

APPROVED: 21 September 2026
doi: 10.2903/j.efsa.2026.10369

Avian influenza overview June–August 2026

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Abstract

Between 5 June and 28 August 2026, 110 highly pathogenic avian influenza (HPAI) A(H5N1) virus detections were reported in domestic (7) and wild (103) birds in 12 countries in Europe. The number of detections remained at a seasonal low throughout the summer, continuing the decline observed since spring. In contrast to previous years, fewer colony-breeding seabirds were affected, and the geographical range of detections was more limited. Further sporadic detections of HPAI A(H5) virus were reported in wild terrestrial carnivores and pinnipeds. Outside Europe, the epidemic continued in the Americas, where also the HPAI A(H7N3) subtype was detected in Mexico. Following its first introduction to mainland Australia, HPAI A(H5N1) virus spread within local wild bird populations and spilled over to terrestrial carnivores and marine mammals. In the US, the number of dairy cattle farms reportedly affected by HPAI A(H5N1) increased, while detections in captive American minks were reported for the first time. Between 5 June and 31 August 2026, 15 cases of avian influenza virus infection were publicly reported in humans (no fatal cases) in three countries and territories: Bangladesh (one A(H5N1) case), Cambodia (one A(H5N1) case) and China (13 A(H9N2) cases). All human cases reported exposure to poultry or a poultry environment prior to detection or onset of illness. Human infections with avian influenza viruses remain rare and no sustained human-to-human transmission has been documented. The risk posed by avian influenza A(H5N1) clade 2.3.4.4b viruses currently circulating in Europe remains low for the general public in the European Union/European Economic Area (EU/EEA) and low-to-moderate for those occupationally or otherwise exposed to infected animals or contaminated environments.

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

Requestor: European Commission

Question number: EFSA-Q-2026-00364 and Commission request 280 to ECDC (SANTE.B.2/IK/mo (2023)2182203)

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Acknowledgements: In addition to the listed authors, EFSA, ECDC and the EURL wish to thank the Member State representatives who provided epidemiological data on avian influenza outbreaks or shared sequence data: Lika Aldin and Erga Shkodra (Albania); Sandra Revilla-Fernández and Irene Zimpernik (Austria); Mieke Steensels and Steven Van Borm (Belgium); Emiliya Ivanova (Bulgaria); Vladimir Savic (Croatia); Vasiliki Christodoulou (Cyprus); Tomáš Jarosil, Klára Jelínková, Petr Kučinský, Alexander Nagy, Hynek Siksta and Ludek Zavada (Czechia); Charlotte Kristiane Hjulsager, Yuan Liang, Pernille Dahl Nielsen and Heidi Huus Petersen (Denmark); Kärt Jaarma and Imbi Nurmoja (Estonia); Tuija Gadd, Ari Kauppinen, Niina Tammiranta and Tiia Tuupanen (Finland); François-Xavier Briand, Thomas Gayen, Béatrice Grasland, Éric Niquex, Audrey Schmitz and Angela Srouf (France); Timm Harder, Anne Pohlmann and Carola Sauter-Louis (Germany); Malik Peter (Hungary); Brigitte Brugger and Vilhjálmur Svansson (Iceland); Laura Garza Cuartero (Ireland); Lara Cavicchio, Marta Dianati, Isabella Monne, Angela Salomoni and Bianca Zecchin (Italy); Juris Kibilds, Marta Lizuma and Žanete Šteingolde (Latvia); Simona Pileviciene, Vilija Grigaliūnienė and Egidijus Pumputis (Lithuania); Vicky Binck and Chantal Snoeck (Luxembourg); Oxana Groza (Moldova); Monika Ballmann, Dennis Bol and Marcel Spierenburg (Netherlands); Aleksandar Dodovski and Igor Dzadzovski (North Macedonia); Britt Gjerset and Ingeborg Slettebø Wathne (Norway); Katarzyna Domańska-Blicharz, Anna Pikula, Aleksandra Podrażka, Magdalena Roman and Krzysztof Śmietanka (Poland); Margarida Duarte, Teresa Fagulha and Margarida Henriques (Portugal); Iuliana Onita (Romania); Dejan Vidanovic (Serbia); Zuzana Dirbakova, Barbora Pavlíková and Martin Tinak (Slovakia); Brigita Slavec (Slovenia); Montserrat Agüero García and María Teresa Barrios Zambrano (Spain); Linnea Lindgren Kero and Siamak Zohari (Sweden); Claudia Bachofen (Switzerland); Michael McMenemy (Northern Ireland)¹. The authors also wish to thank Ron Fouchier from Erasmus Medical Center (Netherlands); Ashley Banyard and Holly Coombes from the Animal and Plant Health Agency (United Kingdom); Camille Delavenne from EpiMundi for conducting the data analysis under the contract EFSA/2025/OP/0014; the authors, originating and submitting laboratories of the sequences from GISAID's EpiFlu™ database, which is used for this assessment (Annex E); Julio Álvarez and Jan Arend Stegeman from EFSA's Panel on Animal Health and Welfare (AHAW); Edoardo Colzani from ECDC, as well as Maya Carvalho Evans and Sasan Fereidouni from EFSA for the support provided to this scientific output.

Suggested citation: EFSA (European Food Safety Authority), ECDC (European Centre for Disease Prevention and Control), EURL (European Union Reference Laboratory for Avian Influenza), Barbezange, C., Ducatez, M., Fusaro, A., Gonzalez, J. L., Kuiken, T., Melilli, R., Mirinavičiūtė, G., Ståhl, K., Staubach, S., Svartström, O., Terregino, C., Willgert, K., Alarcón, E., & Kohnle, L. (2026). Avian influenza overview June–August 2026. *EFSA Journal*, 24(9), e10369, <https://doi.org/10.2903/j.efsa.2026.10369>

ISSN: 1831-4732

¹ In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Windsor Framework, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).

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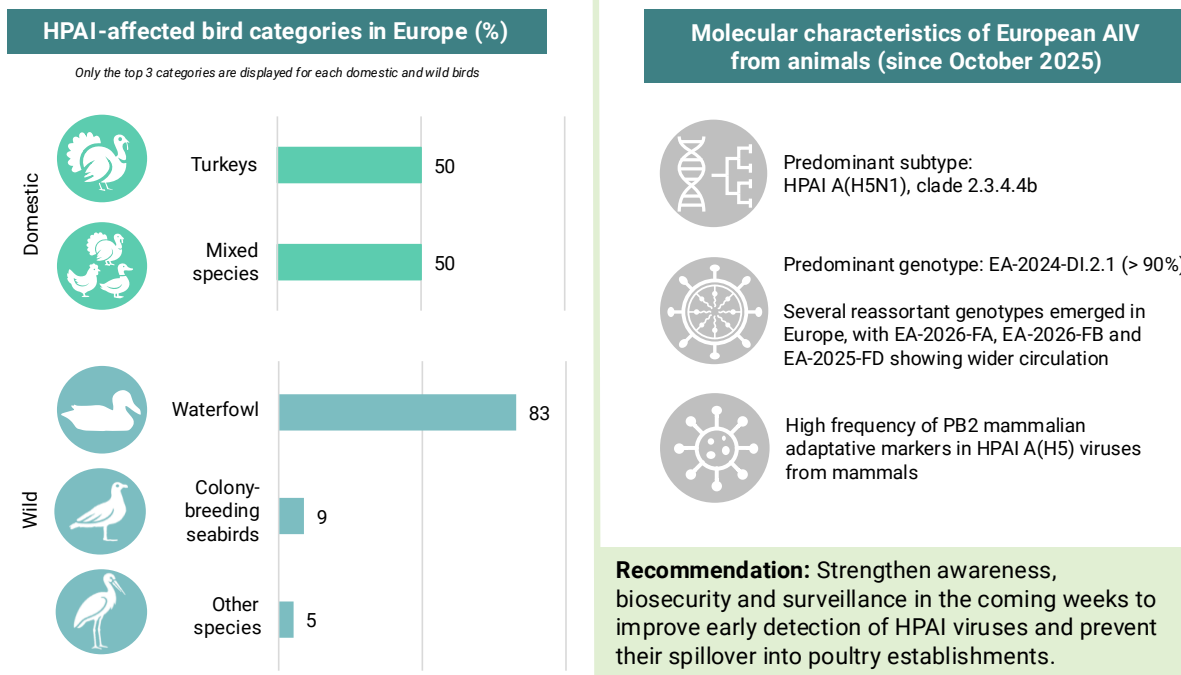
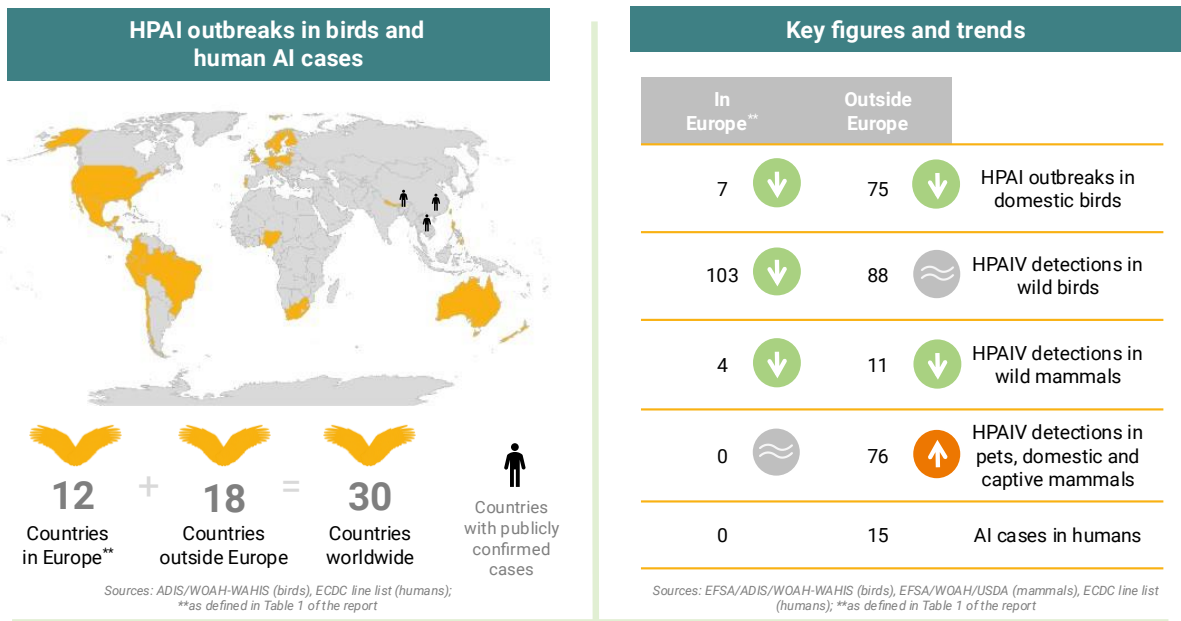
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Avian influenza overview

June–August 2026*



- In Europe, HPAI A(H5N1) virus detections further declined during summer and remained at very low levels in both domestic and wild birds. No new HPAI A(H5N5) virus detections were reported.
- However, HPAI virus detections are expected to increase in the coming weeks with the arrival of migratory birds.
- Outside Europe, HPAI A(H5N1) virus has spread among local wild bird populations in Australia and has further spilled over to mammals following its first introduction to the Australian mainland in June. HPAI A(H5) viruses continued to be detected across the Americas, with Mexico reporting HPAI A(H7N3) virus detections in wild birds.



AI: avian influenza; AIV: avian influenza virus; HPAI: highly pathogenic avian influenza; HPAIV: highly pathogenic avian influenza virus

*5 June to 28 August 2026

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1 Introduction

This Scientific Report provides an overview of highly pathogenic avian influenza (HPAI) virus detections in poultry² and captive birds³ (domestic birds), as well as in wild birds, that occurred in and outside Europe between 5 June and 28 August 2026. In addition, the report includes HPAI virus detections in mammals up until 31 August 2026 and cases of avian influenza infection in humans between 5 June and 31 August 2026. Detections of low pathogenic avian influenza (LPAI) virus in birds are discussed whenever they are of zoonotic concern or otherwise relevant.

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

2 Assessment

2.1 HPAI virus detections in birds

2.1.1 HPAI virus detections in birds in Europe

Figure 1 shows all HPAI virus detections in birds in Europe that were reported via the European Union (EU) Animal Disease Information System (ADIS) or the World Animal Health Information System (WOAH-WAHIS) of the World Organisation for Animal Health (WOAH) for the last six and the current epidemiological year⁴ by month of suspicion. For the current epidemiological year 2025–2026, starting on 1 October 2025, data reported are truncated on 28 August 2026.

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

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

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

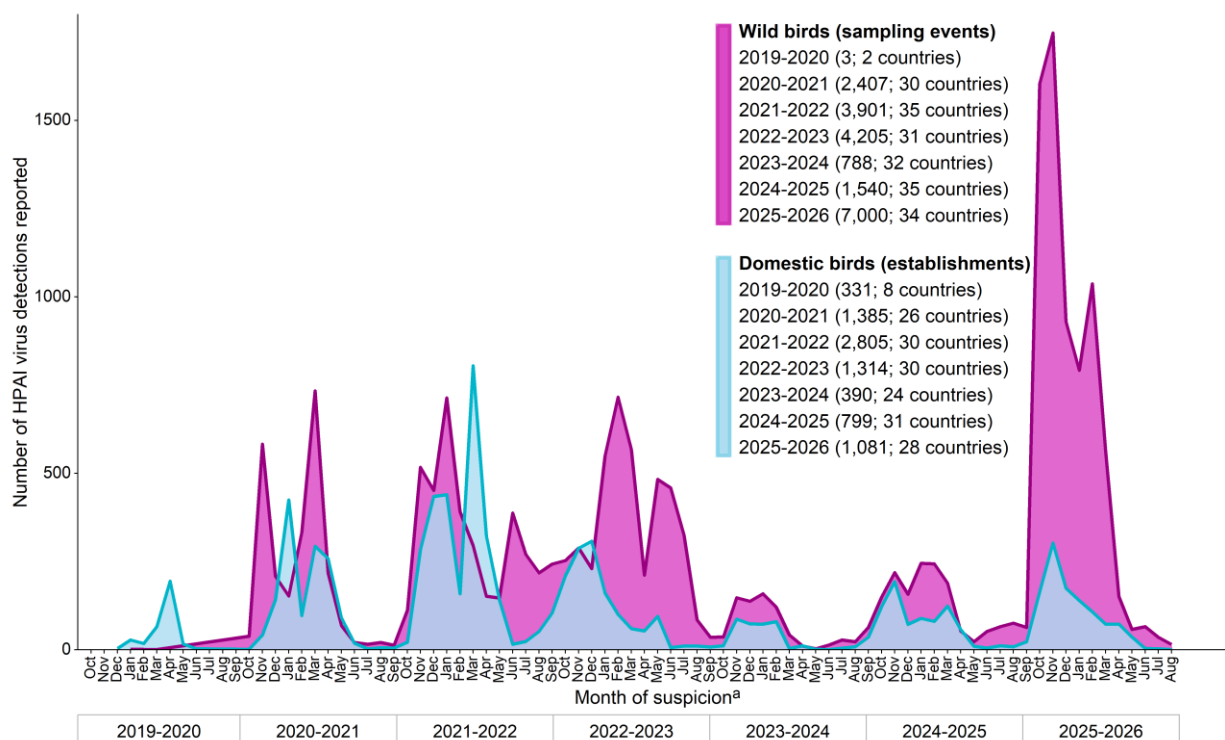


Figure 1: Distribution of the number of HPAI virus detections in wild birds (cumulative n = 19,844) (pink) and establishments keeping domestic birds (cumulative n = 8105) (blue) that were reported in Europe during seven epidemiological years by month of suspicion, from 1 October 2019 to 28 August 2026 (total cumulative n = 27,949).

Note: 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 WOA-H-WAHIS for the United Kingdom (excluding Northern Ireland) and ADNS/ADIS for the United Kingdom (Northern Ireland)⁵.

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

Source: ADNS/ADIS and WOA-H-WAHIS (data extraction carried out on 28 August 2026).

Considering the current reporting period from 5 June to 28 August 2026, 110 HPAI virus detections were reported in poultry (2), captive (5) and wild (103) birds in 12 countries in Europe (Table 1, Figure 2).

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

Table 1: Number of HPAI outbreaks reported in Europe by country, virus subtype and affected sub-population, from 5 June to 28 August 2026. Cumulative numbers since the start of the 2025–2026 epidemiological year are reported in parentheses (1 October 2025 to 28 August 2026).

Country	Captive birds A(H5N1)	Poultry				Wild birds			Total
		A(H5Nx)	A(H5N1)	A(Not typed)	A(H5Nx)	A(H5N1)	A(H5N2)	A(H5N5)	
Austria	0 (4)	-	0 (1)	-	-	1 (92)	-	-	1 (97)
Belgium	0 (3)	-	0 (20)	-	0 (47)	2 (338)	-	-	2 (408)
Bosnia and Herzegovina	-	-	0 (1)	-	-	0 (1)	-	-	0 (2)
Bulgaria	0 (1)	-	0 (15)	-	-	0 (1)	-	-	0 (17)
Croatia	-	-	-	-	-	0 (7)	-	-	0 (7)
Czechia	0 (35)	-	0 (20)	-	-	0 (44)	-	-	0 (99)
Denmark	0 (6)	-	0 (25)	-	0 (1)	3 (232)	-	0 (1)	3 (265)
Estonia	0 (4)	-	-	-	-	0 (29)	-	-	0 (33)
Finland	-	-	-	0 (2)	0 (2)	1 (38)	-	-	1 (42)
France	0 (31)	-	0 (125)	-	-	0 (315)	-	-	0 (471)
Germany	2 (73)	-	1 (200)	-	-	46 (3826)	-	-	49 (4099)
Greece	-	-	-	-	-	0 (1)	-	-	0 (1)
Hungary	-	-	0 (16)	-	-	0 (55)	-	-	0 (71)
Iceland	-	-	-	-	0 (1)	0 (4)	-	0 (3)	0 (8)
Ireland	0 (1)	-	0 (5)	-	-	0 (12)	-	-	0 (18)
Italy	0 (2)	-	0 (65)	-	0 (13)	0 (97)	-	-	0 (177)
Latvia	0 (2)	-	-	-	-	0 (27)	0 (1)	-	0 (30)
Lithuania	1 (1)	-	0 (3)	-	-	0 (30)	-	-	1 (34)
Luxembourg	0 (1)	-	-	-	-	0 (23)	-	-	0 (24)
Moldova	-	-	-	-	-	0 (7)	-	-	0 (7)
Montenegro	-	-	0 (5)	-	-	-	-	-	0 (5)
Netherlands	1 (15)	-	0 (46)	-	-	31 (415)	-	-	32 (476)
North Macedonia	0 (2)	-	-	-	-	-	-	-	0 (2)
Norway	-	-	-	-	0 (9)	11 (78)	-	-	11 (87)
Poland	1 (21)	-	0 (182)	-	-	1 (257)	-	-	2 (460)
Portugal	0 (4)	0 (1)	0 (11)	-	-	2 (14)	-	-	2 (30)
Romania	0 (1)	-	0 (1)	-	-	0 (12)	-	-	0 (14)
Serbia	-	-	-	-	-	0 (1)	-	-	0 (1)
Slovakia	0 (4)	-	0 (4)	-	-	0 (11)	-	-	0 (19)
Slovenia	-	-	-	-	-	0 (18)	-	-	0 (18)
Spain	0 (4)	-	0 (7)	-	0 (1)	0 (115)	-	-	0 (127)
Sweden	0 (2)	-	1 (9)	-	-	2 (114)	0 (1)	-	3 (126)
Switzerland	0 (1)	-	-	-	-	0 (24)	-	-	0 (25)
Ukraine	0 (2)	-	-	-	-	0 (2)	-	-	0 (4)

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United Kingdom (excluding Northern Ireland)	-	-	0 (4)	-	-	0 (6)	-	-	0 (10)
United Kingdom (Northern Ireland) ^a	0 (18)	-	0 (77)	-	-	3 (669)	-	0 (3)	3 (767)
Total	5 (238)	0 (1)	2 (842)	0 (2)	0 (74)	103 (6915)	0 (2)	0 (7)	110 (8081)

–, no HPAI outbreaks were notified via ADIS or WOA-H-WAHIS.

^a 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).

Source: ADIS and WOA-H-WAHIS (data extraction carried out on 28 August 2026).

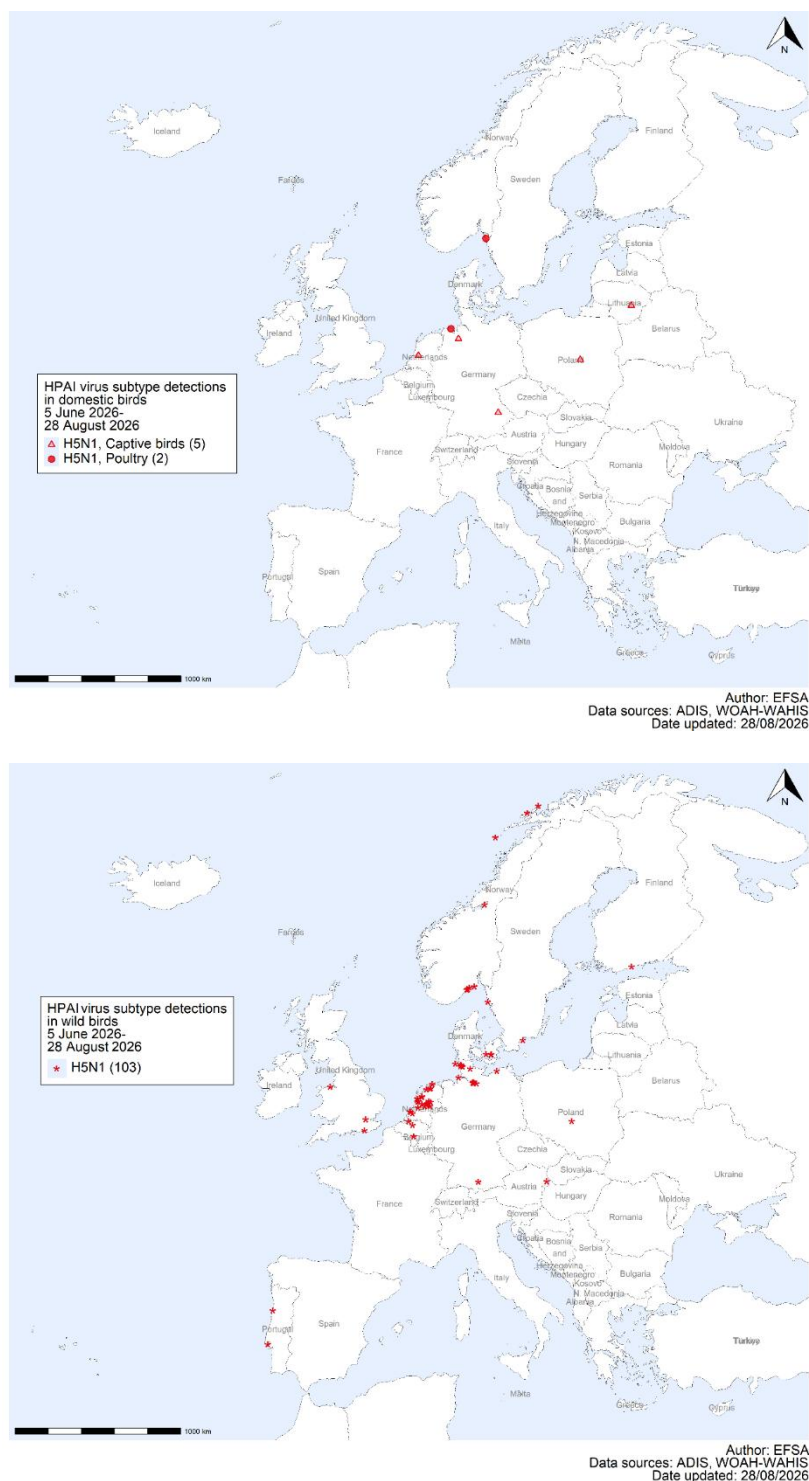


Figure 2: Geographic distribution, based on available geocoordinates, of HPAI virus detections in poultry and captive birds (7) (upper panel), and in wild birds (103) (lower panel), reported by virus subtype in Europe from 5 June to 28 August 2026.

* 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.

Source: ADIS and WOAH-WAHIS (data extraction carried out on 28 August 2026).

The decrease in the number of HPAI virus detections in Europe observed already in spring continued during the current reporting period and reached a very low level (Figure 1, Table 1). The number of detections between 5 June and 28 August (n = 110) was even lower than in the same period last year (72% and 45% lower for domestic and wild birds, respectively).

The number of HPAI outbreaks in domestic birds (Figure 2, upper panel; Figure 3) was too low to allow a meaningful comparison with the geographical and temporal distribution of HPAI virus detections in wild birds, although the few outbreaks reported coincided with areas where HPAI virus was detected in wild birds (Figure 2, lower panel; Figure 3).

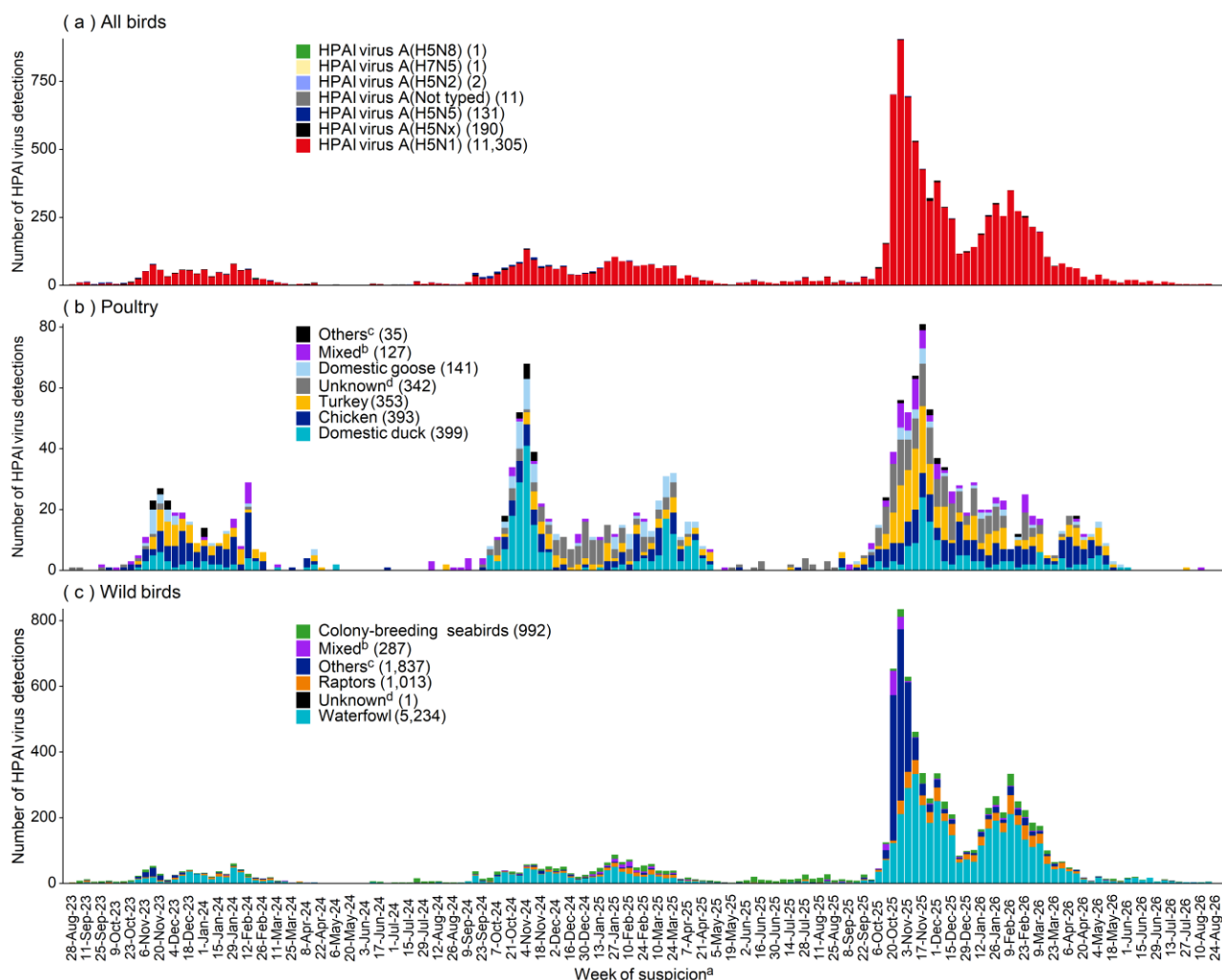


Figure 3: Distribution of the total number of HPAI virus detections reported in Europe by week of suspicion (dates indicate the first day of the week) and virus subtype (a), affected poultry categories (b), and affected wild bird categories (c), from 1 October 2023 to 28 August 2026.

Note: 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 WOA-H-WAHIS for the United Kingdom (excluding Northern Ireland) and ADNS/ADIS for the United Kingdom (Northern Ireland)⁶.

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

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

^b Mixed, outbreaks in which multiple species or categories were involved.

^c Others, all other affected categories which are not indicated in the legend.

^d Unknown, affected categories which were not further specified during reporting.

Source: ADNS/ADIS, EFSA and WOAH-WAHIS (data extraction carried out on 28 August 2026).

The majority of HPAI virus detections in wild birds were in western Europe (Germany, Netherlands), although sporadic detections were also recorded in the far north (Norway) and southwestern Europe (Portugal) (Table 1; Figure 2, lower panel). Compared to the same period last year, fewer colony-breeding seabirds (decrease of 94%) were affected during the current reporting period (Figure 3), which is also reflected in a lower number of detections in western and southwestern Europe (France, Spain, United Kingdom) (EFSA, ECDC, and EURL, 2025a).

All HPAI viruses detected in domestic and wild birds between 5 June and 28 August belonged to subtype A(H5N1). No new HPAI A(H5N5) virus detections were reported during the current reporting period (Table 1, Figure 2, Figure 3).

Considering the entire epidemiological year from 1 October 2025 to 28 August 2026, the end of the current reporting period, Europe recorded its highest number of HPAI virus detections in wild birds to date ($n = 7000$). This represents a 1.8-fold and 1.7-fold increase compared to the 2021–2022 ($n = 3901$) and 2022–2023 ($n = 4205$) epidemiological years, respectively, which had previously been the years with the highest detection numbers since 2016. In contrast, the number of outbreaks in domestic birds ($n = 1081$) was 2.6 and 1.2-fold times lower than in the 2021–2022 ($n = 2805$) and 2022–2023 ($n = 1314$) epidemiological years, respectively (Figure 1).

Spatio-temporal information on all HPAI virus detections reported in Europe since October 2016 is available via EFSA's interactive dashboard⁷.

Poultry

Between 5 June and 28 August 2026, 2 HPAI A(H5N1) outbreaks in poultry were reported in Germany (1) and Sweden (1) (Table 1, Figure 2). Additional data on the characteristics of the affected poultry establishments (i.e. poultry species, purpose of raising, source of introduction, number of exposed people, clinical signs, mortality) were collected and provided by the reporting countries for both outbreaks (Annex B).

In Germany, the outbreak was reported on 28 July in a commercial establishment keeping parent-stock turkeys ($n = 6554$) in the northeast of the country. Indirect contact with wild birds was identified as the most likely source of introduction. Mortality was observed, with a total of 10 (0.2%) dead birds identified via bucket sampling. No clinical signs were reported.

In Sweden, the outbreak was reported on 15 August in a commercial establishment keeping laying hens ($n = 143$) and domestic ducks ($n = 2$) with outdoor access. Mortality and clinical signs were reported, with a total of 62 (42.8%) dead birds recorded. Direct contact with wild birds was identified as the most likely source of introduction. A total of four persons were reported as exposed.

The two HPAI outbreaks in poultry reported during the current reporting period represent a 99% decrease compared to the previous reporting period, when 155 HPAI outbreaks in poultry

⁷ <http://hpaiefsa.eu.vet/>



occurred, particularly in Poland ($n = 102$) (EFSA, ECDC and EURL, 2026a). Following the implementation of specific control measures in domestic birds in the country, which entered into force on 28 May 2026 (European Commission, 2026; Veterinary Inspection of the Republic of Poland, 2026) and prohibited the restocking of establishments within restricted zones, thereby reducing the number of susceptible poultry establishments, no further HPAI outbreaks in poultry were reported in Poland. In addition to the effective control of farm-to-farm transmission, environmental infection pressure declined as waterfowl, in particular, migrated to breeding grounds largely situated outside Europe. In the same period last year, 17 HPAI outbreaks in poultry were recorded in Europe (Figure 3), with outbreaks occurring in Bulgaria, Spain and the United Kingdom.

Considering the entire epidemiological year from 1 October 2025 to 28 August 2026, the end of the current reporting period, a total of 843 HPAI outbreaks were reported in poultry, involving 33,091,685 susceptible birds. Of those, 842 outbreaks were reported as HPAI A(H5N1), while for one A(H5) outbreak, reported in Portugal, the neuraminidase gene (N) could not be determined. The highest number of outbreaks was reported in Germany (200/843, 24%), followed by Poland (182/843, 22%) and France (125/843, 15%). In terms of birds affected, the highest number was reported in Poland ($n = 11,902,520$), followed by Germany ($n = 4,118,200$) and the United Kingdom (excluding Northern Ireland) ($n = 3,690,459$) (Figure 4).

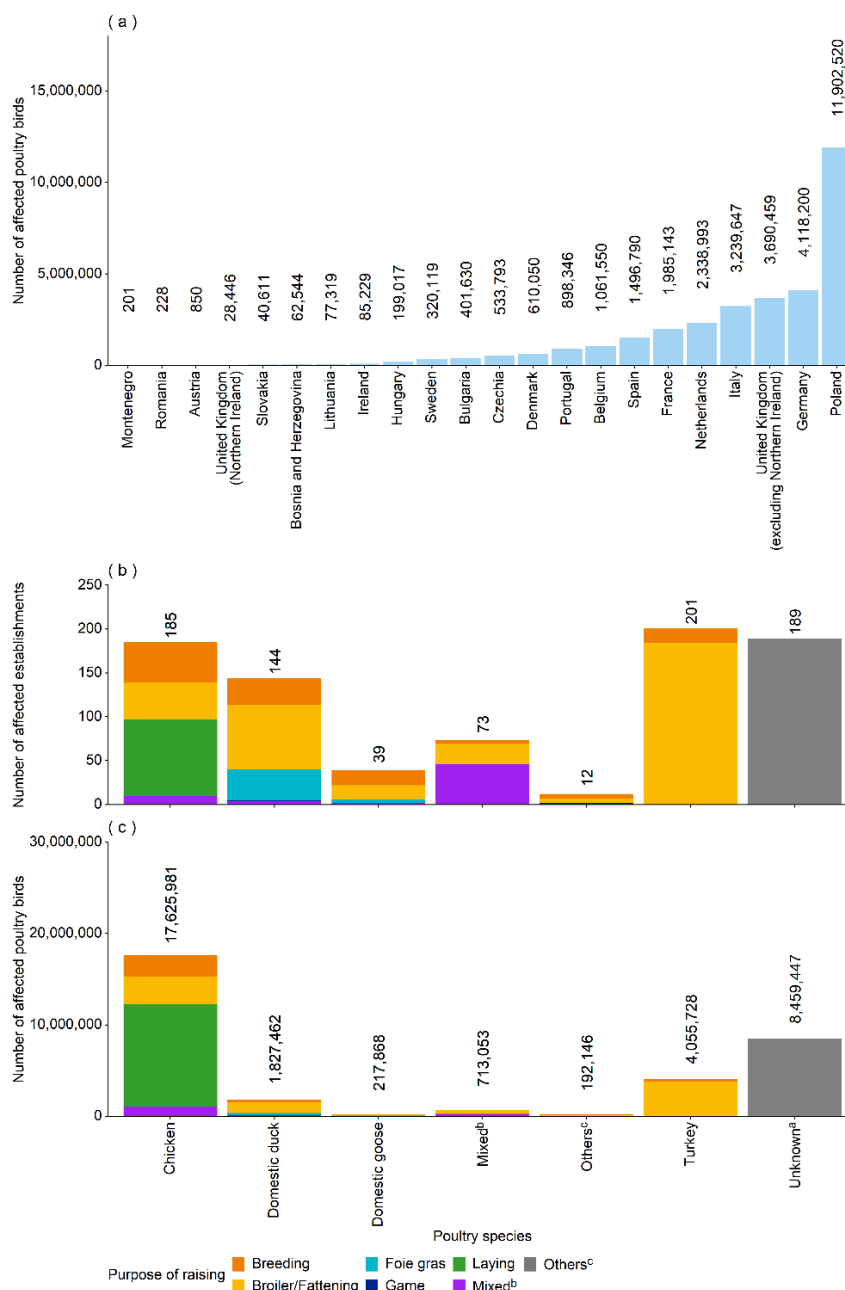


Figure 4: Number of poultry birds in the HPAI-affected establishments per country (total n = 33,091,685; countries are ranked according to the number of poultry birds affected) (a), as well as number of HPAI-affected establishments (total n = 843) (b) and poultry birds (total n = 33,091,685) (c) per poultry species and purpose of raising in Europe between 1 October 2025 and 28 August 2026.

Note: 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).

^a Unknown, affected categories which were not further specified during reporting.

^b Mixed, outbreaks in which multiple species or categories were involved.

^c Others, all other affected categories which are not indicated in the legend.

Source: ADIS, EFSA and WOA-H-WAHIS (data extraction carried out on 28 August 2026).



The most affected poultry category during this period was 'turkey' (201/843, 24%), followed by 'chicken' (185/843, 22%), 'domestic duck' (144/843, 17%), 'domestic goose' (39/843, 5%) and 'others' (12/843, 1%). Mixed poultry species were present in 73 (9%) establishments, while information on the poultry species kept was not available for another 189 (22%) establishments. Most turkeys were kept for fattening (92%, 184/201), while the remaining 8% (17/201) were kept for breeding. Among the 'chicken' category, 47% (87/185) were laying hens, 25% (46/185) were kept for breeding, 23% (42/185) were broilers, and another 5% were kept for mixed (9/185) or other purposes (1/185). Among the 'domestic duck' category, 51% (74/144) were kept for fattening, 24% (35/144) for foie gras production, 21% (30/144) for breeding, 3% (4/144) for mixed purposes and 1% (1/144) were game birds. Among the 'domestic goose' category, 44% (17/39) were kept for breeding, 41% (16/39) for fattening, 10% (4/39) for foie gras production and 5% (2/39) for mixed purposes. Among other poultry, breeding and fattening each accounted for 41.7% (5/12), while 16.6% (2/12) were game birds. For mixed poultry species, 62% (45/73) were kept for mixed purposes, 32% (23/73) for fattening, 5% (4/73) for breeding and 1% (1/73) for other purposes (Figure 4).

Although the current epidemiological year saw the highest number of wild bird detections to date, potentially indicating greater environmental contamination than in 2021–2022 and 2022–2023), HPAI outbreaks in poultry dropped significantly. Particularly in France and Hungary, during the 2021–2022 and 2022–2023 epidemiological years, domestic ducks were heavily impacted, representing 60% (848/1403) and 63% (251/401) of the outbreaks in France, and 49% (145/293) and 55% (95/172) of the outbreaks in Hungary. In the current epidemiological year, outbreaks in domestic ducks fell dramatically (e.g. 58/125 in France and 5/16 in Hungary). Enhanced biosecurity and preventive control measures likely contributed to this drop despite high wild bird infection levels. Particularly in France, the introduction of mandatory preventive vaccination in domestic ducks, alongside improved biosecurity, appears to have effectively reduced outbreaks resulting from both wild bird introductions and farm-to-farm transmission. Hungary also implemented targeted control measures in the duck sector in 2025 to reduce secondary spread, including restocking restrictions, enhanced surveillance of high-risk poultry establishments, improved biosecurity, and incentives to decrease the density of establishments (EFSA, ECDC and EURL, 2026b). These measures appear to have contributed to the reduction in the number of outbreaks.

Overall, between 1 October 2025 and 28 August 2026, 606 (72%) HPAI outbreaks in poultry occurred in commercial establishments, while 11 (1%) occurred in non-commercial establishments. For the remaining 226 (27%) outbreaks, information on the type of establishment was not available. While only 94 (11%) of the affected commercial establishments provided outdoor access to poultry, all 11 affected non-commercial establishments provided outdoor access. Information on outdoor access was not available for 307 (36%) establishments. Regarding the most likely source of introduction, indirect contact with wild birds was identified as the main suspected source (395/843, 46.9%), followed by indirect contact with poultry (47/843, 5.5%), direct contact with poultry (11/843, 1.3%) and direct contact with wild birds (6/843, 0.8%). For the remaining 384 (45.5%) outbreaks, information on the most likely source of introduction was not available.

Clinical signs accompanied by mortality were reported in half of the outbreaks (50%, 422/843), while mortality without clinical signs was reported in 136 (16%, 136/843) outbreaks (Figure 5). Clinical signs without mortality were observed in 56 (7%, 56/843) outbreaks, predominantly in turkeys for fattening (29/56, 52%). No clinical signs or mortality were reported in 32 outbreaks

(4%), half of which (16/32, 50%) were detected via outbreak-related surveillance. These outbreaks involved primarily ducks for foie gras production (18/32, 56%). Information on the occurrence of clinical signs and mortality was not available for 197 (23%) outbreaks.

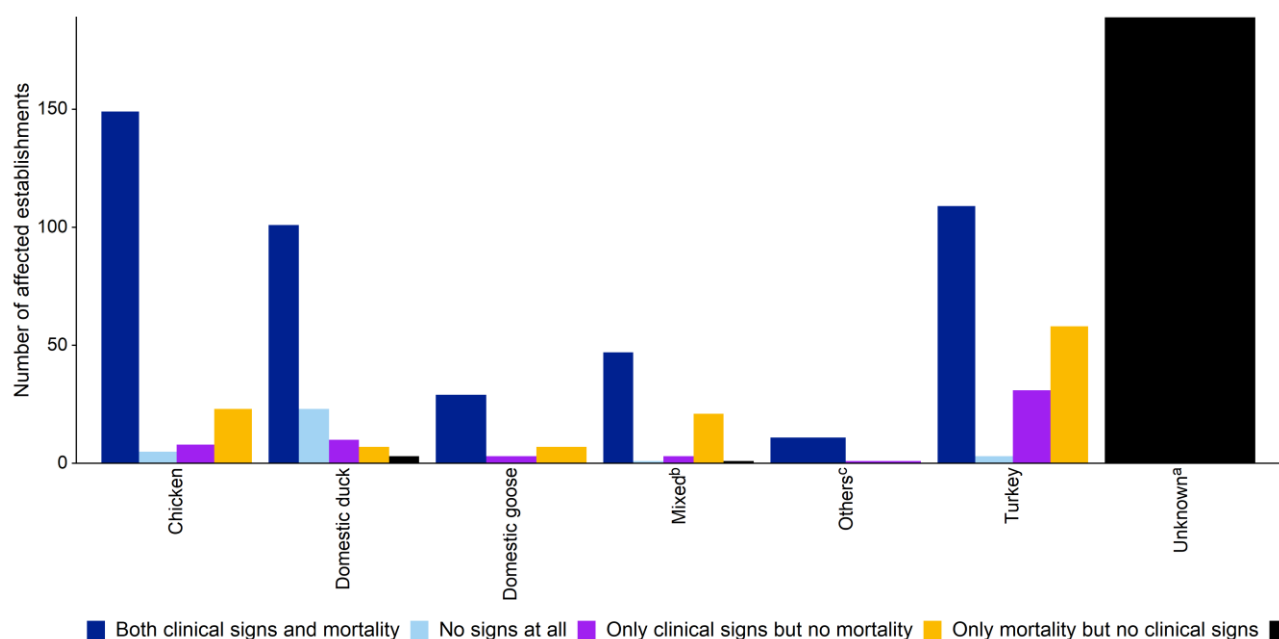


Figure 5: Number of HPAI-affected poultry establishments (n = 843) classified according to the presence of clinical signs and mortality, by poultry species, in Europe between 5 June and 28 August 2026.

^a Unknown, affected species which were not further specified during reporting.

^b Mixed, outbreaks in which multiple species were involved.

^c Others, all other affected species which are not listed separately.

Source: ADIS, EFSA and WOA-H-WAHIS (data extraction carried out on 28 August 2026).

Captive birds

Between 5 June and 28 August 2026, 5 HPAI A(H5N1) outbreaks in captive birds were reported in 4 countries in Europe: Germany (2), Lithuania (1), Netherlands (1) and Poland (1) (Table 1, Figure 2). Additional data on the characteristics of the affected captive bird establishments (i.e. species, purpose of raising, source of introduction, clinical signs, mortality) were collected and provided by the reporting countries for all 5 outbreaks (Annex B).

All outbreaks occurred in non-commercial backyard or hobby establishments keeping small numbers of mixed poultry species for private consumption and recreational purposes. The two outbreaks in Germany involved laying hens (n = 13) and a mix of laying hens (n = 25) and ducks (n = 20), both with outdoor access, while the outbreak in Lithuania concerned a mix of chickens (n = 57) and turkeys (n = 3) without outdoor access. In the Netherlands, mute swans (n = 15) and greylag geese (n = 10) were affected alongside ducks (n = 135) and chickens (n = 12) in a hobby establishment with outdoor access. In Poland, a non-commercial establishment with 500 laying hens was affected. In three outbreaks (60%), indirect contact with wild birds was considered the most likely source of introduction, while direct contact with wild birds was suspected in one outbreak (20%). In the Polish outbreak (20%, 1/5), no outdoor access was provided, and indirect contact with poultry was identified as the most likely source of

introduction. Mortality was reported in almost all affected establishments (80%, 4/5), with clinical signs only observed occasionally.

Considering the entire epidemiological year from 1 October 2025 to 28 August 2026, the end of the current reporting period, a total of 238 HPAI A(H5N1) outbreaks were reported in captive birds, with non-commercial backyard and hobby establishments providing outdoor access accounting for the largest proportion of affected establishments. However, several outbreaks in zoos and similar establishments exhibiting birds to the public were reported during the autumn and winter periods. Most outbreaks in captive birds during this period occurred in Germany (31%, 73/238), followed by Czechia (15%, 35/238) and France (13%, 31/238).

Wild birds

During the current reporting period from 5 June to 28 August 2026, 103 HPAI A(H5N1) virus detections in wild birds (with one HPAI virus detection potentially including more than one wild bird species) were reported in 11 countries in Europe: Germany (46), Netherlands (31), Norway (11), Denmark (3), United Kingdom (excluding Northern Ireland) (3), Belgium (2), Portugal (2), Sweden (2), Austria (1), Finland (1) and Poland (1) (Table 1, Figure 2).

This number represented an 87% reduction compared to the previous reporting period (797) (Figure 3) and a 45% reduction compared to the same period of the previous epidemiological year, when the virus was more widespread across the continent (EFSA, ECDC and EURL, 2026a). Regarding the wild bird categories involved and considering that more than one wild bird species can be included in a single HPAI virus detection, HPAI A(H5N1) was mostly recorded in waterfowl (82.5%, 85/103), followed by colony-breeding seabirds (8.7%, 9/103), 'other' wild bird species (4.9%, 5/103) and raptors (3.9%, 4/103) (Figure 6).

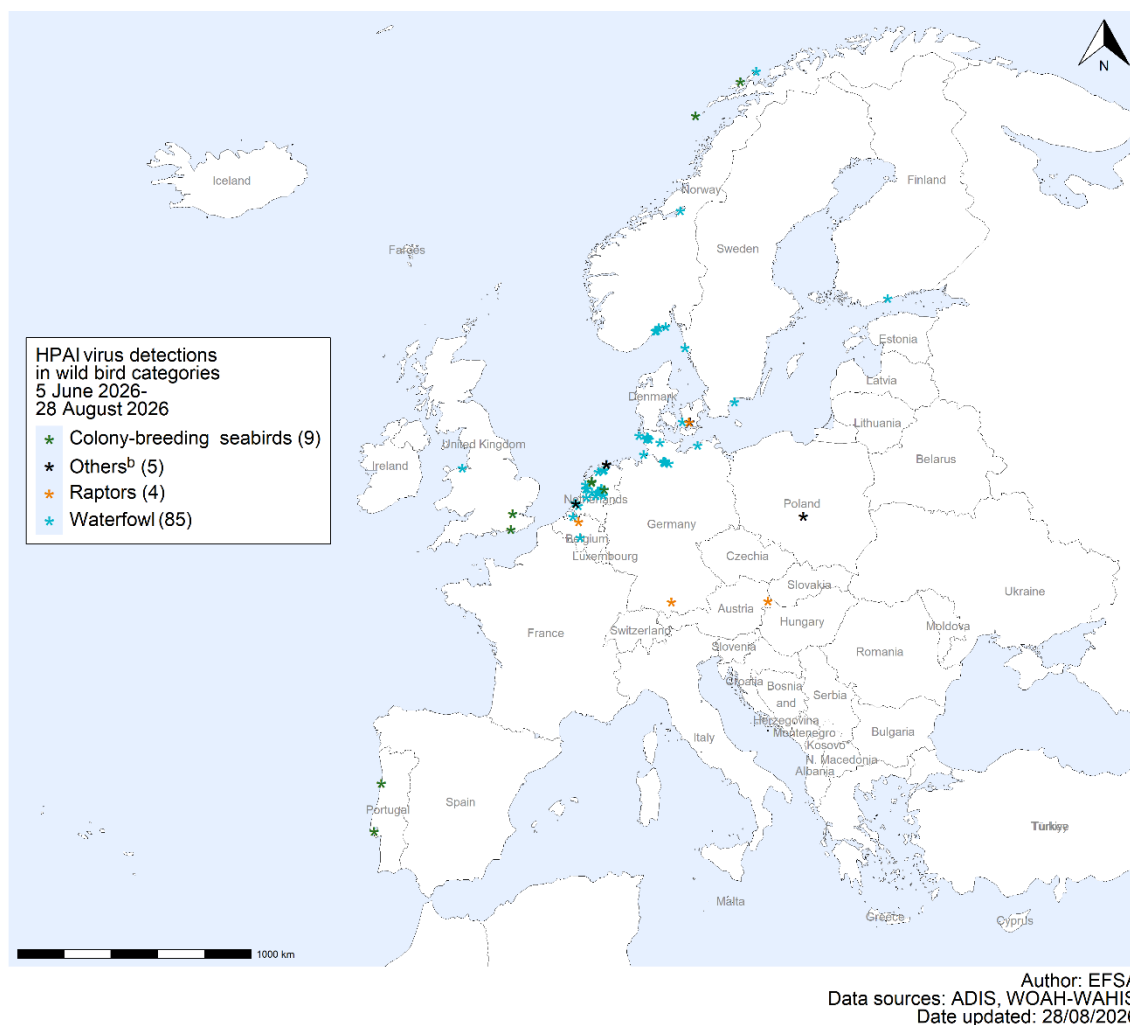


Figure 6: Geographic distribution, based on available geocoordinates, of HPAI virus detections in different categories of wild birds in Europe, by species category, from 5 June to 28 August 2026.

Note: 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).

^a Mixed, outbreaks in which multiple species or categories were involved.

^b Others, all other affected categories which are not indicated in the legend.

* 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.

Source: ADIS and WOA-H-WAHIS (data extraction carried out on 28 August 2026).

The proportion of HPAI virus detections in waterfowl was higher during the current (82.5%) compared to the previous reporting period (65%), while in raptors it was lower (3.9% vs 18%). For colony-breeding seabirds (8.7% vs 10%) and 'other' wild bird species (4.9% vs 6%), the proportions were nearly the same. The HPAI virus detections in the far north (Norway) and southwestern Europe (Portugal) were reported in colony-breeding seabirds, while the few detections in raptors were not co-localised with those in other wild bird species. This distribution

is strikingly different from that in the same period last year, when HPAI was mainly detected in colony-breeding seabirds (75%, 139/186) and much less frequently in waterfowl (12%, 23/186).

The wild bird species in which HPAI viruses were detected between 5 June and 28 August 2026 belonged mainly to the order Anseriformes (83%, 85/103), among which the main Anseriformes identified to species level were the greylag goose (49 during the current vs 198 during the previous reporting period), mute swan (9 vs 127) and Canada goose (7 vs 33) (Figures A.1–A.2⁸ in Annex A). Indeed, breeding bird indices for greylag geese have steadily increased in recent years in parts of northwestern Europe, including Norway, Sweden, Denmark and the Netherlands (EGMP Data Centre, 2026). Among the colony-breeding seabirds, at least 5 different species of gulls were affected: European herring gull (2 vs 25), Caspian gull (2 vs 1), yellow-legged gull (2 vs 2), black-headed gull (1 vs 13) and great black-backed gull (1 vs 3). One other bird of the order Laridae could not be identified to species level. The complete list of wild bird species affected by HPAI between 5 June and 28 August 2026 is reported in Figure A.1 in Annex A. The proportion of HPAI-affected wild birds that could not be identified to species level was 16% (16/103), comparable to that reported during the previous reporting period (15%, 121/814) (Figures A.1–A.2 in Annex A).

During the current reporting period, there were no reports (in the media or elsewhere) of unusual mortality events of wild birds from HPAI in Europe. The picture of HPAI-associated mortality of wild birds is, however, incomplete, as reporting counts of dead wild birds in association with HPAI is not part of the current avian influenza surveillance system in Europe. Available data largely rely on voluntary efforts in some countries and media reports. Additionally, only a small proportion of wild birds found dead are submitted for HPAI testing. Therefore, HPAI virus detections in wild birds generally underestimate the number of wild birds actually dying from A(H5) virus infection.

Between 5 June and 28 August 2026, no further HPAI A(H5N5) virus detections were reported in wild birds in Europe. However, a total of seven HPAI A(H5N5) virus detections were reported in wild birds in the 2025–2026 epidemiological year up to 28 August 2026, distributed across colony-breeding seabirds (3/7), raptors (2/7) and other wild bird species (2/7) (Table 2). The two Eurasian buzzards and the European herring gull were reported in the United Kingdom, the two common ravens and the black-legged kittiwake were reported in Iceland, and the black-headed gull was reported in Denmark.

⁸ Note that Figures A.1–A.2 in Annex A provide information on the numbers of wild bird orders/families/species that were detected as HPAI-affected at single bird level, as more than one bird can be involved in a single HPAI virus detection reported.

Table 2: Number of HPAI A(H5N5)-affected birds per wild bird category and species in the 2025–2026 epidemiological year.

Wild bird category	Species	Number of affected birds
Colony-breeding seabirds (3)	Black-headed gull	1
	Black-legged kittiwake	1
	European herring gull	1
Raptors (2)	Eurasian buzzard	2
Others (2)	Common raven	2
Total		7

Source: ADIS and WOA-H-WAHIS (data extraction carried out on 28 August 2026).

Considering the entire epidemiological year from 1 October 2025 to 28 August 2026, the end of the current reporting period, the most frequently HPAI-affected wild bird category was waterfowl (57.5%, 4029/7000), followed by ‘other’ wild bird species (mostly common cranes) (23%, 1630/7000), raptors (10.5%, 737/7000) and colony-breeding seabirds (6%, 419/7000). Another 185 (3%) outbreaks involved mixed wild bird species. During this time, the most striking aspects were the high number of HPAI virus detections in common cranes along the West European flyway in autumn 2025, and the high number of HPAI virus detections in waterfowl between October 2025 and April 2026, with two peaks (one in November 2025, the other in February 2026) (Figure 3).

As part of the SENTINEL Wild Birds project (Söderquist et al., 2026), 18,851 samples collected from 11,017 trapped or hunted apparently healthy wild birds were analysed between 15 August 2025 and 15 August 2026. The sampled birds represented 98 species across 14 countries and nine surveillance nodes in and near Europe. During this period, 1,031 birds tested positive to avian influenza virus (AIV), corresponding to an overall bird-level prevalence of 9.4%. Mallards (3269 individuals sampled) and Eurasian teals (2300 individuals sampled) were the most frequently sampled species, with AIV prevalences of 19% and 11%, respectively. HPAI virus was detected in 93 samples from 89 birds across eight countries, with most HPAI-positive samples reported from the Netherlands, Italy and Sweden. Among the HPAI-affected birds were mallards (n = 58), Eurasian teals (n = 24), Eurasian spoonbills (n = 3), common pochards (n = 2), a Tundra bean goose (n = 1), a mute swan (n = 1), a northern shoveler (n = 1), a gadwall (n = 1), a Eurasian wigeon (n = 1) and a great crested grebe (n = 1). Genomic analyses generated 204 avian influenza virus sequences, including 72 H5 and 132 non-H5 viruses representing a wide diversity of subtypes. Most HPAI viruses belonged to the HPAI A(H5N1) clade 2.3.4.4b EA-2024-DI.2.1 genotype, which was also the predominant genotype reported in Europe during the 2025-2026 epidemiological year. The project moreover generated a large proportion of the European LPAI genomic sequences currently available in GISAID.

2.1.2 HPAI virus detections in birds outside Europe

An overview of HPAI virus detections in birds reported to WOA-H from countries outside Europe between 5 June and 28 August 2026 is presented in Table 3 and Figure 7.

Table 3: Number of HPAI virus detections in non-European countries notified to WOA, by virus subtype and country, from 5 June to 28 August 2026. Cumulative numbers since the start of the 2025–2026 epidemiological year are reported in parentheses (1 October 2025 to 28 August 2026).

Region (total in season)	Country	Domestic birds					Wild birds							Total
		A(H5N1)	A(H5N9)	A(H5Nx)	A(H7N3)	A(Not typed)	A(H5N1)	A(H5N5)	A(H5N6)	A(H5N9)	A(H5Nx)	A(H7N3)	A(Not typed)	
Africa (64)	Côte d'Ivoire	0 (1)	-	-	-	-	-	-	-	-	-	-	-	0 (1)
	Namibia	-	-	-	-	-	0 (2)	-	-	-	-	-	-	0 (2)
	Nigeria	1 (30)	-	-	-	-	-	-	-	-	-	-	-	1 (30)
	Senegal	0 (1)	-	-	-	-	-	-	-	-	-	-	-	0 (1)
	South Africa	0 (6)	-	-	-	-	1 (19)	-	-	-	-	-	-	1 (25)
	Togo	5 (5)	-	-	-	-	-	-	-	-	-	-	-	5 (5)
Americas (846)	Argentina	0 (20)	-	-	-	-	0 (4)	-	-	-	-	-	-	0 (24)
	Brazil	1 (4)	-	-	-	-	2 (3)	-	-	-	-	-	-	3 (7)
	Canada	0 (109)	-	-	-	-	0 (2)	0 (5)	-	-	0 (1)	-	-	0 (117)
	Cayman Islands	0 (1)	-	-	-	-	-	-	-	-	-	-	-	0 (1)
	Chile	1 (38)	-	-	-	-	0 (10)	-	-	-	-	-	-	1 (48)
	Colombia	1 (9)	-	-	-	-	-	-	-	-	-	-	-	1 (9)
	Costa Rica	-	-	-	-	-	1 (1)	-	-	-	-	-	-	1 (1)
	Ecuador	-	-	-	-	-	1 (1)	-	-	-	-	-	-	1 (1)
	Guatemala	0 (1)	-	-	-	-	-	-	-	-	-	-	-	0 (1)
	Honduras	1 (1)	-	-	-	1 (1)	-	-	-	-	-	-	5 (6)	7 (8)
	Mexico	0 (1)	-	-	0 (6)	-	0 (5)	-	-	-	-	3 (3)	-	3 (15)
	Peru	28 (75)	-	-	-	-	7 (17)	-	-	-	-	-	-	35 (92)
	Uruguay	7 (478)	-	0 (7)	-	-	0 (5)	-	-	-	0	-	-	7 (514)
	US	-	-	-	-	-	-	-	-	-	(24) 0 (8)	-	-	0 (8)
Antarctica (1)	Heard Island and McDonald Islands	-	-	-	-	-	0 (1)	-	-	-	-	-	-	0 (1)
Asia (559)	Bhutan	1 (4)	-	-	-	-	-	-	-	-	-	-	-	1 (4)
	Cambodia	0 (6)	-	-	-	-	-	-	-	-	-	-	-	0 (6)
	China	-	-	-	-	-	0 (1)	-	-	-	0 (1)	-	-	0 (2)
	India	0 (26)	-	-	-	-	0 (5)	-	-	-	-	-	-	0 (31)
	Indonesia	0 (15)	-	-	-	-	-	-	-	-	-	-	-	0 (15)
	Iraq	0 (4)	-	-	-	-	-	-	-	-	-	-	-	0 (4)
	Israel	0 (2)	-	-	-	-	0 (12)	-	-	-	-	-	-	0 (14)
	Japan	0 (24)	-	-	-	-	0	0 (1)	-	-	0	-	-	0 (188)
							(137)				(26)			

Avian influenza overview June–August 2026

Oceania (67)	Mongolia	-	-	-	-	-	0 (1)	-	-	-	-	-	-	0 (1)
	Nepal	24 (91)	-	-	-	-	1 (2)	-	-	-	-	-	-	25 (93)
	Philippines	2 (44)	-	0 (1)	-	-	-	-	-	-	-	-	-	2 (45)
	Russia	-	-	-	-	-	0 (2)	-	-	-	-	-	-	0 (2)
	South Korea	0 (56)	0 (5)	-	-	-	0 (52)	-	0 (1)	0 (10)	-	-	-	0 (124)
	Taiwan	2 (26)	-	-	-	-	0 (2)	-	-	-	-	-	-	2 (28)
	Viet Nam	0 (2)	-	-	-	-	-	-	-	-	-	-	-	0 (2)
	Australia	-	-	-	-	-	64 (64)	-	-	-	-	-	-	64 (64)
	New Zealand	-	-	-	-	-	3 (3)	-	-	-	-	-	-	3 (3)
Total		74 (1080)	0 (5)	0 (8)	0 (6)	1 (1)	80 (351)	0 (6)	0 (1)	0 (10)	0 (60)	3 (3)	5 (6)	163 (1537)

–, no HPAI outbreaks were notified via WOA–WAHIS.

Source: WOA–WAHIS (data extraction carried out on 28 August 2026).

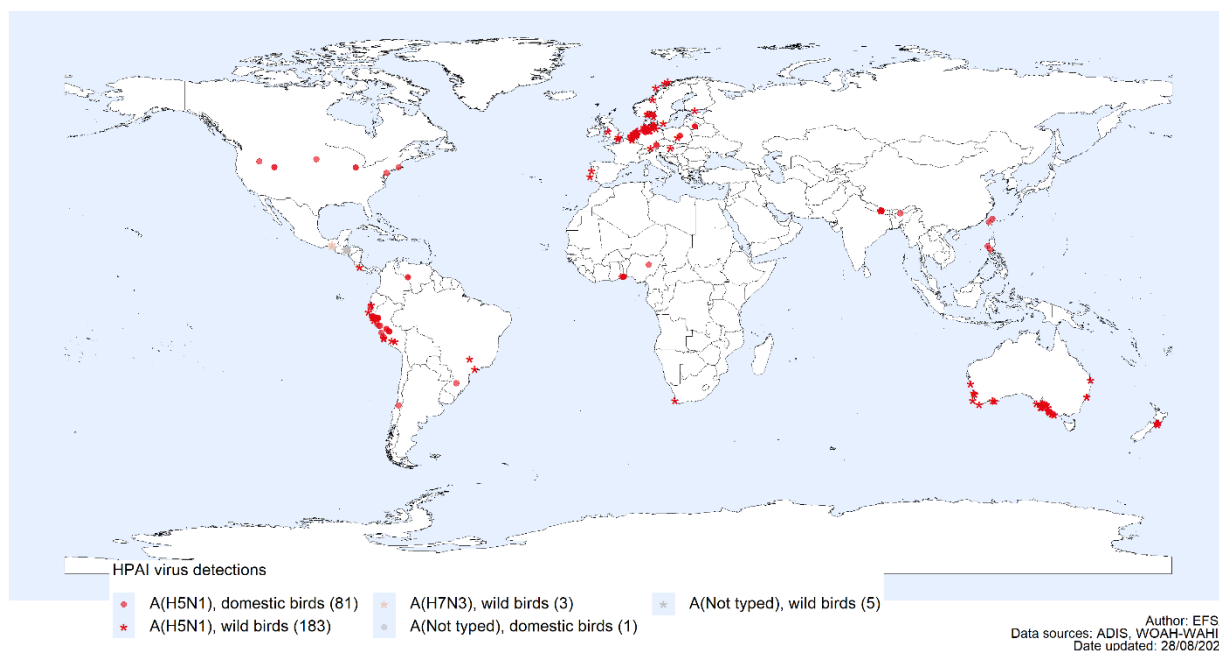


Figure 7: Geographic distribution, based on available geocoordinates, of HPAI virus detections reported worldwide in domestic (82) and wild (191) birds by virus type, from 5 June to 28 August 2026.

Source: ADIS and WOA-H-WAHIS (data extraction carried out on 28 August 2026).

Compared to the previous reporting period, the total number of HPAI virus detections in domestic and wild birds officially notified to WOA-H from outside Europe decreased from 448 to 163 (decrease of 64%), and the number of reporting countries outside Europe also decreased from 23 to 18 (Table 3, Figure 7). Compared to the same period last year, the number of official notifications to WOA-H during the current reporting period was about 46% higher than the number of outbreaks reported between 5 June and 28 August 2025 (163 vs 112 outbreaks).

The tables and figures presented in this report only include data extracted from WOA-H-WAHIS on 28 August 2026. However, HPAI virus detections in domestic and wild birds are also reported to the public via different means. Information on these detections obtained from additional sources has been incorporated into the text below.

In Africa, the number of HPAI outbreaks officially notified to WOA-H declined from 14 during the previous reporting period to seven during the current reporting period. All seven outbreaks were caused by HPAI A(H5N1) viruses, with the majority (6/7) reported from West Africa. As described in the previous report (Table A.1 in Annex A), the epidemic in poultry continued in Nigeria, with one small establishment (1400 birds) affected this time. In Togo, five small-sized establishments (500–6040 birds per establishment) were involved. During the current reporting period, South Africa officially notified WOA-H of a single HPAI outbreak in a wild bird, affecting a Hartlaub's gull.

In the Americas, the number of HPAI virus detections in domestic and wild birds officially reported to WOA-H from North America declined substantially between the previous and current reporting periods, decreasing from 103 to 7 in the US and from 10 to none in Canada (Table A.1 in Annex A). In the US, six outbreaks in poultry (wide range of establishment sizes: 81 to more than 1.2 million birds) and one outbreak in captive birds (48 birds) were officially notified to WOA-H. The United States Department of Agriculture (USDA), in the same period, reported 16



outbreaks in all types of poultry establishments (USDA, online-a), including also three outbreaks in live bird markets. While no reports of HPAI virus detections in wild birds were available via WOAHA-WAHIS, the USDA reported 176 detections of HPAI A(H5) virus in wild birds, including American crow, bald eagle, black vulture, blue-winged teal, Canada goose, Caspian tern, cinnamon teal, common eider, common tern, Eurasian collared dove, gadwall, goose, greater white-fronted goose, herring gull, killdeer, mallard, mute swan, Northern pintail, pelican, peregrine falcon, redhead duck, red-shouldered hawk, red-tailed hawk, rock pigeon, sandhill crane and wood duck. A total of 27 wild bird species were affected, and most cases were reported in mallard (82 cases), common eider (15 cases) and Canada goose (14 cases) (USDA, online-b). In contrast, no HPAI virus detections have been reported on the website of the Canadian Food Inspection Agency since May 2026 (CFIA, online). However, the media reported an HPAI A(H5N1) virus detection in a herring gull (CBC, online). In Central and South America, as a continuation from the previous reporting period, Brazil officially reported to WOAHA three HPAI A(H5N1) virus detections, comprising one outbreak in a captive bird flock (198 birds) and two outbreaks in wild white-faced whistling ducks. The media furthermore reported HPAI A(H5N1) in wild birds in Ibirapuera Park, São Paulo, with a collared teal (G1 Sao Paulo, online), a mallard and a white-faced whistling duck affected (UOL Notícias, online). After reporting a larger number of outbreaks during the previous reporting period, Chile notified WOAHA of one HPAI A(H5N1) outbreak in captive birds, affecting a flock of 201 birds. The media also reported HPAI A(H5N1) in black-necked swans from the Los Ríos region (Chilevision, online; Informa al minuto, online), a turkey vulture (Está Pasando, online), a Peruvian booby from Iquique (Vilas Radio, online) and a Garuma gull from Coquimbo (SAG, online). During the current reporting period, Colombia officially notified WOAHA of one outbreak in a captive bird flock comprising 190 birds. Costa Rica and Ecuador each officially reported one outbreak in a wild bird, affecting a blue-footed booby and a Peruvian pelican, respectively. Honduras officially reported to WOAHA seven HPAI outbreaks between 5 June and 28 August 2026, with an A(H5N1) outbreak in a large poultry establishment (> 42,000 birds), an outbreak (not typed) in captive birds (684 birds), as well as five outbreaks (not typed) in wild birds, all affecting black vultures. The media mentioned a poultry outbreak in which 2800 breeding birds died (Beacon, online), as well as 320 dead wild birds (most of which were black vultures) in western Honduras (El Heraldo, online; Hondudiario, online). Mexico officially reported three HPAI A(H7N3) outbreaks to WOAHA during the current reporting period, all in plain chachalacas. Over the January–July 2026 period, the media reported both HPAI A(H5N1) and A(H7N3) in Mexico, with 11 outbreaks and 23,881 birds affected for A(H5N1) in poultry, while A(H7N3) was reported in a backyard farm, subsequently in two poultry establishments with vaccinated birds and laying hens (Diario de Yucatán, online) and wild chachalacas (Pulso, online; Tiempo, online). Peru officially reported 28 HPAI A(H5N1) outbreaks in poultry and seven detections in wild birds during the current reporting period. The poultry outbreaks occurred predominantly in very small establishments, including two commercial poultry establishments with fewer than 400 birds and 26 captive bird establishments housing between 1 and 81 birds. Among wild birds, detections were reported in both waterfowl and colony-breeding seabirds, including two outbreaks in Andean geese, three in Peruvian pelicans, one in a Peruvian booby and one in a sooty shearwater. For Peru, still, the media reported outbreaks in many backyard establishments (e.g. in the Lambayque region) (Infobae, online-a), as well as outbreaks in fighting cocks (Infobae, online-b; MPU, online).

No new HPAI outbreaks were reported from Antarctica between 5 June and 28 August 2026.

However, HPAI A(H5) outbreaks continued to be officially reported to WOAHA from Asia, with a total of 30 outbreaks recorded during the current reporting period, representing a marked



decrease compared to the previous reporting period (193 reported outbreaks then; Table 3, Table A.1 in Annex A). In Bhutan, a small-sized poultry establishment (1100 birds) was affected. As reported in the previous reporting period (Table A.1 in Annex A), the poultry epidemic in Nepal continued during the current reporting period, with 25 HPAI A(H5N1) outbreaks officially notified to WOA across establishments ranging in size from 400 to 18,000 birds. An HPAI A(H5) virus detection was also reported in a black-faced ibis. Media reports also provided details on an outbreak at Kathmandu Zoo from mid-June 2026, affecting 65 animals. Mortality was reported among birds belonging to more than 20 species (e.g. barn owl, common pigeon, greylag goose, Himalayan griffon, house crow, swan, sarus crane), with HPAI A(H5) virus infection confirmed in affected birds (Mongabay, online a-b). In addition, media reports summarised the outbreaks reported over recent months, with 162 affected establishments and approximately 835,000 birds involved across 12 districts (The Kathmandu Post, online). The Philippines and Taiwan each officially reported two HPAI A(H5N1) outbreaks to WOA during the current reporting period. The outbreaks in the Philippines occurred in small poultry establishments, while those in Taiwan affected establishments comprising approximately 25 and 120,000 birds, respectively. According to the media, 100,278 quails were affected and unusual mortality was observed (Central News Agency, online). Finally, the media reported outbreaks in ducks in Viet Nam, with 1100 ducks affected in Lai Thanh commune (Danviet, online) and 400 ducks in Tan Thoi commune (Saigon, online). Media reports also provided a summary of outbreaks reported since the beginning of 2026, indicating that 80 outbreaks had occurred across 17 provinces and cities, resulting in the death or compulsory culling of more than 349,400 poultry (Channuoi, online). Due to the high HPAI A(H5N1) virus burden in 2026, the Vietnamese Department of Livestock and Veterinary Services has called for strengthened measures to prevent and control the disease.

In Oceania, the first detection of HPAI A(H5N1) virus in a brown skua on mainland Australia, located on the country's western coast, was reported in June 2026 and is described in the previous report (EFSA, ECDC and EURL, 2026a). Between 5 June and 28 August 2026, Australia officially notified 64 HPAI A(H5N1) virus detections in wild birds to WOA. The five affected species or orders were greater crested tern (46 cases), southern giant petrel (15 cases), Procellariidae (2 cases), brown skua (1) and northern giant petrel (1 case). According to the Australian Government (Australian Government, online), further detections were reported in Australasian gannet, Australian magpie, Australian raven, black-faced cormorant, brown falcon, fluttering shearwater, forest raven, great pied cormorant, Hutton's shearwater, little penguin, little raven, Pacific gull, peregrine falcon, silver gull, sooty oystercatcher, southern boobook, white-fronted tern and white-headed petrel, most of which were reported from South Australia and Victoria. In parallel, the Australian media and governmental sources reported mass mortality events, particularly in greater crested tern colonies in South Australia, where more than 1000 birds died across several breeding sites (Australia Government, online; The Guardian, online-a), with indication of spread to local wild bird species (The Maitland Mercury, online). Mortality of 28 little penguins was reported on King Island in Tasmania (News24, online). As a response, preventive vaccination of approximately 5000 little penguins was implemented on Phillip Island to protect this vulnerable species (Agriculture Victoria, online). New Zealand officially reported two HPAI A(H5N1) virus detections in wild birds to WOA during the current reporting period, involving a brown skua and a swamp harrier. In addition, the media reported HPAI A(H5N1) virus infection in a northern giant petrel (Xinhua News, online). Following these detections, mandatory biosecurity measures were introduced (Devdiscourse, online), and a vaccination programme targeting approximately 300 breeding individuals of five critically endangered bird species was initiated (CNN Brasil, online).

The incursion of HPAI A(H5N1) virus into Oceania initially affected a small number of migratory seabirds on the west coast of Australia and subsequently spread to local seabird species in the south of the country. To date, however, the outbreak has remained largely confined to a limited number of species. Given that several seabird species winter along the southern coast of Australia and migrate to New Zealand, including the white-fronted tern, further outbreaks in wild birds may occur in Oceania, particularly in New Zealand, in the coming months.

A list of all wild bird species that were reported to WOA as HPAI-affected from outside Europe between 5 June and 28 August 2026 is presented in Table A.2 in Annex A.

Considering the past seven epidemiological years, the timing and heights of the peaks of HPAI virus detections officially reported to WOA between 2019–2020 and 2025–2026 were variable between wild and domestic birds, as well as among continental regions (Figure 8).

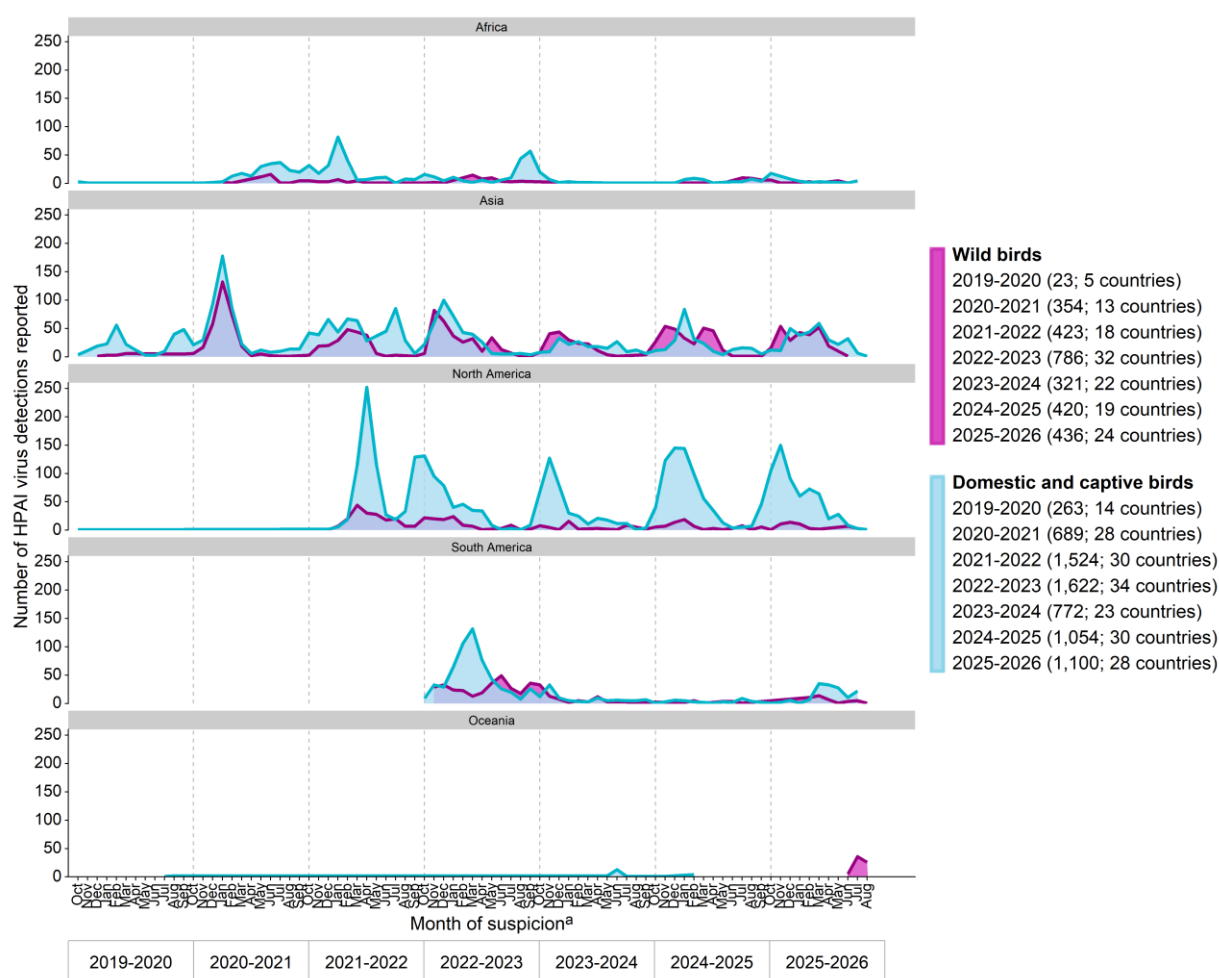


Figure 8: Distribution of the number of HPAI virus detections in wild birds (cumulative $n = 2763$) (pink) and domestic birds (cumulative $n = 7024$) (blue) that were reported to WOA from non-European countries during seven epidemiological years by month of suspicion, from 1 October 2019 to 28 August 2026.

Source: WOA-WAHIS (data extraction carried out on 28 August 2026).

In Africa, detections occurred at generally low levels, with irregular peaks reported in different months, such as February and September, without a consistent seasonal pattern in either wild



or domestic birds. Similarly, in South America, the timing of peaks was sporadic and variable, occurring in months such as March, May, September and November in both wild and domestic birds. In contrast, Asia exhibited a clear seasonal pattern, characterised by annual peaks during the winter months (November to February) that were synchronised between wild and domestic birds. Additional, smaller increases in detections among wild birds were observed during spring and summer. North America also showed a distinct seasonal trend, with recurrent peaks occurring during autumn and winter (September to January) in both wild and domestic birds. No clear seasonal pattern was evident in Oceania. HPAI detections remained at very low levels throughout the period, with only a minor peak observed in wild birds in July 2026 and a single, similarly low peak in domestic birds in June 2024.

Taking also the seasonal patterns observed in Europe (Figure 1), the pattern of virus detections in continental regions of the northern hemisphere (Europe, Asia, North America) showed some similarities. In most epidemiological years, there were annual winter peaks of virus detection in both wild and domestic birds. Also, in Europe and Asia these winter peaks in wild birds generally coincided with those in domestic birds. This pattern fits with increased circulation of HPAI virus in wild waterfowl in the boreal autumn and winter (when they migrate from their breeding areas to their wintering areas), and higher risk of transmission from wild birds to domestic birds. Besides winter peaks, there also were additional spring or summer peaks of virus detection in wild birds in Europe and Asia, which were not temporally associated with peaks of virus detection in domestic birds. This pattern fits, at least in Europe, with increased circulation of HPAI virus in colony-breeding seabirds in the boreal spring and summer (when they aggregate and raise their young at breeding colony sites). In continental regions of the southern hemisphere (Africa, South America, Oceania), a clear seasonal pattern in the peaks of virus detections in wild or domestic birds is not apparent. In part, this could be due to the absence of a significant seasonal migration of waterfowl in those regions.

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. (2024a) and the tool GenIn2 (<https://github.com/izsvenezie-virology/genin2>). Mutation analyses of the HPAI A(H5N1) viruses have been performed using FluMut (Giussani et al., 2025) with the FluMutDB v6.4 mutation database (<https://github.com/izsvenezie-virology/FluMutDB>).

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

Since October 2025, more than 2600 complete genome sequences of European viruses from 31 countries have been characterised. All the viruses belong to clade 2.3.4.4b, which is the only clade detected in Europe since 2016.

Based on the genetic data available as of 9 September 2026, during the 2025–2026 epidemiological year, the vast majority (> 90%) of the sequenced viruses belonged to a single genotype, EA-2024-DI, sublineage EA-2024-DI.2.1. This genotype has been detected in wild (mainly Anseriformes) and domestic birds from all 31 European countries for which data are available, representing the most widespread genotype in Europe, extending north from Iceland to Finland and south from Portugal to Bulgaria, reaching as far as Ukraine and Georgia. In addition to EA-2024-DI.2.1, since September 2025, A(H5N1) genotypes circulating during the previous epidemic waves, namely EA-2024-DI.2, EA-2024-DT, EA-2022-BB, EA-2023-DA and the



A(H5N5) genotype EA-2021-I have been sporadically identified in a few geographical areas. Genotype EA-2024-DI.2 has been detected in wild (mainly Anseriformes) and domestic birds in western Europe (United Kingdom, France, Spain, Portugal), as well as in backyard flocks in Slovakia and Austria. The viruses collected in western Europe cluster together with EA-2024-DI.2 viruses that had been circulating over the spring and summer months in these areas, suggesting a persistent viral circulation in the wild bird population. In contrast, the sequences of viruses collected in Slovakia and Austria cluster alongside viruses identified in eastern Europe during the 2024–2025 epidemiological year. The most recent detection of this genotype dates back to February 2026.

Genotypes EA-2024-DT and EA-2022-BB continue to circulate mainly among Laridae and other colony-breeding seabirds in separate geographical areas: EA-2024-DT in France, Spain and Portugal; EA-2022-BB in Belgium, France, Norway and the United Kingdom. Genotype EA-2023-DA continues to be detected exclusively in poultry in Bulgaria and Czechia; this genotype had not been detected in wild birds during the previous (2024–2025) and the current epidemiological years in other regions of Europe or outside Europe. The viruses collected in Bulgaria and Czechia cluster separately in the phylogenetic trees suggesting an ongoing separate circulation in an unknown ecological or domestic niche in the two countries. The most recent detection of the EA-2023-DA genotype dates back to January 2026. The A(H5N5) genotype EA-2021-I was detected at the end of January 2026 in a black-headed gull in Denmark.

In addition to the known genotypes, several reassortant viruses, in almost all cases originating from reassortment events involving mainly the PB2, PB1 and NP gene segments between the EA-2024-DI.2.1 and LPAI viruses have been characterised in Europe. All these new reassortants have been sporadically detected in one or very few outbreaks within one or two countries, likely indicating low epidemiological relevance, except for three genotypes, namely EA-2026-FA, EA-2026-FB and EA-2025-FD, which have been identified since October 2025 in wild and domestic birds from 3–5 central and eastern European countries. Specifically, genotype EA-2026-FA has been detected in Romania, Germany, Czechia, Switzerland and Italy, genotype EA-2026-FB circulated in Poland, Denmark and Sweden, while genotype EA-2025-FD was detected in Germany, Czechia and Slovakia.

Based on the data currently available (< 35 genomic sequences) from nine countries (Belgium, Denmark, France, Germany, Lithuania, Netherlands, Norway, Sweden and the United Kingdom), during the current reporting period (June–August 2026), the majority (approximately 85%) of the characterised viruses belong to the EA-2024-DI.2.1 genotype, which has been identified in wild birds (mainly Anseriformes) and domestic birds in eight countries; approximately 9% belong to the EA-2022-BB genotype, identified in gulls in Norway and Belgium, while two viruses are new reassortants originating from the EA-2024-DI.2.1 and EA-2022-BB genotypes.

The global spread of the HPAI A(H5N1) of European EA-2024-DI.2 and DI.2.1 genotype

Outside Europe, the EA-2024-DI.2 was identified between the end of 2024 and the beginning of 2025 in wild and domestic birds in Israel, and more recently in West and South Africa (Abolnik, 2025; Hamunyela et al., 2026; FAO, online). The EA-2024-DI.2.1 genotype was detected in October 2025 in wild Anseriformes in Kazakhstan. Recently, two novel EA-2024-DI.2.1 reassortant viruses have been characterised from wild and domestic birds in different geographic areas in Japan (EPI_ISL_20448872 and EPI_ISL_20447464). Specifically, the PB1, PA, HA, NA and NS genes of both viruses are highly related to EA-2024-DI.2.1 viruses collected at the beginning of the current epidemiological year in Europe, while the remaining gene segments originated from separate reassortment events with LPAI viruses circulating in Asia. These

findings suggest that the genotype EA-2024-DI.2.1 spread from Europe to East Asia, where it has undergone reassortment with other viruses.

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 2025 indicate that these viruses do not contain critical mutations detected in previous pandemic strains in the receptor binding site of the HA protein, meaning that they continue to be well-adapted to avian species. Several mutations previously described in literature (Du et al., 2018; Suttie et al., 2019; Pinto et al., 2023) have been identified as being associated with i) enhanced polymerase activity and replication in mammals or mammalian cells, ii) increased virulence, iii) increased/conferred resistance towards antiviral drugs, iv) increased in vitro binding to human-type receptors $\alpha 2,6$ -SA, v) decreased antiviral response in ferrets, vi) evasion of human butyrophilin subfamily 3 member A3 (BTN3A3) and vii) disruption of the second sialic acid (SIA) binding site in the neuraminidase protein, with a frequency varying by distinct mutations. The net effect of these mutations on the biological characteristics of the viruses remains unclear, and further research is needed to improve existing knowledge.

Similar to the viruses collected during the previous epidemiological years (2020–2021, 2021–2022, 2022–2023, 2023–2024, 2024–2025), circulating European viruses contain some of the mutations in the receptor binding domain of the HA protein that have demonstrated to promote, to varying degrees, the recognition of human-type receptors of specific H5 viruses in vitro. In particular, some of them (i.e. S133A, S154N, T156A, H5 numbering) have been identified in the majority of the 2025–2026 A(H5N1) viruses, whilst others (i.e. D94N, G139R, HA1:S123P and HA2:R167K, T188I, N189D/T, P235S, E251K, S155N, V210I) have only sporadically been observed (≤ 53 viruses). The impact of these HA mutations on the biological characteristics of the circulating viruses is still unknown. Besides the mutations in the HA protein, it is important to mention that most of the A(H5N1) viruses belonging to the EA-2022-BB and EA-2023-DT genotypes contain mutations NP-Y52N and NA-A369I, which may increase their zoonotic potential due to the evasion of innate immunity and mammalian restriction factors or disruption of the second sialic acid binding site (2SBS).

Mutations associated with a reduced susceptibility of A(H5N1) viruses to the available antiviral drugs authorised for use in humans have rarely been identified in the circulating strains. Specifically, mutations associated with resistance to amantadine and rimantadine, NA and PA inhibitors (WHO, online-a) have been detected in approximately 1.2%, 0.9% and 0.4% of the analysed A(H5Nx) viruses collected in Europe since October 2025 ($n > 2600$), respectively. However, for PA inhibitors, it is important to mention that mutations have been studied in seasonal influenza viruses and not specifically in A(H5N1) viruses; the threshold of ≥ 3 IC₅₀ fold-change was used for the assignment of viruses with a reduced susceptibility to PA inhibitors.

Since October 2025, the K526R, E627K, M631L and D701N mutations in the PB2 protein associated with virus adaptation in mammals (Suttie et al., 2019) have been detected in 13 European viruses collected from outbreaks in birds, more specifically in i) twelve A(H5N1) viruses collected from domestic ($n = 5$), captive ($n = 1$) and wild birds ($n = 6$, mainly raptors) from nine different countries and ii) one A(H5N5) virus (genotype EA-2021-I) collected from a wild bird. Based on the available data, a decreased frequency of detection of such mutations has been observed in birds, from about 4% in the 2024–2025 epidemiological year to about 0.5% in the 2025–2026 epidemiological year (based on data available up to 9 September 2026). Of note, all the A(H5N5) viruses of genotype EA-2021-I that have been collected in Europe since November 2024 contain the PB2 E627K/V molecular marker of mammalian adaptation, suggesting that this mutation may have become fixed in this virus population.

2.1.4 Genetic characteristics of other avian influenza viruses with zoonotic potential in avian species

Low pathogenic avian influenza A(H9N2) clade G5.6 (Fusaro et al., 2024a) has been recently characterised from a sample collected in July 2025 from a backyard farm in Moldova. The virus clusters separately from H9 viruses commonly circulating in wild and domestic birds in Europe, which belong to clade Y8, as well as to the recently detected A(H9N2) viruses in poultry in Hungary and a human case in Italy, which belong to clade G5.5. Clade G5.6 is circulating mainly in domestic birds in the Middle East and Russia, and has not previously been detected in birds in the EU/EEA. Specifically, the virus from Moldova clusters with A(H9N2) viruses detected in domestic and wild birds in Russia between 2018 and 2025. The long branches separating the Hungarian viruses from their progenitors suggest a significant gap of data. No human cases have been associated with this clade.

Similarly to the majority of the A(H9N2) viruses of lineages G and B, they possess the HA-Q226L mutation (H3 numbering), which is associated with preferential binding to human-like α 2-6-linked sialic acid (SA α 2-6) receptors. In addition, the virus possesses the PB2-E627V mutation, which has been described as a potential marker for zoonotic spread (Guo et al., 2025).

2.2 HPAI virus detections in non-human mammals

Between 5 June and 31 August 2026, HPAI A(H5) virus detections were reported in wild mammals in Europe, while detections outside Europe involved wild, captive and domestic mammals. The data described in this report were actively collected from Member States and other European countries, retrieved via WOA-H-WAHIS and from the USDA websites (for cases that occurred in the US), and supplemented with information from media reports (Table 4).

During the current reporting period, all HPAI A(H5) virus detections in mammals reported in Europe involved wild species. Through passive surveillance, HPAI virus infection was detected in two grey seals in Denmark (A(H5N1)), one harbour seal in Sweden (A(H5N1)) and one European pine marten in Finland (A(H5Nx)), all of which were found dead.

HPAI A(H5N1)-positive red foxes were retrospectively reported from Denmark ($n = 2$) and Finland ($n = 1$). Norway moreover retrospectively reported the detection of HPAI A(H5) virus in an Arctic fox that was trapped during active surveillance activities in November 2025. Additionally, a second polar bear from Svalbard was found positive to HPAI A(H5N5) virus, following an earlier report from the same area (Norwegian Veterinary Institute, online). According to an unpublished study, antibodies against HPAI A(H5) viruses were detected in 75% of polar bears from the area sampled in 2023 ($n = 36$) and in 97% of those sampled during 2024–2025 ($n = 65$). These findings suggest widespread circulation of HPAI A(H5) viruses in the polar bear population following the first detections in birds in 2022. In contrast, no antibodies were detected in samples collected between during 2014–2022 ($n = 243$) (Madslien et al., 2026).

At the same time, several European countries with variable testing efforts actively reported the absence of HPAI viruses in mammals during the current reporting period: Germany, Luxembourg, Slovakia. Austria moreover shared detailed test results of analyses performed in mammals, all of which resulted negative: pig ($n = 61$), fox ($n = 13$), horse ($n = 12$), badger ($n = 1$), marten ($n = 1$), sheep ($n = 1$) (personal communication by Sandra Revilla-Fernández, AGES).

Considering the entire epidemiological year from 1 October 2025 to 28 August 2026, the end of the current reporting period, HPAI virus detections in mammals were reported in Europe during most months, albeit at low levels. The number of detections peaked in late 2025 and remained relatively frequent through March 2026 before declining during spring and early summer.

Although only a few detections were reported at the beginning of June, numbers increased slightly again in August 2026. Most cases occurred in wild mammals, predominantly red foxes and raccoons, while detections in captive mammals and pets remained limited (Figure 9).

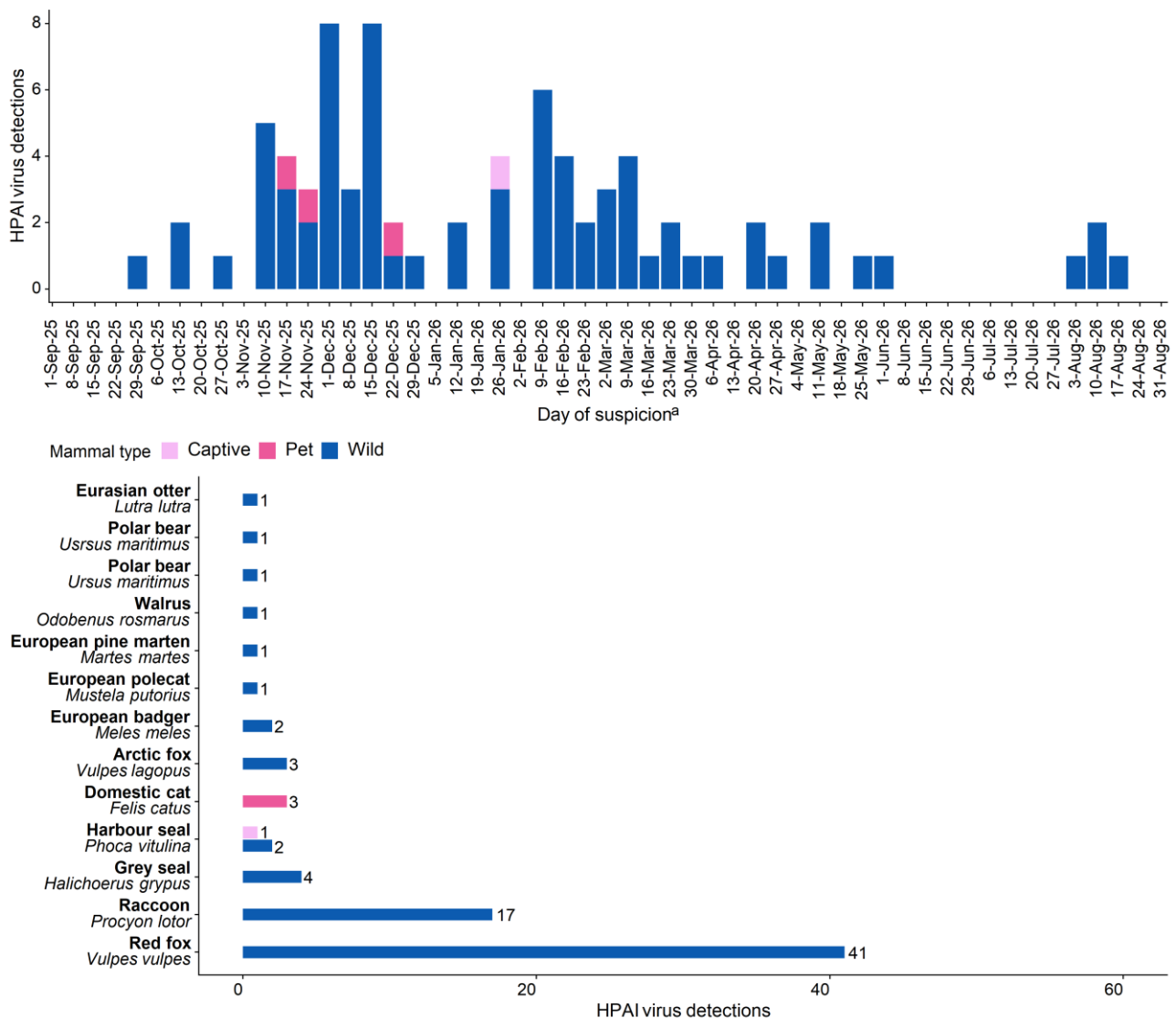


Figure 9: HPAI virus detections in mammals in Europe by date of suspicion and species, from 1 October 2025 to 28 August 2026.

Source: EFSA (data extraction carried out on 28 August 2026).

Outside Europe, most HPAI A(H5N1) virus detections in mammals continued to be reported from the US. As of 28 August 2026, the number of dairy cattle farms reportedly affected by the ongoing epidemic had increased by 67 to 1176 farms across 19 states, with most newly affected establishments located in Idaho, Texas and Utah (USDA, online-c). In addition, seven cases in captive American minks, likely from fur farms, were reported in Utah, representing the first detection of HPAI A(H5N1) virus in captive American minks in North America (USDA, online-d). Further detections were reported in two domestic cats and two striped skunks, all in Utah (USDA, online-d). The occurrence of HPAI A(H5N1) virus in captive American minks is of particular

concern given the species' susceptibility to influenza viruses and the potential implications for animal and public health. However, limited information is currently available on these cases.

Apart from the US, Australia reported the first detections of HPAI A(H5N1) virus in three long-nosed fur seals (Australian Government, online; RNZ, online; The Guardian, online-b), three red foxes (ABC, online-a; Australian Government, online), two common dolphins (ABC, online-b; Australian Government, online) and a bottlenose dolphin (Australian Government, online). These detections were reported in areas where mass die-offs of wild birds had also been observed. The long-nosed fur seal represents a newly affected species, with no previous reports of HPAI infection.

A retrospective report from Nepal indicated that, in mid-June 2026, avian influenza affected 65 animals from more than 20 species at Kathmandu Zoo, including civets, common leopards, jungle cats and leopard cats (Mongabay, online-a, b). According to media reports, all affected felids tested positive for A(H9) virus only, while birds in the zoo tested positive for both HPAI A(H5) and A(H9) virus (Mongabay, online-a).

Table 4: Avian influenza A(H5Nx) virus detections in mammalian species other than humans related to circulating viruses worldwide, 2016–2026.

A(H5N1) or A(H5Nx) clade 2.3.4.4b	Virus	Animal (order, family, species)		Country	Reference ^a
	Artiodactyla	Bovidae	Cattle (<i>Bos taurus</i>)	Netherlands ^b , US	Ballmann et al. (2026)
			Goat (<i>Capra hircus</i>)	US	
			Sheep (<i>Ovis aries</i>)	Norway, UK	Fosse et al. (2025), GovUK (online-a,b)
		Camelidae	Alpaca (<i>Lama pacos</i>)	US	
		Suidae	Pig (domestic) (<i>Sus scrofa</i>)	Italy ^b , US	Rosone et al. (2023)
	Pig (wild boar) (<i>Sus scrofa</i>)		Germany ^b	Günther et. al (2026)	
	Carnivora	Canidae	Arctic fox (<i>Vulpes lagopus</i>)	Finland, Norway	
			Common raccoon dog (<i>Nyctereutes procyonoides</i>)	Finland, Germany ^b , Japan, Sweden ^b	Günther et. al (2026)
			Coyote (<i>Canis latrans</i>)	US	
			Dog (<i>Canis lupus familiaris</i>)	Canada, Italy ^b , Poland	Szaluś-Jordanow et al. (2024)
			Gray fox (<i>Urocyon cinereoargenteus</i>)	US	
			Island fox (<i>Urocyon littoralis</i>)	US	
			Japanese raccoon dog (<i>Nyctereutes viverrinus</i>)	Japan	
			Red fox (<i>Vulpes vulpes</i>)	Australia, Austria, Belgium, Canada, Denmark, Estonia, Finland, France, Germany ^c , Ireland, Italy, Japan, Latvia, Luxembourg, Netherlands, Norway, Slovenia, Spain, Sweden ^c , UK, US	Günther et. al (2026) Australian Government (online)
			South American bush dog (<i>Speothos venaticus venaticus</i>)	UK	
		Felidae	Bobcat (<i>Lynx rufus</i>)	US	
			Canadian lynx (<i>Lynx canadensis</i>)	US	
			Caracal (<i>Caracal caracal</i>)	Poland, US	
			Cat (<i>Felis catus</i>)	Belgium, Canada, France ^c , Germany,	DutchNews (online), TF1 Info (online)

Virus	Animal (order, family, species)	Country	Reference ^a
		Hungary ^c , Italy ^b , Netherlands ^c , Poland, South Korea, US	
	Cheetah (<i>Acinonyx jubatus</i>)	US	
	Eurasian lynx (<i>Lynx lynx</i>)	Finland, Sweden ^b , US	
	Leopard (<i>Panthera pardus</i>)	India, US, Viet Nam	The Times of India (online-a)
	Leopard cat (<i>Prionailurus bengalensis</i>)	South Korea	
	Lion (<i>Panthera leo</i>)	India, Peru, US, Viet Nam	Hindustan Times (online), The Times of India (online-b)
	Mountain lion (<i>Puma concolor</i>)	US	
	Serval (<i>Leptailurus serval</i>)	Bangladesh, US	
	Tiger (<i>Panthera tigris</i>)	India, US, Viet Nam	Hindustan Times (online), The Times of India (online-a,b)
	Mephitidae	Striped skunk (<i>Mephitis mephitis</i>)	Canada, US
	Mustelidae	American marten (<i>Martes americana</i>)	US
		American mink (<i>Neovison vison</i>)	Canada, Finland, Spain, US
		Beech marten (<i>Martes foina</i>)	Netherlands
		Eurasian otter (<i>Lutra lutra</i>)	Finland, France, Netherlands, Sweden, UK
		European badger (<i>Meles meles</i>)	Germany ^c , Netherlands, Sweden
		European pine marten (<i>Martes martes</i>)	Finland, Germany
		European polecat (<i>Mustela putorius</i>)	Belgium, Denmark, Netherlands
		Ferret (<i>Mustela furo</i>)	Belgium, Poland, Slovenia
		Fisher (<i>Pekania pennanti</i>)	US
		Long-tailed weasel (<i>Neogale frenata</i>)	US
		Marine otter (<i>Lontra felina</i>)	Chile
		North American river otter (<i>Lontra canadensis</i>)	US
		Sea otter (<i>Enhydra lutris</i>)	US
		Southern river otter (<i>Lontra provocax</i>)	Chile
		Stoat (<i>Mustela erminea</i>)	US
	Odobenidae	Walrus (<i>Odobenus rosmarus</i>)	Norway
	Otariidae	Antarctic fur seal (<i>Arctocephalus gazella</i>)	South Georgia and the South Sandwich Islands, Uruguay
		California sea lion (<i>Zalophus californianus</i>)	US
		Long-nosed fur seal (<i>Arctocephalus forsteri</i>)	Australia
		Northern fur seal (<i>Callorhinus ursinus</i>)	Russia
		South American fur seal (<i>Arctocephalus australis</i>)	Argentina, Brazil, Peru, Uruguay
		South American sea lion (<i>Otaria flavescens</i>)	Argentina, Brazil, Chile, Peru, Uruguay
	Phocidae	Caspian seal (<i>Pusa caspica</i>)	Russia

Virus	Animal (order, family, species)	Country	Reference ^a
	Crabeater seal (<i>Lobodon carcinophaga</i>)	Joinville Island	Phys.org (online)
	Grey seal (<i>Halichoerus grypus</i>)	Canada, Denmark, Germany, Netherlands, Poland, Sweden ^c , UK, US	
	Harbour seal (<i>Phoca vitulina</i>)	Canada, Denmark, Germany, Japan, Netherlands, South Georgia and the South Sandwich Islands, Sweden, UK, US	The Mainichi (online)
	Northern elephant seal (<i>Mirounga angustirostris</i>)	US	
	Southern elephant seal (<i>Mirounga leonina</i>)	Argentina, South Georgia and the South Sandwich Islands, Possession Island	Banyard et al. (2024), Bennison et al. (2024) PASTAAF (online-a,b)
	Procyonidae		
	Raccoon (<i>Procyon lotor</i>)	Canada, Germany ^c , US	Günther et. al (2026)
	South American coati (<i>Nasua nasua</i>)	Germany, Uruguay	
	Ursidae		
	American black bear (<i>Ursus americanus</i>)	Canada, US	
	Asian black bear (<i>Ursus thibetanus</i>)	France	
	Brown bear (<i>Ursus arctos</i>)	US	
	Kodiak grizzly bear (<i>Ursus arctos horribilis</i>)	US	
	Polar bear (<i>Ursus maritimus</i>)	US	
	Cetacea		
	Delphinidae		
	Bottlenose dolphin (<i>Tursiops truncatus</i>)	Australia, Peru, US	
	Chilean dolphin (<i>Cephalorhynchus eutropia</i>)	Chile	
	Common dolphin (<i>Delphinus delphis</i>)	Australia, Peru, UK	Leguia et al. (2023) Australian Government (online)
	White-sided dolphin (<i>Lagenorhynchus acutus</i>)	Canada	
	Phocoenidae		
	Burmeister's porpoise (<i>Phocoena spinipinnis</i>)	Chile	
	Harbour porpoise (<i>Phocoena phocoena</i>)	Sweden, UK	
	Didelphidae		
	Virginia opossum (<i>Didelphis virginiana</i>)	US	
	Lagomorpha		
	Leporidae		
	Desert cottontail (<i>Sylvilagus audubonii</i>)	US	
	Rodentia		
	Cricetidae		
	Deer mouse (<i>Peromyscus</i> spp.)	US	
	Muskrat (<i>Ondatra zibethicus</i>)	US	
	Prairie vole (<i>Microtus ochrogaster</i>)	US	
	Black rat (<i>Rattus rattus</i>)	US	

Virus	Animal (order, family, species)		Country	Reference ^a
	Muridae	Brown rat (<i>Rattus norvegicus</i>)	Egypt, US	Kutkat et al. (2024)
		House mouse (<i>Mus musculus</i>)	US	
		House rat (<i>Rattus rattus</i>)	Egypt	Kutkat et al. (2024)
	Sciuridae	Abert's squirrel (<i>Sciurus aberti</i>)	US	
		Eastern gray squirrel (<i>Sciurus carolinensis</i>)	US	
		Round-tailed ground squirrel (<i>Xerospermophilus tereticaudus</i>)	US	
		Thirteen-lined ground squirrel (<i>Ictidomys tridecemlineatus</i>)	US	
A(H5N1) clade 2.3.2.1a	Carnivora	Felidae Cat (<i>Felis catus</i>)	India	Raut et al. (2025) The Times of India (online-c)
A(H5N5) clade 2.3.4.4b	Carnivora	Canidae Arctic fox (<i>Vulpes lagopus</i>)	Iceland, Norway	
		Red fox (<i>Vulpes vulpes</i>)	Canada, Norway	
		Felidae Bobcat (<i>Lynx rufus</i>)	Canada	
		Cat (<i>Felis catus</i>)	Canada, Iceland	
		Eurasian lynx (<i>Lynx lynx</i>)	Norway	
		Mephitidae Striped skunk (<i>Mephitis mephitis</i>)	Canada	
		Mustelidae American mink (<i>Neovison vision</i>)	Iceland	
		Eurasian otter (<i>Lutra lutra</i>)	Norway	
		European pine marten (<i>Martes martes</i>)	Netherlands	
		Odobenidae Walrus (<i>Odobenus rosmarus</i>)	Norway	
		Phocidae Grey seal (<i>Halichoerus grypus</i>)	UK	
A(H5N6) clade 2.3.4.4b	Carnivora	Ringed seal (<i>Pusa hispida</i>)	Canada	Yao et al. (2023) Zhao et al. (2024)
		Procyonidae Raccoon (<i>Procyon lotor</i>)	Canada	
A(H5N8) clade 2.3.4.4b	Carnivora	Ursidae Polar bear (<i>Ursus maritimus</i>)	Norway	Shin et al. (2019), Floyd et al. (2021) Floyd et al. (2021) Ärzteblatt (online), Avian Flu Diary (online), Outbreak News Today (online)
		Canidae Dog (<i>Canis lupus familiaris</i>)	China	
	Artiodactyla	Mustelidae American mink (<i>Neovison vison</i>)	China	
		Suidae Pig (domestic) (<i>Sus scrofa</i>) ^b	France	
		Pig (wild boar) (<i>Sus scrofa</i>) ^b	Germany	
	Carnivora	Canidae Red fox (<i>Vulpes vulpes</i>)	UK	
		Phocidae Grey seal (<i>Halichoerus grypus</i>)	Poland, Sweden, UK	
		Harbour seal (<i>Phoca vitulina</i>)	Denmark, Germany, UK	

^a References other than those mentioned under source.

^b Serological detection.

^c Both virological and serological detection.

Source: EFSA, USDA (USDA, online-c,d) and WOA-H-WAHIS (data extraction carried out on 28 August 2026).

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

Details on the nomenclature of the HPAI A(H5) viruses used in this section are reported in Appendix B. Genotypes are assigned using the criteria described in Fusaro et al. (2024b) and the tool GenIn2 (<https://github.com/izsvenezie-virology/genin2>). Mutation analyses of the A(H5N1) viruses have been performed using FluMut (Giussani et al., 2025) with FluMutDB v6.4 mutation database (<https://github.com/izsvenezie-virology/FluMutDB>).

Based on the genetic data available as of 9 September 2026, since October 2025 the complete or partial genome sequences of 43 HPAI A(H5N1) viruses of clade 2.3.4.4b collected from eight distinct mammalian species (beech marten, domestic cat, Eurasian otter, European badger, European polecat, harbour seal, grey seal, red fox) in 11 different European countries have been analysed. One virus collected in February from a red fox in the Netherlands belongs to a rare genotype, namely EA-2026-FE, while four viruses collected in March from a red fox, a Eurasian otter and a grey seal in Sweden, and a red fox in Denmark, belong to the A(H5N1) genotype EA-2026-FB. All the other characterised viruses from mammals belong to the A(H5N1) genotype EA-2024-DI.2.1. All the mammalian viruses cluster with viruses collected from wild or domestic birds from the same geographic area.

Of note, 37/43 (86%) viruses contain one or two of the PB2 molecular markers of mammalian adaptation (E627K, D701N, T271A, M631L), which have not been identified in the phylogenetically related viruses collected from avian species. Additionally, one virus acquired the PB2 substitutions E192K and Q591K (Yamada et al., 2010; Taft et al., 2015).

Finally, two HPAI A(H5N5) viruses collected in May 2026 on Svalbard, Norway, from a walrus and a polar bear were characterised. Both viruses belong to genotype EA-2021-I and cluster with a group of A(H5N5) viruses of the same genotype collected between November 2024 and April 2025 in northern Europe and Canada. All these viruses share the mammalian adaptive marker PB2-E627V.

2.3 Avian influenza virus infections in humans

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

Since 5 June and as of 31 August 2026, 15 new cases of human infection with avian influenza viruses have been publicly reported from four countries and territories: Bangladesh (n = 1), Cambodia (n = 1), China (n = 12 in Mainland China, n = 1 in the Hong Kong Special Administrative Region of China). These infections were caused by the following two subtypes: A(H5N1) and A(H9N2) (Table 5). All cases had either direct or indirect exposure to poultry (Table 6). Sequences were available in GISAID's EpiFlu™ database (Shu and McCauley, 2017) from the cases in Cambodia and Hong Kong Special Administrative Region of China described during the current reporting period. In addition, the sequences from cases in Bangladesh and India described in the previous report (EFSA, ECDC and EURL, 2026a), as well as from two viruses from Bangladesh collected in 2025 (EFSA, ECDC and EURL, 2025a), were included and analysed (Table 7).

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

Subtype	Cases reported 5 June–31 August 2026			Cases reported since first report			
	Cases reported	Deaths	Reporting countries	First reported	Cases reported	Deaths	Reporting countries
H5N1^a	2	0	2	1997	1022	479 ^b	25
H5N2	0	0	0	2024	2	1	1
H5N5	0	0	0	2025	1	1	1
H5N6	0	0	0	2014	94	58 ^c	2
H7N7	0	0	0	2003	93	1	3
H9N2	13	0	1	1998	219	2	11
H10N3	0	0	0	2021	7	0	1

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

^b Deaths among a total of 1002 cases reported 2003–31 August 2026. Mortality data are not available for cases reported prior to 2003 (WHO, online-b).

^c The number of deaths among A(H5N6) cases was updated by China through the International Health Regulations (2005) mechanism (WHO, online-a), resulting in an increase in the reported number of deaths compared with previous reports.

Source: line list maintained by ECDC.

Table 6: Identified exposure associated with human cases of avian influenza, reported globally 5 June–31 August 2026 by zoonotic influenza subtype.

Subtype	Reported exposure ^a	Cases
A(H5N1)	Poultry	2
A(H9N2)	Poultry	13

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

Source: line list maintained by ECDC.

Table 7: Human strains of avian influenza included in phylogenetic and mutation analysis. Sequences include those deposited in GISAID’s EpiFlu™ database (Shu and McCauley, 2017) from 5 June 2026 to 31 August 2026.

Isolate name	Clade	Collection date	Country	Accession ID
A(H5N1) subtype				
A/Bangladesh/3250508010/2025	2.3.2.1a	2025-05-21	Bangladesh	EPI_ISL_20482895
A/Bangladesh/3250811006/2025	2.3.2.1a	2025-08-04	Bangladesh	EPI_ISL_20482897
A/India/Malda_NIV-26-497/2026	2.3.2.1a	2026-03-21	India	EPI_ISL_20485252
A/Bangladesh/IEDCR-icddr-b-3260311024/2026	2.3.2.1a	2026-03-29	Bangladesh	EPI_ISL_20457925
A/Cambodia/KBP00686206/2026	2.3.2.1e	2026-07-10	Cambodia	EPI_ISL_20492853
A(H9N2) subtype				
A/Hong Kong/447/2026	B4.7.3	2026-06-10	Hong Kong	EPI_ISL_20490503
A/Hong Kong/VM26010145/2026	B4.7.3	2026-06-10	Hong Kong	EPI_ISL_20468323

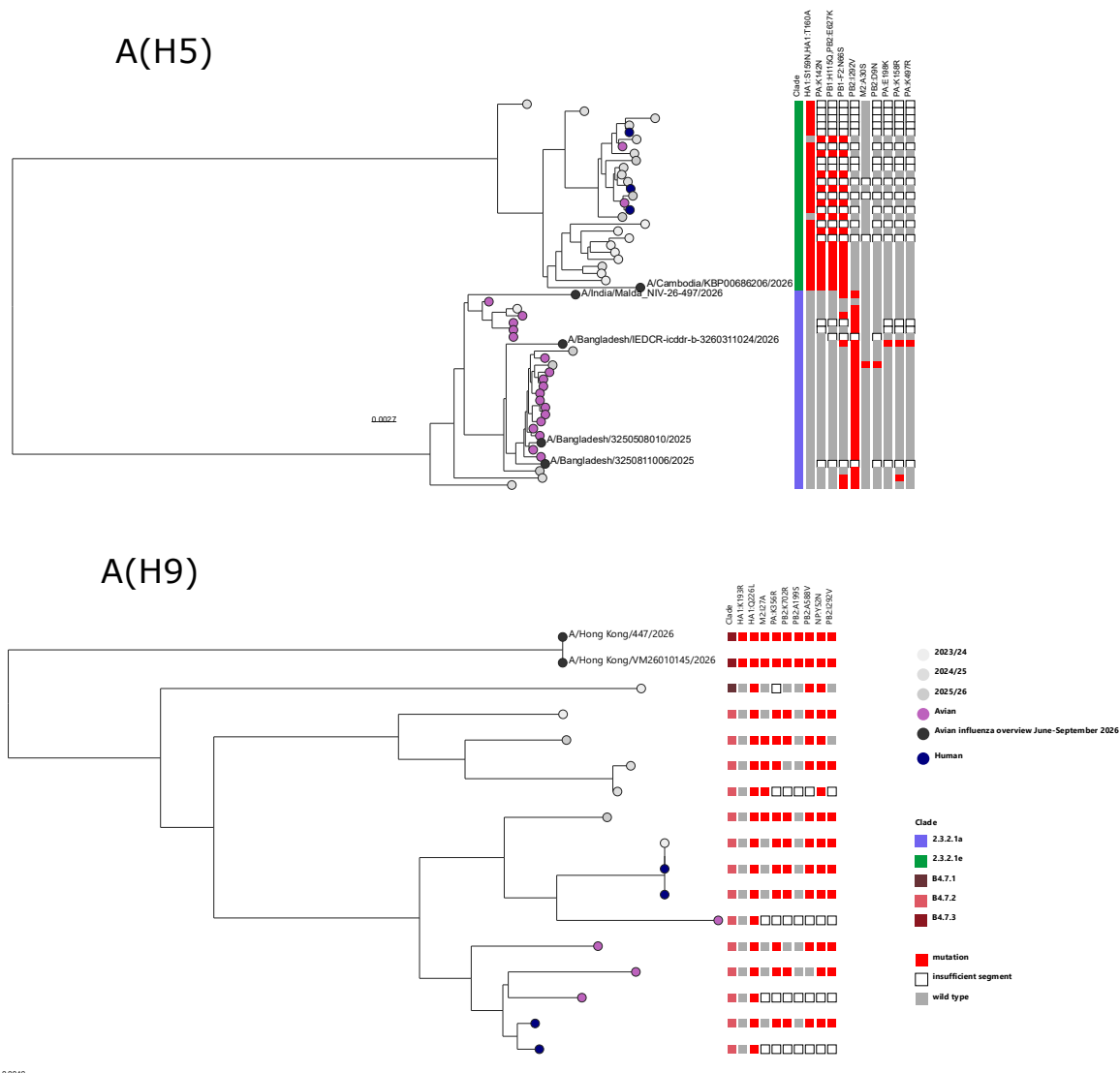


Figure 10: Phylogenetic tree of avian influenza virus strains from human cases, reconstructed from nucleotide alignment of the HA segment and annotated with significant mutation marker findings (H3 numbering) across all segments. Strains from human cases described in previous reports since December 2023 are included and annotated according to epidemiological year. Closely related non-human strains are annotated according to their host.

2.3.2 Human A(H5N1) cases

Between 5 June and 31 August 2026, two new human cases of influenza A(H5N1) virus infection were reported, including one case from Bangladesh and one from Cambodia. Both cases involved children.

Clade 2.3.2.1a in Bangladesh

On 17 May, a child from Sylhet Division developed respiratory symptoms, and a clinical sample collected on 20 May as part of influenza-like illness (ILI) surveillance tested positive for influenza A(H5) virus using real-time RT-PCR on 11 June. The patient received outpatient medical care and recovered (WHO, online-c). The virus subtype was subsequently confirmed as influenza



A(H5N1) (WHO, online-d). Although no history of exposure to poultry was reported for this case, dead poultry were found in the area surrounding the child's residence. Samples from selected close contacts, together with animal and environmental specimens, were collected and tested. No symptoms were reported among the identified contacts and all samples tested negative for influenza virus (WHO, online-c).

The sequenced virus A/Bangladesh/IEDCR-icddr-b-3260311024/2026 belonged to clade 2.3.2.1a and carried several substitutions previously reported, such as N66S in PB1, I292V in PB2 and K158R in PA. In addition, the PA had acquired the E198K substitution associated with baloxavir susceptibility in human seasonal flu virus (Takizawa and Momose, 2022) and the K497R substitution associated with increased polymerase activity in mammalian cells for A(H7N9) viruses (Suttie et al., 2019). The two analysed sequences from the viruses collected in 2025 had a mutation profile commonly observed in similar strains.

In Bangladesh, a total of 15 laboratory-confirmed human cases of infection with influenza A(H5N1) virus have been reported to WHO since 2003, including two deaths (WHO, online-b, c).

In addition, the sequence of the virus responsible for the case in India described in the previous report (EFSA, ECDC and EURL, 2026a), isolate A/India/Malda_NIV-26-497/2026, was recently deposited in GISAID. Sequence analysis showed that the virus belonged to clade 2.3.2.1a and had a substitution profile similar to that of A/India/Mangalgiro_NIV_25_594/2025 reported in 2025 (EFSA, ECDC and EURL, 2025b), although the HA segment sequence appeared more distant on the phylogenetic tree.

Clade 2.3.2.1e in Cambodia

On 30 June, a child under five years from Phnom Penh developed fever, which did not improve despite treatment. The case was hospitalised with bronchopneumonia on 7 July. Respiratory specimens collected on 8 July tested positive for influenza A(H5N1) virus using RT-PCR on 10 July. The patient received antiviral therapy (oseltamivir) and subsequently recovered. Neighbouring households kept fighting cocks and free-range chickens, including one household visited by the case before illness onset. The case was also exposed to environments contaminated with poultry droppings. Three environmental samples collected from poultry kept in neighbouring households tested negative for influenza A(H5N1). All identified contacts of the case tested negative for influenza A(H5N1) (Communicable Disease Control Department, Ministry of Health Cambodia, online; WHO, online-d, e).

The sequence from the corresponding isolate A/Cambodia/KBP00686206/2026 fell in a distinct sub-branch of clade 2.3.2.1e human and avian strains from Cambodia and had a mutation profile similar to that of the A/Cambodia/SVH240441/2024 virus described previously (EFSA, ECDC and EURL, 2024).

In Cambodia, a total of 95 laboratory-confirmed human cases of infection with influenza A(H5N1) virus have been reported to WHO since 2003 as of 7 August 2026, including 53 deaths (WHO, online-b).

Overall, since the first report of human infection with avian influenza A(H5N1) virus in 1997, a total of 1022 cases have been reported globally to WHO by 25 countries (Figure 11). Since 2003, among 1002 cases, 479 deaths have been reported.

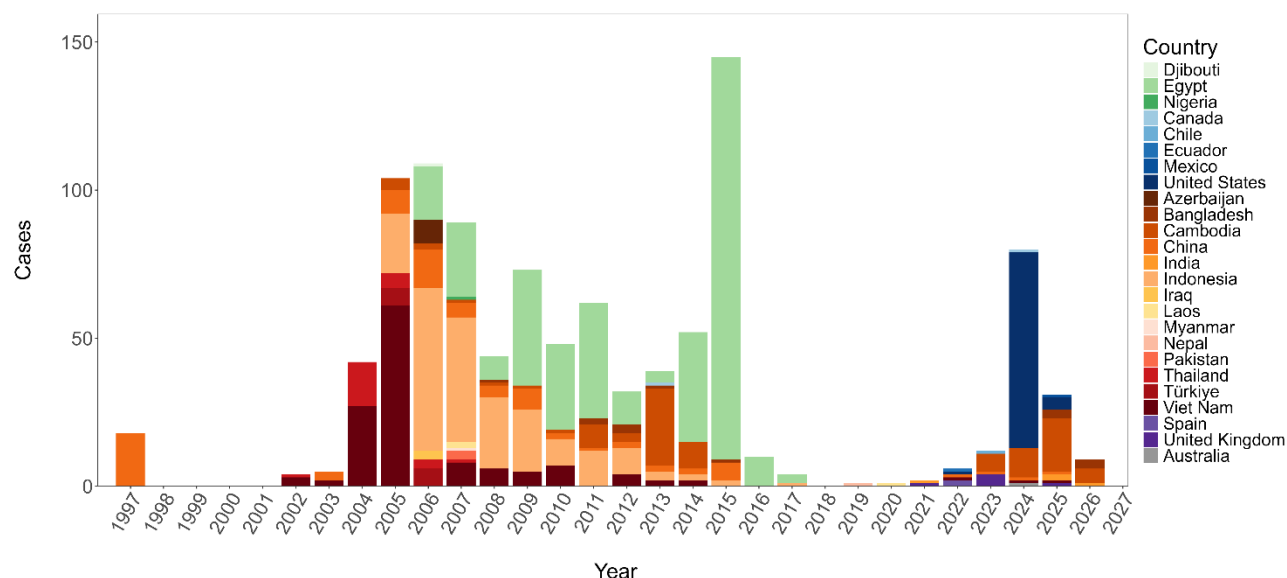


Figure 11: Distribution of reported human cases of A(H5N1) virus infection by year of onset or detection and reporting country from 1997 to 31 August 2026.

Note: The figure includes detections of A(H5N1) due to suspected environmental contamination reported in 2022 by Spain (2) and the US (1), and in 2023 by the United Kingdom (three detections, one inconclusive). Human cases of A(H5) epidemiologically linked to A(H5N1) outbreaks in poultry and dairy cattle farms in the US are included in the number of A(H5N1) cases.

Source: line list maintained by ECDC.

2.3.3 Human A(H9N2) cases

Between 5 June and 31 August 2026, 13 new human cases of influenza A(H9N2) virus infection were reported from China, including one case reported from Hong Kong Special Administrative Region. In Mainland China, cases were reported from Anhui (n = 1), Beijing (n = 1), Gansu (n = 1), Guangdong (n = 2), Guangxi (n = 2), Jiangsu (n = 2), Jiangxi (n = 1) and Yunnan (n = 2) provinces (CHP, online-a,b; WHO, online-c,d,e,f,g,h,i,j,k).

Among the reported cases, three were adults (age range: 44 to 72 years) and 10 were children, eight of which were < 5 years of age. Four cases, including three adults and one child, had known underlying medical conditions. Cases had onset of symptoms between 31 May and 15 August. Nine cases were detected through ILI surveillance. One adult without ILI symptoms presented for medical attention in the context of a follow-up for an underlying medical condition. Another case, also an adult, had underlying medical comorbidities and was hospitalised. Seven cases were admitted to hospital, including one adult requiring intensive medical care. No fatal cases were reported.

All cases had a history of direct or indirect exposure to poultry in local live bird markets and/or household or backyard settings. Environmental samples collected from the likely areas of exposure for 11 of the cases tested positive for influenza A(H9) virus. No new cases have been detected among identified contacts of the affected individuals.

Two A(H9N2) sequenced virus isolates from Hong Kong were available in GISAID. However, based on the patient information, the collection date and the fact that their HA segments and substitution profiles were identical, these are most likely sequences for the same, single case

reported in Hong Kong. The virus was classified as clade B4.7.3 and had a high number of genetic differences compared to previously described strains of low pathogenic subtype A(H9N2). The substitutions include some not described for A(H9) viruses so far, such as K193R in HA associated with increased virus binding to $\alpha 2-6$ and A199S in PB2 associated with increased virulence in mice in in vitro studies performed on A(H5N1) subtype (Suttie et al., 2019).

Overall, since the first report of human infection with avian influenza A(H9N2) virus in 1998, a total of 219 cases, including two deaths, have been reported globally to WHO by 11 countries (Figure 12).

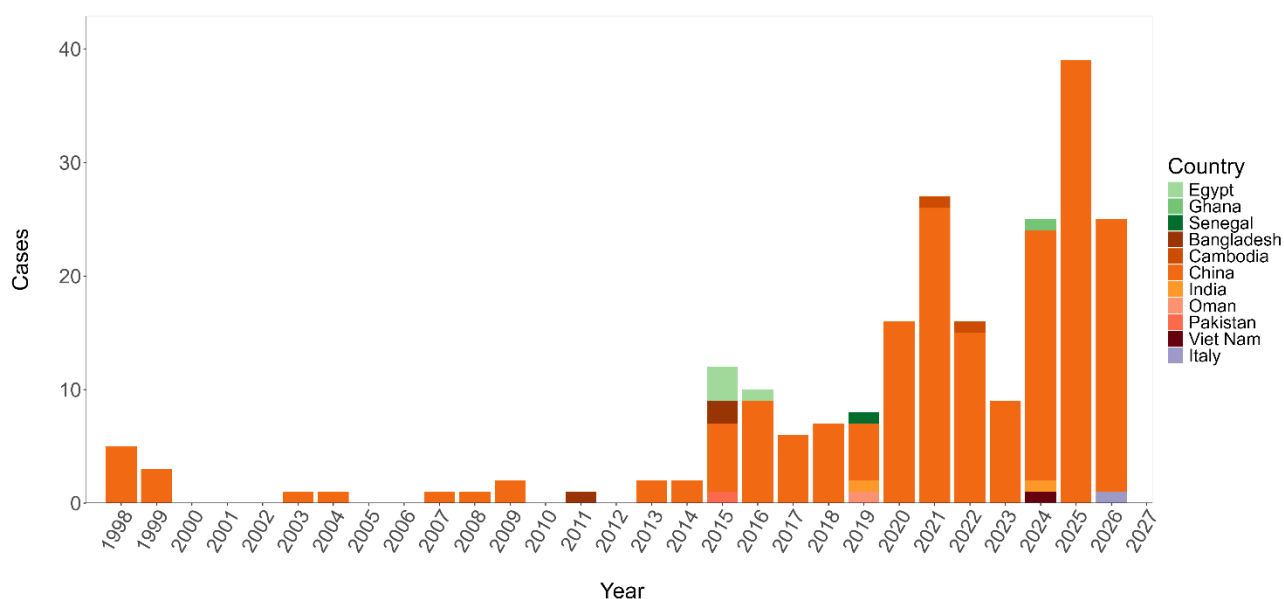


Figure 12: Distribution of reported human cases of A(H9N2) virus infection by year of onset or detection and reporting country, from 1998 to 31 August 2026.

Source: line list maintained by ECDC.

2.3.4 Additional information relevant for public health and international risk assessments

Over the past few years, the epidemiological situation with A(H5N1) clade 2.3.4.4b in birds and mammals has led to the reinforcement of the surveillance of zoonotic transmission. The results from studies following exposed people were recently published. The United Kingdom Health Security Agency (UKHSA) conducted a study over a two-year period (April 2023–March 2025) that included more than 400 exposed people, representing half of those exposed during more than 30 poultry outbreaks of A(H5N1) clade 2.3.4.4b avian influenza. The recruited individuals were requested to answer a questionnaire and collect (self-sampling) a nasopharyngeal swab for several days after exposure. Only three participants were found to be infected with influenza A(H5N1) virus after exposure, representing a positivity rate below 1%. Three additional participants were found positive, but the timing of sampling ruled out a true infection, and they were considered as an environmental contamination. The study also showed that nearly all those exposed after outbreak confirmation wore personal protective equipment and that in-person recruitment of study participants at the outbreak site was more successful than remote recruitment (Halford et al., 2026). The public health authorities from Taiwan reported the 2025 results of the serological surveillance of professionals occupationally exposed to avian influenza virus during poultry outbreaks. The study used paired sera to detect seroconversion as a marker



of infection. No seroconversion was observed among the 122 participants (from 76 avian influenza outbreaks), most of whom were exposed to A(H5N1) clade 2.3.4.4b avian influenza virus (28/76 outbreaks). Nearly all participants reported using personal protective equipment during the exposure activity (Lin et al., 2026). Similar results were reported for 41 farm workers in South Korea, exposed and enrolled during A(H5N1) avian influenza virus outbreaks in the 2024–2025 season (49 outbreaks). Analysis of paired sera did not show any seroconversion (An et al., 2026).

A scoping review focusing on the reported modes of transmission of A(H5N1) avian influenza viruses to humans was recently published (Billias et al., 2026). The study identified 120 literature sources and provided a comprehensive summary of the knowledge for three main routes of transmission: animal-to-human, environment-to-human, human-to-human. The study highlighted the fact that the infection routes described in the literature were reported only as biologically plausible pathways, with no inference regarding their likelihood or causation.

Following the human case of A(H5N5) avian influenza virus infection detected in November 2025 in the US, two independent studies have recently been published evaluating the risk for humans (Pulit-Penaloza et al., 2026; Vu et al., 2026). Overall, the pandemic risk is considered low, mainly based on the lack of direct contact transmission in the ferret model. However, the risk assessment highlighted that the genotype of A(H5) clade 2.3.4.4b viruses seems to play an important role in determining the capacities of the viruses to infect human cells or transmit in the ferret model.

Growing efforts to improve the surveillance of A(H9N2) avian influenza viruses both in birds and humans are highlighted by the recent publication of the results of several studies. Changsha Municipal Centre for Disease Control and Prevention (Hunan province, China) provided a retrospective analysis of the 11 human cases reported between 2015 and 2025 (Chen et al., 2026). Serological monitoring of human populations in 2024 in the Jiangsu province (China) found positivity rates of 4% in exposed populations (n = 370) and 2.5% in non-exposed populations (n = 240) (Gao et al., 2026). In addition, studies focusing on viruses from animal or environmental samples emphasised the diversity of genetic lineages circulating in birds, as well as an increased capacity to bind human $\alpha 2-6$ receptors for some A(H9N2) viruses (Deng et al., 2026; Nyarko et al., 2026; Pang et al., 2026; Ren et al., 2026; Tan et al., 2026).

The Food and Agriculture Organization of the United Nations (FAO), WHO and WOAHA tripartite assessment of the global public health risk posed by HPAI A(H5) viruses has not been updated since 18 May 2026 (FAO, WHO AND WOAHA, online-a). The risk remains unchanged and is considered low for the general public and low-to-moderate for occupationally or frequently exposed individuals. In the latest summary and risk assessment of 'Influenza at the human-animal interface', WHO's assessment of the risk to public health for the current H5N1 and H9N2 avian influenza viruses has not changed and is still considered to be low (WHO, online-d).

During the reporting period, the US Centers for Disease Control and Prevention (CDC) assessment of the public health risk posed by avian influenza A(H5) viruses has not been updated. The last report dates from March 2026 when the risk for public health was still considered low in the US (CDC, online).

The United Kingdom Health Security Agency (UK HSA) risk assessment of HPAI A(H5) to the general public, available in 'Bird flu (avian influenza): latest situation in England' updated on 20 August 2026, has remained unchanged during the reporting period and is still considered to be very low (GovUK, online-c).

2.3.5 ECDC risk assessment

ECDC's assessment of the risk of human infection with HPAI A(H5N1) clade 2.3.4.4b viruses currently circulating in animals in Europe remains unchanged. Overall, ECDC assesses the risk posed by HPAI A(H5N1) clade 2.3.4.4b viruses to be low for the general public in the EU/EEA, and low-to-moderate for those occupationally or otherwise exposed to infected animals or contaminated environments. The assessment considers the risk of infection at population level in the EU/EEA, taking into account the likelihood of human infection and transmission and the potential impact of such an infection, based on ECDC's framework for risk assessments (ECDC, 2019).

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

The likelihood of human infection with HPAI A(H5N1) clade 2.3.4.4b viruses in the EU/EEA:

- Despite the extensive circulation of avian influenza A(H5N1) virus in animal populations in Europe over the past few years, with frequent opportunities for human exposure, there have been no confirmed cases of A(H5N1) clade 2.3.4.4b infection in humans in the EU/EEA, and transmission from infected animals to humans remains a rare event globally.
- In Europe, mutations associated with viral adaptation to mammalian hosts have been identified in sequences of A(H5N1) clade 2.3.4.4b viruses from mammals and birds. However, circulating viruses retain a binding preference for $\alpha 2-3$ sialic acid (avian-type) receptors and are still considered to be avian-like. There is currently no evidence of the viruses being more capable of infecting humans or having the ability to transmit between humans. Further understanding of the implications of such mutations for mammalian adaptation, infection and transmission will help in assessing any change in the associated risk to humans.
- Sporadic cases of infection with avian influenza A(H5N1) virus have been reported in humans globally, often with a history of unprotected exposure to poultry, cattle, or contaminated environments. Both human cases of influenza A(H5N1) publicly reported worldwide between 5 June and 31 August 2026 had documented direct or indirect exposure to poultry.
- To date, there has been no evidence of human-to-human transmission of influenza A(H5N1) clade 2.3.4.4b viruses.

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

- Clinical presentations of individuals infected with A(H5N1), including clades other than 2.3.4.4b, have ranged from asymptomatic or mild (such as conjunctivitis and upper respiratory tract symptoms) to severe illness resulting in death, with a case fatality estimated at 48% since 2003. However, this figure is only based on reported cases and may be overestimated.
- The majority of human cases of infection with influenza A(H5N1) clade 2.3.4.4b reported in the US between April 2024 and February 2025, as well as the human case reported in the United Kingdom in January 2025, experienced mild symptoms, such as conjunctivitis or mild respiratory illness. Between 5 June and 31 August 2026, no new cases of human infection with an A(H5N1) clade 2.3.4.4b virus were reported globally. The most recent

reported case of human infection with influenza A(H5N1), characterised as clade 2.3.4.4b, was reported by Mexico in April 2025 (WHO, online-l).

- The reasons for the variation in outcome following infection with influenza A(H5N1) virus are likely to be multi-factorial and may be attributed to the virus genotype, duration of exposure, viral load, transmission route, individual health status, personal protective measures taken, and medical treatment provided (FAO, WHO and WOA, online-b). The detection of several mild cases of A(H5N1) virus infection and seropositive individuals without a history of clinical symptoms in the US suggests that mild and asymptomatic cases may be more common than previously reported for A(H5N1). Targeted surveillance of individuals exposed to infected animals is therefore recommended (EFSA AHAW Panel and ECDC, 2025).
- Most of the circulating A(H5N1) clade 2.3.4.4b viruses detected in Europe in the epidemiological year 2025–2026 remain susceptible to antiviral medicines available to treat humans, including adamantanes, neuraminidase inhibitors (e.g. oseltamivir) and polymerase acidic inhibitors (e.g. baloxavir marboxil).

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

3 Summary and conclusions

3.1 Birds

- In line with the seasonal dynamics of avian influenza, the number of HPAI virus detections in wild birds in Europe was low during the current reporting period. These HPAI virus detections occurred predominantly in waterfowl, contrasting with the previous year, when most detections were reported in colony-breeding seabirds. No unusual mortality events associated with HPAI were reported in wild birds in Europe during the current reporting period.
- The number of HPAI virus detections in wild birds in Europe is expected to increase in the coming months, as the arrival of migratory birds and the addition of immunologically naïve juvenile birds to the wild bird populations provide the circumstances for higher circulation of avian influenza viruses in wild birds.
- During the current reporting period, only two HPAI outbreaks were reported in poultry in Europe, one each in Germany and Sweden, representing a 99% decrease compared to the previous reporting period, when also farm-to-farm transmission was observed (e.g. in Poland). HPAI outbreaks in captive birds in Europe continued to occur predominantly in non-commercial or backyard establishments keeping mixed poultry species. Indirect or direct contact with wild birds remained the main source of HPAI virus introduction into domestic bird establishments.

- Across the current epidemiological year, despite sustained high levels of HPAI infection in wild birds, a marked reduction in outbreaks was observed in domestic ducks, a sector known from previous years (particularly 2021–2022 and 2022–2023) to carry a high risk for HPAI infection and transmission. Of note, France's implementation of mandatory preventive duck vaccination (not utilised in those previous years), paired with strict biosecurity, likely contributed effectively to curbing both wild bird spillover and farm-to-farm transmission.
- No new HPAI A(H5N5) virus detections in birds were reported in or outside Europe during the current reporting period.
- In line with the prevailing circulation among waterfowl, EA-2024-DI.2.1 remains the predominant genotype during the current reporting period, as it has been throughout the entire epidemiological year, while the genotypes circulating predominantly among colony-breeding seabirds continue to be detected at a low frequency.
- LPAI A(H9N2) virus of clade G5.6 was reported for the first time in July 2025 in a backyard flock in Moldova. Similarly to the majority of the A(H9N2) viruses of lineage G, the identified virus possesses the HA-Q226L mutation (H3 numbering) associated with preferential binding to human-like α 2-6-linked sialic acid (SA α 2-6) receptors.
- The frequency of detection of PB2 mammalian adaptive mutations in A(H5) viruses collected from birds decreased from about 4% in the 2024–2025 epidemiological year to about 0.5% in the 2025–2026 epidemiological year.
- Outside Europe, HPAI A(H5N1) outbreaks continued to be reported from Central and South America, affecting multiple countries and indicating sustained virus circulation across the continent. Outbreaks in domestic birds were frequently reported in non-commercial and backyard establishments. In addition, a mortality event involving black vultures was reported in Honduras. In Mexico, three HPAI A(H7N3) virus detections were reported, affecting both plain chachalacas and poultry.
- During the current reporting period, Nepal continued to report a substantial number of HPAI outbreaks in poultry. Furthermore, HPAI A(H5) and A(H9) viruses were detected in a zoo, where a large variety of avian and mammalian species were affected.
- In general, and as previously reported, low numbers of wild birds infected with HPAI virus were reported from outside Europe via official notifications to WOA.
- Following its initial detection in seabirds likely arriving from the sub-Antarctic region, HPAI A(H5N1) virus has now spread to several resident wild bird species in Australia and has been associated with unusual mortality events in greater crested terns.
- Both in Australia and New Zealand, vaccination programmes targeting a limited number of protected or vulnerable wild bird species are ongoing (e.g. little penguins in Australia).

3.2 Mammals

- In Europe, the number of HPAI A(H5N1) and A(H5) virus detections in wild terrestrial carnivores and pinnipeds remained low and comparable to that reported in previous months. No new HPAI virus detections in pets, domestic or captive mammals were reported.
- Although no such cases were reported during the current reporting period, a second polar bear found dead in Svalbard, Norway, tested positive for HPAI A(H5N5) virus infection in October 2025. Furthermore, serological studies have indicated a high prevalence of A(H5) antibodies among polar bears in the region since 2023 (Madslien et al., 2026).
- Outside Europe, HPAI virus detections in mammals were mainly reported from the US, where 67 additional dairy cattle farms were reportedly affected by HPAI A(H5N1),

alongside domestic cats and other wild terrestrial carnivores. The detection of HPAI A(H5N1) virus in captive American minks in the US constitutes the first reported occurrence in North America and is of concern for both animal and public health.

- In Australia, spillover of HPAI A(H5N1) virus to marine mammals and red foxes was reported in areas with high levels of virus circulation in the wild bird population.
- A(H5Nx) viruses collected from wild and domestic mammals in Europe during the current epidemiological year fall within clade 2.3.4.4b, and the majority of them (84%) belong to genotype EA-2024-DI.2.1. In total, 87% of the characterised viruses differ from genetically related viruses circulating in avian species for the presence, in the PB2 protein, of molecular markers of adaptation to mammals.

3.3 Humans

- Despite the widespread occurrence of HPAI A(H5N1) in wild birds, poultry and some mammals in recent years, with many potential exposures of humans to infected animals, there have been no confirmed human cases of influenza A(H5N1) in the EU/EEA.
- The majority of human infections with avian influenza viruses reported since 1997 have been associated with unprotected exposure to poultry, live poultry markets, or contaminated environments. In addition, since March 2024, there have been 41 human cases of influenza A(H5) reported following exposure to dairy cattle infected with A(H5N1) virus. To date, there has been no evidence of sustained human-to-human transmission.
- During the reporting period from 5 June to 31 August 2026, two human cases of avian influenza A(H5N1) infection were publicly reported worldwide. All cases had direct or indirect exposure to poultry.
- With the extensive circulation of avian influenza viruses in bird populations globally, sporadic transmission to humans is likely to continue in settings where people have unprotected exposure to infected animals or their environment.

4 Options for response

The following sections focus on options for response that are particularly relevant for the coming months. Considering the predictable seasonal increase in HPAI A(H5) risk observed in previous years, heightened preparedness may be indicated. A comprehensive list of general options for response from earlier reports is provided in Annex D.

4.1 Birds

- Given that the level of HPAI virus contamination of the environment is expected to increase in the coming months, biosecurity measures in domestic bird establishments should be optimised and maintained at high level both during the production cycle and culling operations. This also applies to vaccinated poultry and is particularly important for establishments under the same ownership, part of an integrated production chain, or located in densely populated poultry areas.
- EFSA's Bird Flu Radar may be consulted to monitor the probability of HPAI virus introduction into wild bird populations over space and time, especially now at the beginning of autumn: <https://app.bto.org/hpai>
- Surveillance in domestic birds should be maintained at a level that ensures early detection of infected establishments.
- Given the recent detections of LPAI A(H9N2) viruses belonging to clades G5.5 and G5.6 in Hungary and Moldova, respectively, together with the endemic circulation of these

clades in several countries outside Europe and their potential zoonotic risk, any further events involving these viruses should be promptly reported. In addition, virus characterisation and assessments of the risk of establishment in domestic bird populations are recommended.

- For wild birds, options for response include accurate and comprehensive recording of HPAI-associated mortality events (to estimate the impact on wild bird populations) and preventing disturbance of areas undergoing HPAI outbreaks to reduce virus spread (e.g. hunting activities, tourism, leisure activities, use of drones).
- Artificial feeding of wild birds should be avoided during high-risk periods to reduce the level of crowding of these species.
- Given the currently high levels of West Nile virus circulation in parts of Europe (ECDC and EFSA, 2026), West Nile fever should be considered as a differential diagnosis during passive surveillance when neurological signs are observed in wild birds, particularly corvids, raptors and birds kept in zoos.
- Strengthening the genetic characterisation of viruses is recommended to quickly identify molecular markers of adaptation to mammals, which could indicate potential virus circulation in mammals and subsequent mammal-to-avian transmission. Viruses carrying such mutations may have an increased zoonotic potential and their biological characteristics should be further evaluated to assess the actual impact of the acquired mutations. To serve as an effective early warning system, sequences should be generated and shared in public databases as promptly as possible. Genetic data are also instrumental to track the virus spread, support epidemiological investigations in the distinction between primary and secondary outbreaks, and identify novel incursions of viruses that may represent a threat for human or animal health.

4.2 Mammals

- In the coming months, the risk of involvement of mammals in the circulation of HPAI viruses is expected to increase. Therefore, surveillance of HPAI viruses in wild (e.g. red foxes) and free-roaming domestic carnivores (e.g. cats and dogs), as well as in farmed mammals in high-risk areas or establishments (e.g. zoos and mixed-species establishments), is indicated.
- In high-risk areas, private veterinarians should be adequately informed and encouraged to participate in the surveillance of potential spillover events in domestic carnivores (e.g. cats and dogs). If suspect clinical signs are observed (e.g. neurological or respiratory signs), these animals should be tested for HPAI.
- In light of a potential spillovers of HPAI A(H5N1) virus from wild birds to dairy cattle in Europe, 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 or wild animals in/around farms keeping ruminants. In addition, HPAI should be considered as a differential diagnosis in cases of undiagnosed or unresolved compatible clinical signs during periods of HPAI virus circulation in the area where ruminants are kept.

4.3 Humans

- The risk of human exposure to avian influenza viruses can be reduced by implementing some of the preventive measures suggested below (highlights for the coming months) and in Annex D (general options).
- Countries should remain vigilant for potential human cases of avian influenza, especially in geographical areas where the virus is known to circulate in poultry, wild birds or other animals.
- In areas with ongoing avian influenza outbreaks in animals, healthcare workers (including primary care providers) should be made aware of the epidemiological situation in animal populations and the range of symptoms associated with avian influenza infection in humans (e.g. symptoms of upper or lower respiratory tract infection, but also non-respiratory symptoms, such as conjunctivitis, gastrointestinal or neurological symptoms).
- Detections of human cases of zoonotic avian influenza through surveillance systems for seasonal influenza highlight the importance of typing and subtyping samples. All influenza-positive specimens collected through seasonal influenza sentinel surveillance from both primary and secondary care sources should be typed and subtyped.
- During periods of high seasonal influenza virus circulation (typically during the winter months in EU/EEA countries), exhaustive subtyping of influenza type A-positive samples might not be possible. Testing and subtyping for avian influenza virus could then be performed using a risk-based approach, depending on the epidemiological situation in animal populations and focusing on cases from outbreaks, or with severe respiratory signs or neurological symptoms of unknown aetiology. Further guidance is available in ECDC's technical report on targeted surveillance to identify human infections with avian influenza virus during the influenza season (ECDC, 2024).
- The options for response are based on currently available evidence, the epidemiological situation and the risk assessment for the EU/EEA. Recommended measures may need to be adapted if the epidemiological situation changes, or new evidence becomes available.

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

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

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

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

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

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

- ECDC's current risk assessment that focuses on the immediate risk of avian influenza for human health fulfilling ECDC's new mandate and the Regulation (EU) 2022/2371⁹ aiming to prevent and prepare for cross-border health threats, including epidemics; and
- EFSA's latest scientific opinions and reports coupled by measures taken (i.e., surveillance, prevention and control measures) under the Animal Health Law (i.e., Commission Delegated Regulation (EU) 2020/689¹⁰ and Commission Delegated Regulation (EU) 2020/687¹¹).

⁹ 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.

¹⁰ 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.

¹¹ 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) 2022/2370¹² and Articles 29 and 31 of Regulation (EC) No 178/2002¹³, 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 Terms of Reference 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 5 June and 28 August 2026, based on notifications submitted by Member States and third countries via ADIS and WOA-H-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 affected by HPAI outbreaks in poultry and/or captive birds provided EFSA with additional epidemiological information, which was used to analyse the characteristics of the affected 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 28 February to 4 June 2026 (EFSA, ECDC and EURL, 2026a) and that might affect the interpretation of risks related to avian influenza introduction and/or spread in Europe.

¹² Regulation (EU) 2022/2370 of the European Parliament and of the Council of 23 November 2022 amending Regulation (EC) No 853/2004 establishing a European centre for disease prevention and control. OJ L 314, 6.12.2022, p. 1–25.

¹³ 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, HPAI outbreaks in Europe reported via ADIS between 5 June and 28 August 2026 by Member States and other European countries were taken into account. Data extraction was carried on 28 August 2026. WOA-H-WAHIS was consulted to complement the information for European countries not notifying HPAI via ADIS (United Kingdom (excluding Northern Ireland)). Additionally, countries affected by HPAI were asked to provide EFSA with more detailed epidemiological information on HPAI outbreaks in poultry and captive birds. The information collected included details on the affected species and production systems and was provided as supplementary variables to complement the data reported via ADIS. All information gathered is presented in Annex B. In addition, since summer 2023, European reporting countries have been requested to notify EFSA directly of any HPAI virus detections in mammals. The data collected during the current reporting period are summarised in Annex C. Finally, the information HPAI-affected European countries presented to the Standing Committee on Plants, Animals, Food and Feed (SCOPAFF), and the evidence on HPAI outbreaks provided in the info notes from affected countries to the 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.3, and the common and scientific names of wild bird species described in this report for Europe are reported in Table A.4 (both in Annex A). For mammals, the common and scientific names of the species involved are listed in Table 4. GISAID's EpiFlu™ database (Shu and McCauley, 2017) was accessed to download newly released avian influenza virus sequences.

The annexes to this Scientific Report are available here: <https://doi.org/10.5281/zenodo.22893263>

B.1.2. Overview of avian influenza outbreaks outside Europe

Data from WOA-H-WAHIS on HPAI A(H5) and A(H7) in domestic and wild birds, as well as in mammals, were used to describe and map the geographic distribution of HPAI virus detections in animals in other regions of the world based on their observation dates. Data were retrieved from WOA-H-WAHIS and extracted on 28 August 2026. They were used and reproduced with permission. WOA-H bears no responsibility for the integrity or accuracy of the data contained therein, 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 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 the genetic



clustering described in 2018 by Lee and co-authors, who recognised four groups (a–d) within clade 2.3.4.4, was used (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 were collected by ECDC. As part of epidemic intelligence activities at ECDC, multiple sources are scanned regularly to collect information on laboratory-confirmed human cases. Data were extracted and line lists developed to collect case-based information on virus type, date of disease onset, country of reporting, country of exposure, sex, age, exposure, clinical information (hospitalisation, severity) and outcome. All cases included in the line list and mentioned in the document have been laboratory-confirmed. Data are continuously checked for double entries and validity. The data on human cases cover the full period since the first human case was reported. Therefore, data on human cases refer to different time periods. Relevant information on human infections, risk factors, and the results from studies on infection and transmission with relevance for human health are included.

B.2.1. Method for phylogenetic and mutation analysis

GISAID's EpiFlu™ database (Shu and McCauley, 2017) was accessed on 31 August 2026 to retrieve sequences from human cases of avian influenza reported since 5 June 2026. In cases where the same strain had multiple submissions, the ones with the most complete segment data were chosen. Mutations were retrieved using FluMut (Github izsvenezie-virology, online-a, b) with the FluMutDB v6.4 mutation database (<https://github.com/izsvenezie-virology/FluMutDB>). For markers where FluMut reported an undefined amino acid, the marker received the annotation insufficient segment. Mutations found in less than 10% of the background sequences were considered significant as well as others deemed relevant based on literature searches. Clade information was retrieved from GISAID or assigned according to specified literature. Genin2 (<https://github.com/izsvenezie-virology/genin2>) and GenoFLU (Youk et al., 2023) were used to assign genotypes.

Annex A – Data on HPAI virus detections in birds

Annex A includes additional figures and tables on HPAI virus detections in birds. The Annex is available on the EFSA Knowledge Junction community on Zenodo at: <https://doi.org/10.5281/zenodo.22893263>

Annex B – Characteristics of the HPAI-affected poultry and captive bird establishments

Annex B presents the HPAI outbreaks in poultry and captive birds for which additional information on the characteristics of the affected establishments was collected and provided by reporting countries in Europe during the current reporting period. It also includes data on outbreaks that occurred too close to the publication of the previous report and are therefore included this time. The Annex is available on the EFSA Knowledge Junction community on Zenodo at: <https://doi.org/10.5281/zenodo.22893263>

Annex C – Data on HPAI virus detections in mammals

Annex C includes data on HPAI virus detections in mammals for which additional data were collected and provided by reporting countries in Europe during the current reporting period. The Annex is available on the EFSA Knowledge Junction community on Zenodo at: <https://doi.org/10.5281/zenodo.22893263>

Annex D – General options for response

Annex D contains general options for response that are valid throughout the year, irrespective of the current reporting period.

The Annex is available on the EFSA Knowledge Junction community on Zenodo at: <https://doi.org/10.5281/zenodo.22893263>

Annex E – Acknowledgements

All genome sequences and associated metadata linked in the below dataset are published in GISAID's EpiFlu™ database (Shu and McCauley, 2017). To view the contributors of each individual sequence with details such as accession number, virus name, collection date, originating and submitting lab, and the list of authors, visit: <https://doi.org/10.55876/gis8.260624dr>, <https://doi.org/10.55876/gis8.260916mk> and <https://doi.org/10.55876/gis8.260902sa>.