SCIENTIFIC REPORT

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Avian influenza overview June–September 2024

European Food Safety Authority,
European Centre for Disease Prevention and Control,
European Union Reference Laboratory for Avian Influenza, Leonidas Alexakis, Hubert Buczkowski, Mariette Ducatez, Alice Fusaro, Jose L Gonzales, Thijs Kuiken, Karl Ståhl, Christoph Staubach, Olov Svartström, Calogero Terregino, Katriina Willgert, Roxane Delacourt and Lisa Kohnle

Abstract

Between 15 June and 20 September 2024, 75 highly pathogenic avian influenza (HPAI) A(H5) and A(H7) virus detections were reported in domestic (16) and wild (59) birds across 11 countries in Europe. Although the overall number of detections in Europe continued to be low compared to previous epidemiological years, an increase in cases along the Atlantic, North Sea and Baltic coasts was notable, particularly an increase in the detection of HPAI viruses in colony-breeding seabirds. Besides EA-2022-BB and other circulating genotypes, these detections also included EA-2023-DT, a new genotype that may transmit more efficiently among gulls. In Germany, HPAI A(H7N5) virus emerged in a poultry establishment near the border with the Netherlands. No new HPAI virus detections in mammals were reported in Europe during this period, but the number of reportedly affected dairy cattle establishments in the United States of America (USA) rose to > 230 in 14 states, and HPAI virus was identified in three new mammal species. Between 21 June and 20 September 2024, 19 new human cases with avian influenza virus infection were reported from the USA (six A(H5N1) cases and five A(H5) cases), Cambodia (five A(H5N1) cases, including one fatal), China (one fatal A(H5N6) case and one A(H9N2) case), and Ghana (one A(H9N2) case). Most of the human cases (90%, n = 17/19) had reported exposure to poultry, live poultry markets, or dairy cattle prior to avian influenza virus detection or onset of illness. Human infections with avian influenza viruses remain rare and no evidence of human-to-human transmission has been documented in the reporting period. The risk of infection with currently circulating avian A(H5) influenza viruses of clade 2.3.4.4b in Europe remains low for the general public in the European Union/European Economic Area (EU/EEA). The risk of infection remains low-to-moderate for those occupationally or otherwise exposed to infected animals or contaminated environments.

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

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Correspondence: biohaw@efsa.europa.eu and ECDC.influenza@ecdc.europa.eu

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Declarations of interest: If you wish to access the declaration of interests of any expert contributing to an EFSA scientific assessment, please contact interestmanagement@efsa.europa.eu

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Table of Contents

1. Introduction

This Scientific Report provides an overview of highly pathogenic avian influenza (HPAI) virus detections in poultry[1], captive[2] and wild birds that occurred in and outside Europe between 15 June and 23 September 2024, as well as HPAI virus detections in mammals up until 23 September 2024, and human cases due to avian influenza infection between 21 June and 20 September 2024. Detections of low pathogenic avian influenza (LPAI) virus are discussed whenever they are of concern and relevant.

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

2. Assessment

2.1 HPAI virus detections in birds

2.1.1 HPAI virus detections in birds in Europe

Figure 1 shows all HPAI virus detections in birds in Europe that were reported via the European Union (EU) Animal Disease Information System (ADIS) or the World Animal Health Information System (WOAH-WAHIS) of the World Organisation for Animal Health (WOAH) for the last four and the current epidemiological year[3] by month of suspicion. For the current epidemiological year 2023–2024, starting on 1 October 2023, data reported are truncated on 20 September 2024.

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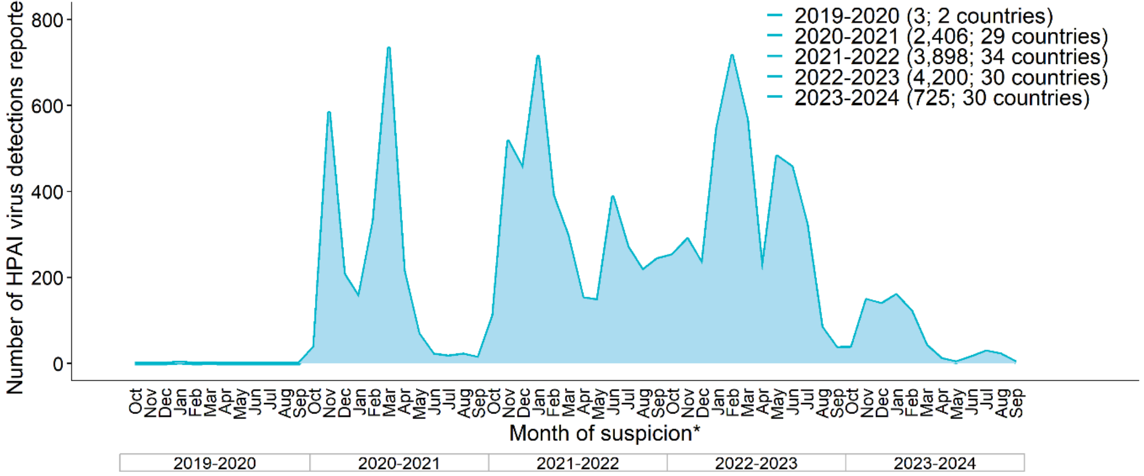
[1] According to Regulation (EU) 2016/429 of the European Parliament and of the Council of 9 March 2016, point (9), 'poultry' means birds that are reared or kept in captivity for: (a) the production of: (i) meat; (ii) eggs for consumption; (iii) other products; (b) restocking supplies of game birds;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

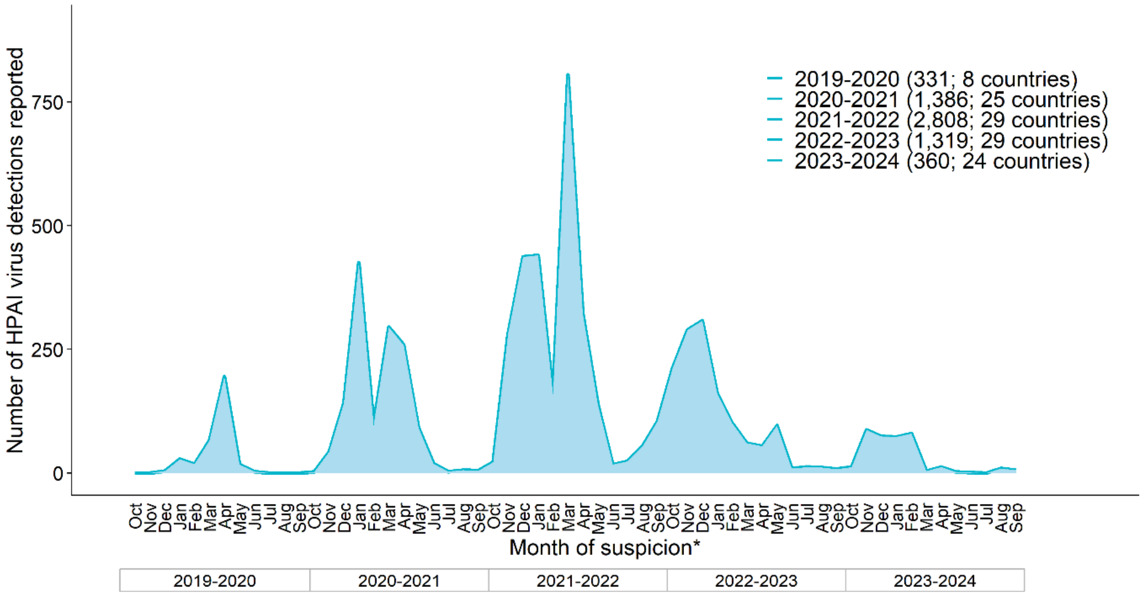
[2] According to Regulation (EU) 2016/429 of the European Parliament and of the Council of 9 March 2016, point (10), 'captive birds' means any birds other than poultry that are kept in captivity for any reason other than those referred to in point (9), including those that are kept for shows, races,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

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

(a) Wild birds



(b) Domestic birds



*If the date of suspicion was not available, the date of confirmation was used to assign the week of suspicion. United Kingdom data are from the Animal Disease Notification System (ADNS, former ADIS) up until 31 December 2020. From 1 January 2021 onwards, the data source was WOAH for the United Kingdom (excluding Northern Ireland) and ADNS/ADIS for the United Kingdom (Northern Ireland)[4].
Source: ADNS/ADIS and WOAH (data extraction carried out on 20 September 2024).

Figure 1: Distribution of the number of HPAI virus detections in wild (cumulative number n = 11,232) (a) and domestic (n = 6,204) (b) birds reported in Europe during five epidemiological years by month of suspicion, from 1 October 2019 to 20 September 2024 (total n = 17,436)

The very low number of HPAI virus detections reported in both wild and domestic birds in Europe between 15 June and 20 September continued from the previous reporting period, between 16 March and 14 June 2024, and is consistent with the trend observed since the beginning of the epidemiological year 2023–2024. Of note, the total number of HPAI virus detections in wild and domestic birds during an epidemiological year has not been this low since the 2019–2020 epidemiological year. In addition, the number of HPAI virus detections in the current reporting period was much lower than in the same periods

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

in the previous two epidemiological years 2021–2022 and 2022–2023 (Figure 1). However, HPAI viruses continue circulating in wild birds year-round, albeit at lower levels than in previous years.

Among the possible reasons for this change are flock immunity acquired by certain wild bird species, depletion of some wild bird populations, reduced viral contamination of the environment, changing composition of circulating HPAI virus genotypes, decreased HPAI-induced mortality and reduced effectiveness in detecting dead or infected wild birds.

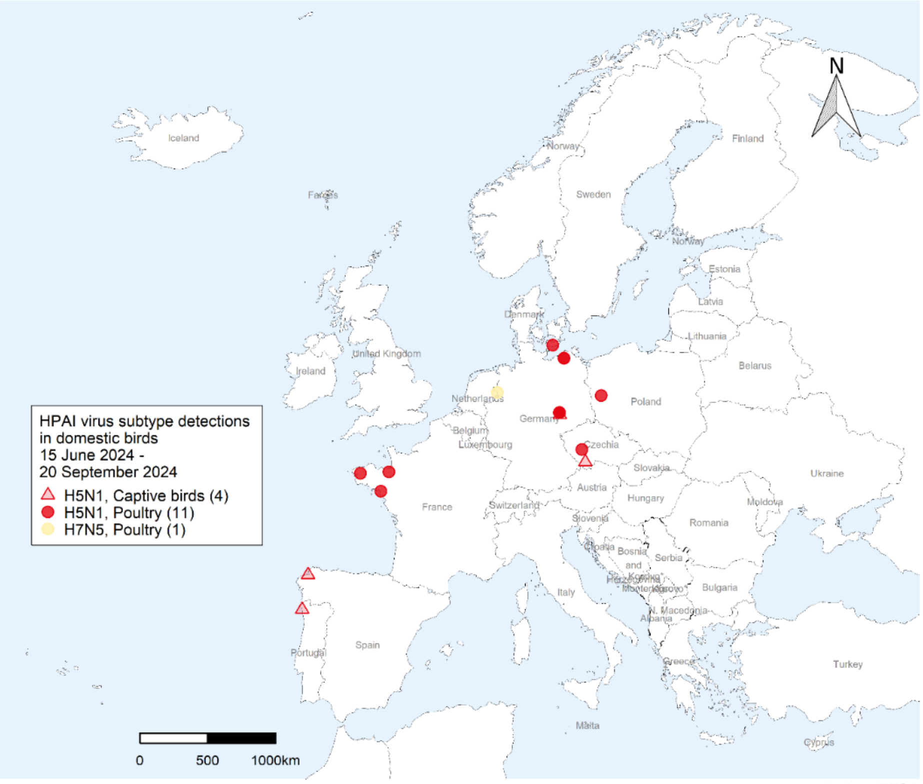
Considering the current reporting period from 15 June to 20 September 2024, 75 HPAI virus detections were reported in poultry (12), captive (4) and wild birds (59) (Table 1, Figure 2).

Table 1: Number of HPAI outbreaks reported in Europe by country, virus subtype and affected sub-population, from 15 June to 20 September 2024. Cumulative numbers since the start of the 2023–2024 epidemiological year are reported in parentheses (1 October 2023 to 20 September 2024)

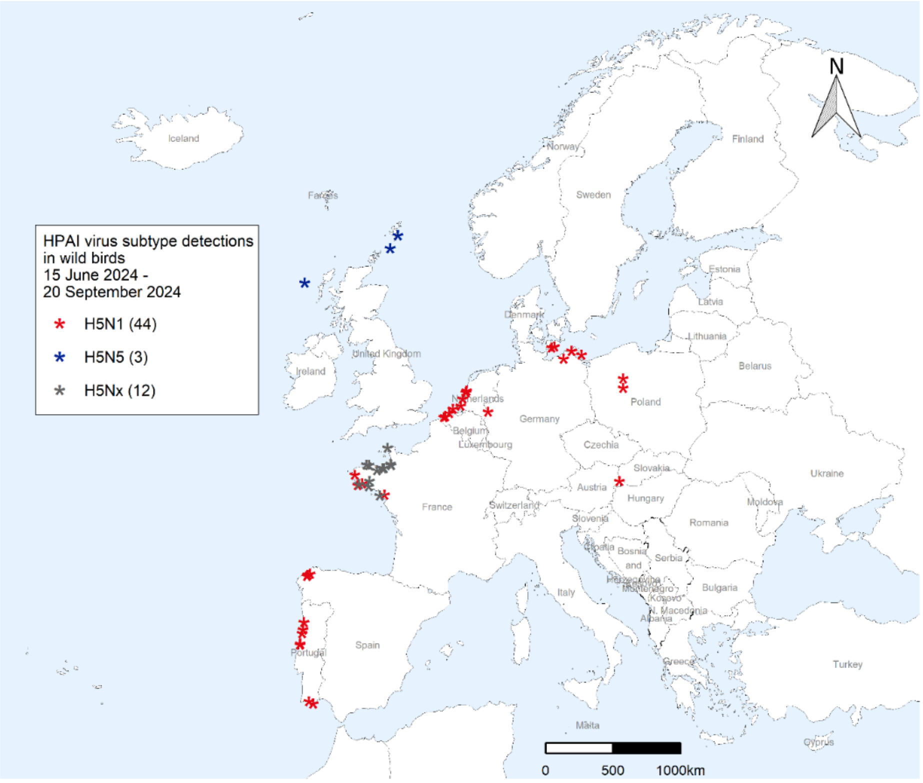
Reporting country	Captive birds		Poultry				Wild birds					Total
	A(H5N1)	A(H5N5)	A(H5N1)	A(H5Nx)	A(H7N5)	A(Not typed)	A(H5N1)	A(H5N5)	A(H5N8)	A(H5Nx)	A(Not typed)	
Austria	- (4)	-	-	-	-	-	1 (24)	-	-	- (2)	-	1 (30)
Belgium	-	-	- (4)	-	-	-	5 (11)	-	-	- (1)	-	5 (16)
Bosnia and Herzegovina	-	-	-	-	-	-	- (1)	-	-	-	-	- (1)
Bulgaria	-	-	- (5)	- (19)	-	-	-	-	-	- (1)	-	- (25)
Croatia	-	-	- (2)	-	-	-	- (7)	-	-	-	-	- (9)
Cyprus	-	-	-	-	-	-	- (1)	-	-	-	-	- (1)
Czechia	1 (24)	-	1 (6)	-	-	-	- (7)	-	-	-	-	2 (37)
Denmark	- (1)	-	1 (12)	-	-	-	2 (82)	-	-	-	-	3 (95)
Faroe Islands	-	- (1)	-	-	-	-	-	-	-	-	-	- (1)
Finland	-	-	-	-	-	-	- (4)	-	-	-	-	- (4)
France	-	-	3 (13)		-	-	4 (4)	-	-	12 (28)	-	19 (45)
Germany	1 (12)	-	5 (31)	-	1 (1)	-	13 (188)	- (2)	- (1)	- (2)	-	20 (237)
Hungary	-	-	- (84)	-	-	-	- (50)	-	-	-	-	- (134)
Iceland	-	-	-	-	-	-	-	- (4)	-	-	-	- (4)
Italy	-	-	- (6)	-	-	-	- (19)	-	-	-	-	- (25)
Kosovo*	-	-	- (1)	-	-	-	-	-	-	-	-	- (1)
Latvia	-	-	-	-	-	-	- (1)	-	-	-	-	- (1)
Lithuania	-	-	- (1)	-	-	-	- (1)	-	-	-	-	- (2)
Moldova	-	-	- (51)	-	-	- (7)	- (31)	-	-	-	-	- (89)

Netherlands	- (2)	-	- (3)	-	-	-	5 (47)	- (1)	-	- (1)	-	5 (54)
Norway	- (1)	-	- (1)	-	-	-	- (3)	- (4)	-	- (3)	-	- (12)
Poland	- (3)	-	1 (34)	-	-	-	2 (25)	-	-	-	-	3 (62)
Portugal	1 (1)	-	-	-	-	-	8 (14)	-	-	-	-	9 (15)
Romania	-	-	- (4)	-	-	-	- (34)	-	-	-	-	- (38)
Serbia	-	-	-	-	-	-	- (9)	-	-	-	-	- (9)
Slovakia	- (3)	-	- (6)	-	-	-	- (9)	-	-	-	-	- (18)
Slovenia	-	-	-	-	-	-	- (14)	-	-	-	-	- (14)
Spain	1 (1)	-	-	-	-	-	4 (20)	-	-	-	-	5 (21)
Sweden	-	-	- (3)	-	-	-	- (29)	-	-	- (4)	-	- (36)
Switzerland	-	-	-	-	-	-	- (1)	-	-	-	-	- (1)
Ukraine	- (7)	-	-	-	-	-	- (6)	-	-	-	-	- (13)
United Kingdom	-	-	- (6)	-	-	-	- (18)	3 (10)	-	-	- (1)	3 (35)
Total	4 (59)	- (1)	11 (273)	- (19)	1 (1)	- (7)	44 (660)	3 (21)	- (1)	12 (42)	- (1)	75 (1,085)

*This designation is without prejudice to positions on status and is in line with United Nations Security Council Resolution 1244 and the International Court of Justice Opinion on the Kosovo Declaration of Independence.
'-' means that no HPAI outbreaks were notified via ADIS.



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 20/09/2024



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 20/09/2024

*This designation is without prejudice to positions on status and is in line with United Nations Security Council Resolution 1244 and the International Court of Justice Opinion on the Kosovo Declaration of Independence. United Kingdom data are from ADNS up until 31 December 2020. From 1 January 2021 onwards, the data source was WOAH for the United Kingdom (excluding Northern Ireland) and ADNS/ADIS for the United Kingdom (Northern Ireland)[5].
Source: ADIS, EFSA and WOAH (data extraction carried out on 20 September 2024).

Figure 2: Geographic distribution, based on available geocoordinates, of HPAI virus detections in poultry and captive birds (16) (upper panel), and in wild birds (59) (lower panel) reported by virus subtype in Europe from 15 June to 20 September 2024

During the current reporting period, HPAI outbreaks in poultry and captive birds were mostly located along the Atlantic (France, Portugal, Spain) and Baltic (Germany) coastlines. However, a few of them were also located inland, such as the HPAI A(H7N5) outbreak in Germany near the border with the Netherlands (Figure 2). Similarly, HPAI virus detections in wild birds were concentrated along the coastlines of the Atlantic Ocean (France, Portugal, Spain), Baltic Sea (Germany), and North Sea (Belgium, Germany, Netherlands, United Kingdom) (Figure 2). The majority of these HPAI virus detections concerned colony-breeding seabirds (Figure 3), similar to the picture observed in summer 2023, although there was a much lower number of HPAI virus detections in wild birds in general during this reporting period (Figure A.1 in Annex A).

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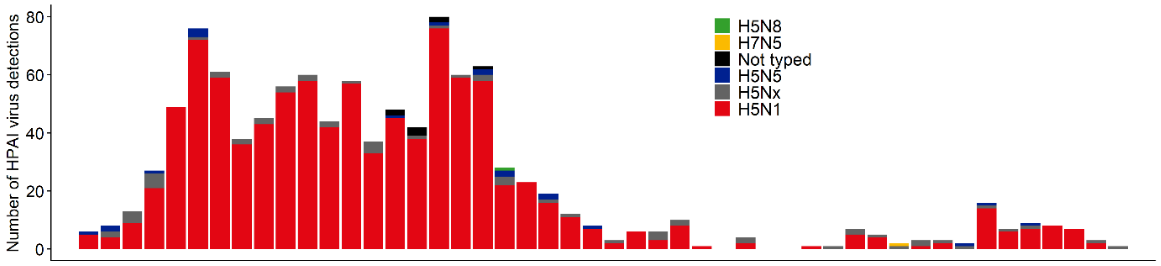
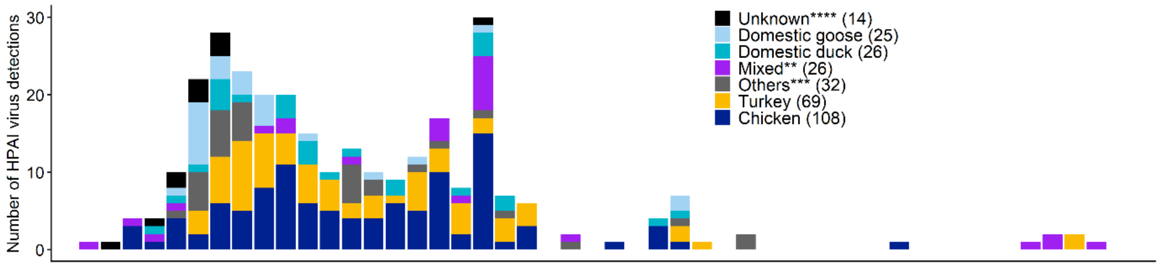
[5] In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Windsor Framework, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).

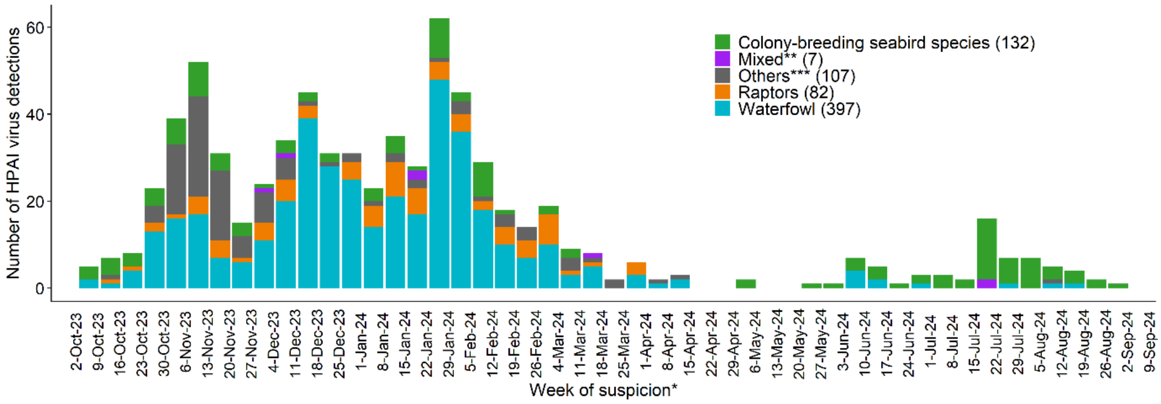
(a) All birds



(b) Poultry



(c) Wild birds



*If the date of suspicion was not available, the date of confirmation was used to assign the week of suspicion.
**'Mixed' refers to outbreaks in which multiple species or categories were involved.
***'Others' groups all other affected categories that are not indicated in the legend.
****'Unknown' refers to affected categories that were not further specified during reporting.
Source: ADNS/ADIS, EFSA and WOAH (data extraction carried out on 20 September 2024).

Figure 3: Distribution of the total number of HPAI virus detections reported in Europe by week of suspicion (dates indicate the first day of the week) and virus subtype (a), affected poultry categories (b) and affected wild bird categories (c), from 1 October 2023 to 20 September 2024

While the majority of HPAI virus detections in birds during this reporting period can be attributed to A(H5N1) viruses, A(H5N5) viruses were still sporadically found in colony-breeding seabirds (great black-backed gull, great skua) in the United Kingdom (Table 1, Figure 2, Figure 3). In addition, a single HPAI outbreak caused by A(H7N5) virus was detected in poultry in Germany.

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

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

Poultry

Between 15 June and 20 September 2024, 12 HPAI outbreaks in poultry were reported from five countries in Europe: Czechia, Denmark, Germany, France and Poland (Table 1, Figure 2). This compares to a total of 25 A(H5) outbreaks during the same period in the previous epidemiological year, when the majority of outbreaks were reported from the United Kingdom, and is the lowest number recorded for this period since 2021. Ten of these outbreaks were reported as primary and two as secondary. For seven out of 12 of these outbreaks, indirect contact with wild birds was considered the most likely source of introduction, while it was indirect contact with poultry for another one, and no information was available for the remaining four outbreaks. Half (n = 6) of the poultry establishments kept multiple species (Figure 3). In total, approximately 125,000 birds died or were culled in the HPAI-affected poultry establishments.

In the following paragraphs, a brief description of the HPAI outbreaks in poultry is given by country. This description is based on information collected by EFSA from ADIS, reporting countries (in form of additional data submitted and personal communications) and media reports. In the period from 15 June to 20 September 2024, 12 HPAI outbreaks in poultry were reported in Europe via ADIS. Additional data on the characteristics of the affected poultry establishments and poultry species reared were collected for nine out of these 12 outbreaks from Denmark, France, Germany and Poland (Annex B). The remaining three outbreaks in poultry occurred too shortly before the publication of this report, which is why additional data on these outbreaks will only be collected from the reporting countries for the next report.

Czechia

During the current reporting period from 15 June to 20 September 2024, one outbreak in poultry was reported in Czechia via ADIS. On 13 September, an A(H5N1) outbreak was detected in a multi-species establishment keeping domestic geese for fattening (n = 700) and laying hens (n = 300) in separate buildings. Increased mortality and clinical signs, including convulsions, spastic movements and twitching, were reported in the geese. No additional information was collected for this outbreak, as it occurred too close to the time of publication of this report.

Denmark

During the current reporting period from 15 June to 20 September 2024, one outbreak in poultry was reported in Denmark via ADIS. On 8 September, an A(H5N1) outbreak was detected in a multi-species establishment keeping domestic ducks for fattening (n = 3,200) and chickens raised for different purposes (laying hens and broilers, n = 2,800). Increased mortality as well as respiratory and neurological signs, including a decrease in feed and water intake, were only described in the ducks. Outdoor access was available for ducks, but the chickens were kept indoors. The most likely source of introduction remained unknown at the time of publication of this report. In total, 43 people were reported as exposed. Out of these, 38 professionals in disease control measures performed the culling, destruction and cleaning with protective equipment. Five people were staff members from the establishment.

France

During the current reporting period from 15 June to 20 September 2024, three outbreaks in poultry were reported in France via ADIS, all located in the same ecological region on the coast of Brittany. On 7 August, an A(H5N1) outbreak was detected in a small multi-species establishment keeping chickens, guinea fowl, domestic ducks and domestic geese (n = 1,200). Increased mortality was reported in all species except geese, but it remains unknown whether clinical signs were present. Given that the birds had outdoor access and related viruses were detected along the coast of Brittany, with seabirds testing positive to viruses of the same genotype in neighboring counties, the most likely source of introduction was indirect contact with wild birds. On 19 August, A(H5N1) virus was detected in an establishment keeping turkeys for fattening (n = 4,650), approximately 150 km south of the first outbreak. The establishment did not provide outdoor access and the most likely source of introduction was indirect contact with wild birds. Increased mortality and clinical signs, including a decrease in feed and water intake, were observed. On 31 August, A(H5N1) virus was once again detected in an establishment keeping domestic ducks for fattening (n = 425), chickens for fattening (n = 190), domestic guinea fowl for fattening (n = 18), domestic geese for fattening (n = 12), domestic pigeons for fattening (n = 7), and one turkey for fattening. Increased mortality was reported in all these species except geese. Clinical signs were observed in the chickens and guinea fowl, but not in the ducks, geese, domestic pigeons and turkeys. Outdoor access for birds was provided, with the most likely source of introduction being direct or indirect contact with wild birds. None of the birds of the three affected establishments were vaccinated. More information on the French HPAI vaccination campaign implemented in the epidemiological year 2023–2024 can be found in Annex A.

Germany

During the current reporting period from 15 June to 20 September 2024, six outbreaks in poultry were reported in Germany via ADIS. Additional information was collected from the reporting country for four outbreaks out of the six, as the last two were reported too close to the time of publication of this report. On 29 June, an outbreak of A(H7N5) was detected in an establishment keeping laying hens (n = 90,879) near the border with the Netherlands. High mortality (n = 6,000) and the presence of clinical signs, such as a drop in egg production, were reported. The detected HPAI virus is not related to any known strains circulating locally, with the closest relation being an A(H7N5) virus reported in Asia. However, despite the absence of A(H7N5) virus detection in wild birds in Germany (possibly due to the low number of wild birds found dead during the summer), the most likely source of introduction was indirect contact with wild birds, given that outdoor access was available for the birds. On 11 August, two A(H5N1) outbreaks were reported in two establishments belonging to the same owner and located in the same area on the Baltic Sea coast. Both establishments kept multiple species, including domestic ducks for fattening (n = 6,219), domestic geese for fattening (n = 165) and chickens (n = 120) in the establishment reported as the primary outbreak, and domestic ducks for fattening (n = 2,227) and geese for fattening (n = 230) in the establishment reported as the secondary outbreak. Outdoor access was available in both establishments. In the primary outbreak, mortality was observed in all species, and the most likely source of introduction was indirect contact with wild birds. In the second affected establishment, increased mortality was only reported in ducks and the source of introduction was indirect contact with poultry from the first establishment. No information on the presence of clinical signs was available for these two establishments. One month later, A(H5N1) virus was detected in three establishments located approximately 300 km inland from these outbreaks. The establishment identified as the primary outbreak kept domestic ducks (n = 100) and domestic geese (n = 98), with increased mortality being observed in both species. No information on the presence of clinical signs was available. Outdoor access was provided, and the most likely source of introduction was indirect contact with wild birds. This outbreak was reported with another HPAI virus detection in a wildlife park, only 15 km away, on the same day. No additional information was provided regarding the two other outbreaks occurring in the same city in establishments keeping laying hens and ducks (n = 34 and n = 84) at low density. No information on the number of exposed people was available at the time of publication of this report.

Poland

During the current reporting period from 15 June to 20 September 2024, one outbreak in poultry was reported in Poland via ADIS. On 21 August, A(H5N1) virus was detected in an establishment keeping 10-week old turkeys for fattening (n = 14,730). High mortality (n = 7,749) and the presence of clinical signs, including a decrease in feed and water intake, were observed. The establishment did not provide outdoor access, but the most likely source of introduction was indirect contact with wild birds. In total, 22 people were reported as exposed.

Captive birds

Czechia

During the current reporting period from 15 June to 20 September 2024, one outbreak in captive birds was reported in Czechia via ADIS. On 22 August, A(H5N1) virus was detected in laying hens (n = 8) kept by a small hobby owner. High mortality and the presence of clinical signs were reported.

Germany

During the current reporting period from 15 June to 20 September 2024, one outbreak in captive birds was reported in Germany via ADIS. On 11 September, A(H5N1) virus was detected in a swan kept in a zoo. The bird had been rescued by a citizen a few days before and later died at the facility. As part of the control measures taken, the entire poultry population of the zoo was culled following the confirmation of the case.

Portugal

During the current reporting period from 15 June to 20 September 2024, one outbreak in captive birds was reported in Portugal via ADIS. The suspicion was notified by 13 August 13, when sampling was also carried out, and the outbreak of A(H5N1) was confirmed in a backyard establishment keeping laying hens (n = 100) on 14 August, on the northern coast of the country. High mortality (n = 60) and the presence of clinical signs were described. The affected backyard establishment was located about 50 km from the beach where a positive seabird had been detected previously, and since the establishment did not implement a high level of biosecurity, the most likely source of introduction was considered direct or indirect contact with seabirds.

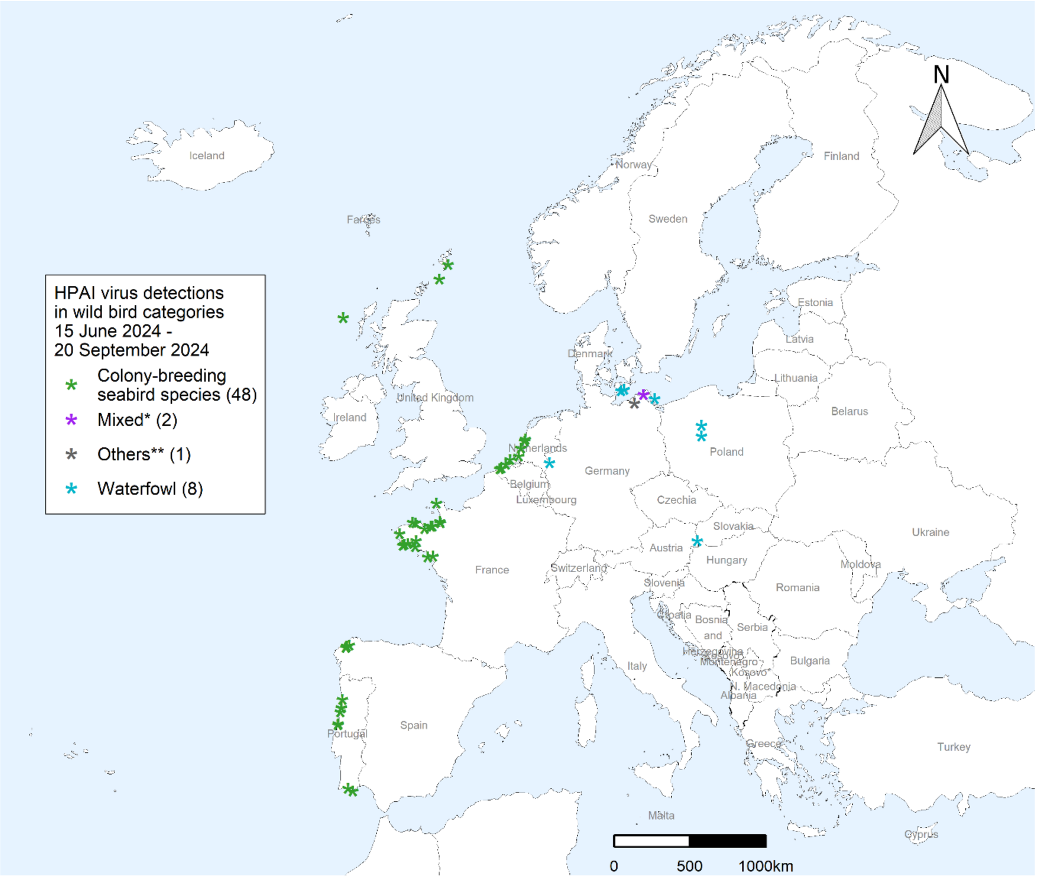
Spain

During the current reporting period from 15 June to 20 September 2024, one outbreak in captive birds was reported in Spain via ADIS. On 8 August, A(H5N1) virus was detected in four yellow-legged gulls in a wildlife recovery center on the Galician coast. The most likely source of introduction was considered an ill yellow-legged gull that was brought to the centre a few days before and later tested positive to HPAI virus (La Opinión, online).

Wild birds

During the current reporting period from 15 June to 20 September 2024, a total of 59 HPAI virus detections in wild birds (sometimes including several wild birds per detection) were reported from France (16), Germany (13), Portugal (8), Belgium (5), the Netherlands (5), Spain (4), the United Kingdom (3), Denmark (2), Poland (2) and Austria (1). Forty-four HPAI virus detections in wild birds were reported as A(H5N1), 12 as A(H5Nx) (all from France) and three as A(H5N5) (all from the United Kingdom) virus detections (Table 1, Figure 2).

While all HPAI virus detections in colony-breeding seabirds during the current reporting period were lined up along the coastlines of the Atlantic Ocean and North Sea, HPAI virus detections in waterfowl (also mixed outbreaks including gannets) were concentrated further east, especially in the Baltic Sea area, but also further inland in eastern and southeastern Europe (Figure 4). Of note, no affected raptors were detected during the current reporting period.



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 20/09/2024

[*] This designation is without prejudice to positions on status and is in line with United Nations Security Council Resolution 1244 and the International Court of Justice Opinion on the Kosovo Declaration of Independence.
Note that the unit reported is the number of HPAI virus detections in different wild bird categories and not the total number of HPAI virus detections in wild birds (as more than one species can be involved in one single HPAI virus detection reported).
[*] ‘Mixed’ refers to outbreaks in which multiple categories were involved.
[**] ‘Others’ groups all other affected categories that are not indicated in the legend.
Source: ADIS, EFSA and WOAH (data extraction carried out on 20 September 2024).

Figure 4: Geographic distribution, based on available geocoordinates, of HPAI virus detections in different categories of wild birds in Europe, by species category, from 15 June to 20 September 2024

The overall number of reported HPAI virus detections in wild birds (59) was almost two times higher than in the previous reporting period (16 March to 14 June 2024, n = 33) (Figure 3). Of note, considering that more than one wild bird species can be included in a single HPAI virus detection, A(H5) was only recorded in five waterfowl identified to species: two mute swans and one bean goose with A(H5N1) in Poland, and another two mute swans with A(H5N1) in Denmark (Figure A.2 in Annex A). In contrast, HPAI virus detections were detected in 38 colony-breeding seabirds identified to species: 34 gulls (see below for details), two northern gannets with A(H5N1) in France, and two great skuas with A(H5N5) in the United Kingdom (Figure A.2 in Annex A).

Although there was a predominance of HPAI virus detections in colony-breeding seabirds (more than one wild bird can be included in a single HPAI virus detection) during the current reporting period, the number (54) was around 15 times lower than during the same time period in 2023 (15 June to 20 September 2023; n = 819), when there was high

HPAI-associated mortality at breeding sites of colony-breeding seabirds (EFSA, ECDC and EURL, 2023). In contrast, there were no reports of increased mortality in this category of wild birds during the current reporting period. For example, there was no evidence of HPAI-associated mortality in the United Kingdom's largest mainland colony of Arctic terns at Long Nanny on the Northumberland coast (BBC, online).

The few wild birds in which HPAI viruses were detected belonged to four orders, namely Charadriiformes (43), Suliformes (11), Anseriformes (11) and Ciconiiformes (1) (Figure A.2 in Annex A). The most common colony-breeding seabird identified to species was the European herring gull (19 in the current vs 3 in the previous reporting period), and a total of 34 out of 43 wild birds identified to species were gull species: European herring gull (19), yellow-legged gull (7), Audouin's gull (2), black-headed gull (2), lesser black-backed gull (2), great black-backed gull (1) and mew gull (1) (Figure A.2 in Annex A). Among these, HPAI virus was identified for the first time in two Audouin's gulls in Portugal. The only two waterfowl identified to species were the mute swan (4 vs 5) and the bean goose (1 vs 0). The complete list of wild bird species found as HPAI virus-infected from 15 June to 20 September 2024 is reported in Figure A.2 in Annex A. The number of HPAI virus-affected wild birds that were not identified to species was 23/66 (35%), slightly higher than in the previous reporting period (11/34, 32%) (Figure A.3 in Annex A). This was especially the case in Germany, where identification of wild bird species in ADIS is based on the immediate report of the district veterinary officer to the German animal disease information system (TSN) shortly after confirmation in the national reference laboratory (NRL). The more precise information on the species is later entered into the German AI surveillance database (AI-DB) by the federal state laboratory.

The overall picture is similar to that of the previous reporting period, namely that HPAI viruses were only circulating at a low level in wild bird populations in Europe without causing mass mortality events. Possible explanations are acquired flock immunity after previous infections, depletion of certain wild bird populations, and underreporting due to decreased detection of dead wild birds in certain countries. HPAI virus detections in wild birds are generally underestimated. Therefore, the numbers provided most likely do not reflect the number of wild birds that actually died from A(H5) virus infection.

Note that Figures A.2–A.3 in Annex A provide information on the numbers of wild bird categories/families/species that were detected as HPAI virus-infected at single bird level, as more than one bird can be involved in one single HPAI virus detection reported.

2.1.2 HPAI virus detections in birds outside Europe

An overview of the HPAI virus detections in birds that were notified from other countries not reporting via ADIS but via WOAH from 15 June to 20 September 2024 is presented in Table 2 and Figure 5.

Table 2: Number of HPAI virus detections in non-European countries, by virus subtype and country, from 15 June to 20 September 2024. Cumulative numbers since the start of the 2023–2024 epidemiological year are reported in parentheses (1 October 2023 to 20 September 2024)

Region (total in season)	**Country**	**Domestic birds**									**Wild birds**					**Total**
		A(H5N1)	**A(H5N2)**	**A(H5N6)**	**A(H5Nx)**	**A(H7N3)**	**A(H7N6)**	**A(H7N8)**	**A(H7N9)**	**A(Not typed)**	**A(H5N1)**	**A(H5N5)**	**A(H5N6)**	**A(H5Nx)**	**A(Not typed)**	
Africa (40)	Burkina Faso	- (2)	-	-	-	-	-	-	-	-	-	-	-	-	-	- (2)
	Gabon	- (1)	-	-	-	-	-	-	-	-	-	-	-	-	-	- (1)
	Nigeria	1 (4)	-	-	-	-	-	-	-	-	-	-	-	-	-	1 (4)
	South Africa	-	-	-	-	-	1 (23)	-	-	- (8)	-	-	-	-	- (2)	1 (33)
Americas (618)	Argentina	- (2)	-	-	-	-	-	-	-	-	- (8)	-	-	- (1)	-	- (11)
	Brazil	-	-	-	-	-	-	-	-	-	- (45)	-	-	-	-	- (45)
	Canada	- (52)	-	-	-	-	-	-	-	-	4 (14)	1 (5)	-	1 (2)	-	6 (73)
	Colombia	-	-	-	- (13)	-	-	-	-	-	-	-	-	- (1)	-	- (14)
	Costa Rica	-	-	-	-	-	-	-	-	-	-	-	-	- (2)	-	- (2)
	Ecuador	- (2)	-	-	-	-	-	-	-	-	- (2)	-	-	-	-	- (4)
	Mexico	1 (9)	- (1)	-	-	- (8)	-	-	-	-	- (9)	-	-	-	-	1 (27)
	Peru	-	-	-	14 (82)	-	-	-	-	-	-	-	-	- (15)	-	14 (97)
	United States of America	18 (333)	-	-	-	-	-	-	-	-	2 (11)	-	-	-	-	20 (344)
	Uruguay	-	-	-	-	-	-	-	-	-	- (1)	-	-	-	-	- (1)
Antarctica (8)	Antarctica	-	-	-	-	-	-	-	-	-	- (1)	-	-	- (1)	-	- (2)
	Falkland Islands	-	-	-	-	-	-	-	-	-	- (1)	-	-	-	-	- (1)
	South Georgia and the South Sandwich Islands	-	-	-	-	-	-	-	-	-	- (5)	-	-	-	-	- (5)
Asia (320)	Bhutan	2 (2)	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (2)
	Cambodia	2 (14)	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (14)
	China	-	-	-	-	-	-	-	-	-	- (3)	-	- (1)	- (1)	-	- (5)
	Hong Kong	-	-	-	-	-	-	-	-	-	- (6)	-	-	-	-	- (6)
	India	2 (12)	-	-	-	-	-	-	-	-	-	-	-	-	-	2 (12)

Region (total in season)	**Country**	**Domestic birds**									**Wild birds**					**Total**
		A(H5N1)	**A(H5N2)**	**A(H5N6)**	**A(H5Nx)**	**A(H7N3)**	**A(H7N6)**	**A(H7N8)**	**A(H7N9)**	**A(Not typed)**	**A(H5N1)**	**A(H5N5)**	**A(H5N6)**	**A(H5Nx)**	**A(Not typed)**	
	Iraq	-	-	-	-	-	-	-	-	-	- (1)	-	-	-	-	- (1)
	Israel	2 (5)	-	-	-	-	-	-	-	-	- (9)	-	-	-	-	2 (14)
	Japan	- (12)	-	- (1)	-	-	-	-	-	-	- (110)	- (31)	- (1)	-	-	- (155)
	Kazakhstan	-	-	-	-	-	-	-	-	-	-	-	-	- (1)	-	- (1)
	Republic of Korea	- (7)	-	- (26)	-	-	-	-	-	-	- (6)	-	- (11)	-	-	- (50)
	Philippines	- (7)	-	-	-	-	-	-	-	-	-	-	-	-	-	- (7)
	Russia	- (3)	-	-	-	-	-	-	-	-	-	-	-	-	-	- (3)
	Taiwan	5 (47)	-	-	-	-	-	-	-	-	- (3)	-	-	-	-	5 (50)
Oceania (16)	Australia	-	-	-	-	1 (7)	-	8 (8)	- (1)	-	-	-	-	-	-	9 (16)
Total		33 (514)	- (1)	- (27)	14 (95)	1 (15)	1 (23)	8 (8)	- (1)	- (8)	6 (235)	1 (36)	- (13)	1 (24)	- (2)	65 (1002)

'-' means that no HPAI outbreaks were notified to WOAH.
Source: WOAH (data extraction carried out on 23 September 2024).

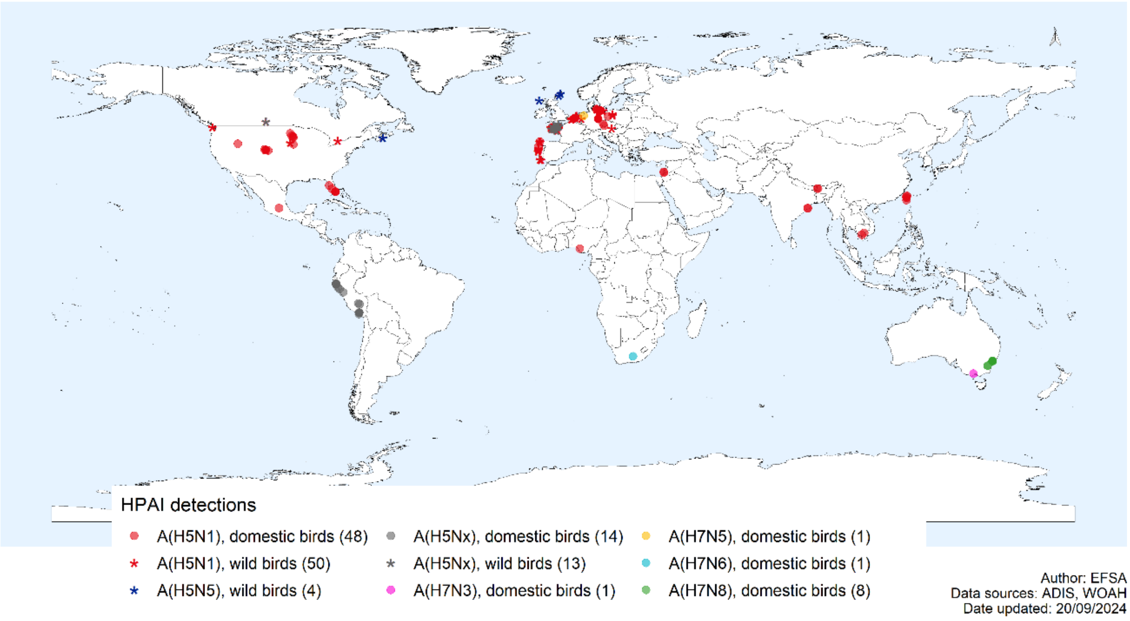


Figure 5: Geographic distribution, based on available geocoordinates, of HPAI virus detections reported worldwide in domestic (73) and wild (67) birds by virus type, from 15 June to 23 September 2024

In the tables and figures of the present report, only data extracted from WOAH on 23 September 2024 are presented. However, HPAI virus detections in poultry and wild birds are also reported to the public via different means. This additional information on HPAI virus detections available from sources other than WOAH-WAHIS has been integrated in the text below.

In comparison to the previous reporting period from 16 March to 14 June 2024 (EFSA, ECDC and EURL, 2024a), the total number of HPAI virus detections reported in domestic and wild birds officially notified to WOAH from outside Europe dropped from 141 to 65, and the number of countries outside Europe from 15 to 12 (Table 2, Figure 5). The official figures reported to WOAH during the current reporting period were about five times lower than the number of HPAI virus detections reported in the same period in 2023 (between 15 June and 20 September; 65 HPAI virus detections in the current vs 304 in the previous epidemiological year). In contrast to the previous reporting period, only eight cases in wild birds were officially reported to WOAH worldwide in the period from 15 June to 23 September 2024. Canada and the United States of America (USA), which notified A(H5N1) in domestic and wild birds, contributed almost 20% of all cases worldwide (and 40% of the cases outside Europe). In addition, A(H5N1) virus detections in wild birds were only reported from these two countries outside Europe. Overall, HPAI virus detections in domestic birds officially reported to WOAH decreased notably from the previous to the current reporting period (96 vs 57), in particular the number of cases in wild birds (45 vs 8).

In Africa, during the current reporting period, two HPAI outbreaks in domestic birds were officially reported to WOAH: one A(H5N1) outbreak in a poultry establishment (n = 1,590) in Nigeria in late August (Food Business Africa, online), and another A(H7N6) outbreak in South Africa in mid-June. In addition, a social media report revealed an ongoing A(H5N1) outbreak in a live bird market in Libreville, Gabon, in June (Devdiscourse, online).

The large epidemic of A(H5N1) in the USA continued on a high level in poultry establishments of all sizes, including several establishments with more than 150,000 birds and one establishment with 1.3 million laying hens. Furthermore, medium- and some small-scale establishments were affected by the epidemic as well as live bird markets in Florida (CDC, online-a). The United States Department of Agriculture (USDA) estimates that more than 20 million birds of different species pass through 150 known storefront live bird markets just in northeastern US metropolitan areas every year, which are monitored with the help of various surveillance schemes (The Humane Society of the United States, 2007; USDA VS, online). The USDA also reported the detection of A(H5) in six captive and 463 wild birds, comprising a total of 43 different species, in the period from 15 June to 20 September 2024 (USDA, online-a). Furthermore, social media reported about a combined outbreak of A(H5N1) and botulism with thousands of birds dying in Tule Lake National Wildlife Refuge in northern California (OPB, online). Canada detected A(H5N1) and A(H5Nx) only in wild birds, such as the American crow, cackling goose, Canada goose, dunlin, golden eagle, great horned owl, merlin, northern fulmar and Ross’s goose. There was also a single detection of A(H5N5) in a mixed outbreak concerning a European herring gull, a great black-backed gull and an Iceland gull. Besides Canada and the USA, only Mexico and Peru notified outbreaks of A(H5Nx) and A(H5N1), respectively, in the Americas. The disease was detected in several backyard farms and in captive European wild birds (Gestión, online; Infobae, online). In contrast to the previous reporting period, Brazil did not report any further outbreaks from previously affected locations on the Brazilian Atlantic coast.

In Asia, the outbreaks of A(H5N1) of clade 2.3.4.4b in poultry and quail establishments of all sizes in Taiwan continued (WOAH; CNA, online). However, in contrast to the reports of 2023, no further outbreaks of the Taiwanese lineage A(H5N2) virus were reported to WOAH. At the beginning of September, Israel detected the first outbreak of A(H5N1) in 2024 in a large turkey establishment (n = 8,700) in the northern part of the country (WOAH; Xinhua News, online-a). About two weeks later, another HPAI outbreak was confirmed 20 km north of the previous outbreak, in another establishment keeping turkeys (n = 34,000) (Xinhua News, online-b). In Southeast Asia, Bhutan and Cambodia notified outbreaks of A(H5N1) in large poultry establishments to WOAH. The previous outbreak in Bhutan occurred over a year ago (WOAH, online). India notified two A(H5N1) outbreaks in domestic birds to WOAH, but also wild birds were mentioned in the media (Business Insider India, online; Times Now, online). Furthermore, only the media reported the continuation of A(H5N1) virus detections in domestic and wild birds in the Philippines (Philstar, online), another country that was affected in previous reporting periods. The China Ministry of Agriculture and Rural Affairs reported the detection of A(H5Nx) in wild waterfowl in Zhejiang Province (MOA, online). This report and China's notification from the previous reporting period are of concern, as wild birds migrate to breeding areas in northern Asia and subsequently south to the Americas, Asia and Europe in autumn.

The outbreaks of A(H7N3) and A(H7N8) continued in domestic birds in Australia. One outbreak of A(H7N3) was detected in a large poultry establishment in the state of Victoria (WOAH; Agriculture Victoria, online). Furthermore, Australia notified for the first time several outbreaks of A(H7N8) in the greater Sydney and Canberra area, a subtype different from the outbreaks of the A(H7N3) and A(H7N9) strains first detected in the state of Victoria (ABC News, online; The Guardian, online-a). With the aim to protect endangered bird species, New Zealand started vaccinating captive wild birds against A(H5N1) for the first time (The Guardian, online-b).

On 20 September 2024, one dead gentoo penguin was found positive to HPAI virus at Surf Bay on the Falkland Islands (Falkland Islands Department of Agriculture, online; RSOE, online). Although no further cases from the Antarctic region were reported to WOAH during the current and previous reporting periods, since 16 March 2024, the detection of HPAI virus has been confirmed in further 14 bird carcasses, such as in skua, penguin and snowy sheathbill, from which samples had been collected on the Antarctic peninsula and northern area of the Weddell Sea back in March 2024 (Sabemos, online). Furthermore, research expeditions and studies exploring the impact of A(H5N1) on birdlife of the Antarctic region are still ongoing (FLI, online; IAATO, online).

The list of wild bird species that were reported to WOAH as HPAI virus-infected from outside Europe between 15 June and 20 September 2024 is presented in Table A.1 in Annex A.

2.1.3 Genetic characteristics of HPAI viruses of the A(H5Nx) subtype in avian species

Details on the nomenclature of the HPAI A(H5) viruses used in this section are reported in Appendix B. Genotypes are assigned using the criteria described in Fusaro et al. (2024). Mutation analyses of the A(H5N1) viruses have been performed using FluMut (Github izsvenezie-virology, online-a, b) with FluMutDB v5.0 mutation database.

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

Since October 2023, complete genome sequences of > 630 clade 2.3.4.4b A(H5) viruses collected from 24 European countries have been characterised. The vast majority (> 90%) belong to six different A(H5N1) and one A(H5N5) genotypes, namely:

- EA-2021-AB (H5N1 A/duck/Saratov/29-02/2021-like)
- A-2022-BB (H5N1-A/Herring_gull/France/22P015977/2022-like)
- EA-2023-DA (H5N1-A/mute_swan/Slovenia/PER1486-23TA_23VIR10323-22/2023-like)
- EA-2023-DB (H5N1-A/herring_gull/Germany-NI/2023AI08764/2023-like)
- EA-2023-DG (H5N1-A/Gallus_gallus/Belgium/11307_0002/2023-like)
- EA-2023-DI (H5N1 A/mute_swan/Poland/MB008-1/2024-like)
- EA-2021-I (H5N5 A/whooper_swan/Romania/10123_21VIR849-1/2021-like).

Based on the current available data, three genotypes have mainly been circulating in Europe during the summer months (June–August 2024), namely EA-2023-DI, EA-2022-BB and EA-2023-DT (H5N1-A/gull/Spain/5061-23_24VIR4860-8/2023-like). The A(H5N5) genotype EA-2021-I, which was reported in multiple European countries in the first half of the current epidemiological year (October 2023–February 2024), has been detected since June 2024 only in great skuas on the islands off the northern coast of the United Kingdom.

Since June 2024, a rapid increase in the frequency of the EA-2022-BB genotype has been observed along the northern European coasts of France, Belgium and the Netherlands, with most cases detected among Laridae. In contrast, all characterised viruses detected in seabirds (Laridae) along the Atlantic coast of Spain and Portugal belong to genotype EA-2023-DT, which originated from a reassortment event between the EA-2022-BB (PB2/HA/NP/NA/M/NS) and a gull-adapted H13 subtype (PB1/PA). Indeed, compared to EA-2022-BB (5:3 – PB2/PB1/HA/NA/M from H5N1 and PA/NP/NS from H13), the EA-2023-DT genotype has an additional gene segment originating from the H13 subtype (4:4 – PB2/HA/NA/M from H5N1 and PB1/PA/NP/NS from H13). EA-2023-DT was detected for the first time in Spain in November 2023 and during the winter it had co-circulated with the EA-2022-BB genotype among Laridae and Sulidae in the country. However, since May 2024, it is the only genotype detected in this geographic area, suggesting it has rapidly replaced the EA-2022-BB genotype. Of note, the analysis of the partial genome obtained from an A(H5N1) virus collected in August 2024 from a European herring gull suggests that the EA-2023-DT genotype has also spread to France.

The EA-2023-DI genotype emerged at the end of 2023 and had been extensively circulating in wild (mainly Anseriformes) and domestic birds in eastern and southern Europe during the winter. Since June 2024, this genotype has been detected mainly in mute swans in Denmark, Germany and Poland.

The genetically characterised A(H5N1) viruses responsible for the domestic bird outbreaks during the current reporting period in Denmark, France, Poland and Portugal were very closely related to the viruses circulating in wild birds in the respective country and belong to three distinct genotypes: EA-2022-BB (France), EA-2023-DT (Portugal) and

EA-2023-DI (Denmark and Poland). Differently, the virus collected from a backyard farm in Czechia belongs to genotype EA-2021-AF. Since October 2022, this genotype has been detected only in domestic birds in Eastern Europe.

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

Molecular analyses of the A(H5N1) viruses circulating in birds in Europe during the 2023–2024 epidemiological year indicate that these viruses continue to be well-adapted to avian species, as they retain a preferential binding for avian-like receptors. However, 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 alpha2,6-SA; v) decreased antiviral response in ferrets; vi) evasion of human butyrophilin subfamily 3 member A3 (BTN3A3); and vii) disruption of the second sialic acid (SIA) binding site in the neuraminidase protein, with a frequency varying by the distinct mutations. The net effect of these mutations on the biological characteristics of the viruses is still unknown and further studies are needed to improve existing knowledge. Since October 2023, mutations in the PB2 protein associated with virus adaptation in mammals (E627K, D701N or K526R) have been detected in 17 European viruses collected from birds (2.7%), more specifically in i) nine genetically related A(H5N5) viruses (genotype EA-2021-I) collected from wild birds in England, Germany, the Netherlands and Norway in January–February 2024; ii) six A(H5N1) viruses collected between October 2023 and March 2024 from separate outbreaks in domestic birds in Poland (genotypes EA-2022-CH and EA-2021-AB), Denmark (genotype EA-2023-DB), Czechia (genotype EA-2024-DI) and Romania (genotype EA-2023-DA); and iii) two A(H5N1) viruses collected from wild birds in France in February–July 2024 (genotype EA-2022-BB). Of note, the emergence of mutations PB2-E627K and PB2-D701N have been observed also in several A(H5N5) viruses (genotype EA-2021-I) collected from wild birds and mammalian species in Canada and Japan. Phylogenetic clustering suggests that these mammalian adaptive markers have emerged independently in the different continents.

Among the mutations in the HA protein that have proved to increase in vitro binding to human-type receptors, some (i.e. S133A, S154N, T156A, H5 numbering) have been identified in the majority of the A(H5N1) viruses which have been circulating in Europe since October 2023, while others (i.e. E251K, E75K-S123P, P235S, V210I and S155N) have only been sporadically observed (< 5 viruses). The impact of these HA mutations on the biological characteristics of the circulating viruses is still unknown; however, none of them has been demonstrated to cause a shift from avian-like to human-like receptor binding preference. Moreover, most of the A(H5N1) viruses belonging to the EA-2022-BB and EA-2023-DT genotypes contain mutations NP-Y52N and NA-S369I, which may impact upon their zoonotic potential. All the currently circulating A(H5N5) viruses (genotype EA-2021-I) contain a deletion in the NA stalk region, which is a virulence determinant in chickens (Stech et al., 2015). Mutations associated with reduced susceptibility of A(H5N1) viruses to available antiviral drugs authorised for use in humans have rarely been identified in the circulating strains. Specifically, mutations associated with resistance towards adamantanes, NA and PA inhibitors (WHO, online-a) have been detected in approximately 1.1%, 0.2% and 1% of the analysed A(H5N1) viruses, respectively. However, for PA inhibitors, it is important to mention that mutations have been studied in seasonal influenza viruses and not specifically for A(H5N1) viruses, the threshold of ≥ 3 IC50 fold-change was used for the assignment of viruses with reduced susceptibility to PA inhibitors.

Genetic characteristics of HPAI A(H7N5) virus from Germany

The complete genome sequence analysis of the A(H7N5) identified in a laying hen establishment in Germany in June 2024 shows that the virus clusters with LPAI viruses circulating among wild birds in Europe and Asia, suggesting that the evolution from the low pathogenic into the highly pathogenic form has likely occurred within the establishment. Molecular analysis reveals the presence of the PB2-K526R mutation, which has been described in literature as a mammalian adaptive marker, capable of increasing polymerase activity in mammalian cell lines (Suttie et al., 2019).

Genetic characteristics of zoonotic avian influenza viruses in birds outside Europe

The A(H7N3) and A(H7N9) from Australia are genetically related to viruses previously detected in Australian wild birds. They cluster separately for most gene segments, suggesting separate virus origin. The characterised viruses are not related to the zoonotic A(H7N9) viruses from China.

2.2 HPAI virus detections in non-human mammals

2.2.1 HPAI virus detections in non-human mammals worldwide

From 15 June to 23 September 2024, HPAI A(H5N1) viruses were only reported in wild and domestic mammals in North America. The data described were actively collected from Member States and other European countries, retrieved through WOAH-WAHIS and from the USDA websites (for cases occurred in the USA), and supplemented with information from media reports (Table 3).

Table 3: Avian influenza A(H5Nx) virus detections in mammalian species other than humans related to circulating viruses worldwide, 2016–2024

Virus	Animal (order, family, species)			Country	Reference
A(H5N1) or A(H5Nx) clade 2.3.4.4b	Artiodactyla	Bovidae	Cattle (*Bos taurus*)	United States of America	WOAH USDA
			Goat (*Capra hircus*)	United States of America	WOAH USDA
		Camelidae	Alpaca (*Lama pacos*)	United States of America	USDA (online-b)
		Suidae	Pig (*Sus scrofa*)*	Italy	Rosone et al. (2023)
	Carnivora	Canidae	Arctic fox (*Vulpes lagopus*)	Finland	WOAH
			Common raccoon dog (*Nyctereutes procyonoides*)	Finland, Japan, Sweden*	WOAH Personal communication by Malin Grant (SVA)
			Coyote (*Canis latrans*)	United States of America	WOAH
			Dog (*Canis lupus familiaris*)	Canada, Italy*, Poland	WOAH Szaluś-Jordanow et al. (2024)
			Japanese raccoon dog (*Nyctereutes viverrinus*)	Japan	WOAH
			Red fox (*Vulpes vulpes*)	Belgium, Canada, Denmark, Estonia, Finland, France, Germany, Ireland, Italy, Japan, Latvia, Netherlands, Norway, Sweden**, United Kingdom (Northern Ireland), United Kingdom, United States of America	WOAH

Virus	Animal (order, family, species)			Country	Reference
			South American bush dog (*Speothos venaticus venaticus*)	United Kingdom	WOAH
		Felidae	Amur leopard (*Panthera pardus*)	United States of America	WOAH
			Amur tiger (*Panthera tigris*)	United States of America	WOAH
			Bobcat (*Lynx rufus*)	United States of America	WOAH
			Caracal (*Caracal caracal*)	Poland	WOAH
			Cat (*Felis catus*)	Canada, France, Hungary**, Italy*, Poland, Republic of Korea, United States of America	WOAH
			Eurasian lynx (*Lynx lynx*)	Finland, Sweden*	WOAH Personal communication by Malin Grant (SVA)
			Lion (*Panthera leo*)	Peru	WOAH
			Mountain lion (*Puma concolor*)	United States of America	WOAH
		Mephitidae	Striped skunk (*Mephitis mephitis*)	Canada, United States of America	WOAH
		Mustelidae	American marten	United States of America	WOAH
			American mink (*Neovison vison*)	Canada, Finland, Spain	WOAH
			Beech marten (*Martes foina*)	Netherlands	GISAID (online)
			Eurasian otter (*Lutra lutra*)	Netherlands, Finland, Sweden, United Kingdom	WOAH
			European badger (*Meles meles*)	Netherlands	WOAH
			European pine marten (*Martes martes*)	Germany	WOAH
			European polecat (*Mustela putorius*)	Belgium, Netherlands	WOAH
			Ferret (*Mustela furo*)	Belgium, Poland, Slovenia	WOAH Golke et al. (2024)
			Fisher (*Pekania pennanti*)	United States of America	WOAH
			Marine otter (*Lontra felina*)	Chile	WOAH
			North American river otter (*Lontra canadensis*)	United States of America	WOAH
			Sable (*Martes zibellina*)*	Finland	WOAH
			Southern river otter (*Lontra provocax*)	Chile	WOAH
		Otariidae	Antarctic fur seal (*Arctocephalus gazella*)	South Georgia and the South Sandwich Islands, Uruguay	WOAH Bennison et al. (2024), Banyard et al. (2024)
			Northern fur seal (*Callorhinus ursinus*)	Russia	WOAH
			South American fur seal (*Arctocephalus australis*)	Argentina, Brazil, Peru, Uruguay	WOAH
			South American sea lion (*Otaria flavescens*)	Argentina, Brazil, Chile, Peru, Uruguay	WOAH
			Walrus (*Odobenus rosmarus*)	Norway	WOAH
		Phocidae	Caspian seal (*Pusa caspica*)	Russia	WOAH
			Grey seal (*Halichoerus grypus*)	Canada, Germany, Netherlands, Poland, Sweden**, United Kingdom, United States of America	WOAH

Virus	Animal (order, family, species)			Country	Reference
			Harbour seal (*Phoca vitulina*)	Canada, Denmark, Germany, United Kingdom, United States of America	WOAH
			Southern elephant seal (*Mirounga leonina*)	Argentina, South Georgia and the South Sandwich Islands	WOAH Bennison et al. (2024), Banyard et al. (2024)
		Procyonidae	Raccoon (*Procyon lotor*)	Canada, Germany, United States of America	WOAH
			South American coati (*Nasua nasua*)	Germany, Uruguay	WOAH
		Rodentia	Abert's squirrel (*Sciurus aberti*)	United States of America	WOAH
			Black rat (*Rattus rattus*)	Egypt	Kutkat et al. (2024)
			Brown rat (*Rattus norvegicus*)	Egypt	Kutkat et al. (2024)
			Deer mouse (*Peromyscus* spp.)	United States of America	USDA
			House mouse (*Mus musculus*)	United States of America	WOAH USDA
			Prairie vole (*Microtus ochrogaster*)	United States of America	USDA
		Ursidae	American black bear (*Ursus americanus*)	Canada, United States of America	WOAH
			Asian black bear (*Ursus thibetanus*)	France	WOAH
			Brown bear (*Ursus arctos*)	United States of America	WOAH
			Kodiak grizzly bear (*Ursus arctos horribilis*)	United States of America	WOAH
			Polar bear (*Ursus maritimus*)	United States of America	WOAH
	Cetacea	Delphinidae	Bottlenose dolphin (*Tursiops truncatus*)	Peru, United States of America	WOAH
			Chilean dolphin (*Cephalorhynchus eutropia*)	Chile	WOAH
			Common dolphin (*Delphinus delphis*)	Peru, United Kingdom	WOAH Leguia et al. (2023)
			White-sided dolphin (*Lagenorhynchus acutus*)	Canada	WOAH
		Phocoenidae	Burmeister's porpoise (*Phocoena spinipinnis*)	Chile	WOAH
			Harbour porpoise (*Phocoena phocoena*)	Sweden, United Kingdom	WOAH
	Didelphimorphia	Didelphidae	Virginia opossum (*Didelphis virginiana*)	United States of America	WOAH USDA
	Lagomorpha	Leporidae	Desert cottontail (*Sylvilagus audubonii*)	United States of America	USDA
A(H5N5) clade 2.3.4.4b	Carnivora	Canidae	Red fox (*Vulpes vulpes*)	Canada, Norway	WOAH
		Mustelidae	European pine marten (*Martes martes*)	Netherlands	Personal communication by Dennis Bol (NVWA, 2024)

Virus	Animal (order, family, species)			Country	Reference
		Procyonidae	Raccoon (*Procyon lotor*)	Canada	WOAH
A(H5N6) clade 2.3.4.4b	Carnivora	Canidae	Dog (*Canis lupus familiaris*)	China	Yao et al. (2023)
		Mustelidae	American mink (*Neovison vison*)	China	Zhao et al. (2024)
A(H5N8) clade 2.3.4.4b	Artiodactyla	Suidae	Pig (domestic) (*Sus scrofa*)*	France	Herve et al. (2021)
			Pig (wild boar) (*Sus scrofa*)*	Germany	Schülein et al. (2021)
	Carnivora	Canidae	Red fox (*Vulpes vulpes*)	United Kingdom	WOAH
		Phocidae	Grey seal (*Halichoerus grypus*)	Poland, Sweden, United Kingdom	SVA Shin et al. (2019), Floyd et al. (2021) Personal communication by Siamak Zohari (SVA)
			Harbour seal (*Phoca vitulina*)	Denmark, Germany, United Kingdom	WOAH Floyd et al. (2021), Ärzteblatt (online), Avian Flu Diary (online), Outbreak News (online)

*Serological detection.
**Both virological and serological detection.

During the current reporting period from 15 June to 23 September 2024, no new HPAI virus detections in mammals were reported in Europe. However, the Netherlands retrospectively reported the detection of A(H5N5) virus in a European pine marten that was sampled back in February 2024 (personal communication by Dennis Bol, NVWA, 2024).

Belgium, Cyprus, Czechia, Denmark, France, Germany, Ireland, Luxembourg, the Netherlands, Norway, Romania, Slovakia, Spain, Sweden and Switzerland declared the absence of known HPAI virus infections in mammals during the current reporting period. The other European countries have not confirmed the absence or presence of A(H5N1) viruses in mammals, but they have not reported HPAI virus detections either. In Austria, since the beginning of 2024, 294 mammals (110 pigs, 109 foxes, 47 bats, 8 horses, 5 badgers, 4 goats, 2 cattle, 2 dogs, 2 martens, 2 raccoons, 2 wolves and 1 wild boar) were tested and all found negative (personal communication by Sandra Revilla-Fernández, AGES, 2024). In Belgium, from 14 June to 17 September 2024, 33 foxes were tested and all found negative (personal communication by Ingeborg Mertens, FAVV, 2024).

Outside Europe, the focus of the HPAI situation in mammals is currently still in North America. Since 25 March and as of 25 September 2024, A(H5N1) virus detections have been reported to the Animal and Plant Health Inspection Service of the USDA (USDA-APHIS) in a total of 238 establishments keeping dairy cattle in 14 US states, most of them in Colorado (64), California (40), Idaho (32), Michigan (29) and Texas (26) (USDA-APHIS, online-a). Of note, California is the state with the highest dairy cattle population in the country (n = 1.7 million) (Stat News, online). In unpublished research, scientists at Colorado State University and Iowa State University tested bulk milk samples for HPAI viruses and found that the virus was detectable 14–16 days before farms saw a significant increase in clinical signs such as lethargy, inappetence, fever and a decrease in milk production (Stat News, online), making it challenging to detect the incursion of the disease in establishments early on. The USDA, at the end of August 2024, authorised a field trial of an A(H5N1) vaccine in cattle. The Center for Veterinary Biologics (CVB) has released a notice regarding veterinary biologics product license application and the authorisation of initial field studies with non-viable, non-replicating vaccines targeting HPAI in livestock (USDA CVB, online). In response to the ongoing HPAI situation in dairy cattle in the USA, several European countries have initiated testing of and/or surveillance in cattle and bulk milk, all of which so far resulted in negative test results. Although experimental infection trials with the US isolate and an A(H5N1) virus isolated from a European wild bird in Germany have successfully infected local cattle via the mammary route (Halwe et al., 2024), suggesting that a spillover event similar to that in the USA may also be possible in Europe, the differences in farming practices between the USA and Europe (in particular the use of traceability systems and the lack of movement of lactating dairy cattle in Europe) make extensive between-farm spread as observed in the USA very unlikely in the European context. Such experimental trials have confirmed the importance of milk as a vehicle for transmission of the virus (Baker et al., 2024; Halwe et al., 2024). In addition, experimental research suggests vertical transmission of HPAI virus in mice, in particular from lactating females to their pups (Eisfeld et al., 2024).

Apart from the HPAI virus detections in dairy cattle, the USA also reported for the first time deer mouse, desert cottontail and prairie vole as affected by A(H5N1), species in which the virus had never been identified before (USDA, online-c; Table 3). The detection of HPAI virus in desert cottontail represents the first detection of the virus in the order Lagomorpha. Furthermore, the USDA reported additional A(H5N1) virus detections in domestic cat, house mouse, raccoon, red fox and striped skunk. More information became available for six HPAI virus detections in domestic cats in Colorado: one of these cases was directly associated with an establishment keeping dairy cattle, in three cases the cats had sometimes outdoor access and were reportedly hunting mice and birds, while in the other two cases, the cats had no outdoor access and therefore no direct exposure to potentially infected animals. Five of these cats expressed clinical signs such as lethargy, inappetence, respiratory and neurological signs (CVMA, online).

In Canada, two detections of A(H5N5) virus were retrospectively reported in red foxes that had been found at the beginning of 2024.

In Pakistan, by serological analysis for binding antibodies to the hemagglutinins of influenza A and B viruses in goats (n = 452) and sheep (n = 329), high prevalence of sera with antibodies against A(H5) (23.9–34.0%), A(H7) (13.9–37.1%) and A(H9) (17.0–34.7%) viruses were detected (Wong et al., 2024). However, the breadth of antibody specificity in post-infection goat and sheep antisera is unknown. Therefore, it is difficult to disentangle evidence of multiple infections from cross-reactive antibodies generated after a single infection, which are expected with an antibody binding assay such as the one used.

In the Antarctic region, the Spanish National Research Council (CSIC) confirmed the long-suspected presence of HPAI virus in marine mammals in the area. A carcass of a southern elephant seal that had been sampled on the Coppermine Peninsula on Robert Island back in March 2024 was finally confirmed positive to A(H5) virus (GovES, online; Sabemos, online).

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

Details on the nomenclature of the HPAI A(H5) viruses used in this section are reported in Appendix B. Genotypes are assigned using the criteria described in Fusaro et al. (2024). Mutation analyses of the A(H5N1) viruses have been performed using FluMut (Github izsvenezie-virology, online-b) with FluMutDB v5.0 mutation database.

Genetic diversity of HPAI A(H5Nx) viruses in non-human mammals in Europe

Since October 2020, the complete genome sequences of about 250 A(H5) viruses of clade 2.3.4.4b collected from 17 distinct mammalian species (i.e. American mink, Arctic fox, Asian black bear, beech marten, bush dog, caracal, cat, common raccoon dog, Eurasian lynx, Eurasian otter, European badger, European polecat, ferret, grey seal, harbour porpoise, harbour seal, pine marten, red fox and South American coati) have been generated. The characterised viruses belong to 11 different A(H5N8), A(H5N1) and A(H5N5) genotypes, most of which have been previously identified in birds. During the current epidemiological year and based on the data available so far (n = 7 complete genome sequences), infections in wild animals have been caused by three different A(H5N1) genotypes and the A(H5N5) EA-2021-I, the last one identified in February 2024 in a red fox in Norway and more recently in a pine marten in the Netherlands.

Approximately 44% of the A(H5Nx) viruses that have been characterised since October 2020 from mammals in Europe contain at least one of the adaptive markers associated with an increased virulence and replication in mammals in the PB2 protein (E627K, D701N, T271A or K526R) (Suttie et al., 2019). During the current epidemiological year, seven out of the 10 characterised viruses from mammals contain the PB2-E627K mutation. These mutations have rarely been identified in the A(H5) viruses of clade 2.3.4.4b collected in birds in Europe during the same period. This observation suggests that these mutations with potential public health implications have likely emerged upon transmission to mammals.

HPAI A(H5N1) outbreaks in cattle and other mammal species in the USA

Since its introduction at the end of 2021 in North America, the HA protein of A(H5N1) viruses of clade 2.3.4.4b has evolved accumulating several mutations. In particular, one of these mutations, T199I (H3 numbering), emerged during the second half of 2023 and is present in all the A(H5N1) viruses collected from the ongoing dairy cattle outbreak in the USA. A recent study demonstrated that HA-T199I is responsible for increased binding breadth to glycans bearing terminal α2,3 sialic acids compared to historical and recent 2.3.4.4b A(H5N1) viruses. This mutation has been observed in only one European A(H5N1) virus collected in Europe during the current epidemic wave (Good et al., 2024). Moreover, a recent study demonstrated that the A(H5N1) virus from dairy cattle has the ability to bind to both human and avian receptors and can be inefficiently transmitted by the respiratory droplet route in ferrets (Eisfeld et al., 2024).

Influenza A viruses in fur farms in China

Virus surveillance in dead farmed fur animals conducted in China between 2021 and 2024 identified the co-circulation of several viruses with zoonotic potential, including influenza A viruses (Zhao et al., 2024). Sequences of four viruses retrieved from lung samples collected from two farmed minks, a guinea pig and a muskrat, and belonging to three subtypes, namely A(H5N6), A(H1N2) and A(H6N2), were characterised. The two

A(H5N6) viruses belonged to clade 2.3.4.4b and were closely related to A(H5) viruses collected in birds and humans in the country. These viruses possessed the mammalian adaptive mutation PB2-D701N. Genetic analysis of the A(H1N2) virus indicates a likely swine origin with the HA belonging to the H1N1/pdm09 lineage. The identification of viruses of swine and avian origin suggests fur farm hosts to be an important hub for virus introductions from different sources. These findings highlight the importance of virus surveillance in these animals, which may play a crucial role in the emergence of novel zoonotic strains, given their high densities, and close and frequent contacts with humans.

2.3 Food and feed safety aspects related to HPAI

Given the continued detections of HPAI A(H5N1) viruses in dairy cattle in the USA, the US government has recently released the results of their second retail sampling study from retail locations throughout the USA, comprising 167 milk and dairy products (including pasteurised milk, pasteurised milk products and raw milk aged cheese) (Suarez et al., 2024). These results indicate that, while viral RNA was present in 29 samples, no viable A(H5N1) virus was detected in any sample. At the same time, screening of retail milk conducted "in the Midwest found 58 out of 150 samples were positive [for viral traces], according to Andrew Bowman at the Ohio State University." (NPR, online).

The US government moreover initiated a study to determine the efficacy of continuous flow pasteurisation under conditions that closely resemble commercial milk pasteurisation processing at high temperature short time (HTST), 72°C (161°F) for 15 s (Spackman et al, 2024). In this study, homogenised raw whole milk samples (~ 4.5% milk fat) were artificially contaminated with a mean concentration/titer of A(H5N1) virus of 6.7 ± 0.2 $\log_{10}$ EID (egg infectious doses)$_{50}$ per millilitre; a titer higher than those found in raw bulk tank milk samples from affected dairy herds (ranging from 1.3 to 6.3 $\log_{10}$ EID_{50}/mL). No viable virus was detected post-pasteurisation. Of note is that a mean reduction of ≥ 5.8 ± 0.2 $\log_{10}$ EID_{50}/mL already occurred during the heating phase when the milk was brought to 72.5°C before the holding tube. The authors estimate, based on heat-transfer analysis support, that standard US continuous flow HTST pasteurisation parameters will inactivate > 12 $\log_{10}$ EID_{50}/mL of HPAI virus (Spackman et al, 2024).

A laboratory scale study conducted in China with different influenza A viruses confirms the effectiveness of milk pasteurisation using both HTST (72°C for 15 s) and low temperature long time (LTLT) (63°C for 30 min). It showed that heat treatment can effectively inactivate as much as 7.75 $\log_{10}$ EID_{50}/mL of A(H5) virus in raw milk (Cui et al., 2024; Nooruzzaman et al., 2024).

In the future, the US government plans to continue the testing of retail samples, addressing geographic and product gaps, sample culled dairy cattle in meat processing plants and conduct further research on pasteurisation and other inactivation methods (e.g. temperature thresholds, duration of application).

Regarding the safety of the milk by-product lactose, regularly used as a feed ingredient in domestic animals such as pigs, a study conducted recently showed the successful inactivation of the virus by industrial procedures (i.e. pasteurisation at 63°C and citric acid treatment) in this product (Kwon et al., 2024).

2.4 Avian influenza virus infections in humans

2.4.1 Most recent human infections with avian influenza A(H5N1), A(H5N6) and A(H9N2) viruses

Since the last report and as of 20 September 2024, 19 new human cases of infection with avian influenza virus have been reported from the USA (six cases A(H5N1) and five cases of A(H5)), Cambodia (five A(H5N1) cases, including one fatal), China (one A(H9N2) case and one fatal A(H5N6) case), and Ghana (one A(H9N2) case) (Table 4). This report also includes a case of A(H9N2) with disease onset on 2 May 2024, which was not reported in 'Avian influenza overview March–June 2024' (EFSA, ECDC and EURL, 2024a), and a case of A(H5N1), which was notified to the World Health Organization (WHO) from China via International Health Regulations (IHR) mechanism on 2 April 2024. Most of the cases reported exposure to poultry prior to zoonotic avian influenza virus detection or onset of illness. One case had exposure to infected dairy cattle, while two had no known reported exposure. At the time of writing, there was no evidence of onward transmission of the virus from any of the reported cases.

Table 4: Human cases due to avian influenza viruses reported globally, including virus subtypes reported in 2024

Subtype	New cases reported 21 June–20 September 2024	Number of reports with disease onset or detection in 2024	Total cases (deaths)	Countries reporting human cases
A(H5N1)	Six cases of A(H5N1) and five cases of A(H5) in the USA[*]; five cases in Cambodia (including one death).	27[**]	909 (464) since 2003.	A total of 24 countries reported cases. EU/EEA: Spain, with virus fragment detections in two poultry workers (considered to be contamination and not productive infections).
A(H5N2)	-	1	1 (1) first reported in 2024.	Mexico (1).
A(H5N6)	One fatal case in China.	3	93 (38) since 2014.	China (92), Laos (1).
A(H9N2)	One case in China; one case in Ghana.	10[***]	140 (2) since 1998.	No EU/EEA country. China (124), Egypt (4), Bangladesh (3), Cambodia (2), India (2), Ghana (1), Oman (1), Pakistan (1), Senegal (1), Vietnam (1).
A(H10N3)	-	1	3 (0) since 2021.	China (3)
A(H10N5)	-	-	1 (1) first reported in 2024.	China (1)

[*] Five A(H5) cases reported in the USA are epidemiologically linked to the ongoing A(H5N1) outbreak in commercial poultry and dairy farms.
[**] Includes one case from Vietnam notified to WHO by China on 2 April 2024 which was not reported in the 'Avian influenza overview March–June 2024' (EFSA, ECDC and EURL, 2024a).
[***] Includes one case with disease onset on 2 May 2024, which was not reported in the 'Avian influenza overview March–June 2024' (EFSA, ECDC and EURL, 2024a).
Source: ECDC line list and WHO.

2.4.2 Human A(H5N1) cases, summary

Since 21 June and as of 20 September 2024, 16 new human infections with avian influenza A(H5N1) or A(H5) virus have been reported in the USA (six cases of A(H5N1) and five of A(H5)) and Cambodia (five cases of A(H5N1), including one death).

Of the 11 new cases reported from the USA, nine were associated with exposure to infected poultry, one with exposure to infected dairy cattle, and one had no known exposure to infected animals or humans.

The first human case in the USA in this period was reported in July 2024 (CDC, online-a; WHO, 2024a). The case was a dairy farm worker from Colorado, who had exposure to cattle infected with A(H5N1). This is the fourth case associated with the ongoing A(H5N1) multi-state outbreak in dairy farms. The previous three cases were reported in Texas (1) and Michigan (2). On 26 June 2024, the case developed conjunctivitis while working at a dairy cattle farm, where HPAI A(H5N1) infection in cows had been previously confirmed. The person was treated with oseltamivir and has since recovered. There was no further transmission among the close contacts of the case. Respiratory and conjunctival samples were collected from the case and on 2 July a nasopharyngeal specimen, but not the conjunctival specimen, tested positive for influenza A(H5) virus in reverse transcription-polymerase chain reaction (RT-PCR). Attempts to isolate and sequence the virus from the samples were not successful and, therefore, the neuraminidase (NA) subtype was not determined. Since the case was exposed to cattle with confirmed A(H5N1) infection, the virus was probably of the same N1 subtype.

In July 2024, the US authorities reported nine cases among adult farm workers involved in depopulation of infected poultry at two commercial egg layer farms in Colorado with confirmed A(H5N1) outbreaks in poultry. The first six cases were reported between 12 and 19 July (CDPHE, online-a, b, c), while another three at the second poultry farm were reported on 25 July 2024 (CDC, online-b). Cases reported conjunctivitis and mild respiratory symptoms, such as fever, chills, coughing, sore throat and runny nose. Cases were offered antiviral treatment but did not require hospitalisation. Sequencing results of the sample collected from one of the cases showed a close match to the human case associated with the A(H5N1) outbreak in dairy farms reported in Michigan in May 2024. The virus sequence lacked mutations associated with antiviral resistance and showed close resemblance to the two HPAI A(H5) candidate vaccine viruses (IDCDC-RG78A and IDCDC-RG71A), which have only two to four amino acid changes compared to the Colorado virus. The virus was genotyped as B3.13, clade 2.3.4.4b A(H5N1) (WHO, 2024a), which is closely related to recent outbreaks in poultry and dairy cattle farms. Genetic analysis showed that the virus maintains avian characteristics and lacks mutations that are known to enhance human infection or transmission. The virus sequence displayed a change at PB2 M631L which has been associated with mammalian adaptation, similar to the virus sequences from dairy cattle. However, unlike the Texas case reported in April 2024, this virus lacked the PB2 E627K mutation associated with human adaptation.

The most recent confirmed human A(H5N1) case in the USA was reported by the US Centers for Disease Control and Prevention (CDC) on 6 September 2024. The case was an adult person from Missouri, who was hospitalised due to underlying medical conditions. The patient presented with chest pain, nausea, vomiting, diarrhoea and weakness, but was not severely ill. The person received antiviral treatment (oseltamivir) and has subsequently recovered. The case was identified through the surveillance system for seasonal influenza. The person had no known exposure to animals within 10 days of the onset of illness, including no consumption of unpasteurised dairy products. Both commercial and backyard poultry have been affected by outbreaks of avian influenza A(H5) in the state of Missouri in 2024. In addition, A(H5N1) detections in wild birds have previously been reported in the state. No A(H5) infections have been reported from cattle farms in the state.

One household contact of the case developed symptoms on the same day as onset of illness in the patient, but subsequently recovered and no diagnostic testing was performed at the time. Blood samples have been collected for serological testing as an indication of previous exposure to infection. A second close contact of the case, a healthcare worker, developed mild respiratory symptoms but tested negative for influenza A. In addition, another healthcare worker who experienced mild respiratory symptoms was also identified through contact tracing. The second healthcare worker was not tested for influenza because at the time of investigation they had already recovered, although they will be offered serological testing for the presence of antibodies to avian influenza A(H5) virus (CDC, 2024a, online-c, d, e).

Of all 11 human cases reported from the USA during this reporting period, six were laboratory-confirmed influenza A(H5N1) infections (GISAID, online). Neuraminidase designation was not available for five of the US cases and they were reported as A(H5) infections. However, the five A(H5) cases were epidemiologically linked to ongoing A(H5N1) outbreaks at commercial poultry and dairy cattle farms (WHO, 2024a; CDC, online-b).

In addition to the 11 human cases of infection with influenza A(H5) virus in the USA during this period, there were five human cases of A(H5N1) infection reported from Cambodia. The first case was a male child from Takeo province (Ministry of Health of the Kingdom of Cambodia, 2024a). The case, who suffered from asthma, developed influenza-like symptoms on 29 June 2024. The case was hospitalised on 2 July, received oseltamivir treatment and has since recovered. Nasopharyngeal and oropharyngeal samples were collected on the day of hospitalisation. On 5 July, the samples tested positive for influenza A(H5N1) by RT-PCR performed at the National Institute of Public Health of Cambodia (NIPH). The test results were further confirmed by the Pasteur Institute in Cambodia (IPC).

The second case, a female child, was a cousin of the first case, and lived in the same household (Ministry of Health of the Kingdom of Cambodia, 2024b). The case was asymptomatic but was tested as part of the epidemiological investigation related to the first case. Nasopharyngeal and oropharyngeal samples collected from this case were positive for influenza A(H5N1) by RT-PCR. The case was hospitalised for isolation purposes on 7 July and treated with oseltamivir. At the time of reporting the patient’s condition was mild.

Investigation conducted by public health authorities revealed that on 26 June, prior to the disease onset, both cases had exposure to dead chickens in the backyard of their household. On 9 July 2024, the National Animal Health and Production Research Institute (NAHPRI) in Cambodia notified WOAH that the animal samples, collected from the village where the two cases resided, had tested positive for A(H5N1) virus.

A third human case from Cambodia was reported in August 2024 (Ministry of Health of the Kingdom of Cambodia, 2024c). The case was a male child from Svay Rieng province, who was admitted to an intensive care unit after developing symptoms such as fever, cough, tiredness, difficulty in breathing, and drowsiness. On 30 July 2024, the samples collected from the case were laboratory-confirmed as positive for A(H5N1) by NIPH and IPC. An epidemiological investigation conducted by the local health authorities revealed that 12 days prior to the onset of disease the case had had exposure to a large number of dead chickens and other poultry and brought home some of the dead birds for consumption.

The fourth case, reported on 3 August 2024, was an adolescent girl from Svay Rieng province, who was admitted to an intensive care unit with symptoms of fever, cough, sore throat and difficulty breathing (Ministry of Health of the Kingdom of Cambodia, 2024d). At the time of reporting, the patient was still in hospital in a serious condition. The samples collected from the patient were laboratory-confirmed as positive for A(H5N1) by the NIPH in Cambodia. According to investigation, four days before the onset of illness, the case was exposed to nine dead chickens at her own home and at a neighbour’s house.

The fifth case, and the only fatality due to A(H5N1) infection in this reporting period, was an adolescent female from Prey Veng province (Ministry of Health of the Kingdom of Cambodia, 2024e; WHO, online-b). On 17 August 2024, the case, who had no underlying medical conditions, was admitted to a severe acute respiratory infection (SARI) sentinel hospital in Phnom Penh with symptoms including fever, cough, sore throat, shortness of breath, and fainting. Despite receiving medical care and oseltamivir treatment, the patient passed away on 20 August.

Health authorities reported that five days before the illness began, dead chickens were found in the village where the girl lived. The girl handled and prepared the dead chickens for a meal. Contact tracing, carried out by the Cambodian Communicable Disease and Control Department of the Ministry of Health and a local rapid response team, identified six close contacts. All were treated with oseltamivir and have not shown any signs of respiratory illness. Environmental, public, and animal health response measures were put in place, and at the time of reporting further investigations were being conducted. Test results on samples collected from chickens and ducks in the village are pending.

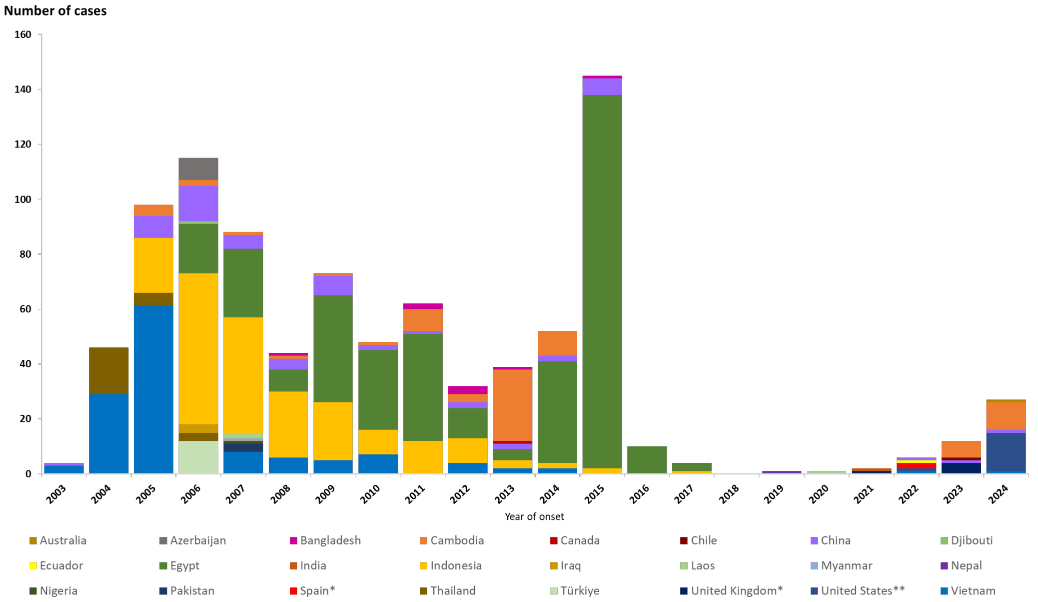
The nasopharyngeal and oropharyngeal samples collected on the day of hospital admission tested positive for influenza A(H5N1) by RT-qPCR on 20 August 2024. On the same day, this initial laboratory diagnosis, conducted by the National Institute of Public Health of Cambodia, was confirmed by the Pasteur Institute in Cambodia. Sequencing analysis of the haemagglutinin (HA) gene showed that the virus belongs to H5 clade 2.3.2.1c, similar to other viruses circulating in Cambodia and Southeast Asia since 2013−2014. However, the internal genes of the sequenced virus belonged to A(H5) clade 2.3.4.4b. This novel influenza A(H5N1) reassortant virus has been reported in human cases from Cambodia since late 2023.

In addition to cases reported by the USA and Cambodia, details of infection with influenza A(H5N1) in a person from Vietnam, previously reported only via the IHR notification system, have become publicly available (WHO, 2024b). The case, which was notified to WHO by China on 2 April 2024, was a female in her thirties, who developed a cough on 26 March. On 28 March, the case, a cargo delivery worker, travelled to China and was tested as part of routine random sampling at a port of entry to Guangxi Autonomous Region. On the same day, the respiratory sample was analysed by RT-PCR at the laboratory of the port of entry and tested positive for A(H5N1). On 30 March, the results were further confirmed by the WHO Collaborating Centre for Reference and Research on Influenza at the Chinese National Influenza Centre (CNIC).

Chinese authorities shared information on the case with the public health authorities in Vietnam on the day of testing. On the same day, the local health authorities visited the case at her residence and transferred her to a health clinic for further examination and isolation purposes. Respiratory samples collected at the clinic were analysed by RT-PCR and tested negative for influenza A(H5N1) on 28 March. The samples also tested negative for SARS-CoV-2, respiratory syncytial virus and influenza A and B viruses.

Epidemiological investigations conducted by Chinese and Vietnamese public health authorities revealed that the case had not travelled elsewhere in China and returned to Vietnam on the same day. The case did not develop any further symptoms, and none of her six close contacts, including household members, reported any illness. According to the results of the investigation, three weeks before disease onset, the case had purchased a chicken at a local market, cooked it and consumed it with her family.

Since 2003 and as of 20 September 2024, there have been 909 human cases, including 464 deaths (case fatality among reported cases: 51%) of influenza A(H5N1) infection notified to WHO from 24 countries (Australia (ex India), Azerbaijan, Bangladesh, Cambodia, Canada, Chile, China, Djibouti, Ecuador, Egypt, Indonesia, India, Iraq, Laos, Myanmar, Nepal, Nigeria, Pakistan, Spain[7], Thailand, Türkiye, Vietnam, United Kingdom and the USA[8] (Figure 6).



*Includes detections due to suspected environmental contamination with no evidence of infection reported in 2022 from Spain (2) and the USA (1), and in 2023 from the United Kingdom (3, 1 inconclusive).
**Includes five A(H5) cases reported in USA which were epidemiologically linked to the ongoing A(H5N1) outbreak in commercial poultry and dairy farms.

Figure 6: Distribution of confirmed human cases of A(H5N1) virus infection by year of onset and reporting country, 2003–2024 (data as of 20 September 2024, n = 909). A(H5) cases from the USA without N designation are included in the total number of cases, as they are epidemiologically linked to ongoing A(H5N1) outbreaks at commercial poultry and dairy cattle farms

2.4.3 Human A(H5N6) cases, summary

Between 21 June and 20 September 2024, one new fatal case of A(H5N6) infection was reported from Anhui province in China (WHO, 2024a). The case was a woman in her seventies, who developed symptoms on 17 June 2024. Two days later, the case was admitted to hospital, where she was diagnosed with severe pneumonia. The case was treated with antivirals from the day of admission, but passed away on 8 July. Nasopharyngeal sample collected on 19 June tested positive for influenza A. On 23 June, A(H5N6) virus was laboratory-confirmed by RT-PCR. The case reported exposure to a live poultry market prior to the onset of disease. No further cases were reported among close contacts and the environmental samples tested negative for influenza A.

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[7] A(H5N1) virus detections in two Spanish poultry workers involved in culling activities are considered contaminations and not productive infections.

[8] Includes five A(H5) cases reported in USA which were epidemiologically linked to the ongoing A(H5N1) outbreak in commercial poultry and dairy farms.

As of 20 September 2024, and since 2014, according to notifications made to WHO, China (92) and Laos (1) have reported a total of 93 human infections with A(H5N6) (Figure 7), including 38 with a fatal outcome (case fatality among reported cases: 40%). Since 2021, the majority of A(H5N6) viruses identified in humans have belonged to clade 2.3.4.4b, although sequence information is not available for all viruses. After the modification of the H5 component in the vaccine used for poultry in China in January 2022, the number of human cases declined. However, with the information available, it is not possible to draw any further conclusions on whether the vaccination has caused the observed decline (Chen et al., 2022; Cui et al., 2022; Gu et al., 2022; Zhu et al., 2022; WHO, 2024a).

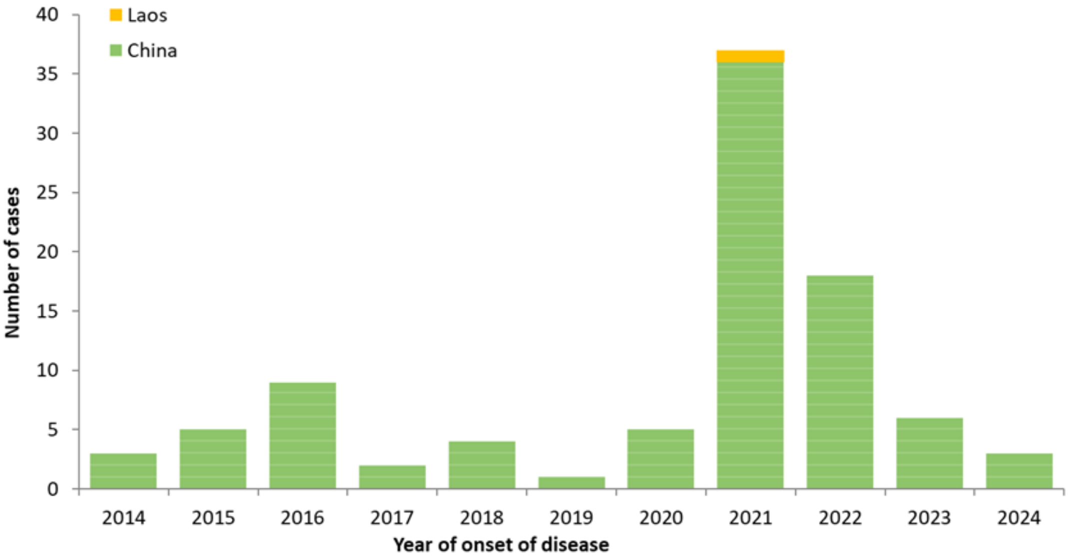

Figure 7: Distribution of confirmed human cases of A(H5N6) virus infection by year of onset and country, 2014–2024 (data as of 20 September 2024, n = 93)

2.4.4 Human A(H9N2) cases, summary

Since 21 June and as of 20 September 2024, one new human case of A(H9N2) infection has been reported by China and one by Ghana.

The first case was a woman in her thirties from Guizhou province, China, who on 15 June 2024 sought medical care after developing symptoms of bronchitis, fever, and cough (WHO, 2024a). She was discharged from hospital after her symptoms were initially linked to asthma. On 20 June, she visited another hospital due to a persistent cough and was diagnosed with an influenza-like illness (ILI). Samples collected on that day were confirmed positive for A(H9N2) on 25 June. However, at the time of writing, details of the sample type and diagnostic tests performed were unavailable. The case has since recovered.

Samples collected from close contacts of the case tested negative, and no other human cases of avian influenza A(H9N2) were linked to this case. Before onset of symptoms, the case had visited a live poultry market, where nine environmental samples tested positive for A(H9) virus in a later investigation.

Another A(H9N2) case had disease onset on 2 May 2024, but was not reported in the previous EFSA report (EFSA, ECDC and EURL, 2024a). The case was a boy from the Guangxi Autonomous Region, who developed a mild illness after a visit to a live poultry market prior to the onset of disease (WHO, 2024b). Samples collected from close contacts tested negative for A(H9). However, environmental samples tested positive for A(H9).

Ghana reported its first human case of avian influenza A(H9N2) in a child from the Upper East region on 26 August 2024. The patient developed symptoms on 5 May 2024, including a sore throat, fever and cough. The case was diagnosed with influenza-like illness at the local hospital and treated with antipyretics, antihistamines and antibiotics. The case has since recovered. Samples collected on 7 May tested positive for seasonal influenza A(H3N2) virus. On 9 July, genomic sequencing by the National Influenza Centre in Ghana revealed avian influenza A(H9) virus. The sample was subsequently confirmed as positive for avian influenza A(H9N2) virus by the US CDC on 6 August.

The case had no known exposure to poultry or any people with similar symptoms before the onset of disease. Samples from close contacts tested negative for influenza and no onward transmission was identified, although the investigation was delayed.

There have been reports of sick poultry in the Upper East region of Ghana, but the cause has not been established. LPAI A(H9N2) virus has been circulating in poultry farms in Ghana since 2017 (WHO, online-c). A(H9N2) viruses have become endemic in poultry (mainly in chicken) since the mid-1990s in many countries in Asia and the Middle East (Alexander, 2007; El Sayes et al., 2022) and since towards the end of the 2010s in Africa (Fusade-Boyer et al., 2021). This circulation of A(H9N2) strains in domestic birds can be linked to zoonotic infections.

As of 20 September 2024, and since 1998, a total of 140 laboratory-confirmed cases of human infection with avian influenza A(H9N2) viruses, including two deaths (both in patients with underlying conditions), have been reported in ten countries (Figure 8): China (124), Egypt (4), Bangladesh (3), Cambodia (2), India (2), Ghana (1), Oman (1), Pakistan (1), Senegal (1) and Vietnam (1). Most of the cases were children with mild disease.

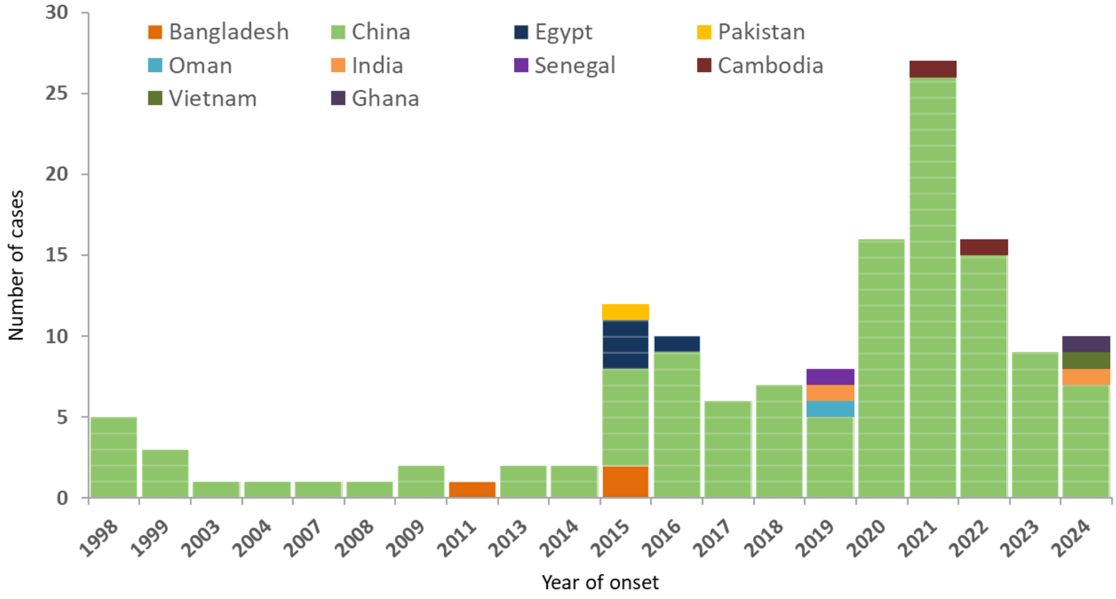

Figure 8: Distribution of confirmed human cases of A(H9N2) virus infection by year of onset and country, 1998–2024 (as of 20 September 2024, n = 140)

2.4.5 Genetic characteristics of avian influenza viruses from humans

The GISAID's EpiFlu™ Database (Shu and McCauley, 2017) was accessed on 20 September 2024 and protein sequences for all available segments from human cases of avian influenza reported since 21 June 2024 were retrieved for 12 cases of A(H5N1) from the USA and Cambodia, one A(H5N6) from China, and two A(H9N2) from Ghana and India (Table 5). The A(H9N2) case A/India/Kol-NIV_24_1519/2024 has been described in a previous report (EFSA, ECDC and EURL, 2024a), but no sequences were available at that time. Clade assignments for A(H9N2) were as proposed by Fusaro et al. (2024a).

Table 5: Overview of isolates included in the genetic analysis within the reporting period

Isolate name	Isolate ID	Subtype	Clade	Continent	Country	Collection date
A/Colorado/109/2024	EPI_ISL_19263923	A(H5N1)	2.3.4.4b	North America	USA	2024-07-11
A/Colorado/134/2024	EPI_ISL_19280426	A(H5N1)	2.3.4.4b	North America	USA	2024-07-15
A/Colorado/138/2024	EPI_ISL_19294962	A(H5N1)	2.3.4.4b	North America	USA	2024-07-19
A/Colorado/137/2024	EPI_ISL_19294963	A(H5N1)	2.3.4.4b	North America	USA	2024-07-19
A/Colorado/139/2024	EPI_ISL_19294964	A(H5N1)	2.3.4.4b	North America	USA	2024-07-22
A/Missouri/121/2024	EPI_ISL_19413343	A(H5N1)	2.3.4.4b	North America	USA	2024-08-22
A/Cambodia/24070331/2024	EPI_ISL_19312043	A(H5N1)	2.3.2.1c	Asia	Cambodia	2024-07-30
A/Cambodia/SVH240441/2024	EPI_ISL_19312044	A(H5N1)	2.3.2.1c	Asia	Cambodia	2024-08-02
A/Cambodia/KSH240409/2024	EPI_ISL_19353003	A(H5N1)	2.3.2.1c	Asia	Cambodia	2024-08-17
A/Cambodia/24020155/2024	EPI_ISL_19270605	A(H5N1)	2.3.2.1c	Asia	Cambodia	2024-02-08
A/Cambodia/24020179/2024	EPI_ISL_19270607	A(H5N1)	2.3.2.1c	Asia	Cambodia	2024-02-10
A/HeFei04171/2024	EPI_ISL_19356984	A(H5N6)	2.3.4.4b	Asia	China	2024-06-23
A/Ghana/FS-24-2641/2024	EPI_ISL_19266347	A(H9N2)	G5.5	Africa	Ghana	2024-05-15
A/India/Kol-NIV_24_1519/2024	EPI_ISL_19280579	A(H9N2)	G5.7	Asia	India	2024-03-05

The sequences were analysed using a script developed in-house, with A/Goose/Guangdong/1/96 (EPI_ISL_1254) as reference to determine mutations of interest and these are referred to by H5 numbering, unless otherwise stated. The analysis was complemented with inspections of alignments produced in CLC Genomics Workbench 24 (QIAGEN).

HPAI A(H5Nx)

Five A(H5N1) viruses from the USA collected in July 2024, as well as one collected in August 2024, were assigned to clade 2.3.4.4b. The single A(H5N6) virus from China collected in June 2024 was also assigned to clade 2.3.4.4b.

The five viruses of A(H5N1) from Cambodia collected between February and August 2024 were of clade 2.3.2.1c, a clade mainly detected in Southeast Asia. A/Cambodia/KSH240409/2024 has been reported as a novel reassortant with internal genes similar to 2.3.4.4b viruses (WHO, online-b). The PB2 and NS segments of A/Cambodia/24020155/2024 and A/Cambodia/24020179/2024 resemble this reassortment. The remaining viruses from Cambodia do not have internal gene sequences reported. Influenza A(H5N1) clade 2.3.2.1c viruses from Cambodia with earlier collection dates (before October 2023) (e.g. A/Cambodia/NPH230032/2023) do not exhibit this internal gene similarity with clade 2.3.4.4b viruses.

The sequences of the five A(H5N1) viruses from cases in Colorado, USA, with exposure to poultry, and the recently submitted virus from Missouri, USA, were closely related to viruses found in dairy cattle in the USA (genotype B3.13) (Eisfeld et al., 2024; Nguyen et al., 2024). The presence of A156T and P136S, observed in a very small fraction of the sequences from dairy cows, that may affect the virus' antigenic properties (CDC, online-d), was confirmed in A/Missouri/121/2024. An S at position 136 (H5 numbering) in HA was also present in all sequences of clade 2.3.2.1c from Cambodia.

The mutation analysis revealed nearly identical profiles among all A(H5N1) viruses from the USA. All viruses from Cambodia, which were also very similar amongst the viruses, had a different profile to those from the USA (Table 6).

Table 6: Amino acid substitutions with known phenotypic associations in avian influenza A(H5) viruses from human cases, submitted 21 June–20 September 2024

	Segment	**HA**										**NA**	**PB2**			**PA**	
Isolate name	**Mutation**	D94	T108	S123	S133	N154	S155	K218	S223	R497	327-328	46-75	Q591	M631	D701	K142	K497
A/Cambodia/24020155/2024		N	I		A		N					46-75del				N	
A/Cambodia/24020179/2024		N	I		A		N					46-75del				N	
A/Cambodia/24070331/2024		N	I		A	D	N			K	328del	-	-	-	-	-	-
A/Cambodia/KSH240409/2024		N	I		A		N		R		328del	-	-	-	-	-	-
A/Cambodia/SVH240441/2024		N	I		A		N			K	328del	46-75del	-	-	-	-	-
A/Colorado/109/2024			I	P	A			Q	R		327-328del		L				R
A/Colorado/134/2024			I	P	A			Q	R		327-328del		L				
A/Colorado/137/2024			I	P	A			Q	R		327-328del		L				R
A/Colorado/138/2024			I	P	A			Q	R		327-328del		L				R
A/Colorado/139/2024			I	P	A			Q	R		327-328del		L				R
A/Missouri/121/2024			I	P	A			Q	R		-		-	-	-	-	-
A/HeFei04171/2024*			I	P	A	D		Q	R		327-328del						

*Subtype A(H5N6)
- No data

All A(H5Nx) viruses carried T108I which, in combination with S107R, has been associated with increased virulence in chickens and mice and increased pH of fusion (Wessels et al., 2018), and S133A, which is linked to increased pseudovirus binding to α2–6 human-type receptors (Yang et al., 2007).

Furthermore, all 2.3.4.4b viruses (with complete available HA sequence) and all except two recent 2.3.2.1c viruses had a deletion at position 328 (a polybasic cleavage motif), which is seen in the vast majority of clade 2.3.2.1c viruses, compared to A/Goose/Guangdong/1/96. Such a deletion may lead to increased pathogenicity of avian influenza viruses (Suttie et al., 2019).

The D94N and S155N substitutions, both associated with increased virus binding to α2–6 human-type receptors (Su et al., 2008; Wang et al., 2010) were present in the five viruses from Cambodia. Furthermore, S123P, K218Q and S223R were present in those from Colorado and Missouri. Acquisition of S123P combined with N193K, and K218Q with S223R increases receptor binding to α2–3 and α2–6 receptors (Guo et al., 2017).

An NA deletion at approximately position 46-75 (stalk region), a virulence determinant in chickens (Stech et al., 2015), occurred in three of the five A(H5N1) viruses from Cambodia. No mutations associated with antiviral resistance were detected in the NA.

Four out of five of the PA segments of the Colorado strains had K497R, which increases polymerase activity in a mammalian cell line, and two out of five of the ones from Cambodia had K142N, associated with increased virulence in mice (Suttie et al., 2019). All viruses with available PA segments had an E at 23, and A at 37, I at 38, and an E at position 199, suggesting no reduced susceptibility to baloxavir marboxil.

A(H9N2)

The HA segments of both A(H9N2) viruses from India and Ghana had leucine at position 226 (H3 numbering), which is associated with increased virus binding to α2–6, enhanced replication in mammalian cells and ferrets, and enhanced contact transmission in ferrets (Wan and Perez, 2007; Wan et al., 2008). Further screening was also carried out for the HA amino acid substitutions T150A, R164Q, N166D and I220T (H9 numbering), which in various combinations are involved in antibody escape, increased viral replication in avian and mammalian cells, and enhanced viral replication in mice (Zhang et al., 2023). The mutations at these positions were the same for both viruses; R164Q was present in combination with I220T. The conjunction of R164Q and I220T has been associated with increased replicative ability in both avian and mammalian cells. For the other segments, the PB2 mutation I292V was detected in A/India/Kol-NIV_24_1519/2024, reported to be associated with increased polymerase activity in mammalian cell lines and increased virulence in mice for A(H9N2) (Gao et al., 2019). Both viruses had the antiviral drug related mutation in S31N in M2, with a phenotype of increased resistance to amantadine and rimantadine (Suttie et al., 2019).

2.4.6 Additional information relevant for public health and international risk assessments

Preliminary results from a seroprevalence study in workers at dairy farms in Michigan, USA, with outbreaks of avian influenza A(H5N1) in cattle found no antibodies specific to avian influenza A(H5N1) viruses in 35 tested farm workers. The authors concluded that the findings suggest asymptomatic infections are not occurring among farm workers on affected farms. Furthermore, the study supports the current testing strategy in which symptomatic people exposed to infected animals are tested (CDC, online-f). However, a pre-print study of two dairy farms in Texas that had experienced infection with A(H5N1) virus in cattle found elevated neutralising antibodies against A(H5N1) in two out of 14 farm workers with recent respiratory symptoms who were tested. Presence of cross-reacting antibodies cannot be excluded (Shittu et al., 2024). The study indicates that there may have been undetected cases occurring among farm workers and highlights the importance of testing all individuals that develop symptoms consistent with zoonotic avian influenza following exposure to infected animals or their environments, as outlined in ECDC's 'Investigation protocol for human cases of avian influenza' (ECDC, 2023a).

Globally, the Food and Agriculture Organization of the United Nations (FAO), WHO and WOAH have assessed the public health risk posed by influenza A(H5N1) viruses characterised since 2021 to be low, while for occupationally exposed individuals the risk of infection was considered low-to-moderate, depending on the protective measures applied (FAO, WHO and WOAH, online-a).

The Influenza Risk Assessment Tool (IRAT) can be used to evaluate various attributes of novel influenza viruses, such as the potential of emergence due to the virus gaining the ability to transmit between humans, and the possible impact on public health (CDC, 2024g). Using IRAT, US CDC scored the future pandemic potential of A(H5N1) viruses from the HA clade 2.3.4.4b, including the virus from a human case in Texas (A/Texas/37/2024), as 'moderate risk', which is a similar risk level to previously assessed influenza A(H5N1) viruses (CDC, 2024b).

US CDC considers that the overall risk for the general public of A(H5N1) viruses currently circulating in animals in the USA is low. In their assessment, the current avian influenza A(H5N1) situation in animals and humans in the USA and internationally was evaluated, taking into consideration sources of human infections, absence of human-to-human transmission, and genetic characteristics of viruses. However, individuals with occupational or recreational exposure to infected animals are considered to be at greater risk of infection (CDC, online-h). The US CDC's current assessment of the human health risk of A(H5N1) to the general public in the USA remains unchanged. Nevertheless, findings from the ongoing investigations following the recent human case in Missouri will determine whether the assessment needs to be revisited (CDC, online-c, d).

The UK Health Security Agency (UKHSA) situational assessment of A(H5N1) clade 2.3.4.4b genotype B3.13 associated with the multi-state outbreak in cattle in the USA, raised the threat to human health from level 3 (limited or facilitated mammalian transmission) to level 4 (sustained and/or multi-species mammalian outbreaks, increasing zoonotic human cases or limited human-to-human transmission associated with zoonotic exposure) on a scale of 6, with moderate confidence (UKHSA, online-a). Based on the likelihood of exposure and impact of infection, UKHSA, together with the joint Human Animal Infections and Risk Surveillance (HAIRS) group, previously assessed the risk to human health from the A(H5N1) clade 2.3.4.4b genotype B3.13 associated with the outbreak in US cattle as very low for people in the United Kingdom (UKHSA, online-b).

2.4.7 ECDC risk assessment

Overall, ECDC assesses the risk of human infection with the HPAI A(H5) clade 2.3.4.4b viruses currently circulating in Europe as low for the general public in the EU/EEA and low-to-moderate for those occupationally or otherwise exposed to infected animals or contaminated environments. The assessment is based on available evidence relating to the transmission, prevalence, and characteristics of A(H5N1) viruses currently circulating in animals in Europe.

Detections of HPAI viruses in wild and domestic birds in Europe continue to be lower than in recent years, with HPAI viruses circulating at low levels particularly in coastal areas. However, detections may increase in the coming weeks with the autumn migration of wild birds. Considering the extensive circulation of avian influenza viruses in animal populations both in Europe and globally in the last few years, with frequent opportunities for human exposure, transmission from infected animals to humans remains rare.

So far, there have been no confirmed cases of A(H5N1) infection in humans in the EU/EEA. In 2022, there were two influenza A(H5N1) virus detections due to suspected environmental contamination in poultry workers in Spain (Aznar et al., 2023). Globally, sporadic cases of infection with avian influenza A(H5N1) virus have been reported in humans, most of which have had a history of unprotected exposure to poultry, contaminated environments, or more recently, dairy cattle. Between 21 June and 20 September 2024, 88% (n = 14/16) of notified A(H5N1) and A(H5) cases in the USA and Cambodia reported exposure to poultry, one case was exposed to cattle infected with avian influenza A(H5N1) virus, and one case had no identified exposure. No sustained transmission between humans has been observed. Sporadic infections with avian influenza in humans are likely to continue occurring in areas where the virus is prevalent and individuals have unprotected contact with animals infected with avian influenza viruses, or their environment.

Clinical presentations of individuals infected with A(H5N1) have ranged from asymptomatic or mild, such as conjunctivitis and upper respiratory tract symptoms, to severe illness resulting in death, with an estimated case fatality of 51% among reported cases. Between 21 June and 20 September 2024, 10 out of 11 A(H5) cases reported in the USA experienced mild symptoms, such as conjunctivitis or mild respiratory illness. One A(H5N1) case, who had underlying medical conditions, was hospitalised but did not experience severe illness. In Cambodia, four out of five A(H5N1) cases reported during the same time period were hospitalised, including one fatal outcome. The reasons for the variation in outcome of infection is likely to be multi-factorial and may be attributed to the virus genotype, duration of exposure, viral load, transmission route, individual health status, personal protective measures taken, and medical treatment provided (FAO, WHO and WOAH, online-b).

With the widespread occurrence of avian influenza A(H5N1) globally, the virus continues to diversify. In Europe, mutations associated with viral adaptation to mammalian hosts have been identified in sequences of A(H5N1) viruses from mammals as well as birds. Nevertheless, A(H5N1) viruses circulating in animal populations in Europe retain a binding preference for α2–3 sialic acid avian-type receptors and are considered to be avian-like. Further understanding of the implications of such mutations for mammalian adaptation, infection and transmission is required to assess any change in the associated risk to humans. However, there have been no identified mutations or reassortments of the virus that would make it human-adapted or enhance transmission between humans. In addition, the vast majority of the circulating A(H5N1) viruses in Europe remain susceptible to antiviral medicines, including adamantanes, neuraminidase inhibitors (e.g. oseltamivir) and endonuclease inhibitors (e.g. baloxavir marboxil).

Events or conditions that increase mammalian or human exposure to avian influenza viruses may lead to spillover events and further transmission, increasing the probability of avian influenza viruses adapting to mammals (EFSA, ECDC and EURL, 2024b). Given the extensive transmission of A(H5N1) in birds and poultry, and in some mammals in certain settings, viral evolution or reassortment may occur which could change the current assessment. As a result, the risk assessment is being regularly reviewed by ECDC, taking into consideration any new developments or information which becomes available.

3. Conclusions

3.1 Birds

- The low number of HPAI virus detections in wild and domestic birds reported in the previous reporting period continued in the current reporting period. However, there was a switch in the main category of wild birds affected, from waterfowl in the previous reporting period to colony-breeding seabirds in the current reporting period. Consequently, most of the reported detections in both wild and domestic birds were located along the coasts of the Atlantic Ocean, North Sea and Baltic Sea. Audouin's gulls were found affected for the first time in Europe. This finding is of great concern, as the Audouin's gull is already experiencing a rapid population decline following the collapse of Europe's largest breeding colonies due to a restriction in food from fishery discards coupled with high level of predation on colonies.

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

- Half of the HPAI-affected poultry establishments in Europe during the current reporting period kept multiple species of birds. Most of these establishments had outdoor access and kept, among other species, ducks and geese. The combination of outdoor access and the higher risk of infection with avian influenza observed in duck and geese establishments compared to chicken establishments have likely contributed to observing more HPAI outbreaks in 'mixed' than other establishments keeping only one poultry species.

- Currently available genetic data indicate a rapid drop in the HPAI A(H5N1) genetic diversity during the summer, with an evident geographic and host segregation among the circulating genotypes: EA-2023-DI genotype has mainly been detected among waterfowl in northeastern Europe (Baltic coast), while the gull-adapted EA-2022-BB and EA-2023-DT genotypes have been mostly circulating among Laridae along the North Sea and Atlantic coasts.

- The HPAI genotype EA-2023-DT, currently circulating in colony-breeding seabirds on the Atlantic coast, emerged in late 2023 from a reassortment event between the EA-2022-BB genotype and LPAI viruses of the gull-adapted H13 subtype, possibly making this genotype even more adapted to Laridae compared to EA-2022-BB. EA-2023-DT is currently widespread in seabirds in Spain and Portugal, where it seems to have been rapidly replacing the EA-2022-BB genotype. Further geographic spread of this genotype in the coming months, with unpredictable impact on seabird populations, is possible.

- The A(H5N5) genotype EA-2021-I continues to circulate at a low level in northern parts of Europe. The reservoir of this subtype remains unknown.

- The HPAI A(H7N5) affecting an establishment keeping laying hens in Germany likely emerged from an LPAI virus initially affecting the farm.

- It is not clear whether the number of HPAI virus detections in Europe will remain low in the coming weeks or whether it will increase in connection with the influx of wintering waterfowl as autumn migration reaches its peak.

- A similar reduction in reported HPAI virus detections in wild and domestic birds as in Europe can be observed worldwide. Compared to the previous reporting period (EFSA, ECDC and EURL, 2024a), the number of HPAI virus detections in both domestic and wild birds decreased, and a lower number of countries reported to WOAH overall. Since a lot of additional information on HPAI virus detections can be retrieved through the screening of government reports and different news media, it is evident that official reports to WOAH have decreased or are delayed. This is particularly true when compared to the same period in the previous epidemiological year. The very low number of officially reported HPAI virus detections in wild birds compared to domestic birds worldwide has been remarkable.

- Most of the HPAI outbreaks reported in poultry worldwide continued to be concentrated in North America, particularly in the USA. Although reported at a lower level, the HPAI situation in domestic and wild birds also continues in the other continents, particularly in Asia, where multiple avian influenza viruses are endemic. Of specific concern are the HPAI A(H5N6) virus detections in wild birds in China due to the potential for long-distance spread to other geographical regions, such as to Europe during their upcoming autumn migration.

- HPAI viruses are expected to continue to spread in the Antarctic region, although the impact thereof can only be assessed during the next breeding season, from about November 2024 onwards. Dependent on epidemiological developments in the Antarctic region, there is a risk of further spread of HPAI A(H5N1) virus to Oceania, including Australia and New Zealand.

- In the 2023–2024 epidemiological year, the detection of 17 HPAI A(H5) viruses in wild and domestic birds collected from eight different European countries containing markers of mammalian adaptation in the PB2 protein (E627K, K526R or D701N) indicates that viruses with an enhanced capacity to infect mammals can replicate and spread in birds. Of particular concern is the spread of HPAI A(H5N5), genotype EA-2021-I, viruses with PB2-E627K mutation, observed in wild bird populations in multiple countries in northern Europe. This poses a threat for host jumps and reassortments with influenza A viruses circulating in mammals.

- The majority of HPAI A(H5N1) viruses circulating in birds in Europe since October 2023 have at least some amino acid substitutions in the HA protein that have proved to increase in vitro binding to human-type receptors. The impact of these HA mutations on the biological characteristics of the circulating viruses is still unknown but may potentially impact their zoonotic potential.

3.2 Mammals

- No new HPAI virus detections in mammals were reported in Europe between 15 June and 20 September 2024. Testing of samples collected from ruminants and bulk milk in Europe have so far only resulted in negative test results.

- The Netherlands retrospectively reported the detection of HPAI A(H5N5) virus in a European pine marten found dead in February 2024.

- The number of establishments keeping dairy cattle in the USA reportedly infected with HPAI A(H5N1) virus, genotype B3.13, continued to increase to > 230 in 14 states during the current reporting period. Importantly, A(H5N1) virus was detected for the first time in dairy cattle in California, which is the US state with the largest dairy cattle population. In relation to other affected domestic mammals in the USA, the source of infection for some domestic cats kept indoors remains unclear.

- HPAI A(H5N1) virus was detected for the first time in deer mouse, dessert cottontail and prairie vole in the USA. The identification of HPAI virus in desert cottontail represents the first report of this kind in a Lagomorpha species.

- HPAI A(H5N1) virus was confirmed for the first time in two wild mammal species (Antarctic fur seal, southern elephant seal) on the Antarctic continent.

- To date, no key mutations associated with the switch in the virus binding preference from avian- to human-type receptors were identified in the A(H5) viruses collected from mammalian species in Europe. However, seven out of the 10 characterised viruses of mammals in Europe from the current epidemiological year contain the PB2-E627K mutation that confers more efficient replication in mammals.

3.3 Humans

- Sporadic cases of zoonotic avian influenza A(H5N1), A(H5N6) and A(H9N2) continued to be reported outside of Europe during the period June−September 2024.

- Despite the widespread occurrence of HPAI A(H5N1) in wild birds, poultry and some mammals in recent years, with many potential exposures of humans to infected animals, there have been no confirmed human cases in the EU/EEA.

- The majority of human infections with avian influenza viruses have been associated with unprotected exposure to poultry, live poultry markets, or contaminated environments. In addition, there have recently been four human cases of A(H5N1) following exposure to dairy cattle presumed or confirmed to be infected with A(H5N1) virus. To date, there has been no sustained human-to-human transmission observed.

- In the reporting period from 21 June to 20 September 2024, two out of 19 human cases of avian influenza reported globally had no known exposure identified following epidemiological investigation. Diagnostic testing of symptomatic contacts of one of the two cases is still ongoing.

- With the extensive circulation of avian influenza viruses in bird populations globally, sporadic transmission to humans is likely to continue occurring in settings where people have unprotected exposure to infected animals or their environment.

4. Options for response

4.1 Birds

- Increased surveillance in wild birds in Europe is indicated in the coming weeks in anticipation of the upcoming autumn migration of waterfowl from different parts of the world, especially from Asia. On the other hand, attention should also be paid to infection and potential mortality of gull species (Laridae) due to a new genotype of HPAI A(H5N1) virus, the EA-2023-DT genotype, which contains additional gene segments of a gull-adapted LPAI A(H13) virus and therefore may transmit more efficiently among gulls.

- Active surveillance in wild birds, especially in those that silently maintain HPAI viruses in the wild (e.g. waterfowl), is indicated to improve knowledge on HPAI viruses circulating in wild bird populations, as well as to estimate viral prevalence and seroprevalence among different species for a better epidemiological understanding of these viruses. Serological studies, combined with mortality data, may also help infer whether some level of flock immunity has been reached in different species.

- It is important to continuously monitor LPAI viruses of the A(H5) and A(H7) subtypes in wild and domestic birds, and introductions of these subtypes into poultry establishments, as it is known that these subtypes are able to mutate into their highly pathogenic forms once circulating in poultry.

- For wild birds, general options for response include accurate and comprehensive recording of HPAI-associated mortality events (e.g. estimating the impact on wild bird populations), preventing disturbance of areas undergoing HPAI outbreaks to reduce virus spread, and, depending on the circumstances, removal of HPAI virus-affected carcasses from areas where wild birds congregate to reduce environmental contamination and further virus spread.

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

- The geographic expansion of HPAI A(H5N5) viruses in wild birds in northern parts of Europe and worldwide should continue to be closely monitored.

- Timely generation and sharing of genome sequence data from avian influenza viruses is of utmost importance to promptly detect the possible emergence of viruses with amino acid changes associated with increased zoonotic potential, resistance toward antiviral drugs or different antigenic properties. The biological characteristics of these variants should be further evaluated to assess the actual impact of acquired mutations. Genetic data are also instrumental to track the virus spread and identify novel incursions of viruses that may represent a threat for human or animal health.

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

4.2 Mammals

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

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

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

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

4.3 Humans

- Measures should be taken to reduce human risk of exposure to avian influenza:
  - The general public should avoid contact with sick or dead birds and other animals susceptible to avian influenza and, if they find dead animals, inform the relevant authorities to ensure safe removal and further investigation, if required.
  - Appropriate personal protective equipment should be used to reduce the risk of infection when in contact with potentially infected animals or highly contaminated environments.

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

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

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

- In the months between seasonal influenza periods, people seeking medical care with respiratory symptoms or other symptoms compatible with zoonotic avian influenza should be asked about exposure to sick or dead animals within two weeks of symptom onset or, if not available, before admission. Additional details on the strengthening of surveillance in the influenza inter-seasonal period are provided in ECDC's report 'Enhanced influenza surveillance to detect avian influenza virus infections in the EU/EEA during the inter-seasonal period' (ECDC, 2024).

- During periods of high seasonal influenza circulation, testing and subtyping for avian influenza virus in humans should be targeted using a risk-based approach based on the epidemiological situation in animal populations, and should focus on outbreaks, severe respiratory signs, and 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, 2023b).

- Recent detections of human cases of zoonotic avian influenza through surveillance systems for seasonal influenza emphasise the importance of typing and subtyping samples and further analysing those which test positive for influenza A that cannot be subtyped. Ideally, all sentinel influenza-positive specimens from both primary and secondary care sources should be typed and subtyped.

- Avian influenza viruses from humans should be sequenced and shared in public databases in a timely manner. Genetic changes in avian influenza viruses that may alter zoonotic potential or susceptibility to available antivirals should be monitored.

- Vaccination against seasonal influenza can be offered to individuals who are occupationally exposed to avian influenza to reduce the risk of reassortment between avian and human influenza viruses. Specific vaccination recommendations are under the remit of national authorities (EFSA, ECDC and EURL, 2024b).

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Appendix A – Terms of Reference

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

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

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

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

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

- ECDC's current risk assessment (ECDC, online) that focuses on the immediate risk of avian influenza for human health fulfilling ECDC's new mandate and the Regulation (EU) 2022/2371[9] aiming to prevent and prepare for cross-border health threats, including epidemics; and
- EFSA's latest scientific opinions and reports (EFSA, online) coupled by measures taken (i.e., surveillance, prevention and control measures) under the Animal Health Law (i.e., Commission Delegated Regulation (EU) 2020/689[10] and Commission Delegated Regulation (EU) 2020/687[11]).

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[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) 2022/2370[12] and Articles 29 and 31 of Regulation (EC) No 178/2002[13], the European Centre for Disease Prevention and Control (ECDC) and the European Food Safety Authority (EFSA) are requested to carry out the following task:

To provide regular quarterly scientific reports, updating on the avian influenza situation within the Union and worldwide, to the Commission by:

1) Analysing the epidemiological data on HPAI and LPAI from Member States and describe the evolution of virus spread from certain regions towards the EU and in case of significant changes in the epidemiology of avian influenza;
2) Analysing the temporal and spatial pattern of HPAI and LPAI, as appropriate, in poultry, captive and wild birds, kept and wild mammals, as well the risk factors involved in the occurrence, spread and persistence in the EU of the avian influenza virus in and at the interface of these animal populations with specific attention to zoonotic risks;
3) Describing the options for adapting preparedness, prevention, and control measures, based on the finding from point 1) and 2).

A.2 Interpretation of the Terms of Reference

In reply to the TORs above, this Scientific Report gives an overview of the HPAI virus detections in poultry, captive and wild birds, as well as in mammals, in Europe and worldwide between 15 June and 20 September (23 September for mammals) 2024, as reported by Member States and third countries via ADIS or WOAH-WAHIS. In addition, LPAI virus detections of specific relevance are included, and possible actions for preparedness in the EU are discussed based on the situation worldwide. Member States and other European countries where HPAI outbreaks have occurred in poultry submitted additional epidemiological data to EFSA, which have been used to analyse the characteristics of the affected poultry establishments.

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

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

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[12] Regulation (EU) 2022/2370 of the European Parliament and of the Council of 23 November 2022 amending Regulation (EC) No 851/2004 establishing a European centre for disease prevention and control. OJ L 314, 6.12.2022, p. 1–25.

[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, data on HPAI outbreaks reported in Europe between 15 June and 20 September 2024, and submitted by Member States and other European countries via ADIS, were taken into account. Data extraction was carried on 20 September 2024. WOAH-WAHIS was consulted to complement the information for European countries not reporting HPAI notifications via ADIS. In addition, HPAI-affected countries were asked to provide more detailed epidemiological information on HPAI outbreaks occurred in poultry directly to EFSA. This information included details on the poultry species and production systems affected by HPAI, which were supplied in form of additional variables to complement the data reported via ADIS. All information is provided in Annex B. In addition, the information European countries affected by HPAI and LPAI presented to the Standing Committee on Plants, Animals, Food and Feed (SCOPAFF), and the evidence on HPAI and LPAI outbreaks provided in the info notes from the affected countries to EC, were consulted to extract relevant information reported in Section 2.1.1. The presentations delivered at the SCOPAFF meetings are available on the EC website (European Commission, online).

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

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

The annexes to this Scientific Report are available here: https://doi.org/10.5281/zenodo.13883775

B.1.2 Overview of avian influenza outbreaks in other countries not reporting via ADIS

Data from WOAH-WAHIS on HPAI A(H5) and A(H7) in domestic and wild birds were used to describe and map the geographic distribution of avian influenza virus detections in domestic and wild birds in all regions of the world based on the observation dates. Data were retrieved on 23 September 2024 and extracted by EFSA. They were used and reproduced with permission. WOAH bears no responsibility for the integrity or accuracy of the data contained herein, but not limited to, any deletion, manipulation, or reformatting of data that may have occurred beyond its control.

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

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

B.2 Data on humans

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

Annex A – Data on Birds

Annex A is available on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.13883775

Annex B – Data on poultry outbreaks

Annex B is available on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.13883775

Annex C – Acknowledgements

Annex C is available on the EFSA Knowledge Junction community on Zenodo at: https://doi.org/10.5281/zenodo.13883775