SCIENTIFIC REPORT

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Avian influenza overview December 2021 – March 2022

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Abstract

Between 9 December 2021 and 15 March 2022, 2,653 highly pathogenic avian influenza (HPAI) virus detections were reported in 33 EU/EEA countries and the UK in poultry (1,030), in wild (1,489) and in captive birds (133). The outbreaks in poultry were mainly reported by France (609), where two spatiotemporal clusters have been identified since October 2021, followed by Italy (131), Hungary (73) and Poland (53); those reporting countries accounted together for 12.8 of the 17.5 million birds that were culled in the HPAI affected poultry establishments in this reporting period. The majority of the detections in wild birds were reported by Germany (767), the Netherlands (293), the UK (118) and Denmark (74). HPAI A(H5) was detected in a wide range of host species in wild birds, indicating an increasing and changing risk for virus incursion into poultry farms. The observed persistence and continuous circulation of HPAI viruses in migratory and resident wild birds will continue to pose a risk for the poultry industry in Europe for the coming months. This requires the definition and the rapid implementation of suitable and sustainable HPAI mitigation strategies such as appropriate biosecurity measures, surveillance plans and early detection measures in the different poultry production systems. The results of the genetic analysis indicate that the viruses currently circulating in Europe belong to clade 2.3.4.4b. Some of these viruses were also detected in wild mammal species in the Netherlands, Slovenia, Finland and Ireland showing genetic markers of adaptation to replication in mammals. Since the last report, the UK reported one human infection with A(H5N1), China 17 human infections with A(H5N6), and China and Cambodia 15 infections with A(H9N2) virus. The risk of infection for the general population in the EU/EEA is assessed as low, and for occupationally exposed people, low to medium.

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

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Note: Kosovo – this designation is without prejudice to positions on status and is in line with United Nations Security Council Resolution 1244 and the International Court of Justice Opinion on the Kosovo Declaration of Independence.

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Figures 1–16, 18–19, 21 and Tables 1, 2 and 3 © EFSA; Figures 17, 20, 22–24 and Table 2 © ECDC.

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1. Introduction

This scientific report provides an overview of highly pathogenic avian influenza (HPAI) virus detections in poultry[1], captive[2] 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 9 December 2021 and 15 March 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 9 December 2021 and 15 March 2022, is presented below.

2.1. Main observations

- In Europe, between 9 December 2021 and 15 March 2022 (based on the Animal Disease Information System (ADIS), OIE World Animal Health Information System (OIE-WAHIS), and information provided by affected countries) 2,652 HPAI A(H5) detections[3] were reported in poultry, and captive and wild birds:
  - 1,030 outbreaks in poultry, in France (603), Italy (131), Hungary (73), Poland (53), Germany (37), UK (32), Spain (29), the Netherlands (26), Czechia (13), Portugal (8), Denmark (6), Bulgaria (5), Sweden (3), Ireland, Kosovo[4] and Slovakia (2 each), Belgium, Croatia, Moldova, Romania and Slovenia (1 each);
  - 1,489 detections in wild birds, in Germany (767), the Netherlands (293), UK (118), Denmark (74), Belgium (52), Spain (28), Austria (22), Sweden (21), France and Hungary (19 each), Ireland and Italy (13 each), Romania (10), Croatia (7), Portugal and Slovakia (5 each), Finland, Luxembourg and North Macedonia (3 each), Bulgaria, Estonia, Greece, Latvia, Lithuania and Norway (2 each), Czechia and Switzerland (1 each);
  - 133 outbreaks in captive birds, in Slovenia (37), Poland (28), France (23), UK (17), Germany and Portugal (5 each), Austria, Czechia and Sweden (3 each), Belgium, Hungary and Slovakia (2 each), Denmark, Norway and Ukraine (1 each).
- Faroe Islands and Moldova reported for the first time detections of HPAI virus in their territory (in wild birds and in poultry, respectively); also, for the first time since 2017, Portugal, North Macedonia and Spain (in poultry) were affected by HPAI viruses.
- During this reporting period HPAI virus was detected in at least 62 wild bird species: at least 17 waterfowl species (1,007 detections), 12 raptor species (241 detections), and 33 other wild bird species (241 detections). The overall temporal pattern showed an increase from the beginning of December reaching a peak in the middle of January.
- Considering outbreaks in poultry, France is by far the most affected country in this reporting period, with 609 outbreaks mainly in the foie gras sector in poultry-dense areas and more than 5.5 million birds having been culled in the affected establishments. France is followed by Italy

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

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

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

[4] This designation is without prejudice to positions on status and is in line with United Nations Security Council Resolution 1244 and the International Court of Justice Opinion on the Kosovo Declaration of Independence.

(127 outbreaks and approximately 5 million birds culled), Hungary (73 outbreaks and more than one million birds culled), and Poland (52 outbreaks and more than 2.2 million birds culled).

- In France, two epidemiological spatiotemporal clusters were identified since October 2021, with no epidemiological links between them: a first cluster in the southwest (southern part of Nouvelle-Aquitaine and Occitanie), with a peak in mid-January, and the second one in western regions (Pays de la Loire and northern part of Nouvelle-Aquitaine) peaking in late February-beginning of March. Nearly all outbreaks involved commercial farms. The vast majority of outbreaks for which information on farmed species was available (373) were duck farms for foie gras production (236/373), followed by ducks for fattening (43/373), and broilers (35/373), nonetheless, chicken breeder farms with high biosecurity levels were also affected. The genetic investigation identified the incursions of at least eight distinct genotypes. However, up to mid-February 2022, a single genotype accounted for most of the virus detections dispersed over the country, both in poultry and birds other than poultry, and also accounted for most poultry outbreaks detected in southwestern France.
- As for the poultry species and production categories affected during this epidemic, there has been an increase in the number of fattening (chickens, domestic ducks and turkey) establishments affected when compared with the 2020-2021 influenza season, whilst the number of outbreaks in breeding and egg-producing establishments has decreased.
- All the HPAI (H5Nx) viruses characterised since October 2021 belong to clade 2.3.4.4b. Whole genome sequencing indicates the persistent circulation of the A(H5N1) and A(H5N8) subtypes in Northern Europe, which have been circulating in the whole Europe since October 2020. Moreover, novel reassortant HPAI A(H5N1) and A(H5N2) genotypes were introduced into Europe through the autumn migration of wild birds or generated from local reassortment events.
- Six additional HPAI A(H5N1) cases in five different mammalian species, red fox (*Vulpes vulpes*), Eurasian otter (*Lutra lutra*), polecat (*Mustela putorius*), ferret (*Mustela furo*) and lynx (*Lynx linx*) were detected in the Netherlands, Slovenia, Finland and Ireland since the las report. Some of these viruses show genetic markers of adaptation to replication in mammals, as previously observed (Manzoor et al., 2009; Kim et al., 2010; Herfst et al., 2012; Suttie et al., 2019).
- In contrast with the last report (EFSA et al., 2021b), the avian influenza situation in non-EU/EEA countries showed an increasing number of reported outbreaks in poultry and detections in wild birds, particularly in Africa and Asia. Furthermore, the number of affected countries increased by one third. The virus subtype HPAI A(H5N1) is now even more dominant than in the previous reporting period (September – December 2021) and infected a broader spectrum of wild bird species also outside Europe. The European lineage of HPAI A(H5N1) was also detected in domestic poultry and wild birds in the east of Canada, suggesting that, for the first time, infected wild birds have carried the virus from Europe westward through Greenland crossing the Atlantic Ocean.
- Seventeen human cases with infections caused by HPAI A(H5N6) have been reported from China since the last report.
- One human asymptomatic infection with HPAI A(H5N1) was reported from the UK since the last report.
- Some of the A(H5N6) viruses responsible for the human cases in China in 2021 were represented by a reassortant virus of clade 2.3.4.4b viruses, which possessed an haemagglutinin (HA) gene closely related to the A(H5) viruses circulating in Europe and Asia.
- Fifteen human infections with A(H9N2) have been reported from China (14) and Cambodia (1) since the last report.

2.2. Conclusions

- The viruses characterised to date retain a preference for avian-type receptors; mutations associated with mammalian adaptation have only been sporadically identified in the analysed viruses from avian species, but they are frequently acquired upon transmission to mammals.
- The transmission of A(H5) clade 2.3.4.4b viruses to humans in UK, Russia and Nigeria, the increasing number of transmission events of A(H5) viruses to wild mammals reported from different European countries together with the recent upsurge of human cases due to A(H5N6) in China underline the continuous risk of avian influenza viruses to transmit to humans also in Europe and that these viruses may adapt further to mammals.
- The risk of infection for the general population in the EU/EEA is assessed as low, and for occupationally exposed people low to medium with high uncertainty due to the high diversity of circulating avian influenza viruses in bird populations.
- The risk of transmission to humans by exposure to contaminated poultry products is considered negligible as also outlined in a previous EFSA assessment (EFSA AHAW Panel, 2017).
- HPAI A(H5) continues to be maintained in wild bird populations in Eurasia, including detection in resident wild birds in Europe. Also, research on various species of dabbling ducks in Italy (Gobbo et al. 2021) showed a high prevalence of HPAI A(H5) infection in winter in geographical areas where no dead birds were detected, indicating that high infection pressure in the environment is possible in absence of wild bird mortality.
- Compared with the same period last year, in addition to migratory waterfowl, HPAI A(H5) was detected in a wider range of other wild bird species, including several terrestrial species. This enlarged host range of HPAI A(H5) in wild birds indicates an increasing and changing risk for virus incursion into poultry farms.
- The dynamics of the current HPAI epidemic compared with those observed in 2016–2017 and 2020–2021 indicate that an elevated environmental pressure of infection will likely persist in the coming months posing a risk for further virus introduction and spread in the poultry sector.
- The frequent occurrence of HPAI A(H5) virus incursions in commercial farms where birds are kept indoors, including poultry production types considered at low avian influenza risk (e.g. broilers), raises concern about the capacity and effectiveness of applied biosecurity measures to prevent virus introduction.

3. Options for response

- The persistence and continuous circulation of HPAI A(H5) viruses in migratory and resident wild birds will continue to pose a risk for the poultry sector in Europe requiring the definition and the rapid implementation of suitable and sustainable HPAI mitigation strategies. In particular, appropriate biosecurity measures, surveillance plan, and early detection strategies must be regularly applied in the different poultry production systems.
- Appropriate early detection and rapid response, together with sustainable and effective biosecurity in poultry and captive birds, should be applied to reduce the high-risk period of an epidemic and to prevent the secondary spread of avian influenza from affected establishments, particularly in densely populated poultry areas and high-risk production sectors. Veterinary authorities in the Member States should ensure high awareness among all stakeholders in the poultry production sector, promoting fast reporting of suspected cases (Gonzales and Elbers, 2018; Elbers and Gonzales, 2021) and the implementation of effective measures to minimise the exposure risk for farmers and other occupationally exposed people.
- Surveillance in mammals and humans that can potentially be exposed to infected birds should be strengthened to facilitate the early identification 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.

- People potentially exposed to infected poultry or captive birds, e.g. during culling operations, should be adequately protected and actively monitored or at least self-monitor for respiratory 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. Antiviral pre-exposure or post-exposure prophylaxis should be considered for exposed people according to national recommendations.
- 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 4.6.1 for more detail).
- Authorities are strongly encouraged to initiate sero-epidemiological studies in exposed people following HPAI outbreaks to identify transmission events and support risk assessments.
- Timely generation and sharing of complete viral genome sequences from wild birds, poultry, and captive birds are crucial to promptly detect novel virus introductions (i.e. distinguishable from viruses that have remained present in birds in Europe since winter 2020–2021) and to detect the emergence of novel reassortant viruses. Continued monitoring together with in-depth analyses on virus evolution and genetic mutations, resulting in changes in viral properties that are relevant for animal and public health, are of utmost importance. More effort should be made by reporting countries to genetically characterise a significant number of samples based on the size, duration, and relevant features of the epidemic in each country.

4. Results

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

Figures 1, 2 and 3 show the HPAI outbreaks in domestic birds (poultry and captive birds) and detections in wild birds that were reported in Europe via ADNS, ADIS or OIE WAHIS for seasons 2016–2017, 2017–2018, 2018–2019, 2019–2020 and 2020–2021 by month of suspicion (Figures 1 and 2) and geographical location (Figure 3). In this document a 'season' refers to the period starting on week 40 (the beginning of October) and ending on week 39 (the end of September) of the following year, based on the dates on which the first HPAI detections were observed in wild birds in Europe in 2016–2017, 2020–2021, and 2021–2022. For the current season, 2021–2022, data reported are truncated at 15 March 2022. Figure 4 shows the comparison between the geographical distribution of HPAI detections from December 2021 to March 2022 and the same period during the 2016–2017 and the 2020–2021 epidemics, which prior to this season were the largest epidemics recorded in the EU/EEA and UK 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 15 March 2022, is reported in Figure 5 by week of suspicion, virus subtype and host population; the distribution of HPAI outbreaks in poultry in Europe by affected bird species and sampling programme leading to the outbreak detection is shown in Figure 6.

Table 1 shows the number of HPAI affected wild bird species and number of HPAI detections by species in the two observed peaks during each of the 2020–2021 and 2021–2022 epidemics. The complete list of HPAI infected wild bird species during those epidemic peaks is presented in Annex C (Table C.1).

The start of the epidemics in the 2016–2017, 2020–2021, and in the current 2021–2022 seasons, all fell within the period between the end of September and beginning of October. There were no evident epidemics in 2017–2018 and 2018–2019, while the end of December was the start of the smaller 2019–2020 epidemic that affected only poultry (Figures 1 and 2). In the 2016–2017 season, the epidemic peaks in wild and domestic (poultry and captive) birds were approximately simultaneous. In the 2020–2021 season, the epidemic peak in wild birds preceded that in domestic birds and, so far, this appears to be the case also in the 2021–2022 season (Figure 2).

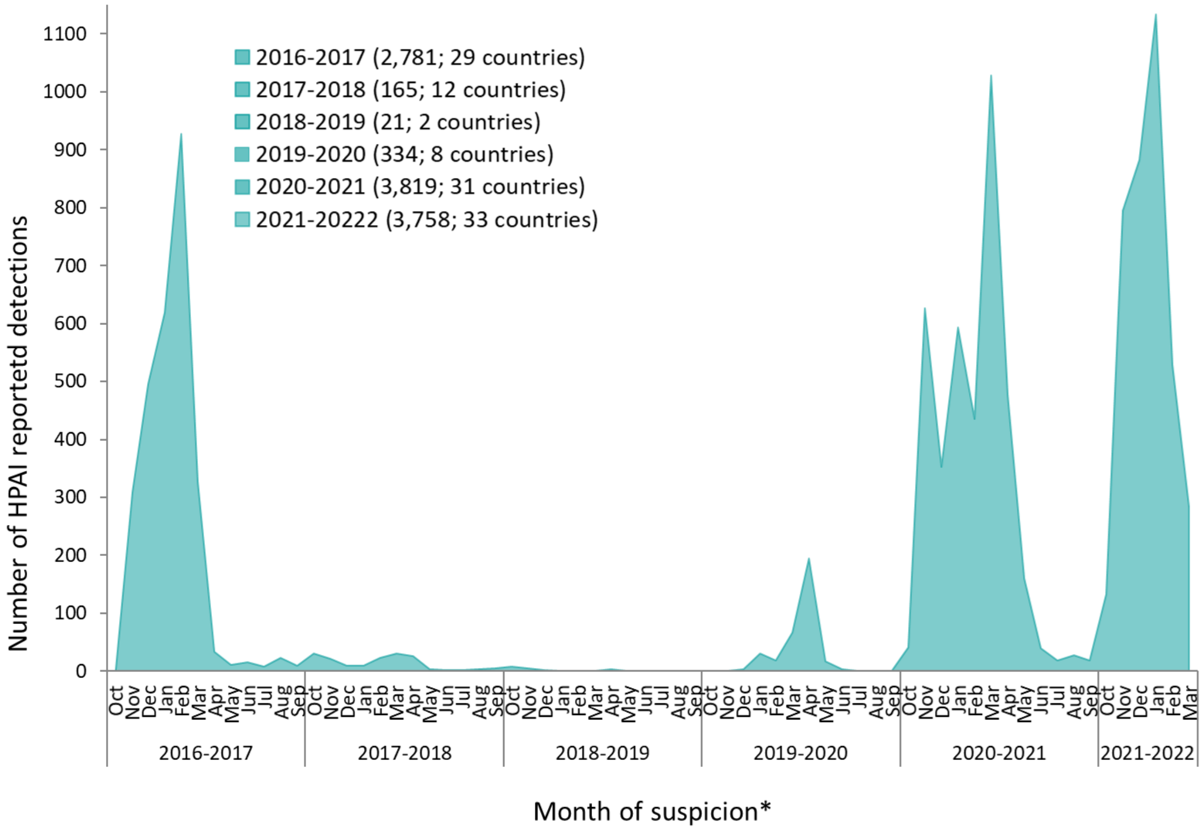
The large 2016–2017 and 2020–2021 epidemics were widespread in Europe and had similar northern (Finland), western (Ireland and the Iberian Peninsula), southern (Italy, Greece) and eastern limits (Ukraine, Romania, Bulgaria). So far, the 2021-–2022 epidemic seems to have become as extensive, with the same northern and southern limits. However, 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).

From December 2021 to March 2022, the virus spreads southward and westward in January to Portugal, Spain, Italy and Greece. The 2021–2022 season stands out with highest frequency of wild bird detections in this reporting period (December 2021 – March 2022) in UK and the Iberian Peninsula. In February and March, the geographical spread was more or less stable. For the number of wild bird detections, the month with the highest detections varies over the seasons: with these peaks being in February in 2016, in March in 2021, and in January in 2022.

The predominant subtype A(H5N8) in the 2020–2021 epidemic season was replaced by subtype A(H5N1) in the current 2021–2022 epidemic. For wild birds, in 2021–2022 HPAI was detected predominantly in waterfowl, but also in a wide range of other wild bird species, including several terrestrial species, and raptors (Figure 5). Similarly to what observed in the 2020–2021 epidemic season, in the current 2021–2022 season there were two peaks of HPAI A(H5) detections in wild birds. In both seasons, the first peak was in the beginning of November, coinciding with the autumn migration of waterfowl and arrival at their wintering grounds in Europe. However, the second peak appeared to be earlier in this season (middle of January) than in the last season (beginning of March) (Figure 5).

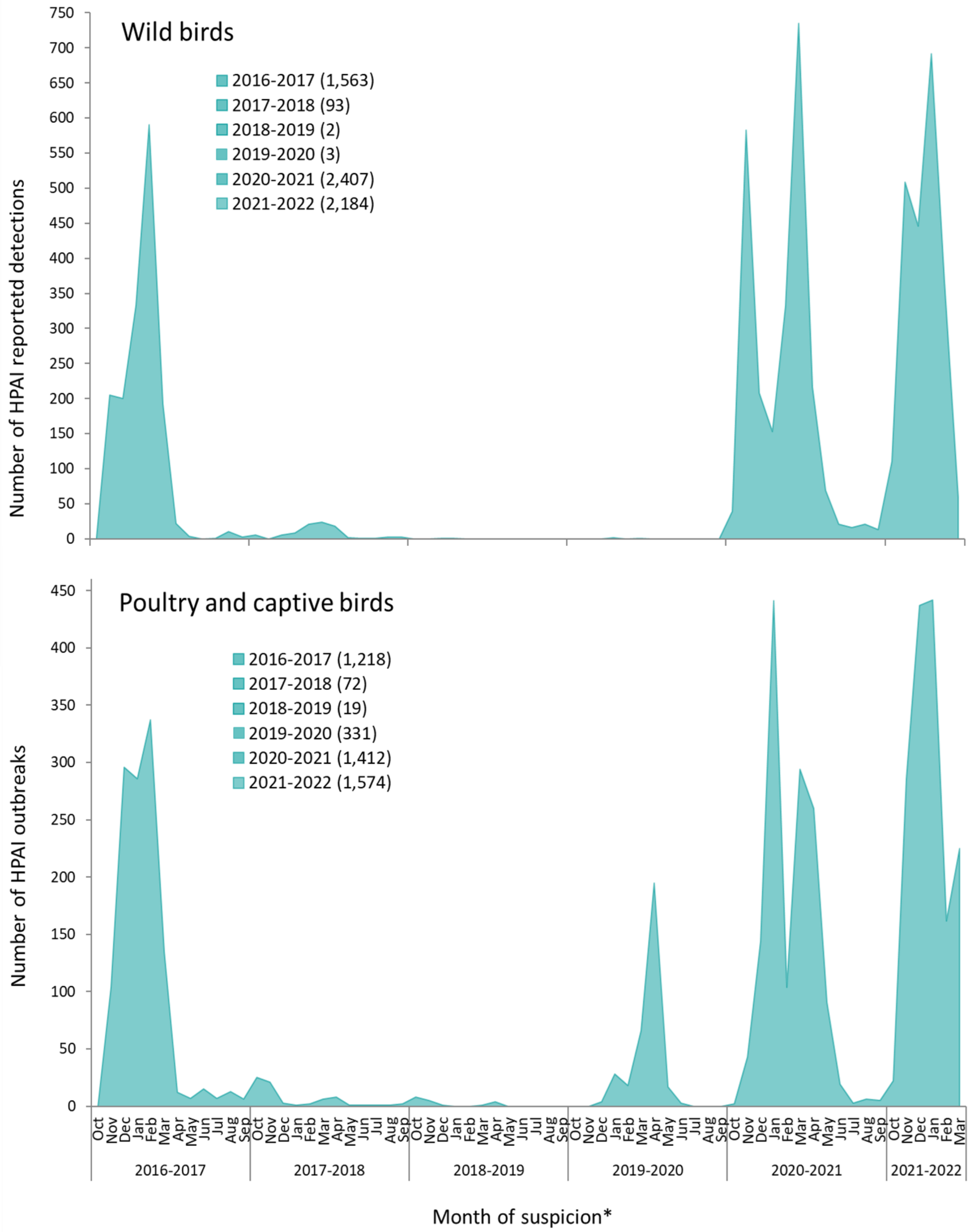
Interestingly, in both seasons the number of HPAI detections in wild birds increased from the first to the second peak during each epidemic, either in terms of number of species detected as HPAI infected and of absolute number of HPAI detections (Table 1). This increasing is particularly evident in this 2021–2022 epidemic season when comparing the number of species and detections observed during the second peak with those observed in the first peak (Table 1). The complete list of HPAI detections in wild birds in the two observed peaks in the 2020–2021 and 2021–2022 epidemic season is reported in Annex C (Tables C.3 and C.4)

Considering only HPAI outbreaks in poultry, so far approximately 31 million of birds have been culled in the HPAI affected establishments in the current epidemic season since October 2021.



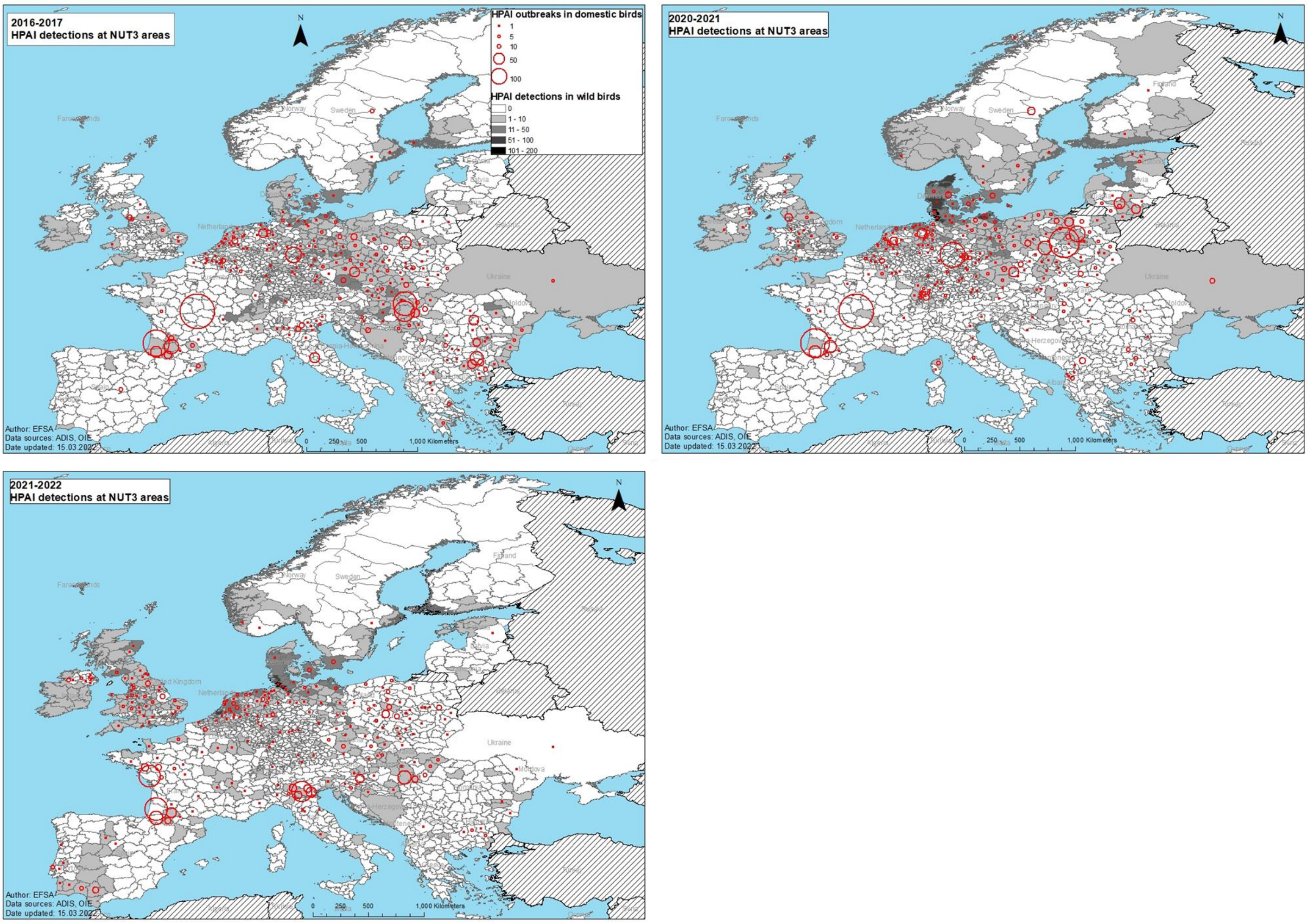
*When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.
UK data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was ADNS for Northern Ireland and World Animal Health Information System (OIE-WAHIS) for Great Britain.
Source: ADIS and OIE (data extraction carried out 15 March 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, 9 December 2021 to 15 March 2022 (10,878)



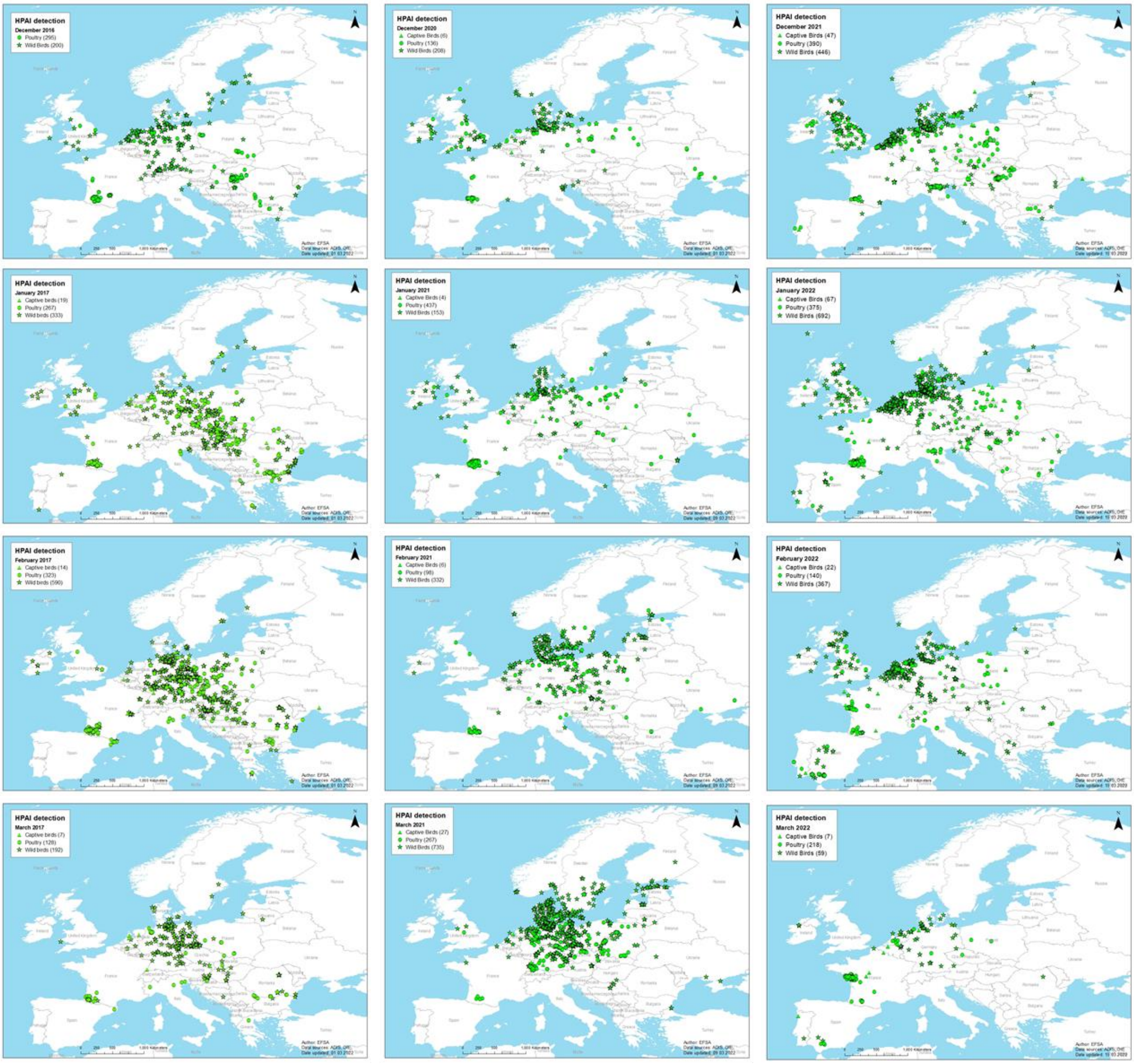
*When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.
UK data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was ADNS for Northern Ireland and World Animal Health Information System (OIE-WAHIS) for Great Britain.
Source: ADIS and OIE (data extraction carried out 15 March 2022).
Note that the scale of the vertical axes is specific to each bird population.

Figure 2: Distribution of total number of HPAI virus detections reported in Europe in the seasons 2016–2017, 2017–2018, 2018–2019, 2019–2020, 2020–2021 and beginning of 2021–2022 by month of suspicion in (upper) wild birds (6,252) and (lower) domestic birds (poultry and captive birds) (4,626), from 9 December 2021 to 15 March 2022



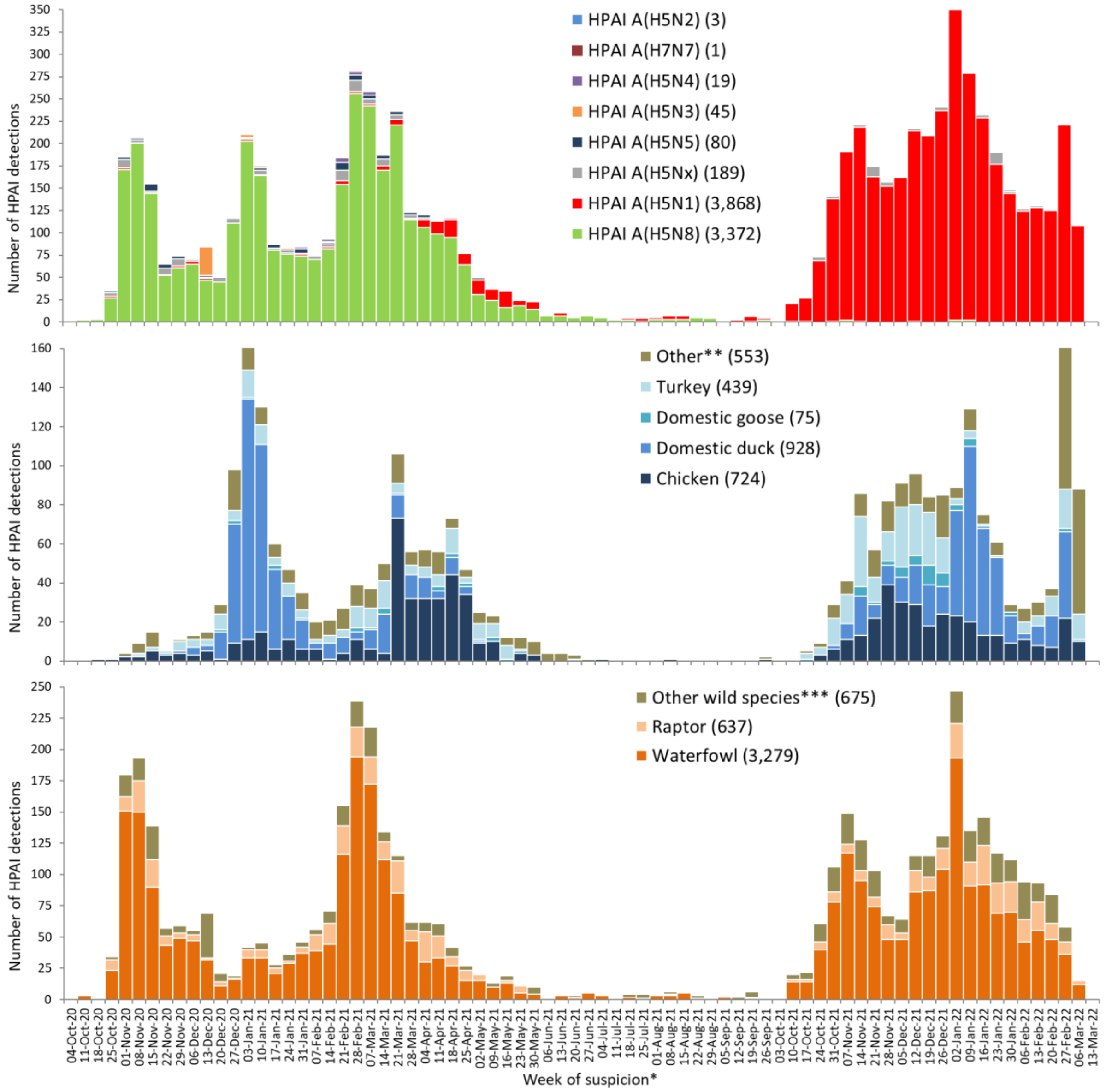
UK data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was ADNS for Northern Ireland and OIE WAHIS for Great Britain.
Source: ADIS and OIE (data extraction carried out 15 March 2022).

Figure 3: Geographical distribution at NUTS3 level of HPAI detections in Europe in seasons 2016-2017 (2,781), 2020–2021 (3,819) and 2021–2022 (3,758) in domestic birds (red circles) and wild birds (grey coloured area), from 1 October 2016 to 15 March 2022



UK data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was ADNS for Northern Ireland and OIE WAHIS for Great Britain.
Source: ADIS and OIE (data extraction carried out 15 March 2022).

Figure 4: Geographical distribution, based on available geocoordinates, of HPAI detections in Europe by month of suspicion in 2016 – 2017 (left column), in 2020 – 2021 (central column) and in 2021 – 2022 (right column). Note that data in March 2022 are up to 15 March

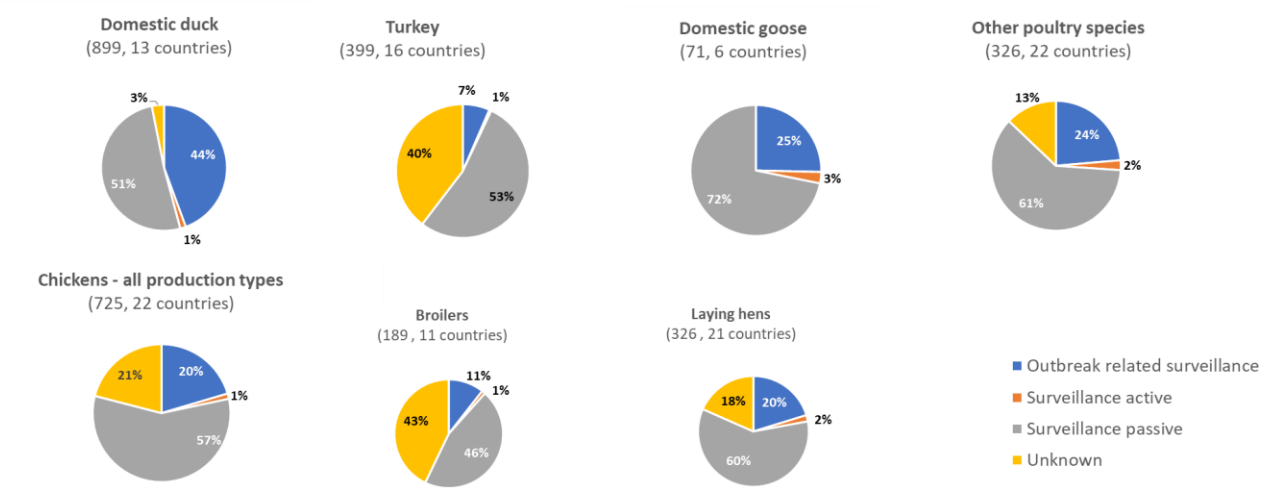


*When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.
**'Other domestic species' category contains mixed, unknown bird species, or categories different from those displayed (i.e. guinea fowl, peacock, pheasant and quail).
***'Other wild species' category contains mixed, unknown bird species, or categories different from those displayed. The complete list of species by each wild bird category is reported in Table C.1 in Annex C.
UK data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was ADNS for Northern Ireland and OIE WAHIS for Great Britain.
The HPAI A(H7N7) outbreak notified by the Lithuanian Health Authorities on 26 March 2021 was not confirmed by AI-ND EURL due to the very low viral load in the samples and the lack of other samples on which to repeat the analysis.
Source: ADNS, ADIS and OIE (data extraction carried on 15 March 2021), EFSA.
Note that the scale of the vertical axes is specific to each category

Figure 5: Distribution of total number of HPAI virus detections reported in Europe by week of suspicion (dates indicate the first day of the week) and (upper) virus subtype (7,577), (middle) affected poultry categories (2,719), (lower) affected wild bird categories (4,591), 9 December 2021 to 15 March 2022

Table 1: Overview of the HPAI detections in wild birds in the two observed peaks in seasons 2020–2021 and 2021–2022

Time period		**Waterfowl species**		**Raptor species**		**Other wild bird species**	
Epidemic season	**Epidemic peak**	**Minimum number of species affected**	**Number of HPAI detections**	**Minimum number of species affected**	**Number of HPAI detections**	**Minimum number of species affected**	**Number of HPAI detections**
2020-2021	1° peak (1/10/2020 to 27/12/2020)	20	601	8	88	20	124
	2° peak (28/12/2020 to 30/5/2021)	21	1,125	11	243	26	154
2021-2022	1° peak (1/10/2021 to 28/11/2021)	17	437	7	41	18	118
	2° peak (29/11/2021 to 15/3/2022)	18	1,081	12	255	33	252



'Other poultry species' contains mixed, unknown, or bird species different from those displayed.
Source: EFSA.

Figure 6: Frequency distribution of HPAI outbreaks in poultry in Europe, by bird species (domestic goose, domestic duck, chicken, turkey and other poultry species) and sampling programme leading to the outbreak detection, in season 2020–2021 from October 2020 to 4 March 2022 (2,416)

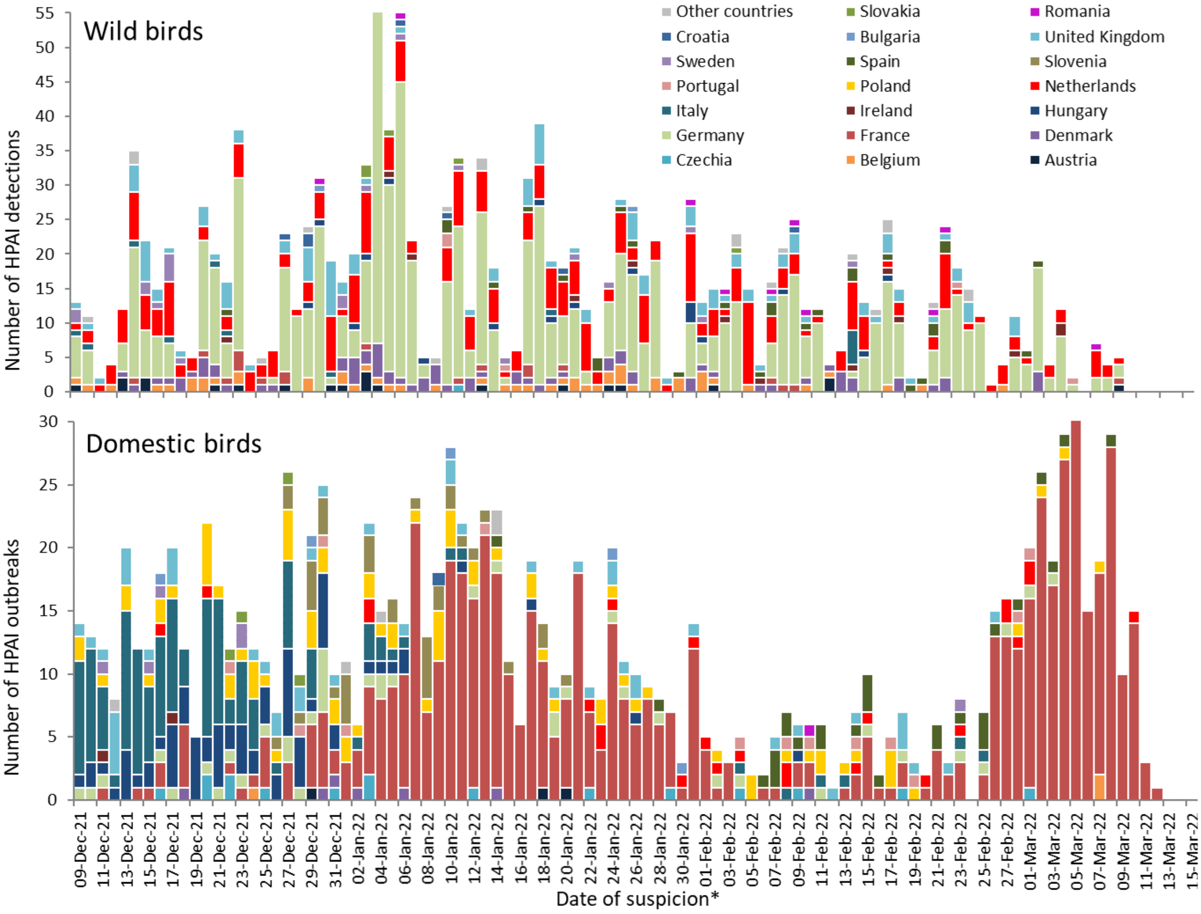
4.2. HPAI and LPAI detections in Europe, 9 December 2021 to 15 March 2022 (ToR 1 and ToR 2)

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

From 9 December 2021 to 15 March 2022, 2,652 HPAI A(H5) virus detections were notified in poultry (1,030), captive (133) and wild birds (1,489) in 33 countries in Europe, and were reported via the ADIS or OIE WAHIS, as presented in Table 1. Overall, approximately 17.7 million birds were culled in the HPAI affected poultry establishments, of which 5.5 million birds in France, 5 in Italy, 1.2 in Hungary and 2.2 in Poland.

The timelines, virus subtypes, locations and the affected bird categories of the avian influenza detections are presented in Figures 7, 8 and 9. This is the first time that HPAI virus has been detected in the Faroe Islands in Denmark (three detections in wild birds) and in Moldova (one detection in poultry); also, the first detections since 2017 in Portugal, North Macedonia and in poultry in Spain. Characterisation of HPAI-affected poultry establishments[5] 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.

In this reporting period, 440 poultry outbreaks were notified to the ADIS as secondary in France (358), Hungary (67), Poland (8), Portugal (4), Spain (2), Germany (1). In France, the between-farm spread was mostly observed in the domestic duck sector.



*When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.
UK data were extracted from ADNS until 31 December 2020. From 1 January 2021 onwards, the data source was ADNS for Northern Ireland and OIE WAHIS for Great Britain.
Source: EFSA, ADIS and OIE (data extraction carried on 15 March 2021).
Countries with a number of outbreaks in domestic birds and detections in wild birds below the median (4 detections in wild birds, 3 outbreaks in domestic birds) are presented aggregated as 'Other countries'.
Note that the scale of the vertical axes is specific to each bird population

Figure 7: Distribution of the highly pathogenic avian influenza detections in wild birds (1,489) (upper panel) and outbreaks in domestic birds (poultry and captive birds) (1,163) (lower panel), in Europe, by day of suspicion and country from 9 December 2021 to 15 March 2022

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[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, p. 1–208.

Table 2: Number of highly pathogenic avian influenza outbreaks in Europe, by country, virus subtype and affected sub-population, 9 December 2021 – 15 March 2022. Cumulative numbers since the start of the 2021-2022 season are reported in parentheses (1 October 2021 – 15 March 2022)

Country	Captive birds		Poultry				Wild birds				Total
	A(H5Nx)	**A(H5N1)**	**A(H5Nx)**	**A(H5N1)**	**A(H5N2)**	**A(H5N8)**	**A(H5Nx)**	**A(H5N1)**	**A(H5N2)**	**A(H5N8)**	
Austria	-	3 (4)	-	-	-	-	-	22 (24)	-	-	25 (28)
Belgium	-	2 (2)	-	1 (3)	-	-	3 (5)	49 (59)	-	-	55 (69)
Bosnia and Herzegovina	-	-	-	-	-	-	-	(1)	-	-	0 (1)
Bulgaria	-	(1)	5 (8)	(1)	-	-	2 (2)	-	-	-	7 (12)
Croatia	-		-	1 (2)	-	-	-	7 (13)	-	-	8 (15)
Czechia	-	3 (3)	-	13 (18)	-	-	-	1 (6)	-	-	17 (27)
Denmark	-	1 (3)	-	5 (6)	-	1 (1)	1 (1)	71 (105)	-	2 (2)	81 (118)
Estonia	-	-	-	-	-	0 (1)	-	2 (8)	-	-	2 (9)
Finland	-	-	-	-	-	-	-	3 (8)	-	(1)	3 (9)
France	-	23 (28)	12 (12)	591 (597)	-	-	2 (2)	17 (26)	-	-	645 (665)
Germany	-	5 (7)	-	37 (66)	-	-	4 (8)	761 (1,082)	2 (2)	-	809 (1,165)
Greece	-	-	-	-	-	-	-	2 (3)	-	-	2 (3)
Hungary	-	2 (3)	-	73 (113)	-	-	-	19 (25)	-	-	94 (141)
Ireland	-	-	-	2 (6)	-	-	2 (2)	11 (41)	-	-	15 (49)
Italy	-	-	4 (4)	127 (311)	-	-	-	13 (23)	-	-	144 (338)
Kosovo[(a)]	-	-	-	-	-	2 (2)	-	-	-	-	2 (2)
Latvia	-	-	-	-	-	-	-	2 (2)	-	-	2 (2)
Lithuania	-	-	-	-	-	-	-	2 (2)	-	-	2 (2)
Luxembourg	-	-	-	-	-	-	-	3 (5)	-	-	3 (5)
Moldova	-	-	-	1 (1)	-	-	-	-	-	-	1 (1)
Netherlands	(1)	(6)	-	26 (34)	-	-	(17)	293 (372)	-	(2)	319 (432)
North Macedonia	-	-	-	-	-	-	-	3 (3)	-	-	3 (3)
Norway	-	1 (1)	-	(2)	-	-	-	2 (6)	-	-	3 (9)
Poland	-	28 (31)	-	52 (90)	1 (1)	-	-	0 (1)	-	-	81 (123)
Portugal	-	5 (6)	-	8 (8)	-	-	-	5 (5)	-	-	18 (19)
Romania	-	-	-	1 (1)	-	-	1 (1)	9 (12)	-	-	11 (14)
Slovakia	-	2 (2)	-	2 (3)	-	-	(1)	5 (6)	-	-	9 (12)

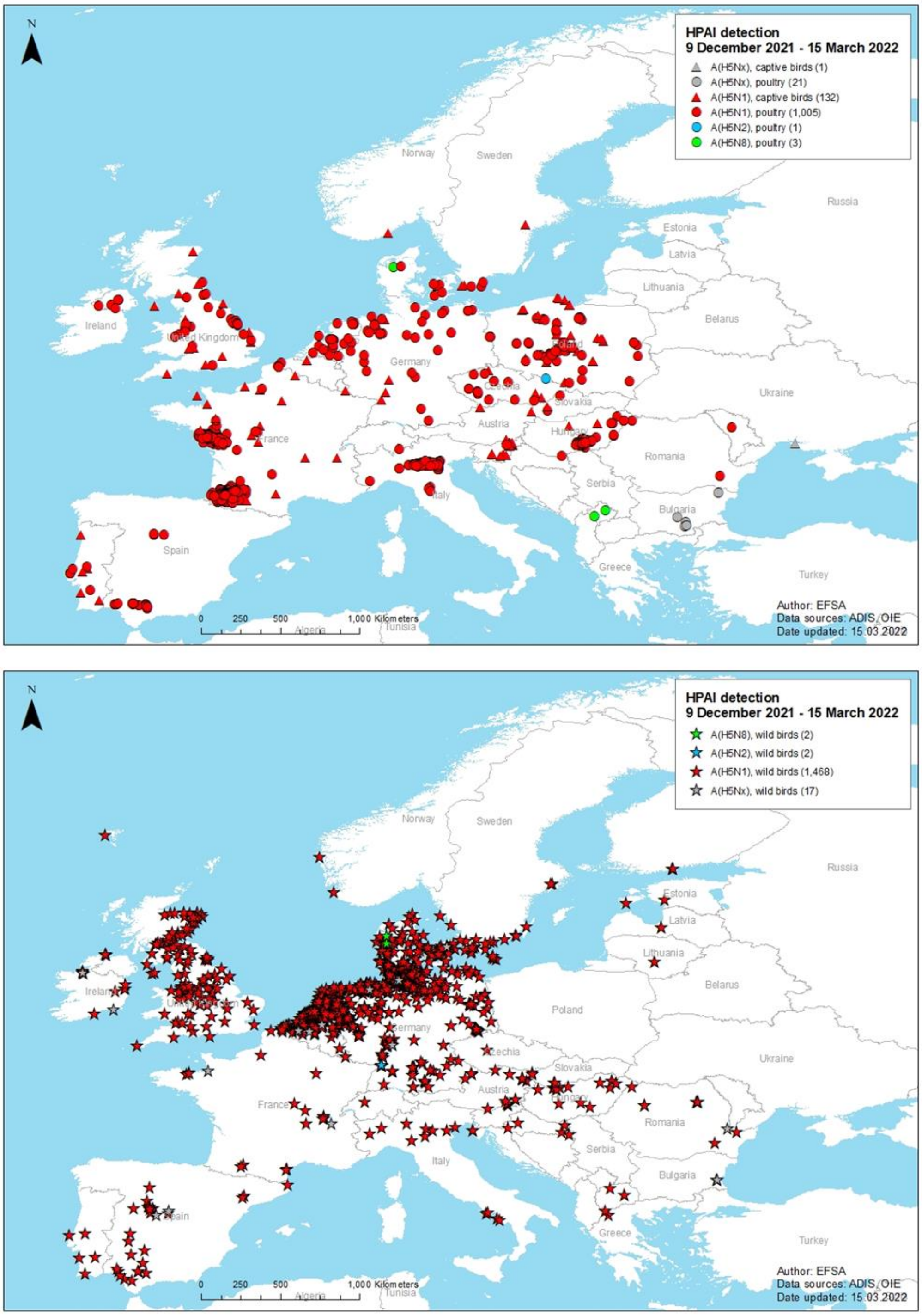
Slovenia	-	37 (37)	-	1 (1)	-	-	-	-	-	-	38 (38)
Spain	-	-	-	29 (29)	-	-	2 (2)	26 (26)	-	-	57 (57)
Sweden	-	3 (4)	-	3 (3)	-	-	-	21 (34)	-	0 (1)	27 (42)
Switzerland	-	0 (1)	-	-	-	-	-	1 (1)	-	-	1 (2)
Ukraine	1 (2)	-	-	-	-	-	-	-	-	-	1 (2)
United Kingdom[b]	-	17 (40)	-	32 (68)	-	-	-	118 (235)	-	0 (1)	167 (344)
Total	1 (3)	132 (179)	21 (24)	1,005 (1,363)	1 (1)	3 (4)	17 (41)	1,468 (2,134)	2 (2)	2 (7)	2,652 (3,758)

(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): UK data were extracted from ADNS until 31 December 2020. From 1 January 2021 onwards, the data source was ADNS for Northern Ireland and OIE WAHIS for Great Britain.

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

Source: EFSA, ADNS and OIE (data extraction carried on 15 March 2022).



UK data were extracted from ADNS until 31 December 2020. From 1 January 2021 onwards, the data source was ADNS for Northern Ireland and OIE WAHIS for Great Britain.
Source: EFSA, ADIS and OIE (data extraction carried on 15 March 2021).

Figure 8: Geographical distribution, based on available geocoordinates, of highly pathogenic avian influenza outbreaks in poultry and captive birds (1,163) (upper panel) and detections in wild birds (1,489) (lower panel) reported by virus subtype in Europe between 9 December 2021 and 15 March 2022

4.2.1.1. HPAI in domestic birds

Characterisation of the HPAI-affected poultry establishments

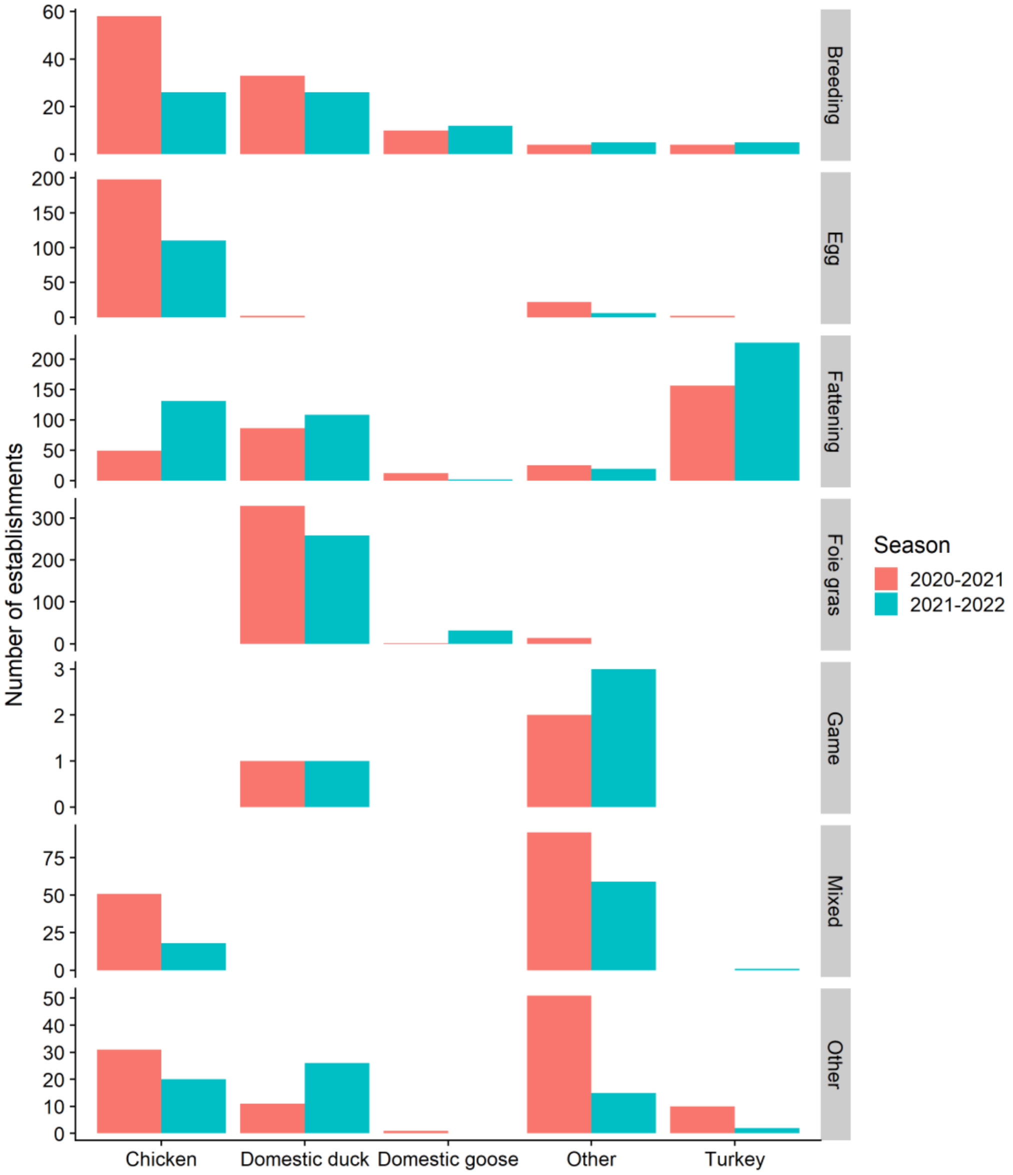
In this section a detailed analysis of the HPAI affected poultry establishments is presented. Due to the time needed to carry out the data collection, the reporting period presented in this section is different and shorter than that of the whole report: only the outbreaks reported between 1 December 2021 and 4 March 2022 are thoroughly described. Outbreaks notified before 1 December 2021 have been described in a previous EFSA report (EFSA et al., 2021b), and the outbreaks that occurred later than 4 March 2022 will be included in the next report.

From 1 December 2021 to 4 March 2022, 893 HPAI outbreaks in poultry were notified in 21 countries through ADIS: 406 in France, 198 in Italy, 83 in Hungary, 57 in Poland, 45 in Germany, 23 each in the Netherlands and Spain, 12 in Czechia, eight each in Bulgaria and Portugal, six each in Denmark and Northern Ireland (UK), four in Ireland, three each in Sweden and Belgium, two each in Slovakia and Kosovo, one each in Romania, Croatia, Moldova and Slovenia (Figure 10A). France accounted for 45% of the outbreaks and 15% of the birds affected, followed by Italy, accounting for 22% of the outbreaks and 46% of the birds affected (Figure 10B).

Compared with the previous reporting period (from 16 September to 1 December 2021), during which 219 outbreaks were reported by 15 affected countries, in this reporting period approximately four times the number of outbreaks were reported, with more than twice the number of birds affected: 18,253,710 in this reporting period *vs* 8,038,099 in the previous period (EFSA et al., 2021a). A similar increasing trend in the number of outbreaks and affected birds between these two reporting periods was also observed in the previous year, with 34 outbreaks (and more than 1,560,000 birds affected) occurring from 16 September to 1 December 2020, and 618 (and more than 7,600,000 birds affected) occurring from 1 December 2020 to 4 March 2021. Compared with the same reporting period from the 2020-2021 epidemic, the number of outbreaks had increased by 45% (893 vs 618).

Three virus subtypes were reported: as in the previous reporting period, the vast majority were A(H5N1) outbreaks (858), while A(H5N8) was reported in three outbreaks (two in Kosovo and one in Denmark), and one A(H5N2) was reported in Poland at the end of February. Thirty-two outbreaks (in Bulgaria, France and Italy) have been reported as A(H5Nx), with no specification on the N-type.

For the species and production type involved in the outbreaks, fattening establishments remain the most affected category, in particular those keeping domestic ducks for foie gras production in France and Hungary, accounting for 32% of the total number of outbreaks (only 1/219 in the previous reporting period), and turkeys (affecting 11 countries, in particular Italy), accounting for 16% of the total number of outbreaks (38% in the previous reporting period). A general increase in the number of affected fattening establishments can be seen comparing this epidemic season with the previous one (Figure 9), whereas no differences were observed considering the distribution of the farm sizes across species and production type in the previous (2020-2021) and current season (2021-2022).

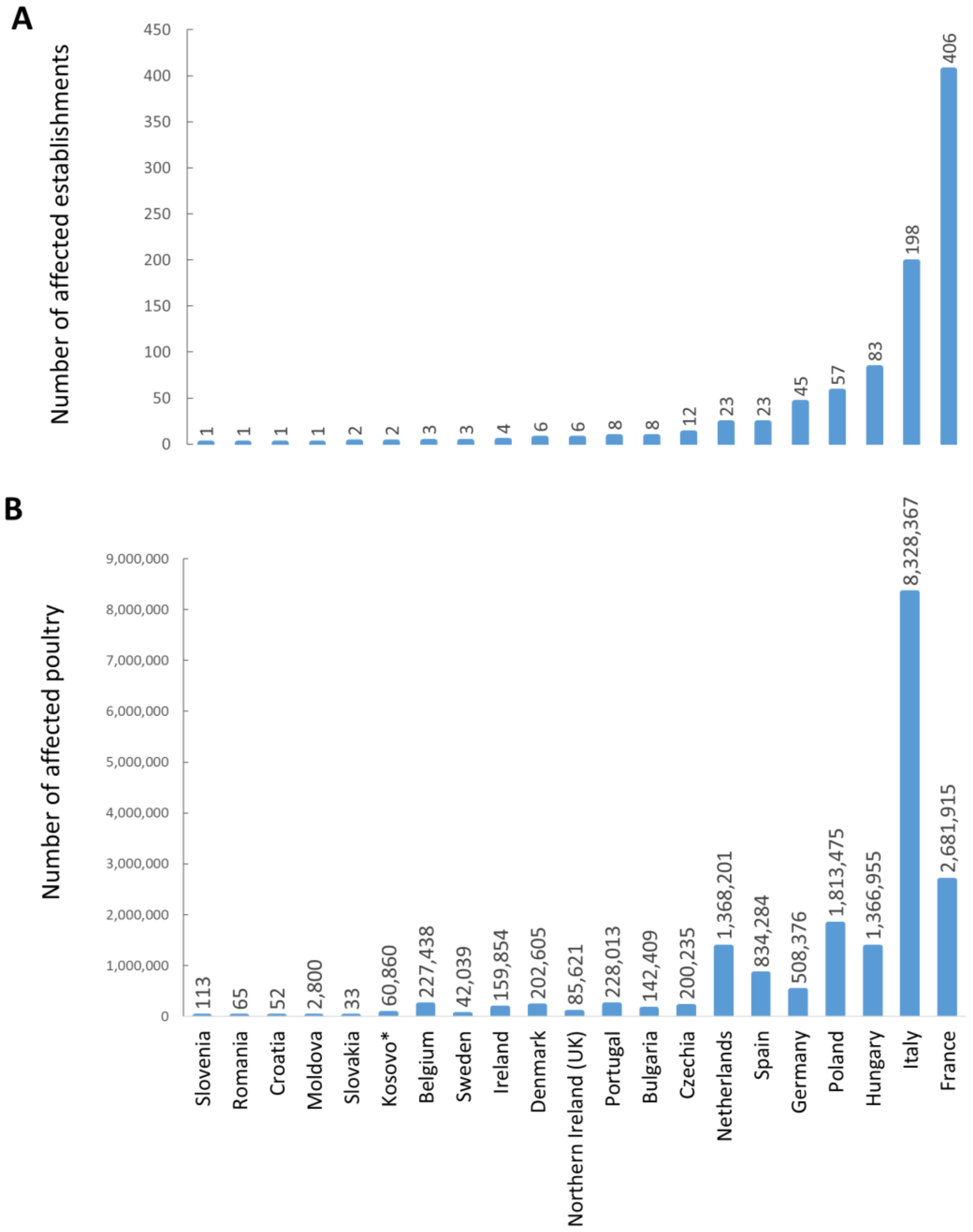


'Other' species category contains mixed, unknown bird species, or categories different from those displayed. 'Other' production type contains unknown or different production type from those displayed.

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

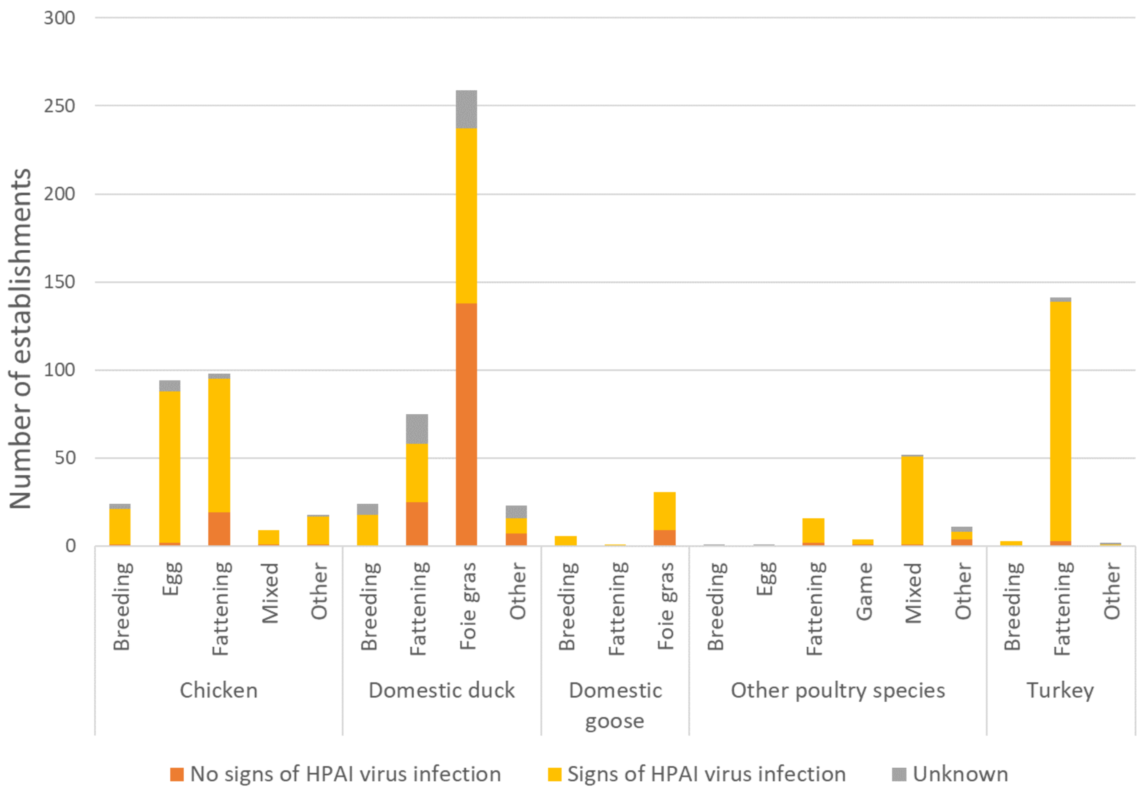
Out of 893 outbreaks, 835 were reported in commercial farms and 57 in non-commercial farms (the information is not known for one farm). Among the primary outbreaks (629), 32 were in farms with outdoor access (10 in Czechia, seven in Poland, three in Northern Ireland (UK), two each in Germany, the Netherlands, Denmark, Slovakia, and one each in Slovenia, Croatia, Kosovo and Portugal), 141 did not have outdoor access and for the remaining 456 farms the information was unknown at the time of publication of this report. More information on the application of housing order at the time of outbreaks suspicion is provided in the specific Member States sections.

Clinical signs, mortality, or other types of signs were not observed in the majority of infected establishments with ducks for which the information was available (170/329) (Figure 11). In contrast, signs were observed in the vast majority of establishments with turkeys (139/143), chickens (206/230) and geese (29/38) (Figure 11).



*This designation is without prejudice to positions on status and is in line with United Nations Security Council Resolution 1244 and the International Court of Justice Opinion on the Kosovo Declaration of Independence.

Figure 10: Number of (A) establishments and (B) poultry affected by HPAI in Europe between 1 December 2021 and 4 March 2022 (893)



'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 11: 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 1 December 2021 and 4 March 2022 (893)

HPAI A(H5N1)-affected poultry establishments in Belgium

Between 9 December 2021 and 3 January 2022, three HPAI A(H5N1) outbreaks were notified in three commercial chicken farms in Vlaanderen region, affecting more than 227,000 poultry. The three farms were keeping chickens for breeding, fattening and egg production, respectively. Birds showed clinical signs and increased mortality, but no drop in feed/water intake. None of the three farms had outdoor access, and the most likely source of introduction of the virus was considered to be indirect contact with wild birds. No data were available on the number of exposed people. The characteristics of the affected establishment and species reared are presented in Annex A.

HPAI A(H5NX)-affected poultry establishments in Bulgaria

Between 2 December 2021 and 1 February 2022, eight H5NX outbreaks were notified in the regions of Haskovo (3), Plovdiv (2), Pazardzhik (1), Stara Zagora (1) and Dobrich (1). Five outbreaks were notified in commercial establishments with laying hens (3/5), Mulard ducks (1/5) and Pekin ducks (1/5). The remaining three outbreaks were notified in non-commercial establishments with mixed poultry species (2/3) and turkeys (1/3). Mortality or clinical signs of disease were reported in all the species, except for Pekin ducks.

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

HPAI A(H5N1)-affected poultry establishments in Croatia

On 14 January 2022, one primary HPAI A(H5N1) outbreak was notified in a backyard farm with 52 poultry (30 laying hens, 10 roosters, three geese, and nine pigeons) located in the Osjecko-Baranjska region. Increased mortality and clinical signs (drop in feed and water intake) were observed in laying hens and roosters (three hens and all the roosters died). No increased mortality nor clinical signs were observed in geese and pigeons. The most likely source of infection remains unknown, but the affected holding had outdoor access, therefore contact with wild birds cannot be excluded. A housing order in the whole territory of Croatia has been in place from 5 December 2021, and at the moment of suspicion of the disease (10/01/22) it was prohibited to keep poultry outdoor. No data were available on the number of exposed people. The characteristics of the affected establishment and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Czechia

Between 17 December 2021 and 22 February 2022, 12 HPAI A(H5N1) were notified in the six regions of Jihočeský (4), Jihomoravský (2), Pardubický (1), Plzeňský (2), Středočeský (1) and Ústecký (2).

Four outbreaks occurred in commercial establishments with breeding ducks, laying hens, mallards, and pheasants. This last farm was also keeping some other poultry (chickens and one peafowl). Mortality and clinical signs were observed in breeding ducks, laying hens, and pheasants.

Two out of the four commercial establishments had outdoor access. The most likely source of virus introduction was considered to be indirect contact with wild birds, as the establishments were located near ponds or rivers.

For the remaining eight backyard establishments, four kept chickens for mixed production, and four mixed species including chickens, ducks, geese, turkeys and guinea fowls. Mortality or clinical signs were observed in all the farms. All the establishments had outdoor access, but housing order has been in place across the entire country since 23 November 2021. The most likely source of introduction was considered to be direct or indirect contact with wild birds.

In total, 309 persons were potentially exposed to the virus in these outbreaks. The characteristics of the affected establishments and species reared are presented in Annex A.

HPAI A(H5N1) and HPAI A(H5N8)-affected poultry establishments in Denmark

Between 20 December 2021 and 11 February 2022, five HPAI A(H5N1) and one HPAI A(H5N8) outbreaks were notified in the regions of Central Jutland (in the part covered by Veterinary Inspection Unit North) and Zealand (in Veterinary Inspection Unit East).

Five of the outbreaks occurred in commercial establishments and one in a backyard holding with mixed species.

For the commercial establishments, two kept turkeys for fattening with, respectively, 33,600 and 63,779 birds, two kept hens for egg production with, respectively, 100,000 and 800 birds, and one kept approximately 4,500 pheasants and 1,500 mallards for re-stocking supplies of game. An increased mortality had been observed in all the species, except for mallards, which also did not show any other kind of sign. Signs were observed in all the farms, except for one farm of laying hens.

The only backyard holding kept 45 birds including laying hens (30), ducks (13) and geese (2). Mortality was observed in laying hens. Clinical signs were observed in both hens and ducks.

Two out of six farms had outdoor access (both commercial establishments). A housing order has been in place across the entire country since 1 November 2021. The source of viral introduction remains unknown, possibly related to direct or indirect contact with wild birds. No data were available on the number of exposed people in the HPAI outbreak.

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

HPAI A(H5N1)-affected poultry establishments in France

Between 7 December 2021 and 4 March 2022, 389 HPAI A(H5N1) and 17 HPAI A(H5NX) outbreaks were notified in France. In total, 238 were primary outbreaks and 168 secondary outbreaks. In particular, two spatiotemporal clusters of outbreaks were identified, with no epidemiological link between each other: a first cluster in the south west area (300 outbreaks in Nouvelle-Aquitaine and 52 in Occitanie), with a peak in mid-January, and a second one in west regions (44 outbreaks in Pays de la Loire) in late February to the beginning of March. Other outbreaks were also notified in Hauts-de-France (7), Centre-Val de Loire (2) and the Normandie region (1).

All the outbreaks involved commercial farms including chicken breeders' farms with high biosecurity level, which were also affected.

The vast majority of farms for which the information on the farmed species was available (404/406) kept ducks for foie gras production (234/404), followed by ducks for fattening (42/404), and broilers (35/404). Other establishments affected were farming laying hens (13), ducks for breeding (11), breeding chickens (8), turkeys for fattening (5), quails for breeding or fattening (3), guineafowls for fattening (4), and mixed species (9). For 30 farms, including domestic ducks (16), chickens (12), one turkey farms, and one farm with mixed species, the production type was not known at the time of publication of this report. Six farms with domestic ducks and one with quails were classified as having "other" production type.

Information on signs was available for 336/406 farms. The majority of farms with chickens for which information on signs was available reported the presence of mortality or other types of signs of HPAI virus infection (47/59), while signs were not identified for most farms with ducks for foie gras production for which information on signs was available (150/257). No information about outdoor access, the most likely source of virus introduction and 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 Germany

Between 2 December 2021 and 3 March 2022, 42 primary and three secondary HPAI A(H5N1) outbreaks were notified in the nine regions of Lower Saxony (17), North Rhine-Westphalia (7), Mecklenburg-Western Pomerania (7), Bavaria (4), Brandenburg (3), Schleswig-Holstein (2), Saxony-Anhalt (2), Thuringia (2) and Rhineland-Palatinate (1).

Most outbreaks involved commercial farms (35/45), while 10 were backyard farms. Mono-species establishments were farming fattening turkeys (17) and chickens (15). Thirteen farms kept multiple species, including chickens (13/13), and in particular laying hens (11/13), fattening ducks (10/13), fattening geese (7/13), fattening turkeys (2/13), breeding ducks (1/13), pheasants (1/13) and pigeons (1/13).

No mortality was observed in pheasants, pigeons, and in approximately half of the duck farms. Clinical signs were observed in fattening establishments of turkeys (7/13), ducks (2/9), and chickens (1/2).

Most farms where primary outbreaks occurred did not have outdoor access (30/42), but access was present for two backyard farms and information remains unknown for the remaining ten farms (three backyard and seven commercial). At the time in which outbreaks were suspected in the two farms with outdoor access, housing order was not in place in the two federal states concerned (Sachsen-Anhalt and Nordrhein-Westfalen), as in that time they were not affected by domestic and wild bird outbreaks.

The most likely source of virus introduction was direct contact with infected poultry for the three secondary outbreaks, indirect contact with wild birds for 13 outbreaks (of which four were backyard and nine commercial) and unknown for the remaining farms at the time of publication of this report.

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

HPAI A(H5N1)-affected poultry establishments in Hungary

Between 6 December 2021 and 27 January 2022, seven primary outbreaks and 76 secondary outbreaks were notified in six regions of Hungary: Bács-Kiskun (50), Csongrád-Csanád (16), Békés (5), Csongrád (4), Hajdú-Bihar (4) and Szabolcs-Szatmár-Bereg (4).

Most of the outbreaks were detected in commercial establishments (78/83) and five in non-commercial establishments with mixed poultry.

Out of the commercial establishments affected, the vast majority were establishments with geese (27) and ducks (25) for foie gras production, followed by ducks for fattening (8), ducks for breeding (5), turkeys for fattening (3), laying hens (3), geese for breeding (3), turkeys for breeding (1), broilers (1) and mixed species (2).

Increased mortality was detected in most domestic goose establishments for foie gras production (20/27) and in domestic duck fattening establishments (7/8), while this was detected only in 8/25 of duck establishments for foie gras production.

Signs (either clinical or a drop in feed/water intake or egg production) were detected in 12/27 domestic geese establishments for foie gras production, 6/25 duck establishments for foie gras production and in 4/8 domestic duck fattening establishments.

None of the commercial establishments had outdoor access and one out of five backyard farms did not have outdoor access. The most likely source of virus introduction was considered to be indirect contact with infected poultry for the secondary outbreaks, and indirect contact with wild birds for the primary ones.

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

HPAI A(H5N1)-affected poultry establishments in Ireland

Between 1 December and 21 December 2021, four HPAI A(H5N1) outbreaks were notified in commercial farms in the Monaghan and Cavan regions. The farms kept, respectively, 100,000 laying hens, 6,500 fattening turkey, 10,354 fattening ducks and 43,000 breeding ducks.

Mortality and clinical signs were observed in all the farms. The establishments had no outdoor access. However, indirect infection via wild birds was considered to be the most likely source of viral introduction as positive A(H5N1) wild birds were found in the area. In total, 115 people were considered to be exposed as a result of these cases. The characteristics of the affected establishment and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Italy

Between 1 December 2021 and 1 March 2022, in total 198 A(H5N1) virus outbreaks were notified in Italy, mostly in the Veneto region (136), followed by Lombardy (56), Tuscany (3), Piedmont (1), Emilia Romagna (1), and Friuli Venice Giulia (1). The outbreaks involved more than 8,300,000 birds (5,379,000 in the last reporting period).

Most of the outbreaks were detected in commercial establishments (186/198), with 12 occurring in backyard holdings.

Out of the commercial establishments affected, the vast majority were establishments for fattening turkeys (79/186), followed by broilers (51/186), and egg production facilities with hens (42/198). Other farms kept guinea fowls for fattening (4/186), domestic ducks for fattening (3/186), breeding turkeys (2/186), pheasants (2/186), quails (1/186), Muscovy duck (1/186) and breeding chickens (1/186).

Mortality or signs were reported for almost all the laying hens for which data were available (39/40) and fattening turkeys (77/79). For broilers, mortality or signs have been reported in most cases (40/51) although these signs were often not present or not evident in the first days after the virus entered the holding.

The 12 non-commercial establishments kept an average number of 54 poultry for home food production or hobby purpose (chickens, turkeys, domestic ducks, domestic geese, guinea fowls, pigeons, swans).

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

HPAI A(H5N8)-affected poultry establishments in Kosovo[2]

On 2 February 2022, two HPAI A(H5N8) outbreaks have been notified in a commercial farm in Gjakova region and a non-commercial farm in Prishtina region.

The commercial farm kept 60,480 laying hens, and the non-commercial farm 380 chickens for mixed production type. Clinical signs were reported in both farms. The non-commercial farm had outdoor access, but the housing order that was introduced on 30 September 2021 in the country is still ongoing.

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

HPAI A(H5N1)-affected poultry establishments in Moldova

On 2 February 2022, one outbreak was notified in a backyard farm in the Telenesti region, affecting a total of 2800 birds. Additional data on the outbreak were not available at the time of publication of this report.

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

Between 17 December and 3 March 2022, 23 HPAI A(H5N1) were notified in commercial establishments in Gelderland (8), Groningen (4), Flevoland (3), North Brabant (2), Overijssel (2), Friesland (1), Limburg (1), North Holland (1), and Utrecht (1) regions.

The establishments were farming chickens (17/23), either for eggs production, fattening, or breeding purposes, turkeys for fattening (4/23), and ducks (2/23) for breeding and fattening. Clinical signs were detected in all farms. A drop in feed and water intake was observed in three chickens' and three turkeys' farms. A drop in egg production was observed in all the laying hens' facilities.

Only two out of 23 farms had outdoor access. The most likely cause of viral introduction has not been determined by the time of publication of this report. No data were available on the number of exposed people in the HPAI outbreak.

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

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

Between 1 December 2021 and 2 March 2022, 56 HPAI A(H5N1) outbreaks were notified in Poland, in the regions of Wielkopolskie (22), Łódzkie (12), Kujawsko-Pomorskie (5), Warmińsko-Mazurskie (5), Dolnośląskie (3), Śląskie (2), Lubuskie (2), Mazowieckie (2), Małopolskie (1), Podkarpackie (1) and Pomorskie (1). In addition, one HPAI A(H5N2) outbreak was notified in the region of Opolskie. Of these outbreaks, 51 were considered as primary and 11 as secondary (in the regions of Wielkopolskie, Łódzkie and Mazowieckie).

In total, 48 outbreaks were in commercial farms, and nine in non-commercial farms. Out of the commercial establishments affected, the most (39/53) were fattening establishments (22 kept domestic ducks, 12 turkeys, three both chickens and domestic ducks, one broiler and one domestic geese). Among the other farms, there were breeding establishments of domestic geese (3), domestic ducks (2), chickens (1), one farm of laying hens, and seven farms with multiple species with different production types.

For the outbreaks detected in fattening establishments, mortality or clinical signs among domestic ducks was observed in 17/19 cases, in 11/12 cases for turkey, and in the only two farms keeping geese and broilers. The backyard farms affected were mainly keeping chickens and ducks. All the species except for pigeons showed mortality or clinical signs of infection.

Two of the commercial farms and five of the backyard farms that were notified as primary outbreaks had outdoor access. A housing order was in place in the country in high-risk areas, and at the date of suspicion of these outbreaks, it was in place only in one of the areas where these farms are located, in the Wielkopolskie voivodeship. However, the most likely source of infection of the outbreak in the backyard farm in this area was considered to be direct contact with wild birds due to free range breeding.

The most likely source of virus introduction in the establishments was considered to be indirect contact with wild birds in 46 cases, indirect contact with poultry in eight cases, direct contact with wild birds in two cases and direct contact with poultry in one case.

In total, 796 people were exposed to the virus during culling and destructions operations in Poland. The characteristics of the affected establishments and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Portugal

Between 24 December 2021 and 3 March 2022, eight A(H5N1) outbreak were notified in seven commercial establishments and one backyard farm in four regions of Portugal, namely Lisbon (one primary and four secondary), Leiria, Beja, and Santarem.

Outbreaks in commercial establishments were detected in two fattening establishments of turkeys, one fattening establishment with both turkeys and chickens, two breeding establishments of chickens, and two breeding establishment of ducks. Mortality and clinical signs were detected in all the outbreaks, while no other type of signs was detected. For secondary outbreaks, the source of introduction was considered to be indirect contact with infected poultry in three cases and was directly identified to be related to movement of vehicles and personnel with another infected farm in one case. For the other three primary outbreaks in commercial farms, it remains unknown at the time of publication of this report.

The backyard farm had outdoor access and was farming mixed species of poultry. The most likely source of introduction was suspected to be contact with wild birds. At the time of the occurrence of the outbreak, a housing order was in place in the country.

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

HPAI A(H5N1)-affected poultry establishments in Romania

On 14 February 2022, one HPAI A(H5N1) outbreak was notified in a backyard farm keeping birds of multiple species (49 chickens, 14 geese and two guinea fowls) in the region of Ialomita. Forty-seven chickens and the two guinea fowls died. Clinical signs have been observed in both chickens and guinea fowls, while no mortality nor clinical signs have been observed for geese. The most likely reason for the outbreak remains unknown. One person was exposed to HPAI virus during the outbreak. The characteristics of the affected establishment and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Slovakia

On 29 and 30 December 2021, two HPAI A(H5N1) outbreaks were notified in backyard farms in the regions of Zilinský and Trnavský, which kept, respectively, 13 and 20 laying hens. Mortality was observed in both the farms, but no clinical or other types of signs were registered. The source of virus introduction remains unknown, and it is possibly due to indirect or direct contact with wild birds, as both the farms had outdoor access. No housing order was in place at the time at which the outbreaks were suspected.

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

HPAI A(H5N1)-affected poultry establishments in Slovenia

On 28 December 2021, one HPAI A(H5N1) outbreak was notified in a backyard farm with outdoor access keeping birds of multiple species (65 chickens, 30 ducks and 11 geese) in the region of Podravska. Mortality and clinical signs were observed only in chickens. The outbreak was identified in the context of outbreak-related surveillance. No housing order was in place at the time at which the outbreak was suspected. The source of introduction remains unknown at the time of publication of this report, and no data were available on the number of exposed people. The characteristics of the affected establishment and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Spain

Between 18 January and 2 March 2022, 21 primary and two secondary HPAI A(H5N1) outbreaks were notified in commercial farms in Andalusia (20) and Castile and León (3) regions.

Affected farms kept turkeys for fattening (14/23), and chickens for breeding, fattening or the production of eggs (9/23). In all the farms, signs and mortality were observed. None of the farms had outdoor access. The source of introduction remains unknown for all the primary outbreaks, and it was related to direct and indirect contact with infected poultry for the two secondary ones. In total, 297 people were considered to be exposed as a result of these cases. The characteristics of the affected establishment and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Sweden

Between 14 and 28 December 2021, three HPAI A(H5N1) outbreaks were notified in commercial farms with no outdoor access in the Skåne region. Two farms kept approximately 6,000 and 16,000 turkeys for fattening, and one 20,000 chickens for breeding. Mortality and clinical signs were observed in all the farms. Indirect infection via wild birds was considered to be the most likely source of viral introduction, as the area is characterised by the presence of large populations of wild geese, with HPAI detected in wild birds. In total, 20 people were considered to be exposed as a result of these cases. The characteristics of the affected establishment and species reared are presented in Annex A.

HPAI A(*H5N1*)*-affected poultry establishments in Northern Ireland* (*UK*)

Between 10 December 2021 and 10 February 2022 six HPAI A(H5N1) outbreaks were notified in four commercial farms and two backyard farms in Northern Ireland.

The four commercial farms kept, respectively, 13,400 laying hens, 27,520 chickens for breeding, 22,100 ducks for breeding and 22,540 ducks for fattening. Increased mortality was observed in chickens, but not in ducks. Signs (clinical signs and a drop in food water intake and/or in egg production) were observed in both laying hens and domestic ducks. Only one of the four commercial establishments had outdoor access prior to the implementation of the housing order (29/11/2021) and within 21 days of the first clinical signs. Considering the vicinity with wild birds' habitats, the most likely source of introduction was considered to be indirect contact with wild birds for three out of four affected farms. Investigations are still ongoing in the remaining farm.

The two backyard farms kept approximately 30 birds each of mixed species and production type (domestic ducks, chickens, domestic geese and guinea fowls). Both farms had outdoor access and the most likely source of virus introduction was considered to be direct contact with wild birds. In one case, it was observed on the site that wild birds were in direct contact with domestic birds. In the other case, the flock was free ranging, having access to local streams where wild birds had occasionally been observed.

A housing order was in place in all Northern Ireland during this reporting period.

In total, 105 people exposure events resulted from these cases, consisting in approximately 30 different people exposed in total, as the same teams were involved in more outbreaks. The characteristics of the affected establishment and species reared are presented in Annex A.

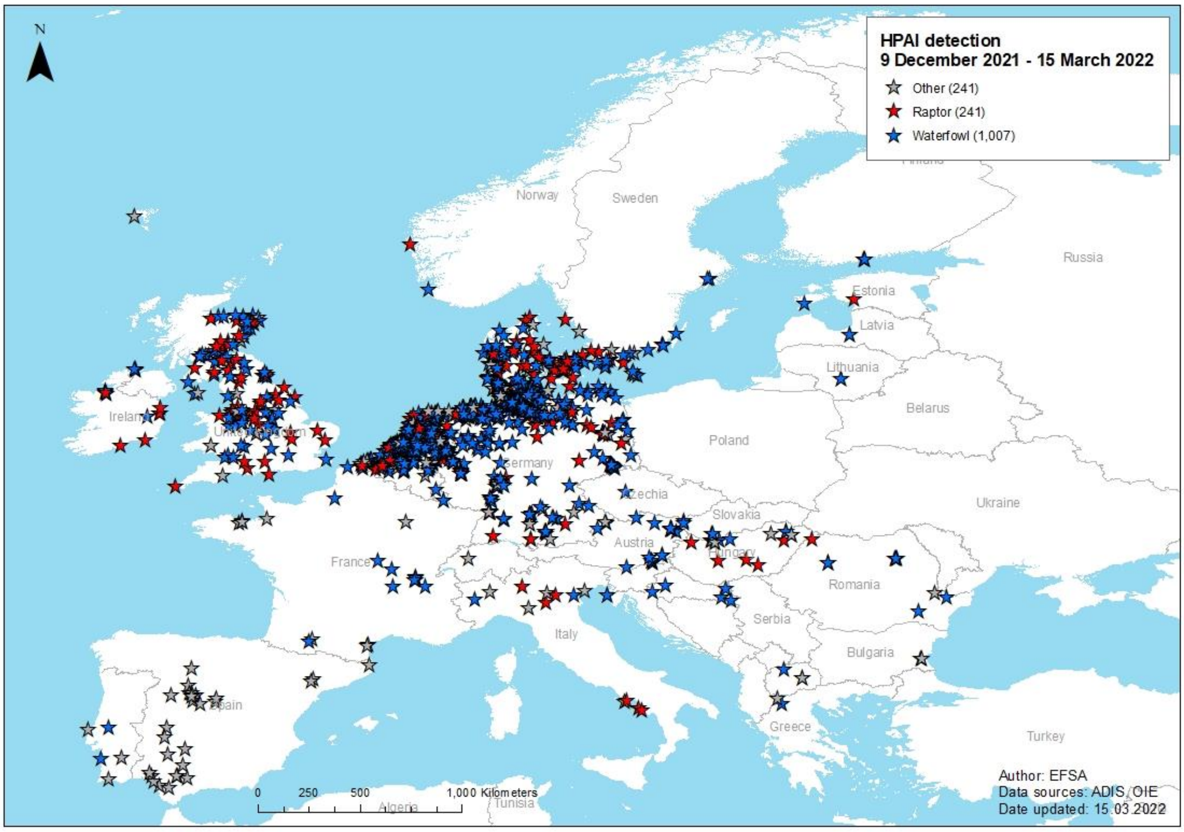
Information extracted from the scientific literature

Elbers and Gonzales (2021) compared data on daily mortality, egg production, feed intake and water intake from broiler and breeder duck flocks not infected (n = 56 and n = 11, respectively) and infected with HPAI A(H5) virus (n = 13, n = 4) between 2007 and 2020 in Europe and the USA to identify threshold values for early detection of HPAI outbreaks. For broiler flocks, daily mortality > 0.3% (after the first week of production) was a sensitive and specific indicator of HPAI virus infection. Drops in mean daily feed or water intake larger than 7 g or 14 ml per duck (after the first week of production), respectively, were sensitive indicators of infection but had poor specificity. For breeders, a consecutive drop in egg production larger than 9% was an effective indicator of a HPAI outbreak. The identified reporting thresholds can be used to update legislation and provide guidelines to farmers and veterinarians to notify suspicions of HPAI outbreaks in commercial duck flocks.

4.2.1.2. HPAI in wild birds

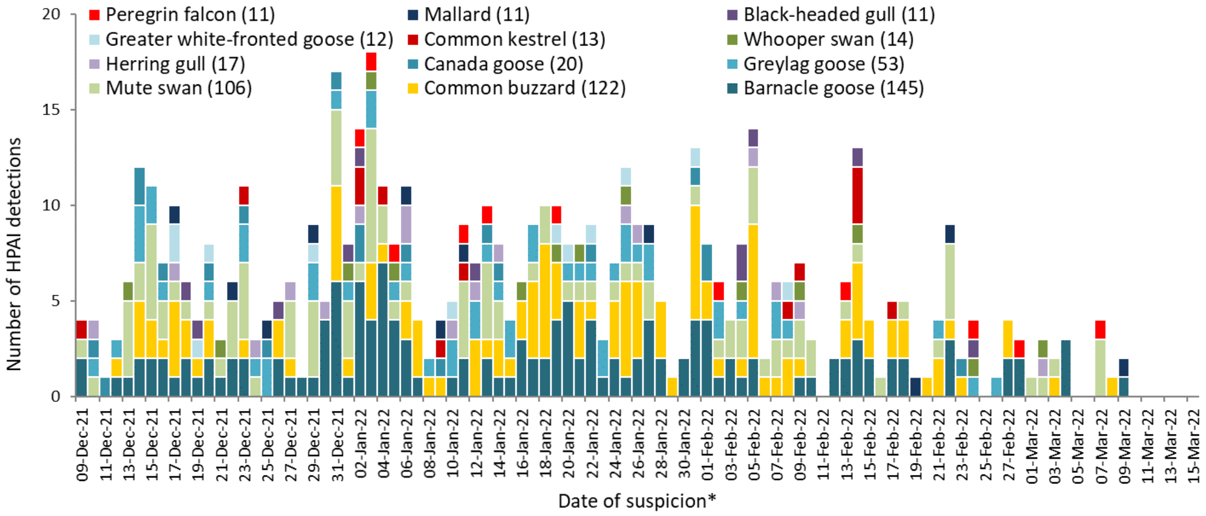
Between 9 December 2021 and 15 March 2022, 1,489 HPAI virus detections in sick, dead or hunted wild birds were reported to the ADIS and OIE by EU/EEA and the UK (Figure 12). The overall geographical pattern shows a concentration of reported cases in a band from the Baltic Sea coasts of southern Sweden, Germany and Denmark in the east, to the north and Wattenmeer coasts of Denmark, Germany and the Netherlands in the west. The overall temporal pattern shows an increase from the beginning of December to a peak in the middle of January, and then a gradual decline in reported cases to the middle of March (Figures 4 and 5). At least 62 wild bird species were involved: at least 17 waterfowl species (1,007 detections), 12 raptor species (241 detections), and 33 other wild bird species (241 detections) (Table C.1). In the same period of the previous year (9 December 2020 to 15 March 2021), at least 56 wild bird species were involved: at least 22 waterfowl species (833 detections), 9 raptor species (135 detections), and 25 other wild bird species (142 detections) were involved (Table C.2). This suggests that in the current reporting period HPAI A(H5) virus was infecting and causing mortality in a wider range of wild bird species than observed in the same period of the previous year. The host range may be even wider than these data suggest, as a larger proportion of wild birds was not identified to species in the current reporting period (829 of 1,489 detections: 56%) compared with the same period last year (285 of 1,110 detections: 26%). The complete list of HPAI detection by wild bird species for the time periods from 9 December 2021 to 15 March 2022 and from 9 December 2020 to 15 March 2021 is reported in Annex C (Tables C.1 and C.2). Of the wild bird species reported, those involved in 10 or more detections were barnacle goose (145), Common buzzard (122), mute swan (*Cygnus olor*, 106), greylag goose (*Anser anser*, 53) Canada goose (*Branta Canadiensis*, 20), herring gull (*Larus argentatus*, 17), whooper swan (*Cygnus cygnus*, 14), common kestrel (*Falco tinninculus*, 13), greater white-fronted goose (*Anser albifrons*, 12), mallard (*Anas platyrhynchos*, 11) (Figure 13). Also, 613 HPAI detections were reported as unspecified Anatidae, 65 as Laridae, 55 as Accipitridae, and 15 as Ardeidae. New species in which HPAI was detected were grey-headed gull (*Chroicocephalus cirrocephalus*, 3), little owl (*Athene noctua*, 1), Anambra waxbill (*Estrilda poliopareia*, 1), pink-backed pelican (*Pelecanus rufescens*, 1), western gull (*Larus occidentalis*, 1), and western sandpiper (*Calidris mauri*, 1). The number of HPAI virus detections was 1.2 times higher than in the same period last year (9 December 2020 to 15 March 2021), when there were 1,110 detections. This difference is mainly due to the higher number of HPAI detections in waterfowl (1,007 compared with 833) and raptors (241 detections including 122 common buzzards, compared with 135 detections including 59 common buzzards).

The numbers provided are not representative for the number of wild birds that died from HPAI A(H5) infection. For example, HPAI was considered the cause of mortality of over 4,000 barnacle goose carcasses counted in the Solway Firth, on the west coast of Scotland, where most barnacle geese breeding on Svalbard spend the winter. The latest population counts of the Svalbard barnacle goose showed a drop in numbers from 43,703 in November last year to 27,133 in this month's counts. This represents a decline of 38% in the Svalbard breeding population of this species from winter 2020-2021 (RSPB, online). Despite these high numbers, there were only 45 HPAI detections in barnacle geese in the UK recorded between October 2021 and 7 March 2022 (DEFRA & APHA, online).



Source: EFSA, ADIS and OIE (data extraction carried on 15 March 2021).

Figure 12: Geographical distribution, based on available geocoordinates, of highly pathogenic avian influenza detections in wild birds in Europe, by species category, 9 December 2021 to 15 March 2022 (1,489)



* When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.
Source: EFSA, ADIS and OIE (data extraction carried on 15 March 2022).
Note that in one single reported detection of HPAI in wild birds more than one bird might be involved

Figure 13: Number of reported detections of highly pathogenic avian influenza virus A(H5) in wild birds of the most affected wild bird species (i.e. those involved in 10 or more detections) in the EU/EEA and the UK, by date of suspicion, from 9 December 2021 to 15 March 2022

Information extracted from the scientific literature

Gobbo et al. (2021) performed virological and serological analyses for avian influenza in 823 hunted and 521 trapped dabbling ducks in northeast Italy in winter 2020-2021. The highest prevalence of infection with the HPAI A(H5) clade 2.3.4.4b in hunted ducks, mainly in Eurasian wigeons (*Mareca penelope*), was found in January 2021 (10.2%). High prevalence of infection with the HPAI A(H5) clade 2.3.4.4b (up to 27.1%) was observed during November–December 2020 in captured Eurasian teals (*Anas crecca*). All HPAI-positive teals were also clinically healthy when recaptured weeks apart. Surprisingly, no mortality events were observed in the HPAI-positive animals or in other species cohabiting or interacting with them (e.g. other waterfowl species, birds of prey, scavengers). These findings confirm subclinical natural infection with HPAI H5Nx GsGd viruses 2.3.4.4b in Eurasian teals and Eurasian wigeons, indicating that these species can act as long-distance vectors of these viruses, and that passive surveillance alone has a poor ability to identify the true level of HPAI virus infection in wild birds.

Caliendo et al., (2022a; 2022b) determined the virus distribution and associated pathological changes in five Eurasian wigeons, nine barnacle geese (*Branta leucopsis*) and 11 common buzzards (*Buteo buteo*) that died with HPAI H5N8 virus clade 2.3.4.4b infection during the 2020 HPAI season in the Netherlands. All animals were systemically infected and had encephalitis as well as necrosis in other organs including liver, pancreas and heart muscle. These studies show that this HPAIV infection can cause severe systemic disease resulting in acute death, with encephalitis as a common lesion. Banyard et al. (2022) diagnosed H5N1 HPAI virus clade 2.3.4.4b as cause of death in great skuas (*Stercorarius skua*) on offshore islands of the UK in summer 2021. Clinical signs suggested neurological disease and included head tilt, inability to fly, incoordination, and twitching of head and wings. Histopathological changes in nine birds included meningoencephalitis and necrosis of heart muscle, adrenal gland, and pancreas colocalising with virus antigen expression. The authors concluded that the HPAI outbreak may have resulted in very low breeding activity in that year and may impact future generations of great skuas.

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 evolved into several subgroups. While a revised nomenclature of clade 2.3.4.4 viruses is pending, in previous reports we used the genetic clustering described in 2018 by Lee and co-authors, who recognised four groups (a–d) within clade 2.3.4.4 (Lee et al., 2018). Recently, an update to the unified nomenclature for clade 2.3.4.4 A(H5) viruses has been proposed by WHO (WHO, 2020d) 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 (2.3.4.4b).

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

The topology of the HA phylogenetic tree shows that all the genetically characterised HPAI viruses collected since the beginning of the current epidemic wave (October 2021 to March 2022) in Europe and Russia fall within clade 2.3.4.4b. Sequences were generated from viruses collected from 19 EU Member States, the UK, Norway, Moldova and Russia (available in GISAID on 3 March 2022, provided by the National Reference Laboratories (NRL) or generated by EURL). To assess the number and variety of co-circulating genotypes, each defined by a unique gene composition, the eight gene segments were phylogenetically analysed.

The results indicate a persistent circulation in Northern Europe of the A(H5N1) and A(H5N8) strains detected during the October 2020 to October 2021 epidemic wave, with the great majority of the viruses belonging to the A(H5N1) subtype. However, the vast majority of the sequenced viruses (approximately 96%) seems likely to be the results of novel virus incursions during the fall migration of wild birds. At least 20 new different A(H5) genotypes originating from multiple inter- and intra-subtype reassortment events were detected: 19 A(H5N1) and one A(H5N2). Except for some of these genotypes identified in September–October 2021 in East and Central Russia, most of them had never been detected in Europe or in other geographic regions before, and this may suggest local reassortment events.

Italy and France are the two countries that have been reporting the highest number of A(H5N1) outbreaks in poultry since October 2021. Based on the analysis of available sequences from a selected number of A(H5N1) viruses detected since November 2021, at least eight distinct genotypes have been circulating in France: all but one single genotype were detected in wild birds and only four genotypes were characterised from poultry outbreaks. Up to mid-February 2022, a single genotype apparently accounted for most virus detections dispersed over the country, in poultry, captive birds, including backyards, and free-living wild birds, and was responsible of most poultry outbreaks detected in southwestern France. Closer investigation suggests that at least five independent virus introductions into the poultry production sector may have occurred in this last area.

Similarly, the investigation on the A(H5N1) viruses, which caused multiple outbreaks in poultry in northern Italy, indicates the occurrence of at least seven distinct virus introductions into the domestic population, with several outbreaks caused by viruses showing a high genetic relationship.

Complete genome sequences of HPAI avian influenza A(H5N1) viruses collected from a human case confirmed in England in January 2022 (Oliver et al., 2022), from three red foxes identified in the Netherlands and Ireland between December 2021 and February 2022 and from a ferret detected in Slovenia in January 2022 were obtained. These viruses show a high genetic identity with the viruses currently circulating in wild and domestic birds in Europe and, in particular, the virus from the human case showed a high genetic identity with the A(H5N1) identified in the domestic ducks reared by the infected individual (Oliver et al., 2022). No mutation associated with adaptation to mammals was observed in the strain detected in human. Conversely, some of the A(H5N1) viruses from red foxes possessed a mammalian adaptive marker (e.g. PB2 E627K), associated with an increased virulence and replication in mammals (Manzoor et al., 2009; Kim et al., 2010; Herfst et al., 2012; Suttie et al., 2019). As in previously identified transmission events and with the aim of supporting public health risk assessment, it is important to better understand the impact of viral mutations associated with mammalian adaptation that can rapidly emerge after transmission to mammals.

To date, mutations recognised as being associated with mammalian adaptation have only been sporadically identified in the analysed viruses from avian species collected since October 2020, as previously reported (EFSA et al., 2021b). In the currently circulating A(H5N1) viruses, mutations in the HA protein associated with increased binding to human-type receptors were identified in all the analysed viruses (S137A H3 numbering) or in few (one or two) of them (D101N, S159N/T160A and T192I, H3 numbering) (Yang et al., 2007; Su et al., 2008; Wang et al., 2010). Moreover, mutations associated to increased polymerase activity in mammalian cells (NP-N319K and PB2-K482R) have been detected in some (4/5) H5N1 viruses identified in wild birds in Italy and Sweden (Gabriel et al., 2005; Gabriel et al., 2008; Yamayoshi et al., 2014; Yamayoshi et al., 2018).

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

Since 2 December 2021 as of 4 March 2022, data from six countries have been collected and reported on the total number of people exposed to infected birds (e.g. during culling activities). They reported, in total, 1,451 exposed people.

In December 2021, a human infection with a A(H5N1) virus of clade 2.3.4.4b was identified in the UK following seven A(H5N8) cases reported from Russia in 2020 and three A(H5) in Nigeria (Pyankova et al., 2021; WHO, 2021a). ECDC published a Threat Assessment Brief in February 2021 that assessed the risk as very low for the general public and low for occupationally exposed people (ECDC, 2021a)and revised the risk to low for the general population and low to medium for occupationally exposed people in December due to the increase in transmission events to mammal species including sporadic human cases with no or mild symptoms. The high diversity and ongoing reassortment events add a high uncertainty to the assessment and transmission events to humans cannot be excluded.

No human infection with avian influenza viruses, as currently detected in wild birds and poultry in Europe, has been identified in the EU/EEA countries during the period covered by this report or has been previously reported (EFSA et al., 2021b). Other transmission events to different mammal species have been increasingly reported as mentioned above and in previous reports (Table 3). So far foxes have been majorly found to be infected with avian influenza viruses of clade 2.3.4.4b and displaying neurological sign leading to death or have already found dead.

The United States Centers for Disease Control and Prevention (US CDC) issued previously a risk assessment using the Influenza Risk Assessment Tool (IRAT) and placed the risk of clade 2.3.4.4b viruses in the low to moderate category (CDC, online-b, c). The risk of the A(H5N1) clade 2.3.4.4 viruses currently circulating in the US bird and poultry populations, which are closely related to European viruses, were assessed by the US CDC to be of low risk for human health in the general population and higher for people occupationally or recreationally exposed to birds (CDC, online-a).

The World Health Organization (WHO) assessed the risk associated with A(h5N6) virus as low (WHO, online-a). The WHO issued a risk assessment on the increase in human cases due to A(H5N6) virus infections in 2021 and recommend to remain vigilant about zoonotic infections and share unsubtypable influenza A viruses from human infections with the WHO Collaborating Centres (WHO, 2021b). Also, a recent publication aimed to raise awareness among clinicians in the EU on zoonotic avian influenza virus infections (Adlhoch et al., 2021).

Table 3: Avian influenza A(H5Nx) virus detections in other mammal species related to circulating viruses in Europe, 2016–2021

Date	Country	Animal (species)	Virus	Reference
November 2016, April 2017	Poland	2 grey seals (*Halichoerus grypus*)	A(H5N8) clade 2.3.4.4b	Shin et al., 2020
December 2016 to May 2017	France	Domestic pigs (*Sus scrofa*), serological detection	A(H5N8) clade 2.3.4.4b	Herve et al., 2021
2017; August 2021	Germany	Wild boar serological detection; three harbour seals (*Phoca vitulina*)	A(H5N8); A(H5N8) clade 2.3.4.4b	Schülein et al., 2021; Ärzteblatt, online
Late 2020	UK	4 juvenile common seals (*Phoca vitulina*), 1 juvenile grey seal (*Halichoerus grypus*), 1 juvenile red fox (*Vulpes vulpes*)	A(H5N8) clade 2.3.4.4b	Floyd et al., 2021
April, February, and September 2021	Sweden	1 grey seal (*Halichoerus grypus*), 2 red foxes (*Vulpes vulpes*)	A(H5N8) clade 2.3.4.4b, A(H5N1) clade	SVA, online; Personal communication by Siamak Zohari, SVA

			2.3.4.4b, A(H5N1)*	
September 2021	Denmark	1 harbour seal (*Phoca vitulina*)	A(H5N8) clade 2.3.4.4b	Outbreak News Today, online; Avian Flu Diary, online; SSI, online.
May 2021 **2022**	Netherlands	2 red fox cubs (*Vulpes vulpes*) Foxes, otter, polecat (*Mustela putorius*)	A(H5N1) clade 2.3.4.4b	Rijks et al., 2021; dwhc, online; Resource WUR, online; WUR, online
September and November 2021 February 2022	Finland	2 foxes (*Vulpes vulpes*), 1 otter (*Lutra lutra*) 1 lynx (*Lynx lynx*)	A(H5N1) clade 2.3.4.4b A(H5N1)*	FFA, online
November 2021	Estonia	Fox (*Vulpes vulpes*)	A(H5N1) clade 2.3.4.4b	OIE, online-a
November 2021	Italy	Domestic pigs (*Sus scrofa*) (serological detection in HPAI poultry outbreak)	A(H5N1) clade 2.3.4.4b	EURL
January 2022	Slovenia	Ferret (*Mustela furo*)	A(H5N1) clade 2.3.4.4b	Slovenian National Reference Laboratory for Avian Influenza, personal communication
February 2022	Ireland	Fox (*Vulpes vulpes*)	H5N1) clade 2.3.4.4b	Irish National Reference Laboratory for Avian Influenza, personal communication

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

4.4. Prevention and control measures applied in Europe, 2 December 2021 to 4 March 2022 (ToR 3)

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

4.5. The avian influenza situation in other countries not reporting via ADNS, 9 December 2021 to 15 March (ToR 4)

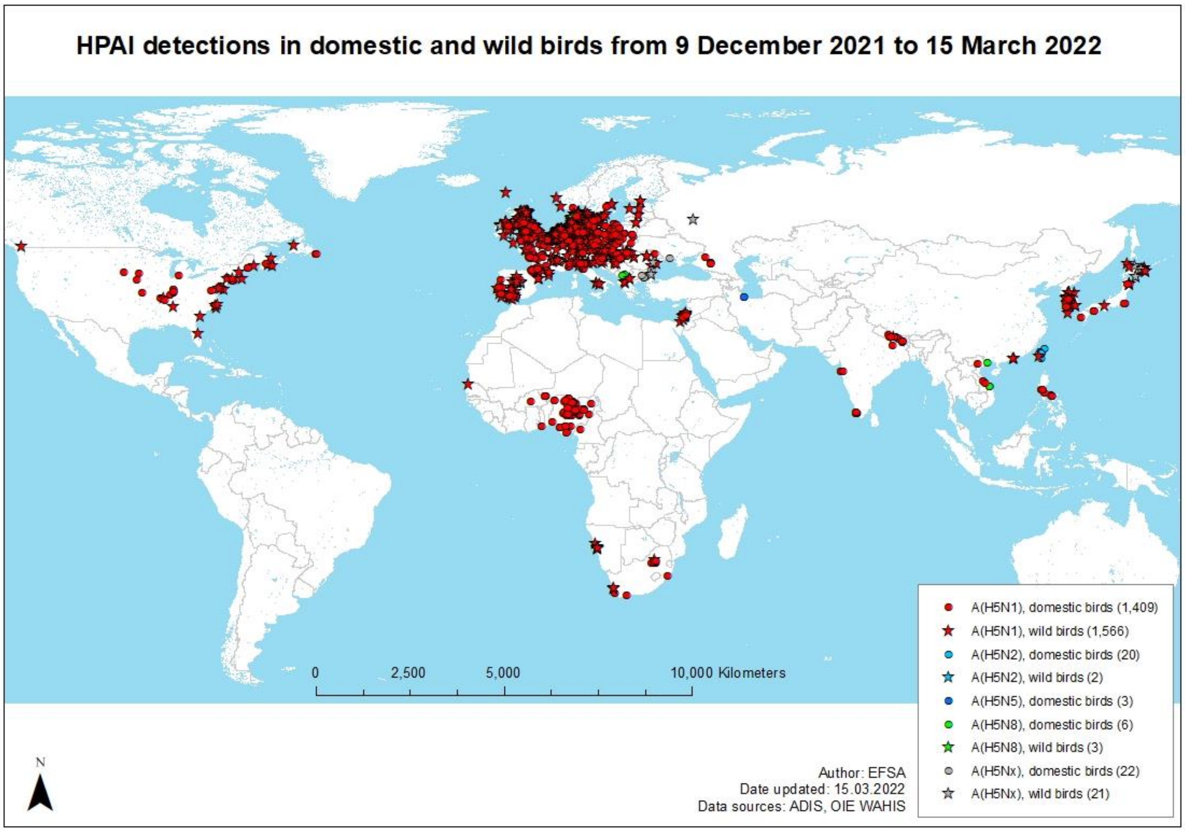
An overview of the HPAI detections notified from other countries not reporting via ADIS but via the OIE or national authorities from 9 December 2021 to 15 March is presented in Table 4 and Figure 14. For the purposes of this report, only findings of avian influenza viruses occurring in countries that are considered to be of epidemiological interest for the EU/EEA or of public health relevance are described.

Table 4: Number of HPAI detections in other countries not reporting via ADIS, by virus subtype and country, 9 December 2021 to 15 March 2022

Region	**Country**	**Domestic birds (297)**				**Wild birds (103)**			**Total**
		A(H5N1)	**A(H5N2)**	**A(H5N5)**	**A(H5N8)**	**A(H5N1)**	**A(H5N8)**	**A(H5Nx)**	
Africa (150)	Burkina Faso	1							1
	Cameroon	1							1
	Namibia					7			7
	Niger	3							3
	Nigeria	123							123
	Senegal					1			1
	South Africa	10				3			13

	Togo	1							1
Americas (47)	Canada	5				5			10
	USA	22				15			37
Asia (197)	Chinese Taipei		19	1		1			21
	Hong Kong					2			2
	India	10							10
	Iran			2					2
	Israel	13				14			27
	Japan	8				20		3	31
	Korea	36				29	1		66
	Nepal	17				1			18
	Philippines	12							12
	Vietnam	5			3				8
Europe (6)	Russia	5						1	6
Total		**272**	**19**	**3**	**3**	**98**	**1**	**4**	**400**

Source: ADIS and OIE WAHIS (data extraction carried out on 15 March 2022).


HPAI detections in domestic and wild birds from 9 December 2021 to 15 March 2022

Author: EFSA
Date updated: 15.03.2022
Data sources: ADIS, OIE WAHIS

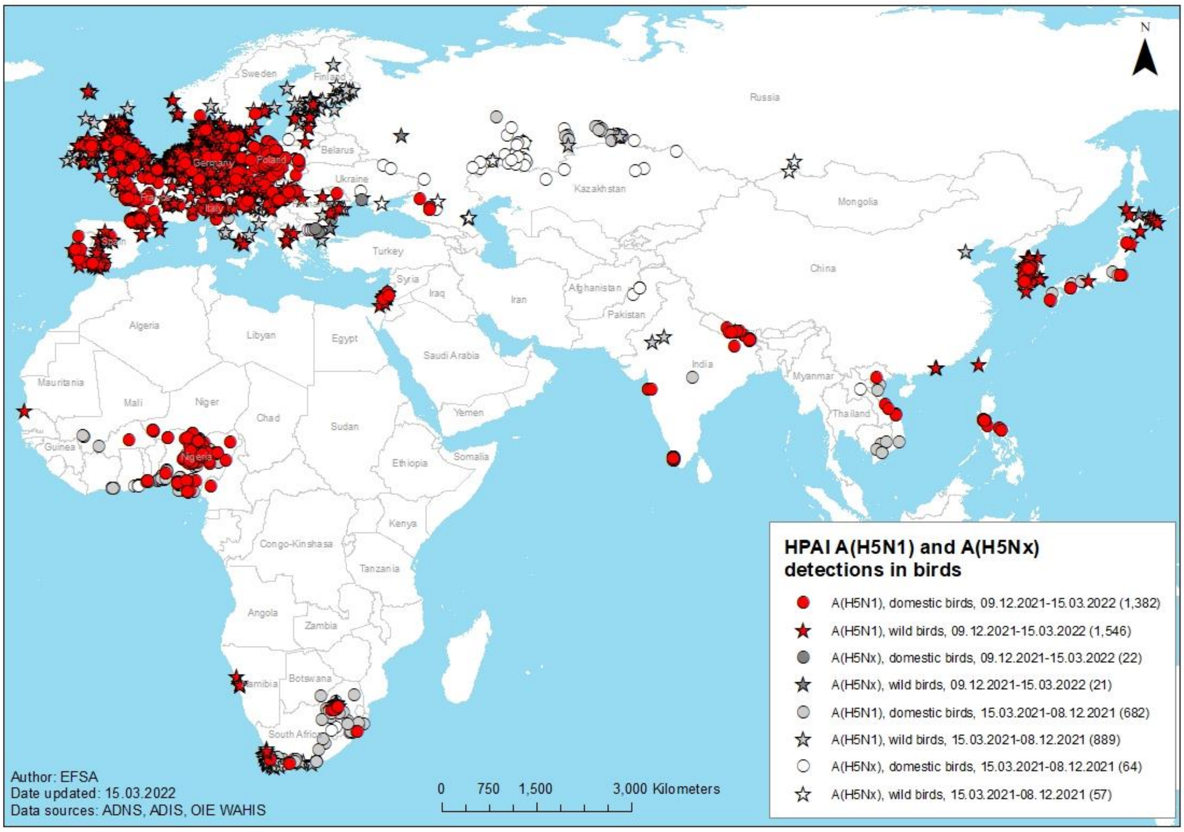
Figure 14: Geographical distribution, based on available geocoordinates, of HPAI detections reported in domestic birds (1,460) and wild birds (1,592) by virus type, 9 December 2021 to 15 March 2022

4.5.1. HPAI A(H5N1)

4.5.1.1. Domestic and wild birds

Detections

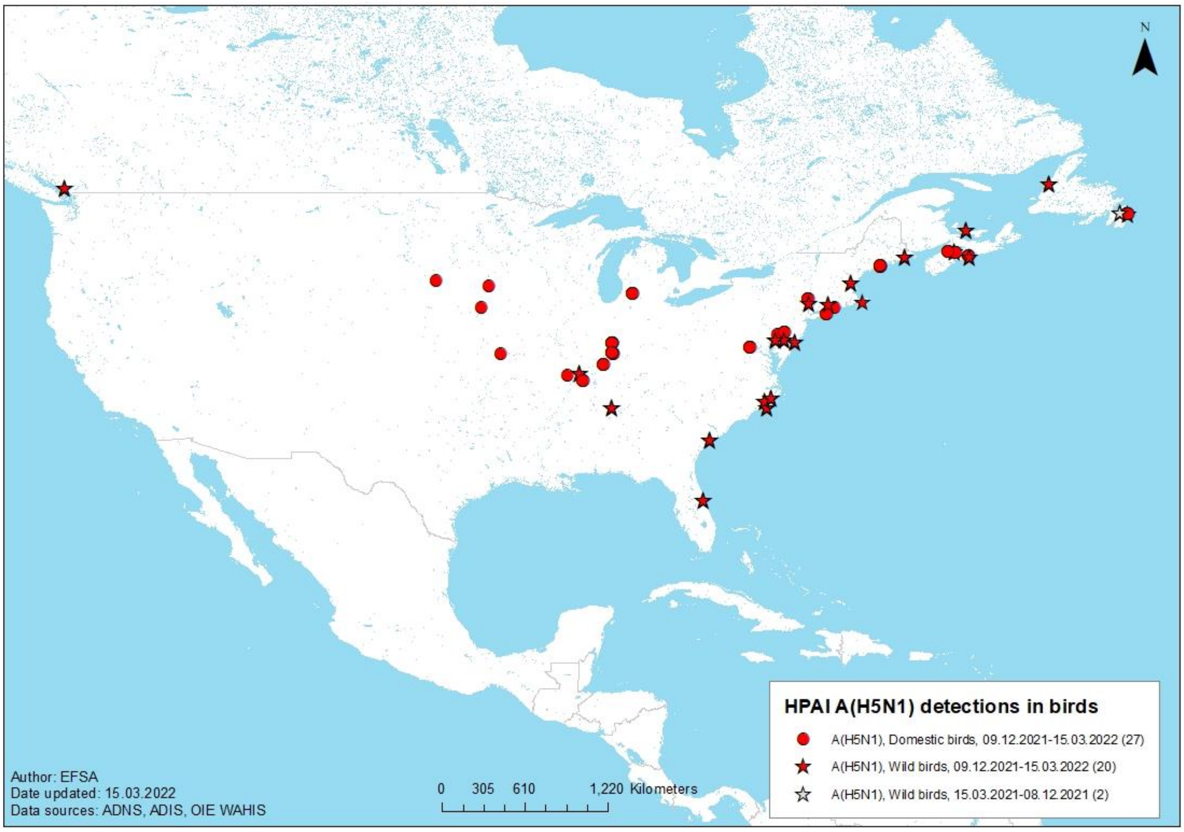
The main focus of the HPAI A(H5N1) epidemic in Africa continues to be Nigeria and South Africa, but five more countries (Burkina Faso, Cameroon, Namibia, Niger and Senegal) notified outbreaks in domestic poultry and wild birds to the OIE in the relevant time period of the report. Nigeria recorded a significant increase in detected outbreaks, mainly in commercial medium-sized and large farms. Namibia, Senegal and South Africa detected cases of HPAI A(H5N1) in several wild bird species as e.g., Cape cormorant (*Phalacrocorax capensis*), common tern (*Sterna hirundo*), great white pelican (*Pelecanus onocrotalus*), and white stork (*Ciconia ciconia*). The HPAI A(H5N1) epidemic continued in several countries in Asia, the Middle East and Russia, but compared to the last report, Chinese Taipei, Hongkong, Nepal, Philippines and Vietnam also recorded outbreaks between the 9 December 2021 and 15 March 2022. Asian countries, Israel and Russia detected HPAI A(H5) and HPAI A(H5N1) in several wild bird species as e.g., mallard (*Anas platyrhynchos*), Indian spot-billed duck (*Anas poecilorhyncha*), gadwall (*Mareca strepera*), greater white-fronted goose (*Anser albifrons*), bean goose (*Anser fabalis*), ruddy shelduck (*Tadorna ferruginea*), whooper swan (*Cygnus cygnus*), great egret (*Ardea alba*), little egret (*Egretta garzetta*), common crane (*Grus grus*), white-naped crane (*Antigone vipio*), black-faced spoonbill (*Platalea minor*), Eurasian curlew (*Numenius arquata*), great white pelican (*Pelecanus onocrotalus*), common buzzard (*Buteo buteo*), eastern buzzard buzzard (*Buteo japonicus*), common kestrel (*Falco tinnunculus*), white-tailed eagle (*Haliaeetus albicilla*), hooded crow (*Corvus cornix*), large-billed crow (*Corvus macrorhynchos*) and house crow (*Corvus splendens*) (Figure 15). However, outbreaks of HPAI A(H5N1) were not only reported from Africa, Asia, the Middle East and Russia, but also for the first time from Canada and the United States of America. HPAI A(H5N1) was detected in small to very large poultry establishments and several wild bird species as e.g. mallard (*Anas platyrhynchos*), American wigeon (*Mareca americana*), green-winged teal (*Anas carolinensis*), northern shoveler (*Spatula clypeata*), blue-winged teal (*Spatula discors*), American black duck (*Anas rubripes*), lesser scaup (*Aythya affinis*), redhead (*Aythya americana*), snow goose (*Anser caerulescens*), Canada goose (*Branta canadensis*), red-tailed hawk (*Buteo jamaicensis*), black vulture (*Coragyps atratus*), bald eagle (*Haliaeetus leucocephalus*) and American crow (*Corvus brachyrhynchos*) on the east coast and one bald eagle (*Haliaeetus leucocephalus*) on the west coast of America in Canada (Figure 16).



Author: EFSA
Date updated: 15.03.2022
Data sources: ADNS, ADIS, OIE WAHIS

Red and dark grey symbols indicate outbreaks that occurred between 9 December 2021 and 15 March 2022, grey and withe symbols indicate outbreaks that occurred between 15 March 2021 and 8 December 2021.

Figure 15: Geographical distribution, based on available geocoordinates, of HPAI A(H5N1) and AH(H5Nx) detections reported in domestic birds (circles) and wild birds (stars) (4,712)



Red symbols indicate outbreaks that occurred between 9 December 2021 and 15 March 2022, grey symbols indicate outbreaks that occurred between 15 March 2021 and 8 December 2021.

Figure 16: Geographical distribution, based on available geocoordinates, of HPAI A(H5N1) and AH(H5Nx) detections reported in domestic birds (circles) and wild birds (stars) (49)

Information extracted from the scientific literature

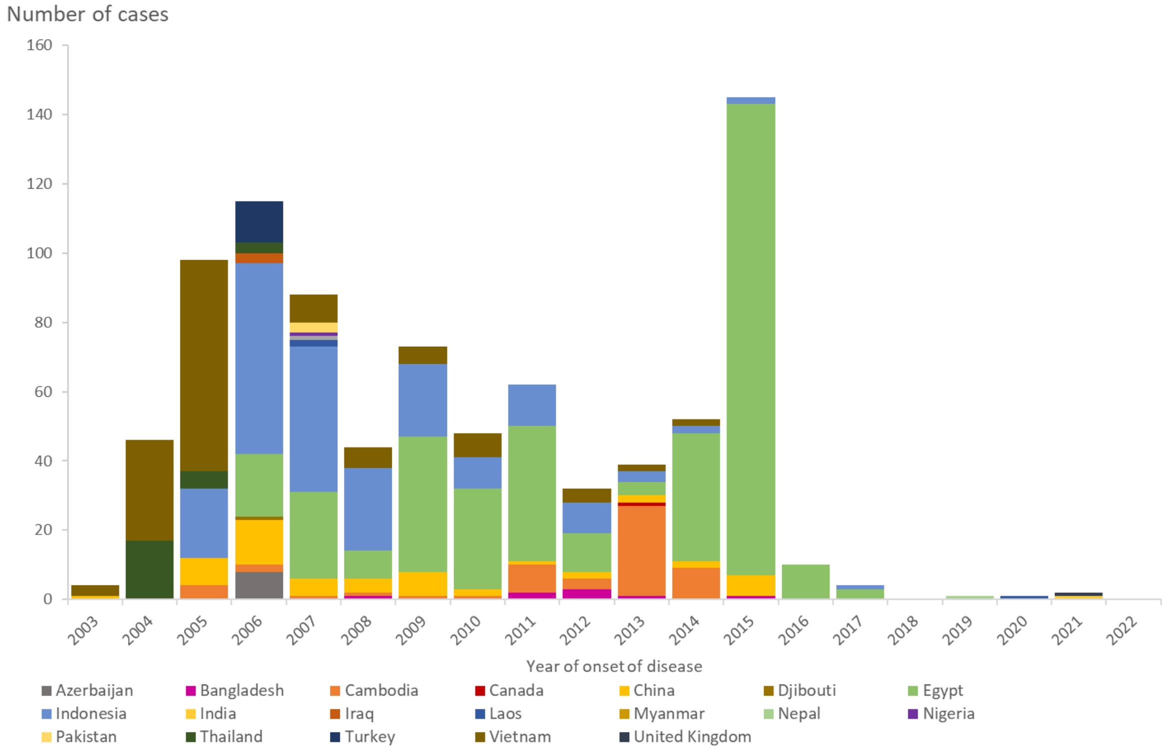
Two recent articles identified the close phylogenetic relationships between HPAI A(H5N1) viruses identified in western and southern Africa between December 2020 and May 2021, and pointed to a probable incursion of this virus from Europe to Africa in fall 2020.

Lo et al. (2022) generated full genome sequences of viruses detected from cloacal swabs collected during an outbreak in domestic laying hens (reported mortality rate of 58%) that occurred in late December 2020 and from an oropharyngeal swab collected in late January 2021 on a great white pelican (*Pelecanus onocrotalus*) found dead during a large-scale mortality event that affected this species in the Djoudj wetland region: both events had taken place in Senegal. All these sequences clustered together and were closely related for all their segments with clade 2.3.4.4b HPAI A(H5N1) viruses detected in the Netherlands, UK and Italy during October–December 2021. The mean time to the most recent common ancestor of the A(H5N1) viruses detected in Senegal was estimated to November 2021 and genetic spatial analysis indicated that the virus had spread from Europe to Senegal, probably through infected wild bird descending migration.

Makalo et al. (2022) reported the detection of the first two outbreaks of HPAI A(H5N1) in Lesotho. Full genome sequences were generated from oropharyngeal swab samples collected in two farms, from layer chickens recently bought from a common supplier in South Africa. High mortality was observed in each farm (10 % and 5%, respectively) and observed clinical signs included diarrhea, cephalic edema, wattle and comb cyanosis and paralysis. Both sequences were highly related to each other, to the clade 2.3.4.4b HPAI A(H5N1) described above in Senegal and to A(H5N1) viruses identified in chickens in Nigeria in 2021. Except a single substitution in the PB1 protein, associated with increased polymerase activity in mice and mammalian cells, there was no mention of other determinants of shift to human-like receptor affinity or of increased virulence and transmission in poultry or mammals. Whereas a 22 amino-acid deletion in the N1 stalk was present in some of the viruses detected in Nigeria, both viruses characterized in Lesotho had a full-length N1 sequence.

4.5.1.2. Human infections due to A(H5N1)

Since the publication of the previous report, one human case due to avian influenza A(H5N1) was reported in January 2022 with zoonotic transmission happening in December 2021 in the UK. The identified asymptomatic person had very close contact with a large number of A(H5N1) infected domestically kept birds, which occurred in mid-December 2021. All birds were subsequently culled. No onward transmission to other people was detected through contact tracing. Since 2003, and as of 15 March 2022, 864 laboratory-confirmed cases of human infection with avian influenza A(H5N1) virus, including 456 deaths, have been reported from 19 countries outside the EU/EEA, no human infection has been reported from an EU/EEA country so far (WHO, 2022a; GovUK, online; WHO, online-c) (Figure 17).



Source: WHO and ECDC line list (WHO, 2021e, d, 2022a, online-b).

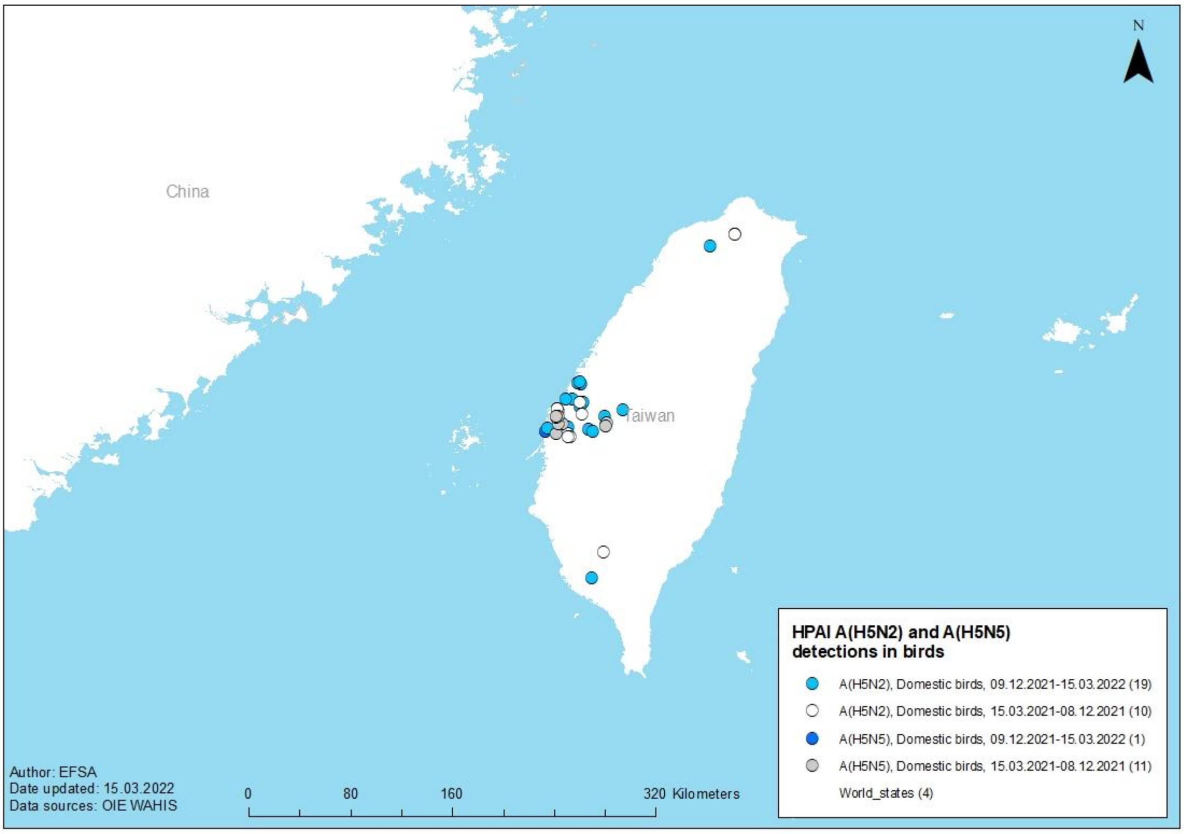
Figure 17: Distribution of confirmed human cases of A(H5N1) by year and country of reporting, 2003 to 15 March 2022 (864)

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

4.5.2.1. Domestic and wild birds

Detections

In contrast with the previous reporting period, Taiwan notified only one new outbreak of the Taiwanese lineage HPAI A(H5N5) in a medium sized poultry farm to the OIE. The outbreak of the Taiwanese lineage HPAI A(H5N2) continued and 19 outbreaks in poultry establishments were detected between 9 December 2021 and 15 March 2022. Furthermore, Iran reported two outbreaks of the Eurasian lineage HPAI A(H5N5) in a medium sized poultry and one backyard farm to the OIE. The Taiwanese lineages of HPAI A(H5N2) and HPAI A(H5N5) (clade 2.3.4.4) differed from the Eurasian HPAI A(H5N2) and A(H5N5) lineages (Li et al., 2020); the latter belonging to clade 2.3.4.4b, which has been detected, with different genotypes, in Egypt and Russia as well as in Asian countries between 2016 and 2019 (EFSA et al., 2019) and in Bulgaria in 2020. No wild bird cases were reported in the relevant time period of the report (Figure 18).



White and grey symbols indicate HPAI A(H5N2) and A(H5N5) detections between 15 March and 8 December 2021, respectively, light and dark blue symbols indicate HPAI A(H5N2) and A(H5N5) detections between 9 December 2021 and 15 March 2022 .

Figure 18: Geographical distribution, based on available geocoordinates, of HPAI A(H5N2) and AH(H5N5) detections reported in domestic birds (circles) in Taiwan (41)

Information extracted from the scientific literature

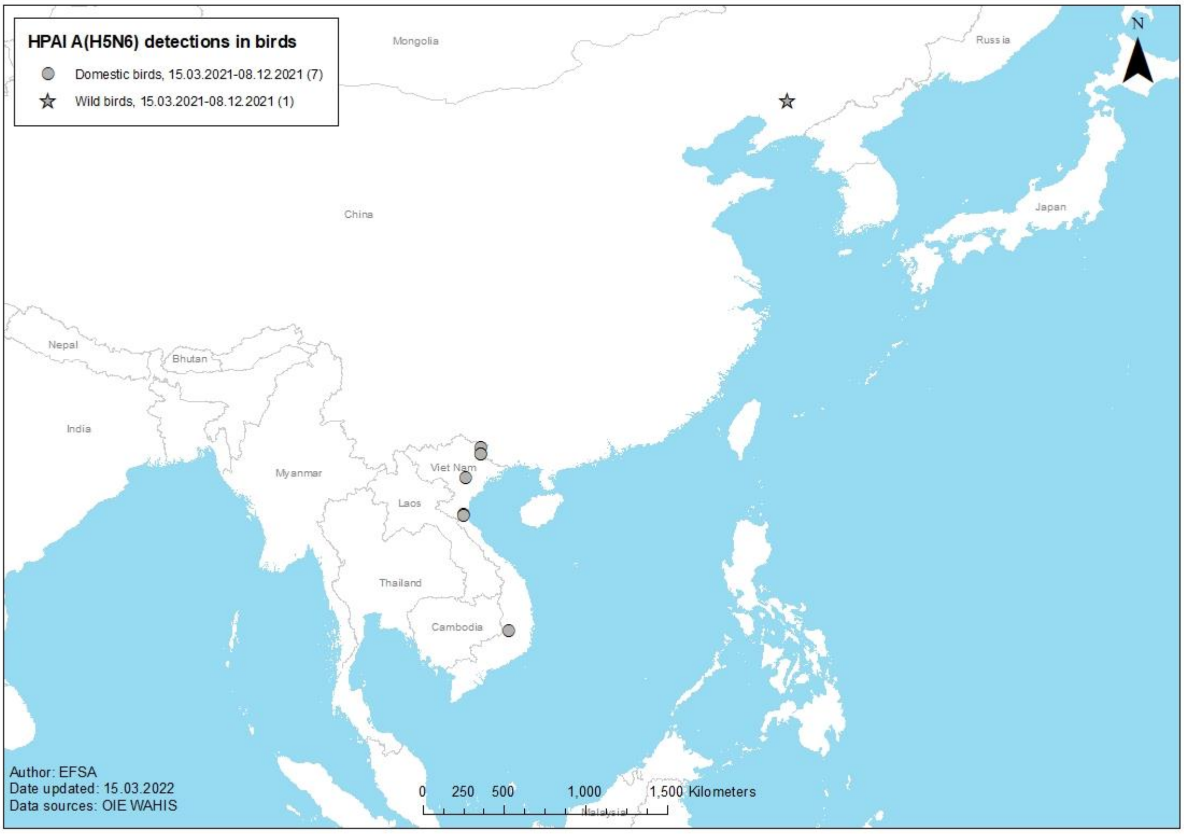
Li et al. (2022) described a reassortant HPAI A(H5N2) virus, isolated in November 2020 from samples collected during an intensified environment and passive wild bird surveillance program in central China, Shanxi Province, on a whooper swan (*Cygnus cygnus*). This virus clustered for its HA and NS gene segments with clade 2.3.4.4b A(H5N8) viruses that were detected in Central Europe, early 2020. The remaining six gene segments shared a high nucleotide identity with a LPAI A(H9N2) virus also isolated from the same species at the same sampling date and location: for these segments, both viruses shared a common ancestor derived from a poultry LPAI gene pool. Although major determinants of human type receptor affinity of the HA protein and of mammalian adaptation in the PB2 protein were not observed for this virus, the presence of several substitutions in the HA, PB1, PA, NP, M1 and NS1 proteins suggested that this virus may be able to bind to human-type receptors and may have acquired increased polymerase activity and enhanced virulence in mice (this latter property associated with the M1 and NS1 mutations).

4.5.3. HPAI A(H5N6)

4.5.3.1. Domestic and wild birds

Detections

As in the last report, no outbreaks of the zoonotic reassortment of HPAI A(H5N6) clade 2.3.4.4c were notified to the OIE between 9 December 2021 and 15 March 2022. New human cases of A(H5N6) from China in the current reporting period (section 4.5.3.2) might suggest underreporting of poultry outbreaks in the Asian region (Figure 19).



Grey symbols indicate outbreaks that occurred between 15 March and 8 December 2021.

Figure 19: Geographical distribution, based on available geocoordinates, of HPAI A(H5N6) detections reported in domestic birds (55)

Information extracted from the scientific literature

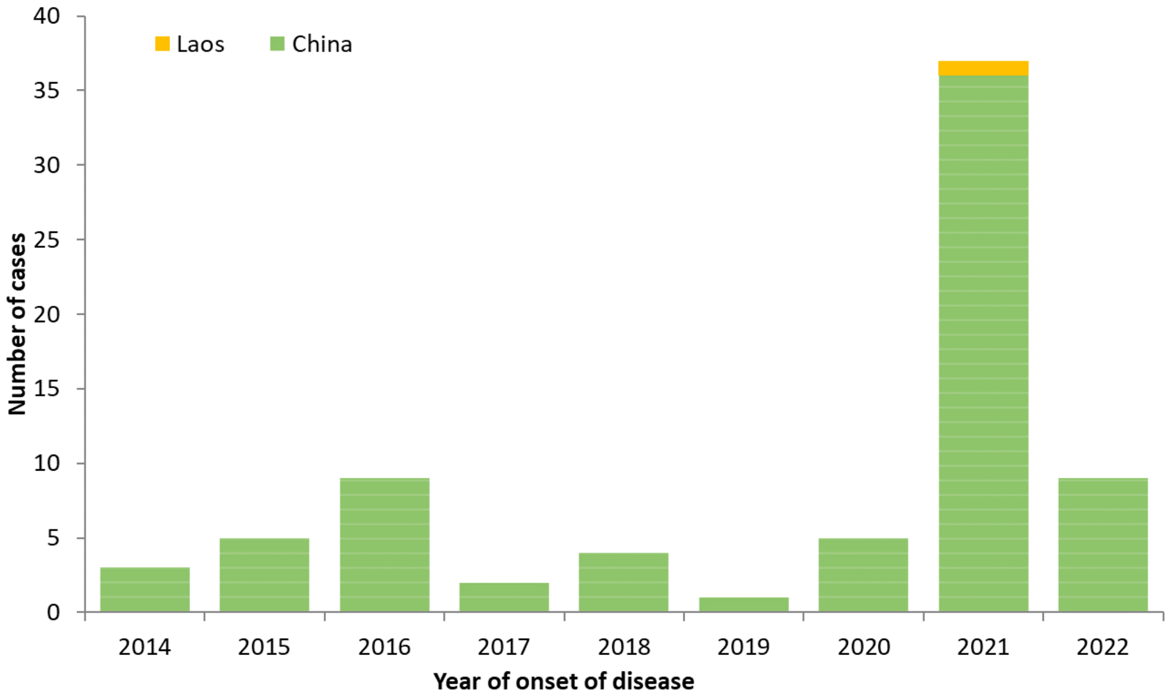
During the reporting period, no new relevant information was published on the phenotypic and genetic characterisation of HPAI A(H5N6) viruses circulating in countries outside the EU/EEA, for domestic and wild birds.

4.5.3.2. Human infections due to A(H5N6)

Seventeen new human cases due to avian influenza A(H5N6) have been notified since the last EFSA report, all from China (CHP, 2022b, a, g, f, e; WHO, 2022a).

The genome of a single additional H5N6 virus was submitted to GISAID The HA gene sequence belongs to clade 2.3.4.4b. Overall, 42 H5N6 viruses of clade 2.3.4.4 collected from humans in China between 2014 and 2021 were deposited in GISAID, 9 of these viruses fall within clade 2.3.4.4b, 1 collected in 2017 and 8 collected in 2021. Among the viruses collected in 2021 (N=10), 8 belong to clade 2.3.4.4b and 2 belong to clade 2.3.4.4h.

Since 2014, and as of 24 March 2022, 75 laboratory-confirmed cases of human infection with avian influenza A(H5N6) viruses of clade 2.3.4.4 circulating in South-East Asia have been reported in China (74 cases) and Laos (1) with 32 of them being fatal (CHP, 2022d; The Government of the Hong Kong Special Administrative Region Press Releases, 2022; WHO, 2022b) (Figure 17). Twelve deaths due to A(H5N6) had been reported between 2014 and 2017 (Jiang et al., 2017). A household cluster with two infections was observed in a couple preparing a duck for meal purchased from a live-bird market. The overall case fatality ratio is estimated to be 43% (limitation: case reports might not have been a complete picture previously reported as severe and lacking updated information).



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

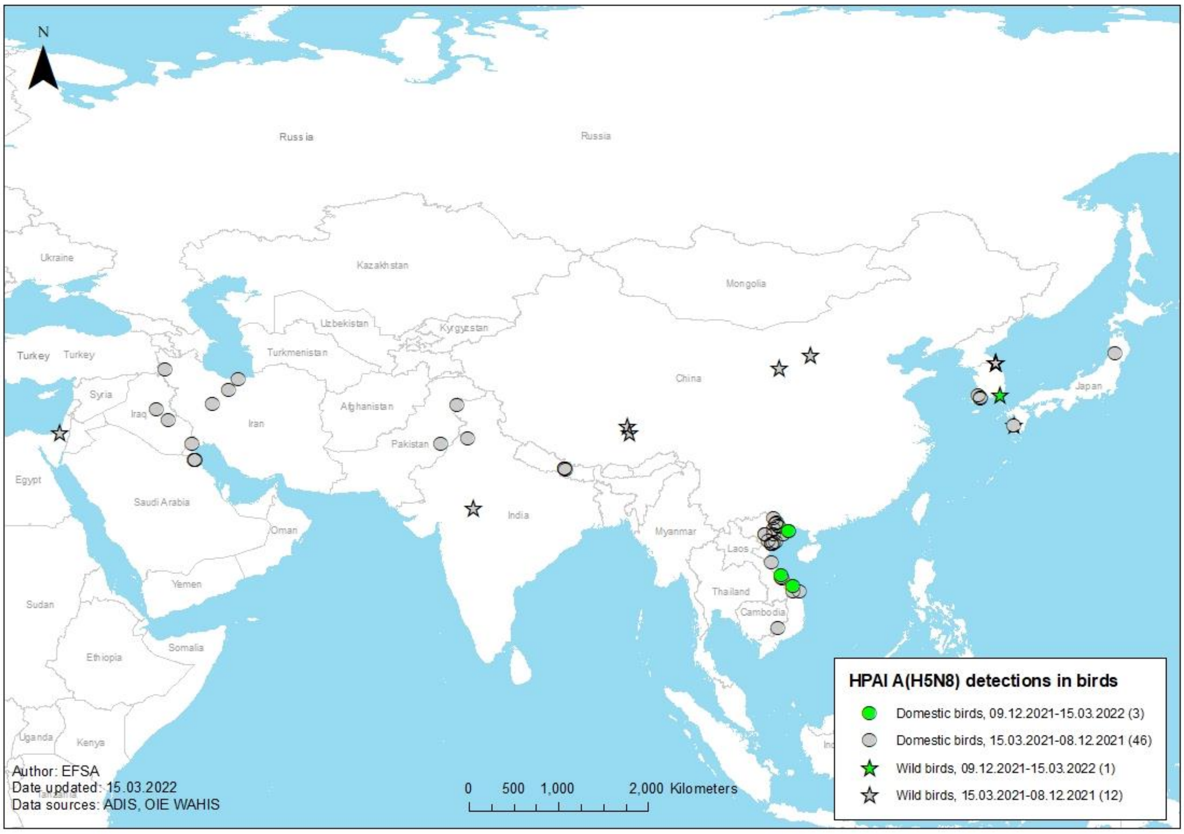
Figure 20: Number of human cases due to A(H5N6) infection by year of onset, 2014 to 24 March 2022 (75)

4.5.4. HPAI A(H5N8)

4.5.4.1. Domestic and wild birds

Detections

The number of reported cases of HPAI remained at a low level again in this reporting period. Vietnam notified three outbreaks of HPAI A(H5N8), clade 2.3.4.4b, from poultry in medium-sized farms. In contrast with the previous reporting, only one case of HPAI A(H5N8) in wild birds was reported by the Republic of Korea, a Whooper Swan (*Cygnus cygnus*) in the southeast of the country (Figure 19).



Grey symbols indicate outbreaks that occurred between 15 March and 8 September 2021, green symbols indicate outbreaks that occurred between 9 December 2021 and 15 March 2022.

Figure 21: Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N8) outbreaks in domestic birds (circles) and wild birds (stars) (62)

Information extracted from the scientific literature

Li et al. (2022) reported the detection of 40 HPAI A(H5N8) viruses during an intensified environment and passive wild bird surveillance program in central China, in October-November 2020. These viruses were isolated from migratory waterbird species: whooper swan, tundra swan (Cygnus columbianus), mute swan (*C. olor*), common teal (*Anas crecca*), bean goose (*Anser fabalis*), whiskered tern (*Chlidonias hybrida*) and from Eurasian eagle-owl (*Bubo bubo*). All full genome sequences clustered together and were closely related to the major genotype of clade 2.3.4.4b A(H5N8) HPAI viruses initially detected in Iraq in May 2020 and that circulated in Eurasia from late 2020 onwards. Phylodynamic analysis suggested that Russia was the most plausible source of introduction of these viruses into central China and that whooper swans were likely involved in the initial introductions during fall migrations. Although no major determinants of human type receptor affinity of the HA protein and of mammalian adaptation in the PB2 protein were observed for these viruses, several substitutions were present in the HA, PB1, PA, NP, M1 and NS1 proteins suggesting that they may have acquired binding ability to human-type receptors, increased polymerase activity and enhanced virulence in mice.

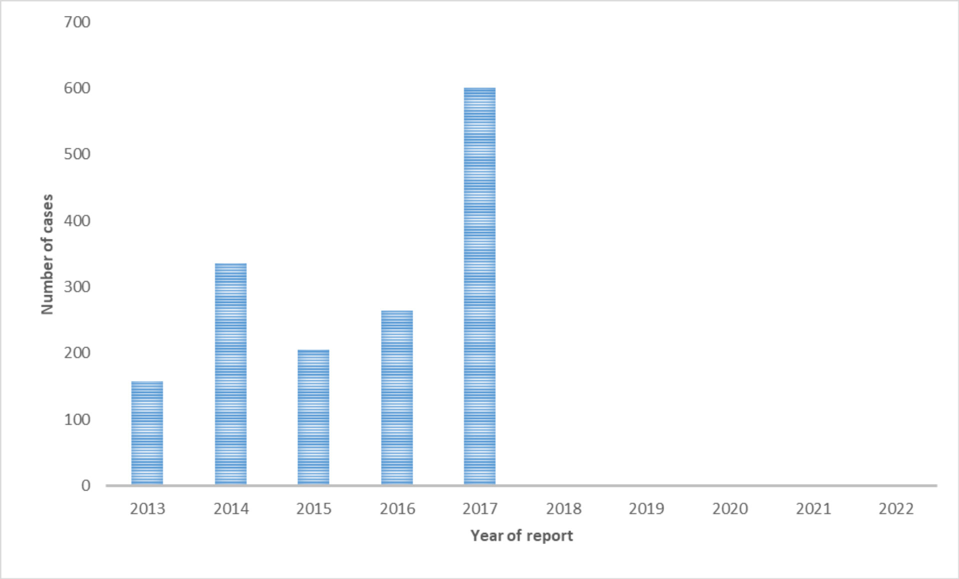
4.5.5. HPAI–LPAI A(H7N9)

4.5.5.1. Domestic and wild birds

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

4.5.5.2. 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, 2020a, b). Since February 2013, in total, 1,568 human cases have been reported from outside of Europe (Figure 22), including at least 615 deaths (39%) (CHP, 2021b; WHO, 2019a, b). The last case was reported in March 2019. Of all human cases, 32 had been infected with HPAI virus A(H7N9), and 13 of them were fatal, according to the Chinese National Influenza Center (Chinese National Influenza Center et al., 2018).



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

Figure 22: Number of human cases due to A(H7N9), infection by year, 2013 to 2022 (1,568)

4.5.6. LPAI A(H9N2)

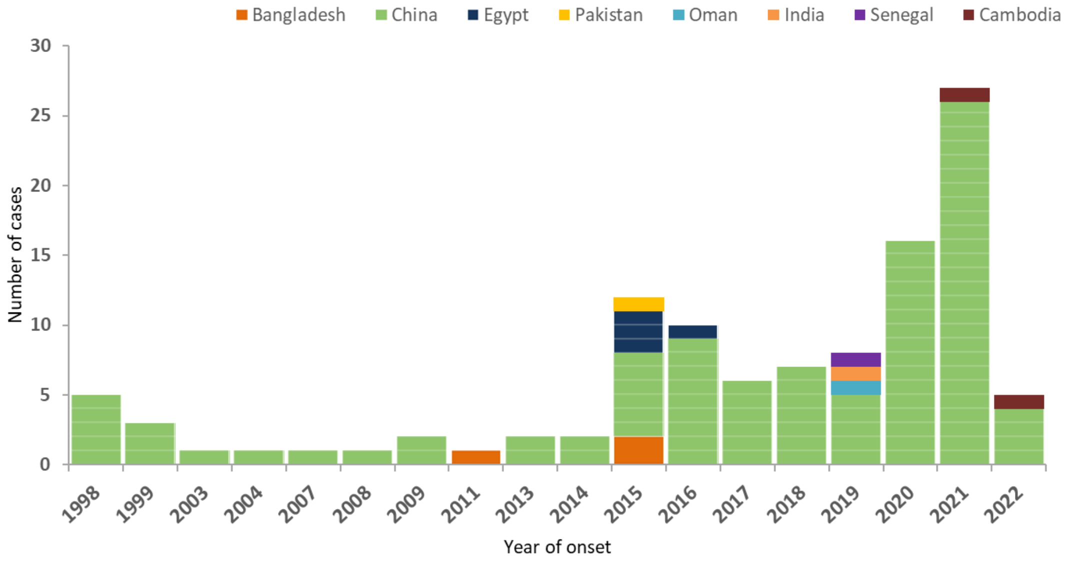
4.5.6.1. Domestic and wild birds

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 15 March 2022.

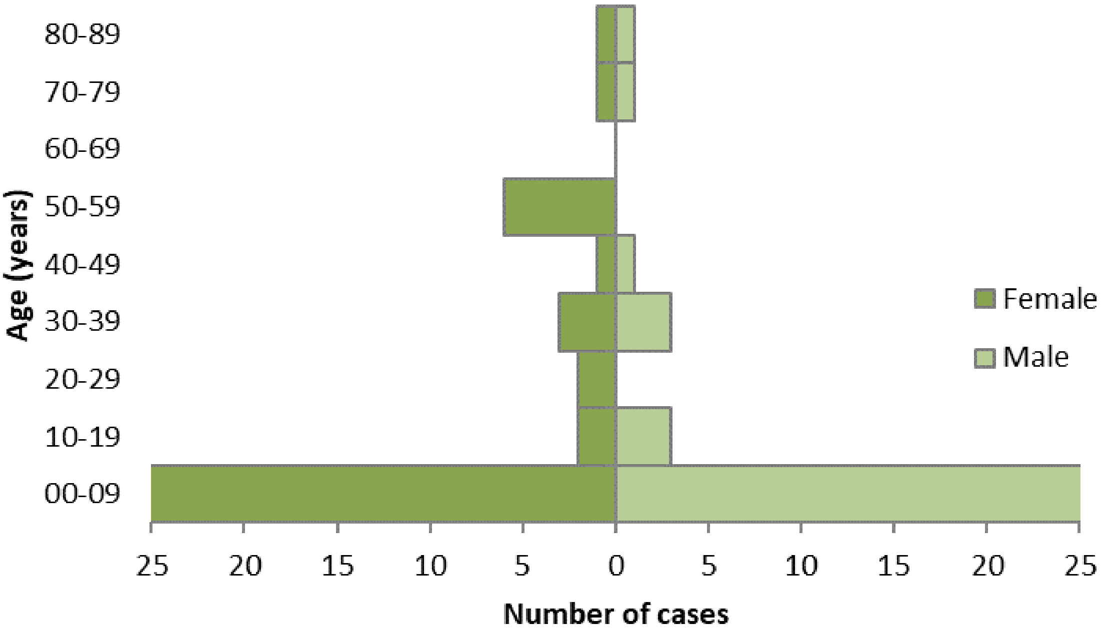
4.5.6.2. Human infections due to A(H9N2)

Since the last EFSA report, 15 human cases of infections with A(H9N2) have been reported from China (14) and Cambodia (1) (WHO, 2020c; CHP, 2021b; ECDC, 2021a). A recent human infection was detected in Cambodia in 2022 in a 1-year-old girl hospitalised with pneumonia (CHP, 2022c; WHO, 2022b). Since 1998, and as of 24 March 2022, 110 laboratory-confirmed human infections with avian influenza A(H9N2) virus, including two deaths, have been reported globally. Cases were reported from China (97), 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 23). Exposure to live or slaughtered poultry or contaminated environment has been reported. The age group most affected by A(H9N2) infections in humans was children under 10 years of age, who developed only mild symptoms (WHO, 2020c; CHP, 2021a; ECDC, 2021b) (ECDC line list; please refer to Appendix B.2) (Figure 24).



Source: ECDC line list

Figure 23: Distribution of confirmed human cases of A(H9N2) by reporting country, 1998 to 24 March 2022 (110)



Source: ECDC line list.

Figure 24: Distribution of confirmed human cases of A(H9N2) by age group, 1998 to 24 March 2022 (110)

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

Since 2014, HPAI A(H5) virus incursions into the European territory have occurred almost every year. These incursions have shown a similar temporal pattern, starting around the end of September or the beginning of October, with the arrival of migratory waterbirds at the wintering areas in Europe. The impact on the poultry industry and wild bird populations has been variable, but two devastating epidemics with hundreds of outbreaks in poultry, heavy mortality in wild birds, and the involvement of numerous European countries have occurred in 2016–2017 and 2020–2021. Furthermore, in the 2020–2021 epidemic season, two HPAI A(H5) virus subtypes persisted in sedentary wild bird populations during summer, mainly in northern Europe (EFSA et al., 2021b).

Since late summer 2021, with the new migratory season, HPAI viruses of the A(H5N1) subtype have been introduced in Europe again, affecting 33 countries. The Faroe Islands and Moldova reported for the first time HPAI virus in their territory (in wild birds and poultry, respectively). Also, for the first time since 2017, Portugal, North Macedonia, and Spain (in poultry) were affected by HPAI viruses. So far, hundreds of HPAI outbreaks in domestic (1,582 outbreaks) and detections in wild birds (2,177 detections) have already occurred, and approximately 31 million domestic birds have either died from the infection or have been culled in the affected establishments.

Both epidemiological and genetic analysis indicate that HPAI A(H5) continues to be maintained in the wild bird populations in Eurasia, including detection in resident wild birds in Europe. Similarly, to the 2020–2021 epidemic season, there have been two peaks of HPAI A(H5) detections in wild birds in the current 2021–2022 season. In both seasons, the first peak was at the beginning of November, coinciding with the autumn migration of waterfowl and arrival at their wintering grounds in Europe. However, the second peak in this season appeared to have occurred earlier (mid- January) than in the last season (beginning of March). The reason for this is not clear. Research on hunted and live-captured dabbling ducks in Italy (Gobbo et al. 2021) showed a high prevalence of HPAI A(H5) infection in common teals and Eurasian wigeons during winter in geographical areas where no dead birds were detected, indicating that high infection pressure in the environment is possible in the absence of wild bird mortality. In addition to migratory waterfowl, HPAI A(H5) was detected in a wider range of other wild bird species compared with last year, including several terrestrial species. This enlarged host range of HPAI A(H5) in wild birds indicates an increasing and changing risk for virus incursion into poultry farms.

Considering the outbreaks in poultry, France and Italy have been the most affected countries since the beginning of the 2021–2022 epidemic season, with 609 and 315 outbreaks, respectively (66% of the total outbreaks that were notified in poultry in the EU since October 2021).

In particular, since 2015, France has been affected by four HPAI A(H5) epidemics. In the 2021–2022 one, two epidemiological clusters have been identified, with no epidemiological links: a first cluster in the south-west area (southern part of Nouvelle-Aquitaine and Occitanie), with a peak in mid-January; and the second one in west regions (Pays de la Loire and northern part of Nouvelle-Aquitaine) in late February-beginning of March. Approximately 5.5 million birds have been culled in the affected poultry establishments, with 5.2 million birds in the western regions (Nouvelle-Aquitaine, Occitanie and Pays de la Loire). All the reported poultry outbreaks have involved commercial farms. The vast majority of the affected establishments for which the information on the farmed species and production type was available (373) farmed domestic ducks for foie gras production (236/373), followed by ducks for fattening (43/373) and broilers (35/373). However, chicken breeder farms with high biosecurity levels have also been affected. Although at least eight distinct genotypes have been circulating in France, a single genotype accounted for most of the virus detections dispersed over the country, up to mid-February 2022 in poultry, captive and wild birds, and also accounted for most of the poultry outbreaks detected in the southwestern region. In this latter area, closer investigation suggested that at least five independent virus introductions into the poultry production sector may have occurred.

In Italy, from October 2021 to the end of February 2022, 315 HPAI A(H5N1) outbreaks affecting more than 14.6 million birds occurred mainly in commercial poultry establishments in areas with high poultry densities in the Po Valley (Veneto and Lombardy regions). The emergence of infection was related to at least seven new virus introductions into the poultry population of these areas, but, similar to France, a single genotype accounted for most of the outbreaks. After the notification of the first outbreak the infection rapidly spread among establishments characterised by highly susceptible poultry species and different poultry production systems (e.g. fattening turkeys and layers). However, an unusually high number of outbreaks (25.4% of the outbreaks in Italy) occurred in broiler establishments (EFSA et al., 2021b) that are historically considered at lower avian influenza risk (Busani et al., 2009).

HPAI A(H5) viruses are still circulating in wild and domestic bird populations in several European countries. The dynamics of the current epidemic compared with those observed in 2016–2017 and 2020–2021 (Figures 1 – 4) indicated that an elevated environmental pressure of infection will likely persist in the coming months posing a risk for further virus introductions and spread in the poultry sector. The rampant spread of the disease observed in some EU countries (e.g. France, Italy, Poland, and Hungary), also due to between-farm transmission of infection, has caused vast economic losses to the poultry industry, jeopardising its sustainability. The prolonged persistence of HPAI A(H5) viruses in wild migratory waterfowl require the definition and the rapid implementation of suitable and sustainable HPAI mitigation strategies. In particular, appropriate biosecurity, surveillance, and early detection measures must be regularly applied in the different poultry production systems.

Biosecurity – HPAI A(H5) viruses have affected poultry establishments without outdoor access and even highly biosecured poultry farms (e.g. breeders). Traditionally, biosecurity measures had been implemented in commercial farms, primarily to reduce the risk of avian influenza virus introduction from infected premises. Measures were applied to mitigate the possible introduction of the virus within the farm perimeter. The persistence for long periods of high environmental avian influenza infection risk requires the systematic application of strict biosecurity and hygienic practices at the line of separation between the environment inside each poultry house, where birds are raised, and the outer farm environment. These measures shall include at least the regular maintenance and repair of buildings, the implementation of a Danish custom at the entrance of each shed (i.e. measures as changing boots and clothes), the definition and systematic implementation of reliable cleansing and disinfection procedures to be systematically applied to decontaminate any equipment brought into the shed, and the storage of materials (e.g. bedding materials) in areas protected from direct or indirect contact with wild birds. Furthermore, the implementation of sustainable levels of biosecurity must be guaranteed and checked along the entire poultry production chain, taking into account that the persistent circulation of HPAI viruses and the possible reduction of biosecurity compliance, might increase the risk of avian influenza incursions with potential further spread between farms.

Surveillance and early detection – The early detection of any avian influenza virus exposure is fundamental to reduce the high-risk period of an epidemic and to limit the secondary spread of avian influenza from affected establishments, particularly in high-risk areas and production sectors. The efficacy of a passive surveillance system is strongly related to the level of awareness, and veterinary authorities should continuously ensure high awareness among all stakeholders in the poultry sector. This is crucial for the immediate reporting of any increase in daily mortality and drop in production parameters, such as egg production and food and water intake. As an example, threshold levels for the compulsory notification of suspect cases of avian influenza infections in layer and duck farms have been defined and provided for in the national legislation in the Netherlands (Gonzales and Elbers, 2018; Elbers and Gonzales, 2021).

In contrast with the last report (EFSA et al., 2021b), in non-EU/EEA countries from 9 December 2021 to 15 March 2022, there was an increasing number of HPAI outbreaks that were reported in poultry and wild birds, particularly in Africa and Asia. Furthermore, the number of affected countries increased by one third, and HPAI virus spread was observed in the southern hemisphere despite the current summer climate conditions. The virus subtype HPAI A(H5N1) was even more dominant than in the previous reporting period and infected a broader spectrum of wild bird species (section 4.5.1). This subtype was also detected in Canada and the USA in domestic and wild birds. It is the second time that HPAI A(H5) viruses of the Eurasian lineage have been introduced via infected wild birds into the American continent. But in the season 2014–2015, the virus spread eastward from Eurasia through the Bering strait, whereas in this epidemic season, it appears that, for the first time, infected wild birds have carried the virus from Europe westward through Greenland crossing the Atlantic Ocean.

In this reporting period, six additional HPAI A(H5N1) cases were detected in wild mammal species in four EU countries. Since October 2020, 26 cases were reported in mammals, 11 caused by the A(H5N8) subtype and 15 by the A(H5N1) subtype. The A(H5N8) subtype was identified in three mammalian species from four Northern European countries between December 2020 and September 2021, while the A(H5N1) subtype affected six different species sampled from seven different countries between February 2021 and February 2022. Some of these viruses present adaptive markers that are associated with an improved replication in mammals (Manzoor et al., 2009; Kim et al., 2010; Herfst et al., 2012; Suttie et al., 2019). The continuous detection of HPAI virus 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 H5Nx viruses of clade 2.3.4.4b reported in the last two years, highlight the need to intensify surveillance in mammals, particularly in high-risk areas with 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 applied[6]. Appropriate PPE should be provided by employers and workers should be trained in its use and disposal. PPE should be properly stored. At poultry farms, it should be ensured that living areas are not contaminated, for example through work clothing, e.g. to avoid additional risk to family workers and relatives.

4.7.2. Monitoring and options for public health measures

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

4.7.3. Diagnosis

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

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

4.7.4. Reporting

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[6] 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.

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/EU[7]. 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-d).

4.7.6. Candidate vaccine viruses

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

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

Avian influenza A(H5N8) viruses have caused large outbreaks in birds and poultry since 2014. ECDC has published a Threat Assessment Brief on 24 February 2021 (ECDC, 2021a).

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 the UK 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.

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

Avian influenza virus transmission to humans is a rare event and the risk is considered very low for viruses adapted to avian species, which viruses currently circulating in bird populations in Europe are considered. However, the detection of viruses carrying markers for mammal adaptation, and correlated with increased replication and virulence in mammals, is of concern. The additional reports of transmission events to mammals, e.g. seals and foxes in several EU countries as well as seroepidemiological evidence of transmission to wild boar and domestic pigs, could indicate evolutionary processes including mammal adaptation with the possibility to acquire the ability to transmit to humans.

However, direct and unprotected exposure to possible infected birds and poultry and their products including blood, remains limited to particular mostly occupationally exposed groups of people in the European countries. Also, other groups of people such as backyard farmers or wild bird hunters with possible exposure to infected poultry or wild birds should be made aware of the potential risk of transmission and reminded to wear protective equipment. Such unprotected exposure to infected backyard birds was the source of infection in the recent human A(H5N1) infection in the UK (GovUK, online; WHO, online-c).

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[7] 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 (notified under document C(2012) 5538) - OJ L 262, 27.9.2012

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 when unprotected or wear PPE when in direct contact. Workers should be protected following an updated workplace risk assessment and prevention measures set accordingly[8]. 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.

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[8] 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.

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Abbreviations

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

PCR	Polymerase chain reaction
PIP	Pandemic Influenza Preparedness
PPE	Personal protective equipment
PZ	Protection zone
RA	Risk assessment
SBA	Swedish Board of agriculture
SVFA	State Veterinary and Food Administration
SZ	Surveillance zone
ToR	Term of Reference
WHO	World Health Organization

Appendix A – Terms of Reference

Background and Terms of Reference as provided by the requestor

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

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

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

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

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

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

There is knowledge, legislation[9], technical and financial tools in the EU to effectively deal with outbreaks of avian influenza in poultry and captive birds. However, the very wide virus spread by wild birds and the increased risk of direct or indirect virus introduction into poultry or captive bird holdings has led to the largest HPAI epidemic in the EU so far. This situation calls for a reflection and evaluation how preparedness, risk assessment, early detection and control measures could be improved.

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

Therefore, in the context of Article 31 of Regulation (EC) No. 178/2002[10], 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.

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

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).

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 between 9 December 2021 and 15 March 2022 and reported by Member States and neighbouring countries via ADNS or OIE. 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 AHAW Panel, 2017).

If HPAI outbreaks in poultry are detected in the EU, a description of the applied prevention and control measures (ToR 3) is given in the case report provided by representatives from the affected Member States and attached as an annex. Information was collected for outbreaks that occurred from 1 December 2021 to 4 March 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 OIE WAHIS. The description focuses only on findings of avian influenza viruses occurring in countries that are considered to be of epidemiological interest for the EU/EEA and the UK or of public health relevance, specifically on HPAI A(H5N1), HPAI A(H5N2), HPAI A(H5N5), HPAI A(H5N6), HPAI A(H5N8), HPAI/LPAI A(H7N9) and LPAI A(H9N2). The background and epidemiology, detections, phenotypic and genetic characterisations are described based on information from confirmed human, poultry and wild bird cases that occurred between 9 December 2021 and 15 March 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 September to December 2021 (EFSA et al., 2021b) 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 9 December 2021 to 15 March 2022 submitted by Member States to the ADIS (European Commission, online) were taken into account for this report. Data extraction was carried on 15 March 2022. The OIE's World Animal Health Information Database (OIE, online-b) was consulted to complement the information for European countries not reporting HPAI notifications to ADIS. In addition, HPAI-affected European countries were asked to provide more detailed epidemiological data directly to EFSA on the avian influenza outbreaks that occurred in poultry during the same period. Wild bird species have been categorised according to Table B1. The public GISAID's EpiFlu Database was accessed to download newly released avian influenza sequences. A descriptive analysis of the data collected is reported in Section 4.2.

Table B1. Categorisation of wild bird species for detection between 5 October 2020 and 15 March 2022

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

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

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 23 November 2021 to 2 March 2022 were searched; the search was run on 2 March 2022.

Relevance criteria Scientific articles added to the database from 23 November 2021 to 2 March 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 142 papers. The articles were subsequently screened against the relevance and eligibility criteria. Five of the screened papers was 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.6400615.

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

Data from OIE WAHIS (OIE, online-b) on HPAI A(H5N1), HPAI A(H5N2), HPAI A(H5N5), A(H5N6), A(H5N8), HPAI and LPAI A(H7N9) in domestic and wild birds were used to describe and to map the geographical distribution of avian influenza detections in domestic and wild birds in Africa, Americas, Asia and Europe based of the observation dates. Data were extracted on 15 March 2022.

B.1.2.1. Literature review on phenotypic and genetic characterisation of HPAI viruses circulating on other continents

Information on phenotypic and genotypic characterisation of HPAI viruses circulating on other continents and in other regions (Africa, Asia, the Middle East) in domestic or wild birds or mammals (excluding humans) were extracted from the scientific literature by performing a literature review.

Review questions Update on the phenotypic and genetic characterisation of HPAI viruses circulating on other continents and in other regions (Africa, Asia, the Middle East) in domestic or wild birds or mammals (excluding humans) within the last 3 years.

Search The PubMed database was searched by using subject index terms and free-text terms combined with the appropriate Boolean operators. Scientific articles added to the database from 23 November 2021 to 2 March 2022 were searched; the search was run on 2 March 2022.

Relevance criteria Scientific articles added to the database from 23 November 2021 to 2 March 2022that report information on the presence or absence of clinical signs, pathological changes or mortality or genotypic characterisation (only new information) due to HPAI infection with viruses circulating within the last 3 years in Asia, Africa or the Middle East in domestic or wild birds or mammals other than humans.

Eligibility criteria Host species all domestic birds or wild birds present in the EU or mammals other than humans; 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 127 papers. The articles were subsequently screened against the relevance and eligibility criteria. Three papers were in the end taken into consideration in the description of phenotypic and genotypic characterisation of HPAI viruses circulating on other continents and in other regions (Africa, Asia, the Middle East) in domestic or wild birds or mammals (excluding humans) in the reporting period.

The search protocol and the results can be consulted at https://doi.org/10.5281/zenodo.6400615.

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.6400451

The annexes contain the following information:

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

The Annex contains table with the characteristics of the HPAI A(H5Nx)-positive poultry establishments by affected EU Member State from 1 December 2021 to 4 March 2022.

Annex B – Applied prevention and control measures on avian influenza

The Annex contains an overview of specific prevention and control measures applied in Belgium, Bulgaria, Croatia, Czechia, Denmark, France, Hungary, Ireland, Italy, Moldova, Kosovo, Netherlands, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden, Northern Ireland (UK) from 1 December 2021 to 4 March 2022 in relation to HPAI outbreaks in poultry and in wild birds.

Annex C – Data on wild birds

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