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## Avian influenza overview March – April 2023

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### Abstract

Between 2 March and 28 April 2023, highly pathogenic avian influenza (HPAI) A(H5Nx) virus, clade 2.3.4.4b, outbreaks were reported in domestic (106) and wild (610) birds across 24 countries in Europe. Poultry outbreaks occurred less frequently compared to the previous reporting period and compared to spring 2022. Most of these outbreaks were classified as primary outbreaks without secondary spread and some of them associated with atypical disease presentation, in particular low mortality. In wild birds, black-headed gulls continued to be heavily affected, while also other threatened wild bird species, such as the peregrine falcon, showed increased mortality. The ongoing epidemic in black-headed gulls, many of which breed inland, may increase the risk for poultry, especially in July–August, when first-year birds disperse from the breeding colonies. HPAI A(H5N1) virus also continued to expand in the Americas, including in mammalian species, and is expected to reach the Antarctic in the near future. HPAI virus infections were detected in six mammal species, particularly in marine mammals and mustelids, for the first time, while the viruses currently circulating in Europe retain a preferential binding for avian-like receptors. Since 13 March 2022 and as of 10 May 2023, two A(H5N1) clade 2.3.4.4b virus detections in humans were reported from China (1), and Chile (1), as well as three A(H9N2) and one A(H3N8) human infections in China. The risk of infection with currently circulating avian H5 influenza viruses of clade 2.3.4.4b in Europe remains low for the general population in the EU/EEA, and low to moderate for occupationally or otherwise exposed people.

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## 1 Background

This scientific report provides an overview of highly pathogenic avian influenza (HPAI) virus detections in poultry<sup>1</sup>, captive<sup>2</sup> and wild birds as well as mammals and noteworthy outbreaks of low pathogenic avian influenza (LPAI) virus in poultry and captive birds, and human cases due to avian influenza virus that occurred in and outside Europe between 2 March and 28 April 2023.

The background, Terms of Reference and their interpretation are described in Appendix A, and the data and methodologies are reported in Appendix B.

## 2 Results

### 2.1 HPAI virus detections in birds

#### 2.1.1 HPAI virus detections in birds in Europe

Figure 1 shows all HPAI outbreaks in birds that were reported in Europe via ADIS or WOA-WAHIS for the last six and the current epidemiological years<sup>3</sup> by month of suspicion. For the current epidemiological year 2022–2023, starting on 1 October 2022, data reported are truncated on 28 April 2023.

The HPAI epidemic observed in the 2021–2022 epidemiological year was so far the largest observed in Europe, with a total of 6,684 HPAI virus detections in 37 European countries, 2,761 of which in domestic birds and 3,923 in wild birds. In the current 2022–2023 epidemiological year and as of 28 April 2023, a total of 3,849 HPAI virus detections were reported over 31 countries: 1,175 in domestic birds and 2,674 in wild birds (Figure 1, [Table A.7 in Annex A](#)).

Considering the current reporting period, from 2 March to 28 April 2023, 716 HPAI virus detections were reported in poultry (92), captive (14) and wild birds (610) (Figure 2, [Table A.7 in Annex A](#)).

#### Domestic birds

HPAI outbreaks in poultry were all identified as A(H5N1) and reported in Hungary (60), Italy (10), Germany (6), United Kingdom (4), Czechia (3), Denmark (2), France (2), Poland (2), Bulgaria (1), Sweden (1), and Switzerland (1) (Figure 3). With the exception of Hungary, most outbreaks were reported as primary outbreaks, and thus not attributed to secondary spread. The most likely source of infection reported by countries was indirect contact with wild birds or unknown. Overall, almost 2.2 million birds died or were culled in the HPAI-affected poultry establishments with Italy accounting for 49% of the birds that died or were culled (due to the large size of some of the Italian affected holdings), followed by Hungary (36%) and the United Kingdom (9%) (Figure 4).

Below, a brief description of HPAI outbreaks in poultry is given by country. Some of the information on the HPAI-affected establishments that is here reported was collected from the affected countries up to outbreaks that occurred by 3 April 2023; the outbreaks that occurred later were too close to the publication of this report to collect the data, therefore, for those

<sup>1</sup> 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).

<sup>2</sup> 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.

<sup>3</sup> In this document an 'epidemiological year' refers to the period starting on week 40 (the beginning of October) and ending on 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.

poultry outbreaks some of the information presented was unknown at the time of publication and will be included in the next report.

Details on the characteristics of the affected poultry establishments and species reared are presented in [Annex C](#), which also reports information on poultry outbreaks that occurred before the current reporting period but was not included in the previous EFSA report (EFSA et al., 2023) (i.e. from 18 November 2022 to 3 April 2023).

### *Bulgaria*

One outbreak was reported in Bulgaria during this reporting period, a primary outbreak in a non-commercial farm keeping chickens and domestic ducks for mixed production. The birds had outdoor access and the source of introduction was reported as unknown. Affected chickens showed increased mortality, whereas affected ducks did not. No data on the number of people exposed to the virus was available.

### *Czechia*

During this reporting period, three primary poultry outbreaks were reported in Czechia. Information was collected and is here described for only two of those poultry outbreaks, as the last one occurred too close to the publication of this report and will be included in the next report. Those two outbreaks occurred in non-commercial farms keeping several species of poultry including chickens, domestic ducks, domestic geese, domestic guineafowls and peafowls. The birds had outdoor access on both farms and the most likely source of introduction was indirect contact with wild birds. The number of exposed people was five. On both farms the chickens showed increased mortality, presence of clinical signs, and one farm reported a drop in egg production. For domestic geese, domestic ducks and domestic guineafowls, presence of clinical signs was reported. For peafowls, presence of clinical signs and increased mortality were reported.

### *Denmark*

Two primary poultry outbreaks were reported in Denmark during this reporting period and, for one of them, information to characterise the outbreak was collected. This outbreak occurred in a non-commercial farm keeping chickens, Muscovy ducks and domestic geese were the animals had outdoor access. The source of introduction was unknown but was most likely from wild birds. The chickens and domestic geese showed increased mortality and presence of clinical signs, while for Muscovy ducks no signs of disease were reported.

### *France*

Two primary poultry outbreaks were reported in France during this reporting period and both occurred in commercial farms keeping turkeys and chickens for fattening. In the farm keeping chickens, the birds had outdoor access and increased mortality and presence of clinical signs were reported. The farm keeping turkeys reported increased mortality, presence of clinical signs as well as drop in feed and water intake. No data on the number of exposed people or the source of introduction were available at the time of publication of this report.

Compared to the previous 2021-2022 epidemiological year where 78% of the total 1,395 poultry outbreaks detected were due to secondary spread, during the ongoing 2022-2023 epidemiological year only 3% of the 294 poultry outbreaks reported in France were due to secondary spread. This decrease in the overall number of poultry outbreaks and of secondary spread of virus infections in poultry might be the consequence of a voluntary reduction in southwestern France of the density of poultry establishments involved in domestic duck production. Only 30-50% of the premises, present in the 68 localities where poultry establishments are at their highest density, were restocked between mid-December 2022 and mid-January 2023, resulting in a global 80% size reduction of the corresponding duck flocks; by mid-March 2023, only 70% of the duck premises in the same area had been restocked. During the mid-December to mid-March higher risk period, in western France, shortage in duckling availability had also imposed to reduce restocking to about only 50% of the domestic duck production establishments.

## *Hungary*

During this reporting period, 60 poultry outbreaks were reported in Hungary, three of which were primary and 57 secondary outbreaks. At the time of publication detailed information was available for 27 of those outbreaks, as the ones that occurred after 3 April were too close to the publication of this report and will be included in the next report. Among those 27 outbreaks, three were chicken farms, two domestic duck farms, ten mulard duck farms, and twelve were domestic goose farms. The birds did not have outdoor access on any of these farms. All affected farms were commercial establishments except from one keeping chicken.

For two primary outbreaks keeping domestic geese the most likely source of introduction was indirect contact with wild birds, while for the third primary outbreak keeping mulard ducks and the 24 secondary outbreaks the most likely source of introduction was indirect contact with poultry.

Two of the farms keeping chickens reported increased mortality, among which, one farm also reported a drop in egg production, feed, and water intake. On the third chicken farm the animals showed no sign of disease. The two farms keeping domestic ducks reported increased mortality and presence of clinical signs. Of the 12 farms keeping domestic goose and the 10 keeping mulard duck, 10 and 7 farms respectively, reported increased mortality, presence of clinical signs drops in feed and water intake, and, where applicable, a drop in egg production. The other two domestic goose farms and three mulard duck farms reported no signs of disease in the birds. No data on the number of exposed people was available at the time of publication of this report.

## *Italy*

During this reporting period, 10 HPAI poultry outbreaks were reported in Italy. Complete information was available for five of them, information for the remaining outbreaks will be included in the next report. The five outbreaks were all primary introductions, four in commercial establishments and one in a non-commercial establishment. Among the commercial farms, two kept chickens for egg production and the other two turkeys for fattening. These farms had no outdoor access, and the most likely source of introduction was considered to be indirect contact with wild birds. On the non-commercial farm the birds had outdoor access and the most likely source of introduction was direct contact with wild birds. No data on the number of exposed people were available at the time of publication of this report.

During this reporting period, and more generally throughout the 2022-2023 epidemic year, the overall number of outbreaks in Italy (39) was significantly lower than in the previous epidemic year (318), as most of the cases in the previous epidemic were linked to secondary spread. One of the factors that may have played an important role was the lower density of poultry holdings in densely poultry populated areas in the current epidemic year compared to the previous one (up to about 20% less for some productive categories). At the time of detection of the first four outbreaks in commercial poultry farms low mortality, very low prevalence of infection, and almost no noticeable drops in egg production, or reduction in feed consumption or water intake were observed. These outbreaks, as well as all the others identified in Italy in 2023, except one, were detected in densely poultry populated areas within days/weeks from a HPAI mass mortality event in black-headed gulls. All these poultry and gulls cases were caused by the BB genotype (H5N1-A/Herring\_gull/France/22P015977/2022-like).

The reason for the limited clinical observations and low prevalence observed in the affected farms may be explained both by the very early detection of these cases thanks to intensive surveillance performed after the mass mortality events in gulls in the densely poultry populated areas and to the characteristics of the responsible virus.

Phenotyping studies in commercial female turkeys of 8-9 weeks of age were performed at the EURL. Two viruses were used for these experiments, an Italian gull isolate and a turkey isolate originating from the first Italian outbreak detected in this 2022-2023 epidemiological year.

Pathogenesis studies were carried out and the Bird Infectious Dose 50% (BID50) for both viruses was ascertained. The Mean Death Time (MDT) for turkeys challenged with 106 EID50

of the gull and turkey isolates ranged between 6-7 days (mean= 6.7 days) and between 8-15 days (mean=10.20 days), respectively. These MDTs are significantly higher than those recorded for 2.3.4.4b viruses associated with outbreaks in turkey farms in Italy in the period 2017-2021, which ranged between 4.56-5.33 days. Preliminary results indicate that for both these BB-genotype viruses high levels of shedding occur via the tracheal route but only modestly via the cloacal route. A worrying aspect was the delayed recognition of signs of disease (depression) in turkeys, only 4-5 days after the experimental infection, while high-level shedding from the tracheal route started 2 days post infection.

The BID50 in turkeys ranged between 5.6-5.8 EID50, which is slightly higher than the one recorded for the viruses isolated in the latest Italian epidemics (4.5-5.6 EID50).

Due to the possibility of an outbreak caused by the BB genotype in poultry species, which may be difficult to detect with passive surveillance in the first phase of infection, it was decided to sample and test carcasses collected in different areas of the pen and over several days every week (weekly bucket sampling) from all the turkey and laying hen farms located in the high-risk area and during the risk period.

### *Sweden*

One primary poultry outbreak was reported in Sweden during this reporting period, in a commercial establishment with breeding chickens where the birds had no outdoor access. The most likely source of introduction was indirect contact with wild birds. Approximately fifteen people were exposed to the virus. The farm reported increased mortality and presence of clinical signs in the chickens.

### *Switzerland*

One primary poultry outbreak was reported in Switzerland during this reporting period in a commercial farm (40 old laying hens) where the animals had outdoor access. The outdoor run was protected against wild birds, however the selling point of eggs was inside the animal location. Customers could enter the stable to pick up eggs. Biosecurity measures were not in place. Hence, the virus most probably entered by means of shoes or cloths of animal keepers and customers. Increased mortality and presence of clinical signs were reported in the chickens. No data on the number of exposed people was available at the time of publication of this report.

The description of the control and prevention measures applied in the affected Member States on HPAI outbreaks occurred up to 3 April 2023 is presented in [Annex B](#), thanks to the countries that were willing to collaborate with EFSA and kindly provided the information reported here.

HPAI virus detections in captive birds, all due to A(H5N1) viruses, were reported in Germany (5), Belgium (3), France (2), Norway (2), Hungary (1), and Lithuania (1) (Figure 2, [Table A.7 in Annex A](#)).

### **Wild birds**

HPAI virus detections in wild birds, six A(H5Nx), one A(H5N5) and 603 A(H5N1) viruses, were reported in Germany (218), the Netherlands (81), Italy (72), Switzerland (64), France (46), Austria (29), Belgium (16), Poland (14), United Kingdom (13), Czechia (9), Denmark (9), Spain (7), Slovenia (7), Sweden (6), Ireland (5), Slovakia (3), Norway (3), Hungary (2), Lithuania (2), Romania (2), and Serbia (2) (Figure 2, [Table A.7 in Annex A](#)).

There was a decrease in the number of detections compared to the previous period (610 vs 1,505 in the period 2 December 2022-1 March 2023) but an increase compared to the same period in the previous year (610 vs 434 in the period 2 March-28 April 2022).

The geographical distribution of reported HPAI virus detections in wild birds was widespread across Europe, from north (Norway, Sweden) to south (Spain, Italy), and from east (Romania, Poland, Lithuania) to west (Ireland, United Kingdom) (Figure 2, Figure 6). Foci of reported HPAI

virus detections were centred in the west of France, the Netherlands, the south of Germany, and the north of Italy. These foci consisted mainly of colonial seabirds, colocalized with smaller numbers of raptors and—except in west France—waterbirds. The complete list of wild bird species found as HPAI virus-infected from 2 March to 28 April 2023 is reported in [Figure A.1 in Annex A](#).

The temporal distribution of reported HPAI virus detections in wild birds in the reporting period (2 March to 28 April) declined rapidly from the peak in January-February (Figure 3). This decline occurred in all categories of wild birds.

As observed during the previous reporting period, the vast majority of reported HPAI virus detections in wild birds during this reporting period was in colony-breeding seabirds (412) (Figure 6), particularly in gulls (family Laridae, 416) (Figure 5). Of the gulls identified to species level, nearly all were black-headed gulls (265), with smaller number of herring gulls (12) (Figure 5, [Figure A.1 in Annex A](#)). Regarding waterfowl (102) (Figure 6), most of the HPAI virus detections were reported in mute swans (25), followed by greylag geese (5) and pink-footed geese (5). Regarding raptors (78) (Figure 6), HPAI virus detections were reported most frequently in peregrine falcons (20) and Eurasian buzzards (12). More than 36% (218/618) of the wild birds reported, in which HPAI virus detections were reported, were not identified to species ([Figure A.1 in Annex A](#)).

Of note, HPAI virus detections in wild birds are underestimated and the numbers provided are not representative for the number of wild birds that died from HPAI A(H5) infection.

The peregrine falcon, whose population in Europe is estimated approximately to 32,200-62,100 mature individuals is listed in CITES Appendix I, CMS Appendix II, Raptor MOU Category 3, and EU Birds Directive Annex I, and is protected by special conservation measures concerning its habitat in order to ensure its survival and reproduction in its area of distribution. Systematic breeding schemes for this species are in place in at least 21 European countries (BirdLifeInternational, online-a).

During this reporting period, mortality events affecting hundreds to thousands of black-headed gulls per event, with HPAI A(H5N1) suspected or confirmed were reported in different media in Belgium, Czechia (European Commission, online), Germany (Zeitung, online) North-Rhein-Westfalia, (Nachrichten, online) Baden-Wuerttemberg, Brandenburg, Hamburg, Mecklenburg-Western Pomerania and Saxony Anhalt), the Netherlands (Group, 2023) Poland (including Silesia region (Group, 2023), Sweden (SVA, online-a), the United Kingdom (Wales, England, (Post, online). These reports strongly suggest that HPAI A(H5N1) virus is widespread in black-headed gulls in Europe and is causing substantial mortality at breeding colony sites.

Historical capture-recapture data from ringing activities from the European Union for Bird Ringing (EURING) and real-time bird abundance data by the EuroBirdPortal on the expected movements of black-headed gulls in the coming weeks/months indicate a general north and north east movement from places where A(H5N1) virus has been confirmed in this species (France, Belgium, the Netherlands, Italy), with larger numbers moving towards Scandinavia and northeastern Europe (e.g. Poland) in the next months (Tables A.1 – A.4). Those data can be consulted in the Migration Mapping Tool developed by the British Trust for Ornithology (BTO) and the Catalan Ornithological Institute (ICO) on behalf of EURING and EuroBirdPortal <sup>4</sup>.

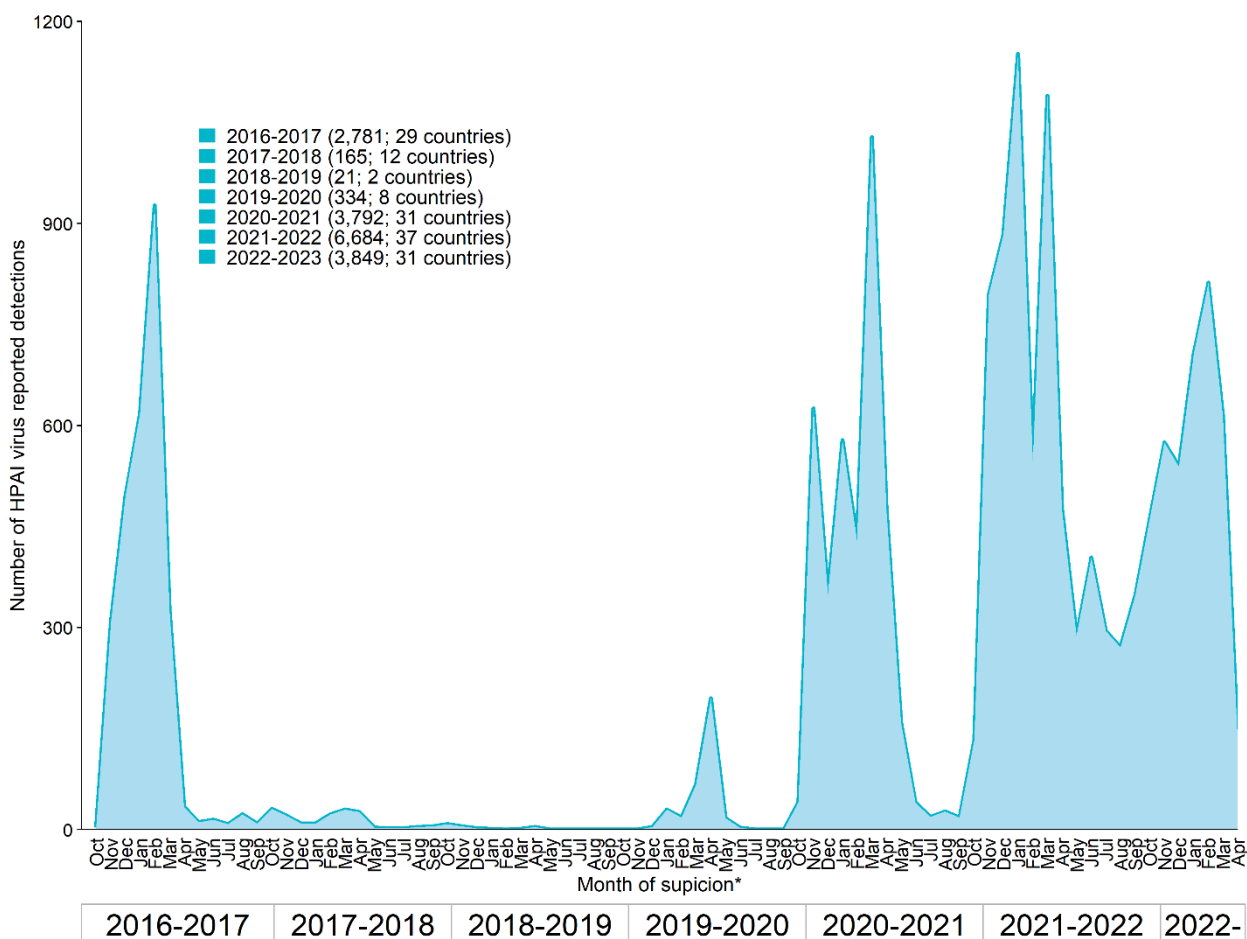
The European population of black-headed gulls (2,670,000-3,980,000 mature individuals) is estimated to have declined moderately between 1990 and 2013. Within the EU, the black-headed gull is listed on Annex II of the Birds Directive, in 43 marine Important Bird Areas, and in 928 Special Protection Areas. There are management plans for protected sites, which include monitoring and enforcement from disturbance and removal of eggs (BirdLifeInternational, online-b). At black-headed gull breeding colonies in the coming months, chicks (about 2-3 per nest) will fledge about in June and disperse from the breeding colonies in July-August. In this

<sup>4</sup> <https://eurring.org/research/migration-mapping>



species, epidemics of LPAI virus subtypes H13 and H16 occur every year in first-year birds, with prevalence rates of up to 72% per week. These epidemics start 1-3 weeks after onset of fledging, possibly due to increased mobility after fledging and, therefore, increased contact rate; due to access to water, facilitating more efficient virus transmission; and to the increased susceptibility of fledglings as a result of immature body condition and loss of maternal antibodies (Verhagen et al., 2014)

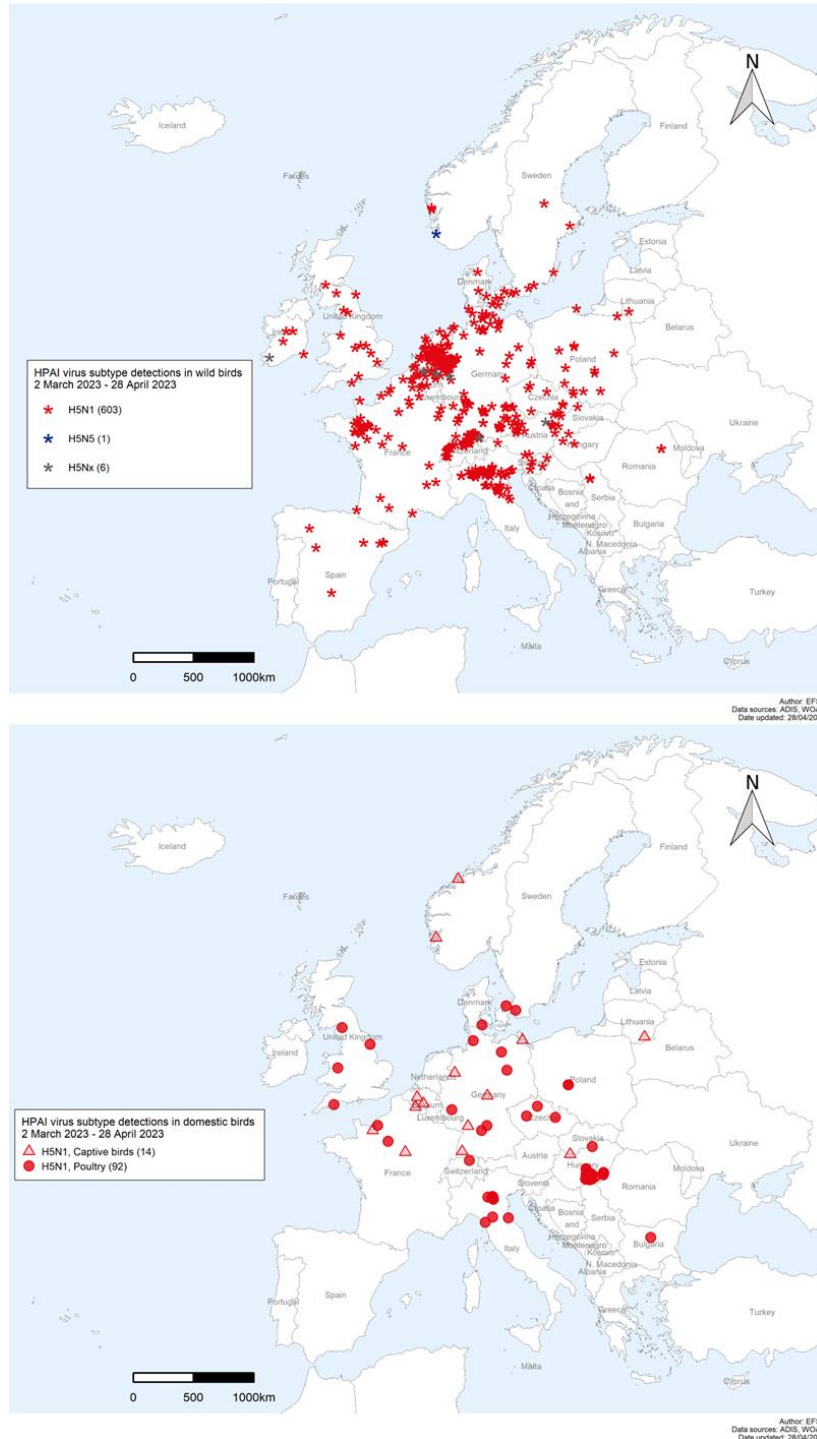
Spatio-temporal information on all HPAI virus detections that have been reported in Europe since October 2016 is available in EFSA’s interactive [dashboard](#).



\*If the date of suspicion is not available, the date of confirmation is used to assign the week of suspicion. United Kingdom data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was the World Animal Health Information System (WOAH-WAHIS) for United Kingdom (excluding Northern Ireland), and ADNS/ADIS for the United Kingdom (Northern Ireland)<sup>5</sup>. Source: ADIS and WOAH (data extraction carried out on 28 April 2023).

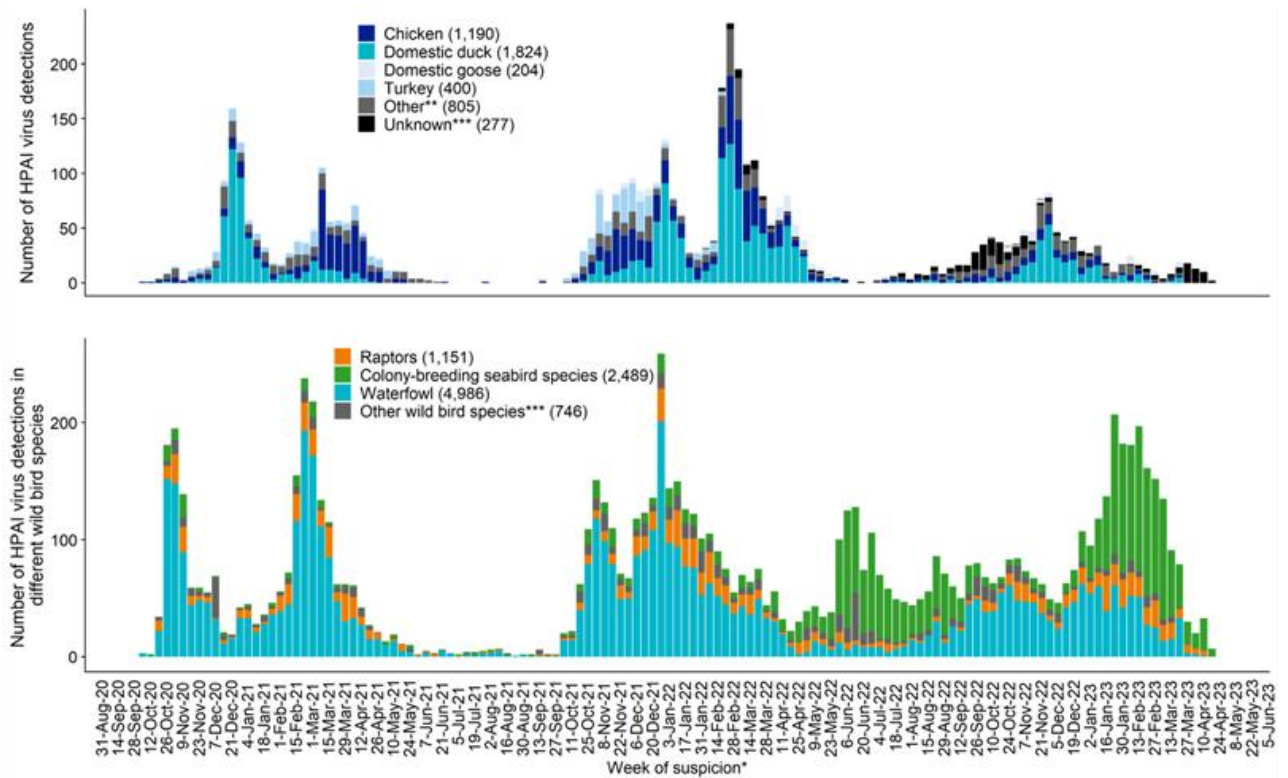
**Figure 1:** Distribution of the number of HPAI virus detections in domestic and wild birds reported in Europe in the epidemiological years 2016–2017, 2017–2018, 2018–2019, 2019–2020, 2020–2021, 2021–2022 and 2022–2023 by month of suspicion, from 1 October 2016 to 28 April 2023 (17,626)

<sup>5</sup> In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Protocol on IE/Ni, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).



Disclaimer: The designations employed and the presentation of material on this map do not imply the expression of any opinion whatsoever on the part of the European Food Safety Authority concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. \* 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 to 31 December 2020. From 1 January 2021 onwards, the data source was the World Animal Health Information System (WOAH-WAHIS) for United Kingdom (excluding Northern Ireland), and ADNS/ADIS for United Kingdom (Northern Ireland)<sup>5</sup>. Source: EFSA, ADIS and WOHIS (data extraction carried out on 28 April 2023).

**Figure 2:** Geographical distribution, based on available geocoordinates, of HPAI virus detection in wild birds (610) (upper panel) and in poultry and captive birds (106) (lower panel) reported by virus subtype in Europe from 2 March to 28 April 2023



United Kingdom data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was the World Animal Health Information System (WOAH-WAHIS) for United Kingdom (excluding Northern Ireland), and ADNS/ADIS for the United Kingdom (Northern Ireland)<sup>5</sup>.

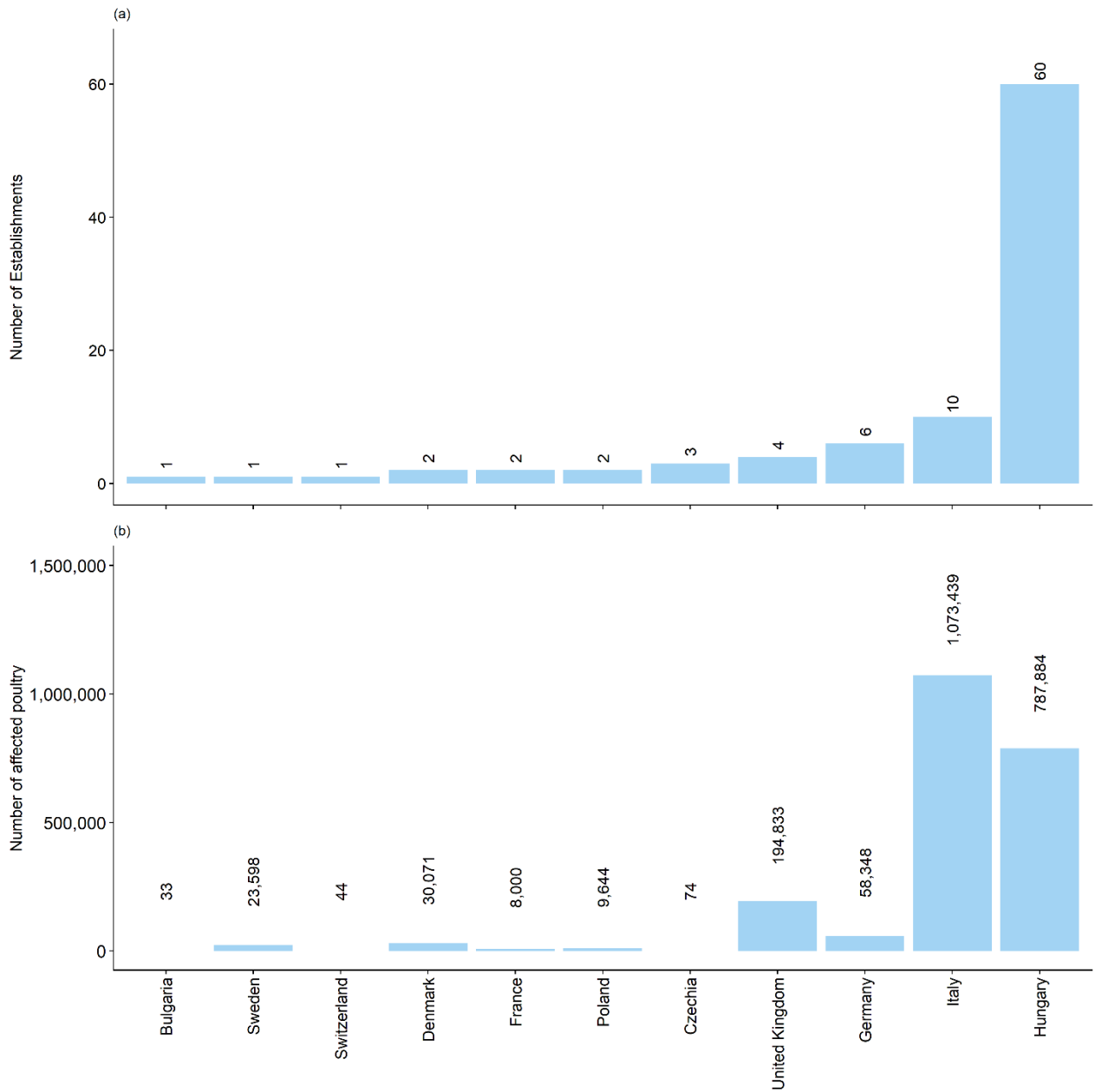
Source: EFSA, ADIS and WOAH (data extraction carried out on 28 April 2023).

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

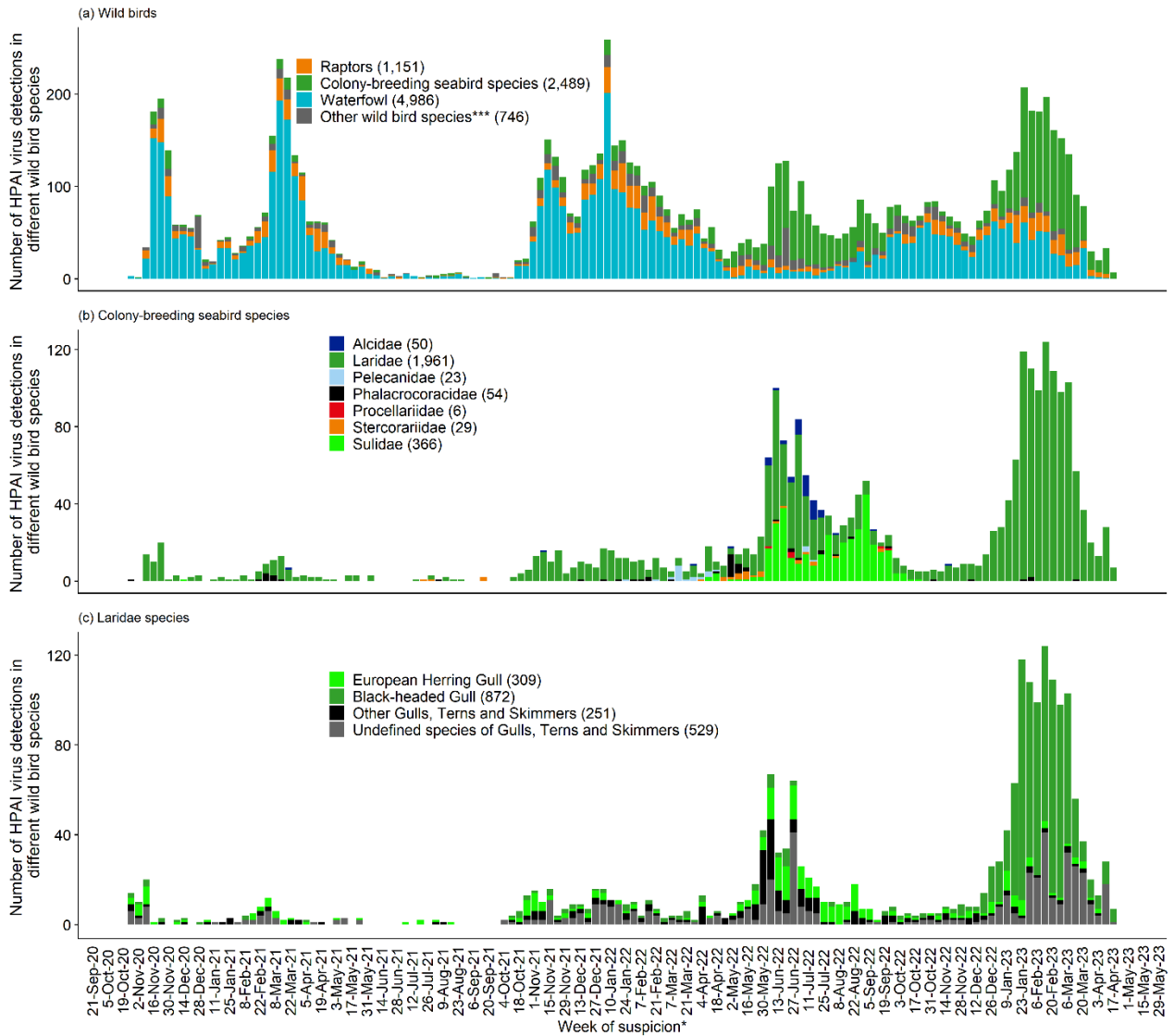
\*\* 'Other' groups all other affected countries that are not indicated in the legend

\*\*\* The information on poultry species affected after 3 April 2023 was collected too close to the publication of this report to be analysed and reported here; therefore, it will be fully described in the next report.

**Figure 3:** Distribution of total number of HPAI virus detections reported in Europe by week of suspicion (dates indicate the first day of the week) and affected poultry categories (4,700) (upper panel), affected wild bird categories (9,372) (lower panel), from October 2020 to 28 April 2023



**Figure 4:** (a) Number of HPAI-affected establishments and (b) number of poultry in the HPAI-affected establishments in Europe between 2 March and 28 April 2023 (92)



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

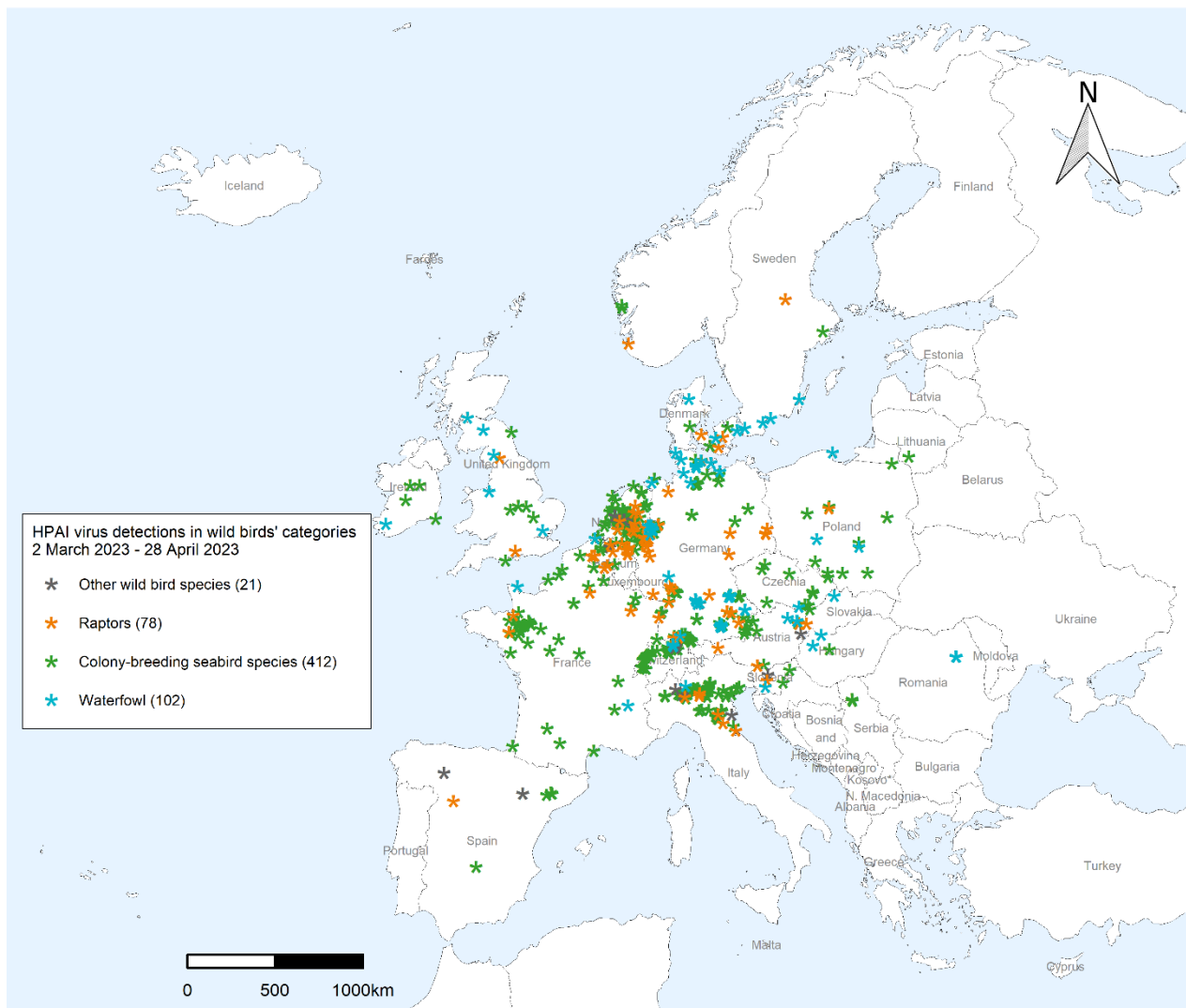
\*\*'Other wild species' category contains unknown bird species, or categories different from those displayed. The complete list of species by each wild bird category is reported in [Table A.8 in Annex A](#).

United Kingdom data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was the World Animal Health Information System (WOAH-WAHIS) for United Kingdom (excluding Northern Ireland), and ADNS/ADIS for the United Kingdom (Northern Ireland)<sup>5</sup>.

Source: ADNS, ADIS and WOAH (data extraction carried out on 28 April 2023), EFSA.

Note that the scale of the vertical axes is specific to each category and that the unit reported is the number of HPAI detections in different wild bird species and not the number of HPAI detections in wild birds (as more than one species can be involved in one single HPAI detection reported).

**Figure 5:** 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 (a) affected wild bird categories (9,372), (b) affected colony-breeding seabird families (2,489), (c) affected *Laridae* species (1,961), from October 2020 to 28 April 2023



Author: EFSA  
Data sources: ADIS, WOA  
Date updated: 28/04/2023

Disclaimer: The designations employed and the presentation of material on this map do not imply the expression of any opinion whatsoever on the part of the European Food Safety Authority concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. \* This designation is without prejudice to positions, or status, and is in line with United Nations Security Council Resolution 1244 and the International Court of Justice Opinion on the Kosovo Declaration of Independence. Source: EFSA, ADIS and WOA (data extraction carried out on 28 April 2023). Note that in one single detection more than one wild bird species might be involved and each wild bird categories detected as HPAI infected is presented in the map.

**Figure 6:** Geographical distribution, based on available geocoordinates, of HPAI detections in different categories of wild birds in Europe, by species category, from 2 March to 28 April 2023

### 2.1.2 HPAI virus detections in birds outside Europe

An overview of the HPAI virus detections in birds notified from other countries not reporting via ADIS but via the WOA from 2 March to 28 April 2023 is presented in Table 1 and Figure 7. Even considering that the relevant time period has halved compared to the previous report (EFSA et al., 2023), significantly fewer outbreaks in poultry and cases in wild birds were reported to WOA overall. Furthermore, the number of countries submitting data to WOA has decreased considerably. In Africa, as well as in Europe, the number of affected countries has remained stable, but in the Americas and Asia, only half as many countries notified HPAI A(H5) virus outbreaks in poultry or cases in wild birds to WOA.

In Africa, two HPAI A(H5N1) virus outbreaks were reported in large poultry farms in Nigeria and Senegal, respectively. Furthermore, in Senegal HPAI A(H5N1) was detected in royal terns (*Thalasseus maximus*), sandwich terns (*Thalasseus sandvicensis*), Caspian terns, grey-headed gulls (*Chroicocephalus cirrocephalus*), and cormorants (unspecified). In Gambia, only wild birds were affected, specifically grey-headed gull, royal tern and Caspian tern (*Hydroprogne caspia*). HPAI A(H5N1) virus was also reported in Russia in wild birds, namely mute swans (*Cygnus olor*) and great white pelicans (*Pelecanus onocrotalus*), as well as in a small poultry farm near to the Caspian Sea.

The HPAI A(H5N1) epidemic continued in Asia, with Japan, Korea and Nepal reporting poultry outbreaks to WOA, differently from the previous reporting period where several countries were affected. Bhutan and Taiwan, which were not affected in the previous reporting period, detected HPAI A(H5N1) virus on large poultry farms. Japan notified several A(H5N1) virus detections in different wild bird species mostly in large-billed crow (*Corvus macrorhynchos*) and very few in carrion crow (*Corvus corone*) hooded crane (*Grus monacha*), northern goshawk (*Accipiter gentilis*), and white-tailed eagle (*Haliaeetus albicilla*).

The actual situation in the Americas is continuously evolving with new HPAI virus detections in wild and domestic birds, as well as in mammal species, despite the lower number of countries reporting to the WOA. HPAI A(H5) virus detections in poultry, mammals and wild birds are also reported to the public via different means, e.g. this is the case of more poultry outbreaks and wild bird cases than those displayed in Table 1 reported by Argentina on 5 May 2023 (SENASA, 2023; Rosario3, online). However, in the tables and figures of the current report only the data extracted from WOA on 28 April 2023 are presented; information available from other sources has not been systematically retrieved and is only described in the text.

As in the last report, Canada and the United States of America detected HPAI A(H5N1) virus in small to very large poultry establishments, but in contrast to the last report only in a small number of wild birds as e.g., glaucous-winged gull (*Larus glaucescens*) and California condor (*Gymnogyps californianus*). In Central America only Panama reported one HPAI A(H5N1) virus detection in brown pelican (*Pelecanus occidentalis*). Along the Pacific coast and west of the Andes Mountains Bolivia, Chile and Colombia detected HPAI (H5N1) virus primarily in large poultry establishments. In contrast to the previous reporting period only one mortality event in brown pelican was notified by Colombia to WOA. East of the Andes Mountains, Uruguay reported outbreaks caused by HPAI A(H5Nx) virus in four backyard farms and one zoo. In the same region HPAI A(H5Nx) virus was also detected in black-necked swan (*Cygnus melancoryphus*). In Argentina, the epidemic continued with a large number of HPAI A(H5) virus outbreaks on farms of all sizes and detections in black-necked swan at two southern locations at 36 and 45 degrees South latitude. The list of wild bird species that have been reported to WOA-WAHIS as HPAI virus infected from 2 March to 28 April 2023 is presented in [Table A.6 in Annex A](#).

Additional information about HPAI virus detections in wild birds, not reported in WOA-WAHIS, was retrieved from different media sources and is reported below.

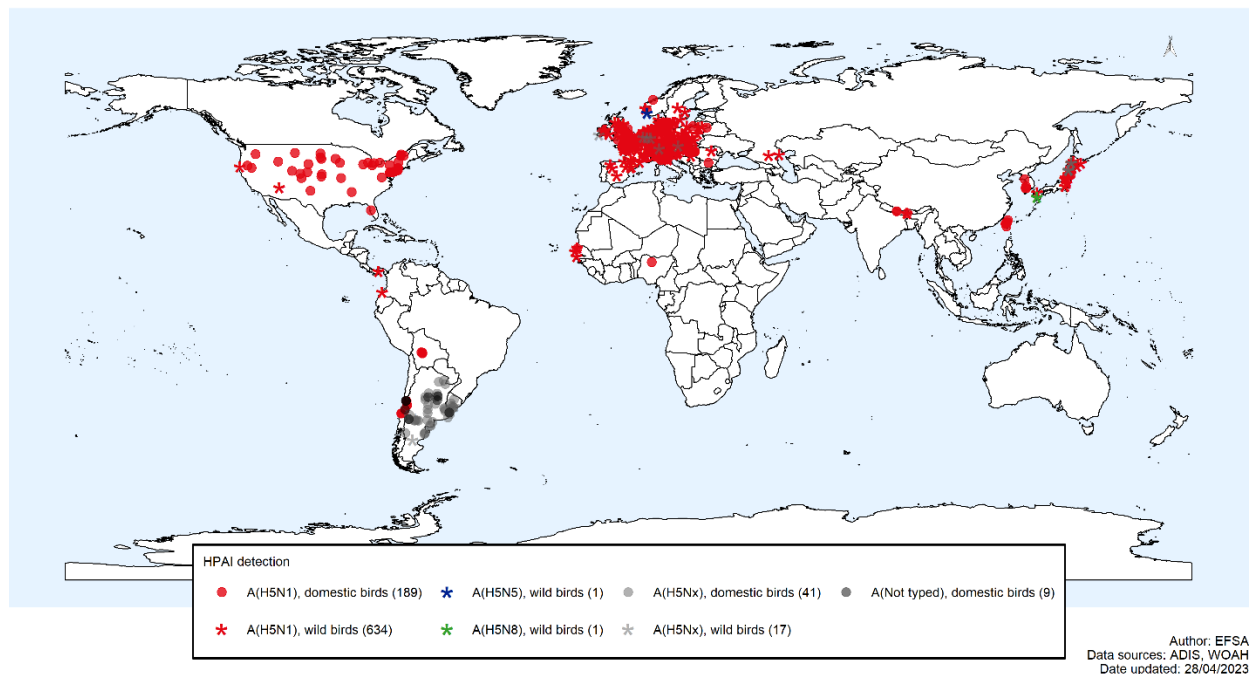
The Servicio Agrícola y Ganadero (SAG) of the Ministry of Agriculture in Chile confirmed HPAI virus in black-necked swans (*Cygnus melancoryphus*) near the town Porvenir, on the island of Tierra del Fuego at southern tip of South America (Patagonia, online). Accordingly, HPAI virus spread south to a latitude of 53 degrees South and actually, is separated from Antarctica only by the Southern Ocean. Furthermore, the Servicio Nacional de Pesca y Acuicultura (Sernapesca) of the Ministry of Economy, Development and Tourism in Chile reported that four more Humboldt penguins (*Spheniscus humboldti*) were found dead (Acuicultura, 2023). This is a worrying situation as Humboldt penguins are very local and with low density in Chile.

The Western Cape Veterinary Services of South Africa confirmed the reoccurrence of HPAI also in the current reporting period. Two large poultry farms were affected in the Western Cape province (News, online).

**Table 1:** Number of HPAI virus detections in non-European countries, by virus subtype and country, from 2 March to 28 April 2023

Region	Country	Domestic birds			Wild birds			Total
		A(H5N1)	A(H5Nx)	A(Not typed)	A(H5N1)	A(H5N8)	A(H5Nx)	
Africa (5)	Gambia	-			1			1
	Nigeria	1						1
	Senegal	1			2			3
Americas (117)	Argentina		36	5			2	43
	Bolivia	5						5
	Canada	9						9
	Chile	7		4				11
	Colombia				1			1
	Panama				1			1
	United States of America	37			2			39
	Uruguay		5				2	7
Asia (52)	Bhutan	1			1			2
	Taiwan	8						8
	Japan	7			21	1	7	36
	Korea	4						4
	Nepal	2						2
Europe (3)	Russia	1			2			3
<b>Total</b>		<b>83</b>	<b>41</b>	<b>9</b>	<b>31</b>	<b>1</b>	<b>11</b>	<b>176</b>

‘-’: means that no HPAI outbreaks or detections were notified to WOAAH.  
 Source: WOAAH-WAHIS (data extraction carried out on 28 April 2023).



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**Figure 7:** Geographical distribution, based on available geocoordinates, of HPAI virus detections reported in domestic birds (239) and wild birds (653) by virus type, from 2 March to 28 April 2023



### 2.1.3 Genetic characteristics of HPAI viruses of the A(H5N1) subtype circulating in Europe in avian species

The description of the nomenclature of the HPAI A(H5) viruses used in this section is reported in Appendix B.

#### *Genetic diversity of A(H5N1) viruses in avian species*

Since October 2022, 20 distinct genotypes have been identified among the characterised viruses (>1000) from 23 European countries. Four of them have been circulating since the 2021-2022 epidemiological year, while the remaining 16 genotypes have newly emerged very likely from reassortment events with avian influenza viruses circulating in Eurasian wild bird populations. Between October 2022 and January 2023, the majority of the characterised viruses belonged to the AB genotype (H5N1-A/duck/Saratov/29-02/2021-like). However, starting from December 2022, a rapid increase in the number of detections of the BB genotype (H5N1-A/Herring\_gull/France/22P015977/2022-like) was observed. Since February 2023, this BB genotype has become the most frequently identified variant. While in domestic birds genotype AB was associated with most of the reported outbreaks, in wild birds an extensive circulation of both the AB and BB genotypes was observed.

Genotype BB emerged in May 2022 through reassortment events with the gull-adapted H13 subtype. In the summer of 2022, it was extensively circulating mainly in sea birds in Northern Europe (France, The Netherlands and Belgium), and the analysed sequences confirmed that the European herring gull represented the most affected species. However, in the 2022-2023 epidemiological year, a rapid northward (UK, Ireland) and southward (Spain, Switzerland, Austria, Italy) expansion of this genotype was observed, and since spring 2023, it has also started to spread eastward (Poland and Czechia), with the black-headed gull representing the most affected species.

#### *Mutations identified in A(H5N1) viruses from avian species*

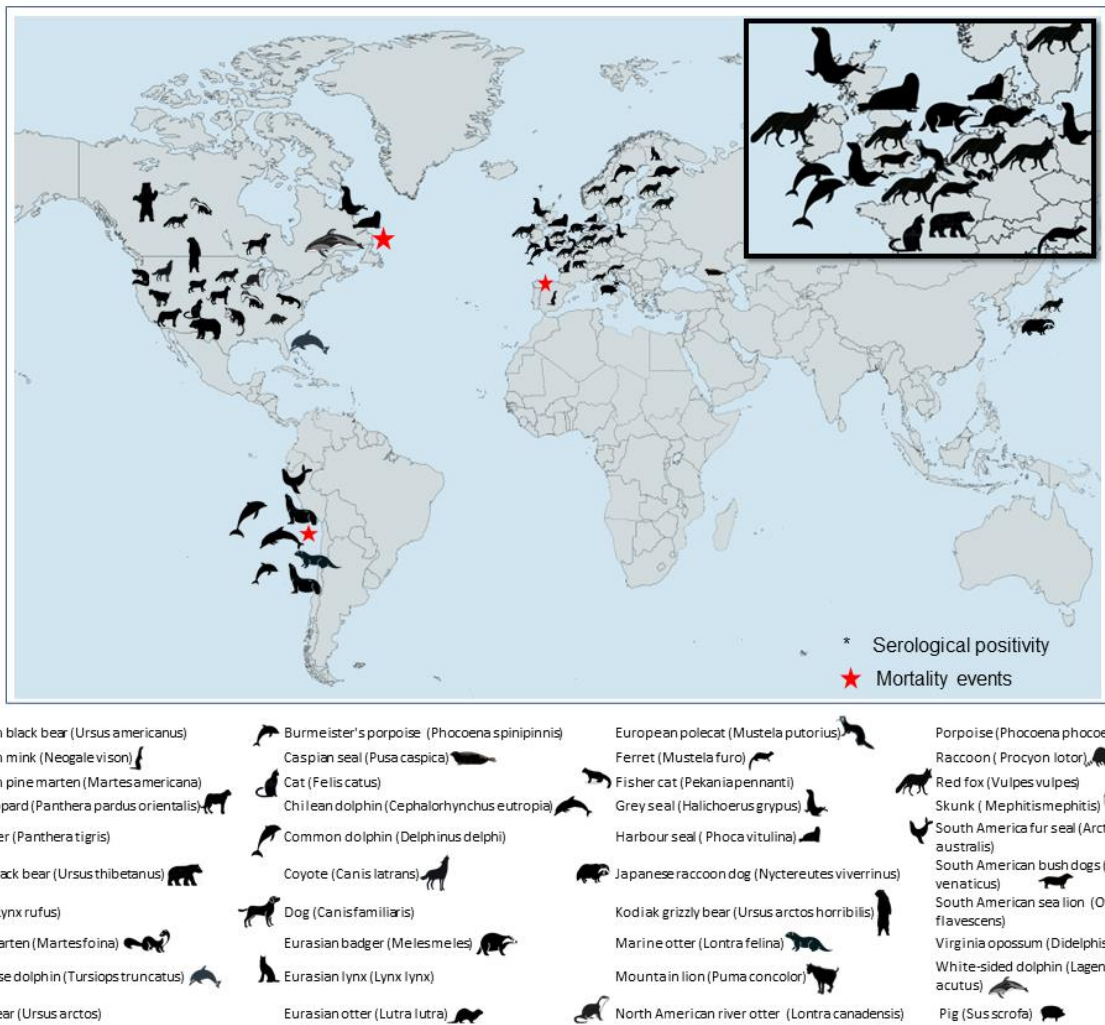
Molecular analyses of the A(H5N1) viruses circulating in birds in Europe during the 2022-2023 epidemiological year indicate that they continue to be well-adapted to avian species, as they retain a preferential binding for avian-like receptors. However, several mutations, previously described in literature (Suttie et al., 2019), were identified as being associated with i) enhanced polymerase activity and replication in mammals or mammalian cells, ii) increased virulence, iii) increased/conferred resistance toward antiviral drugs, iv) increased in vitro binding to human-type receptors alpha2,6-SA, and v) decreased antiviral response in ferrets, with a frequency varying for the distinct mutations. The real effect of these mutations on the biological characteristics of the viruses is still unknown and further studies are needed to improve existing knowledge. Among the identified mutations, molecular markers associated with increased replication and/or virulence in mammals were rarely detected in birds, as observed in the previous epidemiological years. Specifically, since October 2022, mutations E627K, PB2-D701N and PB2-T271A have been observed in four viruses collected from wild (N=1 PB2-627K) and domestic (N=1 E627K, N=1 PB2-D701N and N=1 PB2-T271A) birds in different European countries. Among the mutations in the HA protein which have proved to increase in vitro binding to human-type receptor, some of them (i.e. S137A, S158N, T160A) have been identified in the majority of the A(H5N1) viruses circulating in Europe since October 2022, while others (i.e. T192I, S159N, Q196R, V214I) have only been sporadically observed. The impact of these HA mutations on the biological characteristics of the circulating viruses is still unknown, however, none of them have been demonstrated to cause shift from avian-like to human-like receptor binding preference. Mutations associated with antiviral resistance were identified only occasionally in the circulating viruses. Moreover, all the A(H5N1) viruses belonging to the genotypes BB (H5N1 A/gull/France/22P015977/2022-like) and C (H5N1-A/Eurasian\_Wigeon/Netherlands/1/2020-like) contain the mutation NP-Y52N/H, which allows the evasion of human butyrophilin subfamily 3 member A3 (BTN3A3). BTN3A3 is constitutively expressed in human airways and is a potent inhibitor of avian but not human influenza A viruses (Pinto et al., 2022).

## 2.2 HPAI detections in non-human mammals

HPAI A(H5N1) virus infections during this reporting period were reported in wild mammals in i) Asia: red fox in Japan for the first time; ii) Europe: red fox in Belgium, Germany (first report), France and Italy (first report), beech marten in the Netherlands (first report), common dolphin (first report), harbour porpoise and South American bush dogs (first report) in the United Kingdom, Asiatic black bear in France (first report); iii) North America: red fox, mountain lion, striped skunk, American pine marten (first report) in USA; iv) South America: South American sea lion, marine otter (first report), Chilean dolphin (first report), Burmeister's porpoise in Chile (first report) (Table 2). HPAI A(H5N1) virus infections also were reported in domestic mammals: two cats in the USA and a dog in Canada (first report) (Table 2).

It is worth to be noted how the number of infected mammal species is increasing, in particular marine mammals and mustelids.

The geographical distribution of HPAI A(H5) viruses, clade 2.3.4.4b, that have been reported since 2016 are presented in Figure 8. The mammal species involved are mainly those that hunt wild birds, feed on dead wild birds, or both. The species in which HPAI A(H5N1) virus was reported most frequently is the red fox, which lives all across Europe, north Africa, most of Asia apart from the extreme southeast, and North America except southwest USA and Mexico (GBIF, online; IUCN, online). The frequent detection of HPAI A(H5N1) virus in red foxes is likely a consequence of its wide distribution, which largely overlaps the geographical spread of the HPAI A(H5N1) outbreaks, and its diet, which partly includes both hunted and scavenged wild birds.



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**Figure 8:** Geographical distribution of detections of HPAI in mammals since 2016 (based on Table 2, in the square on top right in the map a zoom on northern Europe situation)

**Table 2:** Avian influenza A(H5Nx) virus detections in mammal species other than humans related to circulating viruses worldwide, 2016–2022

Virus	Animal (order, family, species)			Country	Epidemic season	Reference	
A(H5N8) clade 2.3.4.4b	Artiodactyla	Suidae	Domestic pigs ( <i>Sus scrofa</i> ), serological detection	France	December 2016	(Herve et al., 2021)	
			Wild boar, serological detection	Germany	2017	(Schülein et al., 2021)	
	Carnivora	Phocidae	Grey seals ( <i>Halichoerus grypus</i> )	Poland, United Kingdom, Sweden	November 2016-2020-2021	(Shin et al., 2019; Floyd et al., 2021; SVA, online-c); personal communication by Siamak Zohari, SVA)	
			Harbour seals ( <i>Phoca vitulina</i> )	Germany, United Kingdom; Denmark	December 2020	(Floyd et al., 2021; Ärzteblatt, online; Avian Flu Diary, online-b; Outbreak News, online; SSI, online)	
		Canidae	Red foxes ( <i>Vulpes vulpes</i> )	United Kingdom	December 2020	(Floyd et al., 2021)	
A(H5N1) or A(H5Nx) clade 2.3.4.4b	Carnivora	Canidae	Red foxes ( <i>Vulpes vulpes</i> )	Sweden; Netherlands; Finland; France, Estonia; Ireland; Belgium; Norway; Japan; USA; Canada; Italy; Germany; United Kingdom	2020-2021 2021-2022 2022-2023	(SVA, online-c; USDA, online; WOH, online-a, c); personal communication by Siamak Zohari, SVA; Irish National Reference Laboratory for Avian Influenza, personal communication)	
			Common raccoon dog ( <i>Nyctereutes procyonoides</i> )	Japan	2021-2022	(WOAH, online-c)	
			Dog ( <i>Canis familiaris</i> )	Canada	2022-2023	(WOAH, online-b)	
			Japanese raccoon dog ( <i>Nyctereutes viverrinus</i> )	Japan	2021-2022	(FAO, online)	
			South American bush dog ( <i>Speothos venaticus venaticus</i> )	United Kingdom	2022-2023	((WOAH, online-b)WOAH)	
			Coyote ( <i>Canis latrans</i> )	USA	2021-2022	(WOAH, online-c)	
			Mustelidae	Eurasian otter ( <i>Lutra lutra</i> )	Netherlands; Finland	2021-2022	(WUR, online)
				European badger ( <i>Meles meles</i> )	Netherlands	2021-2022	(WUR, online)
				European polecat ( <i>Mustela putorius</i> )	Netherlands; Belgium	2021-2022 2022-2023	(WUR, online)
				Ferret ( <i>Mustela furo</i> )	Slovenia, Belgium	2021-2022 2022-2023	(WOAH, online-c)
				American mink ( <i>Neovison vison</i> )	Canada, Spain	2021-2022 2022-2023	(WOAH, online-a; Xunta de Galicia, online)
				Beech marten ( <i>Martes foina</i> )	Netherlands	2022-2023	(GISAID, online)GISAID
				Marine otter ( <i>Lontra felina</i> )	Chile	2022-2023	(ProMed, online; WOH, online-b)
			North American River otter ( <i>Lontra canadensis</i> )	USA	2022-2023	(WOAH, online-b)	

Virus	Animal (order, family, species)		Country	Epidemic season	Reference
		Fisher ( <i>Pekania pennanti</i> )	USA	2021-2022	(WOAH, online-c)
	Felidae	Lynx ( <i>Lynx lynx</i> )	Finland	2021-2022	(FFA, online)
		Bobcat ( <i>Lynx rufus</i> )	USA	2021-2022 2022-2023	(WOAH, online-c)
		Amur leopard ( <i>Panthera pardus</i> )	USA	2021-2022 2022-2023	(USDA, online)
		Amur tiger ( <i>Panthera tigris</i> ) <sup>(b)</sup>	USA	2022-2023	(WOAH, online-c)
		Mountain lion ( <i>Puma concolor</i> )	USA	2022-2023	(WOAH, online-c)
		Cat ( <i>Felis catus</i> )	France, USA	2022-2023	(WOAH, online-c)
	Procyonidae	Raccoon ( <i>Procyon lotor</i> )	USA; Canada	2021-2022 2022-2023	(WOAH, online-c)
	Mephitidae	Striped skunk ( <i>Mephitis mephitis</i> )	Canada; USA	2021-2022 2022-2023	(CTV News, online; USDA, online; WOA, online-c, a)
	Otariidae	South American sea lion ( <i>Otaria flavescens</i> )	Peru; Chile	2022-2023	(WOAH, online-b)
		South American fur seal ( <i>Arctocephalus australis</i> )	Peru	2022-2023	(FAO, online)
	Phocidae	Grey seals ( <i>Halichoerus grypus</i> )	USA; Canada; UK, Poland	2016-2017 2021-2022 2022-2023	(AMMI, 2022; WOA, online-a; Shin et al., 2019)
		Harbour seals ( <i>Phoca vitulina</i> )	USA; Canada; UK; Germany, Denmark	2020-2021 2021-2022 2022-2023	(Agriland, online; WOA, online-c)
		Caspian seal ( <i>Pusa caspica</i> )	Russian Federation	2022-2023	(FAO, online)
	Ursidae	American black bear ( <i>Ursus americanus</i> )	Canada USA	2021-2022 2022-2023	(Healthy Wildlife, online; KTOO, online; WOA, online-c)
		Brown bear ( <i>Ursus arctos</i> )	USA	2022-2023	(Kiniradio, online; USDA, online)
		Kodiak grizzly bear ( <i>Ursus arctos horribilis</i> )	USA	2021-2022	(FAO, online)
		Asiatic black bear ( <i>Ursus thibetanus</i> )	France	2022-2023	(GISAID, online; WOA, online-b)
Artiodactyla	Suidae	Domestic pigs ( <i>Sus scrofa</i> ), serological detection <sup>a</sup>	Italy	2021-2022	(Rosone et al., 2023)
Didelphimorphia	Didelphidae	Virginia opossum ( <i>Didelphis virginiana</i> )	USA	2021-2022 2022-2023	(USDA, online; WOA, online-c)
Cetacea	Phocoenidae	Harbour porpoise ( <i>Phocoena phocoena</i> )	Sweden; UK	2021-2022 2022-2023	(SVA, online-b)

Virus	Animal (order, family, species)		Country	Epidemic season	Reference
		Burmeister's porpoise ( <i>Phocoena spinipinnis</i> )	Chile	2022-2023	(FAO, online)
	Delphinidae	Bottlenose dolphin ( <i>Tursiops truncatus</i> )	USA; Peru	2021-2022 2022-2023	(UFHealth, online; WOA, online-c)
		White-sided dolphin ( <i>Lagenorhynchus acutus</i> )	Canada	2022-2023	(Avian Flu Diary, online-a)
		Chilean dolphin ( <i>Cephalorhynchus eutropia</i> )	Chile	2022-2023	(Acuicultura, 2023; FAO, online)
		Common dolphin ( <i>Delphinus delphis</i> )	Peru; UK	2022-2023	(Leguia et al., 2023; WOA, online-b)

(a) Serological detection in a HPAI outbreak in a backyard poultry farm  
 (b) Captive bird into a zoo

### 2.2.1 Genetic characteristics of HPAI viruses of the A(H5N1) subtype circulating in Europe in non-human mammals

The description of the nomenclature of the HPAI A(H5) viruses used in this section is reported in Appendix B.

#### *Genetic diversity of A(H5N1) viruses in non-human mammals*

Since October 2020, the complete genome sequences of HPAI A(H5) viruses of clade 2.3.4.4b collected from 13 distinct mammalian species (badger, Asiatic black bear, bush dog, cat, coati, ferret, fox, lynx, mink, otter, polecat, porpoise and seal) in 15 European countries have been generated. The characterised viruses belong to 9 different A(H5N1) and A(H5N8) genotypes previously identified in birds. During the 2022–2023 epidemiological year, mammalian infections have been caused by the three most widespread genotypes in birds, namely BB (H5N1-A/gull/France/22P015977/2022-like), AB (H5N1-A/duck/Saratov/29-02/2021-like) and CH (H5N1-A/Eurasian\_Wigeon/Netherlands/3/2022-like), with most of the infections caused by the BB and AB genotypes.

#### *Mutations identified in A(H5N1) viruses from non-human mammals*

About half of the characterised viruses contain at least one of the adaptive markers associated with an increased virulence and replication in mammals in the PB2 protein (E627K, D701N or T271A) (Suttie et al., 2019). These mutations have rarely been identified in the HPAI A(H5) viruses of clade 2.3.4.4b collected in birds in Europe since October 2020. This observation suggests that these mutations with potential public health implications have likely emerged upon transmission to mammals.

## 2.3 Avian influenza virus infections in humans

### 2.3.1 Most recent human infections with avian influenza A(H3N8), A(H5N1), A(H5N6) and A(H9N2) viruses

Since 13 March 2022 and as of 10 May 2023, five new human cases with avian influenza infection were reported from Chile (one case A(H5N1)) and China (one A(H3N8); three A(H9N2)) (Table 3):

For the first time Chile reported a human infection with A(H5N1) (clade 2.3.4.4b), marking the second human infection with A(H5N1) in South America after Ecuador reported a human case in December 2022 (ECDC, 2023c, b, a). The virus was detected in a 53-year-old man admitted to hospital due to severe respiratory symptoms including pneumonia who continues to be hospitalized and recovering. The source of infection remains unclear, the investigation identified infected wild birds and sea lions at the coastal area close to where the man lived (ECDC, 2023d).

China reported one new human infection with A(H3N8) in a 56-year-old woman, who was hospitalised following exposure to potentially infected backyard poultry and wild birds. This is the third human infection with A(H3N8) reported from China within one year (ECDC, 2023a).

China also reported three new cases of A(H9N2) infection, two with onset of symptoms in 2023 and one in 2022 (WHO, 2023b). All infections were in children with mild clinical symptoms.

**Table 3:** Most recent human cases due to avian influenza viruses, by virus subtype

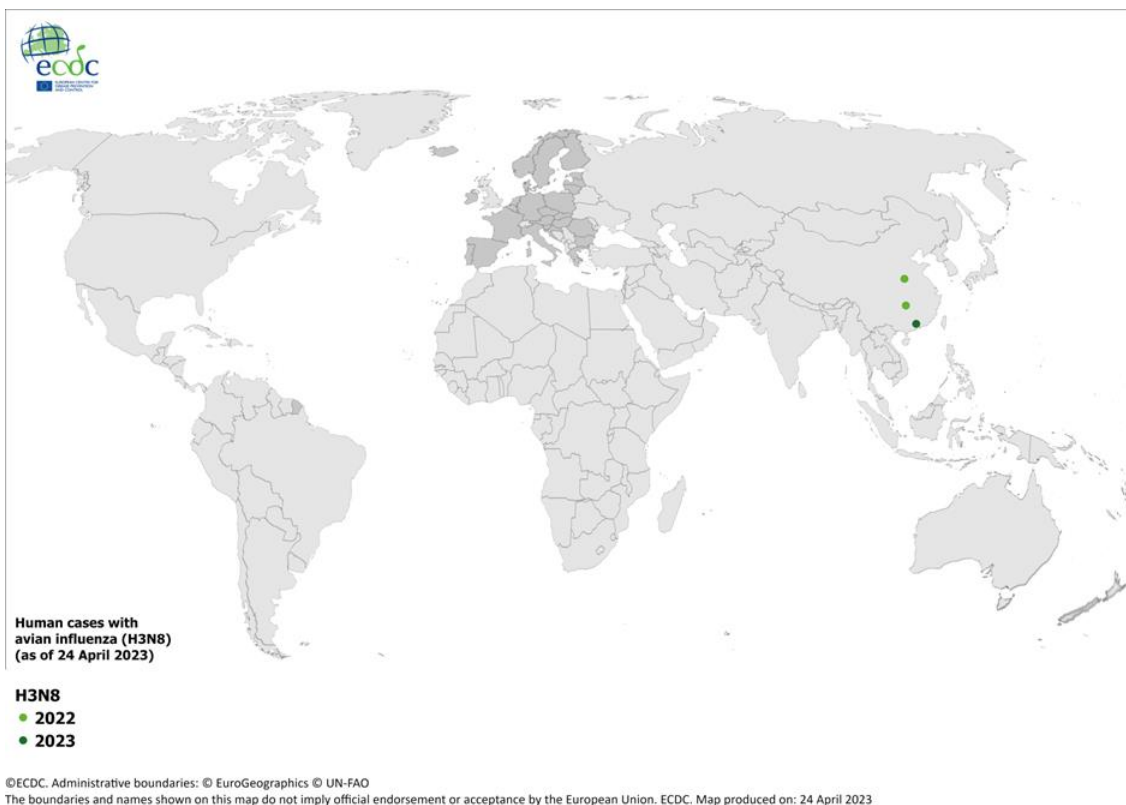
Subtype	New cases reported	Total cases (deaths)	Countries reporting human cases
A(H3N8)	ONE new case from China	3 (0) Since 2022	China
A(H5N1)	ONE new case in Chile - first report from Chile	874 (457) Since 2004	23 countries reported cases, EU/EEA: Spain with virus fragment detections in two poultry workers considered contamination and no productive infections
A(H5N6)	No new case	84 (33) Since 2014	China (83), Laos (1)
A(H9N2)	THREE new cases in China	123 (2) Since 998	No EU/EEA country; China (107), Egypt (4), Bangladesh (3), Cambodia (2), Oman (1), Pakistan (1), India (1), Senegal (1)

Source: ECDC line list

### 2.3.2 Human A(H3N8) cases, summary

As of 10 May 2023, there have been three human infections with A(H3N8), all reported from China within 13 months. Two infections were reported in children (4 and 5 years old) and one adult (56-year-old female) having exposure to either infected backyard poultry or live poultry markets. The infections have been mild in one and more severe or critical in the other two (Bao et al., 2022; Sit et al., 2022). Human-to-human transmission has not been reported and cases were considered sporadic spill-over events.





**Figure 9:** Geographic distribution of human A(H3N8) cases, 2022–2023 (source: ECDC line list)

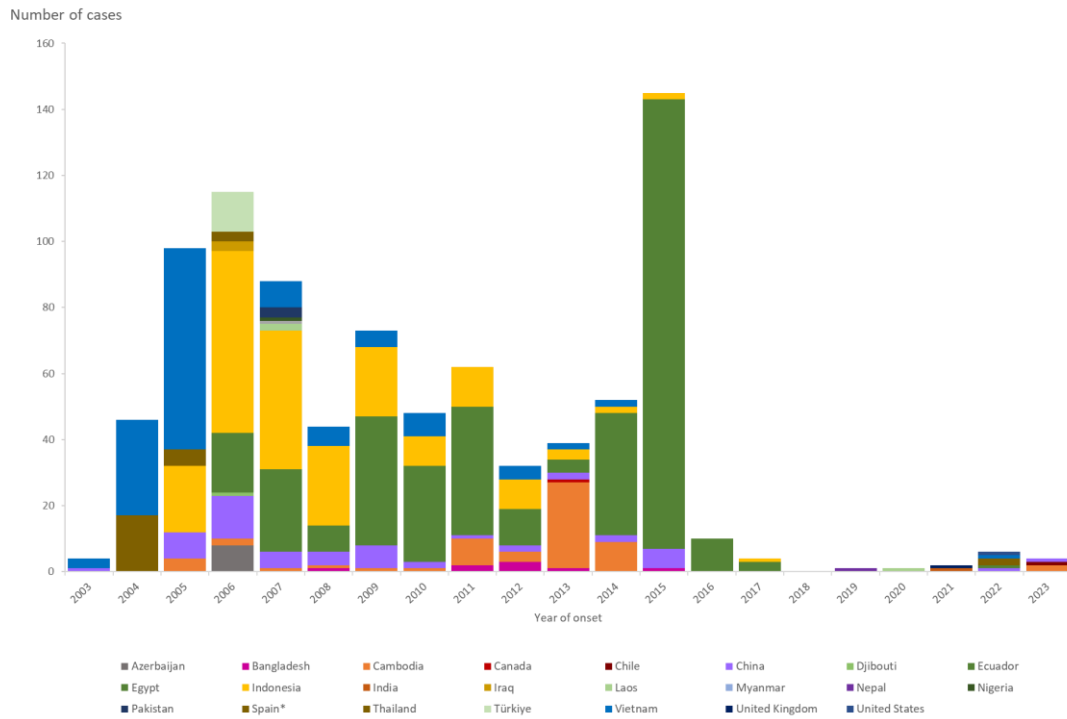
### 2.3.3 Human A(H5N1) cases, summary

As of 10 May 2023, there have been 874 human cases including 457 deaths with A(H5N1) infection notified to WHO from 23 countries (Azerbaijan, Bangladesh, Cambodia, Canada, Chile, China, Djibouti, Ecuador, Egypt, Indonesia, India, Iraq, Laos, Myanmar, Nepal, Nigeria, Pakistan, Spain<sup>6</sup>, Thailand, Türkiye, Vietnam, United Kingdom and United States of America; Figure 10).

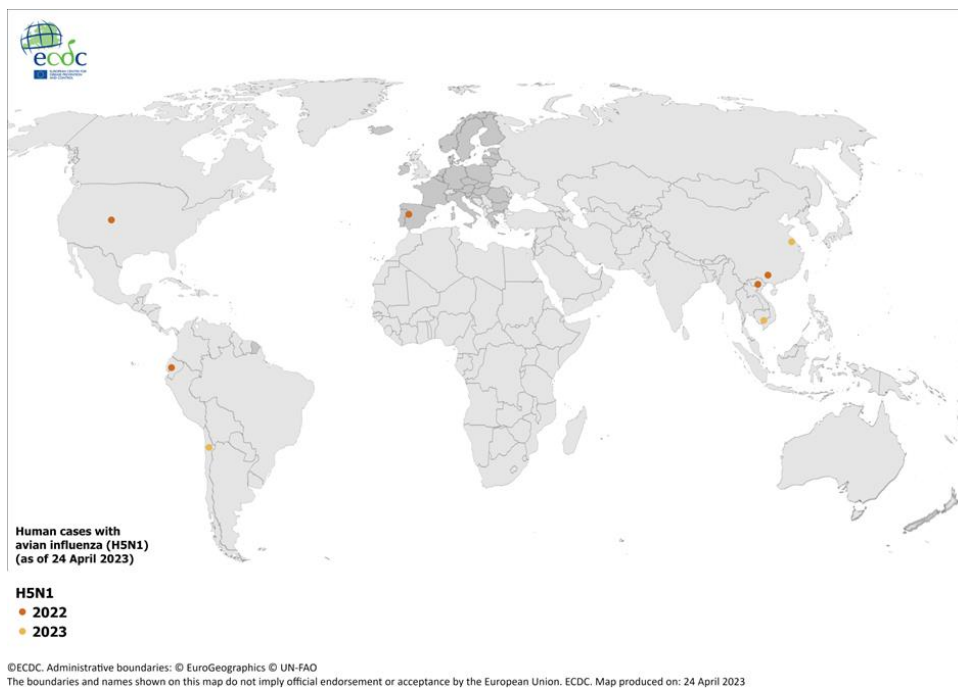
In 2022, five countries reported six human cases (Figures 10 and 11): China (1), Ecuador (1), Spain<sup>6</sup> (2), United States of America (1), Vietnam (1). In 2023, three countries reported four cases: Cambodia (2), Chile (1), China (1).

In 2022, Spain reported the detection of viral A(H5N1) RNA of clade 2.3.4.4b in two asymptomatic poultry farm workers involved in culling activities but epidemiological, laboratory and serological analyses confirmed a mucosal contamination (no sequencing possible, no antibodies against H5 and no virus isolation possible) but no productive infections.

<sup>6</sup> A(H5N1) detections in two Spanish poultry workers involved in culling activities are considered contaminations and not productive infections.



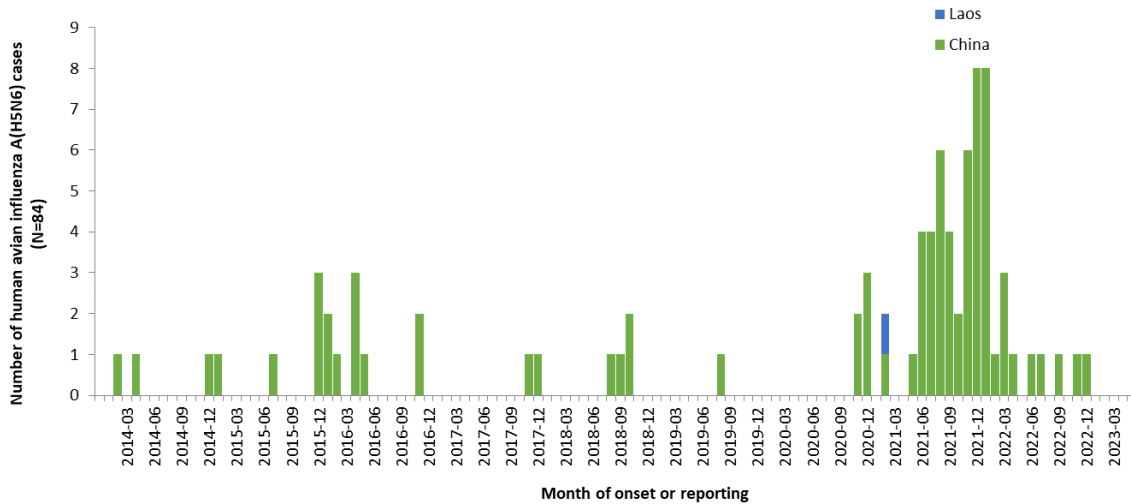
**Figure 10:** Distribution of confirmed human cases of HPAI A(H5N1) virus infection by year of onset and country, 2003–2023 (data as of 10 May 2023, n=874)



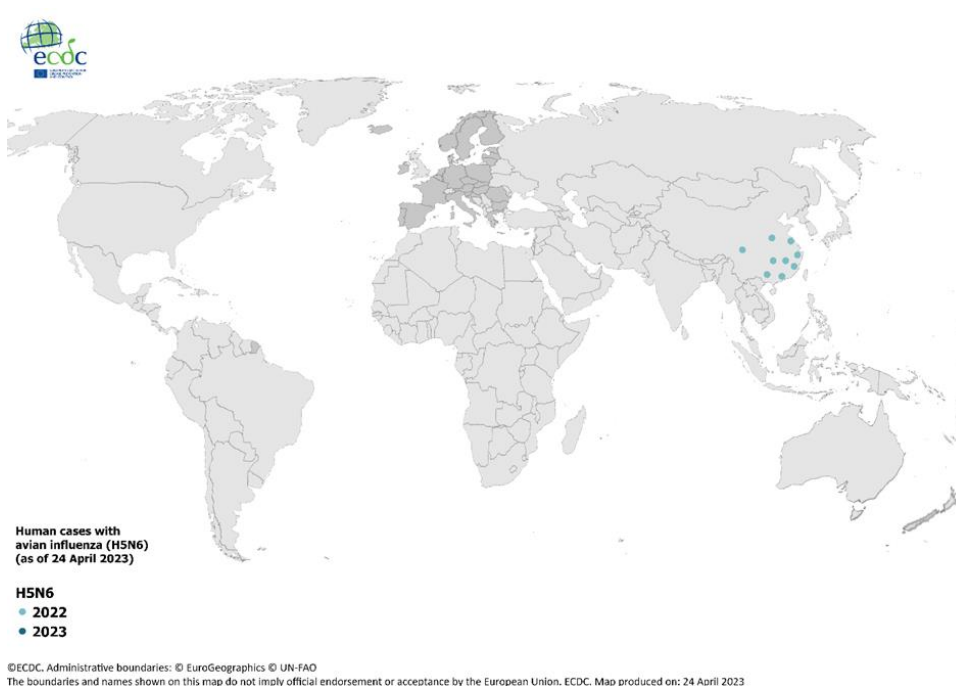
**Figure 11:** Geographic distribution of human A(H5N1), cases, 2022-2023 (source: ECDC line list)

### 2.3.4 Human A(H5N6) cases, summary

As of 10 May 2023 and since 2014, China (83) and Laos (1) reported a total of 84 human infections with A(H5N6), including 29 (35%) with fatal outcome according to notifications to WHO (Figure 12). Since 2021, the majority of A(H5N6) viruses identified in humans belong 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 available information it is not possible to make any further conclusions on causation (Chen et al., 2022; Cui et al., 2022; Gu et al., 2022; Zhu et al., 2022).



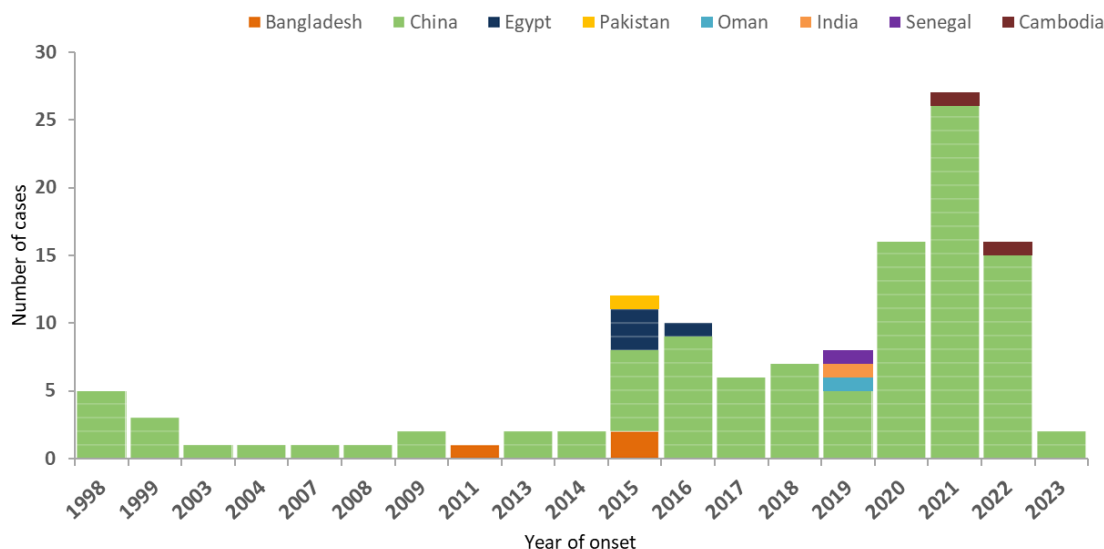
**Figure 12:** Distribution of confirmed human cases of A(H5N6) virus infection by month and year of onset and country, 2014–2023 (data as of 10 May 2023, n=84)



**Figure 13:** Geographic distribution of human A(H5N6) cases, 2022-2023 (data as of 10 May 2023, n= 84; source: ECDC line list).

### 2.3.5 Human A(H9N2) cases, summary

As of 10 May 2023 and since 1998, a total of 123 human infections with A(H9N2) have been reported from eight countries all outside the EU (Figure 14): Bangladesh (3), China (110), Cambodia (2), Egypt (4), Pakistan (1), Oman (1), India (1) and Senegal (1) (Figure 12). The majority of infections were identified in children up to 9 years of age (94; 76%) and women were more affected than men (72 vs. 49; 2 of unknown sex).



**Figure 14:** Distribution of confirmed human cases of avian influenza A(H9N2) virus infection by month and year of onset and country, 1998–2023 (as of 10 May 2023, n=123)

### 2.3.6 Genetic characteristics of HPAI viruses of the A(H5Nx) subtype from humans

Based on the data available from the GISAID EpiFlu database, since 2020 human infections have been caused by four different A(H5) clades of the A/goose/Guangdong/1/1996-lineage, namely 2.3.2.1c (Laos, 2020 and Cambodia, 2023), 2.3.2.1a (India, 2021), 2.3.4.4h (China, 2020–2021), and 2.3.4.4b (China, Europe, North and South America, 2020–2023).

Mutation Q226L was identified in two A(H5N6) viruses of clade 2.3.4.4b collected in China in 2021 (Zhu W Fau - Li et al.). This mutation is associated with the switch in the receptor specificity from avian-type to human-type receptor (Stevens et al., 2006; Chutinimitkul et al.; Russell et al., 2012). This mutation was previously detected in two A(H5N1) viruses of clade 1 collected from human infections in Cambodia in 2013 (Rith et al., 2014) and, based on the available sequence data, it is not present in the clade 2.3.4.4b A(H5Nx) viruses currently circulating in the avian population in Europe. Moreover, six clade 2.3.4.4b A(H5N6) viruses collected from human infections in China in 2021 possessed one of the adaptive markers in the PB2 protein (Q591K, E627K or D701N) associated with an increased virulence and replication in mammals (Zhu W Fau - Li et al., 2022).

### 2.3.7 Additional information and international risk assessments

A study of currently circulating A(H5N1) viruses in North America showed that these viruses are able to replicate efficiently in human respiratory tract cell types and that in ferret infection and transmission studies, animals got infected but showed only very mild symptoms mostly limited to upper respiratory tract and viruses did not transmit to other ferrets kept in a direct-contact setting (Pulit-Penalosa et al., 2022).

Another study with A(H5N1) viruses from North America belonging to different genotypes demonstrated that viruses are able to replicate in primary human airway epithelial cells (Darwyn Kobasa, 2023). These viruses derived from different wild animal species that died following infection. Moreover, one isolate carrying the PB2-E627K mutation efficiently transmitted by direct contact between ferrets, resulting in lethal outcomes.

The previously issued risk assessment using the Influenza Risk Assessment Tool (IRAT) of the United States Centers for Disease Control and Prevention (US CDC) placed the risk of clade 2.3.4.4b viruses in the lower moderate category (CDC, 2021). The risk of the A(H5N1) clade 2.3.4.4b viruses currently circulating in the United States bird and poultry populations, and which are closely related to European viruses, were assessed by the US CDC to be of low risk for human health in the general population and higher for people occupationally or recreationally exposed to birds (CDC, online-a, b). The WHO assessed the risk related to the recent (H5N1) human cases as low for the general public and low to moderate for occupationally exposed people (WHO, 2022, online). WHO previously assessed the risk for A(H5N6) as follows: 'the zoonotic threat remains elevated due to spread of the viruses in birds, based on evidence available so far, the overall pandemic risk is considered not significantly changed in comparison to previous years' (WHO, 2021d). The UK Health Security Agency (UKHSA) assesses the situation to be at level 3 (with limited mammalian transmission that excludes humans but with low confidence) of a scale between 0-6 (GovUK, online-a). A joint EFSA, ECDC, EURL publication from 2021 already described the threat to humans with the objective to raise awareness among clinicians in the EU around zoonotic avian influenza virus infection and consider testing (Adlhoch et al., 2021). Additional information is also available in the Joint ECDC/EFSA/EURL/EU-OSHA document on 'Testing and detection of zoonotic influenza virus infections in humans in the EU/EEA, and occupational safety and health measures for those exposed at work' (ECDC, 2022).

## 2.6 ECDC risk assessment

The risk assessment remains valid and unchanged:

Overall, the risk of infection with avian influenza viruses of the currently circulating clade 2.3.4.4b in Europe for the general public in EU/EEA countries is considered to be low. The risk to occupationally or otherwise exposed groups to avian influenza infected birds or mammals has been assessed as low to moderate.

The viral genotype does not predict the viral phenotype and therefore a high uncertainty is associated with any assessment of the risk for humans, particularly due to the high variability and diversification of the avian influenza viruses of clade 2.3.4.4b with many reassorted subtypes and genetic lineages co-circulating in Europe and globally as well as the sporadic occurrence of various mutations that could increase the transmission to and replication in humans. Reassortment events will likely continue globally leading to a more complex situation.

The risk assessment used the following information:

Viruses continue to spread and diversify globally. Viruses currently circulating in bird populations in Europe are avian-adapted viruses, e.g. they bind to avian-like receptors, transmit and replicate best in bird species.

Mutations associated with mammalian adaptation have been identified sporadically in few birds but emerged more frequently in mammalian hosts after infection. Mammal-to-human or human-to-human transmission has not been observed so far.

Avian influenza transmission from animals to humans is a rare event, but transmission to humans cannot be excluded when avian influenza viruses are present in birds and other animals and people are in direct contact without protection such as gloves. However, despite large number of human exposure events to clade 2.3.4.4b viruses in Europe over the last three years, no symptomatic infection has been identified and reported. In 2022

and 2023, eight human cases related to the circulating 2.3.4.4b viruses in birds have been reported from Chile, China, Ecuador, US, Spain (considered contaminations and no infections) and Vietnam (unknown clade). In 2023 and as of 10 May, only two human infections with A(H5N1) viruses of clade 2.3.4.4b were reported from China and Chile.

The majority of cases had unprotected exposure to infected sick and dead poultry mostly in backyard setting. One case in Chile has an unclear source of transmission with potential exposure to infected wild birds, dead sea lions or contaminated environment being identified close to his residence.

With the current high number of dead wild birds and mammals, ongoing outbreaks in poultry farms or small holdings such as backyard farms with low biosafety measures as well as a high environmental contamination with avian influenza viruses, sporadic human infections with avian influenza viruses can be expected for people in contact with infected sick or dead animals (birds or mammals) not wearing personal protection equipment and related individual severe disease cannot be excluded.

Based on the analyses of known molecular markers associated with resistance toward antiviral drugs in the available sequences, the majority of the circulating A(H5N1) viruses in Europe seem to remain susceptible to licensed antivirals for use in seasonal influenza as well as for pandemic use (neuraminidase inhibitors (oseltamivir, zanamivir), M2 blockers (amantadines) and cap-dependent endonuclease blocker (baloxavir marboxil). All antivirals are available as treatment options and pre- or post-exposure prophylaxis.

The proposed candidate vaccine viruses prepared for pandemic preparedness (to develop H5 vaccines for humans) are antigenically similar to the currently circulating H5 viruses in Europe but human vaccines are not available for use at the moment.

Monitoring of avian influenza viruses in birds and mammals including sharing of sequence data is crucial for updated risk assessment and implementation of measures in the animal-human interface.

Options for response and additional information are available on ECDC webpages: [Avian influenza \(europa.eu\)](https://ecdc.europa.eu/en/avian-influenza).

## 3 Conclusions

### Birds in Europe

- During the current compared to the previous reporting period, a decrease in poultry outbreaks was observed. The number of poultry outbreaks was also lower compared to the same reporting period of the previous year.
- Compared to spring 2022 (EFSA et al., 2023), when 86% of affected poultry establishments reported secondary outbreaks, less poultry outbreaks were attributed to secondary spread this year, which might be linked to the decrease in poultry density adopted in certain areas and poultry production system considered at high risk; this has been the case in West and Southwest France in the domestic duck and foie gras sector and in Northeast Italy in the turkey and laying hen sector.
- Atypical disease presentation, characterised by low mortality and the absence of typical signs of HPAI infection was observed in some of the A(H5N1) outbreaks caused by the BB genotype (H5N1-A/Herring\_gull/France/22P015977/2022-like) in meat turkeys and laying hens in Italy. This atypical disease presentation was further evaluated experimentally. Compared to virus isolates from the previous epidemic years (2017–2021), virus of the BB genotype required a higher infectious dose and the median time to onset of disease, clear clinical signs and mortality was also longer.

- As only a fraction of the wild birds that die of HPAI virus infections are found, and only a fraction of those birds are tested, the number of HPAI virus detections in Europe and worldwide is an underestimation of the real magnitude of the phenomenon in these bird populations.
- The previously observed detections of HPAI A(H5N1) virus in gull species continued with black-headed gulls being most heavily affected and mortality events occurring in Czechia, Germany, Poland, Sweden, Italy and the United Kingdom; this trend is concerning, as the European black-headed gull population has already been declining in recent years.
- If HPAI A(H5N1) virus is still present in black-headed gull colonies around the time of fledging, and follows the same epidemiological pattern as LPAI A(H13 and H16) viruses (Verhagen et al., 2014), a sharp increase in HPAI A(H5N1) virus prevalence, and associated morbidity and mortality, may be expected in first-year black-headed gulls in the second half of the breeding season, approximately in July-August when they start dispersing from their breeding colonies.
- The ongoing and Europe-wide HPAI A(H5N1) virus epidemic in black-headed gulls poses a risk to other seabird species, some of which share colony breeding sites with black-headed gulls, and to marine mammals. This also involves the risk of HPAI virus spreading within seabird colonies.
- Given the number of HPAI virus detection in peregrine falcon, which are an underestimate of the actual number of peregrine falcons that died from HPAI, and their relatively small population in Europe, specific investigation is warranted into the potential impact of mortality from HPAI A(H5N1) virus infection on the peregrine falcon population.
- Of concern is that 37% of wild birds in which HPAI virus detections were reported, were not identified at the species level. Lack of knowledge of the wild bird species involved in the HPAI virus detections severely limits the ability to understand the epidemiology of the virus in wild bird populations and to assess the risk associated with the introduction of HPAI viruses into poultry from wild birds.
- Since December 2022, available genetic data indicate a rapid increase and geographic expansion of the BB genotype (H5N1-A/Herring\_gull/France/22P015977/2022-like) in wild birds, mainly associated with infections in black-headed gulls. The spring migration of this species has caused a recent eastward geographic spread of this genotype, which, to date, has been identified in 11 European countries.
- The A(H5N1) viruses currently circulating in Europe retain a preferential binding for avian-like receptors; however, several mutations associated with increased zoonotic potential have been detected. Their effects on the biological characteristics of the viruses need to be further investigated.
- Very limited information is available on the distribution of LPAI viruses, e.g. A(H3N8) in Europe, as there is no requirement per legislation to diagnose and report avian influenza viruses other than A(H5/H7) viruses.
- The risk for incursion of HPAI virus into poultry farms in the coming months is difficult to predict. On the one hand, environmental virus contamination may be expected to decrease due to higher ambient temperatures and more hours of sunlight. On the other hand, the ongoing and Europe-wide HPAI A(H5N1) virus epidemic in black-headed gulls, many of which breed inland, may increase the risk, especially in July-August, when first-year black-headed gulls disperse from the breeding colonies.

### **Birds outside Europe**

- Compared to the previous reporting period (EFSA et al., 2023), a lower number of outbreaks in poultry and cases in wild birds were reported to WOAHA overall. In Africa the number of affected countries has remained stable, but in the Americas and Asia, only half as many countries were affected by HPAI virus. Although the number of countries reporting to WOAHA in South America has also decreased, a

very dynamic situation in wild and domestic birds can be observed with a continuous spread to the southern tip of Americas. In contrast to the previous reporting period, outbreaks in South America were also increasingly reported from commercial poultry farms.

- Based on the observed temporal and geographical distribution of HPAI (H5N1) virus in wild birds during the reporting period, virus spread in South America corresponds to the Pacific Americas Flyway along the west coast of South America, the Mississippi Flyway along the Caribbean and the north-central part of South America, and the Atlantic Americas Flyway along the east coast of South America.
- During the current reporting period, HPAI A(H5N1) virus reached the island of Tierra del Fuego at the southern tip of South America (latitude: 53 degrees South), and there is a risk that it will spread to seabirds and pinnipeds in the Antarctic in the near future. The Antarctic Wildlife Health Working Group has already provided a guideline for operators interacting with wildlife in the Antarctic (Dewar et al., 2022).
- The results of the genetic analysis conducted on HPAI viruses isolated from South America indicate multiple virus introduction events from North to South America, followed by local spread.

## Mammals

- During this reporting period, several mammal species have been found infected with HPAI viruses for the first time, especially among mustelids and marine mammals: American pine marten (*Martes americana*), Asiatic black bear (*Ursus thibetanus*), Burmeister's porpoise (*Phocoena spinipinnis*), Chilean dolphin (*Cephalorhynchus eutropia*), Marine otter (*Lontra felina*), and South American bush dogs (*Speothos venaticus venaticus*). At the same time, the mass mortality events observed in sea lions in South America continued.
- A(H5) virus infections in mammalian species appear to favour the emergence of molecular markers of virus adaptation to mammals (i.e. PB2 E627K, D701N or T271A).
- A(H5N1) infected cats and dog have been detected highlighting the risk of pets being exposed, infected and developing severe clinical disease, as well as possibly becoming a potential risk for exposure for further animals (e.g. in backyard settings) and the general population.
- The ongoing and Europe-wide HPAI A(H5N1) epidemic in black-headed gulls forms a risk for marine mammals along the coast of Europe, including harbour seals that breed in the international Wadden Sea in the coming months.

## Human cases

- A few sporadic human infections with avian influenza A(H3N8), A(H5N1), and A(H9N2) viruses have been reported from different countries globally since the beginning of 2023.
- Human severe and fatal infections were mainly related to unprotected exposure to sick and dead poultry, particularly in backyard settings, as well as contaminated environment or exposure to live bird markets.
- A human infection with A(H5N1) with undetermined source of infection but potential exposure to contaminated environment, sick or dead wild birds or sea lions has been reported from Chile.



## 4 Options for response

### In birds

- Given the wide geographic expansion and increased number of cases associated with the BB genotype, and considering the atypical (in relation to the A(H5Nx) HPAI infections observed in previous epidemic years) disease presentation reported in some BB-genotype associated outbreaks in poultry and in experimental studies, passive surveillance in poultry might not ensure the prompt detection of the virus when present. Passive surveillance could therefore be complemented by encouraging farmers to collect dead birds to be pooled and tested weekly (bucket sampling) (EFSA AHAW Panel et al., 2020) for a prompt detection of the virus in farms where infected gulls are identified in the surrounding areas; this should be considered in particular for poultry establishments located in densely populated poultry areas. Also, in high-density poultry production areas, regular testing of birds before slaughter is highly recommended to increase early detection.
- Further studies are needed to confirm the atypical presentation of HPAI A(H5N1) virus infection in poultry observed in Italy.
- Close monitoring of seabird breeding colonies, including black-headed gulls, for unusual mortality will allow for the early detection of HPAI virus and, if appropriate, to remove carcasses for the reduction of environmental contamination and therefore reduced mortality.
- Serological surveillance in seabirds, in particular in endangered species, is urgently needed to evaluate the real level of virus circulation in those species as well as their immune protection.
- Species identification remains of utmost importance for the correct interpretation of passive surveillance efforts in wild birds.
- Short-term preparedness and medium- and long-term prevention strategies should be identified and implemented, primarily in densely populated poultry areas and poultry production systems that are highly susceptible to avian influenza exposure. These were described in detail in Avian influenza overview September – December 2021 (EFSA et al., 2021) and include the reinforcement and checking of regular implementation of biosecurity measures, the reduction of the density of commercial poultry establishments, the reorganisation of the poultry production system highly susceptible to avian influenza exposure and the possible application of appropriate vaccination strategies.

### In mammals

- Disease dynamics associated with HPAI virus infection during mass mortality events in mammal species should be thoroughly investigated. Testing a high number of animals and assuring a prompt generation and sharing of viral sequences data are of utmost importance to shed light on the virus origin, evolution and possible transmission between individuals. The latter is also indicated to timely assess the pandemic risk.
- It is recommended to avoid exposure of domestic cats and dogs, and in general carnivore pets, to dead or diseased animals (mammals and birds) in areas where mortality in gulls or other potentially HPAI virus-infected animals are reported. Possible measures are keeping dogs on a leash, and confining cats indoors in areas where extensive circulation of HPAI virus in wild birds has been confirmed.
- Testing against HPAI virus as well as treatment with antivirals should be considered when domestic cats, dogs, or other captive carnivores, e.g. ferrets, show neurological or respiratory signs in areas where HPAI virus has been detected in wild birds.

- Awareness should be raised among people to prevent their exposure to dead or diseased seabirds or mammals in coastal areas.
- Extended and enhanced surveillance of both wild mammals (particularly carnivores and cetacean) and farmed mammals (particularly American mink and domestic pigs) in risk areas where HPAI is present in wild birds and poultry is recommended to promptly identify and characterize HPAI viruses and evaluate the real magnitude of the virus spread in these species.
- Better, 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.

### In humans

- Appropriate personal protective equipment should be used when in contact with potentially infected birds and animals.
- People exposed to sick and dead birds, infected mammals and contaminated environment should be followed-up and tested following onset of respiratory or other symptoms to identify transmission events early.
- Any suspected or confirmed human infection with avian influenza should be reported as early as possible according to regulation on cross border health threats 2022/2071 to the Early warning and response system (EWRS) and international health regulations (IHR).
- Antiviral pre- and post-exposure prophylaxis should be considered following national guidelines.
- Specimens from patients with severe influenza type A infection in hospital settings should be considered for subtyping.
- Patients with viral encephalitis of unknown aetiology could be considered to be tested for influenza type A viruses, and subtyped if positive to identify potential sporadic infections with similar clinical picture as observed in infected mammalian species.
- Timely producing and sharing of virus sequence information is crucial for assessment and development of candidate vaccine viruses.

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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.

Since late October 2016 up to early February 2017, highly pathogenic avian influenza (HPAI) of the subtype A(H5N8) has been detected in wild migratory birds or captive birds on the territory of 21 Member States, namely Austria, Belgium, Bulgaria, Croatia, Czechia, Denmark, Finland, France, Germany, Greece, Hungary, Ireland, Italy, the Netherlands, Poland, Portugal, Slovakia, Slovenia, Spain, Sweden and the United Kingdom. In 17 Member States the virus has spilled over to poultry holdings leading also to lateral spread between holdings in a few Member States, in particular in those with a high density of duck and geese holdings where the poultry cannot sufficiently be protected against contacts with wild birds. A second HP AI subtype A(H5N5) has been detected in wild birds and recently also in poultry holdings in Germany.

The number of infected migratory wild birds found dead and the geographical extent of these findings are posing an immense threat for virus introduction into poultry or captive birds holdings as demonstrated by the high number of outbreaks (~700 as of 08/02/2017).

In the event of an outbreak of avian influenza, there is a risk that the disease agent might spread to other holdings where poultry or other captive birds are kept. As a result, it may spread from one Member State to other Member States or to third countries through trade in live birds or their products.

There is knowledge, legislation<sup>7</sup>, technical and financial tools in the EU to effectively deal with outbreaks of avian influenza in poultry and captive birds. However, the very wide virus spread by wild birds and the increased risk of direct or indirect virus introduction into poultry or captive bird holdings has led to the largest HPAI epidemic in the EU so far. This situation calls for a reflection and evaluation how preparedness, risk assessment, early detection and control measures could be improved.

The Commission and Member States are therefore in need of an epidemiological analysis based on the data collected from the disease affected Member States. The use of the EFSA Data Collection Framework is encouraged given it promotes the harmonisation of data collection. Any data that is available from neighbouring third countries should be used as well, if relevant.

Therefore, in the context of Article 31 of Regulation (EC) No. 178/2002<sup>8</sup>, EFSA should provide the technical and scientific assistance to the Commission based on the following Terms of Reference (TOR):

- 1) Analyse the epidemiological data on highly pathogenic avian influenza (HPAI) and low pathogenic avian influenza (LPAI), where co-circulating or linked within the same epidemic, from HPAI disease affected Member States.
- 2) Analyse the temporal and spatial pattern of HPAI and LPAI as appropriate in poultry, captive birds and wild birds, as well the risk factors involved in the occurrence, spread and persistence of the HPAI virus in and at the interface of these avian populations.
- 3) Based on the findings from the points above, describe the effect of prevention and control measures.
- 4) Provide for regular quarterly reports updating on the avian influenza situation within the Union and worldwide, in particular with a view to describe the evolution of virus spread from certain regions towards the EU. In case of significant changes in the epidemiology of avian influenza, these reports could be needed more frequently. These reports should in particular closely follow the developments of zoonotic avian influenza viruses (such as HPAI A(H5N6) and LPAI A(H7N9)) in collaboration with the European Centre for Disease Prevention and Control (ECDC).

## A.2 Interpretation of the Terms of Reference

In reply to ToR 1 and ToR 2, this scientific report gives an overview of the HPAI and LPAI outbreaks in poultry, captive and wild birds detected in Europe from 2 March to 28 April 2023 and reported by Member States and neighboring countries to the ADIS or WOAHH-WAHIS. Member States where avian influenza outbreaks have occurred in poultry have submitted additional epidemiological data to EFSA, that have been used to analyse the characteristics of the affected poultry establishments.

It was not possible to collect data for a risk factor analysis on the occurrence and persistence of HPAI virus within the EU. Risk factor analysis requires not only case-related information, but also data on the susceptible population (e.g. location of establishments, 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 et al., 2017).

If HPAI outbreaks in poultry are detected in the EU, a description of the applied prevention and control measures (ToR 3) is given in the overview document provided by representatives from the affected Member States and is provided in [Annex A](#). Information was collected for outbreaks that occurred from 3 September to 18 November 2022. The main topics covered are increasing awareness, release and repeal of housing orders, strengthening biosecurity, preventive culling, implementation of a regional standstill, bans on hunting and derogations from restriction zone implementation after a risk assessment.

Monitoring of the avian influenza situation in other countries (ToR 4) is based on data reported to WOAHH-WAHIS. The description focuses only on findings of avian influenza viruses occurring in countries that are considered to be of epidemiological interest for the EU/EEA and the UK or of public health relevance, specifically on HPAI A(H5N1), HPAI A(H5N2), HPAI A(H5N5), HPAI A(H5N6), HPAI A(H5N8), HPAI/LPAI A(H7N9) and LPAI A(H9N2). The background and epidemiology, detections, phenotypic and genetic characterisations are described based on information from confirmed human, poultry and

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<sup>8</sup> 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, pp. 1–24.

wild bird cases that occurred from 2 March to 28 April 2023. Possible actions for preparedness in the EU are discussed.

This report mainly describes information that has become available since the publication of the EFSA report for the period December 2022 to March 2023 (EFSA et al., 2023) and that might affect the interpretation of risks related to avian influenza introduction and/or spread in Europe.

## Appendix B - Data and Methodologies

### B.1 Data on animals

#### B.1.1 Overview of avian influenza outbreaks in Europe (ToR 1 and ToR 2)

Data on the avian influenza outbreaks that occurred in Europe from 2 March to 28 April 2023 submitted by Member States to the ADIS (European Commission, online) were taken into account for this report. Data extraction was carried on 28 April 2023. The WOAH's World Animal Health Information Database ((WOAH, online-b) was consulted to complement the information for European countries not reporting HPAI notifications to ADIS. In addition, HPAI-affected European countries were asked to provide more detailed epidemiological data directly to EFSA on the avian influenza outbreaks that occurred in poultry up to 3 April 2023. Wild bird species have been categorised according to [Table A.8 in Annex A](#), and the common and scientific name of wild bird species described in this report in relation to Europe is reported in [Table A.9 in Annex A](#). The public GISAID's EpiFlu Database was accessed to download newly released avian influenza sequences.

The annexes to this Scientific Report are available on the EFSA Knowledge Junction community on Zenodo at: <https://doi.org/10.5281/zenodo.7919544>

#### B.1.2 Overview of avian influenza outbreaks in other countries not reporting via ADNS (ToR 4)

Data from WOAH-WAHIS ((WOAH, online-b) on HPAI A(H5N1), HPAI A(H5N2), HPAI A(H5N5), A(H5N6), A(H5N8), HPAI and LPAI A(H7N9) in domestic and wild birds were used to describe and to map the geographical distribution of avian influenza detections in domestic and wild birds in Africa, the Americas, Asia and Europe based on the observation dates. Data were retrieved on 28 April 2023 and extracted by EFSA. 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.1.2 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 (WHO, 2020) 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, 2023a).

## B.2 Data on humans

The numbers of human cases caused by infection with avian influenza viruses were collected by ECDC. Multiple sources are scanned regularly as part of Epidemic Intelligence activities at ECDC 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 of time 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.