

APPROVED: 28 September 2022

doi:10.2903/j.efsa.2022.7597

Avian influenza overview June – September 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, Irene Muñoz Guajardo,
Kateryna Chuzhakina and Francesca Baldinelli

Abstract

The 2021–2022 highly pathogenic avian influenza (HPAI) epidemic season is the largest HPAI epidemic so far observed in Europe, with a total of 2,467 outbreaks in poultry, 47.7 million birds culled in the affected establishments, 187 outbreaks in captive birds, and 3,573 HPAI virus detections in wild birds with an unprecedented geographical extent reaching from Svalbard islands to South Portugal and Ukraine, affecting 37 European countries. Between 11 June and 9 September 2022, 788 HPAI virus detections were reported in 16 European countries in poultry (56), captive (22) and wild birds (710). Several colony-breeding seabird species exhibited widespread and massive mortality from HPAI A(H5N1) virus along the northwest coast of Europe. This resulted in an unprecedentedly high level of HPAI virus detections in wild birds between June and August 2022 and represents an ongoing risk of infection for domestic birds. HPAI outbreaks were still observed in poultry from June to September with five-fold more infected premises than observed during the same period in 2021 and mostly distributed along the Atlantic coast. Response options to this new epidemiological situation include the definition and rapid implementation of suitable and sustainable HPAI mitigation strategies such as appropriate biosecurity measures and surveillance strategies for early detection in the different poultry production systems. The viruses currently circulating in Europe belong to clade 2.3.4.4b with seven genotypes, three of which identified for the first time during this time period, being detected during summer. HPAI A(H5) viruses were also detected in wild mammal species in Europe and North America and showed genetic markers of adaptation to replication in mammals. Since the last report, two A(H5N6), two A(H9N2) and one A(H10N3) human infections were reported in China. 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

Requestor: European Commission

Question number: EFSA-Q-2022-00525

Correspondence: biohaw@efsa.europa.eu

Acknowledgements: In addition to the listed authors, EFSA, ECDC and the EURL wish to thank the following: Member State representatives who provided epidemiological data on avian influenza outbreaks or shared sequence data: Lika Aldin (Albania), Irene Zimpernik and Sandra Revilla-Fernandez (Austria), Mieke Steensels and Steven Van Borm (Belgium), Aleksandra Miteva and Gabriela Goujgoulova (Bulgaria), Tihana Miškić, Gordana Nedeljković and Vladimir Savic (Croatia), Charlotte Kristiane Hjulsager (Denmark), Imbi Nurmoja (Estonia), Niina Tammiranta (Finland), Béatrice Grasland, Audrey Schmitz, Karen Bucher, Elisa Bohin, François-Xavier Briand, Axelle Scoizec and Célia Locquet (France), Carola Sauter-Louis and Timm Harder (Germany), George Georgiades (Greece), Georgina Helyes, Bálint Ádám and Malik Péter (Hungary), Laura Garza Cuartero (Ireland), Brigitte Brugger (Iceland), Bianca Zecchin and Isabella Monne (Italy), Armend Cana, (Kosovo), Gediminas Pridotkas (Lithuania), Chantal Snoeck (Luxembourg), Oxana Groza, Vitalie Caraus and Oxana Papa (Moldova), Michael McMenamy (United Kingdom (Northern Ireland)), Britt Gjerset (Norway), Aleksandra Podražka, Krzysztof Śmietanka and Edyta Swieton (Poland), Margarida Duarte, Renata Carvalho, Ana Caria Nunes, Yolanda Vaz and Susana Pombo (Portugal), Marcel Spierenburg, Dennis Bol and Nancy Beerens (the Netherlands), Onita Iuliana, (Romania), Brigita Slavec (Slovenia), Elena García Villacieros, Luis José Romero Gonzalez, Germán Cáceres Garrido and Azucena Sánchez (Spain), Siamak Zohari, (Sweden); Ian Brown from the Animal and Plant Health Agency (United Kingdom); Ilya Chvala from Federal Center for Animal Health (FGBI 'ARRIAH', Russia); Camille Delavenne from AUSVET Europe for conducting the data analysis under the contract OC/EFSA/ALPHA/2021/02; Paolo Tizzani from WOAHP for the support provided with WAHIS data; Paolo Calistri and Karl Stahl from the EFSA AHAW Panel for reviewing the report; Grazina Mirinavičiute from ECDC, Linnea Lindgren Kero, Lisa Kohnle and Gina Cioacata from EFSA for the support provided to this scientific output; we gratefully acknowledge the authors, originating and submitting laboratories of the sequences from GISAID's EpiFlu™ Database, which is used for this assessment.

Suggested citation: EFSA (European Food Safety Authority), ECDC (European Centre for Disease Prevention and Control), EURL (European Reference Laboratory for Avian Influenza), Adlhoch C, Fusaro A, Gonzales JL, Kuiken T, Marangon S, Niqueux É, Staubach C, Terregino C, Aznar I, Chuzhakina K, Muñoz Guajardo I and Baldinelli F, 2022. Scientific report: Avian influenza overview June–September 2022. *EFSA Journal* 2022;20(10):7597, 58 pp. <https://doi.org/10.2903/j.efsa.2022.7597>

ISSN: 1831-4732

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The EFSA Journal is a publication of the European Food Safety Authority, an agency of the European Union.



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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 11 June and 9 September 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 11 June and 9 September 2022, is presented below.

2.1. Main observations

- In Europe, between 11 June and 9 September 2022 (based on the Animal Disease Information System (ADIS), WOA World Animal Health Information System (WOAH-WAHIS), and information provided by affected countries) 788 HPAI A(H5) detections³ were reported in poultry, captive and wild birds:
 - 56 outbreaks in poultry in Germany (15), the Netherlands (14), United Kingdom (10), France (6), Poland (4), Spain (3), Moldova and Portugal (2 each);
 - 710 virus detections in wild birds in Germany (199), France (142), the Netherlands (115), United Kingdom (69), Norway (48), Belgium (32), Sweden (28), Denmark (26), Ireland (15), Spain (11), Finland (9), Lithuania (6), Iceland (5), Portugal (3) and Poland (2);
 - 22 outbreaks in captive birds in the Netherlands (7), France (6), United Kingdom (4), Belgium (2), Portugal (2), Spain (1).
- Considering detections in wild birds, several seabird species exhibited widespread and massive mortality from HPAI A(H5N1) at their breeding colonies, including in Germany, the Netherlands, France and United Kingdom. This resulted in an unprecedentedly high level of HPAI virus detections in wild birds between June and August 2022, a period when no or only a low number of HPAI virus detections had been reported in wild birds in previous years.
- During this reporting period, at least 63 wild bird species were involved: at least 11 waterfowl species (109 detections), 11 raptor species (38 detections), 15 other wild bird species (101 detections) and at least 28 colony-breeding seabird species (541 detections). The latter is a wild bird category firstly used in the current report (in addition to raptors, waterfowls and other wild bird species) to describe the HPAI epidemiological situation during this summer.
- The overall temporal pattern shows an increase in HPAI virus detections in wild birds since the previous reporting period (710 versus 525 detections), which is due to the increased number of detections in colony-breeding seabirds (493 vs 150) and in other wild birds (90 vs 66), while the number of detections in waterfowls (99 vs 224) and raptors (28 vs 85) was lower.
- In the current reporting period, the number of outbreaks in domestic birds rapidly declined after the two peaks of infection observed from fall 2021 to spring 2022. In August, however, a third

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.

minor peak was observed, and the number of infected poultry premises observed between June and September 2022 was five-fold higher than the one detected during the same period in the previous epidemic season. The outbreaks in domestic birds were primarily distributed along coastal areas.

- All the HPAI (H5Nx) viruses characterised since October 2021 in Europe belong to clade 2.3.4.4b. Based on the available genetic information, all the A(H5N1) viruses detected in the summer months belong to seven genotypes, three of which identified for the first time during this reporting period. One of these new genotypes, which resulted from reassortment events with viruses of the gull-adapted A(H13) subtype, has been extensively detected in European herring gulls in the Netherlands, Belgium and France, as well as in a fox in Belgium.
- During the summer months, three additional wild mammal species were affected by HPAI A(H5N1) virus in the EU countries: two red foxes (*Vulpes vulpes*) in Belgium and Norway and a harbour porpoise (*Phocoena phocoena*) in Sweden. Besides Europe, several HPAI A(H5N1) mammalian cases were reported in North America, with harbour seals (*Phoca vitulina*) and grey seals (*Halichoerus grypus*) as the main affected species.
- For the first time HPAI (H5N1) virus infections were reported in a harbour porpoise in Sweden, a bottlenose dolphin (*Tursiops truncatus*) in the USA and in an American black bear (*Ursus americanus*) in Canada.
- As expected during the summer months, the number of HPAI outbreaks and affected countries outside Europe between 11 June and 9 September 2022 has decreased compared to the last report (EFSA et al., 2022), but the number of reported HPAI A(H5N1) virus detections are still high compared to reports from the same period in previous years (EFSA et al., 2019b; EFSA et al., 2020; EFSA et al., 2021a). Furthermore, outbreaks in domestic poultry and wild birds in China and Russia were detected in regions spatially linked to key migration areas.
- During this reporting period five new human infections with avian influenza viruses, all from China, have been reported since the last report: two A(H5N6), two A(H9N2) and one A(H10N3).

2.2. Conclusions

- During the 2021–2022 epidemic a total of 2,467 HPAI outbreaks in poultry with 47.7 million birds culled in the affected establishments, 187 detections in captive birds, and 3,573 HPAI events in wild birds have been confirmed. All of these detections were reported from 37 European countries. This epidemic is the largest so far observed in Europe. Similarly to previous epidemics, the number of reported wild bird events is an underestimate of the total number of wild birds that have been infected and 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.
- 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 virus transmission 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 HPAI epidemic season is still ongoing with virus detections in poultry and wild birds up to September 2022; as in the previous HPAI season, the observed longer persistence of the virus in wild birds, compared with the same period in previous years, indicates a continuous risk for HPAI virus to spread among wild birds and mammals, as well as for virus entry into poultry establishments.
- The high frequency of HPAI virus detections in colony-breeding seabirds along the northwest coast of Europe, together with spillover events to other wild birds sharing the habitat of those seabirds, imply a higher risk of HPAI virus incursion into poultry establishments located in this area.
- As autumn migration will take place in the coming months and the number of migratory wild birds, particularly waterbirds, wintering in European countries increases, it cannot be excluded that they will be at higher risk of HPAI virus infection than in previous years due to the observed persistence of HPAI virus in wild birds in Europe.
- The long duration of the avian influenza risk period represents a challenge for the sustainability of the reinforced biosecurity measures implemented along the poultry chain in high-risk areas or production sectors with a negative welfare and economic impacts (e.g. due to indoor confinement of free-range poultry for a prolonged time period). The persistent presence of HPAI A(H5) viruses in wild birds and in 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.

3. Options for response

- Considering the significant negative impact of these HPAI epidemics in the last years, and the ongoing HPAI risk posed by the sustained virus circulation in wild birds, short-term preparedness and medium- and long-term prevention strategies should be identified and implemented, primarily in densely populated poultry areas and poultry production systems that are highly susceptible to avian influenza exposure. These have been described in detail in the 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) virus, 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 would enhance understanding of these phenomena and provides a factual basis for assessing the ecological impact and coming up with policy decisions to avert HPAI outbreaks not only in poultry and humans but also in wild birds, both migratory and resident.
- 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 underlines the need to expand and strengthen 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 HPAI virus detections in wild birds that were reported in Europe via ADIS or WOA/WAHIS for seasons 2016–2017, 2017–2018, 2018–2019, 2019–2020, 2020–2021 and 2021–2022 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 virus 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 9 September 2022. Figure 4 shows the comparison between the geographical distribution of HPAI virus detections from June to September 2022 and the same period during the 2020–2021 season, which before this season was the largest HPAI epidemic recorded in the EU/EEA and United Kingdom 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 9 September 2022, is reported in Figure 5 by week of suspicion, virus subtype and host population.

The start of the HPAI 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 2016–2017 epidemic season, with a total of 2,781 HPAI virus detections was the largest HPAI epidemic ever recorded at that time. Out of all those virus detections 1,563 were in wild birds. In comparison with this epidemic the number of detections in wild birds in the 2020–2021 and 2021–2022 epidemics were 1.5 (2,406 detections) and 2.2 (3,573 HPAI virus detections so far) times higher. This increased trend may highlight the increased risk over the years of HPAI virus infections for wild bird species (Figure 2). Virus circulation in wild birds is associated with risk for introduction of infection in poultry and potential spread between poultry establishments. In 2016–2017, 1,208 HPAI outbreaks were reported in domestic birds, and the number was similar during the 2020–2021 epidemic season (1,385); however, the number of outbreaks during the current 2021–2022 epidemic season, is so far two times larger than those previous epidemics with a total of 2,654 outbreaks being reported up to 9 September 2022. This increase in the number of outbreaks could be attributed to increased risk of introduction from wild birds to poultry, due to higher levels of circulation in wild birds, resulting in increased number of primary introduction and increased risk of further between farm spread of HPAIV.

The 2021–2022 epidemic also has continued into the summer longer at a higher level than the 2020–2021 epidemic, with 371 HPAI virus detections in June 2022 (versus 21 in June 2021), 261 in July 2022 (16 in July 2021), and 159 in August 2022 (21 in August 2021) (Figures 1 and 4). 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. In the 2021–2022 season, there were three epidemic peaks in wild birds, in October, January and

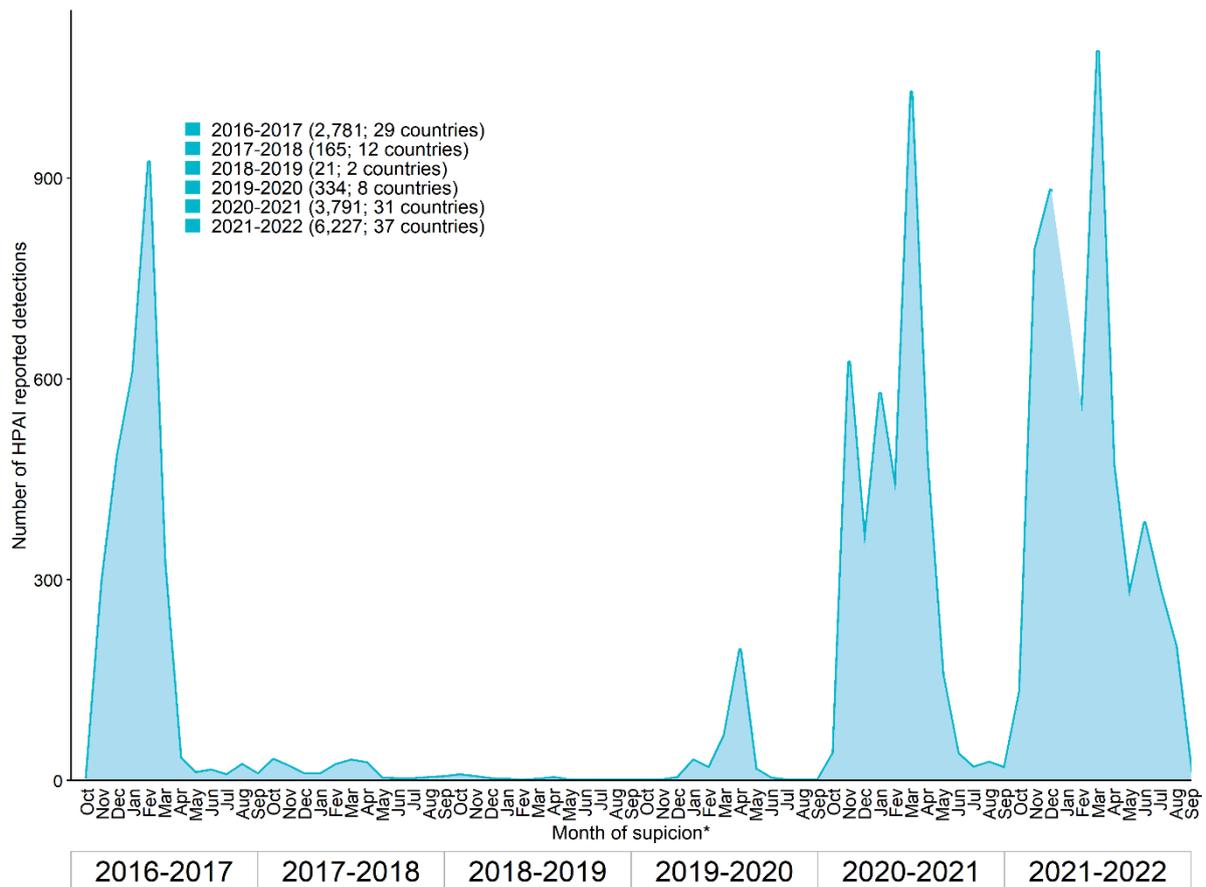
June, and they preceded the epidemic peaks in domestic birds in December, March and August, respectively (Figure 2).

The current 2021–2022 epidemic is widespread in Europe and is even more extensive than the previous 2016–2017 and 2020–2021 epidemics, with a northern limit from Iceland to northern Norway (including the Norwegian islands Svalbard and Jan Mayen) 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).

In poultry, large epidemics occurred in France (1,383 outbreaks), Italy (317), and Hungary (290), but also Poland (98), Germany (89), United Kingdom (83), and the Netherlands (62) were severely affected. After the two peaks of infection observed in winter 2021–2022 (Figure 2B), the number of poultry outbreaks decreased from April to June (Figure 5B). In August, however, a third minor peak of infection was observed, and from June to September 2022, the number of infected premises increased more than five times compared to the same period in the previous epidemic (Table 2). The outbreaks in domestic birds primarily occurred in proximity to coastal areas (Figures 4 and 7).

For wild birds, in 2021–2022 HPAI virus was detected predominantly in waterfowl until the end of April 2022. From the end of April to the middle of August, HPAI virus was detected mainly in colony-breeding seabird species, a category of wild birds that were only affected at a low scale in previous years, and were therefore not categorised separately in the previous published reports. The species included in this seabird category are provided in Appendix B, Table B.1. The high frequency of HPAI virus detections in colony-breeding seabird species lasted from May to August, with a peak in June; this roughly corresponds to the breeding season of seabirds in Europe. As a result, there was an unprecedented high level of HPAI virus detections in wild birds during the summer 2022, which was associated with an – again unprecedented – high number of HPAI virus detections in domestic birds during this period (Figure 5).

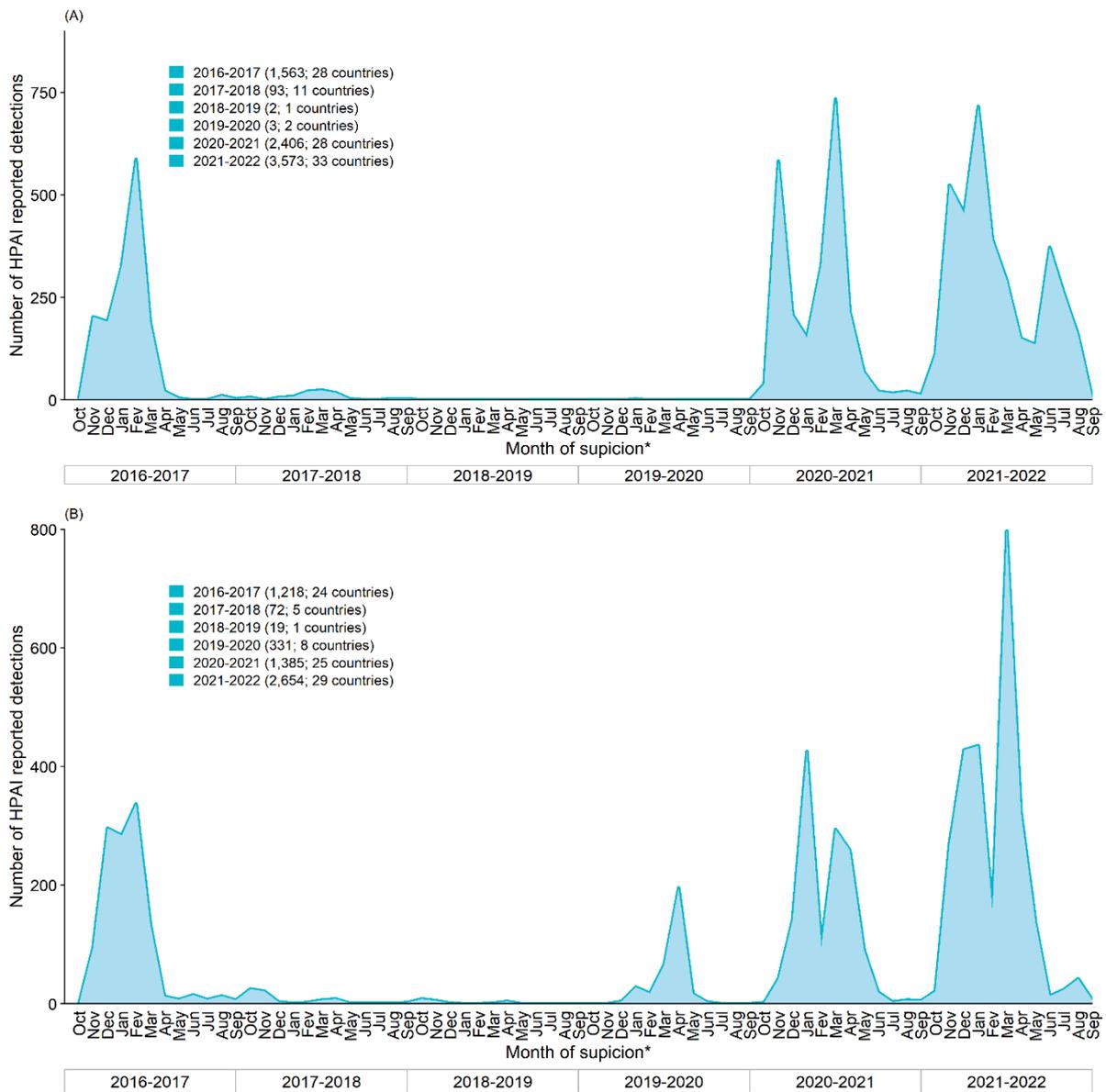
Considering only HPAI outbreaks in poultry, so far ~47.7 million of birds have been culled in the HPAI-affected establishments in the current epidemic season since October 2021.



*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)⁴.
 Source: ADIS and WOA (data extraction carried out on 9 September 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 1 October 2016 to 9 September 2022 (13,319)

⁴ 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).



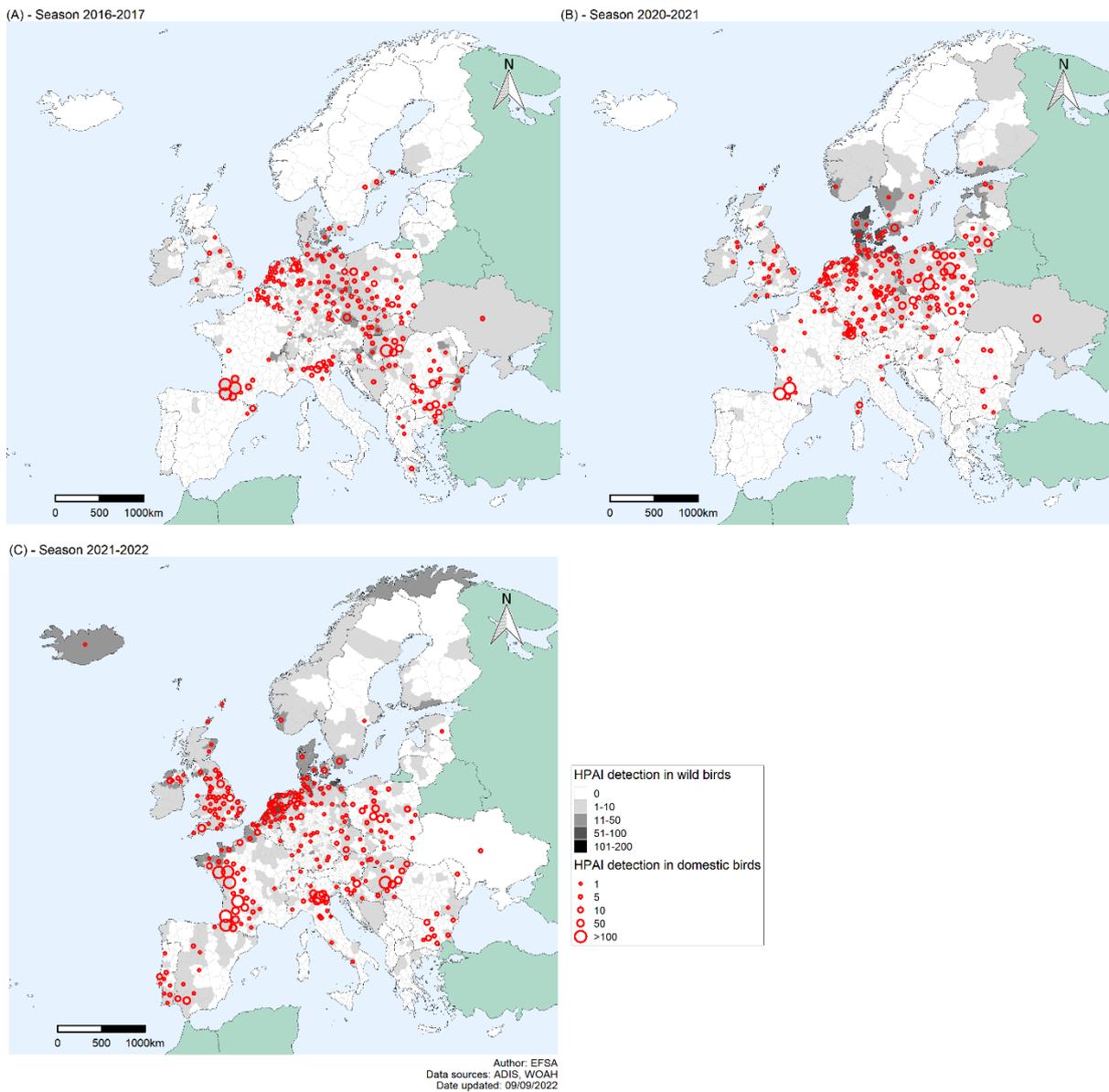
*When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.

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)⁴.

Source: ADIS and WOA (data extraction carried out 9 September 2022).

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

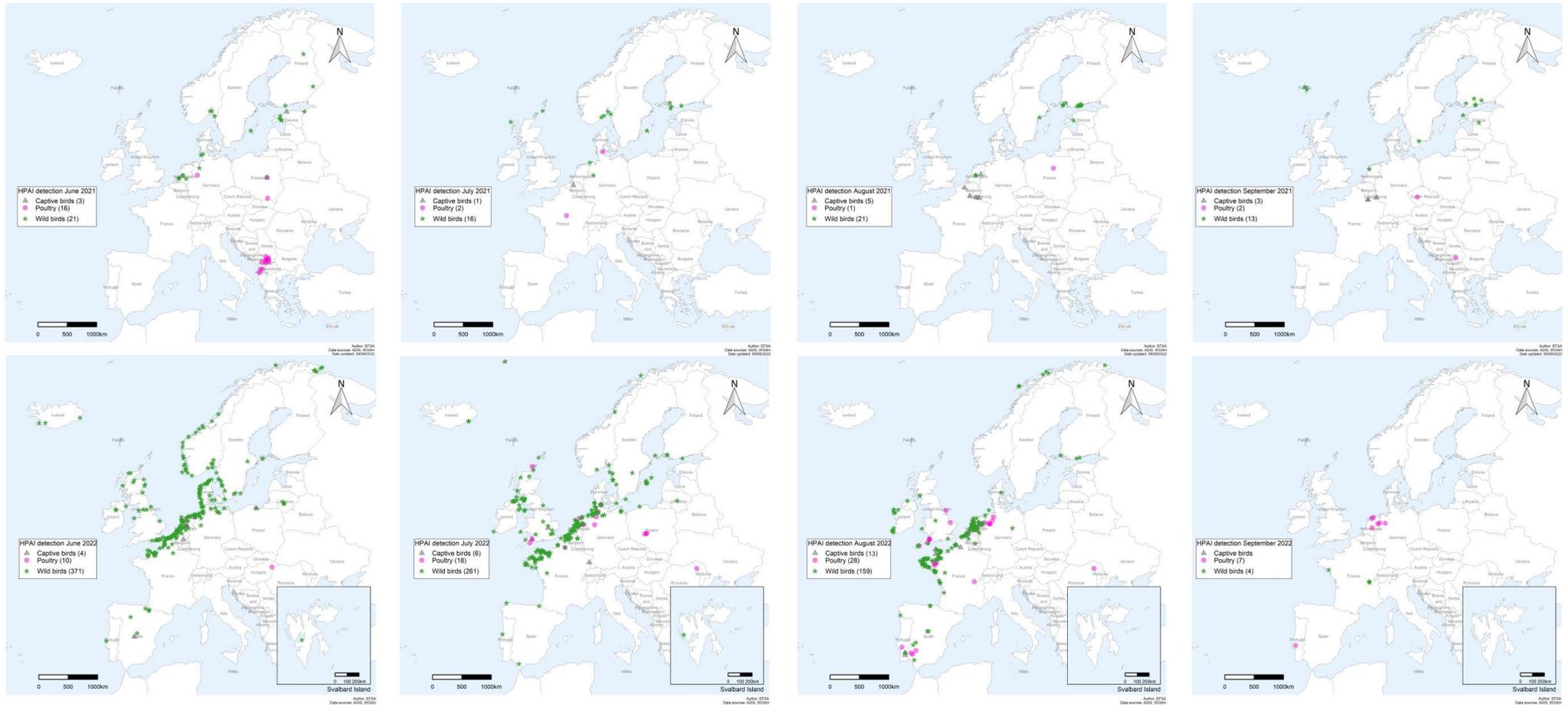
Figure 2: Distribution of number of HPAI virus detections reported in Europe in the seasons 2016–2017, 2017–2018, 2018–2019, 2019–2020, 2020–2021 and 2021–2022 by month of suspicion in (A) wild birds (7,640) and (B) domestic birds (poultry and captive birds) (5,679), from 1 October 2016 to 9 September 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)⁴.

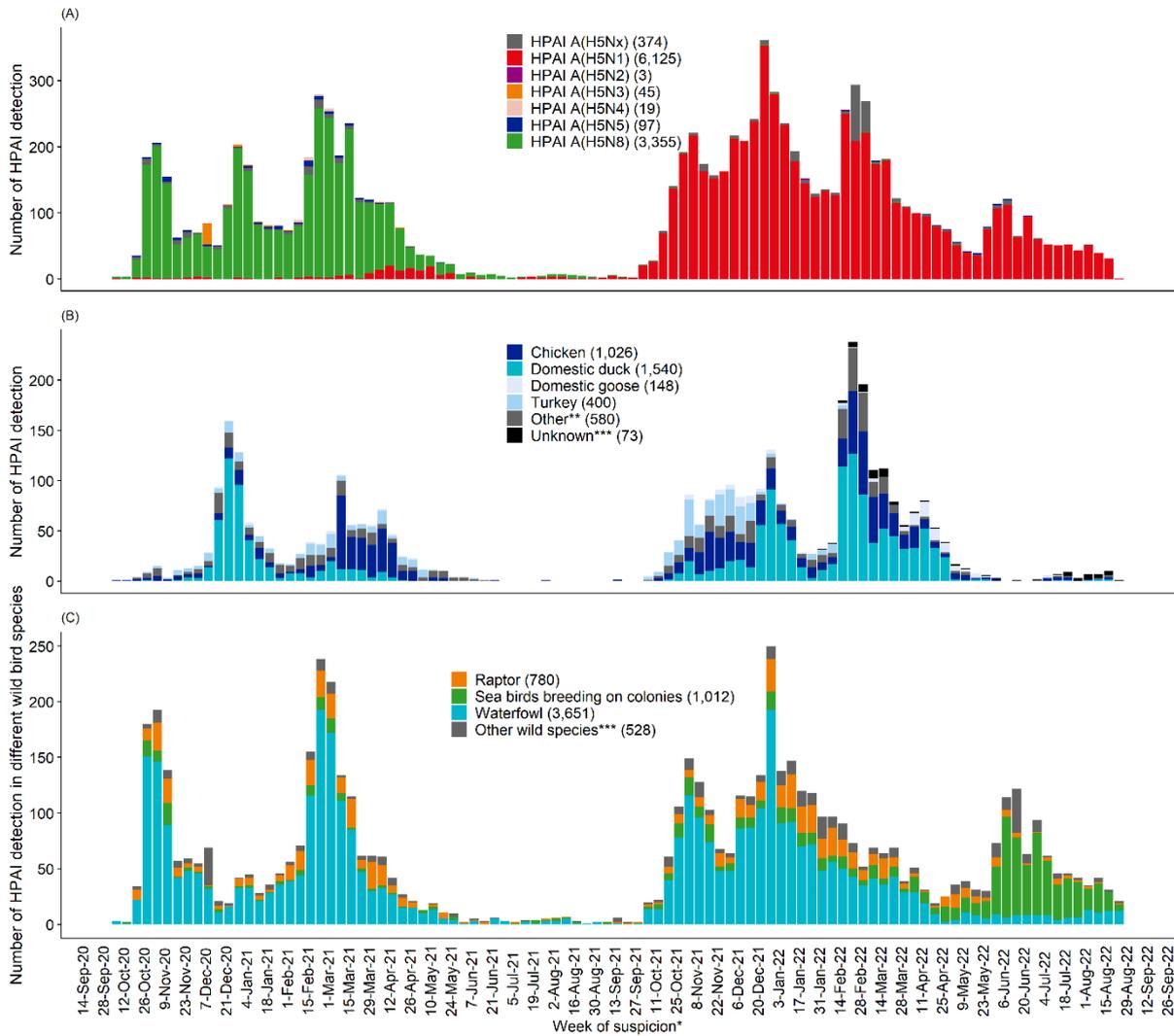
Source: ADIS and WOAH (data extraction carried out on 9 September 2022).

Figure 3: Geographical distribution at NUTS3 level of HPAI detections in Europe in seasons (A) 2016-2017 (2,781), (B) 2020–2021 (3,791) and (C) 2021–2022 (6,227) in domestic birds (red circles) and wild birds (grey coloured area), from 1 October 2016 to 9 September 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)⁴. Note that data in September 2022 are up to 9 September. Source: ADIS and WOA (data extraction carried out on 9 September 2022).

Figure 4: Geographical distribution, based on available geocoordinates, of HPAI detections in Europe by month of suspicion in 2020–2021 (top row) and 2021–2022 (bottom row)



*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 unknown bird species, or categories different from those displayed. The complete list of species by each wild bird category is reported in Table B.1 in Annex 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 the United Kingdom (Northern Ireland)⁴.

Source: ADNS, ADIS and WOA (data extraction carried out on 9 September 2022), EFSA.

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

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 (10,018), (B) affected poultry categories (3,767), (C) affected wild bird categories (5,971), from October 2020 to 9 September 2022

4.2. HPAI and LPAI detections in Europe, 11 June to 9 September 2022 (ToR 1 and ToR 2)

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

From 11 June to 9 September 2022, 788 HPAI A(H5) virus detections were notified in poultry (56), captive (22) and wild birds (710) to the ADIS or WOAH- 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 6, 7 and 8. The reported HPAI virus detections and outbreaks were distributed all over the reporting period and occurred in 16 European countries (Figure 6).

For wild birds, the highest number of HPAI virus reported detections were in Germany (199 detections), France (142), the Netherlands (115), and the United Kingdom (69) (Figure 7A and Table 1). Most of the HPAI virus detections were reported in colony-breeding seabird species that have not been previously affected by HPAI virus and were on the coast rather than inland. Their geographical distribution ranged from the northern tip of Norway and Svalbard and Jan Mayen islands in the north to the southern tip of Spain in the south, involving all countries bordering the north-east Atlantic Ocean with a concentration of detections along the western coasts of Denmark, Germany, the Netherlands, Belgium, and France, (Figure 7A). In contrast, there were no HPAI virus detections in wild birds in south-east Europe in this reporting period. This is the first time that HPAI virus has been detected in Svalbard (3) and Jan Mayen (1) islands (Norway), both in wild birds, far north of the Arctic Circle.

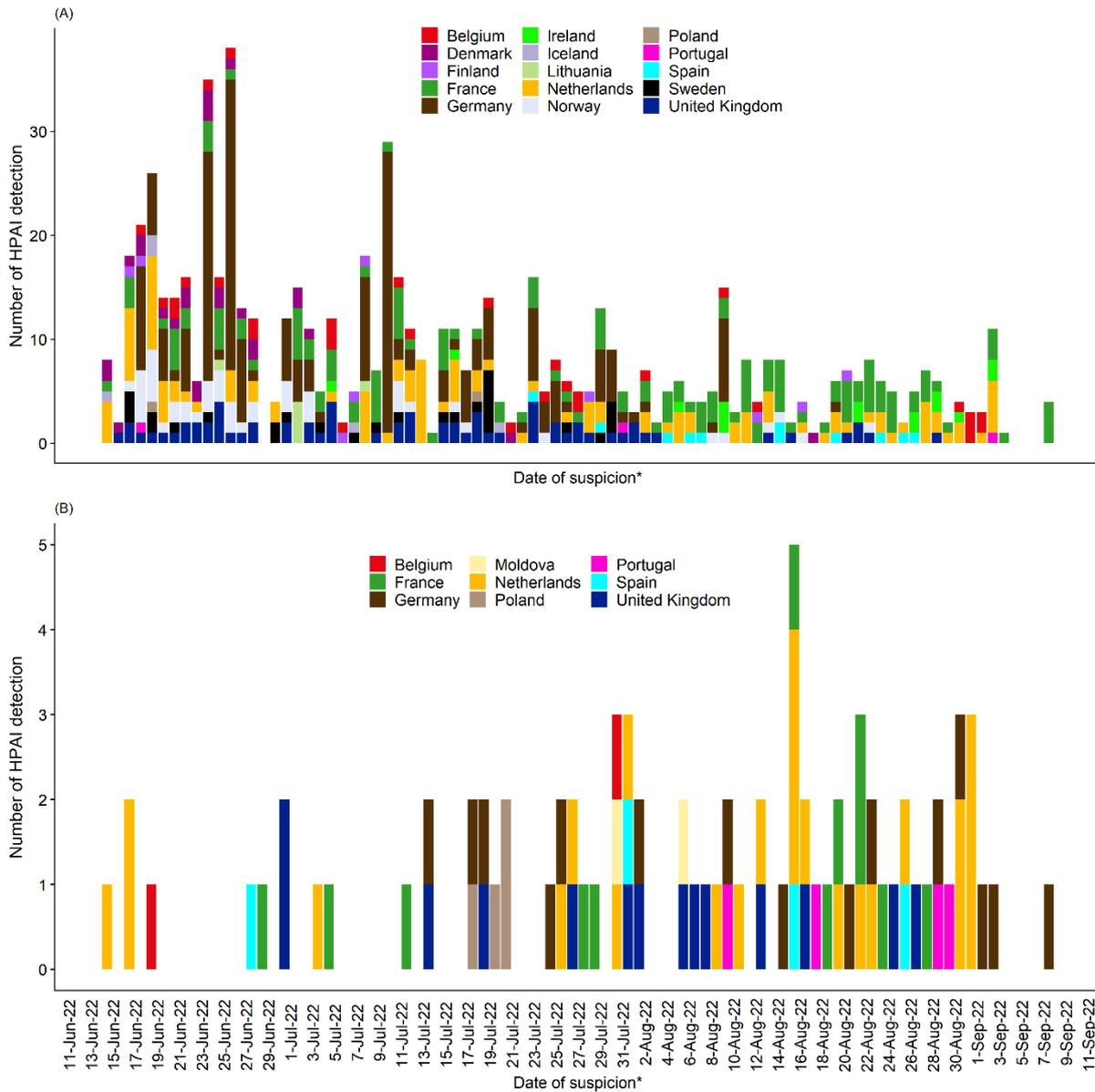
In domestic birds, HPAI outbreaks occurred primarily in north-west Europe (Germany, the Netherlands, United Kingdom, and France), and were mainly distributed along the Atlantic coastal areas, following the distribution of the HPAI events in wild birds, except for outbreaks in Poland and Moldova and to a lesser extent in southern part of Spain and Portugal. For poultry, Germany, the Netherlands and United Kingdom accounted together for 70% of the reported HPAI outbreaks. Overall, 1,9 million birds were culled in the HPAI poultry establishments with the Netherlands accounting for the 43% of the birds culled during this reporting period. In total, three poultry outbreaks were notified to the ADIS as secondary in Germany (1), Moldova (1) and Poland (1).

Characterisation of HPAI-affected poultry establishments⁵ 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.

HPAI A(H5N1) was by far the predominant virus type reported during this reporting period, with few exceptions for A(H5N5) virus detected in Norway in wild birds (6) and non-typed HPAI A(H5Nx) in Norway (15), and Germany (1) (Table 1).

Since 10 September and as of 29 September 2022, 210 HPAI A(H5) outbreaks were confirmed in domestic (33), captive (22) and wild birds (154) outside the reporting period for this report in France (61), the Netherlands (47), Spain (25), Ireland (24), Belgium (21), Germany (17), Northern Ireland (3), Portugal (3), Denmark (3), Norway (2), Poland (1), Finland (1), Italy (1). Those HPAI outbreaks were too close to the publication date to be described in this report and will be fully reported in the next report.

⁵ 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, pp. 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)⁴. Source: EFSA, ADIS and WOA (data extraction carried out on 9 September 2022). Please note that in panel B for the Netherlands, three HPAI outbreaks are erroneously presented as captive birds whereas they should be presented in panel A as HPAI detection in wild birds. This correction of the data was received too close to the publication date of this report to amend this figure. Note that the scale of the vertical axes is specific to each bird population.

Figure 6: Distribution of the highly pathogenic avian influenza virus detections in (A) wild birds (710) and (B) outbreaks in domestic birds (poultry and captive birds) (78), in Europe, by day of suspicion and country from 11 June to 9 September 2022

Table 1: Number of highly pathogenic avian influenza outbreaks in Europe, by country, virus subtype and affected sub-population, from 11 June to 9 September 2022. Cumulative numbers since the start of the 2021–2022 season are reported in parentheses (1 October 2021 to 9 September 2022)

Reporting 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)	-	-	-	(6)	-	(1)	-	-	-	(8)
Austria	-	(4)	-	-	-	-	-	(27)	-	-	-	(31)
Belgium	-	2 (4)	-	(4)	-	-	(6)	32 (105)	-	-	-	34 (119)
Bosnia and Herzegovina	-	-	-	-	-	-	-	(1)	-	-	-	(1)
Bulgaria	(1)	(2)	(9)	(16)	-	-	(2)	-	-	-	-	(30)
Croatia	-	-	-	(3)	-	-	-	(13)	-	-	-	(16)
Czechia	-	-	-	(19)	-	-	-	(9)	-	-	-	(28)
Denmark	-	(4)	-	(6)	-	(1)	(1)	26 (155)	-	-	(2)	26 (169)
Estonia	-	-	-	-	-	(1)	-	(9)	-	-	-	(10)
Finland	-	-	-	-	-	-	-	9 (28)	-	-	(1)	9 (29)
France	1 (3)	5 (43)	(146)	6 (1,237)	-	-	(5)	142 (209)	-	-	-	154 (1,643)
Germany	-	(9)	-	15 (89)	-	-	1 (13)	198 (1,490)	(2)	-	(1)	214 (1,604)
Greece	-	-	-	-	-	-	-	(16)	-	-	-	(16)
Kosovo ^a	-	-	-	-	-	(3)	-	-	-	-	-	(3)
Hungary	-	(4)	-	(290)	-	-	-	(29)	-	-	-	(323)
Iceland	-	-	-	(1)	-	-	-	5 (24)	-	-	-	5 (25)
Ireland	-	-	-	(6)	-	-	(2)	15 (59)	-	-	-	15 (67)
Italy	-	(1)	(4)	(313)	-	-	-	(22)	-	-	-	0 (340)
Latvia	-	-	-	-	-	-	-	(2)	-	-	-	0 (2)
Lithuania	-	-	-	-	-	-	-	6 (11)	-	-	-	6 (11)
Luxembourg	-	-	-	-	-	-	-	(5)	-	-	-	0 (5)
Moldova	-	-	-	2 (4)	-	-	-	-	-	-	-	2 (4)
Netherlands	-	7 (12)	-	14 (62)	-	-	(38)	115 (628)	-	-	(2)	136 (742)
Montenegro	-	-	-	-	-	-	-	(1)	-	-	-	(1)
North Macedonia	-	-	-	-	-	-	-	(3)	-	-	-	(3)
Norway	-	-	-	(2)	-	-	15 (17)	27 (40)	-	6 (19)	-	48 (78)
Poland	-	-	-	4 (97)	(1)	-	-	2 (36)	-	-	-	(134)
Portugal	-	2 (8)	-	2 (10)	-	-	-	3 (9)	-	-	-	7 (27)
Romania	-	-	-	(3)	-	-	(1)	(15)	-	-	-	(19)
Serbia	-	-	-	(3)	-	-	-	(4)	-	-	-	(7)
Slovakia	-	(2)	-	(4)	-	-	(1)	(6)	-	-	-	(13)
Slovenia	-	(37)	-	(1)	-	-	-	-	-	-	-	(38)

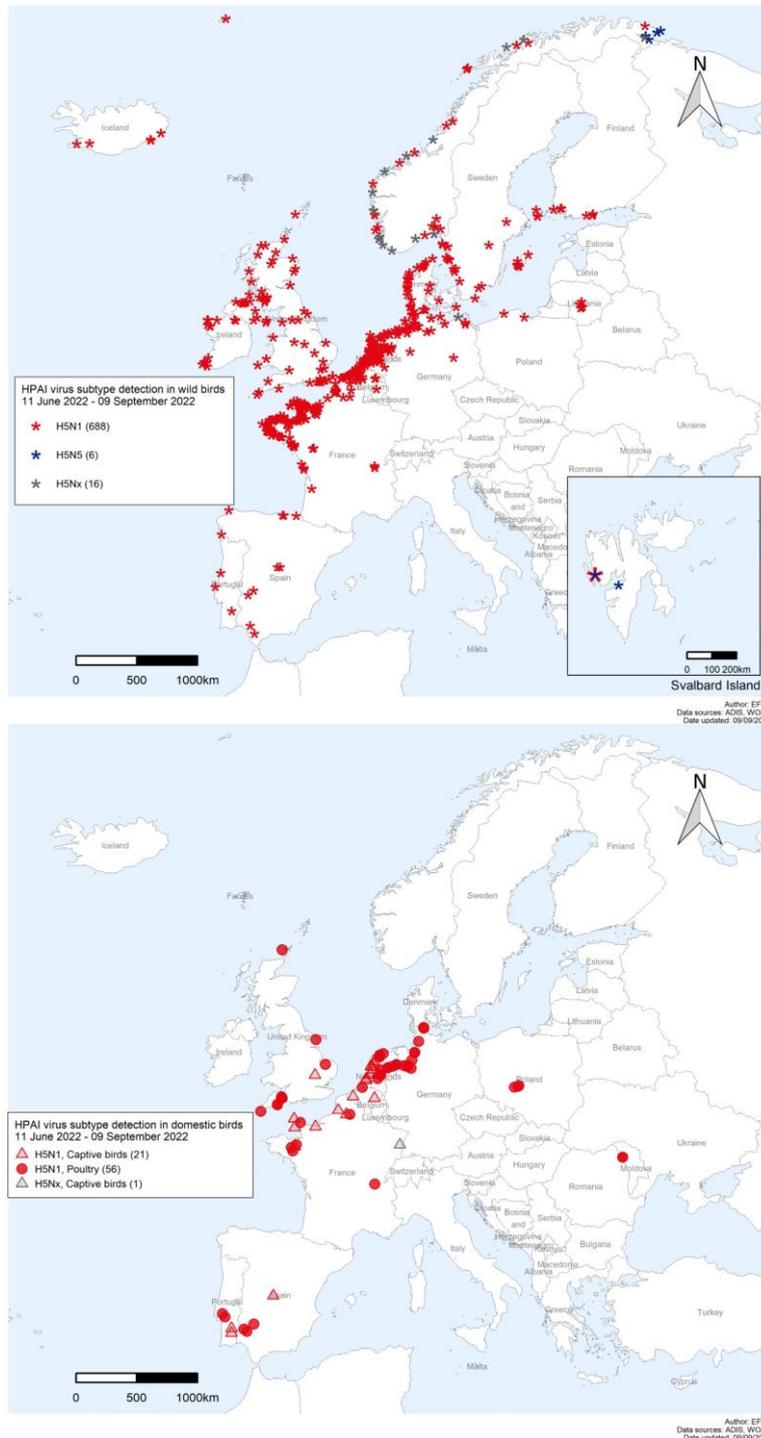
Reporting country	Captive birds		Poultry				Wild birds					Total
	A(H5Nx)	A(H5N1)	A(H5Nx)	A(H5N1)	A(H5N2)	A(H5N8)	A(H5Nx)	A(H5N1)	A(H5N2)	A(H5N5)	A(H5N8)	
Spain	-	1 (3)	-	3 (34)	-	-	(2)	11 (60)	-	-	-	15 (99)
Sweden	-	(4)	-	(3)	-	-	-	28 (78)	-	-	(1)	28 (86)
Switzerland	-	(2)	-	-	-	-	-	(1)	-	-	-	(3)
United Kingdom^b	-	4 (41)	-	10 (89)	-	-	-	69 (360)	-	-	(1)	83 (491)
Ukraine	(2)	-	-	-	-	-	-	-	-	-	-	(2)
Total	1 (6)	21 (181)	(159)	56 (2,296)	(1)	(11)	16 (88)	688 (3,456)	(2)	6 (19)	(8)	788 (6,227)

(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)⁴.

'-' means that no HPAI outbreaks or detections were notified to ADIS or WOAHA.

Source: EFSA, ADNS and WOAHA (data extraction carried out on 9 September 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)⁴.

Source: EFSA, ADIS and WOHIS (data extraction carried out on 9 September 2022).

Figure 7: Geographical distribution, based on available geocoordinates, of highly pathogenic avian influenza virus detections in wild birds (710) (upper panel) and outbreaks in poultry and captive birds (78) (lower panel) reported by virus subtype in Europe from 11 June to 9 September 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 that occurred later than 2 September 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 was 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 2 to 10 June 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 11 June to 9 September 2022, in total, 56 poultry outbreaks were notified in eight countries through ADIS or WOA: 15 in Germany, 14 in the Netherlands, 10 in United Kingdom, six in France, four in Poland, three in Spain and two each in Moldova and Portugal (Figure 9). Overall, 1.9 million birds were culled in the affected establishments. Germany accounted for 27% of the reported outbreaks and 27% of the birds that were culled in the HPAI establishments, followed by Netherlands, 25% of the outbreaks and 43% of the birds culled, United Kingdom 18% and 5% respectively, France 11% and 4% respectively, Poland 7% and 6% respectively, Spain 5% and 3%, respectively, Portugal, 4% and 12% respectively, and Moldova 4% and 0% respectively (Figure 8).

Compared with the previous reporting period (from 16 March to 10 June 2022), during which 757 outbreaks were notified by 18 affected countries, approximately 93% fewer outbreaks were notified during this period (Table 2). A similar decreasing trend was also observed between the same reporting periods in 2021, when 98% fewer outbreaks were reported from 11 June to 9 September 2021 compared with the period from 16 March to 10 June 2021. However, five times more outbreaks were reported in the current reporting period (11 June to 9 September 2022) compared with the same period in 2021 where a total of 10 poultry outbreaks were reported in Europe (Table 2).

Table 2 Number of highly pathogenic avian influenza outbreaks in poultry in Europe, by reporting period and epidemic season

Epidemic season	2020–2021		2021–2022	
	16 March to 10 June	11 June to 9 September	16 March to 10 June	11 June to 9 September
Number of HPAI poultry outbreaks	515	10	757	56

As in the previous reporting period (from 16 March to 10 June 2022) fattening establishments, regardless the species reared, remained the most affected category (Figure 9). It is of note the marked increase in the number of outbreaks in fattening chickens (broilers) during this season compared to previous season.

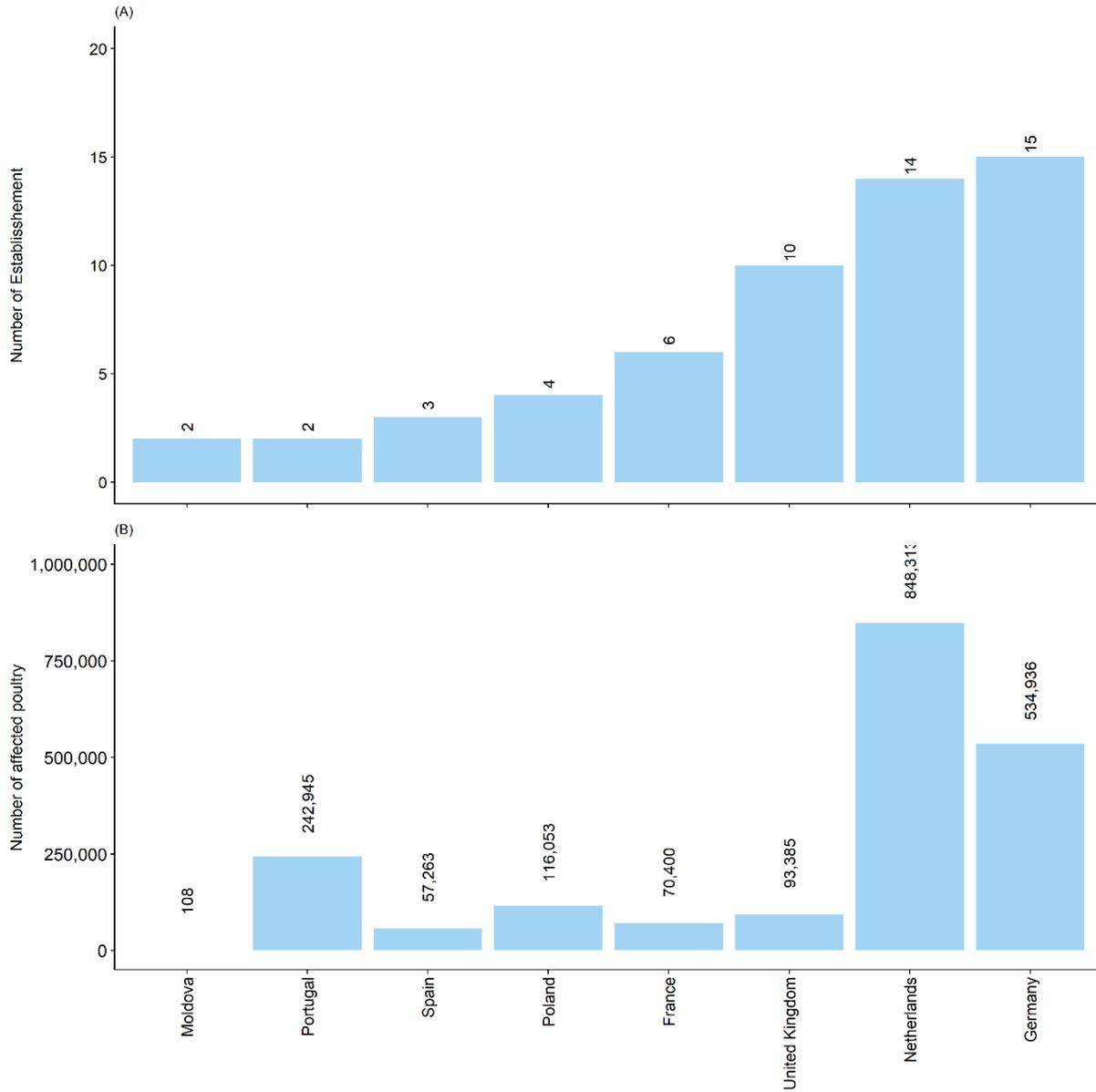
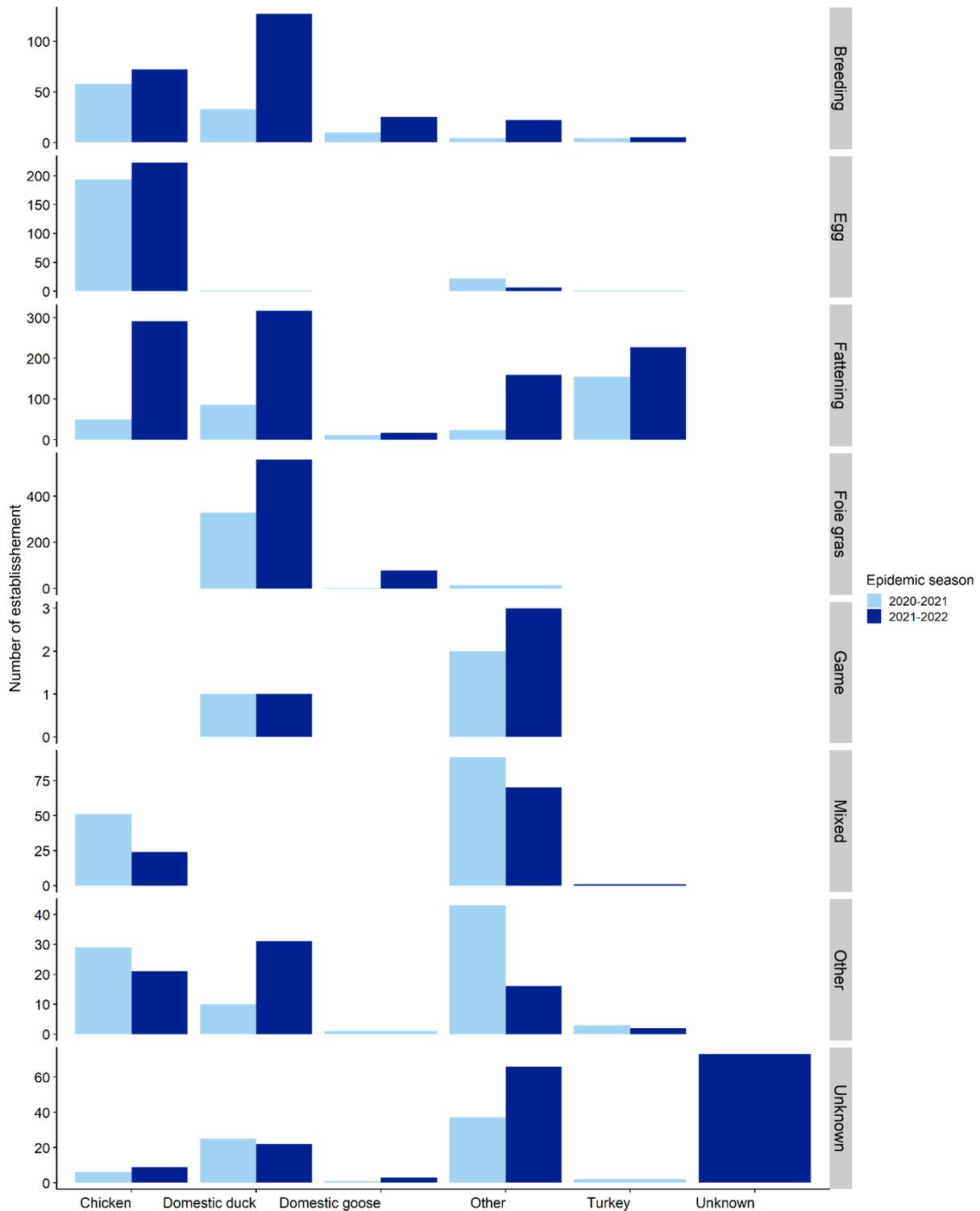


Figure 8: Number of (A) HPAI-affected establishments and (B) number of poultry in the HPAI-affected establishment in Europe between 11 June and 9 September 2022 (56)



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

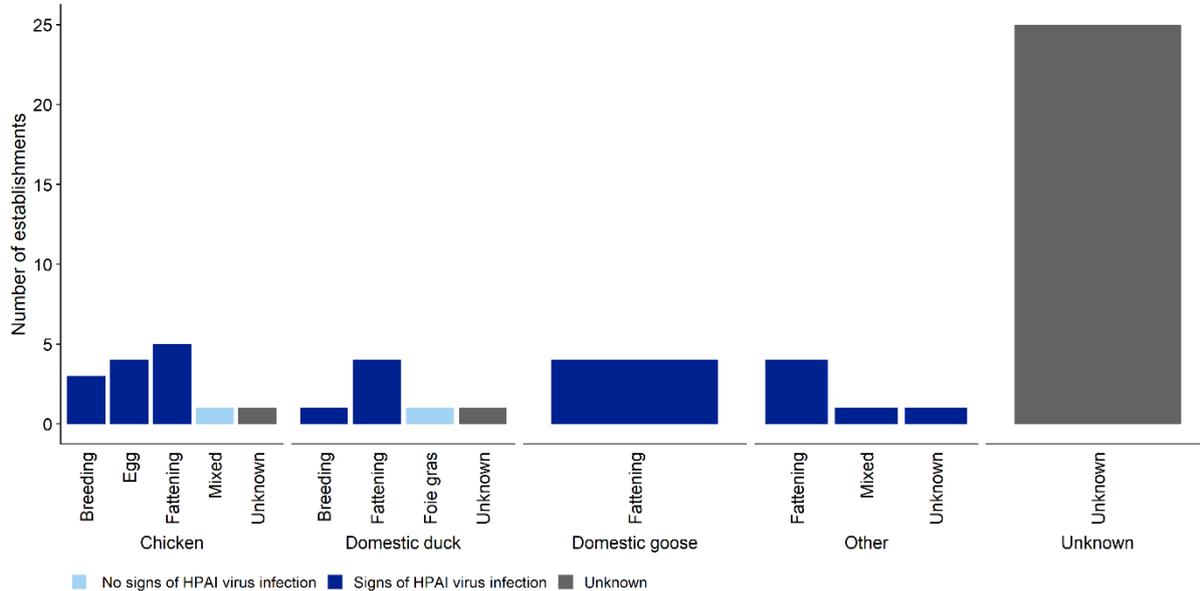
Note that the scale of the vertical axes is specific to each category.

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

Out of 56 outbreaks, 33 were reported in commercial farms, three in non-commercial farms and this information was not available at the time of writing this report for 20 establishments. Three of the outbreaks were secondary outbreaks, two were in commercial establishments (one in Germany with

no outdoor access and one in Poland with outdoor access) and one in a non-commercial establishment (in Moldova, unknown if the poultry had outdoor access).

Increased mortality, or other types of clinical signs were observed in most infected establishments housing chickens, domestic ducks, goose or turkey (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 11 June and 9 September 2022 (56)

HPAI A(H5N1)-affected poultry establishments in France

Between 1 August and 27 August 2022 five primary HPAI A(H5N1) poultry outbreaks were notified in France. The outbreaks were detected in the following regions: Auvergne-Rhône-Alpes (1), Brittany (2), Hauts-de-France (1) and Normandie (1). All outbreaks were in commercial establishments. The type of farmed species was domestic duck for fattening (2), turkey for fattening (2) and mixed species including broiler chickens and domestic ducks (1). Four farms had no outdoor access for poultry and for the farm which kept broilers this data were reported as unknown. The most likely source of virus introduction was identified only for one turkey farm, and it was considered to be indirect contact with wild birds, because of its location in northern France, close to wetland areas (2 km away) where swans had been found dead and tested positive for HPAI A(H5N1) just a few days before the poultry outbreak. All the farms reported increased mortality; clinical signs were reported in the establishments for ducks fattening (2) and turkey fattening (1). No data were available on the drop in feed and water intake. No data on the number of exposed people to the virus were 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 14 July and 3 September 2022, 13 primary and one secondary HPAI A(H5N1) outbreaks were notified in two regions: Schleswig-Holstein (3) and Niedersachsen (11). All outbreaks except one were in commercial farms. The commercial establishments kept laying hens (5), domestic geese for fattening (4), turkeys for fattening (3), chicken for fattening (1) and one had mixed farming holding domestic geese and chicken for fattening. The affected non-commercial farm kept laying hens, domestic geese and domestic ducks for fattening.

The possible source of introduction was reported for two of the outbreaks and was indirect contact with infected poultry and indirect or direct contact with wild birds.

All farms except one that kept geese for fattening reported increased mortality. Similarly, all farms except one that kept turkeys for fattening reported clinical signs. Data on drop in feed and water intake and decreased egg production was not available at the time of publication of this report. No data on outdoor access or number of exposed people were 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(H5)-affected poultry establishments in Moldova

On 31 July and on 6 August 2022, one primary and one secondary HPAI A(H5) outbreaks were notified in the Făleşti region. Both outbreaks were detected in the same village in non-commercial establishments which kept domestic duck and chickens, respectively. None of the farms had outdoor access. The most likely source of infection for those two outbreaks was thought to be indirect contact with wild birds due to presence of HPAI virus in neighbouring countries. Data related to presence of clinical signs or increased mortality as well as drop in feed and water intake, and decreased egg production were not available at the time of publishing this report. The number of exposed people was seven. The characteristics of the affected establishments and species reared are presented in Annex A.

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

Between 15 June 2022 and 1 August 2022, 6 primary HPAI A (H5N1) outbreaks were notified in the Netherlands in the following regions: Overijssel (3), Friesland (2) and Flevoland (1). All affected establishments were commercial farms keeping domestic ducks for fattening (2), chickens for breeding (2) and laying hens (2). Information about outdoor access was not available at the time of publication. The possible sources of all outbreaks were still under investigation at the time of writing this report, however phylogenetic results suggest that most of the establishments were separately infected most likely by exposure to contaminated environments by wild birds. Increased mortality was detected in half of the outbreaks (3/6) in laying hens, breeding chicken and domestic duck establishments. Clinical signs and drop in feed and water intake were reported in four (4/6) of the establishments, including breeding chicken (2), laying hens (1) and domestic ducks for fattening (1). None of the farms reported a decrease in egg production.

No data on the number of people exposed to the virus were 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 Poland

Between 18 and 21 July 2022, three primary and one secondary HPAI A(H5N1) outbreaks were notified in the Wielkopolskie region. All affected establishments were commercial and kept chickens for breeding (2), chicken for mixed production (1) and domestic goose for fattening (1). The two farms that kept chickens for breeding had no outdoor access. The other two farms, which kept chickens for mixed production and domestic goose for fattening respectively, had outdoor access. The most likely source of virus introduction for all establishments were indirect contact with wild birds. Clinical signs and increased mortality were reported for all establishments except from the farm in the secondary outbreak that kept chickens for mixed production. Two establishments farming breeding chickens and fattening domestic geese reported drop in feed and water intake. No farm where it is applicable reported a drop in egg production.

In total 100 people were exposed to the virus in these four outbreaks. The characteristics of the affected establishments and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Portugal

On 31 August and 2 September 2022 two HPAI A(H5N1) primary poultry outbreaks were notified in the Évora and Santarém regions. Both affected establishments were commercial and farmed domestic ducks for fattening. None of the establishments had outdoor access. The most likely sources of the virus were still under investigation at the time of writing this report. All establishments reported presence of clinical signs and increased mortality. Drop in feed and water intake was not reported.

The number of exposed people was 92 in total. The characteristics of the affected establishments and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Spain

Between 1 and 26 of August 2022 three HPAI A(H5N1) primary poultry outbreaks were notified in Andalusia (2) and Extremadura (1). All affected establishments were commercial and kept turkey for fattening (2) and chicken for fattening (1). None of the farms had outdoor access. For three farms the most likely source of virus introduction was indirect or direct contact with wild birds. The farms all reported increased mortality and clinical signs. A drop in feed and water intake was noticed in one establishment farming chickens. In total 52 people were exposed to the virus in these outbreaks. The characteristics of the affected establishments and species reared are presented in Annex A.

Information extracted from the scientific literature

There were three studies on the phenotype of HPAI viruses in poultry in Europe. Gobbo et al. (2022) studied the 'silent infection behaviour' of HPAI A(H5N1) clade 2.3.4.4b in the broiler sector in Italy in the 2021–2022 HPAI epidemic. Monitoring of this epidemic showed increased mortality and clinical signs in turkeys, layer hens, commercial ducks, guinea fowl, quails and pheasants, but not in several broiler chickens, despite the fact that many broiler flocks tested positive for HPAI A(H5N1). Detailed monitoring of a broiler chicken flock that had been tested positive showed no daily cumulative mortality greater than 0.2% during whole production cycle, including in week after HPAI A(H5N1) confirmation. Clinical examination and testing at 3 days after virus confirmation showed no notable respiratory, gastrointestinal, neurological signs; normal drinking and feeding behaviour and negative results in ELISA for AI, despite the fact that 12 of 60 live birds from which tracheal and cloacal swabs collected tested positive for HPAI A(H5N1) by rRT-PCR, with Ct values ranging from 21 to 39. In five moribund or freshly dead birds collected at 3 days after virus confirmation, HPAI A(H5N1) was detected by isolation and immunohistochemistry in multiple organs, and lesions included necrosis and inflammation in lung, pancreas, brain, and lymphoid organs, indicating systemic infection causing multi-organ failure. The authors recommended that during an HPAI A(H5) epidemic, flocks of broilers (like for ducks and geese) should be clinically examined weekly, and tests for HPAI virus should be performed on carcasses/samples of dead birds from each shed collected on the day of sampling, as well as on carcasses/samples from frozen carcasses found dead in the previous 3-5 days, in order to improve early diagnosis of HPAI A(H5) clade 2.3.4.4b.

Grant et al. (2022) described the 2020-2021 HPAI(H5) clade 2.3.4.4b epidemic in wild birds and poultry in Sweden. During the period of the epidemic, 65 suspected outbreaks in poultry (including laying hens, broilers, broiler parents, turkeys and pheasants) and other captive birds were investigated. The most common clinical complaint reported by farmers/bird owners and referring veterinarians was a sudden increase in flock mortality. Depression, inappetence, decreased or increased water intake, respiratory distress, neurologic signs, inactivity and loss of vocalisation, wet litter, faecal staining of eggshells and soft-shelled eggs were reported from occasional flocks.

Lean et al. (2022) studied the gross pathology of HPAI A(H5N1) clade 2.3.4.4b in domestic and wild birds that were naturally infected in the U.K. in 2021-2022. The species studied were poultry (chicken, turkey, pheasant, guineafowl, duck, goose), and captive or wild birds (mute swan, tufted duck, jackdaw, peahen, white-tailed eagle). Pancreatic and splenic necrosis were the most common pathological findings in both Galliformes and Anseriformes. However, there were many instances where gross pathological changes compatible with HPAI were lacking during necropsy. In contrast to the previous season (HPAI A[H5N8] clade 2.3.4.4b), petechiae and haemorrhages were also observed, although infrequently, in chickens. Petechiae and haemorrhages in these coelomic structures, likely a reflection of acute systemic infection and endotheliotropism of HPAI virus, were very subtle and careful examination was needed to identify these changes. In domestic ducks, the lesions observed in HPAI A(H5N1) cases from 2021 to 2022 and 2020–2021 were generally more prominent than those of HPAI A(H5N8) 2020–2021. A continual effort to characterise the pathological impact of the disease is necessary to update on the presentation of HPAI for both domestic/captive and wild birds whilst guiding early presumptive diagnosis.

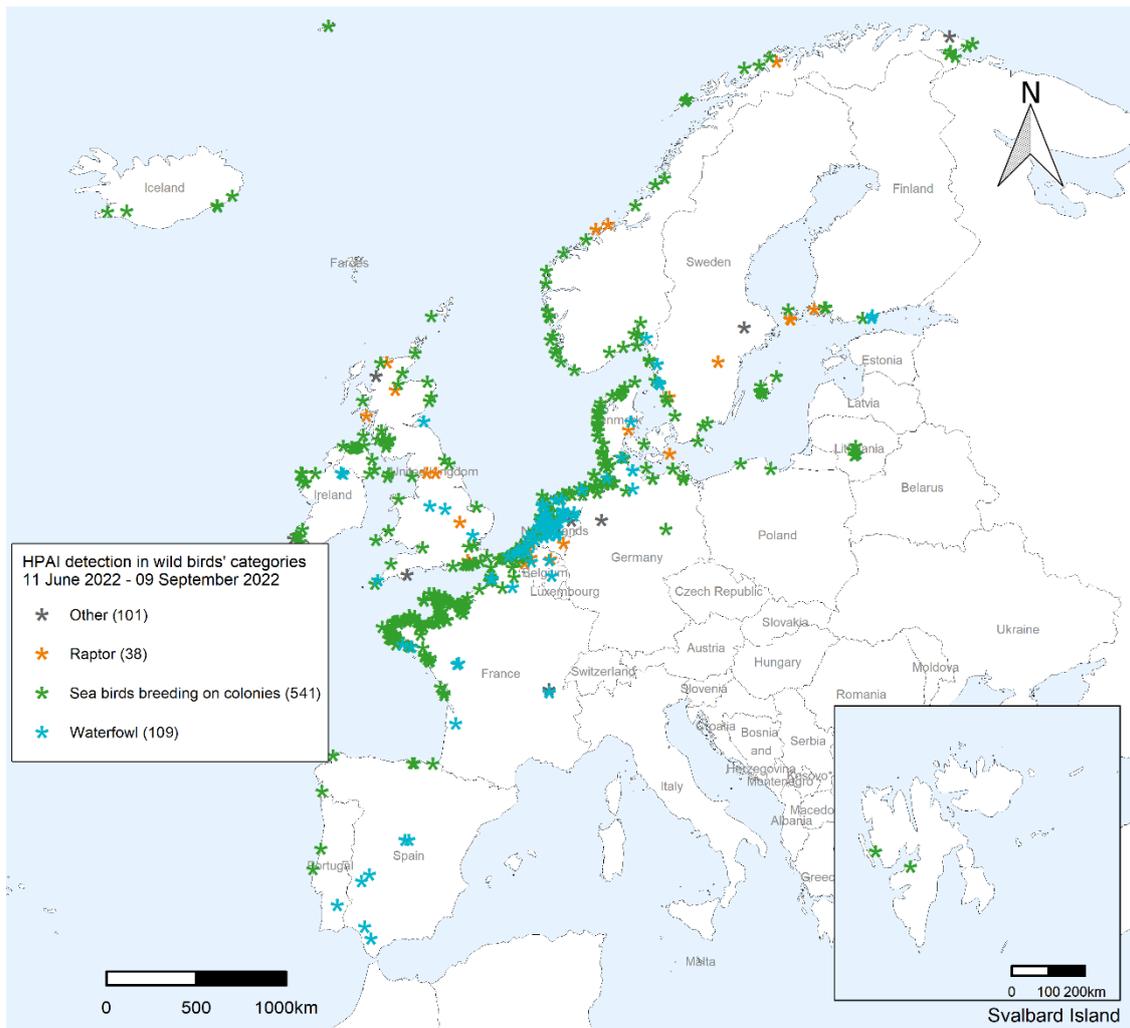
4.2.1.2. HPAI in wild birds

Between 11 June and 9 September 2022, 710 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 an increase since the previous reporting period (from 16 March to 10 June 2022): 525 detections. The HPAI virus detections in wild birds were concentrated in Germany (199), France (142), the Netherlands (112) and

with a lower extent in United Kingdom (69), Norway (48), Belgium (32), Sweden (28) and Denmark (26) (Table 1). Detections were largely restricted to the coasts of these countries, with smaller numbers inland (Table 1 and Figure 11). The overall geographical range of HPAI virus detections in wild birds extended from the northern tip of Norway to the southern tip of Portugal and Spain, and west to Iceland (Figure 11). Locations included several islands in the north-east Atlantic and Arctic Oceans: Orkneys, Shetland, Iceland, Jan Mayen and Svalbard. However, there were no HPAI detections in wild birds in the east and south-east part of Europe in this reporting period. Throughout most of the range, HPAI virus detections consisted mainly of colonial-breeding seabirds interspersed with smaller numbers of waterfowls, raptors and other species (Figure 12). The exception was the Netherlands, where there were substantial numbers of HPAI virus detections in waterfowls in addition to in seabirds.

At least 63 wild bird species were involved: at least 11 waterfowl species (109 detections), 11 raptor species (38 detections), 15 other wild bird species (101 detections) and at least 28 colony-breeding seabird species (541 detections) (Figure 11 and Table C.3 in Annex C). The number of HPAI virus detections was 14 times higher than in the same period last year (11 June to 9 September 2021), when there were 51 detections (Table C.2 in Annex C). This difference is mainly due to the greatly increased number of HPAI detections in seabirds (493 compared with 10, a 49-fold increase). Increased virus detection, but to a lower extent than that observed for seabirds, was also observed in waterfowls (99 compared with 29, 3-fold increase), raptors (28 compared with 7, 4-fold increase), and other wild bird species (90 compared with 5, 18-fold increase). During this reporting period, the main seabird species involved include northern gannets, European herring gulls, greylag goose, common murre, Sandwich terns, mute swans, black-headed gulls, common terns, peregrine falcon, Canada goose, mallard, white stork, grey-headed gulls, with-tailed sea-eagle, great black-backed gulls, great cormorants, and great skuas (Figure 12B). Taken together, the above data show that the marked increase in HPAI virus detections in wild birds in Europe in the current reporting period is mainly due to the virus spreading to breeding colonies of several seabird species, where it caused high mortality. Such die-offs from HPAI had not been seen in seabird breeding colonies in previous years in Europe, with the exception of HPAI in great skuas in different breeding colonies on islands off the shore of Scotland, United Kingdom, during summer 2021 (Banyard et al., 2022). Although the levels of mortality from the HPAI-associated die-offs in seabirds in the current reporting period have yet to be estimated, there are anecdotal reports of HPAI-associated mortality of 2,500 Sandwich terns in a breeding colony of 6,400 birds on Texel, the Netherlands (Banyard et al., 2022); thousands of northern gannets in a breeding colony of 77,000 pairs on Bass Rock, United Kingdom; 70 to 80% of the nests of northern gannet on Heligoland, the only area where this specie breeds in Germany, were abandoned prematurely this year (ntv.de, online), thousands of great skuas in several breeding colonies on islands in Scotland, United Kingdom (Banyard et al., 2022), and approximately half of the birds present in the only breeding colony of northern gannets (around 19,000 couples in northern Brittany) in France (Le Monde, online).

Compared with the previous reporting period (16 March to 10 June 2022), the number of HPAI virus detections showed an overall increase (710 versus 525) in this reporting period, which is due to the increased number of detections in colony-breeding seabirds (493 vs 150) and in other wild birds (90 vs 66), while the number of detections in waterfowls (99 vs 224) and raptors (28 vs 85) was lower (Table C.1 in Annex C). Such an increase in HPAI detections in wild birds during the summer months is unprecedented.



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 09/09/2022

Source: EFSA, ADIS and WOAH (data extraction carried out on 9 September 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 11 June to 9 September 2022

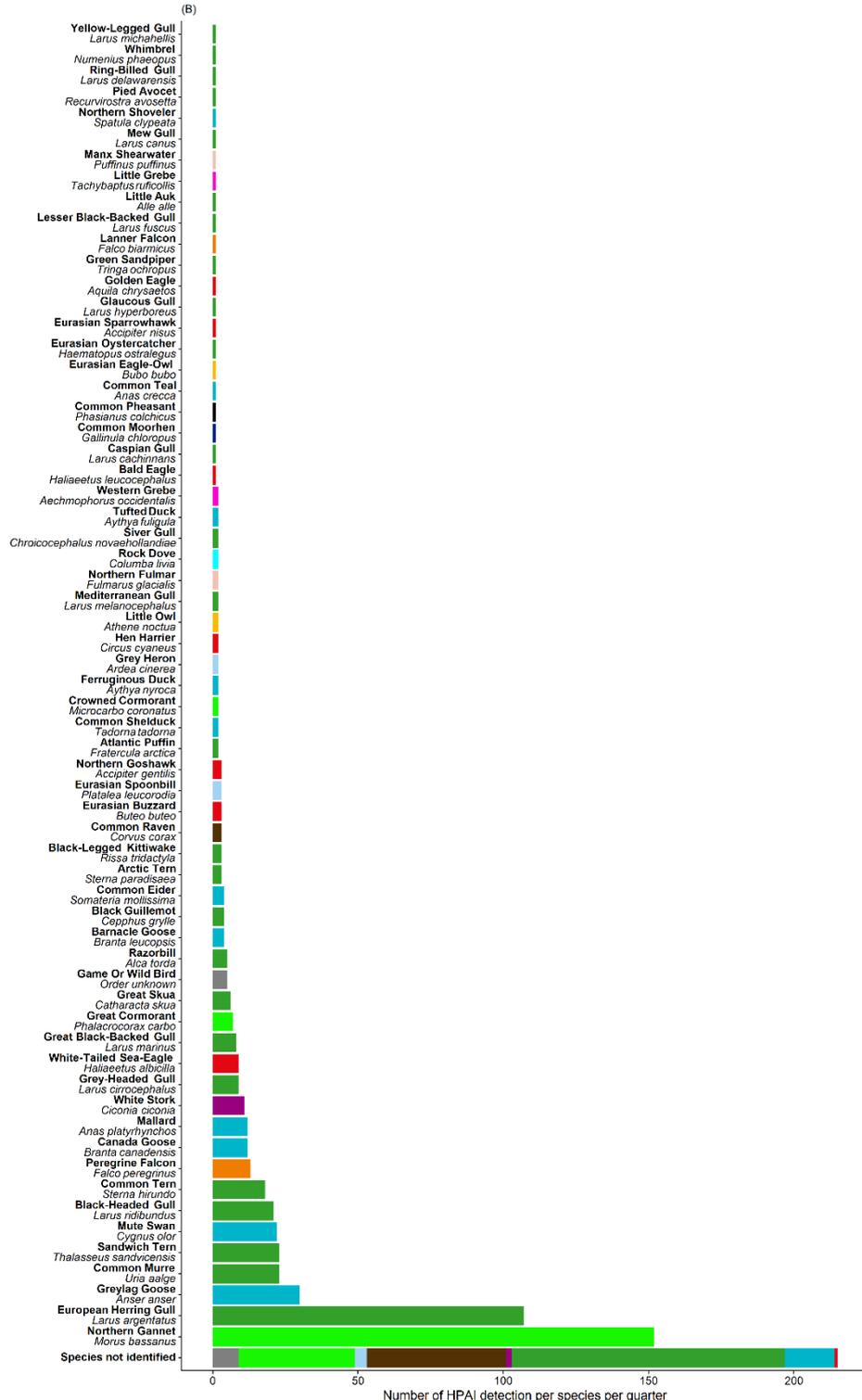
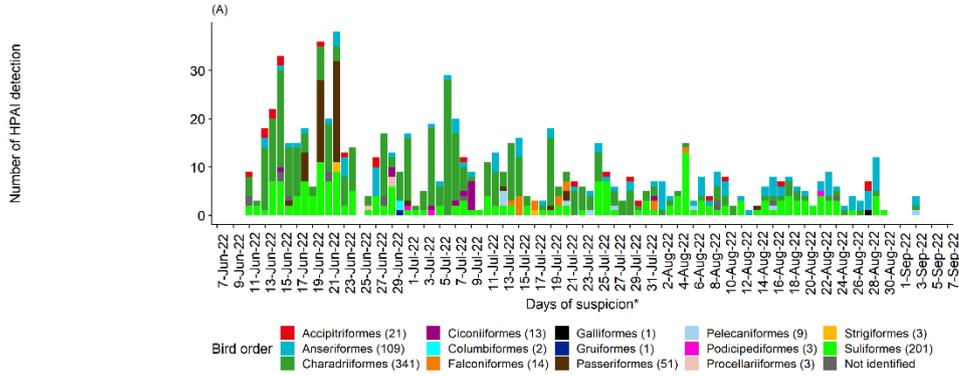


Figure 12: Number of reported detections of highly pathogenic avian influenza virus A(H5) in wild birds by (A) bird order and week of suspicion and (B) wild bird species in the EU/EEA and United Kingdom, from 11 June to 9 September 2022 (fourth quarter)

Information extracted from the scientific literature

There were two studies on the phenotype of HPAI viruses in wild birds in Europe. Pohlmann et al. (2022) performed phylogenetic analysis on HPAI A(H5N1) clade 2.3.4.4b, observed in European wild birds and poultry since October 2021. Phylogenetic analyses of the H5 HA gene revealed that two H5 sublineages within clade 2.3.4.4b, tentatively termed B1 ('branch' 1) and B2, have cocirculated since the autumn of 2021 in Europe. The close phylogenetic relationship of the viruses of the B1 sublineage, (which form a monophyletic branch in the Bayesian HA phylogeny), its stepwise branching pattern throughout the evolutionary period, and a consecutive temporal order support its continuous circulation at a relatively low level in northwestern Europe and Scandinavia during the summer of 2021. The authors hypothesise that sublineage B1 has been maintained, presumably in wild birds, in northern Europe throughout the summer of 2021. This suggests a fundamental shift in the observed epidemiology of HPAI, with the potential for an enzootic status of this HPAI sublineage in northern Europe.

Prosser et al. (2022) studied the movement data of a wild lesser scaup (*Aythya affinis*), captured in winter 2021–2022 during a separate ecology study in the Chesapeake Bay, Maryland, USA, and that tested positive for infection with HPAI A(H5N1) clade 2.3.4.4b virus, highly similar to the virus circulating concurrently in wild birds in Europe. It showed no clinical signs of infection at capture, during surgery, nor upon release. The bird died 3 days later. Analysis of movement data within the 3-day window showed that the infected individual's maximum and average hourly movements (3,894 and 429 m, respectively) were noticeably lower than four non-infected birds of the same species released on the same day (average of 21,595 and 1,098 m, respectively). The authors identified four instances where the infected bird had close contact (fixes located within 25 m and 15 min) with another marked bird during this time. These data suggest that the HPAI-positive bird may have been shedding virus for some period prior to death and there were opportunities for direct bird-to-bird or environmental transmission.

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 the 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 their emergence in the Netherlands in October 2020, the A(H5N1) viruses of clade 2.3.4.4b have spread to many countries in Europe, Africa, Asia and America. While their haemagglutinin gene segment was highly conserved among the circulating viruses, the other genes underwent through multiple reassortment events.

In January 2021, an A(H5N1) related to the 2020–2021 European viruses was reported in West Africa (Lo et al., 2022) and subsequently in Southern African countries (Makalo et al., 2022). Since then, it has been persistently circulating in this geographic area, and in West Africa it reassorted with the A(H9N2) subtype of the zoonotic G1 lineage (Ouoba et al., 2022). Starting from October 2021, different A(H5N1) genotypes, some of them previously identified in Europe, have been detected in South and East Asia, including China (Cui et al., 2022). In December 2021, North America announced the first

detection of an A(H5N1) virus strongly related to the A(H5N1) identified in Northern Europe during the 2020–2021 epidemic season (Bevins et al., 2022; Caliendo et al., 2022b).

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

All the genetically characterised HPAI viruses collected since the beginning of the current epidemic season (October 2021 to September 2022) in Europe fall within clade 2.3.4.4b. Sequences were generated from viruses collected in 23 EU Member States, Albania, Iceland, Kosovo⁶, Moldova, Norway, Russia and the United Kingdom (available in GISAID on 12 September 2022, provided by the National Reference Laboratories (NRL) or generated by the 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 four subtypes originating from multiple inter- and intra-subtype reassortment events have been detected since October 2021: 28 A(H5N1), one A(H5N8), one A(H5N5), and one A(H5N2). The A(H5N1) and A(H5N8) genotypes circulated persistently in several European countries, whereas the A(H5N5) genotype was confined to Norway and the A(H5N2) genotype was detected only in Poland and Germany. Most of these 31 genotypes are likely to have been 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 a persisting circulation in Europe since the 2020–2021 epidemic season.

In the current reporting period (June–September 2022), only the A(H5N1) and A(H5N5) subtypes were identified in Europe. Based on the available genetic information, all the A(H5N1) belong to six genotypes: three persistently circulating in Europe since the beginning of the 2021–2022 epidemic season and three novel genotypes. One of these latter resulted from reassortment events with viruses of the gull-adapted A(H13) subtype and has been extensively detected in colony-breeding seabird species, mainly European herring gulls, and sporadically in other bird species in the Netherlands, Belgium and France. During this epidemic season, all the characterised A(H5N5) viruses from Norway, including Svalbard Island, clustered together and with the A(H5N5) collected during the previous (2020–2021) season, therefore suggesting a persistent but confined circulation of the A(H5N5) genotype in this geographic area.

Three HPAI avian influenza A(H5N1) viruses collected between June and July 2022 from red foxes (*Vulpes vulpes*) in Belgium and Norway and from one porpoise (*Phocoena phocoena*) in Sweden were genetically characterised. The virus from the Belgian fox belongs to the novel A(H5N1) genotype detected mainly in European herring gulls during this reporting period. The A(H5N1) viruses from the Norwegian red fox and from the Swedish porpoise are closely related to one of the most common A(H5N1) genotype circulating in birds in Northern Europe.

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 A(H5) viruses from this reporting period, 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 few of them (T192I, H3 numbering) (Yang et al., 2007). Mutations associated with increased resistance to antiviral drugs were identified in the neuraminidase or ion channel proteins of some of the circulating A(H5N1) viruses.

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

Since 11 June as of 9 September 2022, data from four countries (Moldova, Poland, Portugal and Spain) have been reported on the total number of people exposed to infected birds (e.g. during culling activities). They reported, in total, 251 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-c). The person was involved in culling activities and reported fatigue symptoms but did not require specific treatment. Earlier human

⁶ 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

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, 2021b).

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 in any period previously (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. During the summer period 2022, also likely seal-to-seal transmission accompanied with seal mortality due to avian influenza A(H5N1) viruses were observed in the USA (Puryear et al., 2022). Although seals have been found infected with A(H5N1) viruses in Europe as well, such transmission event between the same mammal species has not been reported so far. A study on currently circulating A(H5N1) viruses in North America showed that these viruses are able to replicate efficiently in human respiratory tract cell types and that in ferret infection and transmission studies, animals got infected but showed only very mild symptoms mostly limited to upper respiratory tract and viruses did not transmit to other ferrets kept in a direct-contact setting (Pulit-Penalosa et al., 2022). Supporting also the previously issued risk assessment using the Influenza Risk Assessment Tool (IRAT) of the United States Centers for Disease Control and Prevention (US CDC) that 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-d, e, c, a). The risk of the A(H5N1) clade 2.3.4.4b viruses currently circulating in the United States bird and poultry populations, and which are closely related to European viruses, were assessed by the 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-b).

The WHO assessed the risk associated with A(H5N6) virus as low (CDC, online-b). 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 unsubtypable influenza A viruses from human infections with the WHO Collaborating Centres (CDC, online-d). 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 3: Avian influenza A(H5Nx) virus detections in mammal species other than humans related to circulating viruses worldwide, 2016–2022

Virus	Animal (order, family, species)		Country	Epidemic season	Reference	
A(H5N8) clade 2.3.4.4b	Artiodactyla	<i>Suidae</i>	Domestic pigs (<i>Sus scrofa</i>), serological detection	France	December 2016	(Herve et al., 2021)
			Wild boar, serological detection	Germany	2017	(Schüle et al., 2021)
	Carnivora	<i>Phocidae</i>	Grey seals (<i>Halichoerus grypus</i>)	Poland, United Kingdom, Sweden	November 2016; 2020-2021	(Shin et al., 2019; Floyd et al., 2021; SVA, online-b; personal communication by Siamak Zohari, SVA)
			Harbour seals (<i>Phoca vitulina</i>)	Germany, United Kingdom; Denmark	December 2020	(Floyd et al., 2021; Ärzteblatt, online; Avian Flu Diary, online; Outbreak News, online; SSI, online)
	<i>Canidae</i>	Red foxes (<i>Vulpes vulpes</i>)	United Kingdom,	December 2020	(Floyd et al., 2021)	
A(H5N1) clade 2.3.4.4b	Carnivora	<i>Canidae</i>	Red foxes (<i>Vulpes vulpes</i>)	Sweden; Netherlands; Finland; Estonia; Ireland; Belgium; Norway; Japan; USA; Canada	2020-2021; 2021-2022	(SVA, online-b; WOH, online-a,b; personal communication by Siamak Zohari, SVA; Irish National Reference Laboratory for Avian Influenza, personal communication)
			Common raccoon dog (<i>Nyctereutes procyonoides</i>)	Japan	2021-2022	(WOAH, online-b)
			Coyote (<i>Canis latrans</i>)	USA	2021-2022	(WOAH, online-b)
		<i>Mustelidae</i>	Eurasian otter (<i>Lutra lutra</i>)	Netherlands; Finland	2021-2022	(WUR, online)
			European badger (<i>Meles meles</i>)	Netherlands	2021-2022	(WUR, online)
			European polecat (<i>Mustela putorius</i>)	Netherlands	2021-2022	(WUR, online)
			Ferret (<i>Mustela furo</i>)	Slovenia	2021-2022	Slovenian National Reference Laboratory for Avian Influenza, personal communication
			American mink (<i>Neovison vison</i>)	Canada	2021-2022	(WOAH, online-b)
		<i>Felidae</i>	Lynx (<i>Lynx lynx</i>)	Finland	2021-2022	(FFA, online)
			Bobcat (<i>Lynx rufus</i>)	USA	2021-2022	(WOAH, online-b)
			Fisher cat (<i>Pekania pennanti</i>)	USA	2021-2022	(WOAH, online-b)
		<i>Procyonidae</i>	Raccoon (<i>Procyon lotor</i>)	USA	2021-2022	(WOAH, online-b)
		<i>Mephitidae</i>	Skunks (<i>Mephitis mephitis</i>)	Canada; USA	2021-2022	(CTV News, online; WOH, online-b)
		<i>Phocidae</i>	Grey seals (<i>Halichoerus grypus</i>)	USA	2021-2022	(WOAH, online-b)
			Harbour seals (<i>Phoca vitulina</i>)	USA; Canada	2021-2022	(WOAH, online-b)
		<i>Ursidae</i>	American black bear (<i>Ursus americanus</i>)	Canada	2021-2022	(Healthy Wildlife, online; WOH, online-b)
		Artiodactyla	<i>Suidae</i>	Domestic pigs (<i>Sus scrofa</i>), serological detection ^a	Italy	2021-2022
Didelphimorphia	<i>Dedelphidae</i>	Virginia opossum (<i>Didelphis virginiana</i>)	USA	2021-2022	(WOAH, online-b)	
Cetacea	<i>Phocoenidae</i>	Porpoise (<i>Phocoena phocoena</i>)	Sweden	2021-2022	(SVA, online-a)	
	<i>Delphinidae</i>	Bottlenose dolphin (<i>Tursiops truncatus</i>)	USA	2021-2022	(UFHealth, online; WOH, online-b)	

(a) Serological detection in a backyard poultry HPAI outbreak

4.4. Prevention and control measures applied in Europe, 2 June to 2 September 2022 (ToR 3)

The description of the control and prevention measures applied in the affected Member States on HPAI outbreaks occurred from 2 June to 2 September 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 June 2022 have been described in the previous EFSA report (EFSA et al., 2022).

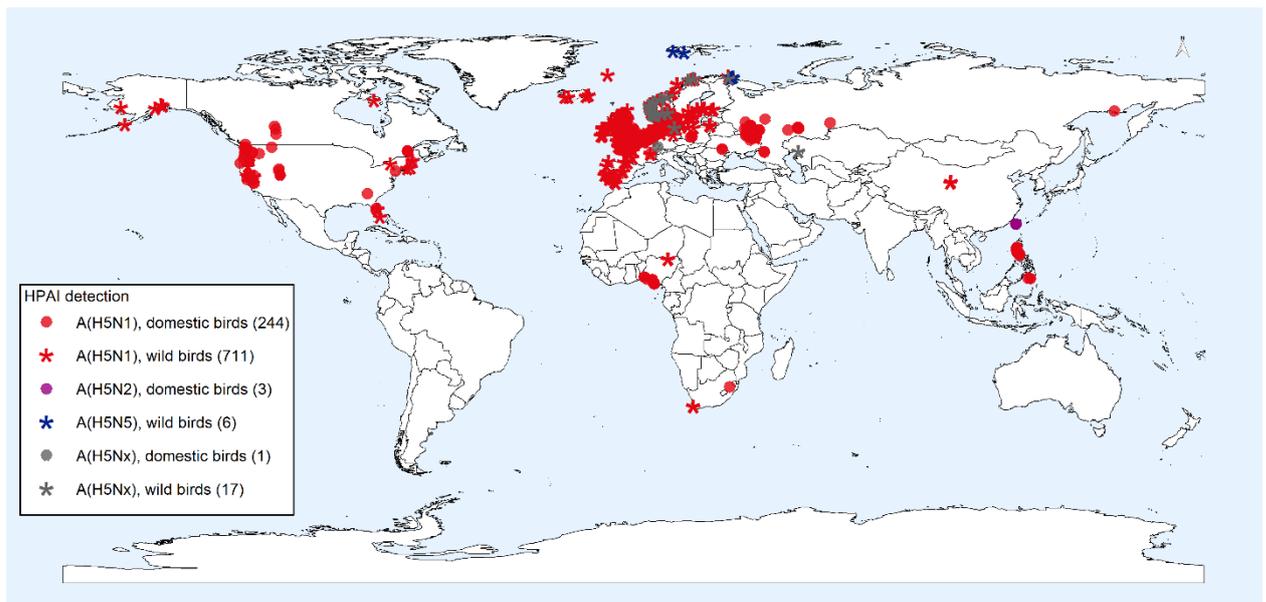
4.5. The avian influenza situation in other countries not reporting via ADIS, 11 June to 9 September 2022 (ToR 4)

An overview of the HPAI detections notified from other countries not reporting via ADIS but via the WOA or national authorities from 11 June to 9 September 2022 is presented in Table 4 and Figure 13. 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 4: Number of HPAI detections in non-European countries, by virus subtype and country, from 11 June to 9 September 2022

Region	Country	Domestic birds (170)		Wild birds (24)		Total
		A(H5N1)	A(H5N2)	A(H5N1)	A(H5Nx)	
Africa (19)	Nigeria	14		2		16
	South Africa	1		2		3
Americas (69)	Canada	9		1		10
	USA	44		15		59
Asia (68)	China			2		2
	Chinese Taipei		3			3
	Kazakhstan				1	1
	Philippines	62				62
Europe (38)	Russia	37		1		38
Total		167	3	23	1	194

Source: WOA-WAHIS (data extraction carried out on 9 September 2022).



Author: EFSA
Data sources: ADIS, WOA
Date updated: 09/09/2022

Figure 13: Geographical distribution, based on available geocoordinates, of highly pathogenic

avian influenza virus detections reported in domestic birds (248) and wild birds (734) by virus type, from 11 June to 9 September 2022

4.5.1. Avian influenza A(H3N8)

4.5.1.1. Human infections with A(H3N8)

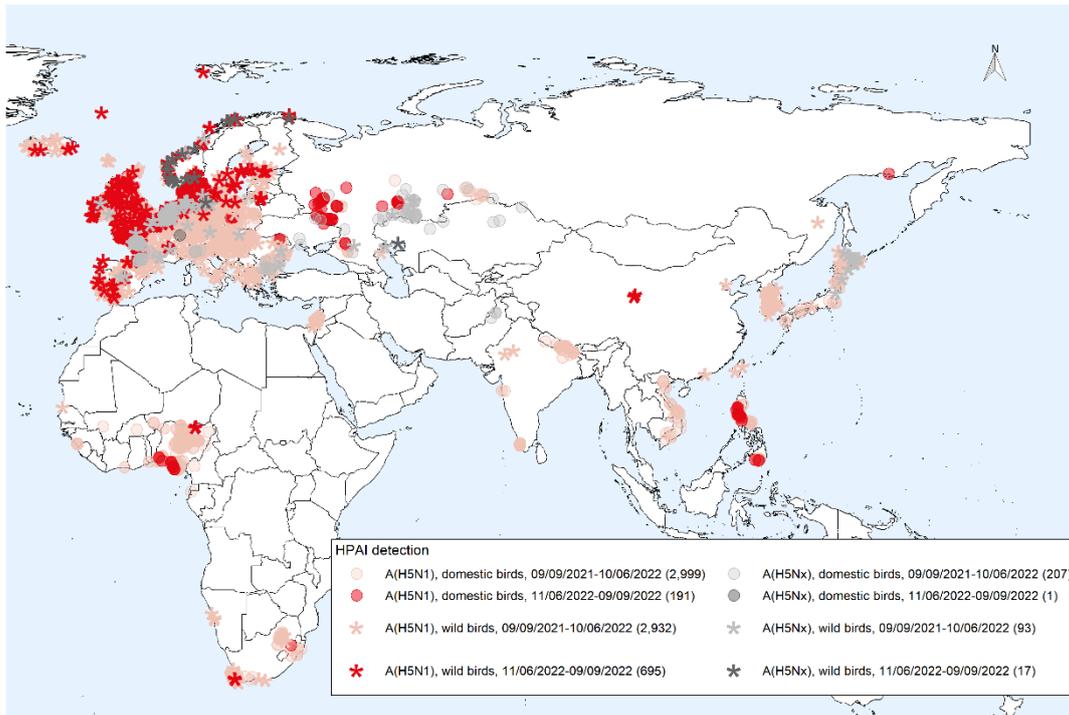
No new cases have been reported due to infection with A(H3N8) since the last report (EFSA et al., 2022). Two human infections with avian influenza A(H3N8) reassortant virus were reported for the first time in a 4-year-old child with critical conditions in April 2022 (WHO, 2022b) and a 5-year-old child in May 2022, both in China (The Government of the Hong Kong Special Administrative Region Press Releases, 2022b). 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 birds and wild animals

Detections

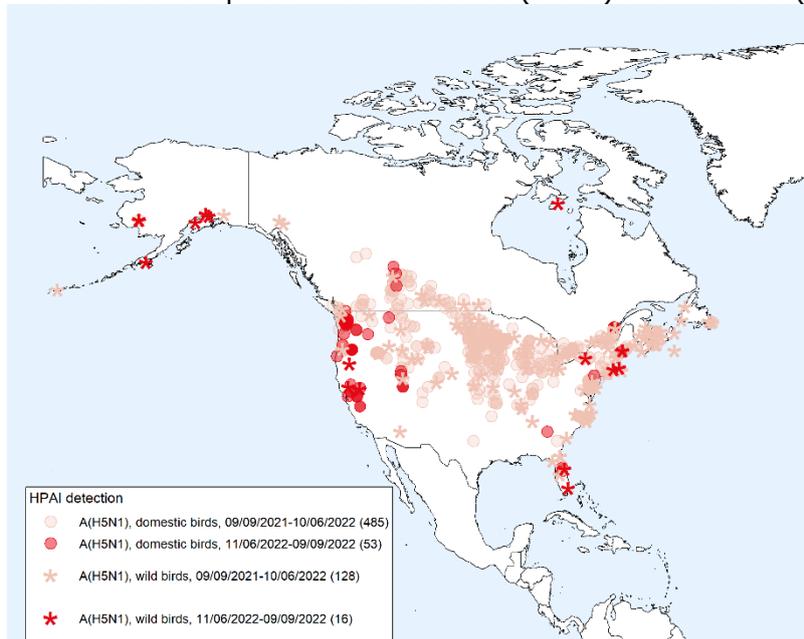
Contrary to the last report, outbreaks of HPAI A(H5N1) in Africa were only notified to the WOAH from previously affected regions in Nigeria and South Africa, affecting mainly medium-sized poultry establishments and several wild bird species (common tern, white-faced whistling duck and nightjars). Compared to the previous reporting period, only three Asian countries reported outbreaks in domestic poultry and wild birds to the WOAH (Figure 14). The outbreak in the Philippines continues with a large number of HPAI A(H5N1) cases on farms of all sizes. Kazakhstan notified the detection HPAI A(H5Nx) in a not determined wild bird species at the Caspian Sea. Furthermore, China reported the confirmation of HPAI A(H5N1) virus in brown-headed gulls at the Qinghai Lake, a location spatially linked with key migration areas. Compared with the period covered by the last report, the number of outbreaks notified to the WOAH by Russia has risen sharply. HPAI A(H5N1) was detected on three medium-sized farms and a large number of backyard holdings as well as in a rock dove from an affected region. The HPAI A(H5N1) epidemic in Canada and the USA continues, but the number of cases in domestic poultry and wild birds decreased significantly (Figure 15). Small to very large poultry establishments and several wild bird species were affected, for example common eider, cinnamon teal, Canada goose, Arctic tern, tree swallow, wood stork, red-necked grebe, dunlin, glaucous gull, Sabine's gull, short-billed gull, thick-billed murre, great black-backed gull, Arctic skua, eastern screech owl, great horned owl and crested caracara. Furthermore, Canada and the USA detected HPAI A(H5N1) virus in red foxes (*Vulpes vulpes*) and the USA additionally confirmed the virus in raccoons (*Procyon lotor*), harbour seal (*Phoca vitulina*), grey seal (*Halichoerus grypus*) and striped skunk (*Mephitis mephitis*) (Table 3).



Author: EFSA
Data sources: ADIS, WOA/H
Date updated: 09/09/2022

Red and dark grey symbols indicate outbreaks that occurred between 11 June and 9 September 2022, light red and light grey symbols indicate outbreaks that occurred between 9 September 2021 and 10 June 2022.

Figure: 14 Geographical distribution, based on available geocoordinates, of HPAI A(H5N1) and A(H5Nx) virus detections reported in domestic birds (circles) and wild birds (stars) (7,136)



Author: EFSA
Data sources: ADIS, WOA/H
Date updated: 09/09/2022

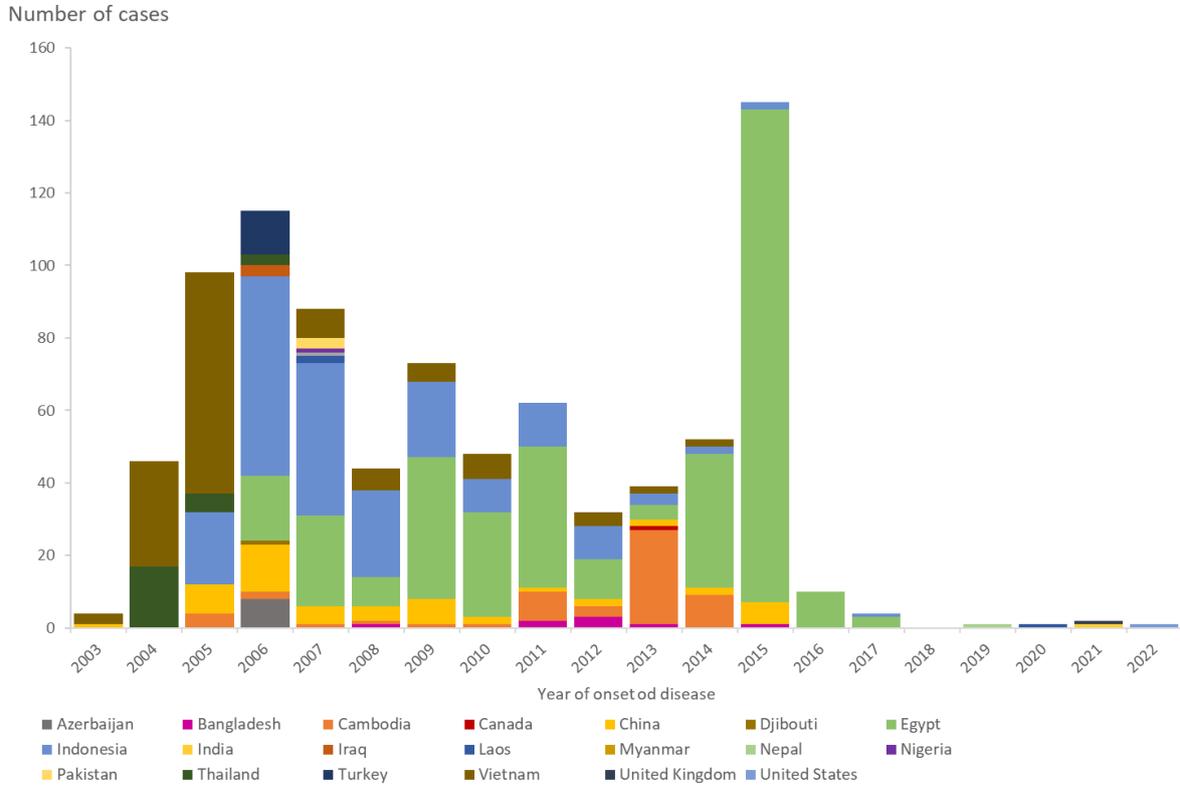
Red symbols indicate outbreaks that occurred between 11 June and 9 September 2022, light red symbols indicate outbreaks that occurred between 9 September 2021 and 10 June 2022.

Figure 15: Geographical distribution, based on available geocoordinates, of HPAI A(H5N1) and A(H5Nx) virus detections reported in domestic birds (circles) and wild birds (stars) (684)

4.5.2.2. Human infections due to A(H5N1)

No new human infection with avian influenza A(H5N1) has been reported over the reporting period. In 2022, one human case was reported in April from the USA with mild symptoms following exposure

during depopulation activities in a commercial poultry facility following an outbreak of influenza A(H5N1) virus. Since 2003, and as of 30 August 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, 2022b) (Figure 16).



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

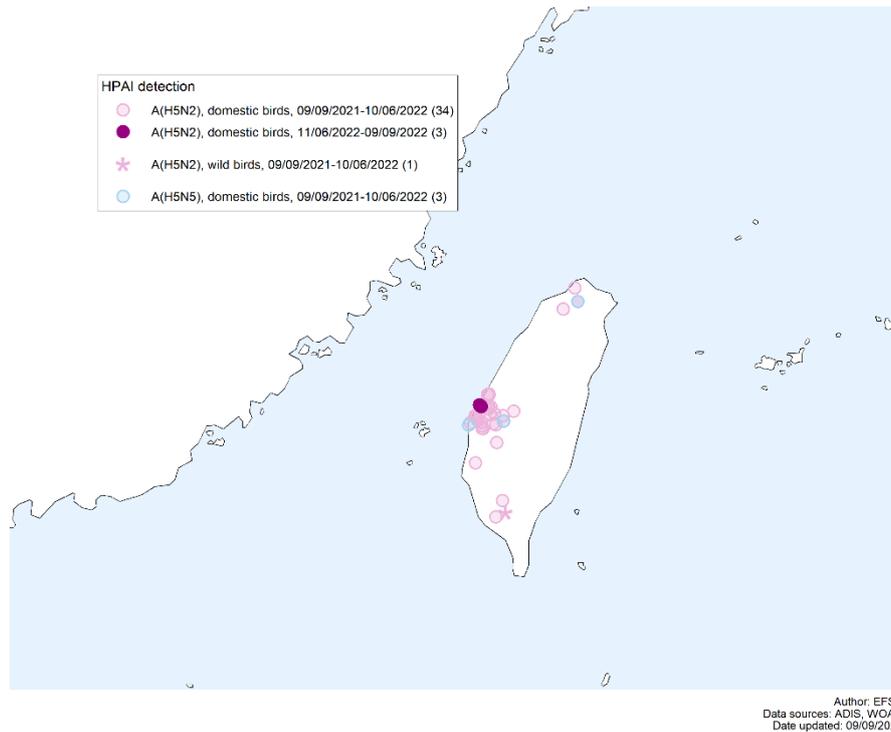
Figure 16: Distribution of confirmed human cases of A(H5N1) by year and country of reporting, 2003 to 30 August 2022 (865)

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

4.5.3.1. Domestic and wild birds

Detections

As in the previous reporting period, Taiwan detected no new outbreaks of the Taiwanese lineage HPAI A(H5N5) virus. However, three outbreaks of the Taiwanese lineage HPAI A(H5N2) in medium-sized poultry farms from the same township were reported to the WOA. 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., 2019a) and in Bulgaria in 2020. No wild bird cases were reported between 11 June and 9 September 2022 (Figure 17).



Purple symbols indicate HPAI A(H5N2) virus detections between 11 June and 9 September 2022, light purple symbols indicate HPAI A(H5N2) virus detections between 9 September 2021 and 10 June 2022, light blue symbols indicate HPAI A(H5N5) virus detections between 9 September 2021 and 10 June 2022.

Figure 17: Geographical distribution, based on available geocoordinates, of HPAI A(H5N2) and HPAI A(H5N5) virus detections reported in domestic birds (circles) and wild birds (stars) in Taiwan (41)

4.5.4. HPAI A(H5N6)

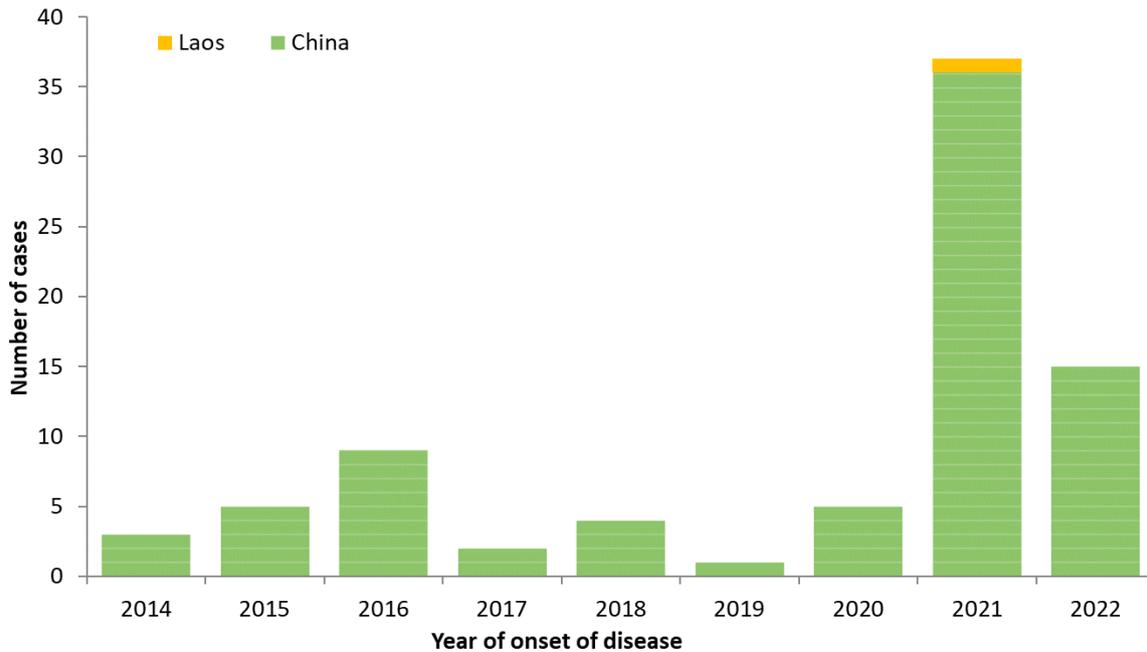
4.5.4.1. Domestic and wild birds

Detections

No new outbreaks of the zoonotic reassortment of HPAI A(H5N6) clade 2.3.4.4c were detected within the relevant time period for this report. New human cases of A(H5N6) from the Hong Kong Special Administrative Region 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)

Two new patients infected with avian influenza A(H5N6) and hospitalised with critical conditions following exposure to poultry at a market have been reported from China since the last EFSA report (WHO, 2022c, a). Since 2014, and as of 14 September 2022, 81 laboratory-confirmed human infections with avian influenza A(H5N6) viruses have been reported from China (80 cases) and Laos (1), 33 of the patients died (CHP, 2022a) (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, 2022a; BNO, online; GovMO, online). 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 14 September 2022 (N = 81)

4.5.5. HPAI A(H5N8)

4.5.5.1. Domestic and wild birds

Detections

In contrast with the last report, no outbreaks of HPAI A(H5N8) in domestic poultry or wild birds were notified outside Europe between 11 June and 9 September 2022.

4.5.6. HPAI–LPAI A(H7N9)

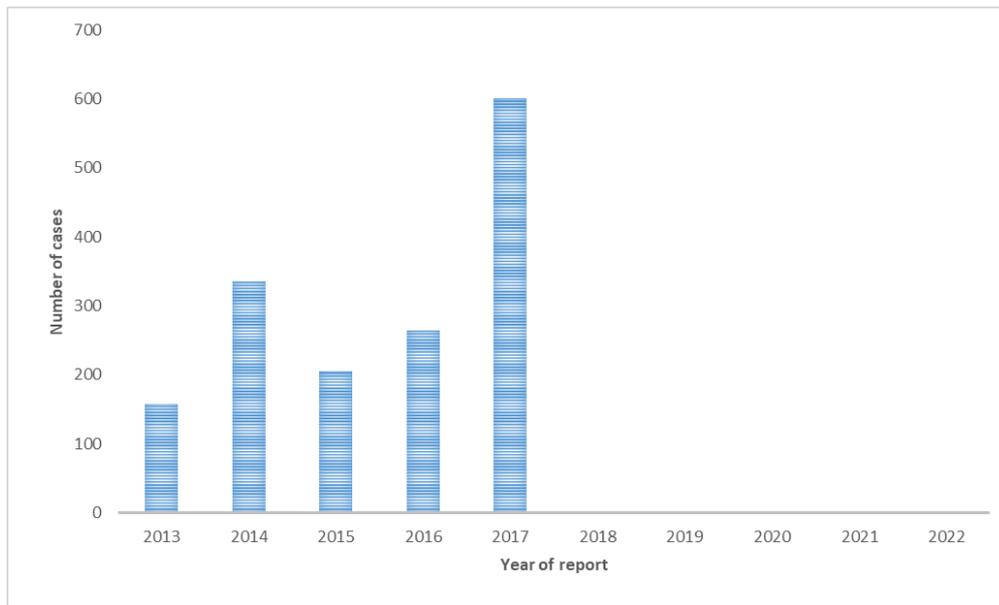
4.5.6.1. Domestic and wild birds

Detection

No LPAI or HPAI A(H7N9) cases had been notified to WOA–WAHIS 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, d). Since February 2013, in total, 1,568 human cases have been reported from outside Europe (Figure 19), including at least 615 deaths (39%) (WHO, 2019a, b; CHP, 2021a). 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 19: Number of human cases due to A(H7N9), infection by year, 2013 to 2022 (1,568) - 2018 (2 cases); 2019 (1 case)

4.5.7. LPAI A(H9N2)

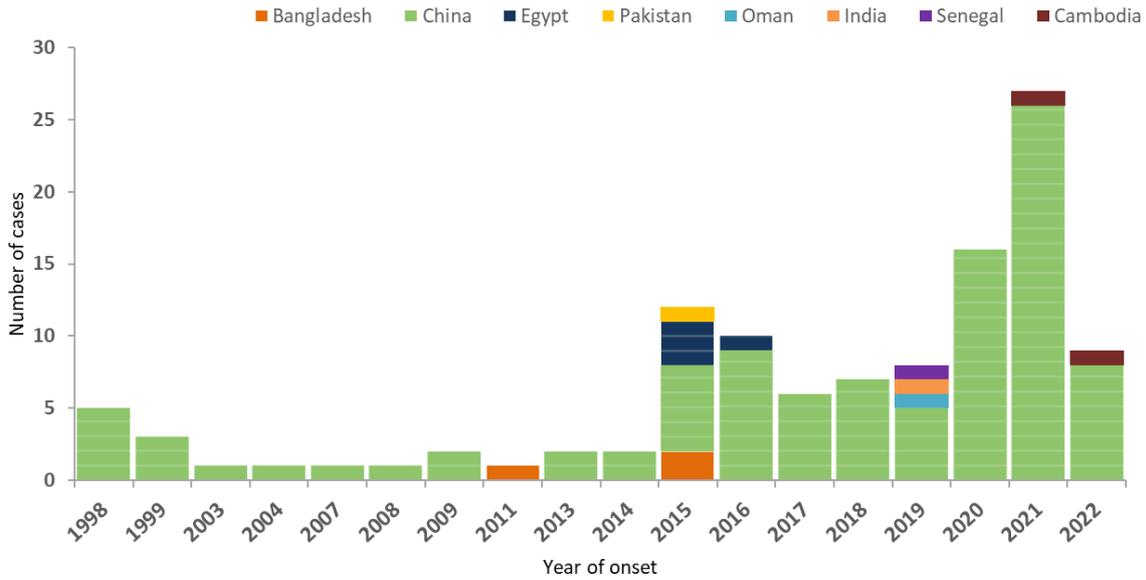
4.5.7.1. Domestic and wild birds

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 9 September 2022.

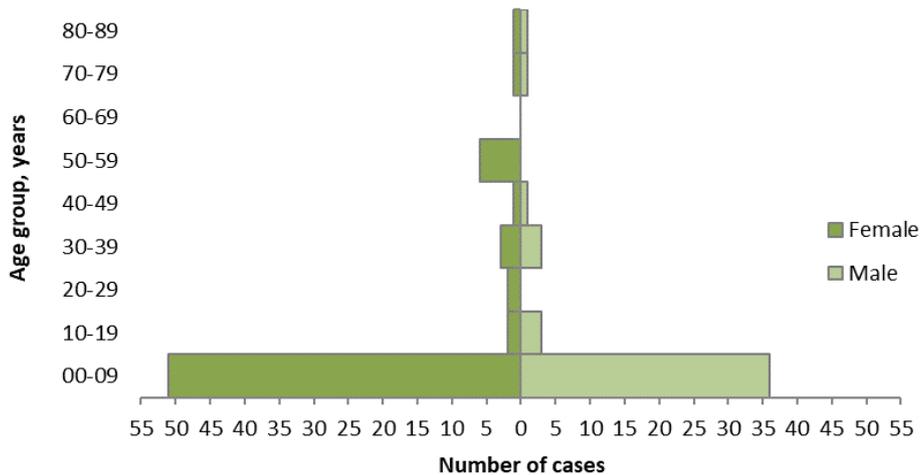
4.5.7.2. Human infections due to A(H9N2)

Two new human infections with A(H9N2) have been reported since the last report. Both cases were children from China (CHP, 2022b). Since 1998, and as of 14 September 2022, 114 laboratory-confirmed human infections with avian influenza A(H9N2) virus, including two deaths, have been reported globally. Infections were reported from China (101), 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 20). 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, 2020c; CHP, 2021b; ECDC, 2021a) (ECDC line list; please refer to Appendix B.2) (Figure 21).



Source: ECDC line list.

Figure 20: Distribution of confirmed human cases of A(H9N2) by reporting country, 1998 to 14 September 2022 (114)



Source: ECDC line list.

Figure 21: Age and sex distribution of confirmed human cases of A(H9N2) by age group, 1998 to 14 September 2022 (114)

4.5.8. Human infections due to A(H10N3) and A(H10N8)

In June 2021, the first human case of A(H10N3) was detected in China (NHCGovCN, online). China reported a second infection in 2022. Both patients were adults between 30 to 45 years of age with unknown exposure to birds or poultry. To date, there were three people infected with influenza A(H10N8) between November 2013 and February 2014, two of whom died (Parry, 2014; GovHK, online). Both adults were above 55 years of age in China and reported exposure to live poultry/poultry market before onset of symptoms.

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

The impact of the 2021–2022 HPAI A(H5) epidemic was unprecedented in the number of detections in wild and domestic birds and the geographic spread of infection. From October 2021 to 9 September

2022, a total of 2,467 HPAI outbreaks in poultry, with 47.5 million birds dead or culled in affected poultry establishments, 187 findings in captive birds, and 3,573 HPAI virus detections in wild birds were detected in 37 European countries. Major epidemics in poultry occurred in France (1,383 outbreaks), Italy (317), and Hungary (290), but also Poland (98), Germany (89), United Kingdom (89), and the Netherlands (62) were severely affected. Considering wild birds, Germany was the most affected country with 1,506 reported detections, followed by the Netherlands (668), United Kingdom (361), France (214), Denmark (157) and Belgium (111).

In autumn 2021, the HPAI A(H5N1) virus also crossed the Atlantic Ocean for the first time and spread from Europe to North America along migration routes, causing a severe epidemic in poultry in several Canadian provinces and US States as well as causing mortality in wild birds (Caliendo et al., 2022b).

Considering the three main HPAI epidemic seasons reported in Europe, an increasing trend was observed in the number of HPAI virus detections in wild birds from the 2016–2017 (1,563) to the 2020–2021 (2,407) and the current 2021–2022 (3,573) epidemic seasons (Figure 2); this might highlight the increased risk over the years for HPAI virus infections for wild bird species. Virus circulation in wild birds is associated with risk for introduction of infection in poultry and potential spread between poultry establishments.

HPAI A(H5) viruses first persisted over the summer months in wild birds in continental Europe during the 2020–2021 epidemic season, but with a low level of virus circulation (Figure 4B). Conversely, in the summer 2022, the HPAI A(H5) virus circulated mainly among seabird colonies at coastal breeding sites in north-western Europe at an unprecedented scale, representing a continuous risk of infection for domestic birds. The very high temperatures of the summer did not fully mitigate the environmental contamination and the consequent HPAI risk due to heavily infected wild bird populations.

The continuous and widespread circulation of HPAI A(H5) viruses in wild bird populations, and the increasing number of birds and wild bird species affected during the last two epidemic seasons indicate that HPAI A(H5) viruses are gradually adapting to the wild reservoir. It appears that HPAI A(H5) viruses can be maintained in the wild independently of domestic bird populations (Caliendo et al., 2022a). The high mortality in wild birds from HPAI virus in recent years has changed the paradigm of wild birds as unaffected agents of HPAI viruses, with increasing concerns about potential effects on their populations (Kleyheeg et al., 2017). International responsibilities regarding migratory bird populations, e.g. Agreement on the Conservation of African-Eurasian Migratory Waterbirds (AEWA, online), should stimulate national authorities to avert HPAI outbreaks not only in poultry and humans but also in wild birds. Given the scale of die-offs from HPAI in colony-breeding seabirds observed in this reporting period, these recommendations are even more widely relevant now, and may apply both to migratory and resident wild birds in HPAI-affected areas.

During the present reporting period, the number of outbreaks in domestic birds sharply declined after the two peaks of infection observed from autumn 2021 to spring 2022 (Figure 2B). However, in the summer 2022, the number of infected poultry premises increased more than five-fold compared with the previous epidemic in 2020–2021 (Table 2). The temporal and spatial distributions of HPAI A(H5) outbreaks during summer (Figures 4 and 7) suggest the presence of a sustained HPAI risk for domestic birds primarily in the vicinity of coastal areas.

Considering the high negative impact of HPAI epidemics in recent years and the ongoing risk of HPAI posed by the sustained virus circulation in wild birds, short-term preparedness and medium- and long-term prevention strategies should be identified and implemented, primarily in densely populated poultry areas and poultry production systems that are highly susceptible to avian influenza exposure. These have been described in detail in the Avian influenza overview September – December 2021 (EFSA et al., 2021b).

As expected in the summer months, the number of outbreaks and affected non-European countries between 11 June and 9 September 2022 has decreased compared to the last report (EFSA et al., 2022), but the number of reported HPAI A(H5N1) virus detections are still high compared to reports from the same period in previous years (e.g., (EFSA et al., 2020; EFSA et al., 2021a). Furthermore, outbreaks in domestic poultry and wild birds in China and Russia were detected in regions spatially linked to key migration areas.

The expanding host range of the HPAI A(H5N1) viruses and their wide circulation in colony-breeding seabird species during the summer months has caused the emergence of at least three new genotypes.

One of them has been extensively detected in seabirds, mainly European herring gulls, in the Netherlands, Belgium and France, and resulted from reassortment events with viruses of the gull-adapted A(H13) subtype. This same genotype was also responsible of a case in hobby chickens and in a red fox in Belgium. In addition to the A(H5N1) subtype, viruses of the A(H5N5) subtype were persistently detected during the summer months in northern Norway, including Svalbard Island. These viruses from 2022 clustered together as well as with the A(H5N5) collected during the previous 2020–2021 season, therefore suggesting a persistent but confined circulation of the A(H5N5) genotype in this geographic area.

Since October 2020, 12 European countries have reported infections of HPAI A(H5) viruses of clade 2.3.4.4b in multiple mammalian species, including red foxes, harbour seals, grey seals, a Eurasian otter, a lynx, domestic pigs, a European badger, a European polecat, and a ferret. In the current reporting period, three additional wild mammal species were affected by HPAI A(H5N1) in European countries: two red foxes (*Vulpes vulpes*) in Belgium and Norway and, for the first time, a harbour porpoise (*Phocoena phocoena*) in Sweden. In addition to Europe, several HPAI A(H5N1) mammalian cases were reported also in the USA, Canada and Japan and for the first time the virus was identified also in a bottlenose dolphin (*Tursiops truncatus*) in the USA and in an American black bear (*Ursus americanus*) in Canada. During the summer period 2022, also likely seal-to-seal transmission accompanied with seal mortality due to avian influenza A(H5N1) viruses were observed in the USA. 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 two 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.

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.

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.

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, also other non-respiratory symptoms might possibly 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.

ECDC jointly with EFSA, EU_OSHA and the EURL published a separate document that outlines the testing of humans for zoonotic influenza viruses and which outlines different exposed groups at risk as well as highlights the likelihood of atypical presentations in people similar to other mammals showing severe infection of the brain with encephalitis or meningoencephalitis (ECDC, 2022).

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-a).

4.7.6. Candidate vaccine viruses

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

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

Sporadic transmission of uncommon avian influenza viruses such as A(H3N8) and A(H10N3) reported in 2022 have 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 viruses. However, the detection of viruses carrying markers for mammalian 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 mammalian adaptation with the possibility to acquire the ability to transmit to humans.

Direct and unprotected exposure to possibly infected poultry or wild birds and their products including blood, remains limited to mostly occupationally exposed groups of people in the EU/EEA 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 United Kingdom (GovUK, online; WHO, online-b). 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
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
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
IVPI	Intravenous pathogenicity index
IVPP	Influenza Viruses with Human Pandemic Potential
LPAI	Low pathogenic avian influenza
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
RA	Risk assessment
SSI	Statens Serum Institut
SVFA	State Veterinary and Food Administration
ToR	Term of Reference
WAHIS	World Animal Health System
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 HP AI subtype A(H5N5) has been detected in wild birds and recently also in poultry holdings in Germany.

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

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

There is knowledge, 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.
- 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.

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, pp. 1–24.

- 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 11 June to 9 September 2022 and reported by Member States and neighbouring countries to the ADIS or WOAH-WAHIS. Member States where avian influenza outbreaks have occurred in poultry have submitted additional epidemiological data to EFSA, that have been used to analyse the characteristics of the affected poultry establishments.

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

If HPAI outbreaks in poultry are detected in the EU, a description of the applied prevention and control measures (ToR 3) is given in the overview document provided by representatives from the affected Member States and attached as an Annex B. Information was collected for outbreaks that occurred from 2 June to 2 September 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 WOAH-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 11 June to 9 September 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 March to June 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 11 June to 9 September 2022 submitted by Member States to the ADIS (European Commission, online) were taken into account for this report. Data extraction was carried on 9 September 2022. The WOAH’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, and the common and scientific name of wild bird species described in this report in relation to Europe is reported in Table B2. 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 4.1 and 4.2.

Table B1. Categorisation of the wild bird species detected as HPAI virus-positive between 1 October 2016 and 9 September 2022

Raptor	Waterfowl	Colony-breeding sea birds	Other wild bird species
Accipitridae	Anatidae	Arctic tern	Anambra waxbill
Accipitriformes	Anatinae	Atlantic puffin	Ardeidae
Bald eagle	Anserinae	Auk	Calidris
Bearded vulture	Barnacle goose	Black guillemot	Carrion crow
Common barn-owl	Bean goose	Black-headed gull	Charadriidae
Common kestrel	Black swan	Caspian gull	Ciconiidae
Eagles	Brent goose	Common murre	Columbidae
Eurasian buzzard	Canada goose	Common tern	Common coot
Eurasian eagle-owl	Common eider	Cormorants and shags	Common crane
Eurasian sparrowhawk	Common goldeneye	crowned cormorant	Common moorhen
Falcons and caracaras	Common pochard	Dalmatian pelican	common pheasant
Golden eagle	Common shelduck	European herring gull	Common raven
Griffon vulture	Common teal	Glaucous gull	Common redshank
Hen harrier	Cygnus	Great black-backed gull	Common starling
Kites, hawks and eagles	Duck	Great cormorant	Common woodpigeon
Lanner falcon	Egyptian goose	Great skua	Corvids, jays and magpies
Little owl	Eurasian wigeon	Grey-headed gull	Cranes
Merlin	Ferruginous duck	Gulls, terns and skimmers	Curlew sandpiper
Montagu's harrier	Gadwall	Lesser black-backed gull	Dunlin
Northern goshawk	Garganey	Little auk	Eurasian blackbird
Northern long-eared owl	Goosander	Manx shearwater	Eurasian bullfinch
Peregrine falcon	Goose	Mediterranean gull	Eurasian collared-dove
Red kite	Greater scaup	Mew gull	Eurasian curlew
Rough-legged buzzard	Greater white-fronted goose	Northern fulmar	Eurasian jackdaw
Short-eared owl	Greylag goose	Northern gannet	Eurasian jay
Spotted harrier	Lesser white-fronted goose	Pelecanidae	Eurasian magpie
Strigidae	Mallard	Razorbill	Eurasian oystercatcher
Strigiformes	Muscovy duck	Ring-billed gull	Eurasian spoonbill
Tawny owl	Mute swan	Sandwich tern	Eurasian woodcock
True owls	Northern shoveler	Silver gull	European greenfinch
Ural owl	Pink-footed goose	Sulidae	Finches

Western marsh-harrier	Tufted duck	Western gull	Great Blue heron
White-tailed sea-eagle	Whooper swan	Yellow-legged gull	Great crested grebe
			Great white egret
			Green sandpiper
			Grey heron
			Haematopodidae
			Hooded crow
			House sparrow
			Little egret
			Little grebe
			Northern bald ibis
			Northern lapwing
			Passeridae
			Pheasants and allies
			Pied avocet
			Rallidae
			Red knot
			Rock dove
			Rook
			Ruddy turnstone
			Sanderling
			Semipalmated sandpiper
			Snipe
			Song thrush
			Turdidae
			Western grebe
			Western sandpiper
			Western water rail
			Whimbrel
			White stork
			White-rumped sandpiper
			Unidentified species

Table B2. Common and scientific name of the wild bird species detected as HPAI virus-positive between 1 October 2016 and 9 September 2022

Common name	Scientific name	Common name	Scientific name
Anambra waxbill	<i>Estrilda poliopareia</i>	Common goldeneye	<i>Bucephala clangula</i>
Arctic tern	<i>Sterna paradisaea</i>	Common kestrel	<i>Falco tinnunculus</i>
Atlantic puffin	<i>Fratercula arctica</i>	Common moorhen	<i>Gallinula chloropus</i>
Bald eagle	<i>Haliaeetus leucocephalus</i>	Common murre	<i>Uria aalge</i>
Barnacle goose	<i>Branta leucopsis</i>	common pheasant	<i>Phasianus colchicus</i>
Bean goose	<i>Anser fabalis</i>	Common pochard	<i>Aythya ferina</i>
Bearded vulture	<i>Gypaetus barbatus</i>	Common raven	<i>Corvus corax</i>
Black guillemot	<i>Cepphus grylle</i>	Common redshank	<i>Tringa totanus</i>
Black swan	<i>Cygnus atratus</i>	Common shelduck	<i>Tadorna tadorna</i>
Black-headed gull	<i>Larus ridibundus</i>	Common starling	<i>Sturnus vulgaris</i>
Brent goose	<i>Branta bernicla</i>	Common teal	<i>Anas crecca</i>
Calidris	<i>Calidris spp.</i>	Common tern	<i>Sterna hirundo</i>
Canada goose	<i>Branta canadensis</i>	Common woodpigeon	<i>Columba palumbus</i>
Carrion crow	<i>Corvus corone</i>	Crowned cormorant	<i>Microcarbo coronatus</i>

Common name	Scientific name	Common name	Scientific name
Caspian gull	<i>Larus cachinnans</i>	Curlew sandpiper	<i>Calidris ferruginea</i>
Common barn-owl	<i>Tyto alba</i>	Dalmatian pelican	<i>Pelecanus crispus</i>
Common coot	<i>Fulica atra</i>	Dunlin	<i>Calidris alpina</i>
Common crane	<i>Grus grus</i>	Egyptian goose	<i>Alopochen aegyptiaca</i>
Common eider	<i>Somateria mollissima</i>	Eurasian blackbird	<i>Turdus merula</i>
Eurasian bullfinch	<i>Pyrrhula pyrrhula</i>	Mew gull	<i>Larus canus</i>
Eurasian buzzard	<i>Buteo buteo</i>	Mediterranean gull	<i>Larus melanocephalus</i>
Eurasian collared-dove	<i>Streptopelia decaocto</i>	Merlin	<i>Falco columbarius</i>
Eurasian curlew	<i>Numenius arquata</i>	Montagu's harrier	<i>Circus pygargus</i>
Eurasian eagle-owl	<i>Bubo bubo</i>	Muscovy duck	<i>Cairina moschata</i>
Eurasian jackdaw	<i>Corvus monedula</i>	Mute swan	<i>Cygnus olor</i>
Eurasian jay	<i>Garrulus glandarius</i>	Northern bald ibis	<i>Geronticus eremita</i>
Eurasian magpie	<i>Pica pica</i>	Northern fulmar	<i>Fulmarus glacialis</i>
Eurasian oystercatcher	<i>Haematopus ostralegus</i>	Northern gannet	<i>Morus bassanus</i>
Eurasian sparrowhawk	<i>Accipiter nisus</i>	Northern goshawk	<i>Accipiter gentilis</i>
Eurasian spoonbill	<i>Platalea leucorodia</i>	Northern lapwing	<i>Vanellus vanellus</i>
Eurasian wigeon	<i>Mareca penelope</i>	Northern long-eared Owl	<i>Asio otus</i>
Eurasian woodcock	<i>Scolopax rusticola</i>	Northern shoveler	<i>Spatula clypeata</i>
European greenfinch	<i>Chloris chloris</i>	Peregrine falcon	<i>Falco peregrinus</i>
European herring gull	<i>Larus argentatus</i>	Pied avocet	<i>Recurvirostra avosetta</i>
Ferruginous duck	<i>Aythya nyroca</i>	Pink-footed goose	<i>Anser brachyrhynchus</i>
Finches	<i>Fringillidae</i>	Razorbill	<i>Alca torda</i>
Gadwall	<i>Mareca strepera</i>	Red kite	<i>Milvus milvus</i>
Garganey	<i>Spatula querquedula</i>	Red knot	<i>Calidris canutus</i>
Glaucous gull	<i>Larus hyperboreus</i>	Ring-billed gull	<i>Larus delawarensis</i>
Golden eagle	<i>Aquila chrysaetos</i>	Rock dove	<i>Columba livia</i>
Goosander	<i>Mergus merganser</i>	Rook	<i>Corvus frugilegus</i>
Great black-backed gull	<i>Larus marinus</i>	Rough-legged buzzard	<i>Buteo lagopus</i>
Great blue heron	<i>Ardea herodias</i>	Ruddy turnstone	<i>Arenaria interpres</i>
Great cormorant	<i>Phalacrocorax carbo</i>	Sanderling	<i>Calidris alba</i>
Great crested grebe	<i>Podiceps cristatus</i>	Sandwich tern	<i>Thalasseus sandvicensis</i>
Great skua	<i>Catharacta skua</i>	Semipalmated sandpiper	<i>Calidris pusilla</i>
Great white egret	<i>Ardea alba</i>	Short-eared owl	<i>Asio flammeus</i>
Greater scaup	<i>Aythya marila</i>	Silver gull	<i>Chroicocephalus novaehollandiae</i>
Greater white-fronted goose	<i>Anser albifrons</i>	Song thrush	<i>Turdus philomelos</i>
Green sandpiper	<i>Tringa ochropus</i>	Spotted harrier	<i>Circus assimilis</i>
Grey heron	<i>Ardea cinerea</i>	Tawny owl	<i>Strix aluco</i>
Grey-headed gull	<i>Larus cirrocephalus</i>	Tufted duck	<i>Aythya fuligula</i>
Greylag goose	<i>Anser anser</i>	Ural owl	<i>Strix uralensis</i>
Griffon vulture	<i>Gyps fulvus</i>	western grebe	<i>Aechmophorus occidentalis</i>
Hen harrier	<i>Circus cyaneus</i>	Western gull	<i>Larus occidentalis</i>
Hooded crow	<i>Corvus coronus</i>	Western marsh-harrier	<i>Circus aeruginosus</i>
House sparrow	<i>Passer domesticus</i>	Western sandpiper	<i>Calidris mauri</i>
Lanner falcon	<i>Falco biarmicus</i>	Western water Rail	<i>Rallus aquaticus</i>
Lesser black-backed gull	<i>Larus fuscus</i>	Whimbrel	<i>Numenius phaeopus</i>

Common name	Scientific name	Common name	Scientific name
Lesser white-fronted goose	<i>Anser erythropus</i>	White stork	<i>Ciconia ciconia</i>
Little auk	<i>Alle alle</i>	White-rumped sandpiper	<i>Calidris fuscicollis</i>
Little egret	<i>Egretta garzetta</i>	White-tailed sea-eagle	<i>Haliaeetus albicilla</i>
Little grebe	<i>Tachybaptus ruficollis</i>	Whooper swan	<i>Cygnus cygnus</i>
Little owl	<i>Athene noctua</i>	Yellow-legged gull	<i>Larus michahellis</i>
Mallard	<i>Anas platyrhynchos</i>		
Manx shearwater	<i>Puffinus puffinus</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 3 June to 5 September 2022 were searched; the search was run on 8 August and 5 September 2022.

Relevance criteria Scientific articles added to the database from 3 June to 5 September 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 143 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.7120286>.

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

Data from WOA-H-WAHIS (WOAH, 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 9 September 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.7124008>

The annexes contain the following information:

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

The Annex contains a table with the characteristics of the HPAI A(H5Nx)-positive poultry establishments by affected EU Member State from 2 June to 2 September 2022.

Annex B – Applied prevention and control measures on avian influenza

The Annex contains an overview of specific prevention and control measures applied in France, Moldova, the Netherlands, Poland, Portugal and Spain, from 11 June to 2 September 2022 in relation to HPAI outbreaks in poultry. In addition, Bulgaria and Hungary reported on the specific prevention and control measures applied on their territory for HPAI poultry outbreaks that occurred before 11 June that were not included in the previous published report as they were too close to the publication date to be collected; those overviews are also included in Annex B.

Annex C – Data on wild birds

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