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Avian influenza overview March – June 2022

European Food Safety Authority,
European Centre for Disease Prevention and Control,
European Union Reference Laboratory for Avian Influenza,
Cornelia Adlhoch, Alice Fusaro, José L Gonzales, Thijs Kuiken, Stefano Marangon,
Éric Niqueux, Christoph Staubach, Calogero Terregino, Inma Aznar, Irene Muñoz
Guajardo and Francesca Baldinelli

Abstract

The 2021–2022 highly pathogenic avian influenza (HPAI) epidemic season is the largest epidemic so far observed in Europe, with a total of 2,398 outbreaks in poultry, 46 million birds culled in the affected establishments, 168 detections in captive birds, and 2,733 HPAI events in wild birds in 36 European countries. Between 16 March and 10 June 2022, 1,182 HPAI virus detections were reported in 28 EU/EEA countries and United Kingdom in poultry (750), and in wild (410) and captive birds (22). During this reporting period, 86% of the poultry outbreaks were secondary due to between-farm spread of HPAI virus. France accounted for 68% of the overall poultry outbreaks, Hungary for 24% and all other affected countries for less than 2% each. Most detections in wild birds were reported by Germany (158), followed by the Netherlands (98) and the United Kingdom (48). The observed persistence of HPAI (H5) virus in wild birds since the 2020–2021 epidemic wave indicates that it may have become endemic in wild bird populations in Europe, implying that the health risk from HPAI A(H5) for poultry, humans, and wildlife in Europe remains present year-round, with the highest risk in the autumn and winter months. Response options to this new epidemiological situation include the definition and the rapid implementation of suitable and sustainable HPAI mitigation strategies such as appropriate biosecurity measures and surveillance strategies for early detection measures in the different poultry production systems. Medium to long-term strategies for reducing poultry density in high-risk areas should also be considered. The results of the genetic analysis indicate that the viruses currently circulating in Europe belong to clade 2.3.4.4b. HPAI A(H5) viruses were also detected in wild mammal species in Canada, USA and Japan, and showed genetic markers of adaptation to replication in mammals. Since the last report, four A(H5N6), two A(H9N2) and two A(H3N8) human infections were reported in China and one A(H5N1) in USA. The risk of infection is assessed as low for the general population in the EU/EEA, and low to medium for occupationally exposed people.

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Key words: avian influenza, captive birds, HPAI/LPAI, humans, monitoring, poultry, wild birds

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Correspondence: biohaw@efsa.europa.eu

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Note: Kosovo – 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.

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1. Introduction

This scientific report provides an overview of highly pathogenic avian influenza (HPAI) virus detections in poultry¹, captive² and wild birds as well as 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 16 March and 10 June 2022.

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

2. Main observations and conclusions

A description of the avian influenza outbreaks in European countries and in other countries of interest taking place between 16 March and 10 June 2022, is presented below.

2.1. Main observations

- In Europe, between 16 March and 10 June 2022 (based on the Animal Disease Information System (ADIS), WOAH World Animal Health Information System (WOAH WAHIS), and information provided by affected countries) 1,182 HPAI A(H5) detections³ were reported in poultry, and captive and wild birds:
 - 750 outbreaks in poultry, in France (509), Hungary (177), Bulgaria (15), the Netherlands (13), United Kingdom (11 each), Germany (7), Albania (4), Poland (3), Italy and Romania (2 each), Belgium, Croatia, Czechia, Iceland, Kosovo⁴, Moldova and Slovakia (1 each);
 - 410 detections in wild birds, in Germany (158), the Netherlands (98), United Kingdom (48), Iceland (16), France and Spain (15 each), Norway (13), Denmark (10), Finland (7), Greece (6), Belgium (5), Sweden (4), Hungary and Lithuania (3), Austria, Poland and Romania (2 each), Estonia, Ireland and Montenegro (1 each);
 - 22 outbreaks in captive birds, in France (15), United Kingdom (3), Bulgaria (2) and Albania and Denmark (1 each);
- For the first time Iceland reported detections of HPAI virus in its territory (in wild birds and in poultry); the first case was confirmed in April 2022 in a white-tailed eagle found dead in October 2021; of note, the virus identified was closely related to the HPAI A(H5N1) viruses that have been detected in North America since December 2021.
- Similar to the 2020–2021 epidemic season, in the current A(H5N1) epidemic in Europe the second peak of reported HPAI detections in wild birds in Northern Europe extended to the end of the reporting period (10 June 2022) and will likely last longer.
- During this reporting period HPAI virus was detected in at least 45 wild bird species: at least 11 waterfowl species (206 detections), 9 raptor species (68 detections), and 25 other wild bird species (136 detections). The overall temporal pattern showed a decrease of HPAI detections from January 2022 (which was the second and major peak of the current epidemic season in wild birds) onwards. A downward trend compared to the winter season was expected, however

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 The date of suspicion was used as the reference date, when the date of suspicion was not available then the date of confirmation was used as the reference date.

⁴ 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.

H5N1 detections in wild birds were reported to the end of the current period, with most of them reported in raptors and other wild bird species since the end of April.

- During this reporting period large die-offs of several species of colonial breeding birds associated with H5N1 A(H5) were reported in the Netherlands, Scotland, Iceland, Norway, France, and Greece. H5N1-associated mortality was reported in sandwich terns, Eurasian spoonbills, common terns, black-headed gulls, northern gannets, great skuas and Dalmatian pelicans.
- Considering outbreaks in poultry, France is by far the most affected country in this reporting period and epidemic season, with 509 and 1,371 outbreaks respectively, and more than 6.5 million birds having been culled in the affected establishments in this reporting period. France is followed by Hungary (171 outbreaks and almost three million birds culled), and Bulgaria (15 outbreaks and almost one million birds culled). During this reporting period, 86% of the poultry outbreaks - up to 93% in France and Hungary - were secondary due to between-farm spread of H5N1 virus.
- In France, three epidemiological spatiotemporal clusters have been identified since October 2021, with no epidemiological links between the first one and last two: a first cluster in the southwest (southern part of Nouvelle-Aquitaine and Occitanie), with a peak in mid-January, the second one in western regions (Pays de la Loire and northern part of Nouvelle-Aquitaine) peaking in early March, and the third one in central western regions (north-eastern Nouvelle-Aquitaine and northern Occitanie) with a peak in early April. Nearly all outbreaks involved commercial farms. The southwestern and central western clusters mostly involved duck establishments for foie gras production, whereas outbreaks in the western cluster also affected all types of species and productions in mixed proportions. The genetic investigation identified the incursions of at least eight distinct genotypes. However, up to mid-February, a single major genotype accounted for most detections in poultry in the southwestern cluster (as well as in sporadic detections dispersed over the country, in poultry, captive birds and wild birds). This genotype was afterwards superseded by another one, responsible for the poultry outbreaks in the western and central western clusters.
- As for the poultry species and production categories affected during this epidemic, there has been an increase in almost all type of poultry production systems, particularly in the number of fattening, foie gras and breeding (chickens, domestic ducks and goose) establishments affected when compared with the 2020–2021 epidemic season.
- All the H5N1 (H5Nx) viruses characterised since October 2021 in Europe belong to clade 2.3.4.4b. Whole genome sequencing indicates the persistent circulation of the A(H5N1), A(H5N8) and A(H5N5) virus subtypes in Northern Europe, which have been circulating in Europe since October 2020. Moreover, multiple novel reassortant H5N1 A(H5N1) and A(H5N2) genotypes were introduced into Europe through the autumn migration of wild birds or generated from local reassortment events.
- Since the last reporting period no further H5N1 A(H5Nx) cases were detected in mammalian species in Europe, whereas several cases have recently been observed in other parts of the world: in red foxes and skunks in North America, and a common raccoon dog in Japan.
- Although the number of outbreaks, particularly for the dominant H5N1 A(H5N1) subtype, in non-EU/EEA countries has again increased compared with the last report (EFSA et al., 2022), the distribution across the different continents has shifted considerably. The number of reported outbreaks of domestic and wild birds in Africa and Asia decreased significantly in the relevant time period of this report compared with the months before, whereas the number of reported outbreaks of H5N1 A(H5N1) in Canada and the USA has increased 10-fold.
- Nine new human infections with avian influenza viruses have been reported since the last report: four A(H5N6), two A(H9N2) and two A(H3N8) from China and one A(H5N1) from the USA.

2.2. Conclusions

- The 2021–2022 epidemic with a total of 2,398 outbreaks in poultry, 46 million birds culled in the affected establishments, 168 detections in captive birds, and 2,733 HPAI events in wild birds in 36 European countries is larger than the 2020–2021 epidemic and appears to be the largest so far in Europe. Also, similarly to previous epidemics, the number of reported wild bird events is an underestimate of the total number of wild birds that have died from HPAI during this epidemic, limiting the assessment of the impact of the disease on the wild bird population.
- The viruses characterised to date retain a preference for avian-type receptors; mutations associated with mammalian adaptation have only been sporadically identified in the analysed viruses from avian species, but they are frequently acquired upon transmission to mammals.
- The latest transmission events of A(H5) clade 2.3.4.4b viruses to humans in United Kingdom and USA together with the increasing number of transmission events of A(H5) viruses to wild mammals reported from different European countries underline the continuous risk of avian influenza viruses to transmit to humans also in Europe and that these viruses may adapt further to mammals.
- The risk of infection for the general population in the EU/EEA is assessed as low, and for occupationally exposed people low to medium with high uncertainty due to the high diversity of circulating avian influenza viruses in bird populations.
- The risk of transmission to humans by exposure to contaminated poultry products is considered negligible as also outlined in a previous EFSA assessment (EFSA AHAW Panel, 2017).
- The current 2021–2022 epidemic season is still ongoing with cases in poultry and wild birds up to June 2022.
- As in the previous HPAI season, the observed longer persistence of HPAI in wild birds compared with the same period in the previous years may indicate a continuation of the risk for spread among wild birds and mammals, as well as for virus entry into poultry farms.
- The long duration of the avian influenza risk period could represent a challenge for the sustainability of the reinforced biosecurity measures implemented along the poultry chain (e.g. compulsory indoor confinement of free-range poultry) in high-risk areas or production sectors. The persistent presence of HPAI A(H5) viruses in wild birds and the environment, and the possible reduction of biosecurity compliance might increase the risk of avian influenza incursions with the potential further spread between establishments, primarily in areas with high poultry densities.
- The observed change in the proportions of affected wild bird species from waterfowl to raptors and other wild bird species suggests a shift of infection from winter migrants to wild birds that are resident and/or breeding in Europe, including those that breed in colonies.

3. Options for response

- Considering the high negative impact of these HPAI epidemics in the last years, 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 have been described in detail in Avian influenza overview September – December 2021 (EFSA et al., 2021b).
- Given the substantial mortality of wild birds associated with the detection of HPAI A(H5), it is important for the relevant authorities to ensure careful documentation of the number of wild birds found dead or ill during these HPAI-associated die-offs. Such information enhances our understanding of these phenomena and provides a factual basis to help policy makers to minimise the probability of similar events due to HPAI virus occurring in the future.
- Surveillance in mammals and humans that could potentially be exposed to infected birds should be strengthened to facilitate the early detection of virus transmission events from birds to wild

or domestic mammals and/or humans, and subsequently between humans. Cross-sectoral cooperation and communication between animal and public health and occupational safety and health (OSH) authorities are recommended (One Health approach) to initiate rapid response, follow-up, and control measures. Especially, the inclusion of avian influenza viruses in the differential diagnosis of neurological disease in wild mammals needs to be more widely implemented.

- Occupational health and safety measures should be set according to national legislation. Health monitoring should be offered according to national requirements (please refer to Section 4.7.1 for more detail).
- People potentially exposed to infected poultry or captive birds, for example during culling operations, or workers in close contact to potentially infected mammals such as foxes or other wildlife, for example at rehabilitation centres, should be adequately protected and actively monitored or at least self-monitor for respiratory symptoms, neurological symptoms or conjunctivitis for 10 days following exposure, and immediately inform the local health and occupational health authorities or other preventive services to initiate testing and follow-up in case of symptoms. Antiviral pre-exposure or post-exposure prophylaxis should be considered for exposed people according to national recommendations.
- Timely generation and sharing of complete viral genome sequences from wild birds, poultry, and captive birds are crucial to promptly detect the emergence in or introduction into the EU of viruses relevant for animal and public health. The recent human infections in China caused by a reassortant A(H3N8) virus underline the need to expand and strength the genomic surveillance also on low pathogenic viruses, for a prompt identification of viruses with an increased zoonotic potential. More efforts should be made by reporting countries to monitor and genetically characterise a significant number of samples based on the size, duration, and relevant features of the epidemic in each country or of subtypes of concern for public health.

4. Results

4.1. Overview of HPAI outbreaks in Europe during the previous and current seasons

Figures 1, 2 and 3 show the HPAI outbreaks in domestic birds (poultry and captive birds) and detections in wild birds that were reported in Europe via the Animal Disease Notification System (ADNS), ADIS or WOA/WAHIS for seasons 2016–2017, 2017–2018, 2018–2019, 2019–2020 and 2020–2021 by month of suspicion (Figures 1 and 2) and geographical location (Figure 3). In this document a 'season' 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 detections were observed in wild birds in Europe in 2016–2017, 2020–2021 and 2021–2022. For the current season, 2021–2022, data reported are truncated at 10 June 2022. Figure 4 shows the comparison between the geographical distribution of HPAI virus detections from March to June 2022 and the same period during the 2016–2017 and the 2020–2021 epidemics, which before this season were the largest epidemics recorded in the EU/EEA and GB in terms of number of poultry outbreaks, geographical spread and number of dead wild birds.

The analysis of the characteristics of the previous 2020–2021 and current 2021–2022 avian influenza seasons, from October 2020 to 10 June 2022, is reported in Figure 5 by week of suspicion, virus subtype and host population.

The start of the epidemics in the 2016–2017, 2020–2021, and in the current 2021–2022 seasons, all fell within the period between the end of September and beginning of October. There were no evident epidemics in 2017–2018 and 2018–2019, while the end of December 2019 was the start of the smaller 2019–2020 epidemic that affected only poultry (Figures 1 and 2). The current 2021–2022 epidemic is still ongoing and might be lasting longer than previous ones: so far, 245 HPAI detections have been reported in May 2022 compared with 160 in May 2021 and to 11 in May 2017 (Figure 4). These May

2022 numbers should not be considered as definitive as the season is still ongoing and new detections, particularly in wild birds, might be reported in the coming weeks.

In the 2016–2017 season, the epidemic peaks in wild and domestic (poultry and captive) birds were approximately simultaneous. In the 2020–2021 season, the epidemic peak in wild birds preceded that in domestic birds and, so far, this also appears to be the case in the 2021–2022 season (Figure 2).

The large 2016–2017 and 2020–2021 epidemics were widespread in Europe and had similar northern (Finland), western (Ireland and the Iberian Peninsula), southern (Italy, Greece) and eastern limits (Ukraine, Romania, Bulgaria). So far, the 2021–2022 epidemic seems to have become more extensive, with a northern limit from Iceland to Northern Norway and the southern limit in Portugal and Spain: all countries that were not previously affected, or only partially affected for Norway, in the previous epidemic seasons. Moreover, in the current epidemic a higher number of cases in both poultry and wild birds than in previous epidemics have been identified at the western limits (Figure 3).

During the three large epidemics 2016–2017, 2020–2021 and 2021–2022, secondary spread of HPAI virus between poultry establishments in southwestern France was responsible for clusters of poultry outbreaks that involved mostly the duck for foie gras production farming sector. Although, for all three epidemic seasons, direct or indirect contact with infected wild birds was considered to be the most likely source of primary introductions in this area, the number of reported HPAI virus detections in free-living wild birds has been limited and their timeframe or localisation was not directly related to the poultry clusters (Figure 3).

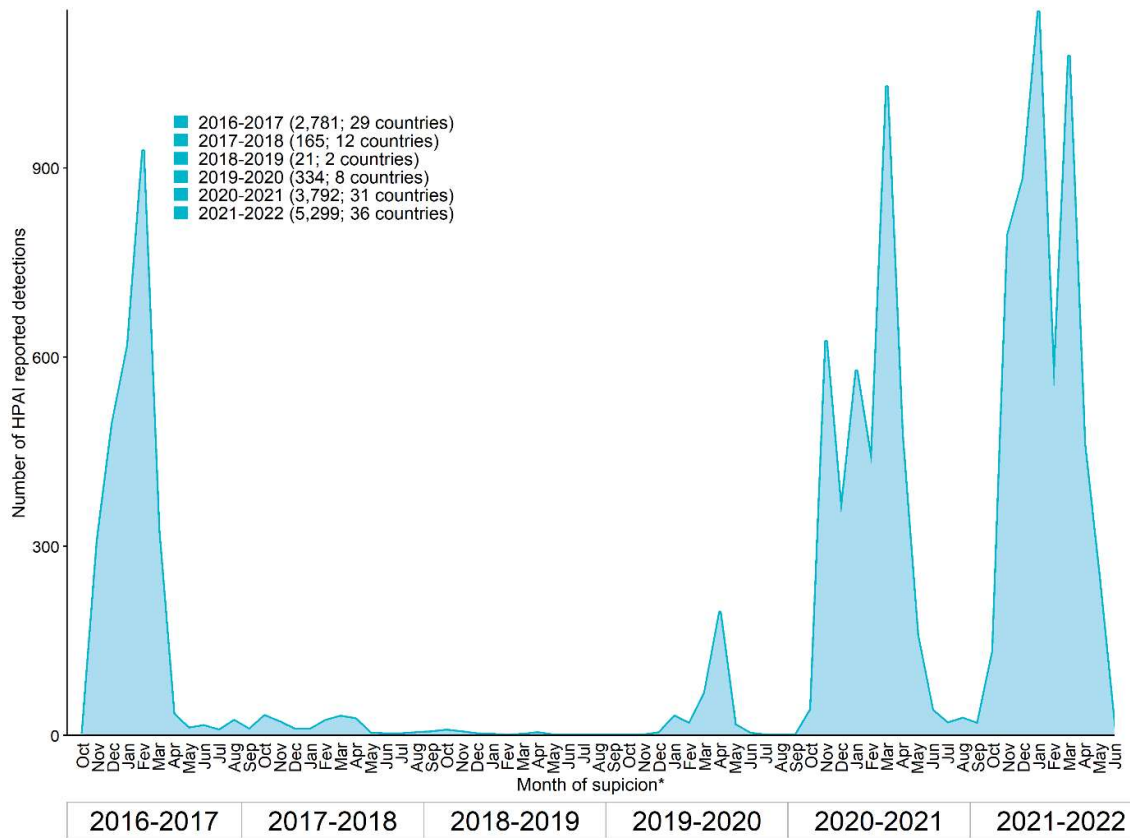
However, the current 2021–2022 season in France stands apart from the previous epidemics: clusters of poultry outbreaks were not restricted to the southwestern area and two other major epidemiological spatiotemporal clusters, unrelated to the former, were identified respectively in the western Pays-de-la-Loire region and in central western areas (north-eastern Nouvelle-Aquitaine and northern Occitanie, respectively). Besides, not only the foie gras sector but also all types of poultry species and productions were affected in the second cluster observed in western areas (Figures 3 and 4).

The predominant subtype A(H5N8) in the 2020–2021 epidemic season was replaced by subtype A(H5N1) in the current 2021–2022 epidemic (Figure 5). During this epidemic season, a total of 16 A(H5N8) virus detections was reported: 9 in poultry in Albania (4), Kosovo (3), Denmark and Estonia (1 each); 7 in wild birds in Denmark and the Netherlands (2 each), and Finland, Sweden and the United Kingdom (1 each). The viruses detected in poultry in Albania and Kosovo in this epidemic season seem to be strictly related to the ones detected from the same countries in May–June 2021.

Norway was the only country where HPAI A(H5N5) virus was detected during this epidemic season (nine wild birds detections) from January to end of May 2022.

For wild birds, in 2021–2022 HPAI was detected predominantly in waterfowl, but also in a wide range of other wild bird species, including several terrestrial species, and raptors. Since January 2022, HPAI virus detections have progressively decreased in waterfowl and since the end of April, most detections have occurred in raptors and other wild bird species, including those breeding in colonies. It cannot be excluded that the persistence of HPAI (H5) virus until June provided new opportunities for the virus to spread in wild bird populations (Figure 5). Similarly to that observed in the 2020–2021 epidemic season, in the current 2021–2022 season there were two peaks of HPAI A(H5) virus detections in wild birds. In both seasons, the first peak was at the beginning of November, coinciding with the autumn migration of waterfowl and arrival at their wintering grounds in Europe. However, the second peak appears to be earlier in this season (middle of January) than in the previous season (beginning of March) and the virus persists longer than in the previous season as there are still wild bird cases being reported at the beginning of June and more cases that have been sampled in June could be reported in the coming weeks (Figure 5).

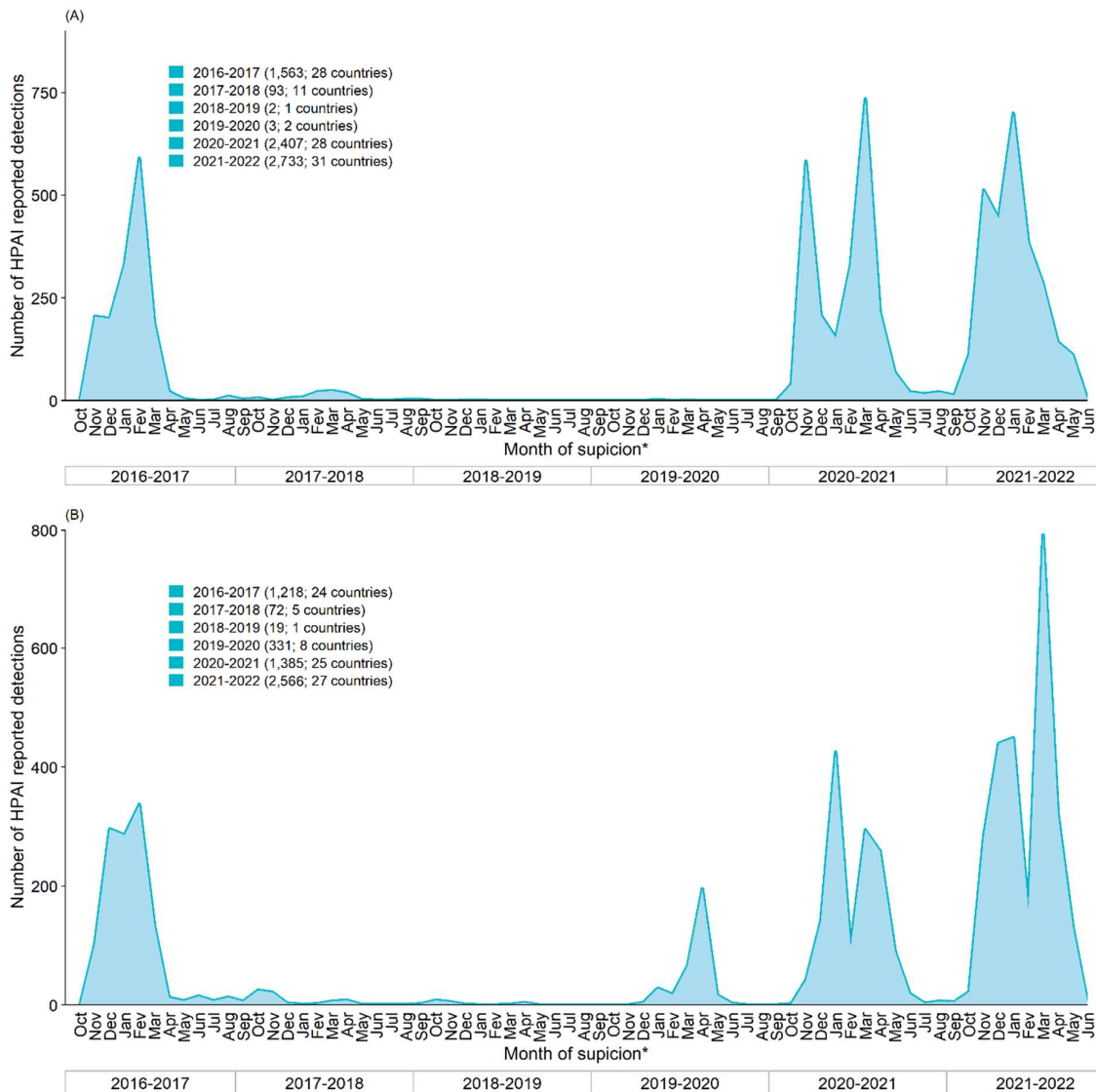
Considering only HPAI outbreaks in poultry, so far approximately 46 million of birds have been culled in the HPAI-affected establishments in the current epidemic season since October 2021.



*When the date of suspicion is not available then 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)⁵.
 Source: ADIS and WOA (data extraction carried out on 10 June 2022).

Figure 1: Distribution of the number of HPAI virus detections reported in Europe in the seasons 2016–2017, 2017–2018, 2018–2019, 2019–2020 and 2020–2021 by month of suspicion, from 16 March to 10 June 2022 (12,392)

⁵ 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).



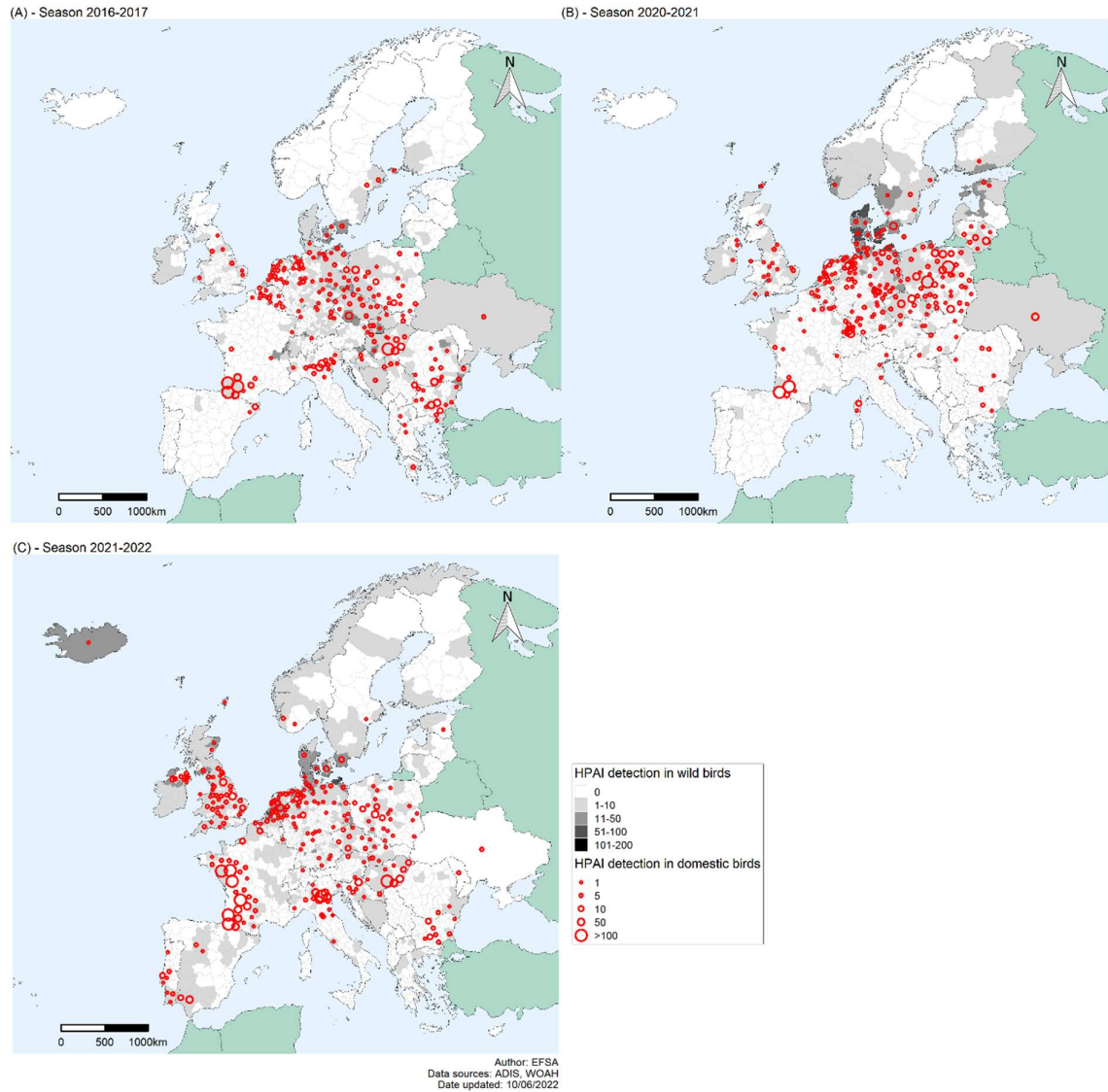
*When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.

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)⁵.

Source: ADIS and WOA (data extraction carried out 10 June 2022).

Note that the scale of the vertical axes is specific to each bird population.

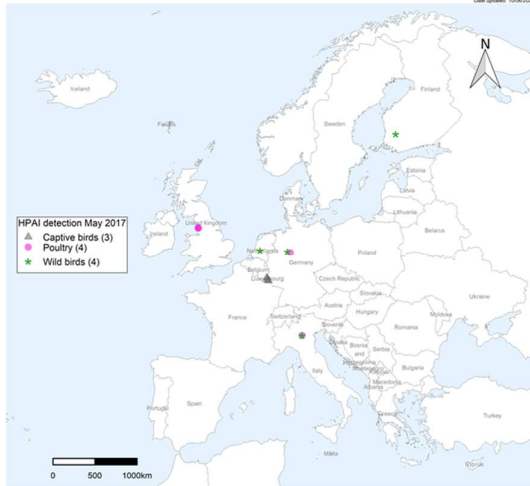
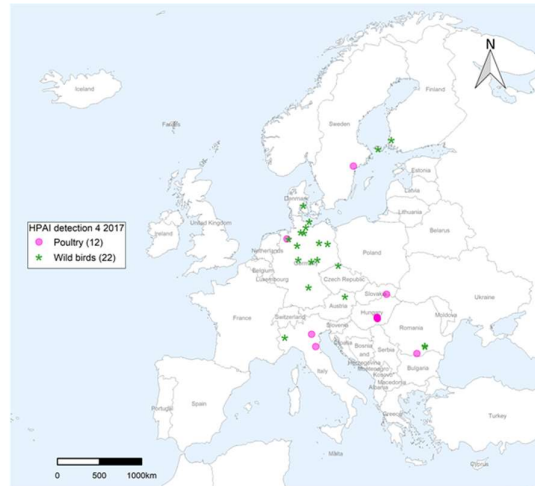
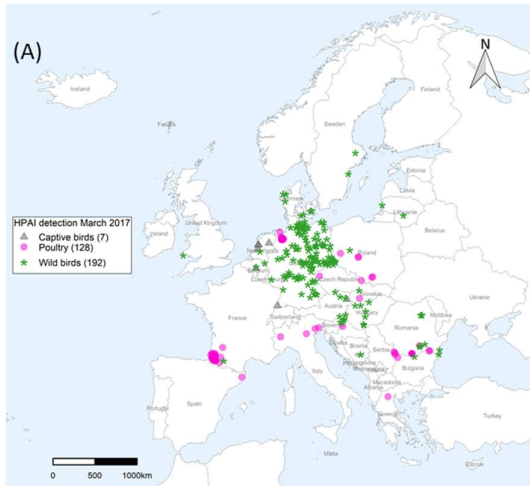
Figure 2: Distribution of total number of HPAI virus detections reported in Europe in the seasons 2016–2017, 2017–2018, 2018–2019, 2019–2020, 2020–2021 and 2021–2022 by month of suspicion in (A) wild birds (6,801) and (B) domestic birds (poultry and captive birds) (5,591), from 16 March to 10 June 2022

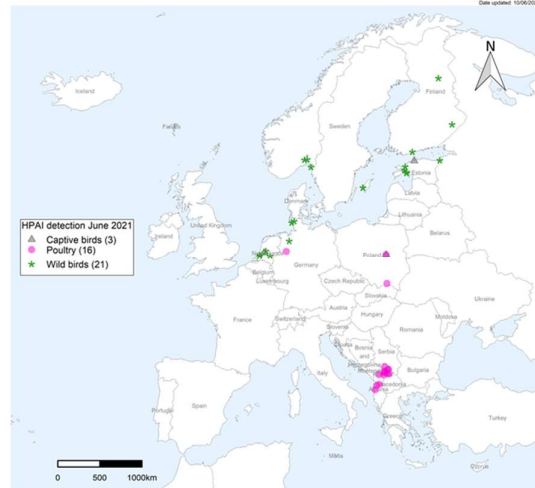
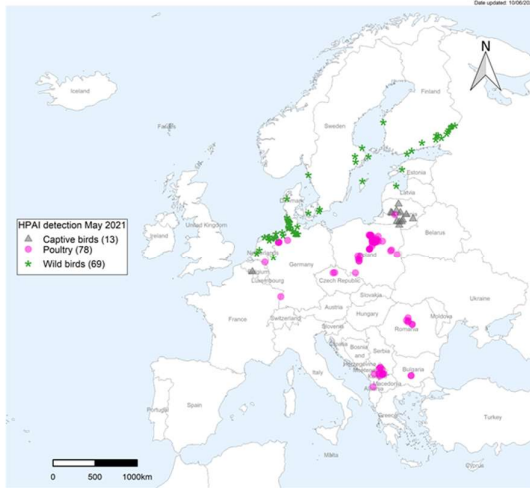
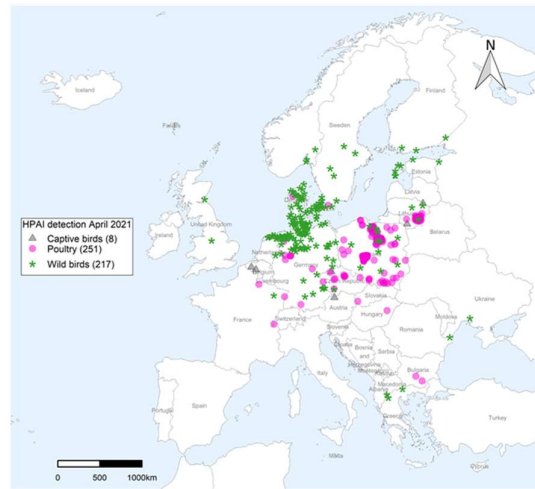
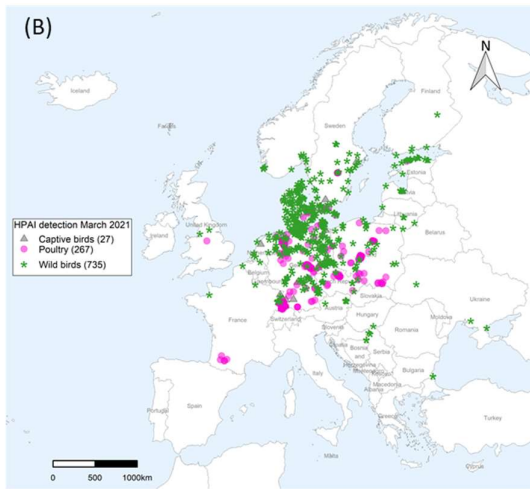


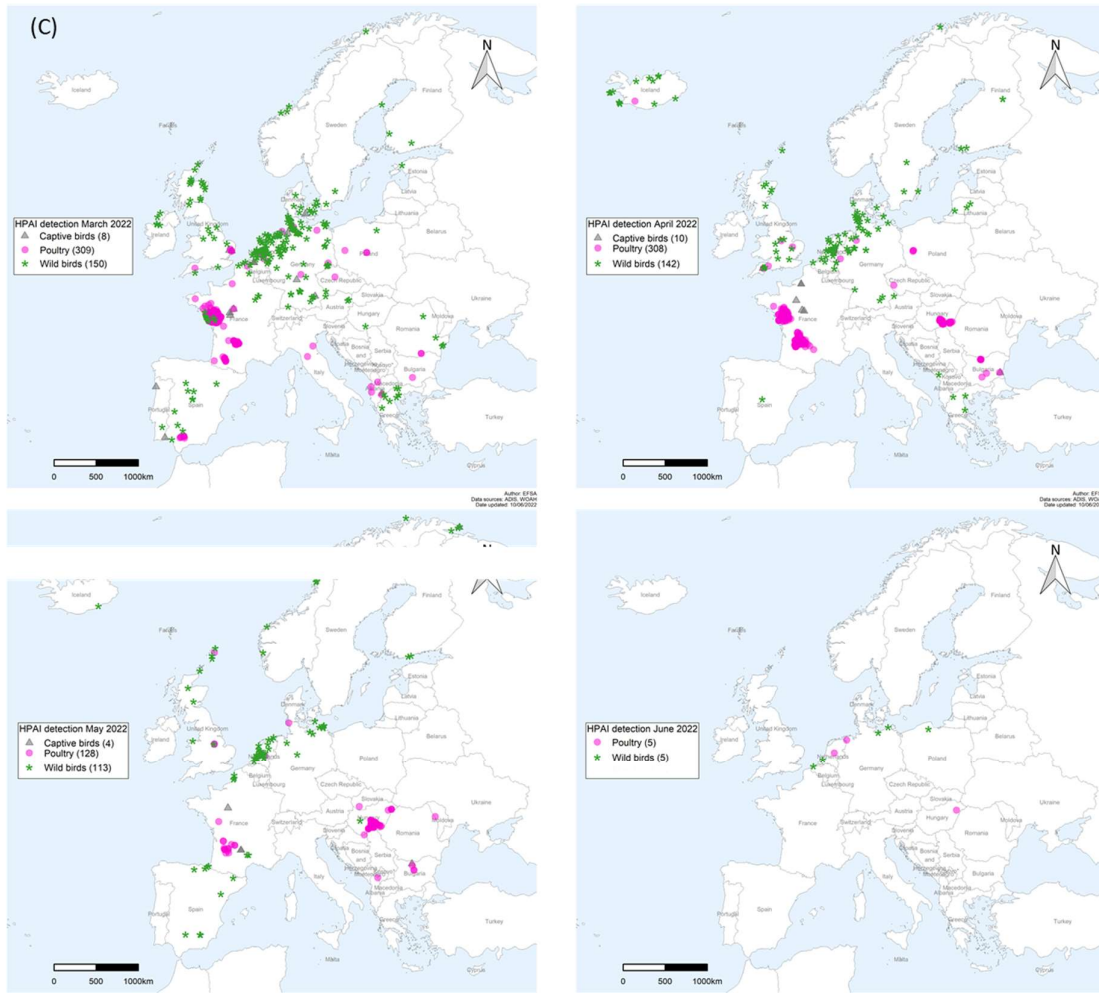
United Kingdom data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was the World Animal Health Information System (WOAH-WAHIS) for United Kingdom (excluding Northern Ireland), and ADNS/ADIS for the United Kingdom (Northern Ireland)⁵.

Source: ADIS and WOAH (data extraction carried out on 10 June 2022).

Figure 3: Geographical distribution at NUTS3 level of HPAI detections in Europe in seasons (A) 2016-2017 (2,781), (B) 2020–2021 (3,792) and (C) 2021–2022 (5,299) in domestic birds (red circles) and wild birds (grey coloured area), from 1 October 2016 to 10 June 2022





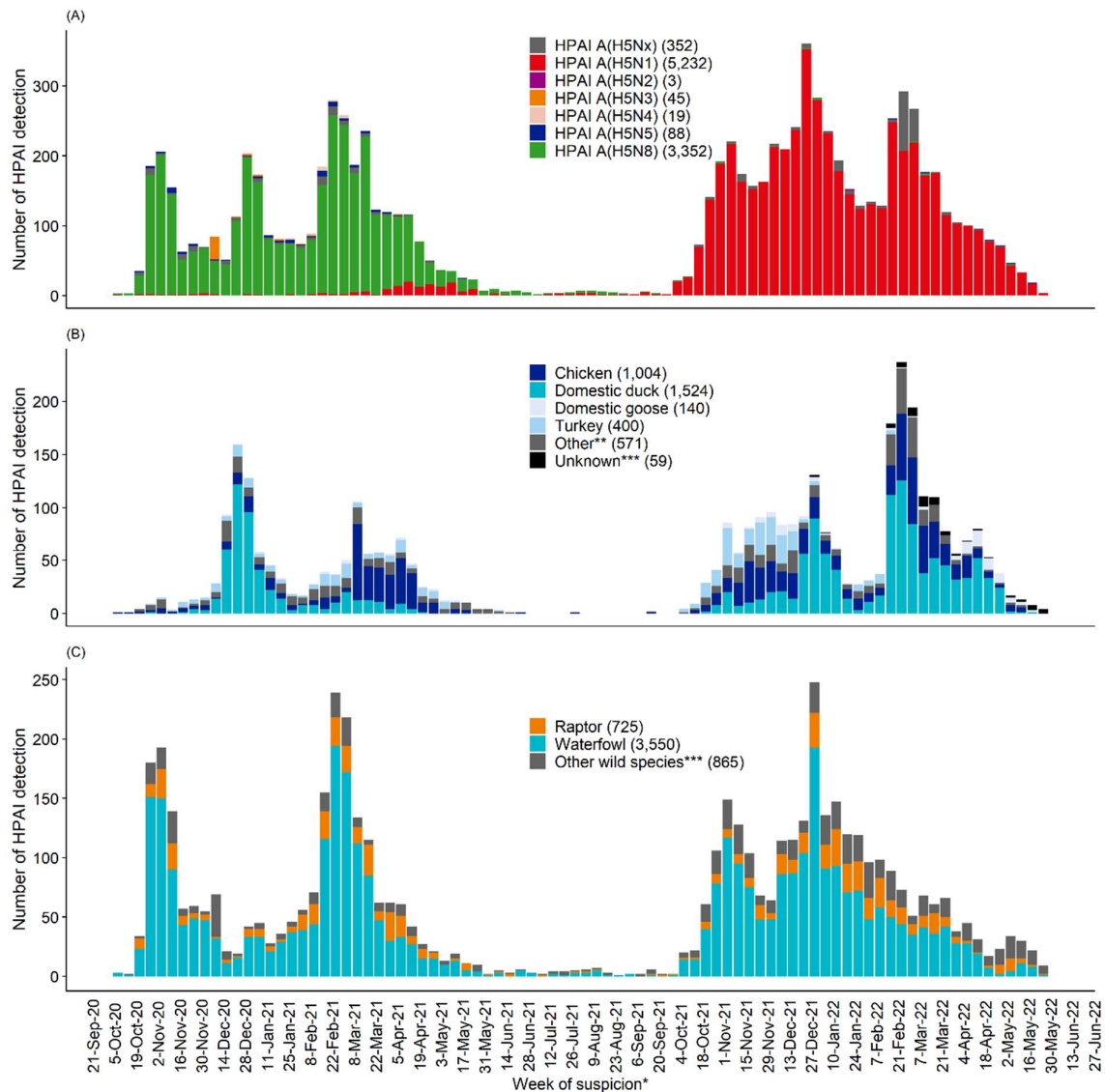


United Kingdom data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was the World Animal Health Information System (WOAH-WAHIS) for United Kingdom (excluding Northern Ireland), and ADNS/ADIS for the United Kingdom (Northern Ireland)⁵.

Note that data in June 2022 are up to 10 June.

Source: ADIS and WOAH (data extraction carried out on 10 June 2022).

Figure 4: Geographical distribution, based on available geocoordinates, of HPAI detections in Europe by month of suspicion in (A) 2016–2017, (B) 2020–2021 and (C) 2021–2022



*When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.

**Other domestic species' category contains mixed, unknown bird species, or categories different from those displayed (i.e. guinea fowl, peacock, pheasant and quail).

***Other wild species' category contains mixed, unknown bird species, or categories different from those displayed. The complete list of species by each wild bird category is reported in Table C.1 in Annex C.

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)⁵.

Source: ADNS, ADIS and WOA (data extraction carried out on 10 June 2021), EFSA.

Note that the scale of the vertical axes is specific to each category.

Figure 5: Distribution of total number of HPAI virus detections reported in Europe by week of suspicion (dates indicate the first day of the week) and (A) virus subtype (9,091), (B) affected poultry categories (3,698), (C) affected wild bird categories (5,140), from October 2020 to 10 June 2022

4.2. HPAI and LPAI detections in Europe, 16 March to 10 June 2022 (ToR 1 and ToR 2)

4.2.1. HPAI detections in poultry, other captive birds and wild birds

From 16 March to 10 June 2022, 1,181 HPAI A(H5) virus detections were notified in poultry (750), captive (22) and wild birds (410) in 28 countries in Europe, and were reported via the ADIS or WOA/WAHIS, as presented in Table 1. The timelines, virus subtypes, locations and the affected bird categories of the HPAI virus detections are presented in Figures 7, 8 and 9. This is the first time that HPAI virus has been detected in Iceland, both in poultry (1) and wild birds (16).

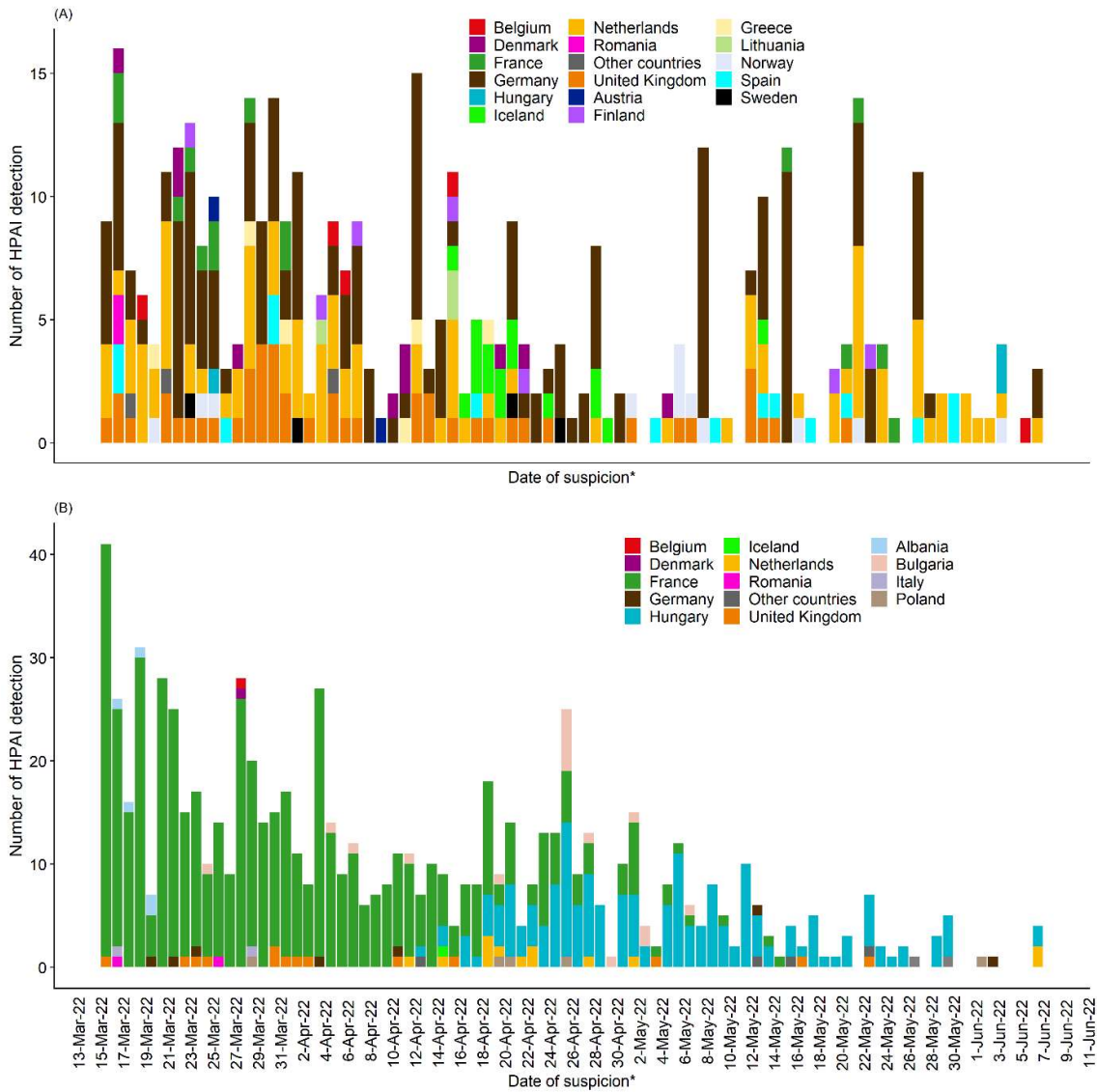
In this reporting period 68% of the overall poultry outbreaks were reported from France, 24% in Hungary, 2% in both Bulgaria and the Netherlands, 1% in United Kingdom and less than 1% in all the other affected countries. In total, 643 poultry outbreaks were notified to the ADIS as secondary in France (472), Hungary (165), Albania (3), Poland (2), Germany (1); in France, the between-farm spread was mostly observed in the domestic duck sector (232/472). Overall, approximately 11.5 million birds were culled in the HPAI-affected poultry establishments, of which 6.5 million birds in France and 2.9 in Hungary.

HPAI A(H5N1) was the only reported virus type during this reporting period, with few exceptions for A(H5N8) and A(H5N5). HPAI A(H5N8) virus was detected only in poultry in Albania and Kosovo without being detected in wild birds; the virus isolated seems closely related to A(H5N8) circulating in domestic birds in these two countries in May–June 2021. During this reporting period A(H5N5) was reported in north Norway in wild birds.

For wild birds, the highest number of HPAI detections were in Germany (158 detections), the Netherlands (98), and the United Kingdom (48) (Figure 7A, Table 1).

Characterisation of HPAI-affected poultry establishments⁶ is reported in Section 4.2.1.1; the description of the HPAI detections in wild birds is reported in Section 4.2.1.2.

⁶ According to Regulation (EU) 2016/429 'establishment' means any premises, structure, or, in the case of open-air farming, any environment or place, where animals or germinal products are kept, on a temporary or permanent basis, except for: (a) households where pet animals are kept; (b) veterinary practices or clinics. Regulation (EU) 2016/429 of the European Parliament and of the Council of 9 March 2016 on transmissible animal diseases and amending and repealing certain acts in the area of animal health ('Animal Health Law'). OJ L 84, 31.3.2016, p. 1–208.



*When the date of suspicion is not available then 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)⁵.

Source: EFSA, ADIS and WOAH (data extraction carried out on 10 June 2021).

Countries with some outbreaks in domestic birds and detections in wild birds below the median (six detections in wild birds, two outbreaks in domestic birds) are presented aggregated as 'Other countries'.

Note that the scale of the vertical axes is specific to each bird population.

Figure 6: Distribution of the highly pathogenic avian influenza detections in (A) wild birds (410) and (B) outbreaks in domestic birds (poultry and captive birds) (772), in Europe, by day of suspicion and country from 16 March to 10 June 2022

Table 1: Number of highly pathogenic avian influenza outbreaks in Europe, by country, virus subtype and affected sub-population, from 16 March to 10 June 2022. Cumulative numbers since the start of the 2021–2022 season are reported in parentheses (1 October 2021 to 10 June 2022)

Country	Captive birds		Poultry				Wild birds				Total	
	A(H5Nx)	A(H5N1)	A(H5Nx)	A(H5N1)	A(H5N2)	A(H5N8)	A(H5Nx)	A(H5N1)	A(H5N2)	A(H5N5)		A(H5N8)
Albania	-	1 (1)	-	-	-	4 (4)	-	-	-	-	-	5 (5)
Austria	-	(4)	-	-	-	-	-	2 (27)	-	-	-	2 (31)
Belgium	-	(2)	-	1 (4)	-	-	1 (6)	4 (67)	-	-	-	6 (79)
Bosnia and Herzegovina	-	-	-	-	-	-	-	(1)	-	-	-	0 (1)
Bulgaria	1 (1)	1 (2)	(8)	15 (16)	-	-	(2)	-	-	-	-	17 (29)
Croatia	-	-	-	1 (3)	-	-	-	(13)	-	-	-	1 (16)
Czechia	-	-	-	1 (19)	-	-	-	(9)	-	-	-	1 (28)
Denmark	-	1 (4)	-	(6)	-	(1)	(1)	10 (121)	-	-	(2)	11 (135)
Estonia	-	-	-	-	-	(1)	-	1 (9)	-	-	-	1 (10)
Faeroe Islands	-	-	-	-	-	-	-	(1)	-	-	-	0 (1)
Finland	-	-	-	-	-	-	-	7 (17)	-	-	(1)	7 (18)
France	-	15 (38)	29 (146)	480 (1,225)	-	-	4 (6)	11 (44)	-	-	-	539 (1,459)
Germany	-	(9)	-	7 (74)	-	-	2 (10)	156 (1,273)	(2)	-	-	165 (1,368)
Greece	-	-	-	-	-	-	-	6 (16)	-	-	-	6 (16)
Hungary	-	(3)	-	177 (290)	-	-	-	3 (30)	-	-	-	180 (323)
Iceland	-	-	-	1 (1)	-	-	-	16 (17)	-	-	-	17 (18)
Ireland	-	-	-	(6)	-	-	(2)	1 (44)	-	-	-	1 (52)
Italy	-	-	(4)	2 (313)	-	-	-	(23)	-	-	-	2 (340)
Kosovo*	-	-	-	-	-	1 (3)	-	-	-	-	-	1 (3)
Latvia	-	-	-	-	-	-	-	(2)	-	-	-	0 (2)
Lithuania	-	-	-	-	-	-	-	3 (5)	-	-	-	3 (5)
Luxembourg	-	-	-	-	-	-	-	(5)	-	-	-	(5)
Moldova	-	-	-	1 (2)	-	-	-	-	-	-	-	1 (2)
Montenegro	-	-	-	-	-	-	-	1 (1)	-	-	-	1 (1)
Netherlands	(1)	(6)	-	13 (47)	-	-	1 (37)	97 (476)	-	-	(2)	111 (569)
North Macedonia	-	-	-	-	-	-	-	(3)	-	-	-	0 (3)
Norway	-	-	-	(2)	-	-	1 (1)	4 (11)	-	8 (10)	-	13 (24)
Poland	-	-	-	3 (93)	(1)	-	-	2 (34)	-	-	-	5 (128)
Portugal	-	(7)	-	(8)	-	-	-	(5)	-	-	-	0 (20)

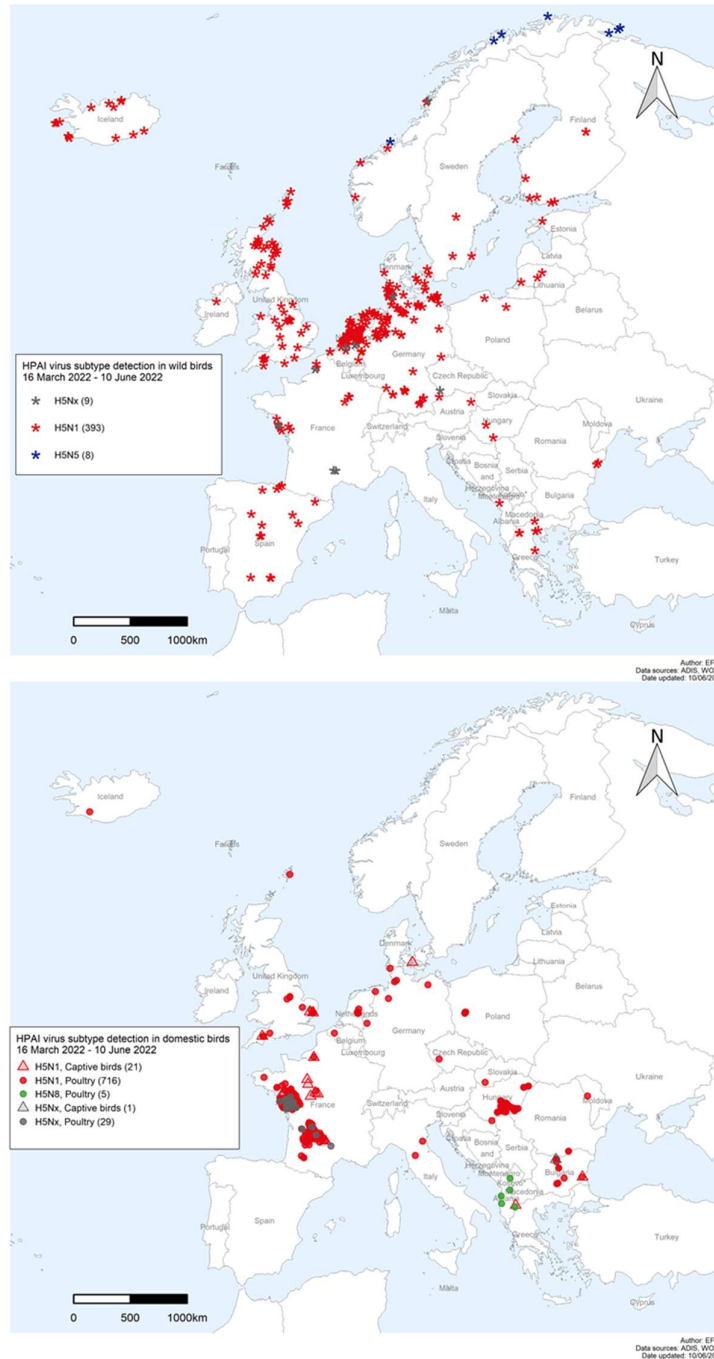
Country	Captive birds		Poultry				Wild birds					Total
	A(H5Nx)	A(H5N1)	A(H5Nx)	A(H5N1)	A(H5N2)	A(H5N8)	A(H5Nx)	A(H5N1)	A(H5N2)	A(H5N5)	A(H5N8)	
Romania	-	-	-	2 (3)	-	-	(1)	2 (15)	-	-	-	4 (19)
Slovakia	-	(2)	-	1 (4)	-	-	(1)	(6)	-	-	-	1 (13)
Slovenia	-	(37)	-	(1)	-	-	-	-	-	-	-	0 (38)
Spain	-	-	-	(31)	-	-	(2)	15 (44)	-	-	-	15 (77)
Sweden	-	(4)	-	(3)	-	-	-	4 (41)	-	-	(1)	4 (49)
Switzerland	-	(1)	-	-	-	-	-	(2)	-	-	-	0 (3)
United Kingdom	-	3 (44)	-	11 (79)	-	-	-	48 (283)	-	-	(1)	62 (407)
Ukraine	(2)	-	-	-	-	-	-	-	-	-	-	(2)
Total	1 (4)	21 (164)	29 (158)	716 (2,230)	(1)	5 (9)	9 (69)	393 (2,645)	(2)	8 (10)	(7)	1,182 (5,299)

(a): 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.

(b): 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)⁵.

‘-’ means that no HPAI outbreaks or detections were notified to ADIS or WOAH.

Source: EFSA, ADNS and WOHA (data extraction carried out on 10 June 2022).



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)⁵.

Source: EFSA, ADIS and WOA (data extraction carried out on 10 June 2021).

Figure 7: Geographical distribution, based on available geocoordinates, of highly pathogenic avian influenza detections in wild birds (410) (upper panel) and (outbreaks in poultry and captive birds (772) lower panel) reported by virus subtype in Europe from 16 March to 10 June 2022

4.2.1.1. HPAI in domestic birds

Characterisation of the HPAI-affected poultry establishments

In this section a detailed analysis of the HPAI-affected poultry establishments is presented. Due to the time needed to carry out the data collection, the outbreaks occurred later than 1 June were too close to the publishing of this report to collect the data, and in many cases, the epidemiological investigations of those outbreaks were still ongoing. Therefore, for those poultry outbreaks some of the information presented in this section were unknown at the time of publication and will be included in the next report.

The information on poultry outbreaks that occurred before the reporting period for this report but too close to the publication of the previous EFSA report (EFSA et al., 2022), i.e. from 4 to 15 March 2022, are reported in Annex A (they have been collected during this reporting period but are not described in the text of this section).

During this reporting period, from 16 March to 10 June 2022, in total, 750 poultry outbreaks were notified in 17 countries through ADIS or WOA: 509 in France, 177 in Hungary, 15 in Bulgaria, 13 in the Netherlands, 11 in United Kingdom, seven in Germany, four in Albania, three in Poland, two in Italy and Romania, one in Belgium, Croatia, Czechia, Kosovo, Iceland, Moldova and Slovakia (Figure 9). Overall, 11.5 million birds were culled in the HPAI poultry establishments.

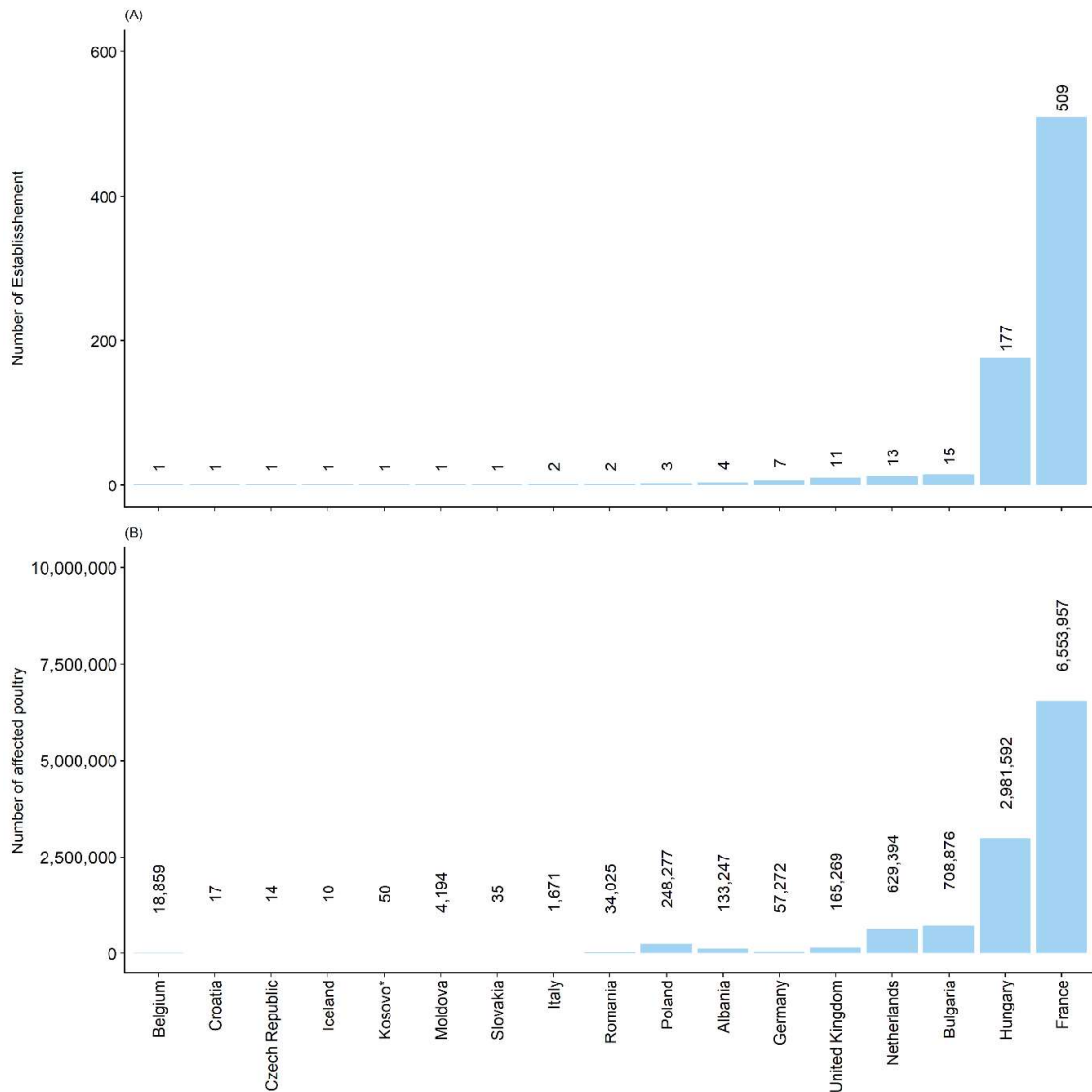
France accounted for 68% of the reported outbreaks and 57% of the birds that were culled in the HPAI establishments, followed by Hungary, accounting for 24% of the outbreaks and 26% of the birds culled, Bulgaria and the Netherlands, accounting for 2% of the poultry outbreaks each and 6% and 5% of the birds culled, respectively; all the other affected countries accounted for 1% or less of the outbreaks and 2% or less of the birds culled (Figure 9).

Compared with the previous reporting period (from 9 December 2021 to 15 March 2022), during which 1,030 outbreaks were reported by 21 affected countries, in this reporting period approximately 25% fewer outbreaks were reported, and 35% fewer birds were culled: 11.5 million birds in this reporting period vs 17.7 in the previous period (EFSA et al., 2021a). A decreasing trend in the number of outbreaks and affected birds between these two reporting periods was also observed in the previous year, 37% and 38% respectively, with 725 outbreaks (and more than 800,000 birds affected) occurring from 9 December 2020 to 15 March 2021, and 462 outbreaks (and more than 500,000 birds affected) occurring from 16 March to 10 June 2021. However, compared with the same reporting period from the 2020–2021 epidemic, the number of outbreaks had increased by 38% (750 vs 462).

Two virus subtypes were reported: as in the previous reporting period, the vast majority were A(H5N1) outbreaks (715) and A(H5N8) was reported in Albania (4) and Kosovo (1). Thirty outbreaks in France (29) and Moldova (1) have been reported as A(H5Nx), with no specification on the N-type.

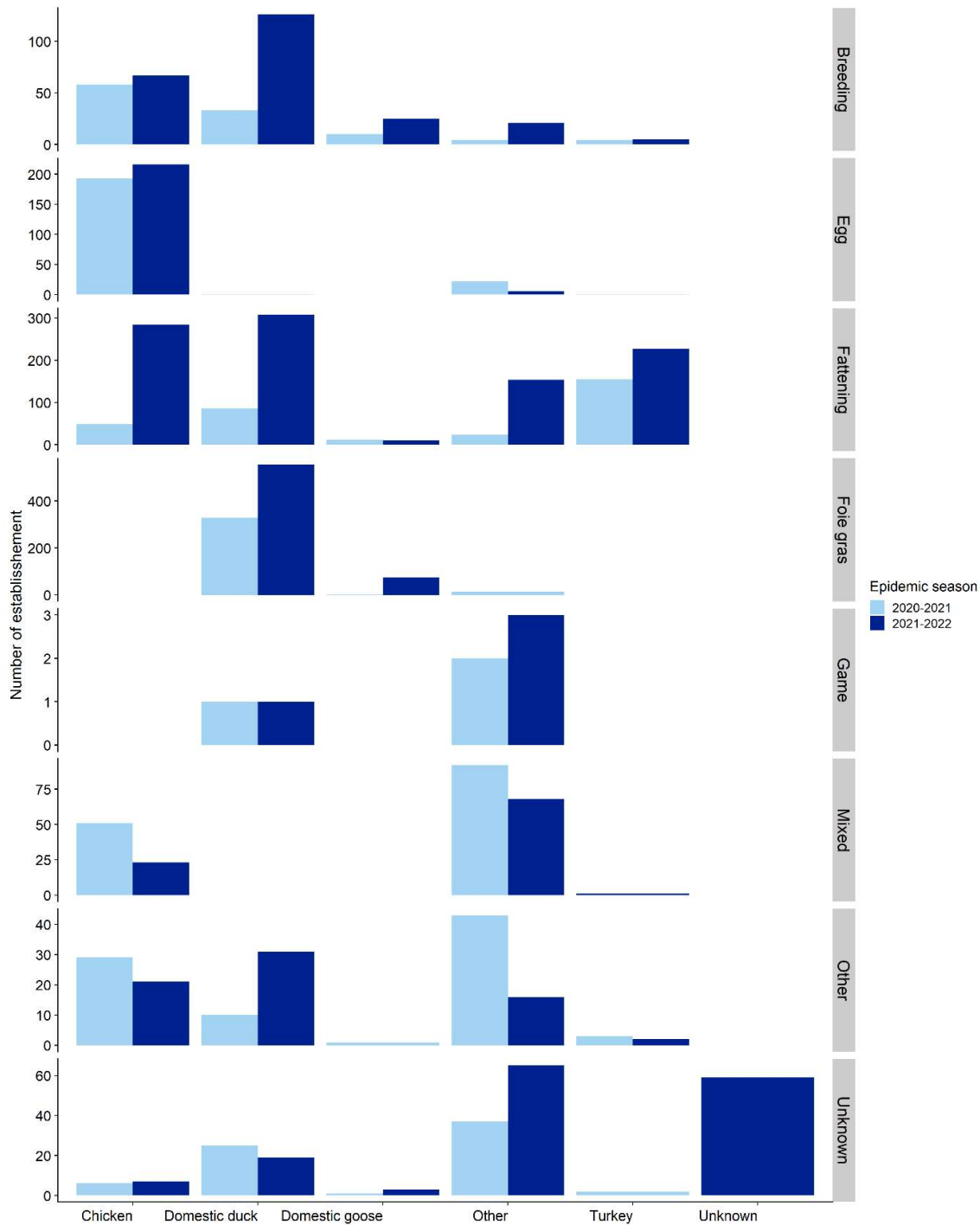
As in the previous reporting period from December to March, for the species and production type involved in the outbreaks, fattening establishments, regardless the species reared, remained the most affected category accounting for 33% of the total number of outbreaks followed by domestic ducks or domestic goose for foie gras production (31%), particularly in France and Hungary; outbreaks in broilers accounted for 13% of the outbreaks and laying hens for the 9% as observed also in the previous reporting period.

A general increase in the number of affected fattening, breeding establishments as well as foie gras and eggs production can be seen comparing this epidemic season with the previous one (Figure 9).



*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.

Figure 8: Number of (A) HPAI affected establishments and (B) number of poultry in the HPAI affected establishment in Europe between 16 March and 10 June 2022 (750)

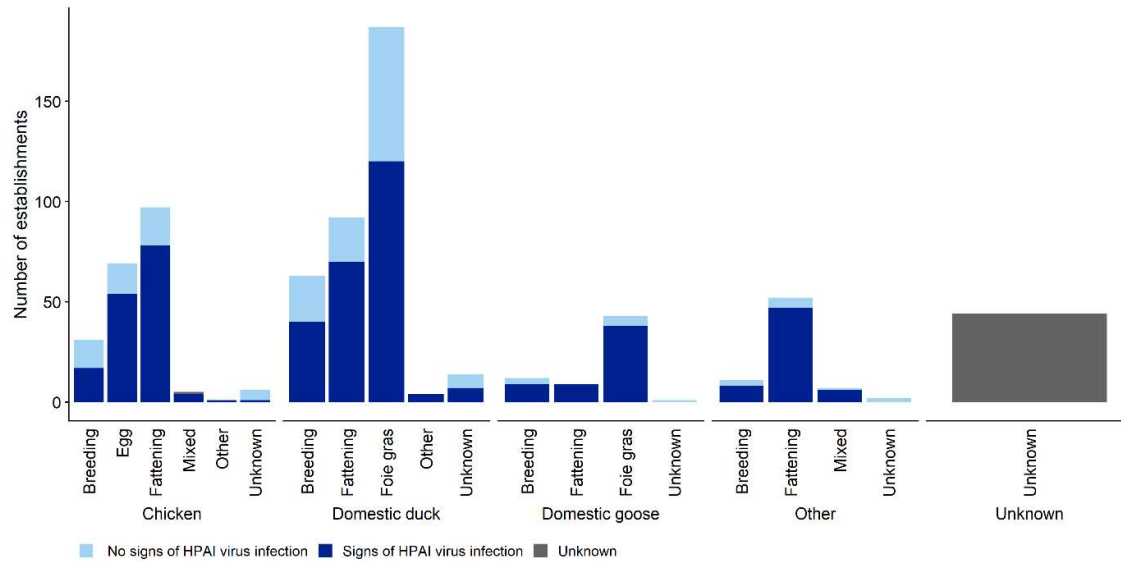


'Other' species category contains mixed, unknown bird species, or categories different from those displayed. 'Other' production type contains unknown or different production type from those displayed.

Figure 9: Number of HPAI poultry outbreaks per farmed species and production category in the 2020–2021 and 2021–2022 epidemic seasons

Out of 750 outbreaks, 709 were reported in commercial farms and 14 in non-commercial farms (the information is not known for 27 establishments). Among the primary outbreaks (95), nine were in farms with outdoor access (three in the Netherlands, one each in Czechia, Iceland, Kosovo, Moldova, Romania and Slovakia), 36 did not have outdoor access and for the remaining 50 farms the information was unknown at the time of publication of this report.

Clinical signs, mortality, or other types of signs were observed in most infected establishments, in chickens, domestic duck and goose and other species (e.g. guinea fowl, quails) (Figure 10).



'Other' species category contains mixed, unknown bird species, or categories different from those displayed. 'Other' production type contains unknown or different production type from those displayed.

Figure 10: Number of HPAI poultry outbreaks with and without reporting of signs of HPAI infection (either mortality, clinical signs, drop in feed/water intake or drop in egg production) per poultry species and production type, between 16 March and 10 June 2022 (750)

HPAI A(H5N1)-affected poultry establishments in Belgium

On 29 March 2022 one HPAI A(H5N1) outbreak was notified on a chicken farm in the Vlaanderen region. The affected farm was keeping commercial breeding chickens. Birds showed clinical signs including drop in feed and water intake and increase in mortality. The most likely source of infection was thought to be direct contact with wild birds although the birds had no outdoor access. No data were available on the number of exposed people. The characteristics of the affected establishment and species reared are presented in Annex A.

HPAI A(H5N8)-affected poultry establishments in Albania

Between 21 and 26 March 2022 one primary and three secondary outbreaks of HPAI A(H5N8) were notified in Albania. The primary outbreak occurred in Durrës, whereas the three secondary outbreaks occurred in Korçë, Dibër and Fier. The primary outbreak was in a commercial establishment, two of the secondary in non-commercial establishments and for the fourth establishment there was no information for holding type. Information on species and clinical signs were available for three of the farms. All farms kept chicken, the commercial was used for egg production and the other two for mixed production. The farms all reported increased mortality and clinical signs, including a drop in feed and water intake. The commercial farm with egg production also reported a drop in egg production.

The source of infection in the establishments had not been determined at the time of publication of this report, and whether the farm had outdoor access and the number of exposed people it is not known. The characteristics of the affected establishments and species reared are presented in Annex A.

HPAI A(H5NX)-affected poultry establishments in Bulgaria

Between 16 March and 1 June 2022, 15 outbreaks of HPAI A(H5N1), all primary, were notified in Bulgaria. The outbreaks occurred in Pleven (11), Gabrovo (2), Burgas (1) and Stara Zagora (1). All except one of the establishments were commercial. The commercial farms kept chickens for egg production (4), chickens for fattening (2), chickens for breeding (1), domestic ducks for fattening (4) and mulard ducks for foie gras (3). The backyard farm kept chicken for mixed production. The

establishments with chickens and domestic ducks reported an increased mortality but there were no other clinical signs. The farms with mulard duck didn't report increased mortality or any other clinical signs.

None of the farms had outdoor access. The most likely source of introduction of the virus on eight of the farms was indirect contact with wild birds. On the remaining farms the most likely source of introduction was indirect contact with poultry, as they had the same owner or another connection to at least one other infected farm. The numbers of exposed persons were unknown.

The characteristics of the affected establishments and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Czechia

On 20 April 2022 one HPAI A(H5N1) outbreak was notified in the Plzeňský region. The outbreak occurred in a non-commercial holding with outdoor access and the way of transmission is thought to be either direct or indirect contact with wild birds. The farm kept chickens for mixed production. On the farm increased mortality and clinical signs were present. In total, two persons were potentially exposed to the virus in the outbreak. The characteristics of the affected establishment and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in France

Between 16 March 2022 and 1 June 2022 442 HPAI A(H5N1) and 26 HPAI A(H5NX) poultry outbreaks were notified in France. In total, 35 were primary and 433 were secondary outbreaks. The outbreaks were detected in the following regions: Pays de la Loire (293), Nouvelle-Aquitaine (122), Occitanie (42), Bretagne (5), Auvergne-Rhône-Alpes (4) and Centre- Val de Loire. All outbreaks except one were on commercial establishments.

The most common type of farmed species, for which information was available (452/468), was domestic duck for foie gras (126/452), breeding (55/452) and fattening (48/452) as well as broiler (90/452), laying hens (35/452) and breeding chickens (25/452). Affected establishments with other types of species included fattening turkey (25/452), breeding turkey (6/452), fattening guineafowl (11/452), breeding guineafowl (1/452), fattening domestic goose (3) and one for foie gras and fattening. Furthermore, there were in total three establishments with quails and two with pigeons. For 16 establishments the species reared was not specified and for 15 the type of production was not specified.

Information on increased mortality was available for 307 farms and information on unspecified clinical signs were available for 342 farms. Of the farms that kept chicken where information was available (81/150), the majority reported increased mortality (78/81) as well as clinical signs (93/100). Of the farms that kept domestic duck where information was available, the majority reported clinical signs (153/189) as well as increased mortality (95/163). No information about outdoor access, the most likely source of virus introduction and the number of people exposed to the virus was available at the time of publication of this report.

The characteristics of the affected establishments and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Germany

Between 16 March and 13 May 2022, six primary and one secondary outbreak of HPAI A(H5N1) were notified in the regions of Schleswig-Holstein (3), Saxony (1), Mecklenburg-Western Pomerania (1), Lower Saxony (1) and North Rhine-Westphalia (1). All except one of the affected farms were commercial. The commercial farms were mono-species farms with laying hens, breeding domestic geese and fattening turkeys. The non-commercial farm kept hens and domestic ducks.

All farms reported increased mortality as well as clinical signs except from one turkey and one domestic geese farm. There is no information about clinical signs or mortality of the domestic ducks kept in the non-commercial farm. It is unknown if the animals had outdoor access. The most likely source of introduction for all of the primary outbreaks is unknown. In the secondary outbreak the most likely source of infection is indirect poultry contact.

Data related to the number of exposed people were not available at the time of publication of this report. The characteristics of the affected establishment and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Hungary

Between 16 March 2022 and 1 June 2022, 10 primary and 162 secondary outbreaks of HPAI A(H5N1) were notified in four regions in Hungary: Bács-Kiskun (132), Csongrád-Csanád (22), Békés (14), and Szabolcs-Szatmár-Bereg (4).

Most of the outbreaks were detected in commercial establishments (170/172) and two in non-commercial establishments with mixed poultry species.

Of the commercial establishments affected, the type of production was as follows: mulard duck for foie gras (50), domestic goose for foie gras (42), domestic duck for fattening (34), domestic goose for fattening (8), laying hens (14), domestic goose for breeding (7), broilers (4), domestic duck for breeding (4), turkey for fattening (4), chicken for breeding and one farm each for pheasant breeding and mixed ostrich production.

Increased mortality was detected in chicken (19/21), domestic goose (48/54), turkey (3/4), mulard duck (31/50), domestic duck (25/37) and ostrich (1/1) establishments.

Clinical signs were not detected in any of the establishments with chicken or the farm with ostriches. For the other species, clinical signs were reported in domestic goose (45/58), domestic duck (25/38), turkey (1/4) and pheasant (1/1). Dropped egg count was present in most chicken farms (9/12) and domestic goose farms (6/7), where it was applicable. On the backyard farm holding domestic guineafowl and domestic pigeon, these species showed no signs of clinical infection.

None of the commercial or non-commercial establishments had outdoor access. The most likely source of infection was thought to be indirect contact with poultry for the secondary outbreaks and in the primary outbreaks indirect contact with wild birds.

No data were available on the number of exposed people in the HPAI outbreaks in Hungary. The characteristics of the affected establishments and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Iceland

On 4 May 2022, one outbreak of HPAI A(H5N1) in the region of Suðurland on a backyard farm was notified. The farm kept chicken and they reported increased mortality and unspecified clinical signs. The poultry had outdoor access and the most likely source of introduction was indirect contact with wild birds as a raven was found dead on the premises six days before the outbreak started. The raven was later found to be positive for HPAI A(H5NX). The number of exposed persons in the outbreak was two. The characteristics of the affected establishment and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Italy

Between 16 March and 10 May 2022 two HPAI A(H5N1) outbreaks were notified in Toscana and Emilia-Romagna regions. The outbreak in Toscana was in a non-commercial holding with laying hens and domestic pigeons. The chicken had an increased mortality and no other clinical signs, whereas the pigeons had no clinical signs at all. The outbreak in Emilia-Romagna was on a commercial farm with domestic duck and 'other species', including ornamental birds, that in many cases had access to the outside. The route of introduction of the virus remains unknown.

Data from epidemiological investigations, and the number of exposed people were not available at the time of publication of this report. The characteristics of the affected establishment and species reared are presented in Annex A.

HPAI A(H5N8)-affected poultry establishments in Kosovo²

On 18 May 2022, one outbreak of HPAI A(H5N8) in the region of Gjakova in a non-commercial farm was notified. The farm kept chicken for mixed production. No information about clinical signs or mortality has been reported. The animals had outdoor access and the most likely source of introduction is unknown.

Data from epidemiological investigations and the number of exposed people were not available at the time of publication of this report. The characteristics of the affected establishment and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Moldova

On 14 May 2022, one outbreak was notified in a backyard farm in the Unghani region. The virus type was unknown at the time of writing this report. The farm kept laying hens and domestic ducks and domestic geese for mixed production. In all the species clinical signs, increased mortality, drop in feed and water intake, and decreased egg production was reported. The farm had outdoor access and the most likely source of infection was indirect contact with wild birds. The number of exposed people was 25. The characteristics of the affected establishments and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in the Netherlands

Between 12 April 2022 and 2 May 2022, 11 A(H5N1) outbreaks were notified in commercial establishments in Gelderland (11).

The establishments were farming chickens (9/11) either for egg production or breeding, or domestic duck (2) for breeding or fattening. Clinical signs were detected in all farms, increased mortality was detected in all but one, drop in feed and water intake in eight and decrease in egg production in two farms.

Three of the 11 farms had outdoor access. The most likely source of virus introduction is unknown. No data were available on the number of exposed people in the HPAI outbreak.

The characteristics of the affected establishments and species reared are presented in Annex A.

HPAI A(H5N1) and A(H5N2)-affected poultry establishments in Poland

Between 16 March 2022 and 10 May 2022, three HPAI A(H5N1) outbreaks were detected in the region of Wielkopolskie. One of the outbreaks were primary and two were considered secondary.

All the outbreaks were in commercial farms. Two of the farms kept turkeys for fattening and one chickens for egg production. All farms reported presence of clinical signs and increased mortality. The turkey farms also reported a drop in feed and water intake.

None of the farms had outdoor access. For all of the outbreaks the most likely source of infection was indirect contact with poultry, either by feed transport (primary) or infection by air during eradication in a neighbouring outbreak.

In total 6 people were exposed to the virus in these outbreaks.

The characteristics of the affected establishments and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Romania

Between 16 March and 10 May 2022, two outbreaks of HPAI A(H5N1) were notified. Both farms were in Giurgiu. One of the farms kept chickens for egg production commercially. The other farm was a non-commercial farm keeping chicken for mixed production, common quail for egg production, as well as pheasants, domestic ducks and domestic guinea fowl for fattening. The commercial farm with chicken noted clinical signs, increased mortality and a drop in feed and water intake, and egg production. The non-commercial farm noted clinical signs and a drop in feed and water intake and production in all species. Increased mortality was only seen in chickens.

The animals in the non-commercial farm had outdoor access, whereas the animals in the commercial farm did not. The most likely routes of infection are direct contact with wild birds and indirect contact with birds due to poor biosecurity. The number of exposed people was four in total. The characteristics of the affected establishment and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Slovakia

On 23 May 2022, one HPAI A(H5N1) outbreak was notified in a backyard farm in the region of Nitriansky. The farm kept chicken for egg production. Clinical signs included increased mortality and drop in feed and water intake. The source of the virus is unknown but, as the animals had outdoor access, this was probably due to direct or indirect contact with wild birds.

No data were available on the number of exposed people. The characteristics of the affected establishment and species reared are presented in Annex A.

Information extracted from the scientific literature

There were two studies on the phenotype of HPAI viruses in poultry in Europe. Smietanka et al. (2022) described the epidemiology of the HPAI H5N8 virus, clade 2.3.4.4b, infection in Poland in 2021/2022 in poultry of different species and purposes: chicken layers (both breeders and hens laying eggs for consumption), meat turkeys, fattening ducks, breeder geese, fattening geese, broiler chickens and breeder ducks. The disease usually began with the drop in feed and/or water consumption that was accompanied (or quickly followed) by increased mortality and a drop in egg production (the latter not always observed in hens at the onset of clinical problems), depression, on some occasions shortness of breath, other respiratory signs (conjunctivitis, nasal discharge, sneezing) and diarrhoea. The neurological signs were very clearly seen in fattening ducks and included a broad spectrum of clinical signs including: ataxia, tremors, lying on the back and pedalling with the legs, torticollis and paralysis. Breeder ducks usually did not display obvious clinical signs, and the drop in feed/water intake and decreased production of eggs (by approximately 50%) were the only observed abnormalities. (Engelsma et al., 2022) determined the intravenous pathogenicity index (IVPI) of an isolate of HPAI H5N8 virus, clade 2.3.4.4b, from an infected poultry farm in the Netherlands in 2020. In six-week-old White Leghorn chickens, the IVPI (2.76) was higher than in 6-week-old Pekin ducks (1.74). Both disease onset and mortality had been observed earlier in chickens compared with ducks in the IVPI experiments. All 10 chickens died within 3 days, whereas two ducks survived the 10-day experiment, and daily probability of mortality was significantly higher in chickens than in ducks. Together, these results indicate that the clinical signs of these HPAI H5N8 virus infections in poultry did not substantially differ from those typically described for HPAI, and that the pathogenicity was higher for chickens than for domestic ducks.

4.2.1.2. HPAI in wild birds

Between 16 March and 10 June 2022, 410 HPAI virus detections in sick, dead or hunted wild birds were reported to the ADIS and WOA by EU/EEA and United Kingdom (Figure 12), which is still a substantial number, although a marked decline since the previous reporting period (from 9 December 2021 to 15 March 2022): 1,622 detections. The HPAI detections in wild birds were concentrated in northern Germany, southern Denmark, and the Netherlands, as well as on the east coast of Scotland (UK) (Figure 12). The overall geographical range of HPAI detections in wild birds was wide: north to northern Norway, east to eastern Romania, south to Greece and Spain, and west to Iceland (Figure 8B). Throughout most of the range, HPAI detections consisted mainly of waterbirds interspersed with smaller numbers of raptors and other species (Figure 12). Exceptions were the coast of Norway, and south-east Europe (Greece, Romania, Montenegro), where HPAI detections were reported only in raptors (white-tailed eagles) and species other than waterbirds and raptors. White-tailed eagles may become infected locally or carry the virus from a more distant location, since they are partial migrants. In both cases, they would most likely have become infected by feeding on contaminated carcasses of wild birds. In Norway, HPAI A(H5N5) was detected from the end of March to the end of May mainly in white-tailed eagles (10); only two detections involved gulls and one detection involved a raven. The raptors were all found dead and reported via passive surveillance as well as other bird species that were found dead/sick in the same time period and that tested negative (a total of 122 birds consisting mainly of black-headed gulls, common gulls, greylag geese, mallards, and common guillemots). In the past weeks, a number of sick (neurological signs) and dead northern gannets have been noticed along the North Sea and along the coastline of Rogaland county; laboratory results are pending at the moment of publication of this report. On the Iberian peninsula, HPAI detections in the months January to June 2022 were reported most frequently in white storks (10 of 34 detections from Spain, 1 of 2 detections from Portugal) and in greylag geese (9 of 34 detections from Spain; 0 detections from Portugal); it is not clear what the role of these two species was in the epidemiology of HPAI on the Iberian peninsula.

This is the first time that HPAI detection in wild birds has been reported from Iceland, where, during this reporting period, in total, 16 A(H5N1) detections were reported in waterfowl (two greylag goose, two pink-footed goose and one barnacle goose) and in other wild species (six northern gannet, two great black-backed gull, two great skua and one black-headed gull). Also, a white-tailed eagle was found dead beginning of October 2021 and confirmed as A(H5N1) virus infected in April 2022; of note, the virus identified was closely related to the HPAI A(H5N1) viruses that have been detected in North America since December 2021. The passive surveillance scheme leading to the reporting of, in addition to the white-tailed eagle, the first wild bird case in 2022 (pink-footed goose) was the same also applied in March 2017 and in March 2021 (active surveillance is not currently in place). This finding, together with the first poultry outbreak that was confirmed few days later received attention from the Icelandic

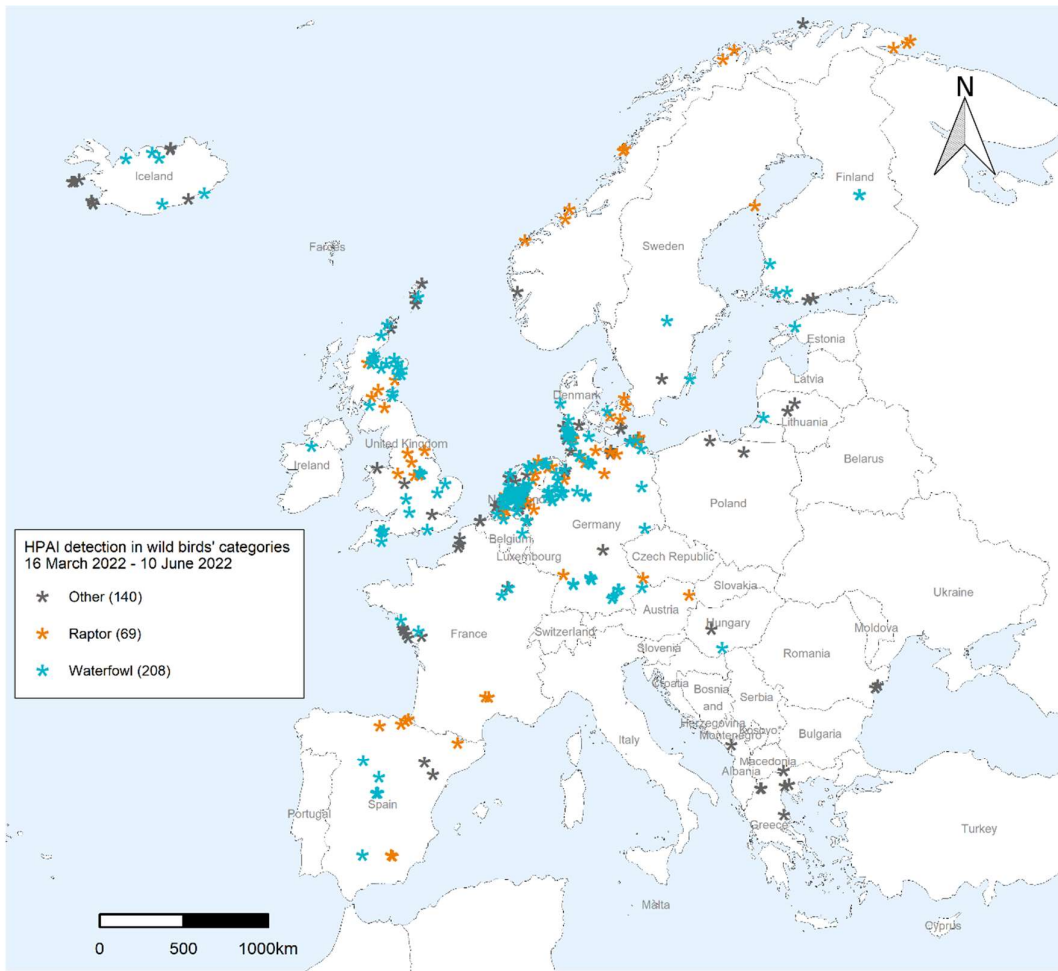
media and raised awareness among the public leading to a marked increase in the reporting of sick and dead wild birds. In the south-west area, an extraordinary die-off of northern gannets was observed, with sick animals found in private gardens, on streets and other very unusual places away from the shore; HPAI was detected in some of the samples taken.

The overall temporal pattern showed that the decline in HPAI detections, which started in January 2022 of the previous reporting period, continued to June 2022, but not to zero: HPAI detections in wild birds were reported to the end of the current reporting period (Figure 5C).

At least 45 wild bird species were involved: at least 11 waterfowl species (206 detections), 9 raptor species (68 detections), and 25 other wild bird species (136 detections) (Figure 11 and Table C.1). In the same period of the previous year (16 March to 10 June 2021), at least 34 wild bird species were involved: at least 11 waterfowl species (332 detections), 9 raptor species (107 detections), and 14 other wild bird species (48 detections) were involved (Table C.2). This suggests that in the current reporting period HPAI A(H5) virus was infecting and causing mortality in a wider range of non-raptor and non-waterfowl wild bird species than observed in the same period of the previous year. The host range may be even wider than these data suggest, as a large proportion of wild birds was not identified to species in the current reporting period (181 of 407 detections: 44%) compared with the same period last year (144 of 487 detections: 30%). The number of HPAI virus detections was 0.84 times lower than in the same period last year (16 March to 10 June 2021), when there were 487 detections. This difference is mainly due to the lower number of HPAI detections in waterfowl (206 compared with 332) and raptors (68 detections, compared with 107 detections). Conversely, the number of other bird species was substantially higher (136, including several colonial breeding birds such as Dalmatian pelicans, northern gannets, and sandwich terns, compared with 48). The occurrence of HPAI (H5) die-offs in several species of colonial breeding birds in the spring of 2022—for northern gannets and sandwich terns for the first time—and not in previous springs may be related to the more widespread presence of HPAI (H5) virus in wild bird populations, and longer persistence this spring leading to overlap with the timing of breeding of the affected species.

The complete list of HPAI detections by wild bird order and species for the time periods from 16 March to 10 June 2022 is presented in Figure 13. New species in which HPAI was detected were bearded vulture (3), griffon vulture (4), Eurasian spoonbill (1), European greenfinch (1), great blue heron (1) and Sandwich tern (3).

It is important to underline that the numbers provided are much smaller than the number of wild birds that have died from HPAI A(H5) infection. Of particular concern during this reporting period are large die-offs of several species of colonial breeding birds associated with HPAI A(H5). In the Netherlands, HPAI-associated mortality was reported in several sandwich tern colonies, including 2,500 dead birds collected from a breeding colony of 6,400 sandwich terns on the island of Texel (Vogelbescherming, online); HPAI-associated mortality also was reported in breeding colonies of Eurasian spoonbills, common terns, and black-headed gulls (Trouw, online). In the United Kingdom, HPAI-associated mortality of many thousands of northern gannets has been reported in several breeding colonies on islands off the coast of Scotland, including Bass Rock, which is the world's largest gannet colony with over 150,000 birds. In addition, HPAI-associated mortality of several hundred great skuas has been reported at multiple breeding colonies on the Shetland Isles and on St Kilda (BBC, online). In Greece, 1,143 carcasses of adult Dalmatian pelicans were collected from the world's largest breeding colony of this species on Lesser Prespa Lake, associated with a HPAI outbreak in February and March 2022 (AEWA, online). There was a contemporaneous outbreak in Dalmatian pelicans on Skadar Lake, Montenegro, where 26 carcasses were found, comprising 10-12% of the breeding population (Vizi, 2022). An unusual number of mortality events (for this period of the year) are also being observed since mid-May 2022 and are still ongoing along the Channel coast in France, initially in its north-eastern part near the Belgian border – in the 'Baie de Somme' – and now extending westward to Cotentin (along more than 500 km of shoreline): European herring gulls were most commonly reported, with up to hundreds of birds, including juveniles, found dead. Other seabird species – *Larus sp.*, common terns and Sandwich terns – were also involved to a lesser extent (Anne Van de Wiele, French Biodiversity Agency, personal communication).



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 10/06/2022

Source: EFSA, ADIS and WOAH (data extraction carried out on 10 June 2022). 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 11: Geographical distribution, based on available geocoordinates, of highly pathogenic avian influenza detections in wild birds' categories in Europe, by species category, from 16 March to 10 June 2022

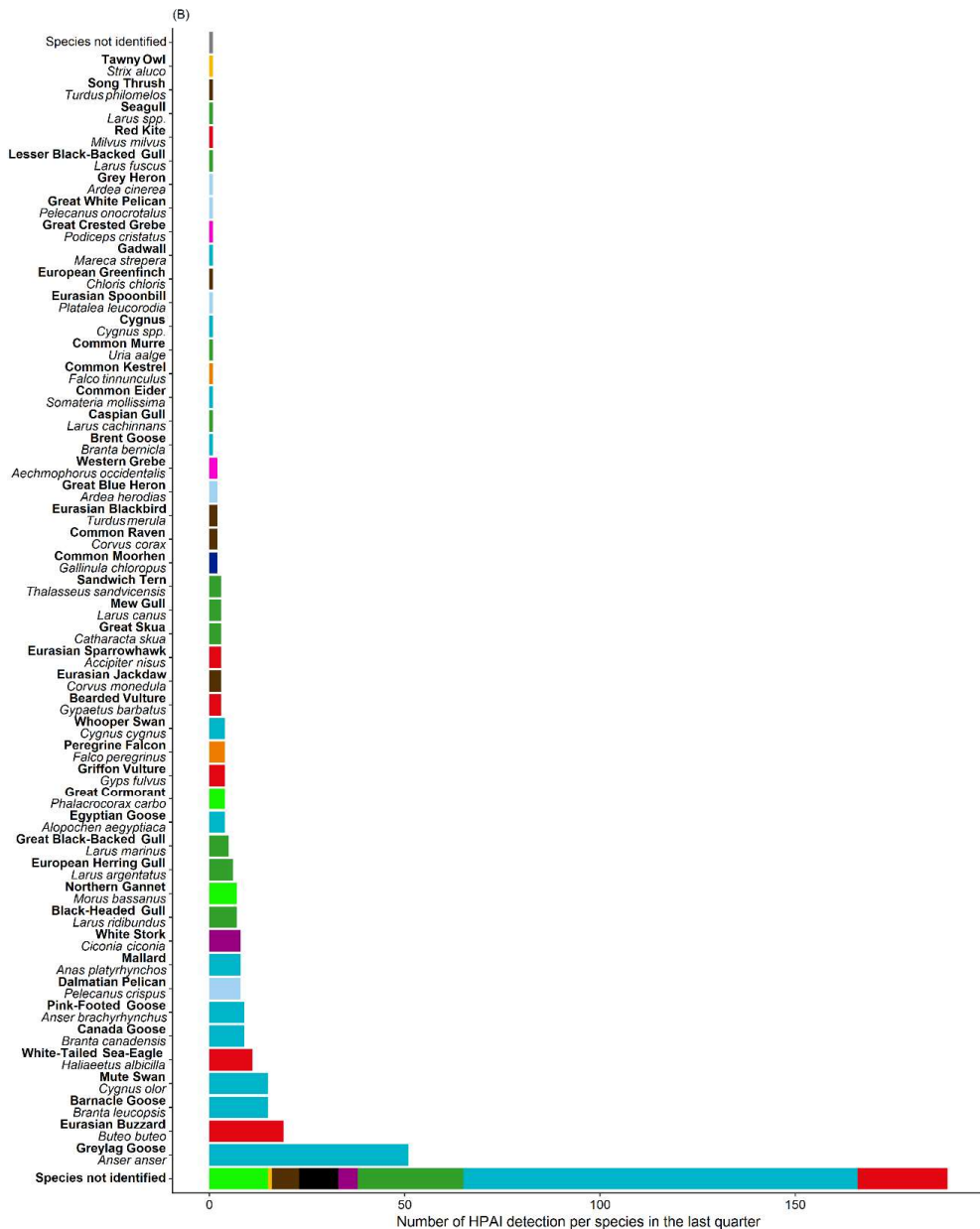
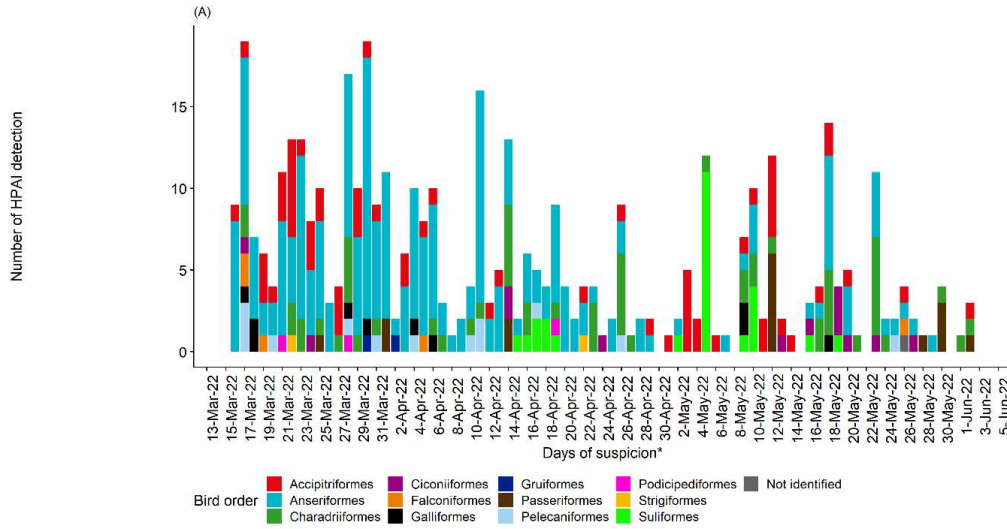


Figure 12: Number of reported detections of highly pathogenic avian influenza virus A(H5) in wild birds by (A) bird order and week of suspicion and (B) wild bird species in the EU/EEA and GB, from 16 March to 10 June 2022 (third quarter)

Information extracted from the scientific literature

Caliendo et al. (2022) studied an outbreak of HPAI H5N8 virus in a wildlife rehabilitation centre in the Netherlands that occurred in the autumn to winter of 2020–2021. Clinical signs compatible with HPAI included lethargy, head shaking, body tremors, torticollis, abnormal gait and corneal opacity. The following species showed these clinical signs: barnacle goose, domestic goose (*Anser anser domesticus*), greylag goose, mute swan, Egyptian goose, and mallard. Peters et al. (2022) described mortality from natural HPAI H5N1 virus infection, clade 2.3.4.4b, in a wood pigeon from Germany in 2022. Postmortem findings were dominated by acute lymphohistiocytic meningoencephalitis, neuronal necrosis in cerebrum and brainstem, and necrotising pancreatitis, associated with virus infection. These findings are unusual because birds belonging to the family Columbidae (pigeons and doves) were previously not found to play a role in the epidemiology of HPAI outbreaks, and any suspect cases in these species should be tested for avian influenza. Bevins et al. (2022) detected HPAI H5N1, clade 2.3.4.4.b, in the period December 2021 to February 2022 in the USA in 292 individual birds of following species American wigeon, all ducks belonging to the family Anatidae: American wigeon, mallard, American black duck, gadwall, northern shoveler, blue-winged teal, American green-winged teal, northern pintail, and wood duck. Given that these birds were apparently healthy before being shot dead by hunters or live-trapped, infection with this virus did not causing clinical signs. The studies described above confirmed that the clinical effects of infections with these HPAI viruses ranged from absence of clinical signs to death, and that we need to be alert for the infection in wild bird species that have not been involved in HPAI epidemiology in the past.

4.2.2. 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 enzootic 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 WHO (WHO, 2020a) 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).

Global overview of HPAI viruses of the A(H5) subtype of clade 2.3.4.4b

Since October 2020, multiple reassortant A(H5) viruses of clade 2.3.4.4b belonging to the A(H5N8), A(H5N1), A(H5N2), A(H5N3), A(H5N5), A(H5N4) subtypes have emerged in Europe. Since then, the A(H5N1) of clade 2.3.4.4b has also been identified in several Asian, African and North American countries. In West Africa, an A(H5N1) virus related to the 2020–2021 European viruses was reported in January 2021 (Lo et al., 2022). In December 2021, North America announced the first detection of the A(H5N1) virus strongly related to the A(H5N1) identified in Northern Europe during the 2020–2021 epidemic season (Bevins et al., 2022).

Genetic characterisation of HPAI viruses of the A(H5) subtype circulating in Europe

The topology of the HA phylogenetic tree shows that all the genetically characterised HPAI viruses collected since the beginning of the current epidemic wave (October 2021 to May 2022) in Europe and Russia fall within clade 2.3.4.4b. Sequences were generated from viruses collected from 23 EU Member States, United Kingdom, Norway, Moldova, Kosovo, Iceland and Russia (available in GISAID on 16 June

2022, provided by the National Reference Laboratories (NRL) or generated by EURL). To assess the number and variety of co-circulating genotypes, each defined by a unique gene composition, the eight gene segments were analysed phylogenetically.

At least 31 different A(H5) genotypes belonging to 4 subtypes that originated from multiple inter- and intra-subtype reassortment events were detected since October 2021: 28 A(H5N1), one A(H5N8), one A(H5N5), and one A(H5N2). These genotypes are likely to be the result of novel virus incursions during the autumn migration of wild birds or of local reassortment events, except for three of them – one A(H5N1), one A(H5N8) and one A(H5N5) – for which the genetic clustering indicates an persisting circulation in Europe since the 2020-2021 epidemic wave. Specifically, the A(H5N1) and A(H5N8) genotypes had circulated persistently in several European countries, whereas the A(H5N5) genotype was detected only in Norway. The A(H5N2) genotype was detected only in Poland and Germany prior to this reporting period.

France and Hungary are the two countries that have reported the highest number of A(H5N1) outbreaks in poultry since October 2021. Based on the analysis of available sequences from a selected number of A(H5N1) viruses detected since November 2021 in France, at least eight distinct genotypes have been circulating in the country: all genotypes were detected in wild birds and only four of them were also characterised from poultry outbreaks. From mid-December 2021 to early March 2022, at least six introductions of HPAI A(H5N1) viruses occurred in poultry in southwestern France. From mid-February to early May 2022, a distinct episode of poultry outbreaks occurred in western France, caused by a single genotype that differed from the ones previously detected in southwestern France. A probably unique virus incursion took place, in a single or few poultry establishments in a localised sector in western Vendée, followed by an extremely fast diffusion within the same region, Pays-de-la-Loire, and to immediate neighbouring areas. Further longer-distance spread of directly related viruses also occurred, resulting in sporadic detections in Brittany and generating a third bout of poultry outbreaks between mid-March and mid-May 2022, which spread from a single primary incursion in a previously HPAI virus infection-free central western area (Cantal/Lot).

Similarly, the investigation into the A(H5N1) viruses, which have caused multiple outbreaks in poultry in Hungary since November 2021, indicated the occurrence of multiple distinct virus introductions into the domestic population. Based on the available genetic information all the recent outbreaks seem to be caused by a single virus strain.

Complete genome sequences of a HPAI avian influenza A(H5N1) virus collected from a lynx in Finland in February 2022 were obtained. This virus had a high genetic identity with the viruses circulating in wild birds in the country. As in previously identified transmission events to mammals (EFSA et al., 2022), this avian virus possesses adaptive markers that were associated with an increased virulence and replication in mammals (Manzoor et al., 2009; Kim et al., 2010; Herfst et al., 2012; Suttie et al., 2019).

To date, mutations recognised as being associated with mammalian adaptation have only been sporadically identified in the analysed viruses from avian species collected since October 2020, as previously reported (EFSA et al., 2021b). In the currently circulating A(H5N1) viruses, mutations in the HA protein that are associated with increased binding to human-type receptors were identified in all the analysed viruses (S137A H3 numbering) or in a few (one or two) of them (D101N, S159N/T160A and T192I, H3 numbering) (Yang et al., 2007; Su et al., 2008; Wang et al., 2010). Mutations that are associated with increased polymerase activity in mammalian cells (NP-N319K and PB2-K482R) have been detected in a few (less than 14) A(H5N1) viruses identified in wild birds (Gabriel et al., 2005; Gabriel et al., 2008; Yamayoshi et al., 2014; Yamayoshi et al., 2018). Moreover, mutations associated with increased resistance to antiviral drugs were identified in the neuraminidase or ion channel proteins of five A(H5N8)/A(H5N1) viruses collected from poultry.

Genetic characterisation of the A(H3N8) virus responsible of a human case in China

On 26 April, the first human infection caused by an A(H3N8) subtype was reported in Henan province, China. Before the onset of the symptoms, the patient had contact with chickens at home and the presence of wild ducks nearby the home was reported. Analysis of the complete genome indicated that the A(H3N8) virus had originated from reassortment events among avian A(H3Nx) viruses of the Eurasian lineage, avian A(HxN8) viruses of the American lineage and the A(H9N2) viruses endemically circulating in poultry in China. The virus possesses the amino acid mutation E627K in the PB2 protein, which is associated with adaptation and increased virulence in mammals. Moreover, all the three sequences available in the GISAID database show a mixture of two aminoacids (G/S) at position 228 of

the HA protein (offlu, 2022). 228S is typical of seasonal human A(H3N2) viruses and is considered a 'hallmark' mutation of the H3 subtype to adapt to the human host (Connor et al., 1994).

4.3. Human cases reported and transmission to other mammal species due to clade 2.3.4.4 A(H5Nx) viruses detected in Europe

Since 16 March 2022 as of 10 June 2022, data from four countries (Czechia, Iceland, Moldova and Romania) have been reported on the total number of people exposed to infected birds (e.g. during culling activities). They reported, in total, 39 exposed people.

In April 2022, a human infection with a A(H5N1) virus was reported linked to the ongoing outbreaks of A(H5N1) clade 2.3.4.4b in poultry and wild birds in the USA (CDC, online-f). The person was involved in culling activities and reported fatigue symptoms but did not require specific treatment. Earlier human infections with A(H5N1) or A(H5N8) viruses of clade 2.3.4.4b were reported in December 2021, in United Kingdom with one A(H5N1) infection, seven A(H5N8) infections were reported from Russia in 2020 and three A(H5) in Nigeria (Pyankova et al., 2021; WHO, 2021c).

ECDC published a Threat Assessment Brief in February 2021 that assessed the risk as very low for the general population and low for occupationally exposed people (ECDC, 2021b) and revised the risk to low for the general population and low-to-medium for occupationally exposed people in December 2021 due to the increase in transmission events to mammal species including sporadic human cases with no or mild symptoms. The assessment remains valid. The high diversity and ongoing reassortment events add a high uncertainty to the assessment, and transmission events to humans cannot be excluded.

No human infection with avian influenza viruses, as currently detected in wild birds and poultry in Europe, has been identified in the EU/EEA countries during the period covered by this report or has been previously reported (EFSA et al., 2022). Other transmission events to different mammal species have been increasingly reported as mentioned in this report and in previous reports (Table 3). So far foxes had been majorly found to be infected with avian influenza viruses of clade 2.3.4.4b and displayed neurological signs leading to death or were already found dead.

The United States Centers for Disease Control and Prevention (US CDC) issued previously a risk assessment using the Influenza Risk Assessment Tool (IRAT) and placed the risk of clade 2.3.4.4b viruses in the low-to-moderate category and issued a Health and Alert Notification message about 'Recommendations for Human Health Investigations and Response' (CDC, online-a, b, c, e). The risk of the A(H5N1) clade 2.3.4.4 viruses currently circulating in the United States bird and poultry populations, and which are closely related to European viruses, were assessed by the United States 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-d).

The World Health Organization (WHO) assessed the risk associated with A(H5N6) virus as low (CDC, online-d). The WHO issued a risk assessment on the increase in human cases due to A(H5N6) virus infections in 2021 and recommended remaining vigilant about zoonotic infections and to share unsubtypeable influenza A viruses from human infections with the WHO Collaborating Centres (CDC, online-a). In addition, a recent publication was produced that aimed to raise awareness among clinicians in the EU of zoonotic avian influenza virus infections (Adlhoch et al., 2021).

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

Date	Country	Animal (species)	Virus	Reference
November 2016, April 2017	Poland	2 grey seals (<i>Halichoerus grypus</i>)	A(H5N8) clade 2.3.4.4b	(Shin et al., 2020)
December 2016 to May 2017	France	Domestic pigs (<i>Sus scrofa</i>), serological detection	A(H5N8) clade 2.3.4.4b	(Herve et al., 2021)
2017; August 2021	Germany	Wild boar serological detection; three harbour seals (<i>Phoca vitulina</i>)	A(H5N8); A(H5N8) clade 2.3.4.4b	(Schülelein et al., 2021); (Ärztblatt, online)

Late 2020	UK	4 juvenile harbour seals (<i>Phoca vitulina</i>), 1 juvenile grey seal (<i>Halichoerus grypus</i>), 1 juvenile red fox (<i>Vulpes vulpes</i>)	A(H5N8) clade 2.3.4.4b	(Floyd et al., 2021)
April, February, and September 2021	Sweden	1 grey seal (<i>Halichoerus grypus</i>), 2 red foxes (<i>Vulpes vulpes</i>)	A(H5N8) clade 2.3.4.4b, A(H5N1) clade 2.3.4.4b, A(H5N1)*	(SVA, online), Personal communication by Siamak Zohari, SVA
September 2021	Denmark	1 harbour seal (<i>Phoca vitulina</i>)	A(H5N8) clade 2.3.4.4b	(Avian Flu Diary, online; Outbreak News, online; SSI, online)
May 2021 January-March 2022	Netherlands	2 red fox cubs (<i>Vulpes vulpes</i>) Red foxes, Eurasian otter (<i>Lutra lutra</i>), European polecat (<i>Mustela putorius</i>), European badger (<i>Meles meles</i>)	A(H5N1) clade 2.3.4.4b	(Rijks et al., 2021; dwhc, online; Resource WUR, online; WUR, online)
September and November 2021 February 2022	Finland	2 foxes (<i>Vulpes vulpes</i>), 1 otter (<i>Lutra lutra</i>), 1 lynx (<i>Lynx lynx</i>)	A(H5N1) clade 2.3.4.4b	(FFA, online)
November 2021	Estonia	Fox (<i>Vulpes vulpes</i>)	A(H5N1) clade 2.3.4.4b	(WOAH, online-e)
November 2021	Italy	Domestic pigs (<i>Sus scrofa</i>) (serological detection in HPAI poultry outbreak)	A(H5N1) clade 2.3.4.4b	EURL
January 2022	Slovenia	Ferret (<i>Mustela furo</i>)	A(H5N1) clade 2.3.4.4b	Slovenian National Reference Laboratory for Avian Influenza, personal communication
February 2022	Ireland	Fox (<i>Vulpes vulpes</i>)	A(H5N1) clade 2.3.4.4b	Irish National Reference Laboratory for Avian Influenza, personal communication
March-April 2022	Japan	1 red fox (<i>Vulpes vulpes</i>) and 1 common raccoon dog (<i>Nyctereutes procyonoides</i>)	A(H5N1)	(WOAH, online-d)
April 2022	Wisconsin, New York, Michigan, (USA)	4, 5, 5 red fox kits (<i>Vulpes vulpes</i>)	A(H5N1)	(WOAH, online-b)
April-May 2022	Ontario, Manitoba (Canada)	3, 6 red fox (<i>Vulpes vulpes</i>)	A(H5N1) clade 2.3.4.4b	(WOAH, online-a)
May 2022	British Columbia (Canada)	1 red fox (<i>Vulpes vulpes</i>)	A(H5N1)	(WOAH, online-a)
May 2022	Wisconsin, Iowa, Alaska, Minnesota, New York, (USA)	5, 2, 2, 2, 1 red fox (<i>Vulpes vulpes</i>)	A(H5N1)	(WOAH, online-b)
May 2022	Alberta (Canada)	Skunks		(CTV News, online)
May 2022	Utah (USA)	2 red foxes		(CBS 58 News, online)

* No information on the clade for HPAI A(H5N1).

4.4. Prevention and control measures applied in Europe, 4 March to 1 June 2022 (ToR 3)

The description of the control and prevention measures applied in the affected Member States on outbreaks occurred from 4 March to 1 June 2022 is presented in Annex B, thanks to the countries that were willing to collaborate with EFSA and kindly provided the information reported here. Outbreaks that occurred before 2 December 2021 have been described in the previous EFSA report (EFSA et al., 2022).

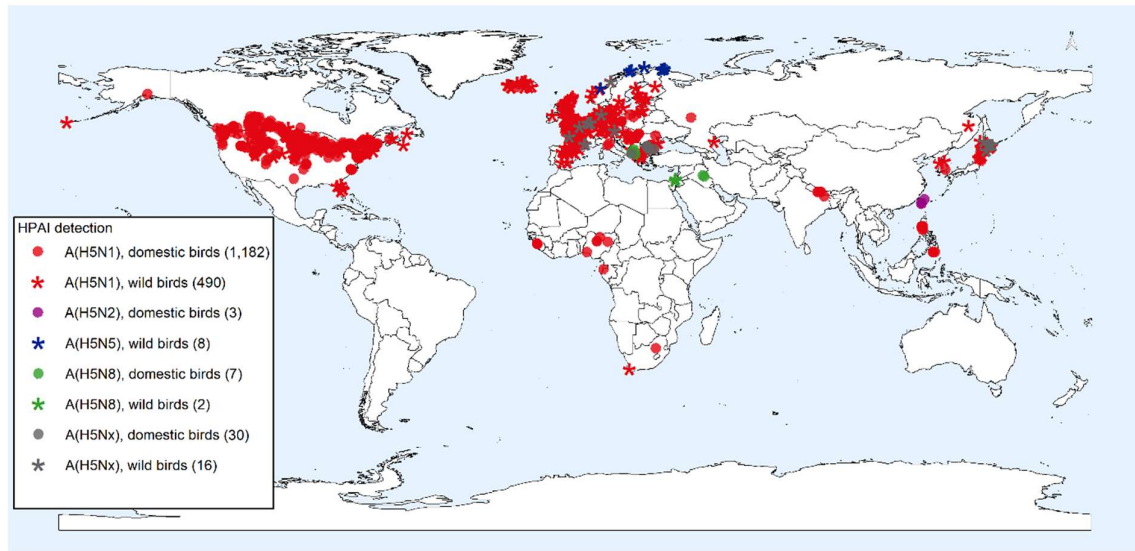
4.5. The avian influenza situation in other countries not reporting via ADNS, 16 March to 10 June 2022 (ToR 4)

An overview of the HPAI detections notified from other countries not reporting via ADIS but via the WOA or national authorities from 16 March to 10 June 2022 is presented in Table 4 and Figure 14. For the purposes of this report, only findings of avian influenza viruses occurring in countries that are considered to be of epidemiological interest for the EU/EEA or of public health relevance are described.

Table 3: Number of HPAI detections in other countries not reporting via ADIS, by virus subtype and country, from 16 March to 10 June 2022

Region	Country	Domestic birds (450)			Wild birds (136)			Total
		A(H5N1)	A(H5N2)	A(H5N8)	A(H5N1)	A(H5N8)	A(H5Nx)	
Africa (14)	Gabon	1						1
	Guinea	6						6
	Nigeria	5						5
	South Africa	1			1			2
Americas (483)	Canada	88			10			98
	USA	311			46			357
Asia (86)	Chinese Taipei		3					3
	India	1						1
	Iraq			2				2
	Israel					2		2
	Japan	9			33		7	49
	Korea	1			5			6
	Nepal	4						4
	Philippines	17						17
Europe (3)	Russia	1			2			3
Total		445	3	2	97	2	7	556

Source: ADIS and WOA WOHIS (data extraction carried out on 10 June 2022).



Author: EFSA
Data sources: ADIS, WOA
Date updated: 10/06/2022

Figure 13: Geographical distribution, based on available geocoordinates, of detections reported in domestic birds (1,222) and wild birds (516) by virus type, from 16 March to 10 June 2022

4.5.1. Avian influenza A(H3N8)

4.5.1.1. Human infections with A(H3N8)

Two human infections with avian influenza A(H3N8) reassortant virus were reported for the first time. The first patient is a 4-year-old child from Henan province in China, who was hospitalised in critical condition in April 2022 (WHO, 2022). A second patient with mild symptoms, a 5-year-old child from Hunan province, China, was diagnosed in May 2022 (The Government of the Hong Kong Special Administrative Region Press Releases, 2022a). Both children had been exposed to live poultry before the onset of symptoms. A preliminary FAO/WOAH/WHO Joint Rapid Risk Assessment ranks the risk for A(H3N8) as low for human health (FAO, 2022).

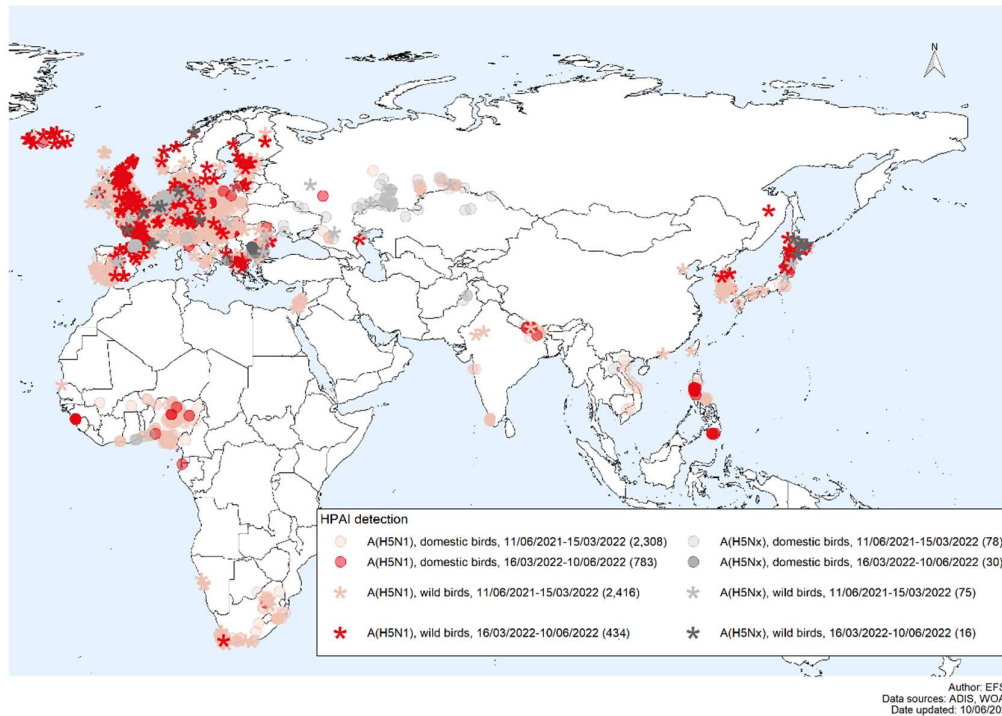
4.5.2. HPAI A(H5N1)

4.5.2.1. Domestic and wild birds

Detections

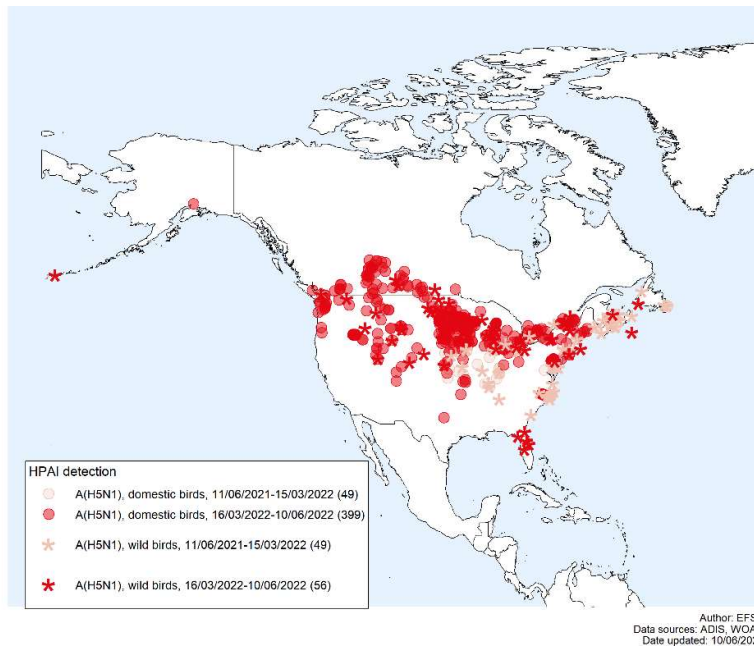
The number of reported outbreaks of HPAI A(H5N1) in Africa decreased in the relevant time period of this report significantly compared with the previous months (Figure 14). Only Guinea and Nigeria notified more than one outbreak to the WOA, affecting mainly medium-sized poultry establishments. Gabon detected one outbreak of HPAI A(H5N1) on a backyard farm and South Africa on a medium-sized poultry establishment in a previously affected region. Furthermore, South Africa reported the detection of HPAI A(H5N1) in a greater crested tern. The HPAI A(H5N1) epidemic in Asia continues but, compared with the last report with a lower number of outbreaks and affected countries (Figure 14). India, the Philippines and Nepal reported several outbreaks of HPAI A(H5N1) on poultry establishments of all sizes. Japan, Korea and Russia notified cases of HPAI A(H5N1) not only in domestic birds, but also in several wild bird species, for example greater white-fronted goose, bean goose, whooper swan, great egret, Caspian tern, Caspian gull, Pallas's gull, Dalmatian pelican, white-tailed eagle, mountain hawk-eagle, large-billed crow and carrion crow. Furthermore, Japan detected HPAI A(H5N1) in two mammal species, common raccoon dog (*Nyctereutes procyonoides*) and red fox (*Vulpes vulpes*), on Hokkaido (Figure 15). Compared with the period covered by the last report, the number of outbreaks of HPAI A(H5N1) in

Canada and the USA has risen sharply (Figure 15). The outbreaks in domestic birds were detected in small to very large poultry establishments and several wild bird species were affected, for example mallard, common goldeneye, ruddy duck, Baikal teal, Muscovy duck, Canada goose, greater white-fronted goose, snow goose, Ross's goose, mute swan, tundra swan, trumpeter swan, common loon, royal tern, great blue heron, sandhill crane, ring-billed gull, laughing gull, great black-backed gull, double-crested cormorant, red-tailed hawk, bald eagle, Harris's hawk, peregrine falcon, Cooper's hawk, sharp-shinned hawk, hen harrier, great horned owl, snowy owl, barred owl, turkey vulture, American crow, common raven, fish crow, wild turkey, great-tailed grackle, black-billed magpie and American robin. Furthermore, Canada and the USA detected HPAI A(H5N1) in red foxes (*Vulpes vulpes*) and Canada additionally detected virus in striped skunk (*Mephitis mephitis*).



Red and dark grey symbols indicate outbreaks that occurred between 16 March and 10 June 2022, grey and white symbols indicate outbreaks that occurred between 10 June 2021 and 15 March 2022.

Figure 14: Geographical distribution, based on available geocoordinates, of HPAI A(H5N1) and A(H5Nx) detections reported in domestic birds (circles) and wild birds (stars) (6,110)

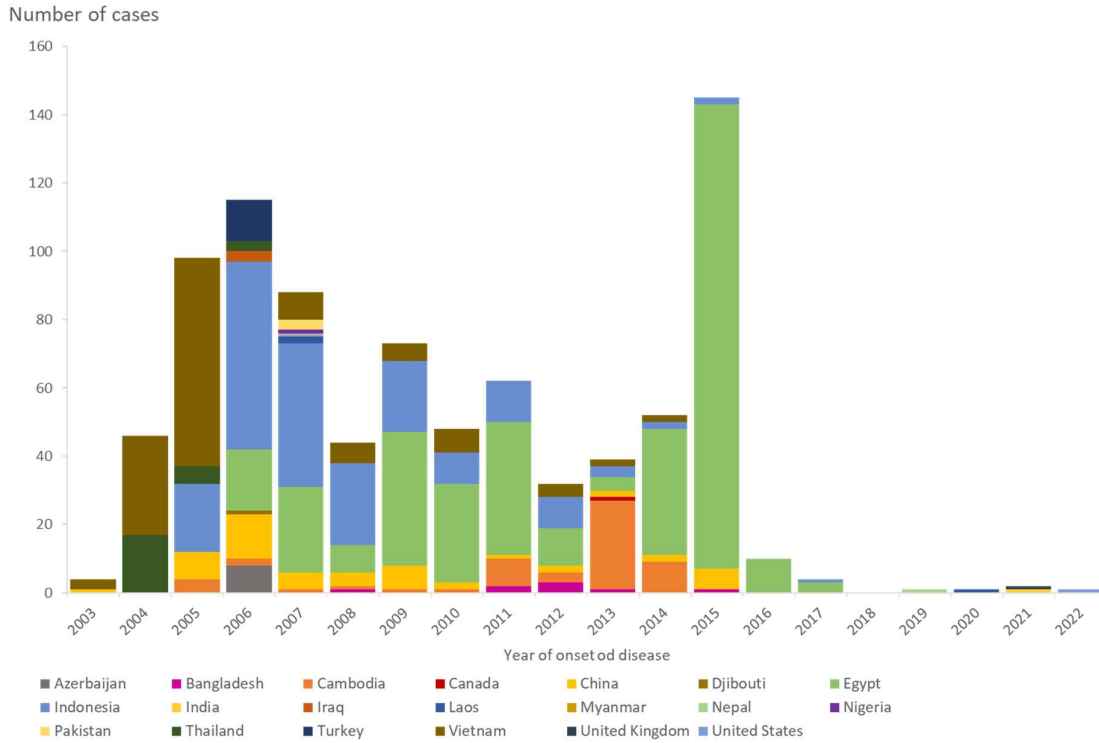


Red symbols indicate outbreaks that occurred between 16 March and 10 June 2022, grey symbols indicate outbreaks that occurred between 10 June 2021 and 15 March 2022.

Figure 15: Geographical distribution, based on available geocoordinates, of HPAI A(H5N1) and AH(H5Nx) detections reported in domestic birds (circles) and wild birds (stars) (553)

4.5.2.2. Human infections due to A(H5N1)

Since the publication of the previous report, one human case due to avian influenza A(H5N1) was reported in April 2022 in the USA. The patient developed mild symptoms (fatigue) during the depopulation activities in a commercial poultry facility where influenza A(H5N1) virus was confirmed in poultry. The patient was not hospitalised and has recovered after receiving antiviral treatment. No additional cases were reported in connection to this person. Since 2003, and as of 16 June 2022, 865 laboratory-confirmed cases of human infection with avian influenza A(H5N1) virus, including 456 deaths, have been reported from 20 countries outside the EU/EEA. No human infection has been reported from an EU/EEA country so far (WHO, 2022) (Figure 16).



Source: WHO and ECDC line list (WHO, 2021d, a, online-a).

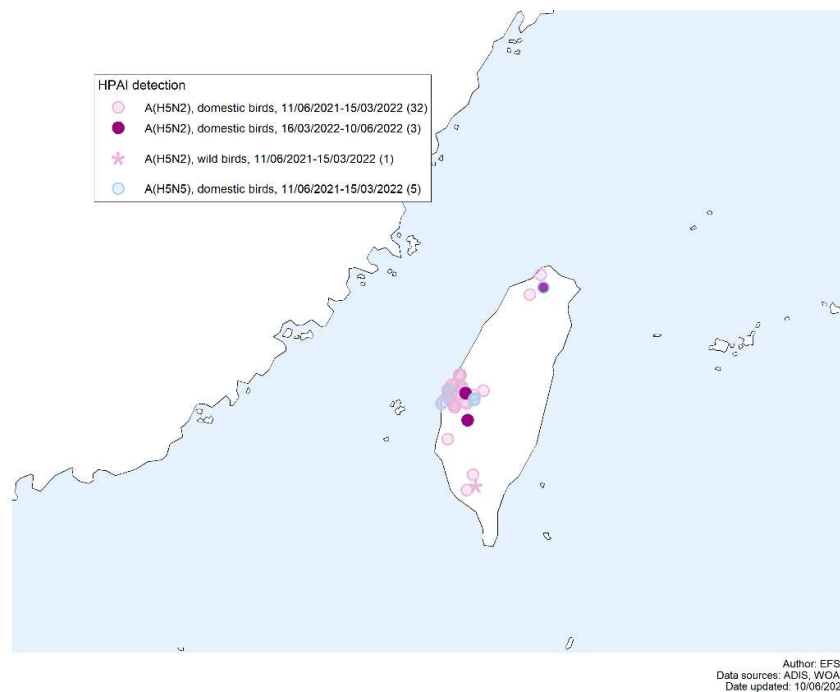
Figure 16: Distribution of confirmed human cases of A(H5N1) by year and country of reporting, 2003 to 16 June 2022 (865)

4.5.3. HPAI A(H5N2) and A(H5N5)

4.5.3.1. Domestic and wild birds

Detections

In the current reporting period, Taiwan reported no new outbreaks of the Taiwanese lineage HPAI A(H5N5) to the WOA. But three outbreaks of the Taiwanese lineage HPAI A(H5N2) in one backyard farm and two medium-sized poultry establishments were detected. The Taiwanese lineages of HPAI A(H5N2) and HPAI A(H5N5) (clade 2.3.4.4) differed from the Eurasian HPAI A(H5N2) and A(H5N5) lineages (Li et al., 2020); the latter belonging to clade 2.3.4.4b, which has been detected, with different genotypes, in Egypt and Russia as well as in Asian countries between 2016 and 2019 (EFSA et al., 2019) and in Bulgaria in 2020. No wild bird cases were reported in the relevant time period of the report (Figure 17).



Grey symbols indicate HPAI A(H5N2) detections between 10 June 2021 and 15 March 2022, blue symbols indicate HPAI A(H5N2) detections between 16 March and 10 June 2022.

Figure 17: Geographical distribution, based on available geocoordinates, of HPAI A(H5N2) detections reported in domestic birds (circles) in Taiwan (41)

4.5.4. HPAI A(H5N6)

4.5.4.1. Domestic and wild birds

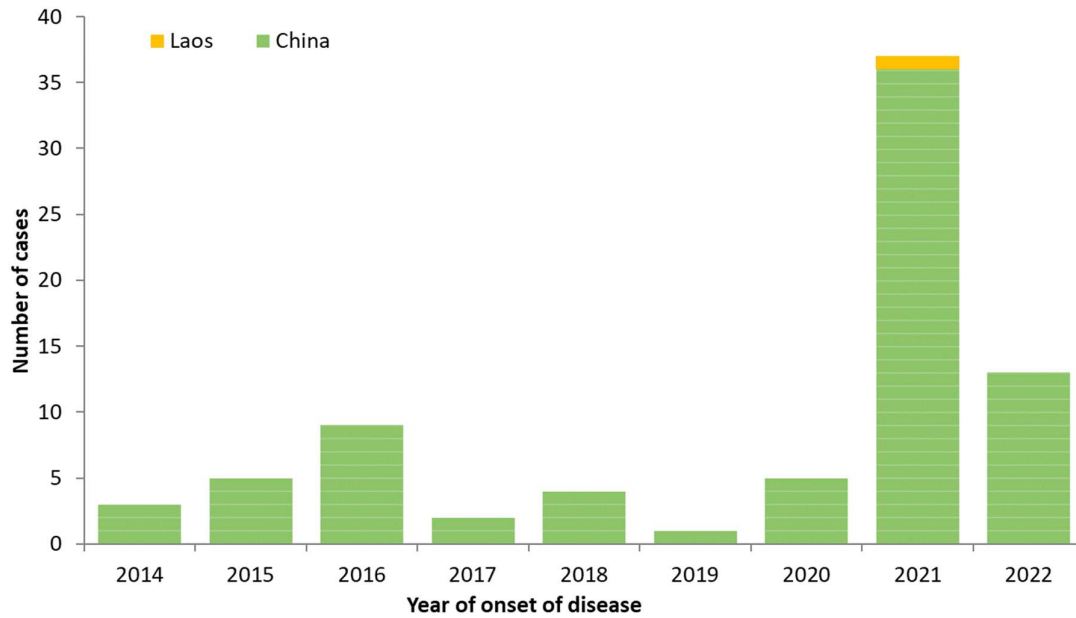
Detections

As in the last reports, no outbreaks of the zoonotic reassortment of HPAI A(H5N6) clade 2.3.4.4c were notified to the WOAHA between 16 March and 10 June 2022. New human cases of A(H5N6) from China in the current reporting period might suggest underreporting of poultry outbreaks in the Asian region.

4.5.4.2. Human infections due to A(H5N6)

Four new human infections, including one death, due to avian influenza A(H5N6) have been reported from China since the last EFSA report.

Since 2014, and as of 16 June 2022, 79 laboratory-confirmed human infections with avian influenza A(H5N6) viruses have been reported from China (78 cases) and Laos (1), 33 of the patients died (CHP, 2022) (Figure 18). Twelve of these 33 deaths due to A(H5N6) had been reported between 2014 and 2017 (Jiang et al., 2017) and at least 17 deaths occurred in the most recent period 2018–2021 (ECDC line list; please refer to Appendix B.2). A household cluster with two infections was observed in a couple preparing a duck purchased from a live-bird market for meal (The Government of the Hong Kong Special Administrative Region Press Releases, 2022b; BNO, online; GovMO, online-a). The overall case fatality ratio of A(H5N6) in humans is estimated to be 42% (limitation: case reports might not have been a complete or lacking updated information).



Source: ECDC line list (please refer to Appendix B.2).

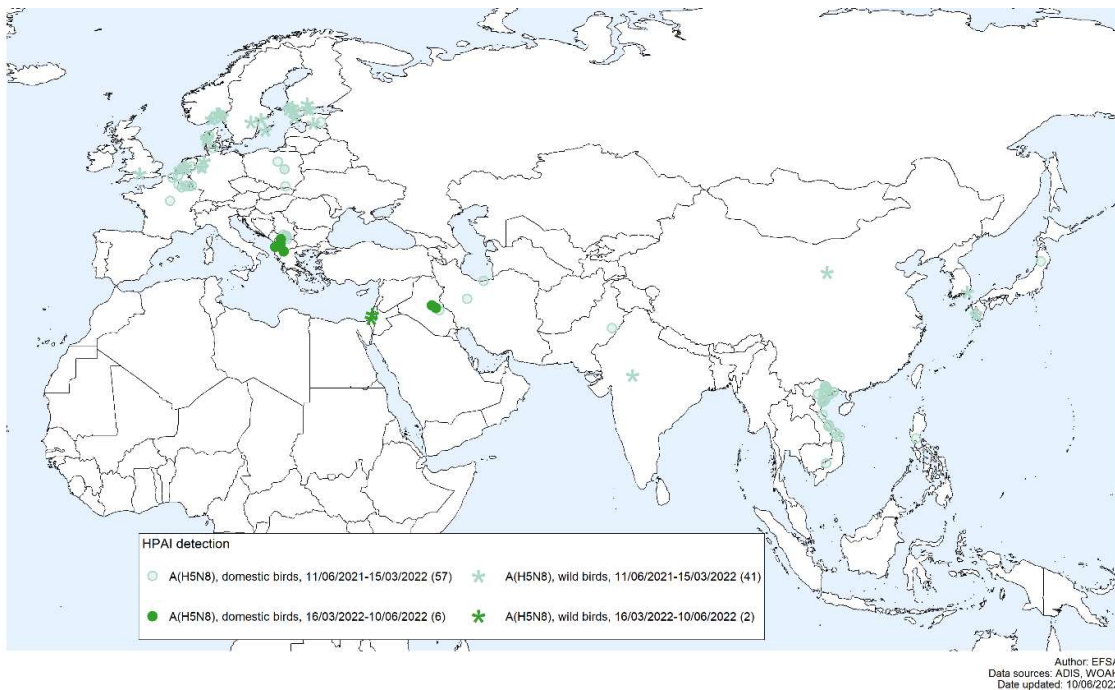
Figure 18: Number of human cases due to A(H5N6) infection by year of onset, 2014 to 16 June 2022 (79)

4.5.5. HPAI A(H5N8)

4.5.5.1. Domestic and wild birds

Detections

Between 16 March and 10 June 2022 and outside Europe, HPAI A(H5N8), clade 2.3.4.4b, was only detected in two large poultry establishments in Iraq and in two wild birds in Israel. In the latter, a Eurasian sparrowhawk and white stork were determined to be the affected species (Figure 19).



Grey symbols indicate outbreaks that occurred between 10 June 2021 and 15 March 2022, green symbols indicate outbreaks that occurred between 16 March and 10 June 2022.

Figure 19: Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N8) outbreaks in domestic birds (circles) and wild birds (stars) (106)

4.5.6. HPAI–LPAI A(H7N9)

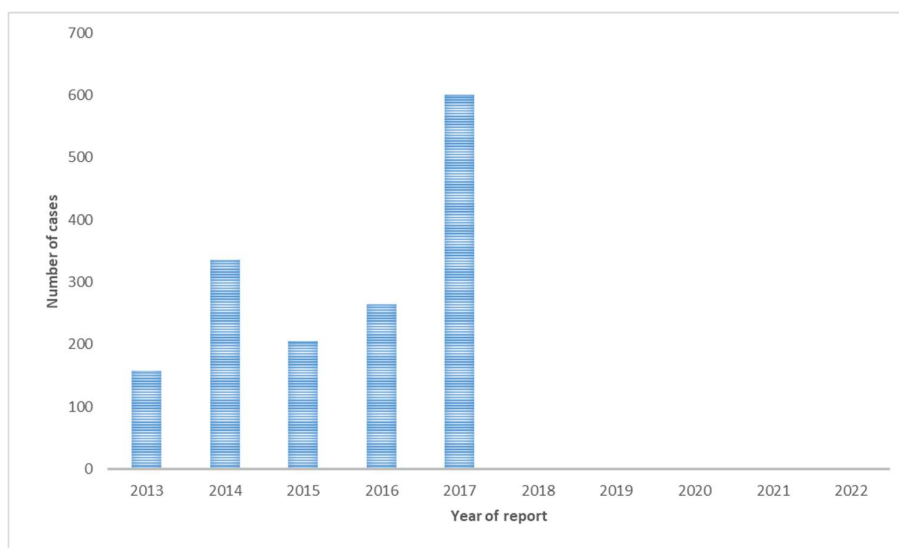
4.5.6.1. Domestic and wild birds

Detection

No LPAI or HPAI A(H7N9) cases had been notified in poultry or wild birds within the relevant time period for this report. The last case was reported from Shandong province, China, in October 2020. The nationwide A(H7N9) vaccination campaigns for poultry, with the exception of poultry in avian influenza-free zones and export farms, started extensively in September 2017 (FAO, online).

4.5.6.2. Human infections due to A(H7N9)

No human cases due to avian influenza A(H7N9) have ever been reported from Europe and no human case has been reported globally since 2019 (WHO, 2020b, c). Since February 2013, in total, 1,568 human cases have been reported from outside of Europe (Figure 20), including at least 615 deaths (39%) (CHP, 2021b) (WHO, 2019a, b). The last case was reported in March 2019. Of all human cases, 32 had been infected with HPAI virus A(H7N9), and 13 of them were fatal, according to the Chinese National Influenza Center (Chinese National Influenza Center et al., 2018).



Source: ECDC line list (please refer to Appendix B.2).

Figure 20: Number of human cases due to A(H7N9), infection by year, 2013 to 2022 (1,568)

4.5.7. LPAI A(H9N2)

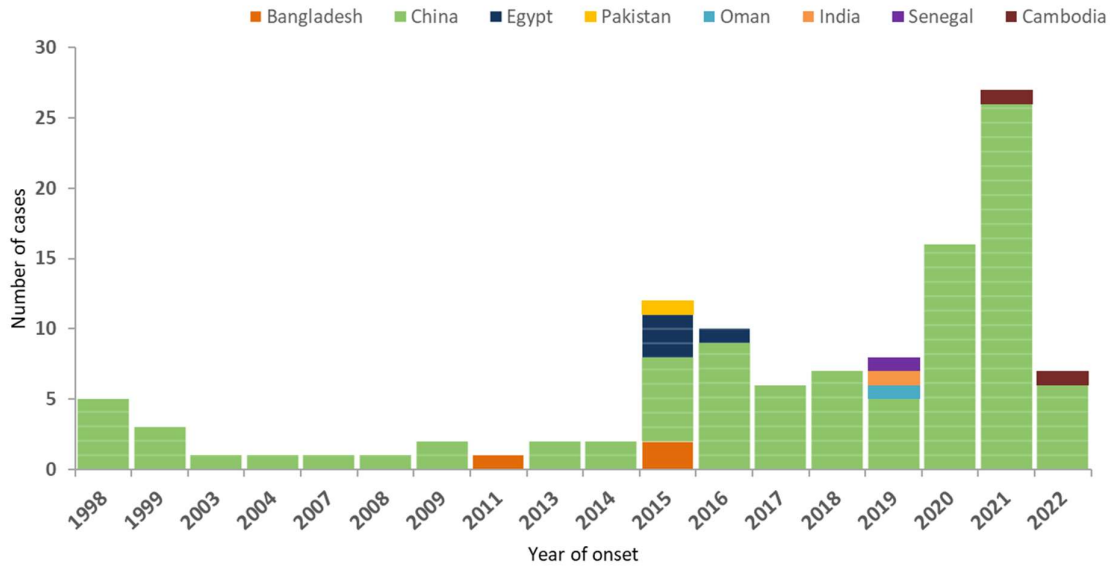
4.5.7.1. Domestic and wild birds

Detection

As mentioned in previous EFSA reports, A(H9N2) is the most commonly detected non-notifiable subtype of influenza virus in poultry in Asia, the Middle East and Africa (Zecchin et al., 2017; Bonfante et al., 2018; Chrzastek et al., 2018; Xu et al., 2018; Zhu et al., 2018; Awuni et al., 2019; Kariithi et al., 2019). These regions remained LPAI (H9N2) endemic at least until 10 June 2022.

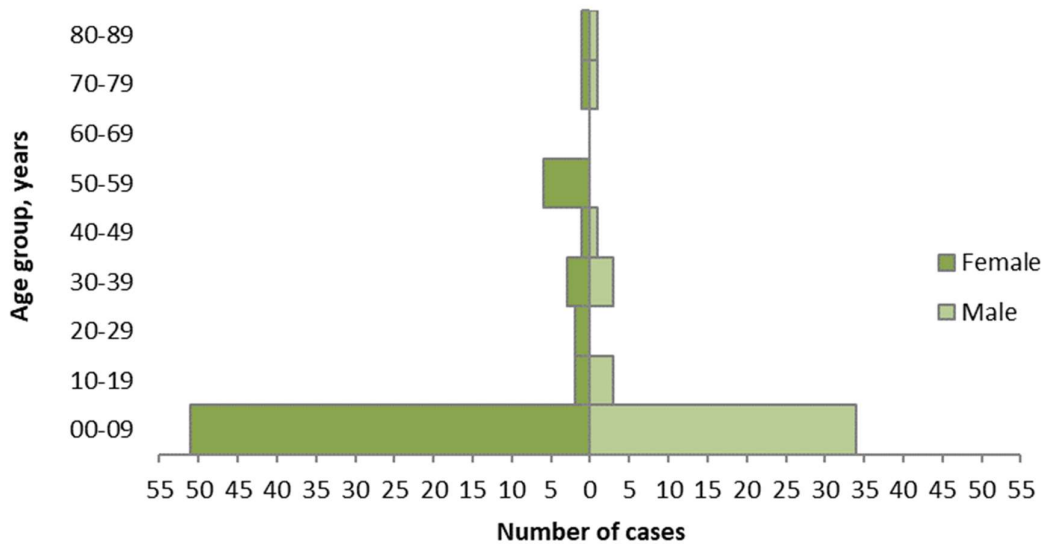
4.5.7.2. Human infections due to A(H9N2)

Two new human infections with A(H9N2) have been reported since the last report. Both cases were children from China (GovMO, online-b). Since 1998, and as of 16 June 2022, 112 laboratory-confirmed human infections with avian influenza A(H9N2) virus, including two deaths, have been reported globally. Infections were reported from China (99), Egypt (4), Bangladesh (3), Cambodia (2), India (1), Oman (1), Pakistan (1) and Senegal (1) (ECDC line list; please refer to Appendix B.2) (Figure 21). Exposure to live or slaughtered poultry or contaminated environment has been reported. The age group mostly affected by A(H9N2) infections in humans was children under 10 years of age, who developed mild symptoms (WHO, 2020d; CHP, 2021a; ECDC, 2021a) (ECDC line list; please refer to Appendix B.2) (Figure 22).



Source: ECDC line list.

Figure 21: Distribution of confirmed human cases of A(H9N2) by reporting country, 1998 to 16 June 2022 (112)



Source: ECDC line list.

Figure 22: Age and sex distribution of confirmed human cases of A(H9N2) by age group, 1998 to 16 June 2022 (112)

4.6. Scientific analysis of avian influenza spread from non-EU/EEA countries and within the EU/EEA

Since 2005, multiple incursions of HPAI (A)H5 viruses through wild migratory waterbirds have occurred in Europe. The frequency of outbreaks in poultry, the number of affected countries, and the impact on the poultry industry have been variable in different years. The 2021–2022 HPAI A(H5) epidemic with a total so far of 2,398 outbreaks in poultry, approximately 46 million birds culled in affected

establishments, 168 detections in captive birds, and 2,733 HPAI detections in wild birds in 36 European countries has been the largest and most devastating HPAI epidemic that has ever occurred in Europe.

The evolution of the epidemic in France, the most affected European country, involving 1,371 poultry establishments since October 2021 and approximately 16 million birds has resulted from the uncontrollable spread of infection among commercial poultry operations after the initial exposure to infected wild birds. Not only in France, but also in other affected EU countries, large HPAI A(H5) epidemics have occurred due to the rapid spread of the virus among highly susceptible poultry species (e.g. domestic ducks, domestic geese, turkeys) and poultry production systems (e.g. layers, foie gras sector) in areas with high poultry densities. Overall, 86% of affected poultry establishments have been reported as secondary outbreaks, particularly in the most affected countries (e.g., France, Hungary, Italy).

In the current reporting period (16 March to 10 June 2022), HPAI A(H5) continues to circulate in wild birds, including in resident wild birds in Europe. Although the number of HPAI A(H5) detections has decreased in the current period compared with the previous period (9 December 2021 and 15 March 2022), the virus continues to be detected in wild birds, indicating it may have become endemic in wild bird populations in Europe. This implies that, like in the 2021-2022 HPAI season (EFSA 2022: Avian influenza overview December 2021 – March 2022), the health risk from HPAI A(H5) for poultry, humans, and wildlife in Europe not only exists in autumn and winter, but remains present all year-round.

To mitigate the risk of AI introduction in the domestic flock, appropriate biosecurity, surveillance, and early detection measures must be maintained in the different poultry production systems:

- **Biosecurity:** The persistence for long periods of an environmental avian influenza infection risk requires the systematic application of strict biosecurity and hygiene practices at the line of separation between the environment inside each poultry house, where birds are raised, and the outer farm environment. These measures shall include at least the regular maintenance and repair of buildings, the implementation of a Danish custom at the entrance of each shed (i.e. measures such as changing boots and clothes), the definition and systematic implementation of reliable cleansing and disinfection procedures to be systematically applied to decontaminate any equipment brought into the shed, and the storage of materials (e.g. bedding materials) in areas protected from direct or indirect contact with wild birds. Furthermore, the application of sustainable levels of biosecurity must be guaranteed and checked along the entire poultry production chain, considering that the persistent circulation of HPAI viruses and the possible reduction of biosecurity compliance might increase the risk of avian influenza incursions with the potential further spread between farms.
- **Surveillance and early detection:** The early detection of any avian influenza virus exposure is fundamental to reducing the high-risk period of an epidemic and to limiting the secondary spread of avian influenza from affected establishments, particularly in high-risk areas and production sectors. The efficacy of a passive surveillance system is strongly related to the level of awareness, and veterinary authorities should continuously ensure high awareness among stakeholders in the poultry sector, promoting fast reporting of suspected cases based on indicators such as increased daily mortality, drops in egg production or in food or water intake (Gonzales and Elbers, 2018).

Considering the high negative impact of these HPAI epidemics in the recent years, 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 have been described in detail in Avian influenza overview September – December 2021 (EFSA et al., 2021b).

In the 2021-2022 epidemic in France, three successive epidemiological spatiotemporal clusters (caused by fast secondary spread of HPAI virus between poultry establishments, following a single or multiple primary incursions) have been identified since December 2021, with no epidemiological links between the first and last two clusters. The first cluster was localised in southwestern France (southern parts of Nouvelle-Aquitaine and Occitanie), following a final local extension pattern that was similar to that of the previous large epidemics in 2016–2017 and 2020–2021, although the latter two had been limited to this single cluster. From mid-December 2021 to early March 2022, at least six introductions of HPAI A(H5N1) viruses occurred in poultry in southwestern France and the peak of outbreak detections was observed in mid-January. The second cluster occurred in western regions (Pays-de-la-Loire and northern

part of Nouvelle-Aquitaine) peaking in early March, and the third one in central western regions (north-eastern Nouvelle-Aquitaine and northern Occitanie) with a peak in early April. Nearly all outbreaks involved commercial farms. The southwestern and central western clusters mostly involved duck establishments for foie gras production, whereas outbreaks in the western cluster also affected all types of species and productions in mixed proportions. At least eight distinct genotypes have been circulating in France but, up to mid-February, a single major genotype accounted for most detections in poultry in the southwestern cluster. This genotype was afterwards superseded by another genotype, responsible for poultry outbreaks in the western and central western clusters.

Although the number of outbreaks in non-EU/EEA countries from 16 March to 10 June 2022 has again increased compared with the last report (EFSA et al., 2022), the distribution across the different continents has shifted considerably. The number of reported outbreaks of the dominant subtype HPAI A(H5N1) in Africa and Asia decreased significantly in the relevant time period of this report compared with the months before, whereas the number of reported outbreaks of HPAI A(H5N1) in Canada and the USA has increased 10-fold. Furthermore, the number of affected wild birds and species has increased compared with the previous reporting period. The broadened host range and infection pressure is underlined by the notification of cases in three mammal species such as the red fox (*Vulpes vulpes*) in Canada, Japan and the USA, the common raccoon dog (*Nyctereutes procyonoides*) in Japan and the striped skunk (*Mephitis mephitis*) in Canada.

In the current reporting period, no additional HPAI A(H5) cases were detected in wild mammal species in EU countries. Since October 2020, 10 European countries have reported more than 25 infections of HPAI A(H5) viruses of clade 2.3.4.4b in eight distinct mammalian species, mostly in red foxes (*Vulpes vulpes*). Some of these viruses present adaptive markers associated with an improved replication in mammals. The continuous detection of HPAI viruses in wild and domestic mammals, the rapid acquisition of viral mutations associated with mammalian adaptation after transmission to mammals, as well as the sporadic human infections with HPAI A(H5Nx) viruses of clade 2.3.4.4b reported in the last 2 years, are all factors that highlight the need to intensify surveillance in mammals and humans, particularly in high-risk areas with an intensive viral circulation.

Genetic surveillance of viruses circulating in birds is also of utmost importance to promptly detect viruses with mutations associated with increased zoonotic potential. The recent human infections in China caused by the A(H3N8) subtype highlight the need not to limit the surveillance to the HPAI viruses alone, but to extend it to low pathogenic viruses belonging to subtypes with a demonstrated high zoonotic potential.

4.7. Monitoring, diagnosis of human infections and public health, occupational health and safety measures for infection prevention and control in the EU/EEA

4.7.1. Occupational health and safety measures

When there is a potential risk of exposure to these viruses from infected birds (whether in an agricultural or other setting), the workplace risk assessment should be revised taking into account all occupational risks, including the increased physical load on workers from wearing PPE, and appropriate measures should be taken, prioritising technical and organisational measures over personal measures. The measures should be agreed in consultation with the health and safety committee when available or with workers' representatives. These measures may include physical distancing, enhanced ventilation, dust- and aerosol-avoiding measures (for example when cleaning and handling litter) and using appropriate PPE, when other more general protective measures do not sufficiently protect workers. Work clothing and street clothing should be stored separately and a separation of potentially contaminated areas from clean areas should be ensured (black/white areas) and appropriate hygiene measures applied. In agricultural settings, care should be taken to avoid contamination of domestic areas, for example through contaminated work clothing. Appropriate PPE should be provided by employers and properly stored and disposed of, and workers should be trained in its use. Specific measures should be set out for culling operations and for the handling of dead animals and waste.

At premises where workers may be exposed to the above-mentioned viruses, for example when directly exposed to birds, their products or droppings, which may potentially be infected or contaminated with avian influenza viruses, the workplace risk assessment should be revised by employers and appropriate

OSH measures should be applied⁷. Appropriate PPE should be provided by employers and workers should be trained in its use and disposal. PPE should be properly stored. At poultry farms, it should be ensured that living areas are not contaminated, for example through work clothing, e.g. to avoid additional risk to family workers and relatives.

4.7.2. Monitoring and options for public health measures

Surveillance and options for public health measures have been outlined in previous reports (EFSA et al., 2021b) and remain valid.

4.7.3. Diagnosis

People in the EU presenting with severe acute respiratory or influenza-like infection and a history of exposure to poultry or wild birds will require careful investigation, management and infection control. Neurological symptoms have also been observed in mammals infected with avian influenza viruses. Should transmission to humans occur, possibly other non-respiratory symptoms might also occur, and clinicians should consider testing severely ill patients for influenza presenting with respiratory but also with other unusual e.g. neurological symptoms. Appropriate samples for influenza tests should be rapidly taken and processed from patients with relevant exposure history within 10 days preceding the symptom onset. If positive specimens cannot be subtyped, those should be shared with the national reference laboratory (National Influenza Centres; NICs).

With routine diagnostic laboratory assays, human infection with A(H5Nx) viruses should be detected as positive for influenza A virus, and negative for influenza B, A(H1), A(H1)pdm09 and A(H3) viruses and therefore classified as unsubtypeable influenza A virus, if no specific A(H5) diagnostic test is performed. Such unsubtypeable influenza A virus isolates or clinical samples that cannot be subtyped should be sent to NICs, and further to a WHO Collaborating Centre for Reference.

4.7.4. Reporting

Human infections with avian influenza viruses are notifiable under EU legislation within 24 hours through the Early Warning and Response System (EWRS) according to EU Decision 1082/2013/EU⁸. Reporting is also required through the International Health Regulations (IHR) notification system (WHO, 2017): 'Each State Party shall notify WHO, by the most efficient means of communication available, by way of the National IHR Focal Point, and within 24 hours of assessment of public health information, of all events that may constitute a public health emergency of international concern within its territory according to the decision instrument, and any health measure implemented in response to those events.'

Information should also be shared with local OSH authorities.

4.7.5. Sharing of sequences

The timely characterisation of viruses and the sharing of sequence information remain crucial for the monitoring of virus evolution and for virus vaccine development. Sharing of sequence data through the GISAID EpiFlu (GSAID, online) or other sequence databases and of virus isolates with WHO Collaborating Centres are important for public health assessment, improvement of diagnostics and the development of candidate vaccines. Sharing of influenza viruses occurs through the Global Influenza Surveillance and Response System (GISRS) (WHO, online-b).

4.7.6. Candidate vaccine viruses

Candidate vaccine viruses (CVV) developed, under development or proposed are listed at WHO (WHO, 2021b).

⁷ An extensive body of occupational safety and health (OSH) legislation applies to the protection of workers. Employers' obligations are set out in the OSH framework Directive 89/391/EC and its daughter directives, in particular directive 2000/54/EC 000 on the protection of workers from risks related to exposure to biological agents at work. These Directives are minimum requirements and are implemented in national regulations. There may be specific guidance for poultry workers in the Member states and they may also include requirements for appropriate health surveillance for instance.

⁸ Commission Implementing Decision of 8 August 2012 amending Decision 2002/253/EC laying down case definitions for reporting communicable diseases to the Community network under Decision No 2119/98/EC of the European Parliament and of the Council. OJ L 262, 27.9.2012, p. 263-319.

4.8. ECDC risk assessment for the general public in the EU/EEA

Avian influenza A(H5Nx) clade 2.3.4.4 viruses have caused large outbreaks in birds and poultry since 2014. ECDC has published a Threat Assessment Brief on 24 February 2021 (ECDC, 2021b).

The risk assessment is based on the likelihood of infection and disease severity: the likelihood of infection is related to direct unprotected exposure to infected wild birds or poultry (or other mammals infected with avian influenza virus such as foxes and seals) and is considered low for the general population and low to medium for people occupationally exposed to infected birds or other potentially infected mammals. The disease severity has been described as asymptomatic or mild in human infections with A(H5N1) in United Kingdom or the USA as well as A(H5N8) infections in Russia and Nigeria, therefore the impact based on severity has been considered low but with high uncertainty due to the high diversity of circulating avian influenza viruses. Human infections with A(H5N6) in China have shown a high level of severity, which has not been observed elsewhere related to clade 2.3.4.4b viruses.

The risk to the general population of human transmission due to avian influenza viruses of the currently circulating clade 2.3.4.4b in Europe is assessed as *low* and to people occupationally or otherwise HPAI virus exposed *low to moderate*.

Sporadic transmission of uncommon avian influenza viruses such as A(H3N8) has been observed before e.g. for A(H6N1), A(H7N4), A(H10N8) and is therefore not an unexpected event. This does not alter the assessment that avian influenza virus transmission to humans is a rare event and the risk is considered very low for viruses adapted to avian species. Viruses currently circulating in bird populations in Europe are considered to be avian-adapted virus. However, the detection of viruses carrying markers for mammal adaptation, and correlated with increased replication and virulence in mammals, is of concern. The additional reports of transmission events to mammals, e.g. seals and foxes in several EU countries as well as seroepidemiological evidence of transmission to wild boar and domestic pigs, could indicate evolutionary processes including mammal adaptation with the possibility to acquire the ability to transmit to humans.

Direct and unprotected exposure to possible infected birds and poultry and their products including blood, remains limited to mostly occupationally exposed groups of people in the European countries. Also, other groups of people such as backyard farmers or wild bird hunters with possible exposure to infected poultry or wild birds should be made aware of the potential risk of transmission and reminded to wear protective equipment. Such unprotected exposure to infected backyard birds was the source of infection in the recent human A(H5N1) infection in the UK (GovUK, online; WHO, online-c). Workers in close contact to potentially infected mammals such as foxes or other wildlife e.g. at rehabilitation centres or in areas with high level of avian influenza outbreaks in wild birds, should also be cautious about possible avian influenza infections and should wear protective equipment when handling such animals.

The uncertainty of this risk assessment is high due to the high variability of the avian influenza viruses of clade 2.3.4.4 with many reassorted subtypes and genetic lineages co-circulating in Europe and globally. Reassortment events will continue and zoonotic transmission of avian influenza viruses cannot be fully excluded in general when avian influenza viruses are present in birds. People should avoid touching sick or dead birds or their droppings and should wear PPE when in direct contact. Workers should be protected following an updated workplace risk assessment and prevention measures should be set accordingly⁹. Using personal protective measures for people exposed to birds infected with avian influenza viruses will minimise any residual risk. Follow-up measures and testing should be initiated as described above.

The risk of travel-related importation of human avian influenza cases from countries where the viruses are detected in poultry or wild birds is *very low*. Sporadic human cases infected with A(H9N2) LPAI or A(H5N6) HPAI viruses outside Europe underline the risk of transmission whenever people are exposed to infected birds.

⁹ Council Directive 2005/94/EC of 20 December 2005 on Community measures for the control of avian influenza and repealing Directive 92/40/EEC. OJ L 10, 14.1.2006, p. 16-65.

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Abbreviations

ADIS	Animal Disease Information System
ADNS	Animal Disease Notification System
AFSVSPP	Administration for Food Safety, Veterinary Sector and Plant Protection
AIPZ	Avian Influenza Prevention Zone
AVO	Authorised Veterinary Organization
CA	Certification authority
CAB	County administrative boards
CAFRE	College of Agriculture, Food and Rural Enterprise
CVO	Chief Veterinary Officer
CVV	Candidate vaccine viruses
DAERA	Department of Agriculture, Environment and Rural Affairs
DDPA	Densely populated poultry area
DVFA	Danish Veterinary and Food Administration
ECDC	European Centre for Disease Prevention and Control
EEA	European Economic Area
EFSA	European Food Safety Authority
EU	European Union
EURL	European Union Reference Laboratory
EWRS	Early Warning and Response System
FAO	Food and Agriculture Organization
FFA	Finnish Food Authority
FRZ	Further restricted zone
GB	United Kingdom
GISRS	Global Influenza Surveillance and Response System
GVI	General Veterinary Inspectorate
HPAI	Highly pathogenic avian influenza
IHR	International Health Regulations
IRAT	Influenza Risk Assessment Tool
IVPP	Influenza Viruses with Human Pandemic Potential
LPAI	Low pathogenic avian influenza
MA	Ministry of Agriculture
MAFF	Ministry of Agriculture, Forestry and Food
NDCC	National disease control centre
NFCSO	National Food Chain Safety Office
NRL	National Reference Laboratory
NVI	National Veterinary Institute
NVWA	Netherlands Food and Consumer Product Authority

OSH	Occupational safety and health
PCR	Polymerase chain reaction
PIP	Pandemic Influenza Preparedness
PPE	Personal protective equipment
PZ	Protection zone
RA	Risk assessment
SBA	Swedish Board of agriculture
SSI	Statens Serum Institut
SVFA	State Veterinary and Food Administration
SZ	Surveillance zone
ToR	Term of Reference
WOAH	World Organisation for Animal Health
WHO	World Health Organization
WUR	Wageningen University Research

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 HPAI 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, legislation¹⁰, 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. 178/2002¹¹, 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.

¹¹ Regulation (EC) No 178/2002 of the European Parliament and of the Council of 28 January 2002 laying down the general principles and requirements of food law, establishing the European Food Safety Authority and laying down procedures in matters of food safety. OJ L 31, 1.2.2002, p. 1–24.

- 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 16 March to 10 June 2022 and reported by Member States and neighbouring countries to the ADIS or WOAHA 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 case report provided by representatives from the affected Member States and attached as an annex. Information was collected for outbreaks that occurred from 5 March to 1 June 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 WOAHA 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 United Kingdom 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 wild bird cases that occurred from 16 March to 10 June 2022. 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 2021 to March 2022 (EFSA et al., 2022) 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 16 March to 10 June 2022 submitted by Member States to the ADIS (European Commission, online) were taken into account for this report. Data extraction was carried on 10 June 2022. The WOA's World Animal Health Information Database (WOAH, online-c) 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 during the same period. Wild bird species have been categorised according to Table B1. The public GISAID's EpiFlu Database was accessed to download newly released avian influenza sequences. A descriptive analysis of the data collected is reported in Section 4.2.

Table B1. Categorisation of wild bird species for detection between 5 October 2020 and 10 June 2022

Other wild bird species	Raptor	Waterfowl
Anambra waxbill	Accipitridae	Anatidae
Ardeidae	Accipitriformes	Anatinae
Black-headed gull	Barn owl	Anserinae
Calidris	Bearded Vulture	Barnacle goose
Carrion crow	Common kestrel	Bean goose
Caspian gull	Common buzzard	Black swan
Charadriidae	Eurasian eagle-owl	Brent goose
Ciconiidae	Eurasian sparrowhawk	Canada goose
Columbidae	Falconidae	Common eider
Common blackbird	Golden eagle	Common goldeneye
Common coot	Griffon vulture	Common guillemot
Common crane	Little owl	Common merganser
Common magpie	Long-eared owl	Common shelduck
Common moorhen	Merlin	Common teal
Common pheasant	Montagu's harrier	Cygnus
Common raven	Northern goshawk	Egyptian goose
Common redshank	Peregrine falcon	Eurasian wigeon
Common starling	Red kite	Ferruginous duck
Common wood-pigeon	Rough-legged hawk	Gadwall
Corvidae	Short-eared owl	Garganey
Curlew sandpiper	Strigidae	Goose
Dalmatian pelican	Strigiformes	Greater scaup
Dunlin	Tawny owl	Greater white-fronted goose
Eurasian collared-dove	Ural owl	Greylag goose
Eurasian curlew	Western marsh harrier	Lesser white-fronted goose
Eurasian jackdaw	White-tailed eagle	Little grebe
Eurasian jay		Mallard
Eurasian oystercatcher		Muscovy duck
Eurasian spoonbill		Mute swan
Eurasian woodcock		Pink-footed goose
European greenfinch		Tufted duck
Fringillidae		Tundra bean goose
Great black-backed gull		Whooper swan
Great blue heron		
Great cormorant		

Great crested grebe		
Great egret		
Great skua		
Green sandpiper		
Grey heron		
Grey-headed gull		
Gruidae		
Haematopodidae		
Herring gull		
House sparrow		
Laridae		
Larinae		
Lesser black-backed gull		
Little egret		
Mediterranean gull		
Mew gull		
Northern gannet		
Northern lapwing		
Passeridae		
Phalacrocoracidae		
Phasianidae		
Pied avocet		
Pink-backed pelican		
Rallidae		
Red knot		
Rook		
Ruddy turnstone		
Sanderling		
Sandwich tern		
Scolopacidae		
Semipalmated sandpiper		
Turdidae		
Water rail		
Western gull		
Western sandpiper		
White stork		
White-rumped sandpiper		
Yellow-legged gull		
Unknown wild bird species		

Table B2. Common and scientific name of the wild bird species

Common name	Scientific name	Common name	Scientific name
Anambra waxbill	<i>Estrilda poliopareia</i>	Barn owl	<i>Tyto alba</i>
American black duck	<i>Anas rubripes</i>	Barnacle goose	<i>Branta leucopsis</i>
American crow	<i>Corvus brachyrhynchos</i>	Barred owl	<i>Strix varia</i>
American green-winged teal	<i>Anas carolinensis</i>	Bean goose	<i>Anser fabalis</i>
American robin	<i>Turdus migratorius</i>	Bearded vulture	<i>Gypaetus barbatus</i>
American wigeon	<i>Mareca americana</i>	Black swan	<i>Cygnus atratus</i>
Baikal teal	<i>Sibirionetta formosa</i>	Black-billed magpie	<i>Pica hudsonia</i>
Bald eagle	<i>Haliaeetus leucocephalus</i>	Black-headed gull	<i>Larus ridibundus</i>

Common name	Scientific name	Common name	Scientific name
Blue-winged teal	<i>Spatula discors</i>	European herring gull	<i>Larus argentatus</i>
Brent goose	<i>Branta bernicla</i>	Ferruginous duck	<i>Aythya nyroca</i>
Canada goose	<i>Branta canadensis</i>	Fish crow	<i>Corvus ossifragus</i>
Carrion crow	<i>Corvus corone</i>	Gadwall	<i>Mareca strepera</i>
Caspian gull	<i>Larus cachinnans</i>	Garganey	<i>Spatula querquedula</i>
Caspian tern	<i>Hydroprogne caspia</i>	Golden eagle	<i>Aquila chrysaetos</i>
Common coot	<i>Fulica atra</i>	Goose	<i>Anser spp.</i>
Common crane	<i>Grus grus</i>	Great blue heron	<i>Ardea herodias</i>
Common eider	<i>Somateria mollissima</i>	Great cormorant	<i>Phalacrocorax carbo</i>
Common goldeneye	<i>Bucephala clangula</i>	Great crested grebe	<i>Podiceps cristatus</i>
Common guillemot	<i>Uria aalge</i>	Great egret	<i>Ardea alba</i>
Common kestrel	<i>Falco tinnunculus</i>	Great horned owl	<i>Bubo virginianus</i>
Common loon	<i>Gavia immer</i>	Great skua	<i>Catharacta skua</i>
Common magpie	<i>Pica pica</i>	Great-tailed grackle	<i>Quiscalus mexicanus</i>
Common merganser	<i>Mergus merganser</i>	Greater scaup	<i>Aythya marila</i>
Common moorhen	<i>Gallinula chloropus</i>	Greater white-fronted goose	<i>Anser albifrons</i>
Common pheasant	<i>Phasianus colchicus</i>	Green sandpiper	<i>Tringa ochropus</i>
Common pochard	<i>Aythya ferina</i>	Grey heron	<i>Ardea cinerea</i>
Common raven	<i>Corvus corax</i>	Grey-headed gull	<i>Larus cirrocephalus</i>
Common redshank	<i>Tringa totanus</i>	Greylag goose	<i>Anser anser</i>
Common shelduck	<i>Tadorna tadorna</i>	Griffon vulture	<i>Gyps fulvus</i>
Common starling	<i>Sturnus vulgaris</i>	Gulls, Terns and Skimmers	<i>Laridae</i>
Common teal	<i>Anas crecca</i>	Hen harrier	<i>Circus cyaneus</i>
Common wood-pigeon	<i>Columba palumbus</i>	Herring gull	<i>Larus argentatus</i>
Cormorants and Shags	<i>Phalacrocoracidae</i>	Harris's hawk	<i>Parabuteo unicinctus</i>
Cooper's hawk	<i>Accipiter cooperii</i>	Hooded crow	<i>Corvus corone</i>
Curlew sandpiper	<i>Calidris ferruginea</i>	House sparrow	<i>Passer domesticus</i>
Dalmatian pelican	<i>Pelecanus crispus</i>	Kites, Hawks and Eagles	<i>Accipitridae</i>
Double-crested cormorant	<i>Nannopterum auritum</i>	Large billed crow	<i>Corvus macrorhynchos</i>
Dunlin	<i>Calidris alpina</i>	Laughing gull	<i>Leucophaeus atricilla</i>
Egyptian goose	<i>Alopochen aegyptiaca</i>	Lesser black-backed gull	<i>Larus fuscus</i>
Eurasian blackbird	<i>Turdus merula</i>	Lesser white-fronted goose	<i>Anser erythropus</i>
Eurasian buzzard	<i>Buteo buteo</i>	Little egret	<i>Egretta garzetta</i>
Eurasian collared-dove	<i>Streptopelia decaocto</i>	Little grebe	<i>Tachybaptus ruficollis</i>
Eurasian curlew	<i>Numenius arquata</i>	Little owl	<i>Athene noctua</i>
Eurasian eagle-owl	<i>Bubo bubo</i>	Long-eared owl	<i>Asio otus</i>
Eurasian jackdaw	<i>Corvus monedula</i>	Mallard	<i>Anas platyrhynchos</i>
Eurasian jay	<i>Garrulus glandarius</i>	Mediterranean gull	<i>Larus melanocephalus</i>
Eurasian oystercatcher	<i>Haematopus ostralegus</i>	Merlin	<i>Falco columbarius</i>
Eurasian sparrowhawk	<i>Accipiter nisus</i>	Mew gull	<i>Larus canus</i>
Eurasian spoonbill	<i>Platalea leucorodia</i>	Montagu's harrier	<i>Circus pygargus</i>
Eurasian wigeon	<i>Mareca penelope</i>	Mountain hawk-eagle	<i>Nisaetus nipalensis</i>
Eurasian woodcock	<i>Scolopax rusticola</i>	Muscovy duck	<i>Cairina moschata</i>
European greenfinch	<i>Chloris chloris</i>	Mute swan	<i>Cygnus olor</i>

Common name	Scientific name	Common name	Scientific name
Northern gannet	<i>Morus bassanus</i>	Sharp-shinned hawk	<i>Accipiter striatus</i>
Northern goshawk	<i>Accipiter gentilis</i>	Short-eared owl	<i>Asio flammeus</i>
Northern lapwing	<i>Vanellus vanellus</i>	Snow goose	<i>Anser caerulescens</i>
Northern pintail	<i>Anas acuta</i>	Snowy owl	<i>Bubo scandiacus</i>
Northern shoveler	<i>Spatula clypeata</i>	Song thrush	<i>Turdus philomelos</i>
Pallas's gull	<i>Ichthyaetus ichthyaetus</i>	Spotted harrier	<i>Circus assimilis</i>
Peregrine falcon	<i>Falco peregrinus</i>	Tawny owl	<i>Strix aluco</i>
Phalacrocoracidae	<i>Phalacrocoracidae</i>	True owls	<i>Strigidae</i>
Pheasant	<i>Phasianus colchicus</i>	Trumpeter swan	<i>Cygnus columbianus</i>
Pheasants and allies	<i>Phasianidae</i>	Tufted duck	<i>Aythya fuligula</i>
Pied avocet	<i>Recurvirostra avosetta</i>	Tundra bean goose	<i>Anser fabalis</i>
Pink-footed goose	<i>Anser brachyrhynchus</i>	Tundra swan	<i>Cygnus columbianus</i>
Red kite	<i>Milvus milvus</i>	Turkey vulture	<i>Cathartes aura</i>
Red knot	<i>Calidris canutus</i>	Ural owl	<i>Strix uralensis</i>
Red-tailed hawk	<i>Buteo jamaicensis</i>	Water rail	<i>Rallus aquaticus</i>
Ring-billed gull	<i>Larus delawarensis</i>	Western grebe	<i>Aechmophorus occidentalis</i>
Rock pigeon	<i>Columba livia</i>	Western gull	<i>Larus occidentalis</i>
Rook	<i>Corvus frugilegus</i>	Western marsh harrier	<i>Circus aeruginosus</i>
Ross's goose	<i>Anser rossii</i>	Western sandpiper	<i>Calidris mauri</i>
Rough-legged hawk	<i>Buteo lagopus</i>	White-rumped sandpiper	<i>Calidris fuscicollis</i>
Royal tern	<i>Thalasseus maximus</i>	White-tailed eagle	<i>Haliaeetus albicilla</i>
Ruddy duck	<i>Oxyura jamaicensis</i>	Whooper swan	<i>Cygnus cygnus</i>
Ruddy turnstone	<i>Arenaria interpres</i>	Wild turkey	<i>Meleagris gallopavo</i>
Sanderling	<i>Calidris alba</i>	Wood duck	<i>Aix sponsa</i>
Sandhill crane	<i>Antigone canadensis</i>	Yellow-legged gull	<i>Larus michahellis</i>
Sandwich tern	<i>Thalasseus sandvicensis</i>	White stork	<i>Ciconia ciconia</i>
Semipalmated sandpiper	<i>Calidris pusilla</i>		

B.1.1.1. Literature review on phenotypic characterisation of HPAI viruses circulating in the EU

Information on the phenotypic characterisation of AI viruses circulating in the EU was extracted from the scientific literature by performing a literature review.

Review question Update on the phenotypic characterisation of HPAI viruses circulating in the EU in domestic and wild birds within the last 2 years.

Search The PubMed database was searched using subject index terms and free-text terms combined with the appropriate Boolean operators. Scientific articles added to the database from 2 March to 3 June 2022 were searched; the search was run on 3 June 2022.

Relevance criteria Scientific articles added to the database from 2 March to 3 June 2022 and reporting information on the presence or absence of clinical signs or pathological changes or mortality due to HPAI infection with viruses circulating within the last 2 years in the EU in domestic or wild birds.

Eligibility criteria Host species all domestic birds or wild birds present in the EU; the virus subtype should be reported; for experimental studies only, the age of the infected animals should be reported (at least as juvenile/adult).

Results The search retrieved 139 papers. The articles were subsequently screened against the relevance and eligibility criteria. Five of the screened papers were finally taken into consideration in the description of the phenotypic characterisation of HPAI viruses circulating in the EU in domestic and wild birds in the reporting period.

The search protocol and the results can be consulted at <https://doi.org/10.5281/zenodo.6769158>.

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

Data from WOAHA WOHIS (WOAHA, online-c) 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 extracted on 10 June 2022.

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.

List of Annexes

The annexes are available on the EFSA Knowledge Junction community on Zenodo at:

<https://doi.org/10.5281/zenodo.6780350>

The annexes contain the following information:

Annex A – Characteristics of the HPAI A(H5Nx)-positive poultry establishments

The Annex contains table with the characteristics of the HPAI A(H5Nx)-positive poultry establishments by affected EU Member State from 4 March to 1 June 2022.

Annex B – Applied prevention and control measures on avian influenza

The Annex contains an overview of specific prevention and control measures applied in Albania, Belgium, Bulgaria, Czechia, France, Hungary, Iceland, Italy, Moldova, Kosovo¹², Netherlands, Poland, Romania, Slovakia, Spain, from 1 December 2021 to 4 March 2022 in relation to HPAI outbreaks in poultry and in wild birds.

Annex C – Data on wild birds

The Annex contains tables and plots on HPAI notifications in wild birds in Europe.

¹² 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