fattening showed clinical signs and mortality (6.4%). Outdoor access was available and direct contact with wild birds was suspected as the source of introduction, as the establishment is located near ponds. Fifteen people were reported as exposed. On 14 November, an A(H5N1) outbreak was detected in a multi-species commercial establishment housing domestic ducks (n = 12,000), pheasants (n = 780), and other species (mallards and partridges) for game purposes (n = 5,580). Only one species, the domestic ducks, showed clinical signs and mortality (2.1%). The birds had no outdoor access and indirect contact with wild birds was the suspected source of introduction, as the establishment is located near ponds. Thirty-five people were reported as exposed. A fourth A(H5N1) outbreak was reported on 15 November in a commercial turkey fattening establishment (n = 12,764), where increased mortality (46.8%) and clinical signs were observed. The birds had no outdoor access and indirect contact with wild birds was the suspected source of introduction, as the establishment is located near a river. Twenty-five people were reported as exposed. No housing order for domestic birds has been put in place. However, recommendations to strengthen biosecurity measures in connection with HPAI virus detections were distributed by veterinary authorities.

### *France*

During the current reporting period from 21 September to 6 December 2024, nine primary outbreaks in poultry were reported in France via ADIS. Additional data were collected and provided by the reporting country for all nine outbreaks. On 26 September, an A(H5N1) outbreak was confirmed in a commercial laying hen establishment (n = 29,500), where mortality (0.3%) and clinical signs with a drop in egg production were observed. The birds had access to the outdoor and the most likely source of introduction was either direct or indirect contact with wild birds. On 12 October, a second A(H5N1) outbreak occurred in a commercial turkey fattening establishment (n = 6,600), with mortality (1.2%) and clinical signs reported. The birds were kept indoor and the most likely source of introduction remained unknown at the time of publication of this report. On 22 October, an A(H5N1) outbreak was reported in a commercial establishment housing laying hens (n = 27,500), where mortality (0.2%) and clinical signs were observed. The birds had outdoor access, but the most likely source of introduction remained unknown. On 23 October, an A(H5N1) outbreak was detected in a commercial establishment keeping mulard ducks for foie gras production (n = 7,500). No mortality or clinical signs had been observed before infection was confirmed, however neurological signs and mortality were recorded for a limited number of birds on the day the establishment was depopulated. The birds were kept indoor and the most likely source of introduction remained unknown. These birds had been vaccinated with two injections and were housed in two separate buildings and an assisted feeding premise, with ages ranging from seven to 14 weeks. The outbreak was detected through post-vaccination active surveillance (EFSA, ECDC and EURL, 2024a). On 25 October, another A(H5N1) outbreak was reported in the same locality in a commercial Muscovy duck fattening establishment (n = 30,192) housing 5-week-old birds, with no mortality or clinical signs observed. No outdoor access was provided and the most likely source of introduction remained unknown. Also these birds were vaccinated with two injections and the outbreak was detected through post-vaccination active surveillance. On 1 November, two additional A(H5N1) outbreaks were reported: one in a commercial chicken fattening establishment (n = 51,000), with mortality (0.004%) and clinical signs observed. No outdoor access was provided and the most likely source of introduction remained unknown; and another outbreak in a commercial establishment keeping several poultry species (n = 250), with increased mortality (20.0%) and clinical signs observed. Outdoor access was available, but the most likely source of introduction remained unknown. On 5 November, an A(H5N1) outbreak was detected in a commercial establishment rearing mulard ducks for foie gras production (n = 6,400) housing 5-week-old and 16-week-old birds in two separate buildings, with no mortality or clinical signs observed. This establishment provided outdoor access and direct contact with wild birds was the suspected source of introduction. The establishment is located in a specific risk area for HPAI introduction from wild birds. These birds were vaccinated with two injections and the outbreak was detected through pre-movement virological testing (EFSA, ECDC and EURL, 2024a), performed before some of the birds were sent to the assisted-feeding fattening establishment. On 13 November, an A(H5N1) outbreak was reported in the same locality in another commercial mulard duck establishment for foie gras production (n = 6,000) housing 8-week-old birds, with no mortality or clinical signs observed before infection was confirmed (neurological signs were only reported on the day the establishment was depopulated). These birds were vaccinated with two injections and the outbreak was identified through outbreak-related surveillance conducted before the animals were moved. Outdoor access was available and direct contact with wild birds was the suspected source of introduction, although genetic analysis suggested an otherwise unidentified link to the outbreak reported on 5 November. For all outbreaks, the number of people exposed remained unknown at the time of publication of this report. Since 31 October 2024, the national risk level increased from moderate to elevated, prompting the implementation of a nationwide housing order for all establishments with 50 or more birds across France.

#### *Germany*

During the current reporting period from 21 September to 6 December 2024, eight primary outbreaks in poultry were reported in Germany via ADIS. Additional data were collected and provided by the reporting country for four out of the eight outbreaks, as the last four occurred too close to the time of publication of this report. On 25 September, an A(H5N1) outbreak was detected in a commercial establishment keeping geese (n = 115) and ducks for fattening (n = 69). High mortality (82.6%) and clinical signs were observed, but only in the goose population. The birds had outdoor access and indirect contact with wild birds was the suspected source of introduction. On 24 October, a second A(H5N1) outbreak occurred in a commercial establishment housing laying hens (n = 5) and geese for fattening (n = 80). While the goose population expressed high mortality (92.5%) and clinical signs, the chickens remained unaffected. The establishment provided outdoor access and indirect contact with wild birds was the suspected source of introduction. On 28 October, a third A(H5N1) outbreak was reported in a commercial multi-species establishment keeping turkeys for fattening (n = 50), laying hens (n = 119), ducks (n = 148) and geese (n = 110) for fattening, and broilers (n = 50). Increased mortality and clinical signs were observed in all species, but mortality was higher in the goose and turkey populations (93.6% and 50.0%, respectively). The birds had outdoor access and indirect contact with wild birds was the suspected source of introduction. On 18 November, a fourth A(H5N1) outbreak was detected in a commercial turkey fattening establishment (n = 15,873), with mortality (0.6%) and clinical signs observed. The birds were kept indoor and indirect contact with wild birds was the suspected source of introduction. For all four outbreaks, the number of exposed people was unknown at the time of publication of this report.

*Hungary*

During the current reporting period from 21 September to 6 December 2024, 186 outbreaks in poultry were reported in Hungary via ADIS. Additional information was collected from the reporting country for 170 out of the 186 outbreaks, as the last 16 were reported too close to the time of publication of this report. All 170 outbreaks were confirmed as A(H5N1) and the majority of these outbreaks (142) were reported as secondary, while only 28 were reported as primary. Almost all outbreaks (159) occurred in commercial establishments and the total number of susceptible birds was 2,705,478. All affected establishments housed only single species, with the majority keeping mulard ducks (76) or geese (26) for foie gras production; followed by ducks (28), turkeys (6), chickens (5), and geese (3) for fattening; ducks (6), geese (3), and chickens (1) for breeding; laying hens (4); pheasants for other purposes (1); and chickens (1) and other bird species (10) for mixed purposes. In all 170 outbreaks, birds with clinical signs were described and mortality was observed in 156 out of the 170 outbreaks. Fifteen establishments provided outdoor access, while in the remaining 155 the birds were kept indoor. The most common suspected source of introduction was indirect contact with poultry, reported for 142 outbreaks, followed by indirect contact with wild birds for 28 outbreaks. Most outbreaks were geographically clustered, with many establishments being located in close proximity to each other. The number of exposed people in all affected establishments was unknown at the time of publication of this report.

*Iceland*

During the current reporting period from 21 September to 6 December 2024, one primary outbreak in poultry was reported in Iceland via ADIS. No additional data to complement this information in ADIS were collected, as the outbreak was reported too close to the time of publication of this report. On 3 December, an A(H5N5) outbreak was suspected in a commercial establishment keeping turkeys for fattening (n = 1,300). Mortality and clinical signs were observed.

*Italy*

During the current reporting period from 21 September to 6 December 2024, 23 outbreaks in poultry were reported in Italy via ADIS. No additional data to complement this information in ADIS were provided by the country. All outbreaks were confirmed as A(H5N1) and all but one (22) were reported as primary. The total number of susceptible birds was more than 1,500,000, with one large establishment housing almost 800,000 laying hens. In commercial establishments, the most affected species were turkeys for fattening (11), followed by laying hens (2), chickens for fattening (1), capons (1), and pheasants for breeding (1). In all cases, the disease manifested itself with a sudden increase in mortality, often in only one sector of the flock, and a clinical picture consistent with HPAI, characterised by a silent group with some individuals showing nervous and enteric (diarrhea) signs. Mortality always increased exponentially in the days following suspicion. Among the peculiarities of this epidemic season in Italy are the high involvement of small rural, non-commercial multi-species establishments, often backyard flocks with a few dozen birds, and the high number of outbreaks in the province of Treviso (Veneto region), which is not a high-density poultry area, nor does it have extensive wetlands, but only small rivers, streams and water canals, which could justify the presence of waterfowl carrying HPAI viruses and be responsible for environmental contamination of poultry establishment surroundings.

### *Netherlands*

During the current reporting period from 21 September to 6 December 2024, one primary outbreak in poultry was reported in the Netherlands via ADIS. Additional data on this outbreak were collected and kindly provided by the reporting country. On 17 November, an A(H5N1) outbreak was detected in a commercial establishment keeping laying hens (n = 22,793). Mortality (0.2%) and clinical signs were observed. The birds were kept indoor and outdoor (free range), and the most likely source of the outbreak remained unknown at the time of publication of this report. No people were reported as exposed. A housing order for all domestic birds has been in place since 20 November 2024.

### *North Macedonia*

During the current reporting period from 21 September to 6 December 2024, one primary outbreak in poultry was reported in North Macedonia via ADIS. No additional data to complement this information in ADIS were provided by the country. On 25 October, an A(H5N1) outbreak was suspected in a small establishment keeping only four birds. Mortality and clinical signs were observed.

### *Poland*

During the current reporting period from 21 September to 6 December 2024, 19 primary outbreaks in poultry were reported in Poland via ADIS. Additional information was collected from the reporting country for 13 out of the 19 outbreaks, as the last six were reported too close to the time of publication of this report. All 13 outbreaks were confirmed as A(H5N1) and occurred in commercial establishments. The total number of susceptible birds was 2,277,898, involving mainly chickens (n = 2,076,519) and ducks (n = 194,133), and to a smaller extent also turkeys (n = 7,246). All affected establishments housed only single species, with the majority keeping laying hens (4); followed by ducks (4), chickens (1), and turkeys (1) for fattening; and ducks (3) for breeding. In all 13 outbreaks, birds with clinical signs were described and mortality was observed in 12 out of the 13. Only two establishments provided outdoor access, while in the remaining 13 the birds were kept indoor. The most common suspected source of introduction was indirect contact with wild birds, reported for eight outbreaks. For the five remaining outbreaks, the suspected source of introduction remained unknown at the time of publication of this report. Presence of wild birds was reported for four affected establishments, and proximity to waterbodies was reported for another four.

### *Romania*

During the current reporting period from 21 September to 6 December 2024, two primary outbreaks in poultry were reported in Romania via ADIS. Additional data on both outbreaks were collected and provided by the reporting country. On 24 October, the first A(H5N1) outbreak occurred in a non-commercial establishment keeping domestic ducks (n = 20) and chickens (n = 27) for mixed purposes. The outbreak resulted in increased mortality (20.0%) and clinical signs among the chicken population only. The birds had outdoor access and direct contact with wild birds was the suspected source of introduction, likely due to the presence of a pond in vicinity and the absence of protective nets to prevent wild birds from accessing the enclosure. The establishment's location near a flowing water source was highlighted, which potentially increased its risk of contamination. Three people were reported as exposed. On 19 November, a second A(H5N1) outbreak was detected in a non-commercial establishment keeping a small number of chickens (n = 33) and domestic geese (n = 7) for mixed purposes. The outbreak resulted in increased and high mortality (45.5% and 57.1%, respectively), and clinical signs in both species. The birds had outdoor access and the most likely source of introduction was direct contact with wild birds. One person was reported as exposed. No housing order for domestic birds has been put in place. However, recommendations were distributed at the national level by veterinary authorities, instructing poultry owners to keep domestic birds confined, prevent access to water bodies, and avoid contact with wild birds.

*Slovakia*

During the current reporting period from 21 September to 6 December 2024, two primary outbreaks in poultry were reported in Slovakia via ADIS. Additional data on both outbreaks were collected and provided by the reporting country. On 16 October, an A(H5N1) outbreak was detected in a commercial chicken breeding establishment (n = 40,260). The outbreak resulted in increased mortality (25.5%) and clinical signs. The birds had no outdoor access and indirect contact with wild birds was the suspected source of introduction. On 21 October, a second A(H5N1) outbreak occurred in a commercial establishment keeping laying hens (n = 385,000). The outbreak resulted in high mortality (94.8%), affecting almost the entire flock, and clinical signs were observed. The birds had no outdoor access and indirect contact with wild birds was the suspected source of introduction. No people were reported as exposed for neither outbreak. No housing order for domestic birds has been put in place, but recommendations were released by veterinary authorities to keep domestic birds indoor.

*Türkiye*

During the current reporting period from 21 September to 6 December 2024, five primary outbreaks in poultry were reported in Türkiye via ADIS. No additional data to complement this information in ADIS were provided by the country. On 31 October, an A(H5N1) outbreak was suspected in a commercial establishment (n = 3,072,458), resulting in mortality and clinical signs. The source of introduction was suspected to be either direct or indirect contact with wild birds. On 1 November, a second A(H5N1) outbreak occurred in a commercial establishment (n = 758,974), with mortality and clinical signs reported. On 6 November, a third A(H5N1) outbreak was suspected in a commercial establishment (n = 69,790), with mortality and clinical signs observed. Two additional A(H5N1) outbreaks were then suspected on 11 November (n = 688,305) and 22 November (n = 35,784), with mortality and clinical signs observed.

*United Kingdom*

During the current reporting period from 21 September to 6 December 2024, two outbreaks in poultry were reported in the United Kingdom via WOAH-WAHIS. At the beginning of November 2024, A(H5N5) virus was detected in a commercial establishment keeping 24,000 laying hens in East Yorkshire that provided outdoor access (FarmingUK, online-a; Sky News, online). Another outbreak involving A(H5N1) virus was detected in mid-November 2024 in a small commercial establishment keeping 42 laying hens in Cornwall (FarmingUK, online-b; GB News, online; GovUK, online-a).

## Captive birds

Between 21 September and 6 December 2024, 67 HPAI outbreaks in captive birds were reported from 14 countries in Europe: Moldova (29), Czechia (12), Ukraine (5), Poland (4), Slovakia (4), Austria (2), France (2), Germany (2), Türkiye (2), and Croatia, Hungary, North Macedonia, Norway, and Slovenia (each 1) (Table 1, Figure 2).

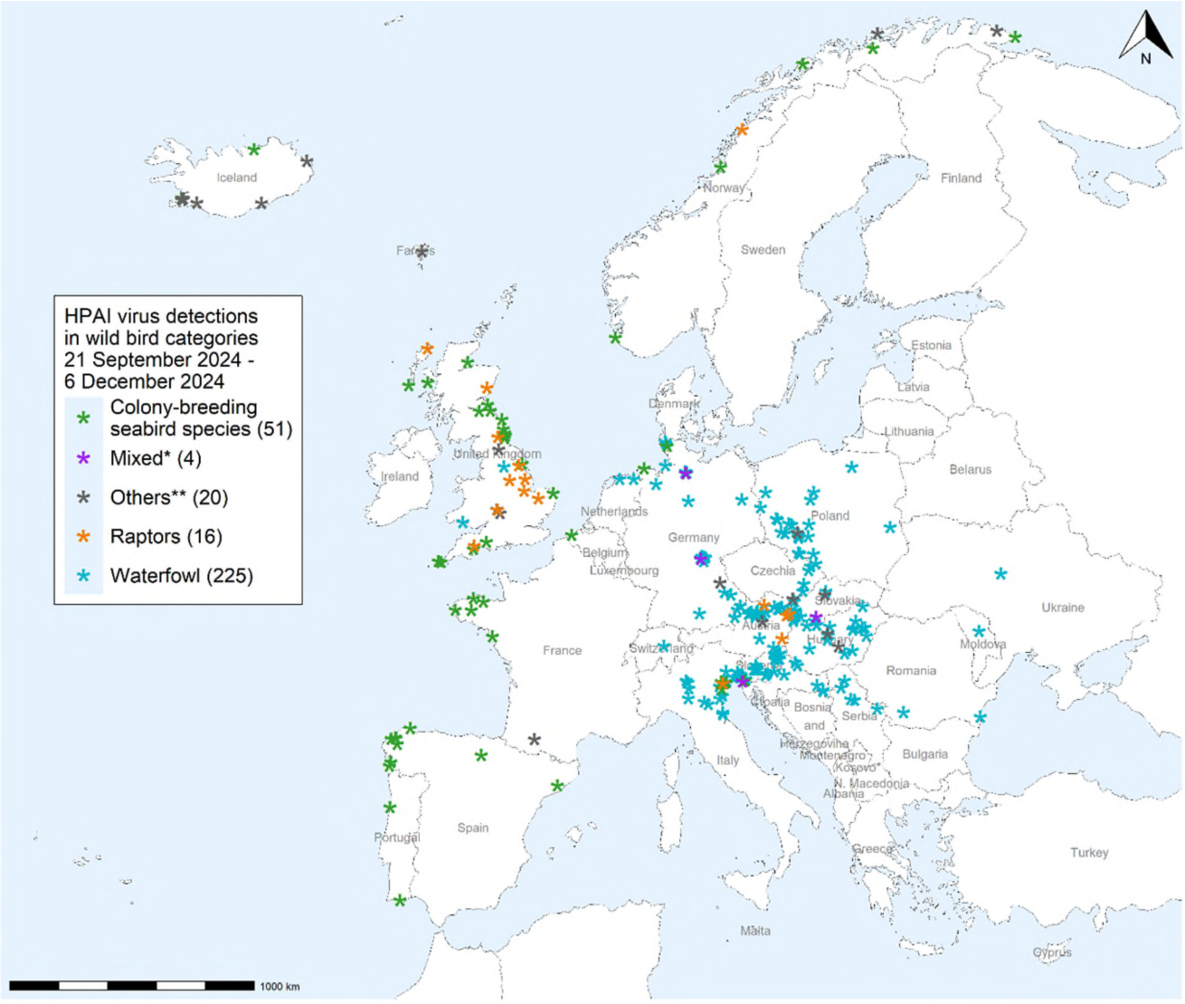
Apart from a large number of non-commercial backyard establishments involved, several HPAI virus detections were reported in zoos. On 5 October, an A(H5N1) outbreak occurred in a zoo in Stralsund, Germany, where pelicans (n = 11) and other wild bird species (n = 802) were kept. The outbreak resulted in mortality (one pink pelican found dead) and clinical signs (WELT, online). Another HPAI virus detection was reported in a zoo in Skopje, North Macedonia, involving one A(H5N1)-infected goose (Ekathimerini, online), and also Croatia reported A(H5N1) in Eurasian spoonbills and a black-crowned night heron in Zagreb zoo. In one out of seven epidemiological unites in the zoo, increased mortality was observed. A housing order to keep the birds indoor as well as other measures were issued.

In Norway, in mid-November 2024, a backyard establishment keeping 94 birds (69 ducks, 22 hens and 3 peacocks) was affected by A(H5N5) virus on Frøya island in Trøndelag county. Several hens (n = 7) were reported to have died suddenly and, at the time of sampling, 16 hens and two ducks were dead (Veterinærinstituttet, online). Outdoor access for birds was available and direct or indirect contact with wild birds was the suspected source of introduction. Domestic mammals present on the farm (23 goats, 5 horses, 3 rabbits and 2 cats) showed no signs of HPAI, except for one goat that was reported as sick at the time the outbreak was confirmed. All mammals tested negative for the virus by qPCR. In addition, available blood samples (23 goats, 5 horses) were serologically tested, with no antibodies to H5 detected.

## Wild birds

During the current reporting period from 21 September to 6 December 2024, a total of 316 HPAI virus detections in wild birds (with a HPAI virus detection potentially including more than one wild bird species) were reported from Austria (54), Germany (54), Italy (41), United Kingdom (33), Slovenia (29), Poland (24), Hungary (18), Spain (10), Iceland (8), Norway (8), Croatia (6), France (6), Serbia (5), Slovakia (5), Czechia (4), Netherlands (2), Portugal (2), Romania (2), and Belgium, Faroe Islands (Denmark), Moldova, Switzerland, and Ukraine (each 1). Overall, 249 HPAI virus detections in wild birds were reported as A(H5N1), 42 as A(H5N5), and 25 as A(H5Nx) (Table 1, Figure 2). The overall number of HPAI virus detections reported in wild birds (316) during this reporting period was more than three times higher than in the previous reporting period (101) (Figure 3) and about one third higher compared to the same period in the previous epidemiological year (212).

Regarding the wild bird categories involved and considering that more than one wild bird species can be included in a single HPAI virus detection, A(H5) was recorded in four times more waterfowl (225) than colony-breeding seabirds (51) (Figure 4). This contrasts with the previous reporting period, when A(H5) was recorded in 1.5 times more colony-breeding seabirds (58) than waterfowl (38) (Figure 3). Similarly to the previous reporting period, almost all HPAI virus detections in colony-breeding seabirds (and in raptors) were located along the Arctic Ocean, Atlantic Ocean and North Sea coasts, while some of them now also occurred on the Adriatic Sea coast. Regarding the increase in HPAI virus detections in waterfowl, the majority were located in South-Central Europe (Figure 4), and part of these HPAI virus detections appear to trace the course of major European rivers, e.g. Danube, Oder, and Po.



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 06/12/2024

[*] This designation is without prejudice to positions on status and is in line with United Nations Security Council Resolution 1244 and the International Court of Justice Opinion on the Kosovo Declaration of Independence.
Note that the unit reported is the number of HPAI virus detections in different wild bird categories and not the 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.
Source: ADIS, EFSA and WOAH (data extraction carried out on 6 December 2024).

**Figure 4:** Geographic distribution, based on available geocoordinates, of HPAI virus detections in different categories of wild birds in Europe, by species category, from 21 September to 6 December 2024

The wild bird species in which HPAI viruses were detected belonged mainly to two orders, Anseriformes (237 HPAI virus detections) and Charadriiformes (52). The main anseriform birds (waterfowl) identified to species were the mute swan (119 in the current vs 12 in the previous reporting period), greylag goose (25 vs 1), mallard (18 vs 1), and Canada goose (20 vs 0). Reports of mortality events in swans were described in some European countries, including Germany (Merkur, online), Poland (RMF24, online), and the

United Kingdom (The Standard, online), in which several or even dozens of deaths were reported. Although information on the age of the affected birds is limited, a report documented the death of several chicks of a single parent pair of swans on a small canal in Slovakia (Teraz, online). Many of these swans were detected nearby waterbodies such as rivers or lakes. Among seven different gull species affected during the current reporting period, the main charadriiform birds (gulls, waders and auks) identified to species were the European herring gull (15 vs 21), yellow-legged gull (12 vs 11), and great black-backed gull (5 vs 4) (Figures A.1–A.2 in Annex A). The complete list of wild bird species found as HPAI virus-infected from 21 September to 6 December 2024 is reported in Figure A.1 in Annex A. The number of HPAI virus-affected wild birds that were not identified to species was 38/335 (11.3%), about two times lower than in the previous reporting period (30/112, 26.8%) (Figures A.1–A.2 in Annex A).

During the current reporting period, A(H5N5) viruses have expanded their geographic and species range and were detected in at least 17 different wild bird species (Table 3).

**Table 3:** Number of HPAI A(H5N5)-affected birds per wild bird category and species, from 21 September to 6 December 2024

| Wild bird category | Species | Number of affected birds |
|---|---|---|
| Colony-breeding seabirds | European herring gull | 8 |
| | Greater black-backed gull | 4 |
| | Black-headed gull | 2 |
| | Mew gull | 2 |
| | Northern fulmar | 2 |
| | Pallas's gull | 2 |
| | Great skua | 1 |
| | Grey gull | 1 |
| | Northern gannet | 1 |
| Others* | Common raven | 5 |
| | Hooded crow | 3 |
| | Ring-necked pheasant | 3 |
| Raptors | Red kite | 3 |
| | Common buzzard | 2 |
| | White-tailed eagle | 2 |
| | Barn owl | 1 |
| Waterfowl | Mallard | 1 |

*'Others' groups all other affected categories.

Given the wide range of wild bird species in which A(H5N5) has recently been reported in Europe, it is not possible to point to a single species in which this subtype is persisting. However, in a study on A(H5N5) viruses in Canada, phylogenetic analysis of host-transmission dynamics suggested northern fulmars to be the source of A(H5N5) virus for European herring gulls, great black-backed gulls, American crows and red foxes (Erdelyan et al., 2024). Mass mortality related to this subtype has been described in several wild bird species and in pheasants in the United Kingdom (FarmingUK, online-c; The Guardian, online). In Norway, these A(H5N5) virus detections coincided with mass mortality among gulls (mostly European herring gulls and great black-backed gulls) and crows. Of a group of about 70 gulls that washed ashore in the Kvænangen fjord, some tested positive, while another 100 dead gulls were observed in the sea (European Commission, online). Abnormal behavior among gulls in the area, including impaired coordination, was observed. In addition to HPAI virus infection, mortality in these birds may also be attributed to bycatch associated with intensive fishing activities in the area and poor weather conditions. Necropsies of ten randomly selected gulls found floating in the sea revealed that these birds were HPAI virus-negative, in good condition, and had changes consistent with drowning. A sudden increase in observations of sick and dead common ravens has also been reported in Iceland since October (personal communication). Some of these birds showed a relatively slow course of the disease with neurological signs involved. Additional mortality events have been reported from northern and north-western parts of the country, although test results are still pending. The A(H5N5) virus detection in Belgium represented the first reported in wild birds in the country so far.

The overall picture in wild bird populations in Europe, compared to the previous reporting period when HPAI viruses were circulating at a low level with an increase from September onwards, shows that the increase in HPAI virus detections in wild birds has continued and was associated with sporadic mass mortality events in mute swans, gulls and crows, but not in other wild bird species. Possible explanations for the latter are acquired flock immunity after previous infections, depletion of certain wild bird populations, and underreporting due to decreased detection of dead wild birds in certain countries. HPAI virus detections in wild birds are generally underestimated. Therefore, the numbers provided most likely do not reflect the number of wild birds that actually died from A(H5) virus infection.

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

### 2.1.2 HPAI virus detections in birds outside Europe

An overview of the HPAI virus detections in birds that were notified from other countries via WOAH from 21 September to 6 December 2024 is presented in Table 4 and Figure 5.

**Table 4:** Number of HPAI virus detections in non-European countries, by virus subtype and country, from 21 September to 6 December 2024. Cumulative numbers since the start of the 2024–2025 epidemiological year are reported in parentheses (1 October 2024 to 30 September 2025)

| **Region** (total in season) | **Country** | **Domestic birds** | | | | **Wild birds** | | | | **Total** |
|---|---|---|---|---|---|---|---|---|---|---|
| | | **A(H5N1)** | **A(H5N2)** | **A(H5Nx)** | **A(H7N6)** | **A(H5N1)** | **A(H5N3)** | **A(H5N5)** | **A(Not typed)** | |
| Americas (123) | Canada | 55 (55) | 2 (2) | - | - | - | - | 3 (3) | - | 60 (60) |
| | Colombia | - | - | 1 (1) | - | - | - | - | - | 1 (1) |
| | Peru | - | - | 1 (1) | - | - | - | - | - | 1 (1) |
| | United States of America | 61 (59) | - | - | - | 3 (2) | - | - | - | 64 (61) |
| Antarctica (1) | Falkland Islands | - | - | - | - | 1 (1) | - | - | - | 1 (1) |
| Asia (80) | Hong Kong | - | - | - | - | 1 (1) | - | - | - | 1 (1) |
| | Israel | 3 (2) | - | - | - | 3 (1) | - | - | - | 6 (3) |
| | Japan | 11 (11) | - | - | - | 54 (54) | - | - | 1 (0) | 66 (65) |
| | South Korea | 3 (3) | - | - | - | 4 (4) | 1 (1) | - | - | 8 (8) |
| | Taiwan | 2 (2) | - | - | - | 1 (1) | - | - | - | 3 (3) |
| Oceania (1) | New Zealand | - | - | - | 1 (1) | - | - | - | - | 1 (1) |

| Region (total in season) | Country | Domestic birds | | | | Wild birds | | | | Total |
|---|---|---|---|---|---|---|---|---|---|---|
| | | A(H5N1) | A(H5N2) | A(H5Nx) | A(H7N6) | A(H5N1) | A(H5N3) | A(H5N5) | A(Not typed) | |
| **Total** | | **135 (132)** | **2 (2)** | **2 (2)** | **1 (1)** | **67 (64)** | **1 (1)** | **3 (3)** | **1 (0)** | **212 (205)** |

'-' means that no HPAI outbreaks were notified to WOAH.
Source: WOAH (data extraction carried out on 6 December 2024).

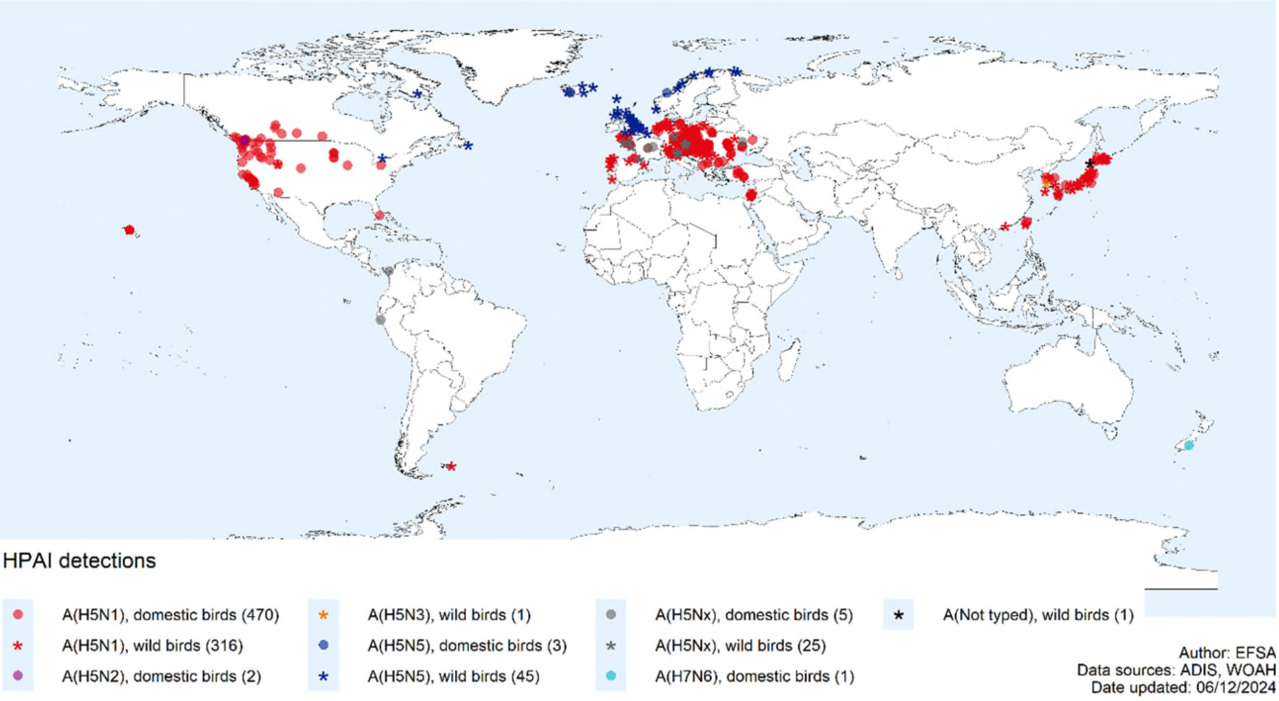


**Figure 5:** Geographic distribution, based on available geocoordinates, of HPAI virus detections reported worldwide in domestic (481) and wild (388) birds by virus type, from 21 September to 6 December 2024

In the tables and figures of the present report, only data extracted from WOAH on 6 December 2024 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 15 June to 20 September 2024 (EFSA, ECDC and EURL, 2024b), the total number of HPAI virus detections in domestic and wild birds officially notified to WOAH from outside Europe almost tripled from 75 to 212, while the number of reporting countries outside Europe decreased (17 in the previous vs 11 in the current reporting period) (Table 4, Figure 5). The number of official notifications to WOAH was about a third lower than the number of outbreaks reported between 21 September and 6 December 2023 (212 vs 330 outbreaks) (EFSA, ECDC and EURL, 2023). Overall, HPAI virus detections in domestic birds officially reported to WOAH from outside Europe increased notably from the previous to the current reporting period (65 vs 140) and the number of cases in wild birds increased from a very low level by more than seven times (10 vs 72). In contrast to previous years, no outbreaks from Africa or Russia were reported to WOAH in the period from 21 September to 4 December 2024, while Canada and the USA contributed 58% of the reported HPAI A(H5) virus detections outside Europe, and 84% when only considering domestic birds.

The large epidemic of A(H5N1) in the USA continued on a high level in poultry establishments of all sizes. Establishments with more than 100,000 birds contributed almost 50% of the outbreaks, and two establishments with approximately 2 million chickens were reported to WOAH. In addition, several medium- and some small-scale establishments were affected by the epidemic. As in the previous reporting period, table-egg producers and turkey operations in various States, mainly in the western part of the country, were once again heavily affected (Feedstuffs, online; News 24, online; ZeroHedge, online). Between 5 November and 5 December 2024, infections were confirmed in 36 commercial establishments and 23 backyard flocks nationwide that together account for 7.15 million birds (USDA, online-a). The USDA also reported the detection of A(H5) in 51 captive and 274 wild birds, comprising a total of 48 different species, in the period from 21 September to 2 December 2024 (USDA, online-b). Furthermore, HPAI virus was not only detected on the mainland but also in the Pacific region for the first time, on the island O'ahu of the state of Hawaii: two backyard flocks with mallards and Muscovy ducks in the county Honolulu and one wild hybrid duck (Anatidae) were tested positive for a different A(H5N1) genotype than the one circulating in dairy cattle (WOAH; Hawaii State Department of Health, online; Star Advertiser, online; USDA, online-b). In contrast to the previous reporting period, Canada officially reported outbreaks of A(H5N1) and A(H5N2) in poultry, and of A(H5N5) in wild birds (great black-backed gull, northern fulmar, turkey vulture). The A(H5N1) outbreaks were mainly detected in medium-scale establishments in western Canada in the border region with the USA (province British Columbia, Fraser valley). Furthermore, the media reported the detection of HPAI virus in a glaucous gull at Resolute Bay, Nunavut territory, in North Canada (Nunatsiaq News, online). In South America, sporadic HPAI virus detections were reported in poultry in Colombia and Peru (WOAH). The outbreak of HPAI A(H5Nx) in Colombia was confirmed in a backyard flock in the rural department of Chocó (Caracol Radio, online).

In Antarctica, HPAI A(H5N1) was confirmed in gentoo penguins in six locations on the Falkland Islands, associated with further mortality of several hundred gentoo penguins between 21 September and 29 November 2024. Furthermore, the detection of HPAI virus has been confirmed in Antarctic terns found dead at Surf Bay on the Falkland Islands (Falkland Islands Department of Agriculture, online). Research expeditions and studies exploring the impact of A(H5N1) on birdlife of the Antarctic region are still ongoing (FLI, online; IAATO, online).

In Asia, the outbreaks of HPAI A(H5N1) of clade 2.3.4.4b in commercial layer establishments in Taiwan continued (WOAH; NOW News, online). In contrast to the previous reporting period, Japan and South Korea notified numerous outbreaks of A(H5N1) in poultry, particularly in duck establishments (WOAH; Hani News, online; Xinhua News, online-a), but also detected HPAI viruses in several wild bird species, such as mandarin duck, northern pintail, Eurasian teal, Eurasian wigeon, tufted duck, whooper swan, red-crowned crane, peregrine falcon, northern goshawk, and white-tailed eagle (WOAH; 373 News, online; YNA, online-a). Additionally, this reporting period is marked by the first confirmation of a HPAI A(H5N3) in South Korea, where it was detected in wild bird faeces near the Mangyeong River in Gunsan (WOAH; YNA, online-b; YTN, online). Israel detected

A(H5N1) virus in chicken and turkey establishments as well as in great white pelicans (WOAH; Israel Hayom, online; Xinhua News, online-b). Hongkong notified A(H5N1) in a European wild bird to WOAH and media reported about a positive environmental sample in a nature reserve (Dimsum Daily, online). Furthermore, media reported the detection of A(H5N1) in migratory birds in the Kaohsiung wetlands (UDN, online). The detection of HPAI A(H5Nx) virus in chickens and ducks in a live bird market in Viet Nam was only reported by the media (Nong Nghiep, online), as well as the HPAI virus detections in a backyard establishment in eastern Russia (Sachalin Island) and in a commercial poultry establishment in south-western Russia (Stawropol) (East Russia, online).

For the first time, New Zealand notified to WOAH an outbreak of HPAI A(H7N6) in commercial layers in rural Otago on the South Island. It was speculated that the strain emerged locally after introduction in the establishment by waterfowl or other wild birds (Ministry for Primary Industries, online).

The list of wild bird species that were reported to WOAH as HPAI virus-infected from outside Europe between 21 September and 6 December 2024 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). Mutation analyses of the A(H5N1) viruses have been performed using FluMut (Github izsvenezie-virology, online-a, b) with FluMutDB v5.0 mutation database.

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

Since October 2023, complete genome sequences of > 820 European clade 2.3.4.4b HPAI A(H5) viruses from 26 countries have been characterised. During the 2023–2024 epidemiological year, the vast majority (> 90%) belonged to six different A(H5N1) and one A(H5N5) genotypes, namely EA-2021-AB (H5N1 A/duck/Saratov/29-02/2021-like), EA-2022-BB (H5N1-A/Herring_gull/France/22P015977/2022-like), EA-2023-DA (H5N1-A/mute_swan/Slovenia/PER1486-23TA_23VIR10323-22/2023-like), EA-2023-DB (H5N1-A/herring_gull/Germany-NI/2023AI08764/2023-like), EA-2023-DG (H5N1-A/Gallus_gallus/Belgium/11307_0002/2023-like), EA-2024-DI (H5N1 A/mute_swan/Poland/MB008-1/2024-like), and EA-2021-I (H5N5 A/whooper_swan/Romania/10123_21VIR849-1/2021-like). During the summer months (June–August 2024), a drop in the genetic diversity was observed, with most of the characterised viruses belonging to three genotypes: EA-2024-DI, EA-2022-BB, and EA-2023-DT (H5N1-A/gull/Spain/5061-23_24VIR4860-8/2023-like). These genotypes showed a clear pattern in their geographic and host distribution, with the EA-2022-BB and EA-2023-DT genotypes detected mainly in seabirds (Laridae) along the northern European coasts of France, Belgium and the Netherlands, and the Atlantic coast of Spain and Portugal, respectively. Differently, genotype EA-2024-DI was detected mainly among Anseriformes in Poland and Germany.

Since September 2024, the analyses of the genetically characterised European clade 2.3.4.4b viruses (n > 200) collected from 15 European countries indicate that the genetic diversity remains low despite the rapid increase in the number of cases. Specifically, the vast majority (> 98%) of characterised viruses belong to three A(H5N1) genotypes, namely EA-2022-BB, EA-2023-DT, and EA-2024-DI, and one A(H5N5) genotype, namely EA-2021-I.

EA-2024-DI emerged at the end of 2023 and during the 2023–2024 epidemiological year circulated mainly in eastern Europe. Since September 2024, EA-2023-DI has become the most widespread genotype in Europe, reported in 11 European countries and responsible for all or almost all the recent outbreaks reported in wild and domestic birds in eastern and central European countries. The phylogenetic analyses of the eight gene segments indicate that the viruses belonging to this genotype form two phylogenetically separate genetic sub-groups, i.e. DI.1 and DI.2. DI.1 has been detected in eight European countries (Austria, Czechia, Denmark, Germany, Italy, Netherlands, Poland, the United Kingdom), while DI.2 has been characterised from nine countries (Austria, France, Czechia, Poland, Germany, Italy, Slovenia, Switzerland, and the United Kingdom). Of note, both groups have been detected in Austria, Germany, Italy, and the United Kingdom. EA-2024-DI is mainly circulating among Anseriformes and has been responsible for most (> 85%) of the genetically characterised poultry outbreaks reported in Europe in the period September–December 2024 (based on sequences available up to 10 December 2024). Besides this genotype, France reported a few outbreaks in wild (Laridae) and domestic birds associated with genotype EA-2022-BB, currently circulating almost exclusively in Brittany. Based on the data available so far, France and the United Kingdom are the only countries where genotype EA-2022-BB has been circulating. In contrast, all characterised viruses detected in seabirds (Laridae) along the Atlantic coast of Spain belong to genotype EA-2023-DT, which originated from a reassortment event between the EA-2022-BB (PB2/HA/NP/NA/M/NS) and a gull-adapted H13 subtype (PB1/PA). Based on the data available, this genotype is circulating only in this geographic area and since May 2024 it has been the only genotype detected in Spain.

Since September 2024, a rapid rise has been seen in the frequency of identification of the A(H5N5) genotype EA-2021-I, mainly in Laridae, in the United Kingdom and Norway. In September this genotype was identified in a northern fulmar in Germany (based on the data available in GISAID, EPI_ISL_19602385) and at the beginning of October it was reported for the first time in a mew gull in Belgium, suggesting a possible southern spread. The last detection of this genotype in Europe dates back to February 2024 in Germany, England, the Netherlands, and Norway. It is still unclear in which reservoir species and geographic areas this genotype circulated in the summer months. Besides Europe, genotype EA-2021-I was also identified in Canada in the first half of 2023, and in Japan in 2023–2024, indicating the spread of this genotype from Europe to northern areas of other continents.

Overall, in comparison to the same period (September–November) in 2023, during which 12 different genotypes were identified in Europe, this year the genetic diversity seems lower, although it needs to be considered that sequencing of samples is ongoing and information on the genetic characteristics of recent viruses is still missing for several countries. Thus, we cannot exclude that some of the previously detected genotypes are still circulating at a low level in some geographic areas.

### 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 2023 indicate that these viruses do not contain critical mutations detected in previous pandemic strains in the receptor binding site of the HA protein and thus they continue to be well-adapted to avian species. However, several mutations previously described in literature (Du et al., 2018, 2021; Suttie et al., 2019; Pinto et al., 2023) as being associated with i) enhanced polymerase activity and replication in mammals or mammalian cells, ii) increased virulence, iii) increased/conferred resistance towards antiviral drugs, iv) increased in vitro binding to human-type receptors α2,6-SA, v) decreased antiviral response in ferrets, vi) evasion of human butyrophilin subfamily 3 member A3 (BTN3A3), and vii) disruption of the second sialic acid (SIA) binding site in the neuraminidase protein, have been identified with a frequency varying by the distinct mutations. The net effect of these mutations on the biological characteristics of the viruses is still unknown and further studies are needed to improve existing knowledge.

Among the mutations in the HA protein that have proved to increase in vitro binding to human-type receptors, some (i.e. S133A, S154N, T156A, H5 numbering) have been identified in the majority of the A(H5N1) viruses circulating in Europe since October 2023, while others (i.e. E251K, E75K-S123P, P235S, V210I, S155N, 189T/D) have only been sporadically observed (≤ 5 viruses). The impact of these HA mutations on the biological characteristics of the circulating viruses is still unknown; however, none of them has been demonstrated to cause a shift from avian-like to human-like receptor binding preference. A recent study demonstrated that a single mutation, G222L (H5 numbering, G228L in H3 numbering), in the HA protein of a clade 2.3.4.4b virus can cause a complete switch the HA binding specificity to human-type receptors (Lin et al., 2024). To date, none of the characterised clade 2.3.4.4b viruses circulating in Europe since October 2020 contains such substitution. Besides 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 impact upon their zoonotic potential. All of the currently circulating A(H5N5) viruses (genotype EA-2021-I) contain a deletion in the NA stalk region, which is a determinant of virus adaptation in chickens (Stech et al., 2015).

Mutations associated with reduced susceptibility of A(H5N1) viruses to available antiviral drugs authorised for use in humans have rarely been identified in the circulating strains. Specifically, mutations associated with resistance towards adamantanes, NA and PA inhibitors (WHO, online-a; WHO, online-b) have been detected in approximately 1%, 0.2% and 0.7% of the analysed A(H5N1) viruses, respectively.

Since October 2023, mutations in the PB2 protein associated with virus adaptation in mammals (E627K/V, D701N or K526R) have been detected in 32 European viruses collected from birds, more specifically in i) 13 A(H5N5) viruses (genotype EA-2021-I) collected from wild and domestic birds in Germany, the Netherlands, Norway, and the United Kingdom in January–February 2024, and in November 2024 (Norway); ii) 11 A(H5N1) viruses collected between October 2023 and November 2024 from outbreaks in domestic birds in Poland (genotypes EA-2022-CH and EA-2021-AB), Denmark (genotype EA-2023-DB), Czechia (genotype EA-2024-DI), Romania (genotype EA-2023-DA), and Italy (genotype EA-2024-DI); iii) eight A(H5N1) viruses collected between February and November 2024 from wild birds in France (genotype EA-2022-BB), Italy (genotype EA-2024-DI), and Austria (genotype EA-2024-DI). Based on the available data, in the current epidemiological year (2024–2025), an increase in the frequency of detection of such mutations in birds can be observed. However, bias cannot be excluded given the limited genetic data available up to date.

## 2.2 HPAI virus detections in non-human mammals

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

From 21 September to 10 December 2024, HPAI A(H5N1) viruses in mammals were only reported outside Europe, in the USA and in Viet Nam. No new HPAI virus detections in mammals have been reported in Europe since spring 2024. The data described were actively collected from Member States and other European countries, retrieved through WOAH-WAHIS and from the USDA websites (for cases occurred in the USA), and supplemented with information from media reports (Table 5).

Outside Europe, HPAI A(H5N1) virus of the B3.13 genotype continued to be detected in high numbers in dairy cattle in the USA, with > 800 confirmed cases in 16 States as of 10 December 2024 (Nevada Department of Agriculture, online). The last State that was added to the list is Nevada, but most of these cases have been located in California (638/838 as of 10 December 2024), the State with the largest dairy cattle population in the country (USDA, online-c). Indeed, 1,117 dairy cattle farms were accounted for in the 2022 census in California (USDA NASS, online), suggesting that nearly 60% of the State's dairy cattle farms have now been affected by A(H5N1). Mortality rates of up to 15% were described by the industry (Los Angeles Times, online). Moreover, the virus has recently been found in two batches of raw milk sold in retail shops in California (Business Insider Netherlands, online). Measures have now been implemented to limit the virus spread out of the State. Interstate-movements of dairy cattle from California are indeed restricted: lactating dairy cattle may only be moved out of California with both a Certificate of Veterinary Inspection and a negative HPAI test from an approved laboratory within 7 days before movement. Dairy cattle with HPAI clinical signs cannot leave the State, and animals from positive herds can only be exported 30 days after all dairy cattle in the herd are HPAI virus-negative (CDFA, online). The national bulk milk testing strategy foresees that, as of the week of 16 December 2024, silo testing will start in all States, which will first assess State's A(H5N1) dairy cattle status, then help detect and respond to outbreaks, demonstrate absence of A(H5N1) virus in unaffected States, and finally, in the long term, demonstrate freedom from A(H5N1) in US dairy cattle (USDA, online-d). At the end of October 2024, a different A(H5N1) virus genotype, D1.2, was detected in two out of five pigs in a mixed livestock-poultry farm in Oregon, where also poultry and wild birds in the surrounding area tested positive for the same virus (USDA, online-e). Shared drinking water was the suspected source of infection. In addition, two more red foxes were found positive for A(H5N1) virus in Alaska (USDA, online-f).

In the southern part of Viet Nam, at the end of September 2024, a total of 41 tigers, three lions and one leopard in a safari park and a zoo were reported positive for HPAI A(H5N1) virus after increased mortality and clinical signs (fatigue, fever, anorexia) were observed in these species (Dan Viet, online; NDTV, online). The suspected source of infection was ingestion of contaminated poultry meat due to the genetic similarity of the virus to other viruses isolated from poultry, wild birds and humans in the same area. Mammal-to-mammal transmission has not been supported, as genetic analysis indicated one single introduction into these animals. A summary of available literature on HPAI virus infections in carnivore species has been published in an earlier report (EFSA, ECDC and EURL, 2024c).

**Table 5:** Avian influenza A(H5Nx) virus detections in mammalian species other than humans related to circulating viruses worldwide, 2016–2024

| Virus | Animal (order, family, species) | | | Country | Reference |
|---|---|---|---|---|---|
| A(H5N1) or A(H5Nx) clade 2.3.4.4b | Artiodactyla | Bovidae | Cattle (*Bos taurus*) | United States of America | WOAH<br>USDA |
| | | | Goat (*Capra hircus*) | United States of America | WOAH<br>USDA |
| | | Camelidae | Alpaca (*Lama pacos*) | United States of America | USDA (online-g) |
| | | 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 |
| | | | Dog (*Canis lupus familiaris*) | Canada, Italy*, Poland | WOAH<br>Szaluś-Jordanow et al. (2024) |
| | | | Japanese raccoon dog (*Nyctereutes viverrinus*) | Japan | WOAH |
| | | | Red fox (*Vulpes vulpes*) | Austria, Belgium, Canada, Denmark, Estonia, Finland, France, Germany, Ireland, Italy, Japan, Latvia, Netherlands, Norway, Sweden**, United Kingdom (Northern Ireland), United Kingdom, United States of America | WOAH<br>Personal communication by Sandra Revilla-Fernandéz (AGES) |
| | | | South American bush dog (*Speothos venaticus venaticus*) | United Kingdom | WOAH |
| | | Felidae | Bobcat (*Lynx rufus*) | United States of America | WOAH |
| | | | Caracal (*Caracal caracal*) | Poland | WOAH |
| | | | Cat (*Felis catus*) | Canada, France, Hungary**, Italy*, Poland, South Korea, United States of America | WOAH |
| | | | Eurasian lynx (*Lynx lynx*) | Finland, Sweden* | WOAH<br>Personal communication by Malin Grant (SVA) |
| | | | Leopard (*Panthera pardus*) | United States of America, Viet Nam | WOAH |
| | | | Lion (*Panthera leo*) | Peru, Viet Nam | WOAH |
| | | | Mountain lion (*Puma concolor*) | United States of America | WOAH |
| | | | Tiger (*Panthera tigris*) | United States of America, Viet Nam | WOAH |
| | | Mephitidae | Striped skunk (*Mephitis mephitis*) | Canada, United States of America | WOAH |
| | | Mustelidae | American marten | United States of America | WOAH |
| | | | American mink (*Neovison vison*) | Canada, Finland, Spain | WOAH |
| | | | Beech marten (*Martes foina*) | Netherlands | GISAID (online) |

| Virus | Animal (order, family, species) | | | Country | Reference |
|---|---|---|---|---|---|
| | | | 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 |
| | | | Marine otter (*Lontra felina*) | Chile | WOAH |
| | | | North American river otter (*Lontra canadensis*) | United States of America | WOAH |
| | | | Southern river otter (*Lontra provocax*) | Chile | WOAH |
| | | 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 |
| | | | Grey seal (*Halichoerus grypus*) | Canada, Germany, Netherlands, Poland, Sweden**, United Kingdom, United States of America | WOAH |
| | | | Harbour seal (*Phoca vitulina*) | Canada, Denmark, Germany, United Kingdom, United States of America | WOAH |
| | | | Southern elephant seal (*Mirounga leonina*) | Argentina, South Georgia and the South Sandwich Islands | WOAH<br>Bennison et al. (2024), Banyard et al. (2024) |
| | | Procyonidae | Raccoon (*Procyon lotor*) | Canada, Germany, United States of America | WOAH |
| | | | South American coati (*Nasua nasua*) | Germany, Uruguay | WOAH |
| | | Ursidae | American black bear (*Ursus americanus*) | Canada, United States of America | WOAH |
| | | | Asian black bear (*Ursus thibetanus*) | France | WOAH |
| | | | Brown bear (*Ursus arctos*) | United States of America | WOAH |
| | | | Kodiak grizzly bear (*Ursus arctos horribilis*) | United States of America | WOAH |
| | | | Polar bear (*Ursus maritimus*) | United States of America | WOAH |
| | Cetacea | Delphinidae | Bottlenose dolphin (*Tursiops truncatus*) | Peru, United States of America | WOAH |
| | | | Chilean dolphin (*Cephalorhynchus eutropia*) | Chile | WOAH |
| | | | Common dolphin (*Delphinus delphis*) | Peru, United Kingdom | WOAH<br>Leguia et al. (2023) |

| Virus | Animal (order, family, species) | | | Country | Reference |
|---|---|---|---|---|---|
| | | | 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 | Brown rat (*Rattus norvegicus*) | Egypt | Kutkat et al. (2024) |
| | | | House rat (*Rattus rattus*) | Egypt | Kutkat et al. (2024) |
| | | | House mouse (*Mus musculus*) | United States of America | WOAH<br>USDA |
| | | Sciuridae | Abert's squirrel (*Sciurus aberti*) | United States of America | WOAH |
| A(H5N5) clade 2.3.4.4b | Carnivora | Canidae | Red fox (*Vulpes vulpes*) | Canada, Norway | WOAH |
| | | Mustelidae | European pine marten (*Martes martes*) | Netherlands | Personal communication by Dennis Bol (NVWA, 2024) |
| | | Procyonidae | Raccoon (*Procyon lotor*) | Canada | WOAH |
| A(H5N6) clade 2.3.4.4b | Carnivora | Canidae | Dog (*Canis lupus familiaris*) | China | Yao et al. (2023) |
| | | Mustelidae | American mink (*Neovison vison*) | China | Zhao et al. (2024) |
| A(H5N8) clade 2.3.4.4b | Artiodactyla | Suidae | Pig (domestic) (*Sus scrofa*)$^{*}$ | France | Herve et al. (2021) |
| | | | Pig (wild boar) (*Sus scrofa*)$^{*}$ | Germany | Schülein et al. (2021) |
| | Carnivora | Canidae | Red fox (*Vulpes vulpes*) | United Kingdom | WOAH |
| | | Phocidae | Grey seal (*Halichoerus grypus*) | Poland, Sweden, United Kingdom | SVA<br>Shin et al. (2019), Floyd et al. (2021)<br>Personal communication by Siamak Zohari (SVA) |
| | | | Harbour seal (*Phoca vitulina*) | Denmark, Germany, United Kingdom | WOAH<br>Floyd et al. (2021), Ärzteblatt (online), Avian Flu Diary (online), Outbreak News (online) |

$^{*}$Serological detection.

$^{**}$Both virological and serological detection.

During the current reporting period, testing efforts in non-human mammals continued and some European countries reported their test results to EFSA. Austria tested a total of

72 mammals (29 pigs, 12 cattle, 9 foxes, 6 wild boar, 4 bats, 2 bisons, 2 badgers, 2 cats, 2 rabbits, 1 beaver, 1 marten, 1 horse, 1 wolf) between September and 20 November 2024, all of which were negative (personal communication by Sandra Revilla-Fernández, AGES, 2024). However, Austria reported the detection of HPAI A(H5N1) virus of the BB genotype in a red fox found dead in the city of Vienna in May 2023. In Belgium, from 18 September to 18 November 2024, 15 foxes were tested and all found negative (personal communication by Ingeborg Mertens, FAVV, 2024).

## 2.3 Avian influenza virus infections in humans

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

Since the last report, and as of 11 December 2024, ten human cases of avian influenza A(H9N2) virus were reported from China, 44 confirmed human cases of avian influenza A(H5N1) from the USA, one A(H5N1) from Canada, and one A(H5) from Viet Nam (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 2024-09-21–2024-12-11** | | | **Cases reported since first report** | | | |
|---|---|---|---|---|---|---|---|
| **Subtype** | Cases reported | Deaths | Reporting countries | First report | Cases reported | Deaths | Reporting countries |
| A(H5N1) | 45* | 0 | 2 | 1997 | 974* | 464** | 24 |
| A(H5Nx) | 1 | 0 | 1 | | | | |
| A(H5N2) | 0 | 0 | 0 | 2024 | 1 | 1 | 1 |
| A(H5N6) | 0 | 0 | 0 | 2014 | 93 | 36 | 2 |
| A(H9N2) | 10 | 0 | 1 | 1998 | 151 | 2 | 10 |
| A(H10N3) | 0 | 0 | 0 | 2021 | 3 | 0 | 1 |
| A(H10N5) | 0 | 0 | 0 | 2024 | 1 | 1 | 1 |

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

**Deaths reported since 2003 out of a total of 954 cases reported 2003—11 December 2024. Mortality data are not available for the cases reported prior to 2003.

### 2.3.2 Human A(H9N2) cases

Since 1998, 151 human A(H9N2) cases have been reported worldwide (Figure 6). During the current reporting period, human A(H9N2) cases were only reported from Asia.

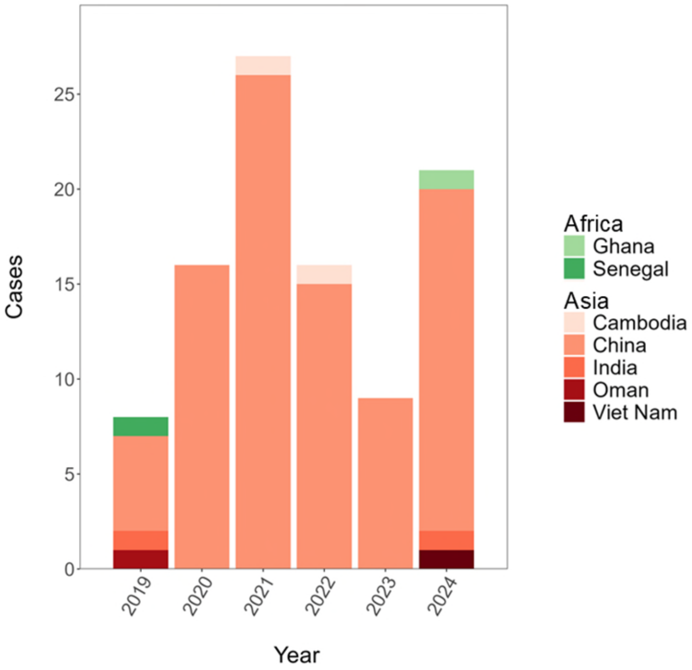


**Figure 6:** Distribution of reported human cases of A(H9N2) virus infection by year of onset or detection and reporting country, 2019–11 December 2024

On 15 October 2024, the Centre for Health Protection in Hong Kong, China, reported one case of avian influenza A(H9N2) in the Avian Influenza Report for week 41 (CHP, online-a). The patient, who is alive, was a three-year-old boy of the Chongqing Municipality (Mainland China) with onset of symptoms on 4 September 2024. No other information is available.

In addition, on 12 November 2024, the Centre for Health Protection in Hong Kong, China, reported seven unrelated cases of human infection with avian influenza A(H9N2) virus detected in four provinces of Mainland China (CHP, online-b). Six of the cases were children between 10 months and 7 years old in Hubei, Huban and Jiangxi, and one was a 67-year-old individual in Sichuan. Onset of symptoms occurred between 23 September and 14 October 2024. All patients are alive. No further information was publicly available.

Finally, on 10 December 2024, the Centre for Health Protection in Hong Kong, China, reported two additional cases of avian influenza A(H9N2) in the Avian Influenza Report for week 49 (CHP, online-c). The patients were two one-year-old girls from the Guizhou and Guangxi provinces, who developed symptoms on 28 October and 18 November 2024, respectively. Both children are alive. No public information was reported about symptoms or a potential exposure to infected animals.

No human sequences deposited since 21 September 2024 (last report) of H9 were available for genomic analysis.

### 2.3.3 Human A(H5N1) cases

Since 1997, 974 confirmed human A(H5N1) cases have been reported worldwide (Figure 7). During the current reporting period, human A(H5N1) cases were mainly reported from North America.

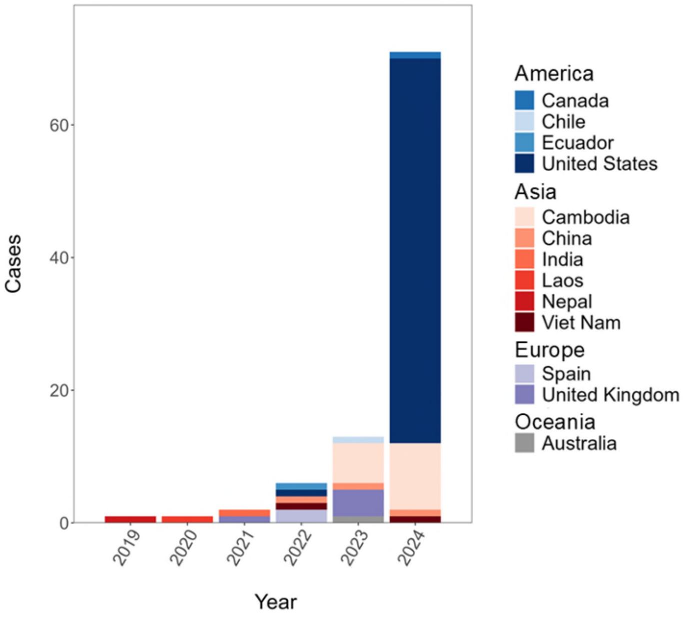


**Figure 7:** Distribution of reported human cases of A(H5N1) virus infection by year of onset or detection and reporting country, 2019–11 December 2024. The figure includes detections of A(H5N1) due to suspected environmental contamination reported by Spain (2) and the USA (1) in 2022, and the United Kingdom (3, 1 inconclusive) in 2023. Human cases of A(H5) cases epidemiologically linked to A(H5N1) outbreaks at poultry and dairy cattle farms in the USA in 2024 are included in the number of cases of A(H5N1).

### In North America

Since the last report, and as of 11 December 2024, 31 individuals were infected with avian influenza A(H5N1) viruses following occupational exposure to infected dairy cattle. These cases were all reported in adult dairy farm workers in California, USA. All cases have been mild, with symptoms including conjunctivitis and typical flu symptoms such as fever, cough, muscle pain and sore throat. The last two cases were reported on 2 December 2024 (CDC, online-a).

In addition, 12 individuals have been infected with avian influenza A(H5N1) viruses following occupational exposure to infected poultry, or heavily contaminated environments where infected birds have been present. All infections were reported in adults residing in the USA. Eleven cases were reported in Washington State (Washington State Department of Health, online) and one in nearby Oregon State (Oregon Health Authority, online). All cases are alive and have presented with mild disease.

Since the last report, the authorities in the USA have been providing information about human infections with A(H5N1) virus mainly in an aggregated manner without detailed information on individual cases.

Finally, two individuals under 18 years old have acquired A(H5N1) avian influenza virus without any evidence of animal exposure. One case was reported in British Columbia, Canada, and the other in California, USA.

On 2 November 2024, a teenager from the Fraser Health region in British Columbia presented to the emergency room with conjunctivitis, fever and cough. By 8 November, the patient's condition deteriorated, leading to hospitalisation for acute respiratory distress and administration of intravenous antivirals. On 9 November, the case was reported by public health authorities as the first locally acquired case of avian influenza A(H5N1) in Canada (BC Gov News, online). The Public Health Agency of Canada confirmed the case on 13 November and indicated that poultry outbreaks were ongoing in the province (PHAC, online). Contact tracing identified 36 individuals, who all tested negative and were offered prophylaxis.

On 22 November 2024, the US CDC confirmed a human infection with avian influenza A(H5N1) in a child in California, who did not have a known exposure to animals and was detected through routine influenza surveillance scheme. The child experienced mild symptoms and received antiviral treatment. Initial tests showed low levels of the virus, and follow-up tests were negative for A(H5N1) but positive for another common respiratory virus. The child has recovered, and all family members tested negative for A(H5N1) with some testing positive for the same common respiratory virus as the child (CDC, online-b).

Sequences deposited since 20 September, and as of 10 December 2024, were available for 38 viruses (Table 7) all being clade 2.3.4.4b. The A/California/174/2024, A/California/192/2024 and A/Oregon/255/2024 viruses were excluded from further analysis due to HA sequence being too short or having gaps.

**Table 7:** Strains included in phylogenetic and mutation analysis. Sequences include those deposited on GISAID's EpiFlu$^{TM}$ Database since 20 September 2024 all belonging to clade 2.3.4.4b

| Isolate Name | Isolate Id | Location | Collection Date |
|---|---|---|---|
| A/British_Columbia/PHL-2032/2024 | EPI_ISL_19548836 | British Columbia, Canada | 2024-11 |
| A/Washington/UW32495/2024 | EPI_ISL_19541397 | Washington, United States | 2024-10-18 |
| A/Oregon/255/2024 | EPI_ISL_19590705 | Oregon, United States | 2024-11-05 |
| A/Washington/253/2024 | EPI_ISL_19531302 | Washington, United States | 2024-10-24 |
| A/Washington/252/2024 | EPI_ISL_19531301 | Washington, United States | 2024-10-24 |
| A/Washington/251/2024 | EPI_ISL_19531300 | Washington, United States | 2024-10-24 |
| A/California/193/2024 | EPI_ISL_19590708 | California, United States | 2024-11-18 |
| A/California/191/2024 | EPI_ISL_19590707 | California, United States | 2024-11-13 |
| A/California/190/2024 | EPI_ISL_19590706 | California, United States | 2024-11-12 |
| A/California/183/2024 | EPI_ISL_19590704 | California, United States | 2024-11-07 |
| A/California/182/2024 | EPI_ISL_19590703 | California, United States | 2024-11-07 |
| A/California/181/2024 | EPI_ISL_19590702 | California, United States | 2024-11-07 |
| A/California/180/2024 | EPI_ISL_19590701 | California, United States | 2024-11-07 |
| A/California/150/2024 | EPI_ISL_19544645 | California, United States | 2024-10-09 |
| A/California/174/2024 | EPI_ISL_19531297 | California, United States | 2024-10-30 |
| A/California/173/2024 | EPI_ISL_19531296 | California, United States | 2024-10-24 |
| A/California/172/2024 | EPI_ISL_19531295 | California, United States | 2024-10-24 |
| A/California/171/2024 | EPI_ISL_19531294 | California, United States | 2024-10-25 |
| A/California/151/2024 | EPI_ISL_19531293 | California, United States | 2024-10-09 |
| A/California/168/2024 | EPI_ISL_19512044 | California, United States | 2024-10-18 |
| A/California/155/2024 | EPI_ISL_19512043 | California, United States | 2024-10-16 |
| A/California/150/2024 | EPI_ISL_19497982 | California, United States | 2024-10-09 |
| A/California/152/2024 | EPI_ISL_19497981 | California, United States | 2024-10-10 |
| A/California/153/2024 | EPI_ISL_19497980 | California, United States | 2024-10-09 |
| A/California/149/2024 | EPI_ISL_19481949 | California, United States | 2024-10-07 |
| A/California/148/2024 | EPI_ISL_19481948 | California, United States | 2024-10-08 |

| | | | |
|---|---|---|---|
| A/California/147/2024 | EPI_ISL_19481947 | California, United States | 2024-10-07 |
| A/California/146/2024 | EPI_ISL_19473581 | California, United States | 2024-10-02 |
| A/California/134/2024 | EPI_ISL_19463619 | California, United States | 2024-09-30 |
| A/California/135/2024 | EPI_ISL_19463618 | California, United States | 2024-10-01 |
| A/Washington/255/2024 | EPI_ISL_19552697 | Washington, United States | 2024-10-29 |
| A/Washington/254/2024 | EPI_ISL_19531303 | Washington, United States | 2024-10-23 |
| A/Washington/240/2024 | EPI_ISL_19531299 | Washington, United States | 2024-10-18 |
| A/Washington/239/2024 | EPI_ISL_19531298 | Washington, United States | 2024-10-18 |
| A/Washington/247/2024 | EPI_ISL_19512047 | Washington, United States | 2024-10-18 |
| A/Washington/240/2024 | EPI_ISL_19512046 | Washington, United States | 2024-10-18 |
| A/Washington/239/2024 | EPI_ISL_19512045 | Washington, United States | 2024-10-18 |
| A/California/192/2024 | EPI_ISL_19597300 | California, United States | 2024-11-12 |

The phylogenetic analysis revealed that most strains from dairy farm workers in California, USA, clustered closely on one branch consisting of genotype B3.13 members, and the strains from Washington, USA, from individuals with various exposure to poultry clustered on a separate branch of genotype D1.1 (Figure 8). The single strain from a patient without any evidence of animal exposure from British Columbia, Canada, was solely placed on a sub-branch within the branch of Washington strains and was also genotype D1.1. On 10 December 2024, US CDC published a technical update (CDC, online-c) on the genetic sequence of the virus identified in the child in California on 22 November. Given the low viral load, the whole genome could not be determined, but analysis of the partial HA sequence indicated that the virus belonged to clade 2.3.4.4b and phylogenetic analysis of the full-length NA and NP segments showed that the virus was similar to genogroup B3.13.

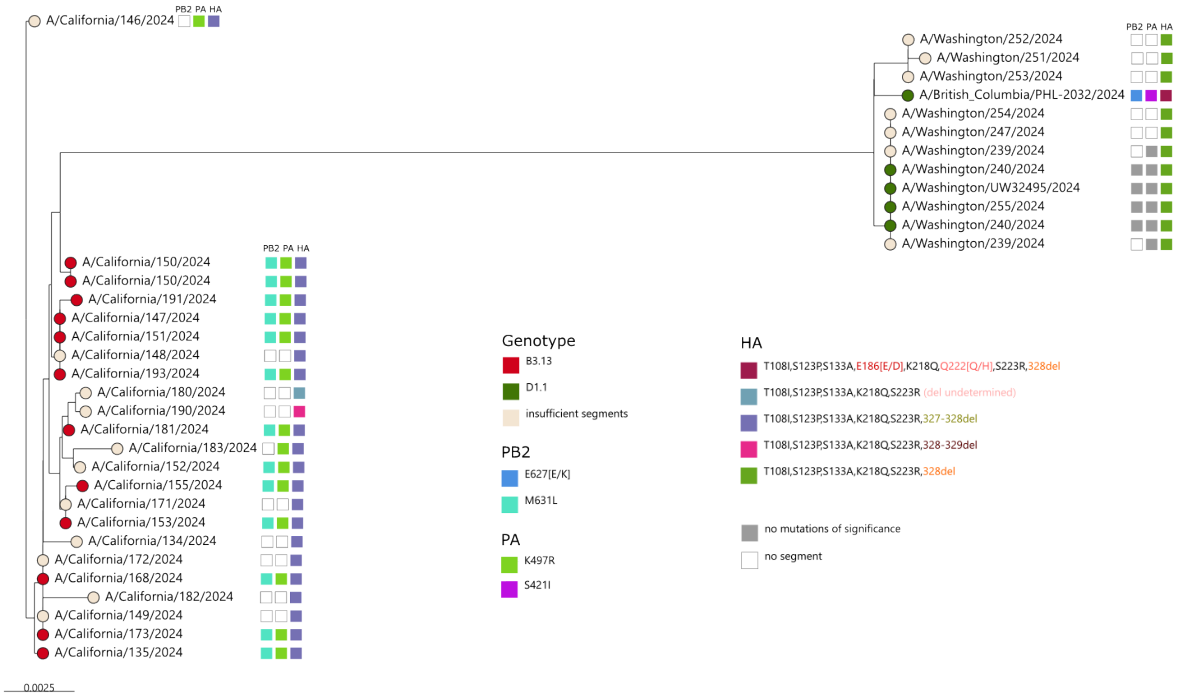


**Figure 8:** Phylogenetic tree of the HA segment annotated with mutation analysis findings from all available segments

Similarly to the findings for clade 2.3.4.4b in the previous report (EFSA, ECDC and EURL, 2024b), the HA amino-acid substitutions T108I, S123P, S133A, K218Q and S223R and a deletion around position 328 were present in all strains. This profile is observed in the vast majority of clade 2.3.4.4b strains submitted to GISAID from the USA since 20 September 2024 with complete HA (n = 745) that involved hosts both from various avian species and dairy cows. These mutations are associated with mammalian adaptations, such as the S133A, which was linked to increased binding to α2–6 human-type receptors in a pseudovirus assay (Yang et al., 2007), and the combination of K218Q with S223R that increases receptor binding to both α2–3 and α2–6 receptors (Guo et al., 2017). However, since these mutations are highly prevalent in 2.3.4.4b viruses from several animal species, it is unlikely that they have an impact on the infectivity of humans. The HA profile of A/British_Columbia/PHL-2032/2024 was unique and had mixed viral populations at the nucleotide level, resulting in either the same amino acid as the reference sequence A/Goose/Guangdong/1/96 at positions 186 and 222, or to substitutions to D and H at these positions, respectively. Substitutions with these specific amino acids at these positions have not been previously described, however E186V was associated with enhanced binding affinity to mammalian cells (Qu et al., 2017) and Q222L with many traits such as increased virus binding to α2–6, enhanced replication in mammalian cells and ferrets and enhanced contact transmission in ferrets (Suttie et al., 2019). The sequence was confirmed by Public Health Agency of Canada to belong to clade 2.3.4.4b and genotype D1.1, but no information on the reason for mixed bases has been provided (PHAC, online).

The PB2 mutation M631L was present in all strains from California with segment available. The M631L, as well as K497R in PA, have been described as highly prevalent in 2.3.4.4b strains in the USA (Chakraborty and Bhattacharya, 2024). The PB2 of A/British_Columbia/PHL-2032/2024 also contained mixed bases resulting in position 627 being either wild type or with a substitution to Lysine (K). The E627K substitution was associated with several phenotypic traits including enhanced polymerase activity, increased virulence in mice and contribution to airborne pathogenicity in ferrets (Suttie et al., 2019). The PA segment of A/British_Columbia/PHL-2032/2024 had S421I which has been reported as coupled with increased virulence in mice (Kim et al., 2010).

None of the viruses with an available PA segment sequence (n = 19) had substitutions suggesting a reduced susceptibility to baloxavir marboxil, except A/California/150/2024 that had a I38M substitution in PA. The clinical significance of this substitution is unclear, but it has been observed after exposure to baloxavir marboxil (WHO, online-b). The NA segment sequence was available for 34 viruses; none had amino acid substitutions associated with reduced treatment efficacy of neuraminidase inhibitors (WHO, online-c).

### In Asia

On 4 December 2024, the Center for Disease Control of Long An province in Viet Nam reported a case of A(H5) in an 18-year-old man (FluTrackers, online). The authorities were informed on 14 November 2024, when the patient was hospitalised with severe pneumonia after developing typical influenza symptoms (fever, headache, muscular pain). The case was reported as A(H5N1), but the confirmation of the N1 neuraminidase subtype is still pending. Epidemiological investigations discovered that poultry mortality had occurred at the patient's family home but had not been reported to the local authorities.

No sequence of the virus for this human case has been deposited in databases yet, but all recent submissions of A(H5N1) viruses from birds from the Mekong Delta in Viet Nam were of the clade 2.3.2.1c.

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

The final results of the seroprevalence study in workers at dairy farms with confirmed infection with avian influenza A(H5N1) in cattle in Michigan and Colorado, USA, were published early November 2024 (Mellis et al., 2024). While the preliminary results in 35 tested farm workers did not find serological evidence of asymptomatic infection (CDC, online-d), the final results based on 115 people showed the presence of antibodies following a recent A(H5) virus infection in 7% of the analysed serum samples. Cleaning the milking station was identified as an activity increasing the risk of getting infected. Half the seropositive people reported being ill at the time when infected cows were detected in the farm. These results based on serology and indicating potential asymptomatic infections are in agreement with similar studies performed in Texas, USA (Shittu et al., 2024), and in Egypt (Gomaa et al., 2023). These studies highlight the importance of monitoring all the individuals who might be occupationally exposed to infected animals or their environments, as outlined in ECDC's 'Investigation protocol for human cases of avian influenza' (ECDC, 2023).

Overall, the Food and Agriculture Organization of the United Nations (FAO), WHO and WOAH tripartite assessment of the public health risk posed by influenza A(H5N1) viruses characterised since 2021 has not changed, and the risk of infection is still considered as low for the general public, and as low-to-moderate for occupationally exposed individuals depending on the protective measures that are applied (FAO, WHO and WOAH, online-a).

Based on the current avian influenza A(H5N1) situation in animals and humans in the USA and internationally, and taking into consideration the sources of the reported human infections, the absence of human-to-human transmission, and the genetic characteristics of the viruses, US CDC's assessment has also not changed (CDC, online-e), with the overall risk of infection with A(H5N1) viruses currently circulating in animals in the USA for the general public still considered as low. Individuals with occupational or recreational exposure to infected animals are however considered to be at greater risk of infection (CDC, online-f). In addition, using the Influenza Risk Assessment Tool (CDC, online-g), US CDC scored the future pandemic potential of A(H5N1) clade 2.3.4.4b viruses as 'moderate risk', which is a similar risk level to previously assessed influenza A(H5N1) viruses (CDC, 2024).

Based on its regular evaluation of the regional epidemiological situation (PAHO, online-a), the Pan American Health Organization (PAHO) increased its public health risk assessment of the potential occurrence of zoonotic avian influenza A(H5N1) clade 2.3.4.4b in Latin American and the Caribbean from low (PAHO, online-b) to moderate (PAHO, online-c) in November 2024, with a moderate confidence.

The UK Health Security Agency (UKHSA) situational assessment of A(H5N1) clade 2.3.4.4b with a specific focus on the genotype B3.13 associated with the multi-state outbreak in cattle in the USA, maintained the overall threat to human health at level 4 (sustained and/or multi-species mammalian outbreaks, increasing zoonotic human cases or limited human-to-human transmission associated with zoonotic exposure) on a scale of

6 (UKHSA, online-a), with the risk of zoonotic infection for the people in the United Kingdom still considered as very low (GovUK, online-b).

### 2.3.5 ECDC risk assessment

ECDC's specific assessment of the risk of human infection with HPAI A(H5) clade 2.3.4.4b viruses remains unchanged. Overall, ECDC assesses the risk of human infection with the HPAI A(H5) clade 2.3.4.4b viruses currently circulating in Europe as low for the general public in the EU/EEA and low-to-moderate for those occupationally or otherwise exposed to infected animals or contaminated environments.

The assessment was based on available evidence and considered the information to evaluate:

- The likelihood of human infection in the EU/EEA with HPAI A(H5) clade 2.3.4.4b viruses:
    - Detections of HPAI A(H5) viruses in wild and domestic birds in Europe are at similar levels compared to last season at the same time of year.
    - Despite the extensive circulation of avian influenza viruses in animal populations in Europe in the last few years, with frequent opportunities for human exposure, there has been no confirmed A(H5N1) infection in humans in the EU/EEA and transmission from infected animals to humans remains a rare event globally. In 2022, two human influenza A(H5N1) virus detections were reported in poultry workers in Spain and were considered as environmental contaminations (Aznar et al., 2023).
    - In North America, between 21 September and 11 December 2024, 95.5% (43/45) of the reported A(H5) cases were related to occupational exposure to dairy cows (31/43) or infected poultry (12/43), with suspectedly no or inappropriate use of personal protective equipment.
    - To date, no sustained transmission between humans has been observed.
- The impact of human infection with HPAI A(H5) clade 2.3.4.4b viruses:
    - Most reported human detections of A(H5) clade 2.3.4.4b viruses since 2020 concerned asymptomatic individuals or individuals with mild disease, including conjunctivitis or typical flu symptoms (fever, cough). In the USA, between 21 September and 11 December 2024, all reported cases had mild symptoms, such as conjunctivitis or mild respiratory illness.
    - The case in Canada originally presented with conjunctivitis, fever and cough, but, following condition deterioration, the patient was later hospitalised with acute respiratory distress.
    - Human infections with other A(H5) clades in the past have shown clinical presentations ranging from asymptomatic or mild disease to severe illness potentially leading to death. The reasons for the variation in outcome of infection 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-b).
    - Despite their widespread circulation globally, A(H5N1) clade 2.3.4.4b viruses circulating in animal populations, including in Europe, retain a binding preference for α2–3 sialic acid avian-type receptors and are still considered to be avian-like. Mutations associated with adaptation to mammalian hosts were only sporadically identified, and there is currently no evidence of the

  viruses being more adapted to infect humans or having the ability to transmit between humans.
  - In addition, 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 endonuclease inhibitors (e.g. baloxavir marboxil).

Sporadic infections with avian influenza in humans are likely to continue occurring in areas where the virus is prevalent and individuals have unprotected contact with animals infected with avian influenza viruses, or their environment. Events or conditions that increase mammalian or human exposure to avian influenza viruses may lead to spillover events and further transmission, increasing the probability of avian influenza viruses adapting to mammals (EFSA, ECDC and EURL, 2024d). 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, the risk assessment will continue to be regularly reviewed by ECDC, taking into consideration any new developments or information that becomes available.

# 3. Conclusions

## 3.1 Birds

- From September 2024, there has been a steep increase in the number of HPAI virus detections in wild and domestic birds with a switch in the main category of wild birds affected, from colony-breeding seabirds in the previous reporting period to waterfowl in the current reporting period. Most of the reported detections in both wild and domestic birds were located in South-Central Europe, partly along the courses of large rivers, and with outbreaks in poultry often taking place in establishments located nearby waterbodies such as ponds and rivers.

- Mortality in mute swans, often in close proximity to waterbodies, was reported in several European countries during the current reporting period.

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

- Based on the available genetic data, all HPAI outbreaks reported in poultry in Europe were caused by viruses closely related to the viruses circulating in wild birds in the same areas.

- HPAI A(H5N5) viruses continued to expand their geographic and species range, and were reported in wild birds in several countries. Further spillover to domestic birds was observed in Iceland, Norway and the United Kingdom. A study on A(H5N5) in wildlife in Canada suggested that northern fulmars were acting as source species for this subtype.

- Secondary outbreaks were mostly reported in Hungary, which reflect an ongoing epidemic affecting mainly duck and goose establishments in a high-density poultry area. This high establishment density together with the poultry species involved are risk factors increasing the risk of secondary spread among farms and may result in major epidemics.

- Several small-scale establishments (backyards) have also been reported affected by several European countries. It is expected that this type of establishments are not likely to transmit the virus to commercial poultry establishments. However, small-scale establishments are of public health relevance, as several spillover events to humans worldwide have been linked to backyard poultry. Similarly, spillover from poultry to pigs was reported in the USA in a backyard establishment.

- HPAI outbreaks in establishments keeping vaccinated ducks were reported in France. Disease in vaccinated flocks is often mild, with clinical signs difficult to be noticed by farmers, thereby reducing the probability of detecting infections via passive surveillance.

- It is expected that the number of HPAI virus detections in Europe will either increase or remain at a similar level in the coming winter months, as in previous years the peak has always taken place between November and February.

- Currently available genetic data of viruses collected since September 2024 indicate the co-circulation of four major genotypes in Europe. Genotype EA-2023-DI is the most widespread genotype and has mainly been detected among waterfowl and domestic birds from 11 countries, with almost all the characterised viruses from South-Central Europe belonging to this genotype. Differently, the gull-adapted EA-2022-BB and EA-2021-I (A(H5N5)) genotypes have been mostly circulating among Laridae and raptors, with occasional spillover to domestic birds, along the Arctic Ocean, Atlantic Ocean and North Sea coasts.

- There has been an increase in the number of HPAI virus detections in both domestic and wild birds reported to WOAH from outside Europe compared to the previous reporting period (EFSA, ECDC and EURL, 2024b).

- Most of the HPAI outbreaks reported in poultry worldwide continued to be concentrated in the Americas, particularly in the USA (now also in Hawaii) and Canada. Although reported at a lower level, the HPAI situation in domestic and wild birds also continues on other continents, particularly in Asia, where multiple avian influenza viruses are endemic.

- Besides the HPAI A(H5) subtypes circulating worldwide, the local emergence of HPAI A(H7N6) in New Zealand was reported to WOAH during the current reporting period. South Korea reported the first detection of HPAI A(H5N3) in wild birds in the country.

- The reported HPAI virus detections in wild birds on the Falkland Islands increased sharply during the current reporting period and were associated with high mortality of gentoo penguins. It remains to be determined what the impact of HPAI will be on Antarctic wildlife in the coming 2024–2025 breeding season. Dependent on epidemiological developments in the Antarctic region, there is a risk of further spread of HPAI A(H5N1) virus to Oceania, including Australia and New Zealand.

- Since October 2023, the detection of 30 HPAI A(H5) viruses in wild and domestic birds collected from eight different European countries containing markers of mammalian adaptation in the PB2 protein (E627K/V, K526R or D701N) indicates that viruses with an enhanced capacity to infect mammals can replicate and spread in birds. Of particular concern is the recent increase of frequency of viruses collected from birds containing such mutations.
- The majority of HPAI A(H5N1) viruses circulating in birds in Europe since October 2023 have at least some amino acid substitutions in the HA protein that have proved to increase in vitro binding to human-type receptors. The impact of these HA mutations on the biological characteristics of the circulating viruses is still unknown but may potentially impact their zoonotic potential.

## 3.2 Mammals

- No new HPAI virus detections in mammals have been reported in Europe since spring 2024. Limited testing activities in different European countries have since then only resulted in negative test results.
- The number of dairy cattle farms in the USA reportedly affected by HPAI A(H5N1) virus of the B3.13 genotype continued to increase to > 800 in 16 states during the current reporting period. Importantly, A(H5N1) virus was detected for the first time in pigs in a mixed livestock-poultry farm.
- Feeding on HPAI virus-contaminated poultry meat may cause mortality in carnivore species.
- No new mammal species have been found positive for HPAI virus during the current reporting period.

## 3.3 Humans

- Sporadic cases of zoonotic avian influenza A(H5N1) and A(H9N2) were reported outside Europe during the period September–December 2024.
- 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 infection cases in the EU/EEA.
- Most human infections with avian influenza viruses reported since 1997 have been associated with unprotected exposure to poultry, live poultry markets, or contaminated environments. To date, no sustained human-to-human transmission has been observed.
- In the reporting period from 21 September to 11 December 2024, only two of 45 reported human cases of avian influenza A(H5N1) virus in North America had no known exposure identified following epidemiological investigation. The 43 other cases have all been occupationally exposed to infected animals (dairy cows or poultry).
- With continued circulation of avian influenza viruses in animal 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

- Continued surveillance in wild birds in Europe is indicated in the coming weeks given the sharp increase in reported HPAI virus detections during the current reporting period. Active surveillance in wild birds is indicated, especially in those silently maintaining HPAI viruses in the wild (e.g. waterfowl), to improve knowledge on HPAI viruses circulating in wild bird populations, as well as to estimate viral and seroprevalence among different species for a better epidemiological understanding of these viruses. Serological studies, combined with mortality data, may also help infer whether some level of flock immunity has been reached in different species.

- 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 are able to mutate into their highly pathogenic forms once circulating in poultry.

- Biosecurity remains a key factor to prevent HPAI virus introduction from wild birds into poultry establishments and further farm-to-farm spread. Sharing farm equipment and personnel, particularly when farms have the same ownership, should be, if possible, avoided, or at least kept to a minimum. In case of shared equipment or personnel, strict biosecurity protocols should be followed. Further research is needed to identify biosecurity breaches in large-scale poultry establishments.

- In poultry, surveillance efforts should also include small-scale establishments, as these may be at higher risk, due to lower biosecurity and the provision of outdoor access, and have important public health relevance.

- Active surveillance in vaccinated flocks is of utmost importance to promptly detect HPAI virus-infected birds without or only mild clinical signs.

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

- 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 acquired mutations. Genetic data are also instrumental to track the virus spread and identify novel incursions of viruses that may represent a threat for human or animal health.

- Reinforcement of genetic characterisation of viruses collected from birds in areas where a high number of infections in mammalian species was identified is recommended to promptly detect possible mammal-to-avian transmission of viruses containing markers of virus adaptation to mammalian species, which may have a higher zoonotic potential.

## 4.2 Mammals

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

- In light of the recent events in the USA and the first results of experimental infections with Eurasian A(H5N1) viruses in dairy cattle, testing of/surveillance in ruminants is recommended when a combination of factors is observed, such as the manifestation of overt and unresolved clinical signs typically associated with HPAI virus infection in ruminants (e.g. undiagnosed severe decrease in milk production and presence of darker, thickened milk), but also the occurrence of HPAI virus infection in other domestic, peridomestic and wild animals in/around cattle farms. In addition, HPAI should be considered as a differential diagnosis in cases of undiagnosed or unresolved clinical signs during periods of HPAI virus circulation in the area where ruminants are kept.

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

- Pet and other captive mammals should not be fed with meat or other animal products (e.g. raw milk) from potentially HPAI virus-infected animals.

- 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 biosafety and biosecurity measures at occupational sites at increased risk of exposure.
  - Provision of information to raise awareness among people at potential risk of exposure and to indicate how it can be mitigated. Guidance should be tailored to specific occupational groups, or people engaged in recreational activities where additional measures may be beneficial. Recommendations for personal protective measures and equipment should take into consideration and be adapted according to the working environment and tasks involved, routes of exposure and environmental factors.
  - Recommendation to the general public to avoid contact with sick or dead birds and other wild animals and to inform the relevant authorities if they find dead animals to ensure safe removal and further investigation.

- People who have been exposed, without appropriate personal protective equipment, to animals with suspected or confirmed avian influenza virus infection should be monitored for symptoms for 10–14 days after the last exposure and tested if symptoms develop. Monitoring of asymptomatic individuals exposed to animals with suspected or confirmed avian influenza virus infection without appropriate protective measures should be assessed on a case-by-case basis, with testing 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) and 'Investigation protocol for human exposures and cases of avian influenza' (ECDC, 2023).

- Countries should remain vigilant for potential human cases of avian influenza, especially in geographic areas where the virus is highly circulating in poultry, wild birds, or other animals. Healthcare workers in primary care in these areas should be made aware of the epidemiological situation and of 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 highlighted the importance of typing and subtyping these samples. Samples collected through seasonal influenza surveillance that are positive for influenza type A virus but cannot be assigned to a seasonal subtype A(H1N1)pdm09 or A(H3N2) should be further analysed to search for avian influenza virus subtypes. This means that all influenza-positive specimens from seasonal influenza surveillance systems in primary and secondary care settings should ideally be typed and subtyped.

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

- Genetic changes in avian influenza viruses that may alter their zoonotic potential (increase capacity to infect humans, increase transmissibility) or their susceptibility to antivirals available to treat humans should be monitored. Avian influenza viruses detected in humans should systematically 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. However, specific recommendations for vaccination remain under the remit of national authorities (EFSA, ECDC and EURL, 2024d).

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# Appendix A – Terms of Reference

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

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

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

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

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

- ECDC's current risk assessment (ECDC, online) that focuses on the immediate risk of avian influenza for human health fulfilling ECDC's new mandate and the Regulation (EU) 2022/2371[7] 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[8] and Commission Delegated Regulation (EU) 2020/687[9]).

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[7] 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.

[8] 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.

[9] 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[10] and Articles 29 and 31 of Regulation (EC) No 178/2002[11], 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 20 September and 6 December (10 December for mammals) 2024, as reported by Member States and third countries via ADIS or WOAH-WAHIS. In addition, LPAI virus detections of specific relevance are included, and possible actions for preparedness in the EU are discussed based on the situation worldwide. Member States and other European countries where HPAI outbreaks have occurred in poultry submitted additional epidemiological data to EFSA, which have been used to analyse the characteristics of the affected poultry establishments.

However, it was not possible to collect data for a comprehensive risk factor analysis on the occurrence and persistence of HPAI viruses within the EU. Risk factor analysis requires not only case-related information but also data on the susceptible population (e.g. location of establishments and population structure), which should be collected in a harmonised manner across the EU. Limitations in data collection, reporting and analysis were explained in the first avian influenza overview report (EFSA, ECDC and EURL, 2017).

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

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[10] 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.

[11] 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 21 September and 6 December 2024, and submitted by Member States and other European countries via ADIS, were taken into account. Data extraction was carried on 6 December 2024. 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.14512202

### 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 December 2024 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 and are included, irrespective of whether there have been any new human cases during the reporting period. Relevant information on human infections, risk factors, and the results from studies on infection and transmission in mammals with relevance for human health are included.

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

The GISAID's EpiFlu™ Database (Shu and McCauley, 2017) was accessed on 10 December 2024 to retrieve sequences from human cases of avian influenza reported since 20 September 2024. 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 1,713 gap free nucleotides. A neighbor joining tree was produced by Jukes-Cantor nucleotide distance measurement with 100 bootstrap replicates. The tree was visualised in microreact (Argimón et al., 2016) and further edited using Inkscape (Inkscape, online). The protein sequences were analysed using a script developed in-house, with A/Goose/Guangdong/1/96 (EPI_ISL_1254) as reference to determine mutations of interest (H5 numbering, unless otherwise stated). Clade information was retrieved from GISAID. Genotype was assigned using GenoFLU (Github USDA-VS, online).

# Annex A – Data on Birds

Annex A is available on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.14512202

# 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.14512202

# Annex C – Acknowledgements

Annex C is available on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.14512202