SCIENTIFIC REPORT

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Avian influenza overview September – December 2022

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Abstract

Between October 2021 and September 2022 Europe has suffered the most devastating highly pathogenic avian influenza (HPAI) epidemic with a total of 2,520 outbreaks in poultry, 227 outbreaks in captive birds, and 3,867 HPAI virus detections in wild birds. The unprecedent geographical extent (37 European countries affected) resulted in 50 million birds culled in affected establishments. In the current reporting period, between 10 September and 2 December 2022, 1,163 HPAI virus detections were reported in 27 European countries in poultry (398), captive (151) and wild birds (613). A decrease in HPAI virus detections in colony-breeding seabirds species and an increase in the number of detections in waterfowl has been observed. The continuous circulation of the virus in the wild reservoir has led to the frequent introduction of the virus into poultry populations. It is suspected that waterfowl might be more involved than seabirds in the incursion of HPAI virus into poultry establishments. In the coming months, the increasing infection pressure on poultry establishments might increase the risk of incursions in poultry, with potential further spread, primarily in areas with high poultry densities. The viruses detected since September 2022 (clade 2.3.4.4b) belong to eleven genotypes, three of which have circulated in Europe during the summer months, while eight represent new genotypes. HPAI viruses were also detected in wild and farmed mammal species in Europe and North America, showing genetic markers of adaptation to replication in mammals. Since the last report, two A(H5N1) detections in humans in Spain, one A(H5N1), one A(H5N6) and one A(H9N2) human infection in China as well as one A(H5) infection without NA-type result in Vietnam were reported, respectively. The risk of infection is assessed as low for the general population in the EU/EEA, and low to medium for occupationally exposed people.

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

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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 10 September and 2 December 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 10 September and 2 December 2022, is presented below.

2.1. Main observations

- In Europe, between 10 September and 2 December 2022 (based on the Animal Disease Information System (ADIS), WOAH World Animal Health Information System (WOAH-WAHIS), and information provided by affected countries) 1,162 HPAI A(H5) detections[3] were reported in poultry, captive and wild birds:
  - 398 outbreaks in poultry in the United Kingdom (115), France (98), Hungary (69), Germany (42), Italy (28), the Netherlands (25), Belgium (8), Norway (2), Ireland (2), Bulgaria, Czechia, Croatia, Cyprus, Denmark, Moldova, Poland, Portugal, and Spain (1 each);
  - 613 virus detections in wild birds in the United Kingdom (160), the Netherlands (97), Germany (86), France (62), Belgium (59), Spain (46), Italy (35), Denmark (20), Norway (9), Iceland (7), Romania (7), Ireland (4), Sweden (4), Serbia (3), Slovenia (3), Portugal (3), Croatia (2), Poland (2), Switzerland (2), Cyprus and Finland (1 each);
  - 151 outbreaks in captive birds in France (52), Germany (32), the United Kingdom (29), Netherlands (18), Belgium (11), Ireland (2), Denmark (2), Austria, Cyprus, Italy, North Macedonia and Switzerland (1 each).
- During this reporting period, HPAI virus has been detected in at least 64 wild bird species in Europe: at least 18 waterfowl species (407 detections), 10 colony-breeding seabird species (117 detections), 12 raptor species (65 detections), and 24 other wild bird species (82 detections).
- The overall temporal pattern has shown a decrease in HPAI virus detections in wild birds since the previous reporting period (613 versus 844 detections), which is mainly due to the decreased number of detections in colony-breeding seabird species (109 versus 581 detections); conversely, the number of detections in waterfowl increased since the previous reporting period (372 versus 129 detections).
- In the current reporting period, the number of outbreaks in domestic birds continued to increase (from its lowest point in June in the previous reporting period) to a peak in October 2022. From 2 September and 10 December 2022, 35% more infected poultry establishments were observed than those observed during the same period in the previous year.
- The high infection pressure due to the continuous circulation of HPAI A(H5N1) virus in the wild reservoir has led to frequent introductions of the virus into poultry populations across Europe. Primary HPAI poultry outbreaks frequently occurred in several EU countries (e.g., France,

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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.

Germany, Italy, the Netherlands), without extensive secondary spread of the virus. Indeed, these countries reported, until now, only a limited number of secondary outbreaks, whereas numerous secondary outbreaks were detected in poultry in Hungary. Primary outbreaks often occurred in establishments without outdoor access, and poultry production systems (e.g. breeders) with high biosecurity standards were also affected.

- All the HPAI A(H5Nx) viruses characterised since October 2020 in Europe belong to clade 2.3.4.4b. Based on the available genetic information, the A(H5N1) viruses detected since September 2022 belong to eleven genotypes, three of which have circulated in Europe during the summer months, while eight represent new genotypes, likely evolved through reassortment events, most likely occurred locally.
- In October 2022 a mink farm in Spain was affected by an A(H5N1) virus belonging to a genotype generated through reassortment events with the gull-adapted H13 subtype. Viruses with this gene constellation have been circulating mainly in wild birds in Northern Europe since May 2022, and were detected in one fox in Belgium. The strain responsible of the outbreak in mink contained a mutation in the PB2 protein that has been demonstrated to enhance the polymerase activity of influenza A viruses in mammals.
- For the first time HPAI A(H5N1) virus infections were reported in an Amur leopard (*Panthera pardus orientalis*) in the USA.
- In comparison to the previous report (EFSA et al., 2022b), in the current reporting period the avian influenza situation in Africa, Asia and Russia showed a comparable level of reported outbreaks in poultry and detections in wild birds. However, the number of notifications to WOAH and of affected countries increased in the Americas by four times, particularly due to the spread of HPAI A(H5N1) to Central (Mexico) and South America (Colombia, Ecuador, Peru and Venezuela). These introductions in South American countries in both wild birds and poultry have been reported for the first time ever.
- During this reporting period six new detections of avian influenza in humans have been reported from three countries: Spain: two A(H5N1); China: one A(H5N1), one A(H5N6), and one A(H9N2); Vietnam: one A(H5) without NA-type.
- The HPAI A(H5N1) virus collected from one human sample in Spain, likely originating from an environmental contamination, clusters with the viruses collected from the infected laying hens' farm where the person was involved in culling activities. No mutation associated with increased zoonotic potential was identified.

2.2. Conclusions

- The HPAI epidemic observed in the 2021–2022 epidemiological year in Europe is the largest in history, involving 37 countries and with a total of 2,520 HPAI outbreaks in poultry and 50 million birds dead or culled in the affected establishments, 227 detections in captive birds, and 3,867 detections in wild birds. The overall number of detections was 1.7 times higher than in the 2020–2021 epidemiological year, and 2.4 times higher than in the 2016–2017 epidemiological year. The epidemic didn't stop during the summer and continued into the 2022–2023 epidemiological year.
- 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.
- Detections of A(H5) clade 2.3.4.4b viruses in humans together with the increasing number of transmission events of A(H5) viruses to wild mammals reported from different European countries, underline the continuous risk of avian influenza virus transmission to humans, also in Europe, and that these viruses may adapt further to mammals.
- The risk of infection for the general population in the EU/EEA is assessed as low, and for occupationally exposed people low to medium with high uncertainty due to the high diversity of circulating avian influenza viruses in bird populations.

- The risk of transmission to humans by exposure to contaminated poultry products is considered negligible as also outlined in a previous EFSA assessment (EFSA AHAW Panel, 2017).
- In contrast to previous epidemiological years, there was no clear start of the HPAI epidemic in October in the epidemiological year 2022–2023, neither in wild nor in domestic birds. This is due to the persistence of the virus in wild birds along the summer months and indicates a continuous risk for HPAI virus to spread among wild birds and mammals, as well as for virus entry into poultry establishments.
- From the previous reporting period (June-September) to the current reporting period (September-December), waterfowl replaced colony-breeding seabirds as the main wild birds in which HPAI virus detection was reported. This switch is likely due to a combination of the post-breeding dispersal of colony-breeding seabirds after their breeding periods in the summer, and the increased number of waterfowl present in Europe as a result of autumn migration. It cannot be excluded that these waterfowl will be at higher risk of HPAI virus infection than in previous years due to the observed persistence of HPAI virus in wild birds in Europe.
- The shape of the epidemic curve in poultry in 2021–2022 resembled that in waterfowl, but not that in seabirds (Figure 5C). This suggests that waterfowl might be more involved than seabirds in the incursion of HPAI virus into poultry establishments, likely because the habitat of waterfowl is more likely to overlap with the location of poultry establishments than seabird colony sites.
- The biosecurity measures implemented along the poultry production chain do not seem effective in preventing all introductions of the HPAI A(H5N1) virus into poultry establishments. In the coming months, the sustained and increasing infection pressure on poultry establishments will further challenge the effectiveness of the applied biosecurity measures.
- The prolonged avian influenza risk period represents a challenge for the sustainability of the reinforced biosecurity measures implemented along the poultry chain in high-risk areas or production sectors. The persistent presence of HPAI A(H5) viruses in wild birds and in the environment and the continuous occurrence of primary outbreaks in several countries, and the possible reduction of biosecurity compliance might increase the risk of avian influenza incursions with the potential further spread between establishments, primarily in areas with high poultry densities.

3. Options for response

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

- Given the substantial mortality of wild birds associated with the detection of HPAI A(H5) virus, it is important for the relevant authorities to enhance the surveillance and to ensure accurate documentation of the number of wild birds dead or ill during these HPAI-associated die-offs. Such information would enhance understanding of these phenomena and provides a factual basis for assessing the ecological impact and coming up with policy decisions to avert future HPAI outbreaks not only in poultry and humans but also in wild birds, both migratory and resident. On the short-term, timely removal of wild bird carcasses in certain situations, e.g. seabird breeding colonies, may reduce virus spread and subsequent mortality of wild birds during the current HPAI outbreak.

- Testing for avian influenza virus should be strongly considered in wild and farmed mammals showing neurological symptoms but also respiratory symptoms, particularly in highly susceptible species for influenza virus, in high risk period and high risk areas, when increased mortality is observed, e.g. at mink farms.

- Surveillance in mammals and humans that could potentially be exposed to infected birds should be strengthened to facilitate the early detection of virus transmission events from birds to wild or domestic mammals and/or humans, and subsequently between humans. Cross-sectoral cooperation and communication between animal and public health and occupational safety and health (OSH) authorities are recommended (One Health approach) to initiate rapid response, follow-up, and control measures. Especially, the inclusion of avian influenza viruses in the differential diagnosis of neurological disease in wild mammals as well as in humans with exposure to potentially infected birds needs to be more widely implemented.

- Occupational health and safety measures should be set according to national legislation. Health surveillance should be offered according to national requirements (please refer to Section 4.7.1 for more detail).
- People potentially exposed to infected poultry or captive birds, for example during culling operations, or workers in close contact to potentially infected mammals such as foxes or other wildlife, for example at rehabilitation centres, should be adequately protected and actively monitored or at least self-monitor for respiratory symptoms, neurological symptoms or conjunctivitis for at least 10 days following exposure, and immediately inform the local health and occupational safety and health authorities and preventive services to initiate testing and follow-up in case of symptoms. Antiviral pre-exposure or post-exposure prophylaxis should be considered for exposed people according to national recommendations.
- Reference viruses and sera against avian influenza reference viruses need to be developed, constantly updated and provided to the countries to investigate transmission events from animals to humans and to confirm serological evidence of infections with a zoonotic virus.
- Timely generation and sharing of complete viral genome sequences from wild birds, poultry, captive birds and mammals are crucial to promptly detect the emergence in or introduction into the EU of viruses relevant for animal and public health. More efforts should be made by reporting countries to monitor and genetically characterise a significant number of samples based on the size, duration, and relevant features of the epidemic in each country or of subtypes of concern for public health.
- Should avian influenza outbreaks in mammalian species involve multiple animals, the genetic characterization of several samples obtained from diverse animals is of utmost importance to shed light on the virus origin, evolution and possible transmission among individuals.

4. Results

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

Figures 1, 2 and 3 show the HPAI outbreaks in domestic birds (poultry and captive birds) and HPAI virus detections in wild birds that were reported in Europe via ADIS or WOAH-WAHIS for the epidemiological years 2016–2017, 2017–2018, 2018–2019, 2019–2020, 2020–2021, 2021–2022 and 2022–2023 by month of suspicion (Figures 1 and 2) and geographical location (Figure 3). In this document an 'epidemiological year' refers to the period starting on week 40 (the beginning of October) and ending on week 39 (the end of September) of the following year, based on the dates on which the first HPAI virus detections were observed in wild birds in Europe in 2016–2017, 2020–2021 and 2021–2022. For the current epidemiological year 2022–2023 that starts on 1 October 2022, data reported are truncated on 2 December 2022. An overview of the epidemiological year 2021–2022, in which before this epidemiological year the largest HPAI epidemic was recorded in the EU/EEA and United Kingdom in terms of number of poultry outbreaks, geographical spread and number of dead wild birds and that conventionally ended on 30 September 2022 is given in Table 1. Figure 4 shows the comparison between the monthly geographical distribution of HPAI virus detections from September to December 2022 and the same period during the 2021–2022 epidemiological year.

The analysis of the characteristics of the previous 2020–2021, 2021–2022 and current 2022–2023 avian influenza epidemiological years, from October 2020 to 2 December 2022, is reported in Figure 5 by week of suspicion, virus subtype and host population. On poultry, the information reported in Figure 5b have been collected from the affected countries up to outbreaks occurred by 18 November 2022; the outbreaks that occurred later were too close to the publishing of this report to collect the data, therefore, for those poultry outbreaks the information presented in Figure 5b was unknown at the time of publication and will be included in the next report.

The start of the HPAI epidemics in the 2016–2017, 2020–2021, and 2021–2022 epidemiological years, all fell within the period between the end of September and beginning of October. There were no evident epidemics in 2017–2018 and 2018–2019, while the end of December 2019 was the start of the smaller 2019–2020 epidemic that affected only poultry (Figures 1 and 2).

In contrast to previous epidemiological years, there was no clear start of the HPAI epidemic in the epidemiological year 2022–2023 expected in October, in neither wild nor domestic birds (Figures 1 and 2). The previously interepidemic pause observed from June to September in 2020 and 2021, was absent in 2022 in wild birds, and restricted to June 2022 in domestic birds (Figure 2).

The HPAI epidemic observed in the 2021–2022 epidemiological year was so far the largest observed in Europe, with a total of 6,614 HPAI virus detections in 37 countries (Figure 1 and Table 1). This is 1.7 times more detections than in the 2020–2021 epidemiological year, and 2.4 times more detections than in the 2016–2017 epidemiological year. Regarding wild birds, the 3,867 detections in the 2021–2022 epidemiological year were 1.6 times more than in the 2020–2021 epidemiological year and 2.5 times more than in the 2016–2017 epidemiological year. Regarding poultry and captive birds, the 2,747 detections in the 2021–2022 epidemiological year were 2.0 times more than in the 2020–2021 epidemiological year and 2.3 times more than in the 2016–2017 epidemiological year (Figure 2). It should be noted that as captive birds also wild birds that are kept in captivity are included.

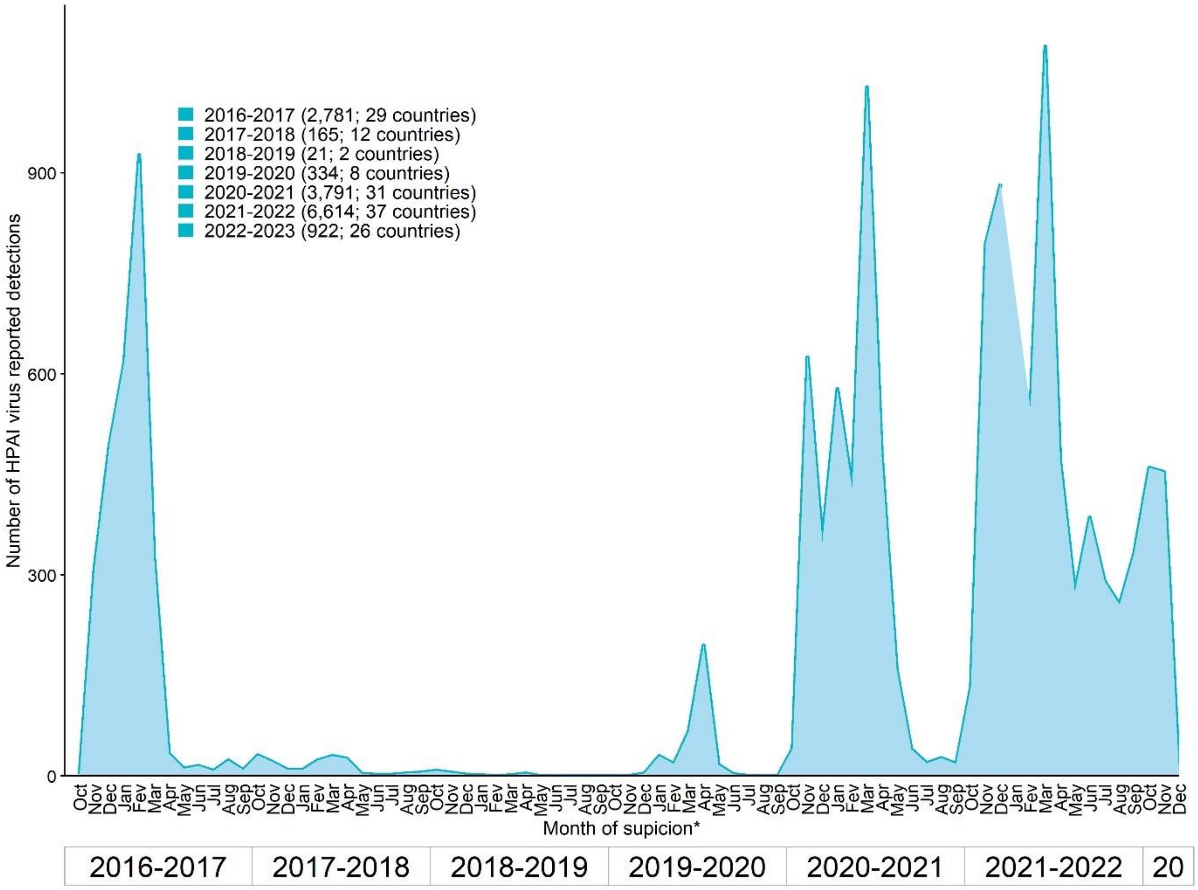
The higher numbers of HPAI virus detections reported in the 2021–2022 epidemiological year compared to the HPAI detections reported in the previous years can be assumed to reflect the higher level of virus circulation in wild birds, resulting in an increased risk of virus transmission from wild birds to poultry, and therefore in a higher number of primary introductions into poultry farms and higher risk of further farm-to-farm spread of HPAI virus.

The epidemic observed in the 2021–2022 epidemiological year was widespread in Europe, extending from Iceland, Ireland, and Portugal in the west to Finland, the Baltic states, Ukraine, Romania and Bulgaria to the east; from northern Norway (including the Norwegian islands Svalbard and Jan Mayen) to the north to southern Spain, Italy and Greece to the south. Compared to the 2020–2021 epidemiological year, HPAI virus detections in the 2021–2022 epidemiological year were reported further north, west and south, with a higher number of detections in both wild and domestic birds than in previous years; most of the virus detections were concentrated along the western coasts of continental Europe and in the British Isles.

In poultry, large epidemics in the 2021–2022 epidemiological year occurred in France (1,395 poultry outbreaks), Italy (318), and Hungary (290), but also United Kingdom (105), Poland (99), Germany (98) and the Netherlands (70) were severely affected (Table 1). After the two peaks of infection observed in winter 2021–2022 (Figure 2b), the number of poultry outbreaks decreased from April to June. From July onwards, however, a third minor peak of infection occurred and continued into the 2022–2023 epidemiological year peaking in October 2022. Since October 2022 HPAI poultry outbreaks have been also detected in inland areas in Hungary, Italy, Czechia, Serbia, Moldova, however in a lower number than those detected in the same period the previous year (Figure 4). Considering the period from 10 September to 2 December 2022, 35% more HPAI virus outbreaks were reported in poultry compared to those reported in the same period in the previous year (398 vs 294) and occurred primarily in the proximity to coastal areas (Figures 3c and Table 2).In wild birds, HPAI virus in the 2021–2022 epidemiological year was detected predominantly in waterfowl until the first half of April 2022. From the second half end of April to the middle of August, HPAI virus was detected mainly in colony-breeding seabird species, a category of wild birds that were only affected at a low scale in previous years. The species included in this seabird category are provided in Appendix B, Table B.1. The high frequency of HPAI virus detections in colony-breeding seabird species lasted from May to August, with a peak in June; this roughly corresponds to the breeding season of seabirds in Europe. As a result, there was an unprecedent high level of HPAI virus detections in wild birds during the summer 2022, which was associated with an – again unprecedent – high number of HPAI virus detections in domestic birds during this period (Figure 5). From September to December 2022, the number of detections in seabirds continued to decline, while the number of detections in waterbirds started to increase, likely in association with the higher number of waterfowl arriving in Europe due to the autumn migration (Figure 5). Interestingly, the increase of the number of HPAI virus detections in waterfowl roughly corresponds to the increase in the number of poultry outbreaks (Figure 5c).

Considering only HPAI outbreaks in poultry, so far ~58.3 million of birds have been died or culled in the HPAI-affected establishments since October 2021.

Information on the HPAI virus detections that have been reported in Europe since October 2016 are available in a new interactive dashboard published by EFSA.



*When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.
United Kingdom data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was the World Animal Health Information System (WOAH-WAHIS) for United Kingdom (excluding Northern Ireland), and ADNS/ADIS for the United Kingdom (Northern Ireland)[4].
Source: ADIS and WOAH (data extraction carried out on 2 December 2022).

Figure 1: Distribution of the number of HPAI virus detections reported in Europe in the epidemiological years 2016–2017, 2017–2018, 2018–2019, 2019–2020, 2020–2021, and 2021-2022 by month of suspicion, from 1 October 2016 to 2 December 2022 (14,629)

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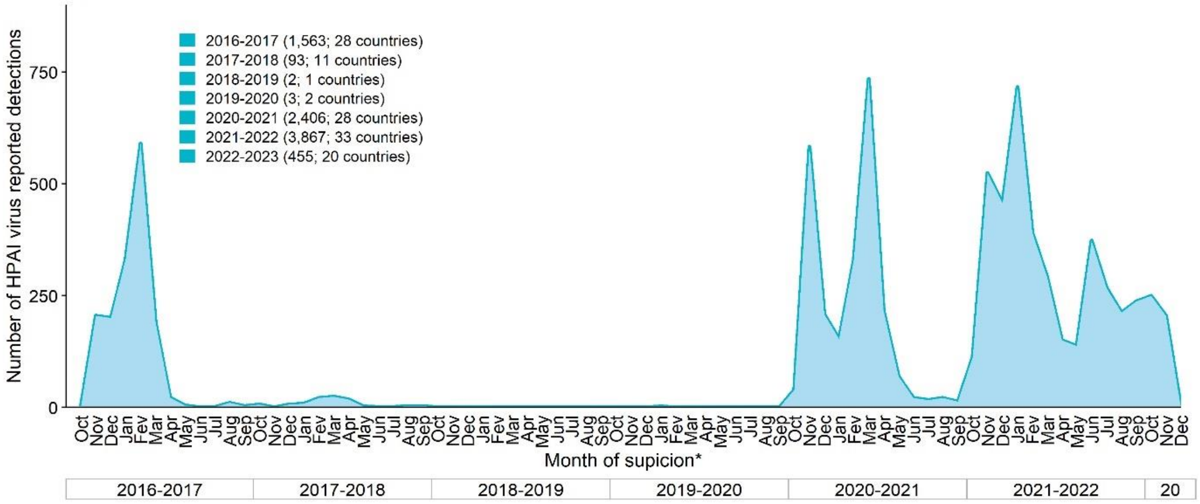
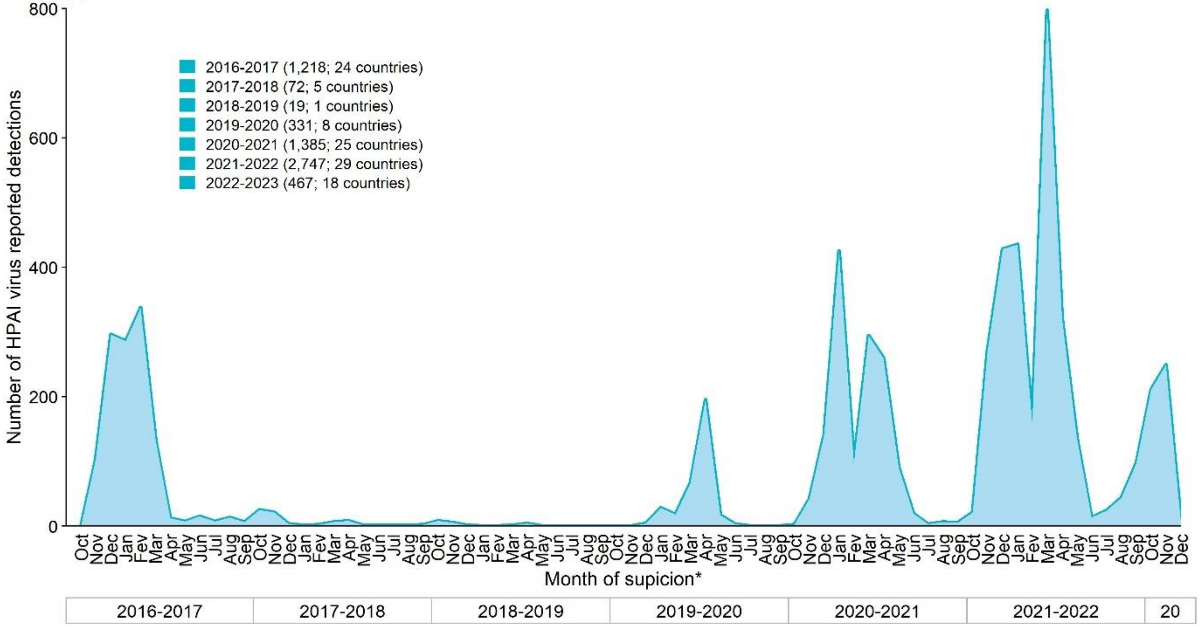
[4] In accordance with the Agreement on the Withdrawal of the United Kingdom from the EU, and in particular with the Protocol on IE/NI, the EU requirements on data sampling are also applicable to the United Kingdom (Northern Ireland).



(a) Wild birds



(b) Domestic birds

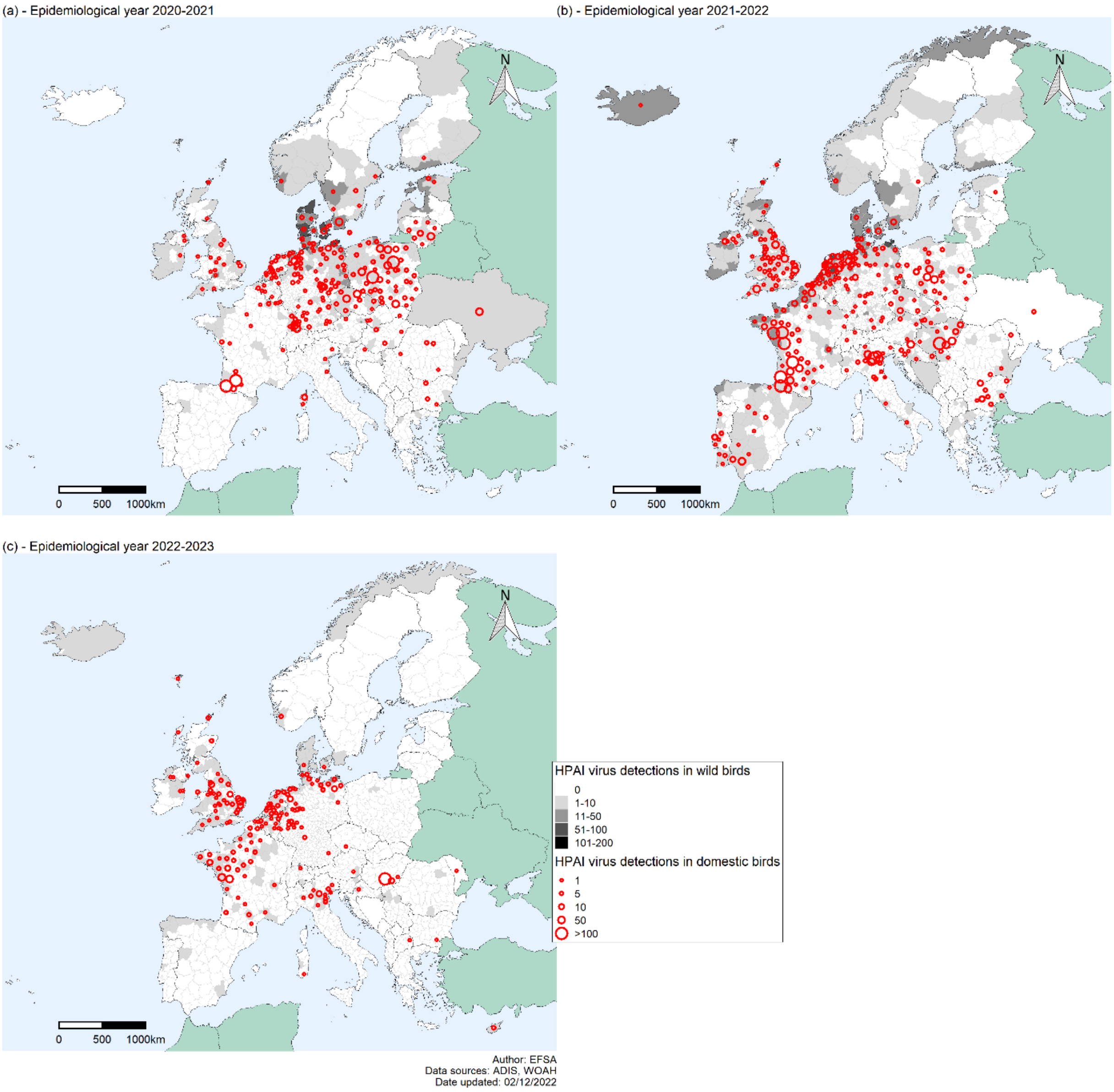
*When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.

United Kingdom data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was the World Animal Health Information System (WOAH-WAHIS) for United Kingdom (excluding Northern Ireland), and ADNS/ADIS for the United Kingdom (Northern Ireland)[4].

Source: ADIS and WOAH (data extraction carried out on 2 December 2022).

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

Figure 2: Distribution of number of HPAI virus detections reported in Europe in the epidemiological years 2016–2017, 2017–2018, 2018–2019, 2019–2020, 2020–2021 and 2021–2022 by month of suspicion in (a) wild birds (8,389) and (a) domestic birds (poultry and captive birds) (6,240), from 1 October 2016 to 2 December 2022



(a) - Epidemiological year 2020-2021

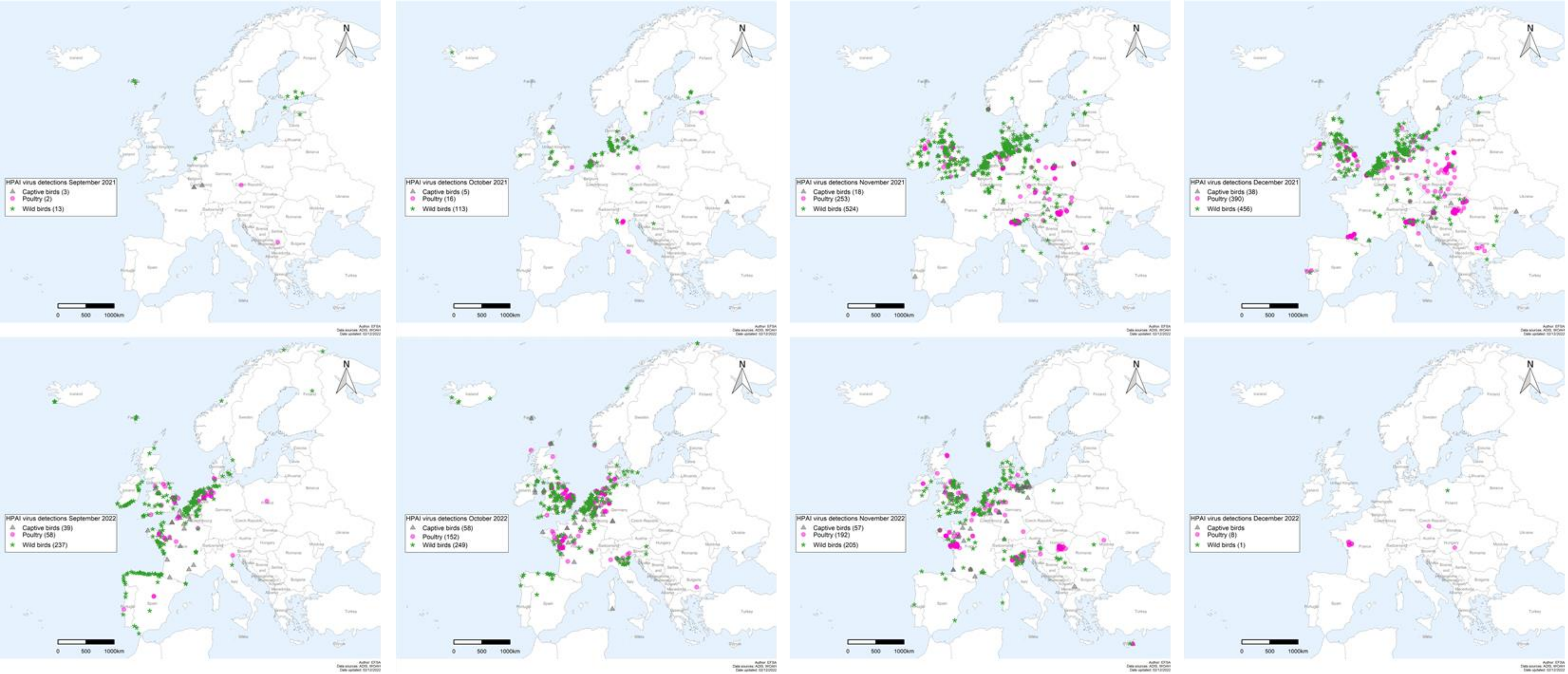
(b) - Epidemiological year 2021-2022

(c) - Epidemiological year 2022-2023

United Kingdom data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was the World Animal Health Information System (WOAH-WAHIS) for United Kingdom (excluding Northern Ireland), and ADNS/ADIS for the United Kingdom (Northern Ireland)[4].

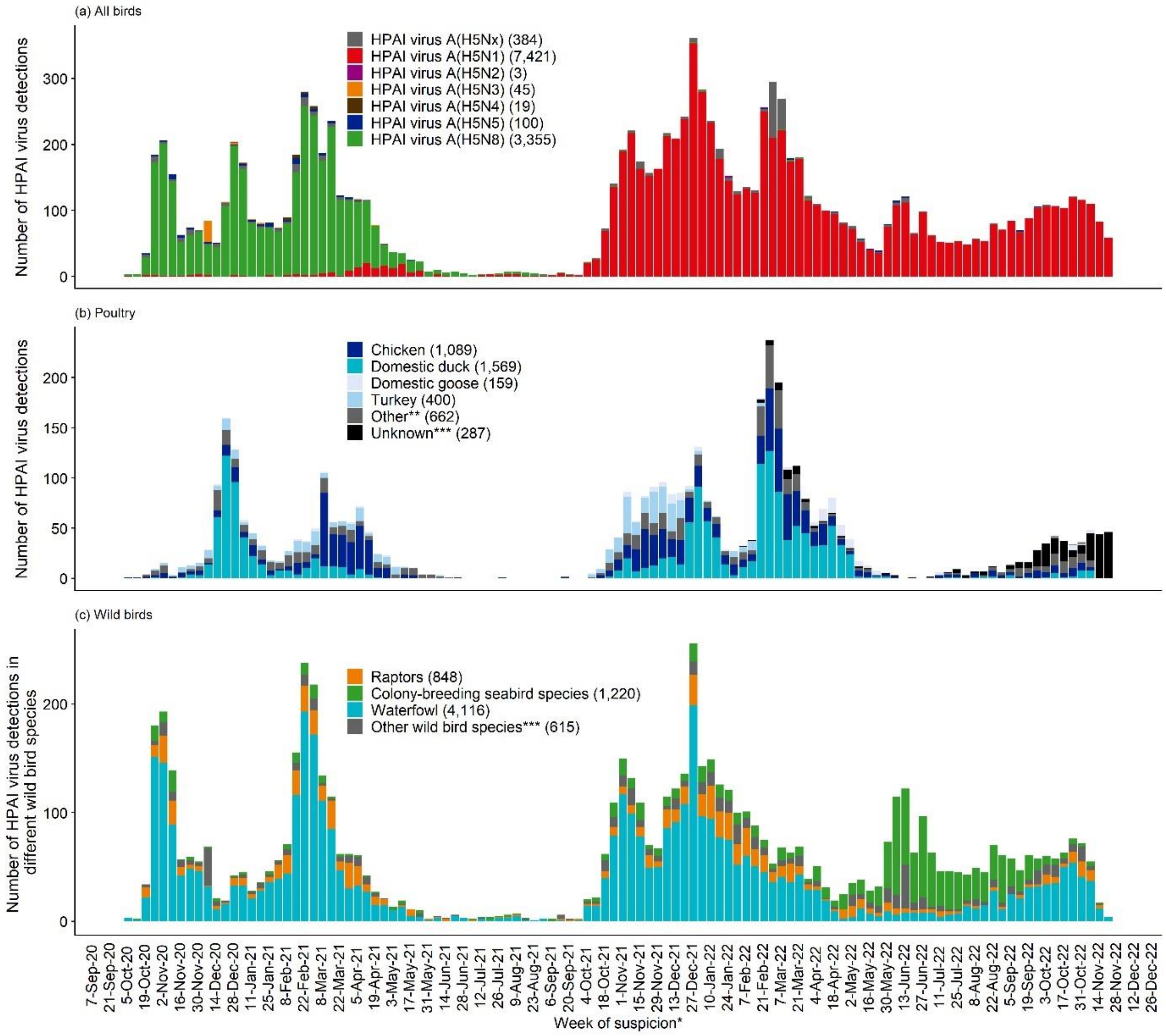
Source: ADIS and WOAH (data extraction carried out on 2 December 2022).

Figure 3: Geographical distribution at NUTS3 level of HPAI detections in Europe in the epidemiological years (a) 2020–2021 (3,791), (b) 2021–2022 (6,614) and (c) 2022 – 2023 (922) in domestic birds (red circles) and wild birds (grey coloured area), from 1 October 2020 to 2 December 2022. An epidemiological year refers to the period starting on 1 October and ending on 30 September of the following year.



One poultry and one captive birds outbreaks reported by France occurred in La Reunion, therefore they are not displayed in the maps. United Kingdom data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was the World Animal Health Information System (WOAH-WAHIS) for United Kingdom (excluding Northern Ireland), and ADNS/ADIS for the United Kingdom (Northern Ireland)[4]. Note that data in December 2022 are up to 2 December. Source: ADIS and WOAH (data extraction carried out on 2 December 2022).

Figure 4: Geographical distribution, based on available geocoordinates, of HPAI virus detections in Europe by month of suspicion from September to December in 2021 (upper row) and 2022 (bottom row)



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

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

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

United Kingdom data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was the World Animal Health Information System (WOAH-WAHIS) for United Kingdom (excluding Northern Ireland), and ADNS/ADIS for the United Kingdom (Northern Ireland)[4].

Source: ADNS, ADIS and WOAH (data extraction carried out on 2 December 2022), EFSA.

Note that the information reported in panel (b) have been collected from the affected countries up to outbreaks occurred by 18 November 2022; the outbreaks that occurred later were too close to the publishing of this report to collect the data, therefore, for those poultry outbreaks the information presented was unknown at the time of publication and will be included in the next report.

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

Figure 5: Distribution of total number of HPAI virus detections reported in Europe by week of suspicion (dates indicate the first day of the week) and (a) virus subtype (11,328), (b) affected poultry categories (4,166), (c) affected wild bird categories (6,799), from October 2020 to 2 December 2022

Table 1: Number of highly pathogenic avian influenza outbreaks in Europe, by country, virus subtype and affected sub-population in the epidemiological year 2021-2022 (from 1 October 2021 to 30 September 2022)

Country	**Captive Birds (227)**		**Poultry (2,520)**				**Wild Birds (3,867)**					**Total**
	A(H5Nx)	**A(H5N1)**	**A(H5N1)**	**A(H5N2)**	**A(H5N8)**	**A(H5Nx)**	**A(H5Nx)**	**A(H5N1)**	**A(H5N2)**	**A(H5N5)**	**A(H5N8)**	
Albania		1			6			1				8
Austria		4						27				31
Belgium		7	7				6	134				154
Bosnia and Herzegovina								1				1
Bulgaria	1	2	16			9	2					30
Croatia			3					13				16
Czechia			19					9				28
Denmark		4	6		1		1	164			2	178
Estonia					1			9				10
Finland								29		1	1	31
France	3	64	1,248			147	5	252				1,719
Germany		10	98				13	1,504	2		1	1,628
Greece								16				16
Hungary		4	290				1	28				323
Iceland			1					32				33
Ireland			6				2	83				91
Italy		1	314			4		23				342
Kosovo[(a)]					3							3
Latvia								2				2
Lithuania								11				11
Luxembourg								5				5
Moldova			4									4
Montenegro								1				1
Netherlands		21	70				38	695			2	826
North Macedonia								3				3
Norway			2				17	42		20		81
Poland			98	1				36				135
Portugal		8	11					12				31
Romania			3				1	15				19
Serbia			3					4				7
Slovakia		2	4				1	6				13
Slovenia		37	1									38
Spain		3	36				4	114				157

Sweden		4	3					79			1	87
Switzerland		2						1				3
Ukraine	2											2
United Kingdom[(b)]		47	105					394			1	547
Total	6	221	2,348	1	11	160	91	3,745	2	21	8	6,614

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

(b): United Kingdom data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was the World Animal Health Information System (WOAH-WAHIS) for United Kingdom (excluding Northern Ireland), and ADNS/ADIS for United Kingdom (Northern Ireland)[4].

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

Source: EFSA, ADNS and WOAH (data extraction carried out on 2 December 2022).

4.2. HPAI and LPAI detections in Europe, 10 September to 2 December 2022 (ToR 1 and ToR 2)

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

From 10 September to 2 December 2022, 1,162 HPAI A(H5) virus detections were notified in poultry (398), captive (151) and wild birds (613) to the ADIS or WOAH- WAHIS, as presented in Table 2. The timelines, virus subtypes, locations and the affected bird categories of the HPAI virus detections are presented in Figures 6, 7 and 8. The reported HPAI virus detections and outbreaks were distributed all over the reporting period and occurred in 16 European countries (Figure 6).

For wild birds, the highest number of HPAI virus reported detections were in the United Kingdom (160 detections), the Netherlands (97), Germany (86), France (62), Belgium (59), Spain (46), Italy (35) and Denmark (20) (Figure 7A and Table 2). Most of the HPAI virus detections were reported in waterbirds (371), followed by colony-breeding seabirds (109). This contrasts with the previous reporting period, when detections in seabirds predominated. This switch probably is associated on the one hand with the post-breeding dispersal of seabirds from their colony sites, and on the other hand with the increased numbers of waterbirds in Europe due to autumn migration. The geographical distribution of HPAI virus detections in wild birds was more limited than in the previous reporting period and was concentrated along the North Sea and Atlantic coasts of continental Europe from Denmark to Spain, as well as the UK and northern Italy. In domestic birds, HPAI virus outbreaks occurred primarily in north-west Europe (Germany, the Netherlands, Belgium, the United Kingdom and France), and were mainly distributed along the Atlantic coastal areas, following the distribution of the HPAI events in wild birds, except for outbreaks in Italy and Hungary. For poultry, Germany, the Netherlands, Belgium, UK and France accounted together for 86% of the reported HPAI outbreaks. In total, 83 poultry outbreaks were notified to the ADIS as secondary mainly in Hungary (64 out of 69 poultry outbreaks), but also in France (10 out of 98) Germany (8 out of 42) and Belgium (1 out of 8).

Overall, 9.8 million birds died or were culled in the HPAI poultry establishments with the UK accounting for 42% of the birds died or culled in the affected establishments during this reporting period, followed by the Netherlands (18%) and France (14%).

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.

HPAI A(H5N1) continues to be by far the predominant virus type reported, with few exceptions for A(H5N5) virus detected in Norway and Finland in wild birds (3) and non-typed HPAI A(H5Nx) in Belgium (1), Bulgaria (1), France (1) and Germany (1) (Table 2).

Since 2 December and as of 16 December 2022, 249 HPAI outbreaks were confirmed in poultry (126), captive (66) and wild birds (57) outside the reporting period for this report in France (99), Germany (74), the Netherlands (19), Hungary (18), Poland (9), Belgium (8), Czechia (5), Denmark (4), Italy (3), Sweden (3), Romania (2), the United Kingdom[6] (2), Luxemburg, Ireland and Switzerland (1 each). Those HPAI outbreaks were too close to the publication date to be described in this report and will be fully reported in the next report.

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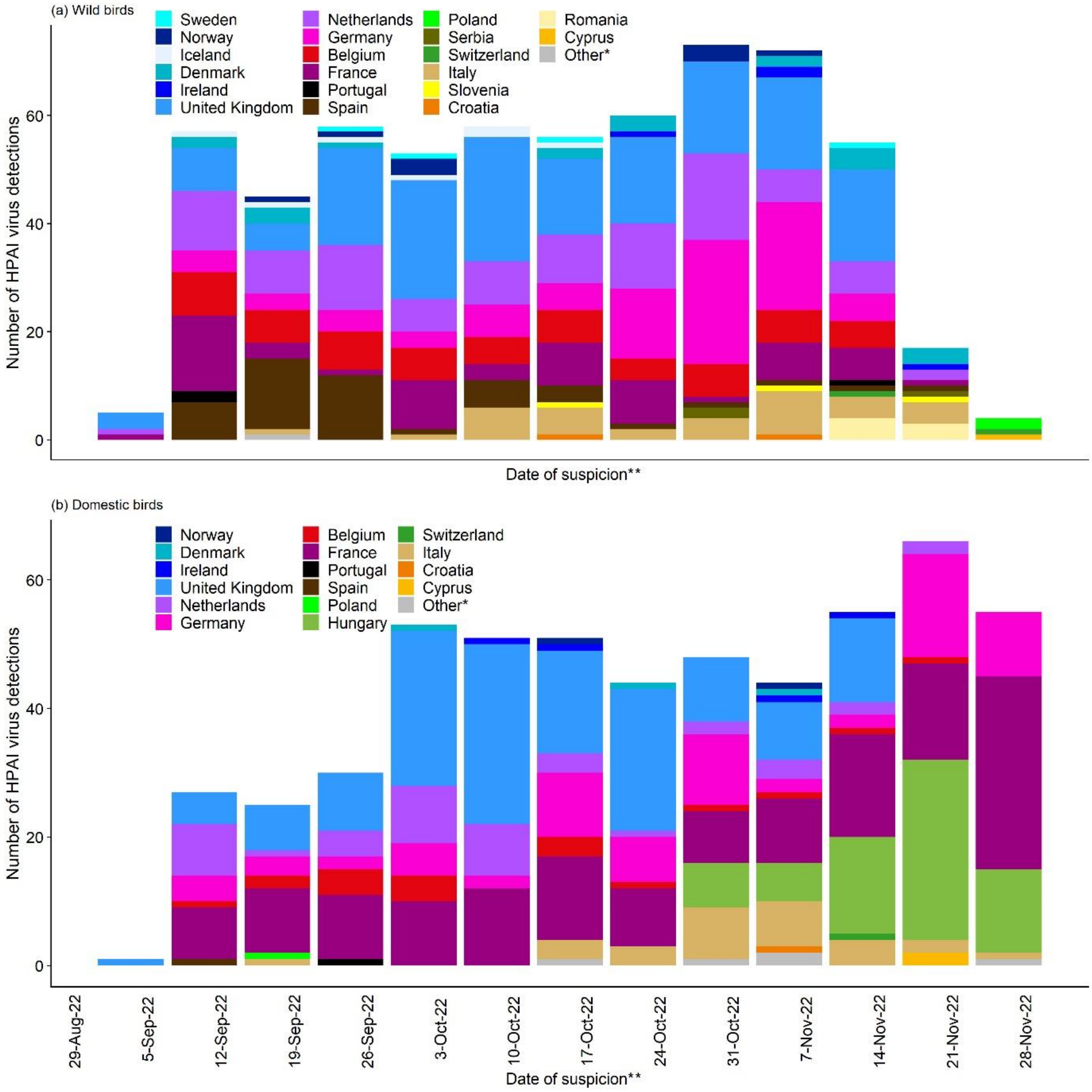
[5] According to Regulation (EU) 2016/429 'establishment' means any premises, structure, or, in the case of open-air farming, any environment or place, where animals or germinal products are kept, on a temporary or permanent basis, except for: (a) households where pet animals are kept; (b) veterinary 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, pp. 1–208.

[6] Only data from United Kingdom (Northern Ireland) from ADIS are included



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

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

United Kingdom data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was the World Animal Health Information System (WOAH-WAHIS) for United Kingdom (excluding Northern Ireland), and ADNS/ADIS for the United Kingdom (Northern Ireland)[4].

Source: EFSA, ADIS and WOAH (data extraction carried out on 2 December 2022).

Note that the scales of the vertical axes are specific to each category of birds.

Figure 6: Distribution of the highly pathogenic avian influenza virus detections in (A) wild birds (613) and (B) outbreaks in domestic birds (poultry and captive birds) (549), in Europe, by day of suspicion and country from 10 September to 2 December 2022

Table 2: Number of highly pathogenic avian influenza outbreaks in Europe, by country, virus subtype and affected sub-population, from 10 September to 2 December 2022. Cumulative numbers since the start of the 2022–2023 epidemiological year are reported in parentheses (1 October 2022 to 2 December 2022).

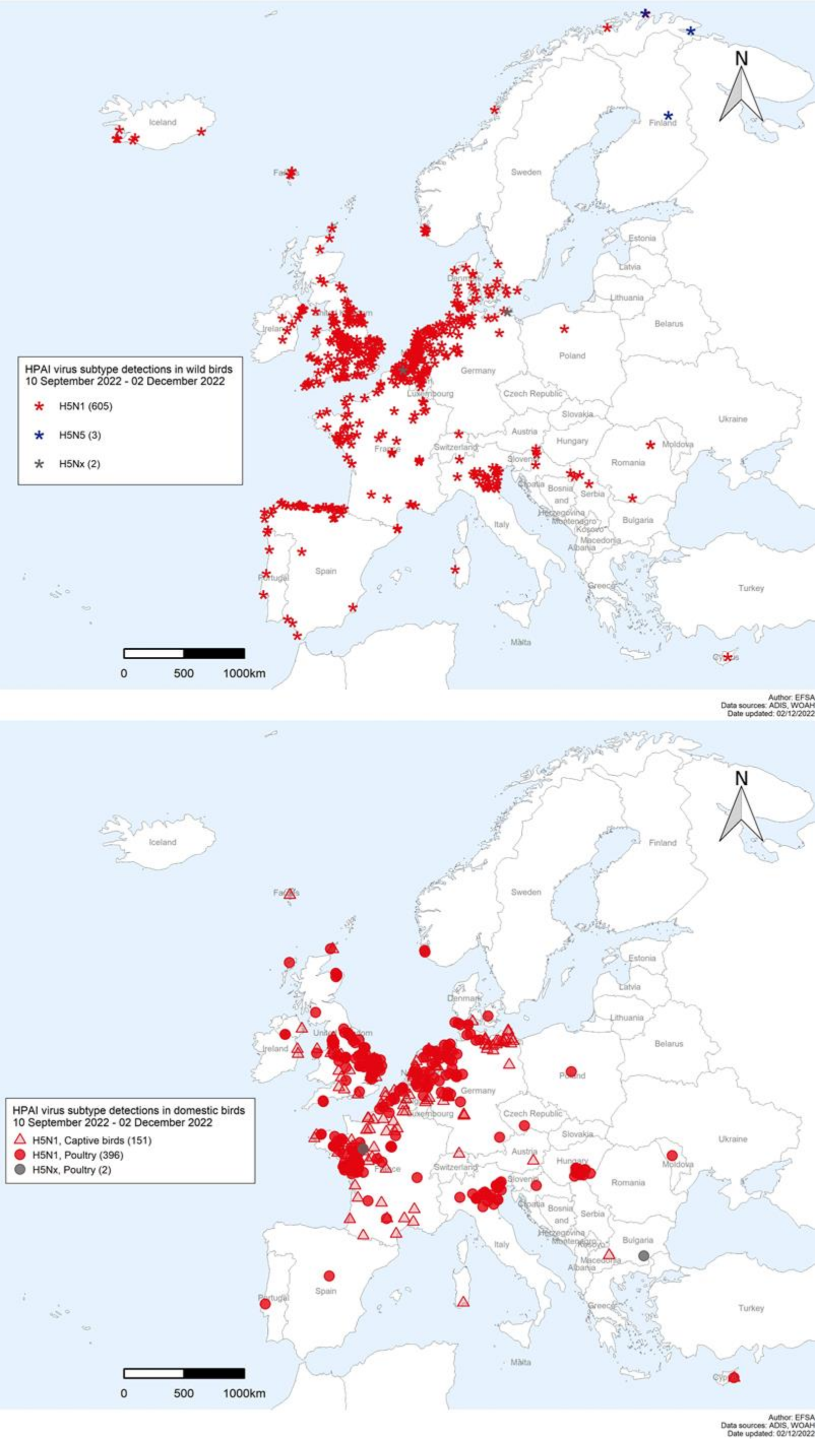
Reporting Country	Captive birds	Poultry		Wild birds			Total
	A(H5N1)	A(H5Nx)	A(H5N1)	A(H5Nx)	A(H5N1)	A(H5N5)	
Austria	1 (1)	-	-	-	-	-	1 (1)
Belgium	11 (8)	-	8 (5)	1 (1)	58 (37)	-	78 (51)
Bulgaria	-	1 (1)	-	-	-	-	1 (1)
Croatia	-	-	1 (1)	-	2 (2)	-	3 (3)
Cyprus	1 (1)	-	1 (1)	-	1 (1)	-	3 (3)
Czechia	-	-	1 (1)	-	-	-	1 (1)
Denmark	2 (2)	-	1 (1)	-	20 (14)	-	23 (17)
Finland	-	-	-	-	-	1	1 (0)
France(a)	52 (33)	1	97 (89)	-	62 (43)	-	212(163)
Germany	32 (31)	-	42 (34)	1 (1)	85 (74)	-	160 (140)
Hungary	-	-	69 (69)	-	-	-	69 (69)
Iceland	-	-	-	-	7 (4)	-	7 (4)
Ireland	2 (2)	-	2 (2)	-	4 (4)	-	8 (8)
Italy	1 (1)	-	28 (27)		35 (34)	-	64 (62)
Moldova	-	-	1 (1)	-	-	-	1 (1)
Netherlands	18 (11)	-	25 (19)	-	97 (67)	-	140 (97)
North Macedonia	1 (1)	-	-	-	-	-	1 (1)
Norway	-	-	2 (2)	-	7 (6)	2 (1)	11 (9)
Poland	-	-	1	-	2 (2)	-	3 (2)
Portugal	-	-	1	-	3 (1)	-	4 (1)
Romania	-	-	-	-	7 (7)	-	7 (7)
Serbia	-	-	-	-	3 (3)	-	3 (3)
Slovenia	-	-	-	-	3 (3)	-	3 (3)
Spain	-	-	1	-	46 (18)	-	47 (18)
Sweden	-	-	-	-	4 (3)	-	4 (3)
Switzerland	1 (1)	-	-	-	2 (2)	-	3 (3)
United Kingdom(b)	29 (23)	-	115 (99)	-	160 (127)	-	304 (249)
Total	151 (115)	2 (1)	396 (351)	2 (2)	608 (452)	3 (1)	1,162 (922)

(a): one poultry and one captive birds outbreaks occurred in La Reunion

(b): United Kingdom data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was the World Animal Health Information System (WOAH-WAHIS) for United Kingdom (excluding Northern Ireland), and ADNS/ADIS for United Kingdom (Northern Ireland)[4].

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

Source: EFSA, ADNS and WOAH (data extraction carried out on 2 December 2022).



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 02/12/2022

Author: EFSA
Data sources: ADIS, WOAH
Date updated: 02/12/2022

One poultry and one captive birds outbreak reported from France were detected in La Reunion, therefore they are not displayed in the above map.

United Kingdom data are from ADNS up to 31 December 2020. From 1 January 2021 onwards, the data source was the World Animal Health Information System (WOAH-WAHIS) for United Kingdom (excluding Northern Ireland), and ADNS/ADIS for United Kingdom (Northern Ireland)[4].

Source: EFSA, ADIS and WOAH (data extraction carried out on 2 December 2022).

Figure 7: Geographical distribution, based on available geocoordinates, of highly pathogenic avian influenza virus detections in wild birds (613) (upper panel) and outbreaks in poultry and captive birds (549) (lower panel) reported by virus subtype in Europe from 10 September to 2 December 2022

4.2.1.1. HPAI in domestic birds

Characterisation of the HPAI-affected poultry establishments

In this section a detailed analysis of the HPAI-affected poultry establishments is presented. Due to the time needed to carry out the data collection, the outbreaks that occurred later than 18 November were too close to the publishing of this report to collect the data, and in many cases, the epidemiological investigations of those outbreaks were still ongoing. Therefore, for those poultry outbreaks some of the information presented in this section was unknown at the time of publication and will be included in the next report.

The information on poultry outbreaks that occurred before the reporting period for this report but too close to the publication of the previous EFSA report (EFSA et al., 2022b), i.e. from 2 to 9 September 2022, are reported in Annex A (they have been collected during this reporting period but are not described in the text of this section).

During this reporting period, from 10 September to 2 December 2022, in total, 398 poultry outbreaks were notified in 18 countries through ADIS or WOAH: 115 in the United Kingdom, 98 in France, 69 in Hungary, 42 in Germany, 28 in Italy, 25 in the Netherlands, 8 in Belgium, two in Ireland and Norway respectively and one each in Bulgaria, Croatia, Cyprus, Czechia, Denmark, Moldova, Poland, Spain and Portugal (Table 2). Overall, 9.8 million birds died or were culled in the affected establishments. The United Kingdom accounted for 29% of the reported outbreaks and 42% of the birds that died or were culled in the HPAI establishments, France accounted for 25% of the reported outbreaks 14% of the birds dead or culled, followed by Germany, 11% and 5% respectively, Italy 7% and 10% respectively, the Netherlands 6% and 18% respectively, Belgium 2% and 5% respectively, Hungary 17% and 4% respectively, (Figure 8).

Compared with the previous reporting period (from 11 June to 9 September 2022), during which 63 outbreaks were notified by eight affected countries, a markable increase of around six times as many outbreaks (398 outbreaks) were notified during this period (Table 3). An increasing trend was also observed between the same reporting periods in 2021-2022, when a lot more outbreaks were reported from 10 September to 2 December 2021 compared to the period from 11 June to 9 September 2021. Also, nearly six times as many cases were reported in the period 11 June to 9 September 2022 compared to the year before (Table 3).

Table 3: Number of highly pathogenic avian influenza outbreaks in poultry in Europe, by reporting period and epidemic season

Epidemic season	**2021-2022**		**2022-2023**	
Reporting period	11 June to 9 September 2021	10 September to 2 December 2021	11 June to 9 September 2022	10 September to 2 December 2022
Number of HPAI poultry outbreaks	10	294	63	398

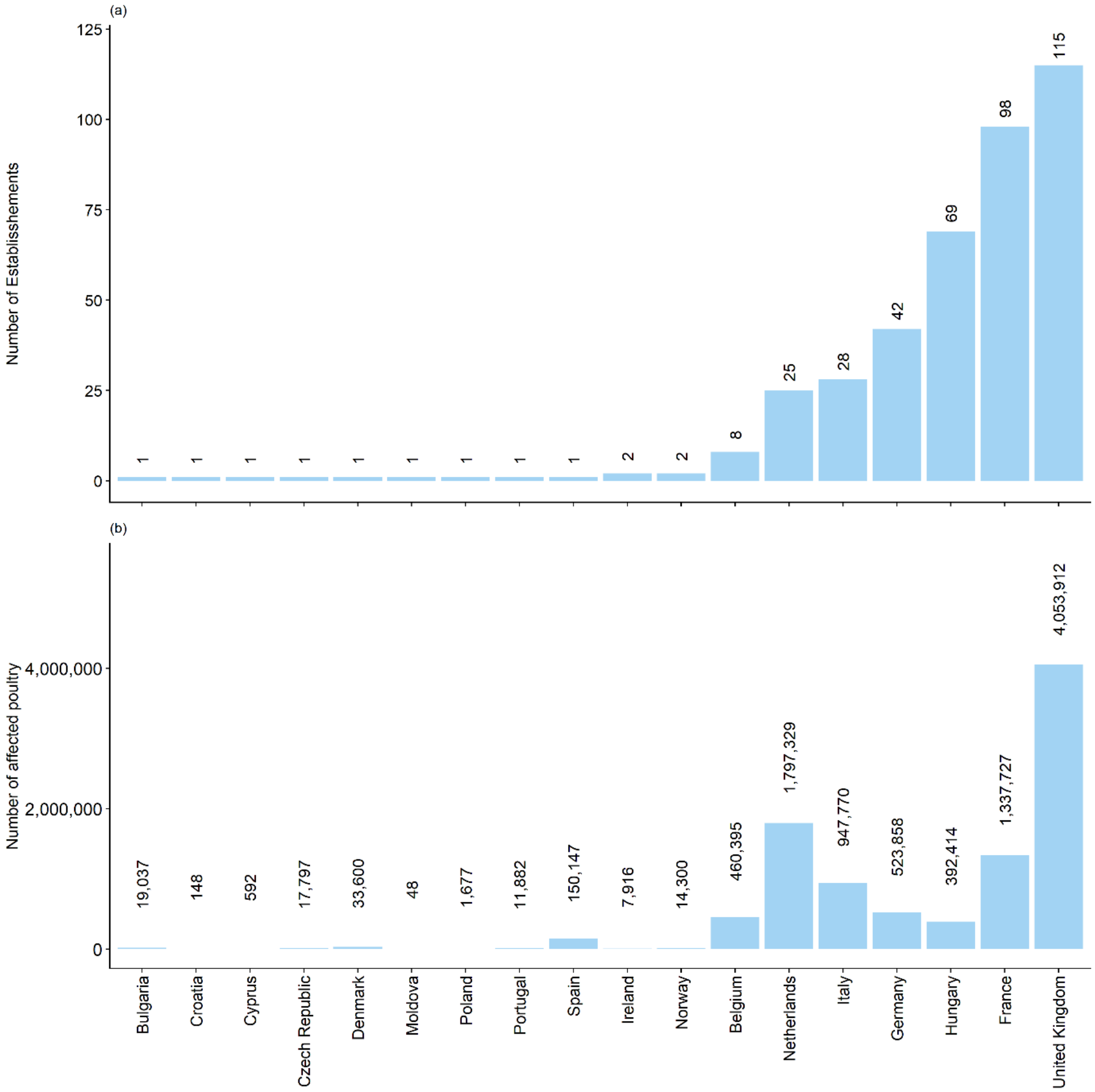
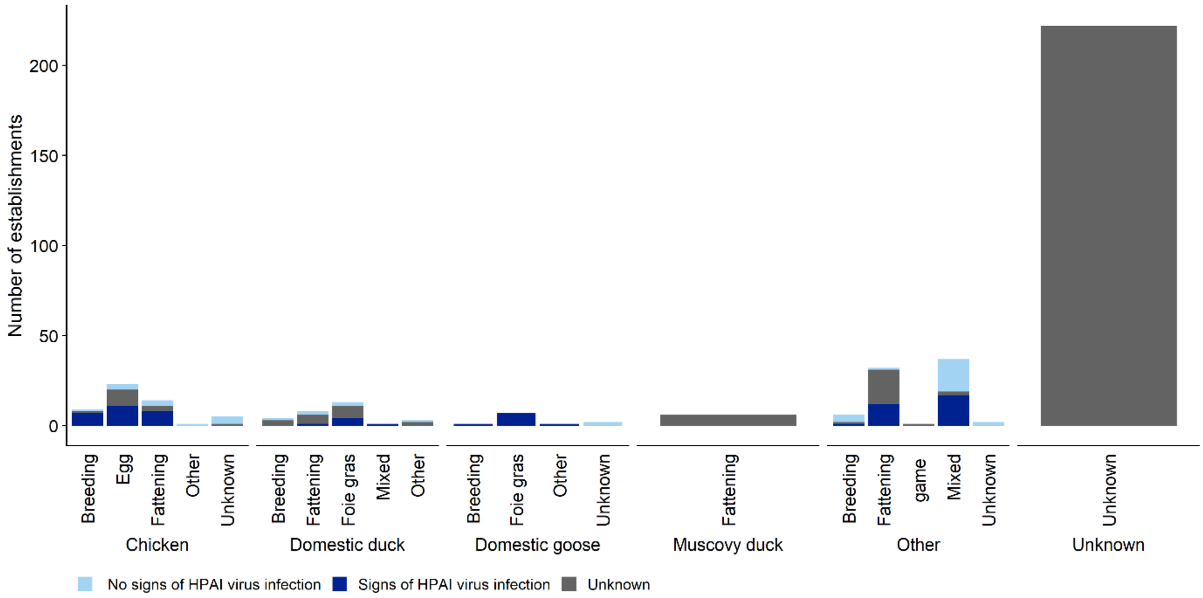


Figure 8: Number of (A) HPAI-affected establishments and (B) number of poultry in the HPAI-affected establishments in Europe between 10 September and 2 December 2022 (398)

Out of 398 outbreaks, 150 were reported in commercial farms, 26 in non-commercial farms and this information was not available at the time of writing this report for 222 establishments. 83 of the outbreaks were secondary outbreaks, 24 in commercial establishments (14 in Hungary, seven in France, two in Germany and one in Belgium) and 4 in non-commercial establishments (in Germany).

Increased mortality, or other types of clinical signs were observed in most of the affected establishments keeping chicken and domestic goose (Figure 9).



'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 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 10 September and 2 December 2022 (398)

HPAI A(H5N1)-affected poultry establishments in Belgium

Between 22 September and 10 November 2022 seven primary and one secondary HPAI A(H5N1) virus outbreaks were reported in Vlaanderen. The affected establishments were commercial farms keeping chickens for breeding (4/7) and egg production (4/7). In none of the establishments the animals had outdoor access. In the primary outbreaks the source of infection was thought to be indirect contact with wild birds and in the secondary outbreak the most likely source was indirect contact with infected poultry because of two outbreaks in the immediate vicinity.

All farms reported increased mortality and three of the four farms keeping laying hens reported clinical signs, while none of the farms keeping chickens for breeding reported no other clinical signs. None of the farms reported a drop in feed and water intake or, where applicable, in egg production.

No data on the number of people exposed to the virus were available at the time of publication of this report. The characteristics of the affected establishments and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Bulgaria

On 21 October 2022 Bulgaria reported one primary HPAI A(H5Nx) virus outbreak in the Haskovo region. The outbreak was on a commercial farm with laying hens without outdoor access. The source of introduction was unknown. No data on observed clinical signs or mortality were available, neither on the number of people exposed to the virus 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 Croatia

On 16 November 2022 one primary HPAI A(H5N1) virus outbreak was notified in the region of Zagreb. The establishment was a non-commercial farm keeping chickens, domestic duck and domestic goose for egg production as well as turkey and peacock. The animals had outdoor access and the most likely source of introduction was direct contact with wild birds since there is a water area in the middle of the affected holding and two dead swans which were found in the area some days before were positive for HPAI A(H5N1). Increased mortality was present in the chickens (except silkie breed) and peacocks. No other clinical signs were present on the farm.

No data on the number of people exposed to the virus were available at the time of publication of this report. The characteristics of the affected establishments and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Denmark

On 9 November 2022 one primary HPAI A(H5N1) virus outbreak was reported in Slagelse. The outbreak was in a commercial farm keeping turkey for fattening without outdoor access. The source of introduction was unknown. Increased mortality, presence of clinical signs and drop in feed and water intake were observed. No data on the number of exposed people was available at the time of publication of this report.

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

HPAI A(H5N1)-affected poultry establishments in France

Between 12 September and 17 November 2022 50 primary and five secondary HPAI A(H5N1) virus outbreaks and one primary HPAI A(H5NX) outbreak was reported. The outbreaks were detected in the following regions: Pays de la Loire (28), Bretagne (10), Nouvelle-Aquitaine (7), Centre-Val de Loire (5), Hauts-de-France (3), Auvergne-Rhône-Alpes (2), Grand Est (1), Île-de-France (1), Normandie (1) and Saint-Paul, La Réunion (1). All outbreaks were in commercial establishments. The type of farmed species were: chicken for egg production (8), chicken for fattening (3), chicken for breeding (1), turkey for fattening (18), turkey for breeding (1), turkey with production type not specified (1), mulard duck for foie gras (7), Muscovy duck for fattening (6) domestic duck for breeding (3), domestic duck for fattening (5), domestic duck for other production type (3) and pheasants for game (1). Two farms kept more than one poultry species: Muscovy ducks for breeding and pheasants and chicken for fattening and domestic guineafowl respectively.

No data on outdoor access, most likely source of introduction, mortality, clinical signs, drop in feed/water intake, egg production or number of exposed people 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 13 September and 15 November 2022 32 primary and six secondary HPAI A(H5N1) virus outbreaks were reported in five regions: Niedersachsen (17), Nordrhein-Westfalen (11), Schleswig-Holstein (8), Bayern (1) and Hessen (1). 24 were commercial farms and 14 were non-commercial. Some establishments were keeping only one species: chicken (10), turkey (7), domestic duck (2) and domestic goose (2); whereas 17 farms kept more than one species, including chicken, domestic goose, domestic duck, domestic pigeon, turkey, pheasant, domestic guineafowl and one species listed as other.

Sixteen establishments had no outdoor access, two had and for the remaining it was unknown. The most likely source of introduction of the virus was indirect contact with wild birds (22), unknown (14), direct contact with poultry because of purchase of animals (5) and direct contact with wild birds (1).

One establishment of domestic ducks detected by outbreak related surveillance showed no mortality or clinical signs in an early stage of infection. Furthermore, a turkey farm without mortality or clinical signs was detected using bucket sampling in a HPAI affected district.

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

HPAI A(H5N1)-affected poultry establishments in Hungary

Between 4 and 17 November 2022 4 primary and 14 secondary outbreaks of HPAI A(H5N1) virus were notified in two regions: Bács-Kiskun (15) and Csongrád-Csanád (3). All establishments were commercial farms keeping domestic goose for foie gras (7), mulard duck for foie gras (6), domestic duck for fattening (2), domestic goose for breeding (1), pheasant for breeding (1) and turkey for fattening (1).

Eight out of the 18 farms had outdoor access. The most likely source of introduction in the primary outbreaks was indirect contact with wild birds and in the secondary outbreaks indirect contact with poultry.

All eight establishments keeping domestic goose reported increased mortality, six reported presence of other clinical signs and two a drop in feed and water intake. Among the establishments keeping mulard duck four (4/6) reported increased mortality, three (3/6) presence of clinical signs and two (2/6) a drop in feed and water intake. The farm keeping pheasant reported increased mortality and presence of clinical signs and the farm keeping turkey reported increased mortality, presence of clinical signs and drop in feed/water intake. None of the two farms keeping domestic ducks reported any signs of disease.

No data on the number of people exposed to the virus were available at the time of publication of this report. The characteristics of the affected establishments and species reared are presented in Annex A.

HPAI A(H5N1)-affected poultry establishments in Ireland

On 14 November and 22 November 2022 two primary HPAI A(H5N1) virus outbreaks were notified in the region of Monaghan. Both establishments were commercial farms keeping turkey for fattening. In one of the establishments the animals had outdoor access. In both outbreaks the most likely source of introduction was indirect contact with wild birds. Both farms reported increased mortality, presence of other clinical signs and a drop in feed and water intake. The total number of exposed people were 37.

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

HPAI A(H5N1)-affected poultry establishments in Italy

Between 23 September and 18 November 2022, 25 primary HPAI A(H5N1) virus outbreaks were notified in Veneto (16), Lombardia (5), Emilia-Romagna (3) and Friuli-Venezia Giulia (1). 15 farms were commercial and ten non-commercial. Nine of the farms kept only chicken for either breeding (2/9), egg production (5/9) or fattening (2/9). Six farms kept only turkey for fattening. Two farms kept only domestic duck for mixed production and domestic goose respectively. The other eight establishments kept more than one poultry species, including chicken (4/8), domestic duck (3/8), domestic goose (3/8), turkey (1/8), domestic guineafowl (1/8) and other species (3/8).

On 15 of the 25 farms the animals had no outdoor access and on ten farms they had outdoor access. The most likely source of infection was indirect contact with wild birds (23/25), direct contact with poultry (1/25) and in one (1/25) establishment it was unknown.

Increased mortality was reported in ten (10/17) of the farms keeping chicken. For two (2/17) farms increased mortality was reported in chicken for egg production but not in those kept for fattening. Four (4/17) reported no increased mortality and for one (1/17) farm it was unknown. All seven farms keeping turkey reported increased mortality. Two farms (2/5) keeping duck reported increased mortality. Two (2/3) farms reported increased mortality in domestic goose and one (1/3) farm reported increased mortality in one of the two species of domestic goose kept on the farm. No increased mortality was reported in the only farm keeping domestic guineafowl. For the species listed as other, no information or unknown was reported for four (4/7), no increase in mortality in two (2/7) and increased mortality for one (1/7).

Presence of other clinical signs were reported in four (4/17) farms keeping chicken and two (2/17) farms reported clinical signs in those kept for egg production but not in those kept for fattening. Three (3/7) turkey farms reported presence of clinical signs. No (0/5) farms keeping domestic duck reported presence of clinical signs. Of the farms keeping domestic goose, one (1/3) reported clinical signs. For the species listed as other, two (2/7) reported presence of clinical signs.

Drop in feed and water intake was reported in two (2/17) farms keeping chicken and in one (1/7) farm keeping turkey. One (1/17) farm keeping chicken reported a drop in egg production.

No data on the number of people exposed to the virus were available at the time of publication of this report. The characteristics of the affected establishments and species reared are presented in Annex A.

HPAI A(H5)-affected poultry establishments in Norway

On 22 October and 12 November 2022 two primary HPAI A(H5N1) virus outbreaks were reported in Rogaland. The affected establishments were commercial farms keeping chicken for breeding and egg production respectively. On neither farm the animals had outdoor access. For the farm keeping chicken for breeding the most likely source of infection was indirect contact with wild birds since the farm is located nearby a wetland area with a dense wild bird population. For the other farm the source of introduction was unknown. The breeding farm reported increased mortality, presence of clinical signs and a decrease in feed and water intake and in egg production while the egg production establishment reported increased mortality and presence of clinical signs. The number of exposed people was 21 for the farm keeping chicken for breeding, for the other farm the number of exposed people was 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(H5)-affected poultry establishments in Moldova

On 14 November 2022 one primary HPAI A(H5N1) virus outbreak was notified in the Teleneşti region. The affected establishment was a non-commercial holding keeping chicken and the animals had outdoor access. The most likely source of infection was direct contact with wild birds. Data related to presence of signs of infection were not available at the time of publishing this report. The number of exposed people was three. The characteristics of the affected establishments and species reared are presented in Annex A.

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

Between 15 September 2022 and 9 November 2022, 22 primary HPAI A (H5N1) outbreaks were notified in the Netherlands in the following regions: Friesland (3), Gelderland (3), Limburg (3), Overijssel (2), Noord- Brabant (2), Zuid-Holland (2) and Drenthe (1). All affected establishments were commercial farms keeping chicken for fattening (7), chickens for breeding (6), laying hens (6), turkey for fattening (2) and domestic duck for fattening. Information about outdoor access was not available at the time of publication. The most likely sources of infection were unknown or the investigation inconclusive for all affected establishments. Presence of clinical signs and drop in feed and water intake was present in all establishments and in all farms keeping laying hens a drop in egg production was reported. In all but two farms increased mortality was reported.

No data on the number of people exposed to the virus were available at the time of publication of this report. The characteristics of the affected establishments and species reared are presented in Annex A.

HPAI A(H5N1) -affected poultry establishments in Poland

On 21 September 2022 one primary HPAI A(H5N1) virus outbreak was notified in Łódzkie. The affected establishment was a commercial farm that kept domestic goose for fattening and chicken for egg production. The animals had outdoor access on the farm and the most likely source of infection was reported to be indirect contact with wild birds.

Increased mortality, presence of clinical signs and drop in feed and water intake was reported in the domestic geese. In the chickens drop in egg production was reported.

The number of exposed people were five.

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

HPAI A(H5N1)-affected poultry establishments in Portugal

On 30 September 2022 one primary HPAI A(H5N1) virus outbreak was notified in the region of Lisbon. The affected establishment was a commercial farm holding turkeys for fattening and the animals had no outdoor access. The source of infection was unknown. The number of exposed people was 18. There was an increased mortality, presence of clinical signs and a decrease in feed intake.

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

HPAI A(H5N1)-affected poultry establishments in Spain

On 17 September one primary HPAI A(H5N1) virus outbreak was reported in the Castilla La Mancha region. The affected establishment was a commercial farm holding laying hens and the animals had no outdoor access. The most likely source of introduction was indirect contact with wild birds due to a river being located nearby. The total number of exposed people was 34. Increased mortality was reported in the farm.

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

Information extracted from the scientific literature

There were four studies relevant for the phenotype of HPAI viruses in poultry in Europe published since the previous EFSA report. Liang et al. (Liang et al., 2022) investigated the pathogenesis and transmission of a HPAI clade 2.3.4.4b A(H5N6) virus infection from 2018 in Denmark in seven-to-nine-week-old ring-necked pheasants (*Phasianus colchicus*) inoculated via the intranasal and intraocular routes, and onward transmission to cohoused six-to-eight-week-old White Leghorn chickens. Clinical signs in infected pheasants ranged from mild to severe neurological signs 24–48 h prior to death or euthanasia. Histopathological changes consisted of necrosis and inflammation in multiple organs colocalised with influenza virus antigen expression. Efficient virus transmission was detected between pheasants over multiple rounds of naïve pheasant introductions and onwards to chickens. Mortality of up to 100% was observed for both infected pheasants and chickens. Intra-species transmission from chicken to chicken was less efficient. The study indicates that game bird premises are at risk of HPAI virus incursion, that these viruses can be maintained within this sector, and that they may subsequently spread to commercial and backyard chickens.

Hayama et al. (2022) estimated the time window from the introduction of HPAI virus into poultry farms using field data from the HPAI A(H5N8) virus outbreak, clade 2.3.4.4b, in the 2020–2021 winter season in Japan. The time window from the introduction of the virus to notification in each farm was estimated at 14.0 days in median (min: 8.6 days, max: 24.1 days) in the deterministic model. In the stochastic model, the upper value of 95% credible interval of the time window ranged from 12 to 34 days, with a median of 21 days. The results suggest that although one to three weeks had elapsed on most farms until notification after the virus introduction, the time window could exceed three weeks. These results provide reliable information for setting up a tracing period for a potential source farm and enhancing the efforts for early detection.

Isoda et al. (2022) investigated the pathogenicity of a major strain of clade 2.3.4.4b HPAI A(H5N1) viruses isolated from wild birds in Japan in winter 2021–2022, which were genetically highly similar to the viruses circulating in Europe. Different virus titres of a representative strain, Crow/Hok, isolated from a crow (presumably *Corvus macrorhynchos*) were intranasally inoculated into 6-week-old chickens. All chickens inoculated with 10^6 or 10^5 EID_{50} died before 4 days post challenge, whereas birds inoculated with $\leq 10^4$ EID_{50} survived for 14 days after the challenge without any apparent clinical manifestations. The median chicken lethal dose of Crow/Hok in 6-week-old chickens was calculated as $10^{4.5}$ EID_{50}, which is similar to that of other HPAI viruses invading Japan in the last decade.

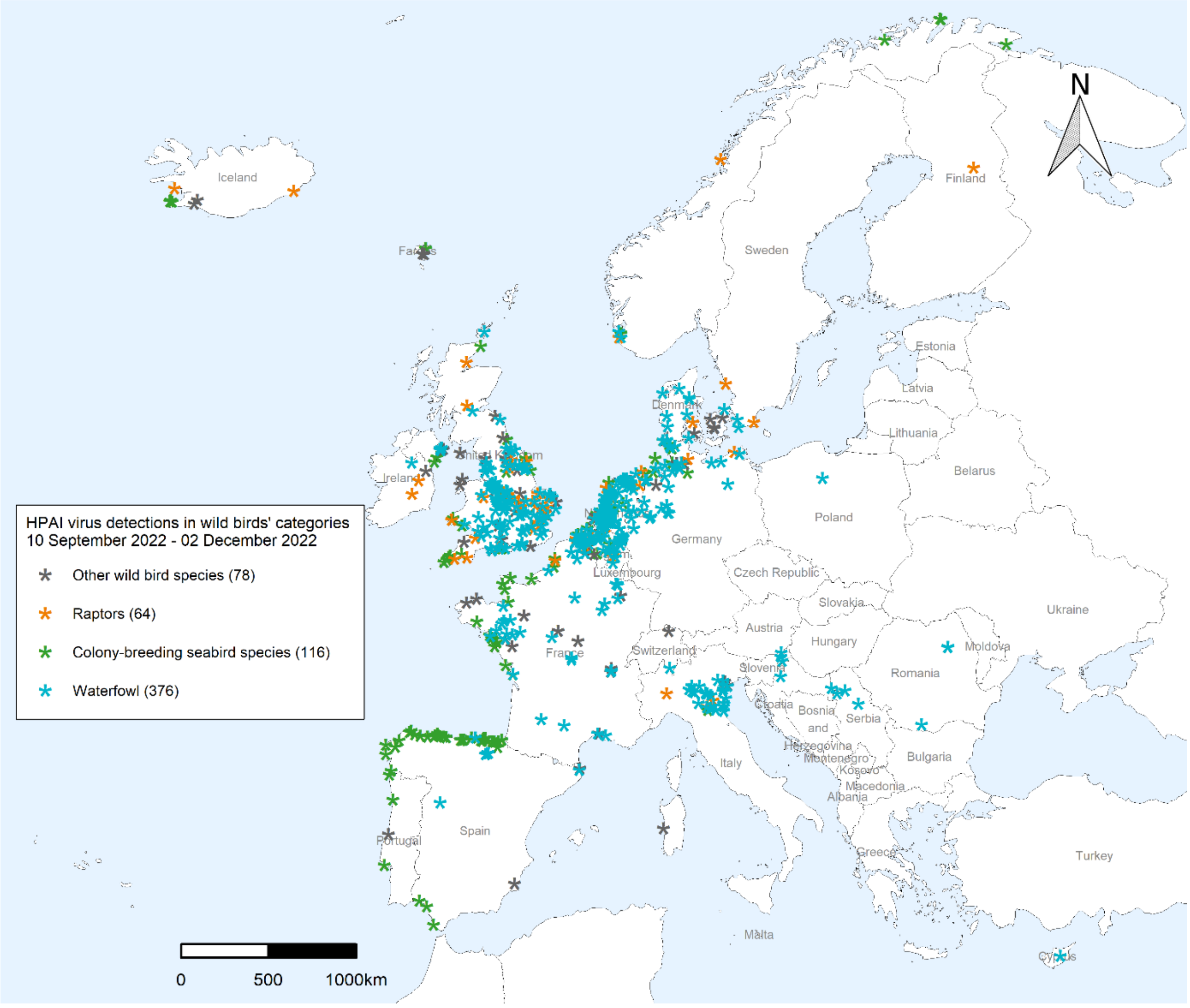
Elsayed et al. (2022) reported that ostriches (*Struthio camelus*) on ostrich farms in Egypt diagnosed with HPAI A(H5N8) virus clade 2.3.4.4b in 2021 showed clinical signs including loss of appetite, drop in production, oculo-nasal discharges, depression, and diarrhea, with different degrees of high mortality. Pathological changes included bleeding from natural orifices and hemorrhage in intestine and trachea. The authors recommend that ostriches should be included in the surveillance of poultry species for HPAI.

4.2.1.2. HPAI in wild birds

Between 10 September and 2 December 2022, 613 HPAI virus detections in sick, dead or hunted wild birds were reported to the ADIS and WOAH by EU/EEA and United Kingdom (Figure 10), which is 73% of the detections in the previous reporting period (from 10 June to 9 September 2022): 844 HPAI virus detections. The HPAI virus detections in wild birds were concentrated in countries bordering the North Sea and the Bay of Biscay: United Kingdom (160), the Netherlands (97), Germany (86), France (62), Belgium (59), and Spain (46) (Table 2). Together, these countries accounted for 82% (502/613) of the detections. In these countries, the detections were predominantly but not exclusively along the sea coasts (Figure 10). The overall geographical range of HPAI virus detections in wild birds extended from the northern tip of Norway to the southern tip of the Iberian Peninsula, and west to Iceland (Figure 10). Locations included the Orkney Islands and Faroe Islands in the north-east Atlantic Ocean. The number of HPAI virus detections in colony-breeding seabirds, predominantly including the orders of Suliformes (64) and Charadriiformes (59) decreased during the course of this reporting period (Figure 11a) and were lower in this reporting period (109) than in the previous reporting period (581) (Table C.1 in Annex C). This is likely due to the post-breeding dispersal of colony-breeding seabirds after their breeding periods in the summer. In contrast, the number of HPAI virus detections in the order of Anseriformes (408) (Figure 11a) was high throughout the reporting period and the number of detections in waterfowl was higher in this reporting period (371) than in the previous reporting period (129) (Table C.1 in Annex

C). This is likely due to the increased number of Anseriformes present in Europe as a result of the autumn migration. Together, Suliformes, Anseriformes and Charadriiformes comprised 79% (531/671) of the HPAI-positive wild bird detected species in the reporting period.

At least 64 wild bird species were involved: at least 18 waterfowl species, 10 colony-breeding seabird species, 12 raptor species, and 24 other wild bird species (Figure 11 and Table C.3 in Annex C). The number of HPAI virus detections was quite similar as in the same period last year (10 September to 2 December 2021), when there were 669 detections (Table C.2 in Annex C). During this reporting period, the main waterfowl species in which HPAI virus was detected were mute swans (117 detections), greylag geese (83), Canada geese (60), and mallards (42); the main colonial seabird species were northern gannets (61), European herring gulls (14), great black-backed gulls and black-headed gulls (11 each); and the main raptor species were European buzzards (29) and peregrine falcons (11).



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 02/12/2022

Source: EFSA, ADIS and WOAH (data extraction carried out on 2 December 2022). Note that in one single detection more than one wild bird species might be involved and each wild bird categories detected as HPAI infected is presented in the map.

Figure 10: Geographical distribution, based on available geocoordinates, of highly pathogenic avian influenza detections in wild birds' categories in Europe, by species category, from 10 September to 2 December2022

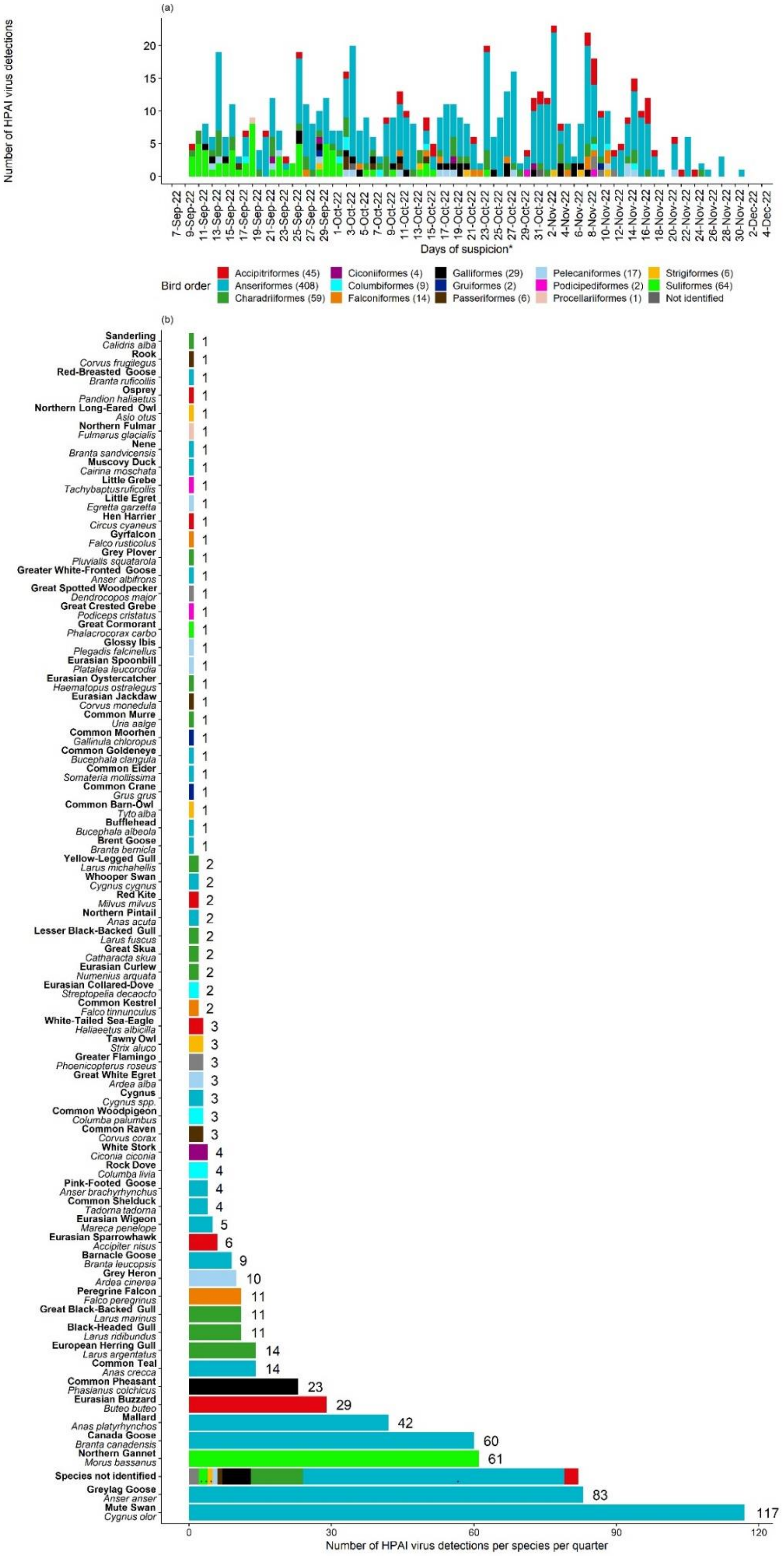


Figure 11: Number of reported detections of highly pathogenic avian influenza virus A(H5) in wild birds by (A) bird order and week of suspicion and (B) wild bird species in the EU/EEA and United Kingdom, from 10 September to 2 December 2022

Information extracted from the scientific literature

There were three studies relevant for the phenotype of HPAI viruses in wild birds in Europe that have been published since the latest EFSA report. Rijks et al. (Rijks et al., 2022) documented the mass mortality in Sandwich terns (*Thalasseus sandvicensis*) during the 2022 breeding season in the Netherlands from HPAI (H5N1) virus clade 2.3.4.4b. In 9 of 10 breeding colonies with mass mortality, 8,001 adult Sandwich terns were found dead out of a total of 18,151 breeding pairs, and only a few chicks fledged. Outside of colonies, another 1,600 adult Sandwich terns were reported dead. Clinical signs in diseased birds included debilitation, lethargy, inability to fly, and opisthotonos. Histopathological changes consisted of necrosis and inflammation in pancreas, duodenum, or lung and nasal tissue, colocalized with influenza virus antigen expression. Like other seabirds, Sandwich terns have low annual reproductive output but relatively long life-expectancy. Therefore, the effect of high adult mortality on population size could be seen for a long time. This mass mortality event exemplifies how severely the continued circulation of HPAI H5N1 viruses in spring 2022 affected populations of colony-breeding birds without flock immunity in Europe.

Fujimoto et al. (2022) diagnosed HPAI H5N8 clade 2.3.4.4b in an adult white-tailed eagle (*Haliaeetus albicilla*) found in Japan in 2021. It showed clinical signs including depression, head shake, and edema in both legs, followed by death. Histopathological examination showed myocardial necrosis throughout the heart and neuronal necrosis throughout the brain, colocalized with influenza viral antigen expression, but no prominent lesions or virus antigen expression in other organs. Comprehensive comparisons of both viral distribution and histopathological observations between experimentally and naturally infected white-tailed eagles imply that viral replication in the brain is responsible for the disease severity and mortality in this species.

Caliendo et al. (2022) inoculated two species of wild ducks—tufted duck (*Aythya fuligula*) and mallard (*Anas platyrhynchos*)—first with 2014 H5N8 HPAI virus and after 9 months with 2016 H5N8 HPAI virus, to test the hypothesis that previous infection with a HPAI virus provides long-term immunity against subsequent infection with another HPAI virus. Both viruses belong to the 2.3.4.4b clade. They found that the previously infected ducks were protected against clinical signs of disease and shed significantly less virus. This finding will help in understanding and potentially predicting the impact that an HPAI virus outbreak may have on wild bird populations, depending on whether they are previously exposed or naive to HPAI virus infections.

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 avian influenza viruses from different regions, and has evolved into several subgroups. While a revised nomenclature of clade 2.3.4.4 viruses is pending, in previous reports we used the genetic clustering described in 2018 by Lee and co-authors, who recognised four groups (a–d) within clade 2.3.4.4 (Lee et al., 2018). Recently, an update to the unified nomenclature for clade 2.3.4.4 A(H5) viruses has been proposed by the WHO (WHO, 2020a) and eight genetic groups (a–h) have been recognised. To align the nomenclature system between international organisations this classification has been adopted for this report. Based on this proposed clustering, A(H5) viruses of clades 2.3.4.4a and d–h have mainly been circulating in poultry in Asia, while clades 2.3.4.4b and 2.3.4.4c have spread globally through wild bird migrations during 2014–2015 (2.3.4.4c) and from 2016 to the present day (2.3.4.4b).

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

A(H5N1) viruses of clade 2.3.4.4b have spread to many countries in Europe, Africa, Asia, and America since their emergence in the Netherlands in October 2020, undergoing multiple reassortment events. In January 2021, an A(H5N1) related to the 2020–2021 European viruses was reported in West Africa and subsequently in South African countries. Since then, it has been persistently circulating in this geographic area, and in West Africa it has reassorted with the A(H9N2) subtype of the zoonotic G1 lineage. From late 2021, different clade 2.3.4.4b A(H5N1) genotypes, one of them previously identified in Europe, have been detected in South and East Asia, including China. In December 2021, the A(H5N1) clade 2.3.4.4b strongly related to the A(H5N1) identified in Northern Europe during the 2020-2021 epidemic season was introduced in North America. At the beginning of 2022, a new introduction in North America from the Pacific flyway of an A(H5N1) related to the viruses circulating in Japan was identified (Alkie et al., 2022). Since then the virus has spread all over North America undergoing reassortment events with LPAI viruses of the American lineages (Alkie et al., 2022). In October 2022, A(H5N1) viruses spread for the first time to Mexico and soon after to South America, including Peru, Colombia, Ecuador and Venezuela, with mass mortality events reported in wild birds (BBC, online) and detections in poultry farms. The characterized viruses belong to clade 2.3.4.4b first detected in January 2022 in the Atlantic coast of North America (ProMed, online-a) and have been described as reassortant viruses between the Eurasian and American lineages (WOAH, 2022).

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

All the genetically characterised HPAI viruses collected since October 2020 in Europe fall within clade 2.3.4.4b. In the current reporting period (September-December 2022) sequences have been generated from viruses collected in nine EU Member States, Norway and in the United Kingdom (available in GISAID on 6 December, provided by the National Reference Laboratories (NRL) or generated by the EURL). Overall, a total of eleven distinct genotypes have been identified among the characterized viruses collected over the period considered, eight of which were detected for the first time. However, the majority of the viruses belongs to a single genotype, which has been circulating in Europe since autumn 2021, indicating a persistent circulation of these viruses in Europe from the 2021-2022 epidemiological year. All the new genotypes identified seem to have evolved through local reassortment events with viruses circulating in the European wild bird population, and each genotype has been identified in one or few viruses in a single country.

The partial genome sequences of a HPAI avian influenza A(H5N1) virus collected in September 2022 from virus detected in an asymptomatic poultry worker in Spain, likely originating from an environmental contamination and not an active replication of the virus in the human host, was genetically characterised. The virus clusters with the viruses collected from infected laying hens in the farm where the person was working and involved in the culling activity. No mutation previously described as associated to increased zoonotic potential has been observed in the viral genome detected in this worker.

In October 2022, an A(H5N1) outbreak in a mink farm was reported in Spain. The virus responsible of this outbreak belongs to a genotype generated through reassortment events for the PA, NP and NS gene segments with the gull-adapted H13 subtype. This genotype has been circulating since May 2022 in wild birds (mainly European herring gulls) in Northern Europe and has caused a poultry outbreak and a case in a fox (*Vulpes vulpes*) during the summer in Belgium. Of note, the characterized viruses from mink carry an amino acid mutation in the PB2 protein that has been previously demonstrated to enhance the polymerase activity of influenza A viruses in mammalian host cells and mice (Bussey et al., 2010). Workers of the mink farm have been tested and no detection of avian influenza virus in humans related to this outbreak in mink has been identified.

To date, few mutations recognised as being associated with mammalian adaptation have been identified in the analysed viruses from avian species collected since October 2020, as previously reported (EFSA et al., 2021) and most of them have only been sporadically detected. In the A(H5N1) viruses from this reporting period, a mutation in the HA protein associated with increased binding to human-type receptors was identified in all the analysed viruses (S137A, H3 numbering) (Yang et al., 2007). Mutations associated with increased resistance to antiviral drugs were observed in the neuraminidase or ion channel proteins of few of the circulating A(H5N1) viruses.

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

Since 10 September as of 18 November 2022, data from six countries (Ireland, Norway, Moldova, Poland, Portugal and Spain) have been reported on the total number of people exposed to infected birds (e.g. during culling activities). In total, 118 exposed people[7] were reported.

During the period covered by this report, avian influenza A(H5N1) virus, as currently detected in wild birds and poultry in Europe, has been detected in two poultry workers in Spain, which were the first human cases related to avian influenza A(H5) viruses reported in the EU/EEA (Table 4). Spanish Authorities reported that two poultry workers involved in culling and cleaning activities exposed to contaminated environment tested positive for A(H5N1) virus on 27 September and 13 October 2022, respectively, following an outbreak on a poultry farm in Guadalajara, in Castilla-La Mancha region, Spain, (ECDC, 2022a, b; Sanidad, 2022; WHO, online-a). Other farm workers involved in the outbreak at the same farm tested negative. Close contacts were followed up and all tested negative, providing evidence that there was no human-to-human transmission. According to the Spanish authorities, the low viral load detected, the absence of clinical symptoms and the absence of serological evidence indicates that both detections were probably due to an environmental contamination and not an active replication of the virus in the human host.

Earlier human infections with A(H5N1) or A(H5N8) viruses of clade 2.3.4.4b were reported since 2021, in the US, the United Kingdom, Russia and Nigeria, all related to outbreaks in poultry or wild birds (Table 4) (Pyankova et al., 2021; WHO, 2021c; CDC, online-c). There are no sequence data available yet from the recently reported human case of A(H5N1) virus infection in China. Sequence data from A(H5N1) viruses detected in China in birds and shared through GISAID have shown that the HA genes of the viruses belong to clade 2.3.4.4b and cluster with viruses collected in Europe, Africa and other Asian countries since 2020, however, the other gene segments indicate a high genetic variability among the circulating viruses in China and differ in at least one gene segment from European viruses. Further analyses are needed to when the genome sequence of the human case will become available.

So far, information from these human A(H5) cases suggest limited evidence of systemic infection and rather amplification of low-level virus RNA following exposure to contaminated environment and infected birds during culling activities (Table 4). Spanish authorities consider these findings the result of an environmental contamination and not an active replication of the virus in the human hosts. This is also reflected in the low virus load in the tested specimens resulting in high Ct values in the initial PCR tests at the detection limit of the assay, the inability to generate full length genomes, the lack of virus cultivation and inconclusive or negative serological findings.

Table 4: Details about human infections with avian influenza A(H5Nx) virus clade 2.3.4.4b related to viruses circulating in Europe, 2021–2022

Date reported	Country (cases, subtype)	Exposure	Symptom	Confirmation
27 Sept, 13 Oct 2022	Spain (2; H5N1) same farm	Culling, cleaning and disinfection	Asymptomatic	PCR, partial sequencing, no virus culture, high Ct Values (>35), no serological evidence (preliminary data)
Apr 2022	USA (1; H5N1)	Culling	Fatigue	PCR, no sequencing or culture possible
Jan 2022	UK (1; H5N1)	Raised birds, “lived with”	Asymptomatic	PCR, reproduced on two successive swabs following days; no serological response identified (UKHSA personal communication)
Apr 2021	Nigeria (3(7); H5) related to H5N1 poultry outbreak	Culling	Asymptomatic	7 type A positive, 3 H5 positive PCR, no full sequencing or culture
Feb 2021	Russia (7; H5N8)	Culling	Asymptomatic	7 PCR, 1 isolated, 4 pos focus reduction neutralisation assay (FRNA) serum titres, 1 4-fold in sample 14d after (1:20), decreased titre 44d after; 5 samples positive for IgG biolayer interferometry

Sources: (Pyankova et al., 2021; WHO, 2021a, e; ECDC, 2022b, a; Sanidad, 2022; CDC, online-e; GovUK, online-b, c; WHO, online-f, a, c)

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

Other transmission events to different mammal species have been increasingly reported as mentioned in this report and in previous reports (Table 5). So far foxes had been majorly found to be infected with avian influenza viruses of clade 2.3.4.4b and displayed neurological signs leading to death or were already found dead. An outbreak of A(H5N1) in a mink farm with increased mortality among the animals also indicates mink-to-mink transmission with spread across the farm through animal contact but also likely through aerosol after possible introduction of the virus through infected wild birds to the open-housed farm (Galicia, online). All workers on this farm were tested negative for influenza. During the summer period 2022, also likely seal-to-seal transmission accompanied with seal mortality due to avian influenza A(H5N1) viruses were observed in the USA (Puryear et al., 2022). Although seals have been found infected with A(H5N1) viruses in Europe as well, such transmission event between the same mammal species has not been reported so far.

A study on currently circulating A(H5N1) viruses in North America showed that these viruses are able to replicate efficiently in human respiratory tract cell types and that in ferret infection and transmission studies, animals got infected but showed only very mild symptoms mostly limited to upper respiratory tract and viruses did not transmit to other ferrets kept in a direct-contact setting (Pulit-Penaloza et al., 2022). Supporting also the previously issued risk assessment using the Influenza Risk Assessment Tool (IRAT) of the United States Centers for Disease Control and Prevention (US CDC) that placed the risk of clade 2.3.4.4b viruses in the low-to-moderate category and issued a Health and Alert Notification message about ‘Recommendations for Human Health Investigations and Response’ (CDC, online-d, f, c, a). The risk of the A(H5N1) clade 2.3.4.4b viruses currently circulating in the United States bird and poultry populations, and which are closely related to European viruses, were assessed by the United States CDC to be of low risk for human health in the general population and higher for people occupationally or recreationally exposed to birds (CDC, online-b). The WHO assessed the risk related to the recent (H5N1) human cases as low for the general public and low to moderate for occupationally exposed people (WHO, online-a). A joint EFSA, ECDC, EURL publication from 2021 already described the threat to humans with the objective to raise awareness among clinicians in the EU around zoonotic avian influenza virus infection and consider testing (Adlhoch et al., 2021).

The UKHSA assesses that ‘at present there are no indicators of increasing risk to human health’ with a low confidence (GovUK, online-c). The WHO assessed the risk associated with A(H5N6) virus as low (CDC, online-b). The WHO issued a risk assessment on the increase in human cases due to A(H5N6) virus infections in 2021 and recommended remaining vigilant about zoonotic infections and to share unsubtypable influenza A viruses from human infections with the WHO Collaborating Centres (CDC, online-d).

Table 5: **Table 5:** Avian influenza A(H5Nx) virus detections in mammal species other than humans related to circulating viruses worldwide, 2016–2022

Virus	**Animal (order, family, species)**			**Country**	**Epidemic season**	**Reference**
A(H5N8) clade 2.3.4.4b	Artiodactyla	*Suidae*	Domestic pigs (*Sus scrofa*), serological detection	France	December 2016	(Herve et al., 2021)
			Wild boar, serological detection	Germany	2017	(Schülein et al., 2021)
	Carnivora	*Phocidae*	Grey seals (*Halichoerus grypus*)	Poland, United Kingdom, Sweden	November 2016; 2020-2021	(Shin et al., 2019; Floyd et al., 2021; SVA, online-b; personal communication by Siamak Zohari, SVA)
			Harbour seals (*Phoca vitulina*)	Germany, United Kingdom; Denmark	December 2020	(Floyd et al., 2021; Ärzteblatt, online; Avian Flu Diary, online-b; Outbreak News, online; SSI, online)
		Canidae	Red foxes (*Vulpes vulpes*)	United Kingdom,	December 2020	(Floyd et al., 2021)
A(H5N1) clade 2.3.4.4b	Carnivora	*Canidae*	Red foxes (*Vulpes vulpes*)	Sweden; Netherlands; Finland; Estonia; Ireland; Belgium; Norway; Japan; USA; Canada	2020-2021; 2021-2022; 2022-2023	(SVA, online-b; WOAH, online-a,b; USDA, online, personal communication by Siamak Zohari, SVA; Irish National Reference Laboratory for Avian Influenza, personal communication)
			Common raccoon dog (*Nyctereutes procyonoides*)	Japan	2021-2022	(WOAH, online-b)
			Coyote (*Canis latrans*)	USA	2021-2022	(WOAH, online-b)
		Mustelidae	Eurasian otter (*Lutra lutra*)	Netherlands; Finland	2021-2022	(WUR, online)
			European badger (*Meles meles)*	Netherlands	2021-2022	(WUR, online)
			European polecat (*Mustela putorius*)	Netherlands	2021-2022	(WUR, online)
			Ferret (*Mustela furo*)	Slovenia	2021-2022	(Slovenian National Reference Laboratory for Avian Influenza, personal communication)
			American mink (*Neovison vison*)	Canada, Spain	2021-2022; 2022-2023	(Galicia, online; WOAH, online-b)
		Felidae	Lynx (*Lynx lynx*)	Finland	2021-2022	(FFA, online)
			Bobcat (*Lynx rufus*)	USA	2021-2022	(WOAH, online-b)
			Fisher cat (*Pekania pennanti*)	USA	2021-2022	(WOAH, online-b)

			Amur leopard (*Panthera pardus*)	USA	2021-2022	(USDA, online)
		Procyonidae	Raccoon (*Procyon lotor*)	USA	2021-2022	(WOAH, online-b)
		Mephitidae	Skunks (*Mephitis mephitis*)	Canada; USA	2021-2022; 2022-2023	(CTV News, online; USDA, online; WOAH, online-b)
		Phocidae	Grey seals (*Halichoerus grypus*)	USA; Canada	2021-2022	(AMMI, 2022; WOAH, online-b)
			Harbour seals (*Phoca vitulina*)	USA; Canada	2021-2022	(WOAH, online-b)
		Ursidae	American black bear (*Ursus americanus*)	Canada USA	2021-2022; 2022-2023	(Healthy Wildlife, online; KTOO, online; WOAH, online-b)
			Brown bear (*Ursus arctos*)	USA	2022-2023	(Kiniradio, online)
	Artiodactyla	*Suidae*	Domestic pigs (*Sus scrofa*), serological detection[a]	Italy	2021-2022	EURL
	Didelphimorphia	*Dedelphidae*	Virginia opossum (*Didelphis virginiana*)	USA	2021-2022; 2022-2023	(USDA, online; WOAH, online-b)
	Cetacea	*Phocoenidae*	Porpoise (*Phocoena phocoena*)	Sweden	2021-2022	(SVA, online-a)
		Delphinidae	Bottlenose dolphin (*Tursiops truncatus*)	USA	2021-2022	(UFHealth, online; WOAH, online-b)
			White-sided dolphin (*Lagenorhynchus acutus*)	Canada	2022-2023	(Avian Flu Diary, online-a)

(a) Serological detection in a HPAI outbreak in a backyard poultry

4.4. Prevention and control measures applied in Europe, 3 September to 18 November 2022 (ToR 3)

The description of the control and prevention measures applied in the affected Member States on HPAI outbreaks occurred from 3 September to 18 November 2022 is presented in Annex B, thanks to the countries that were willing to collaborate with EFSA and kindly provided the information reported here. Outbreaks that occurred before 3 September 2022 have been described in the previous EFSA report (EFSA et al., 2022b).

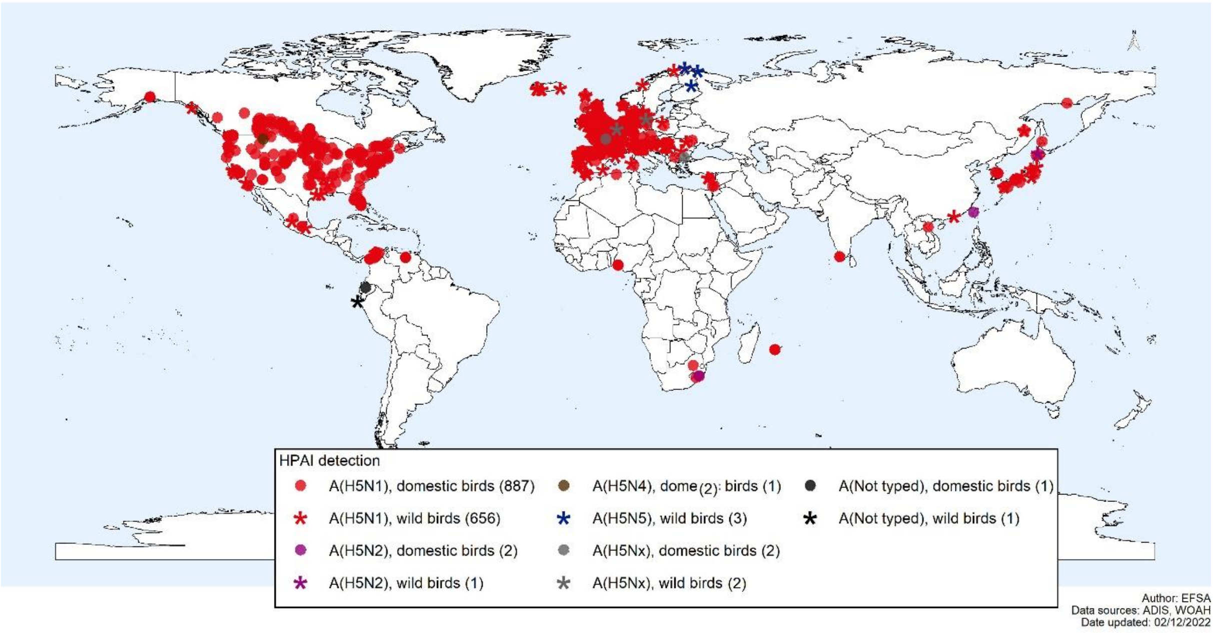
4.5. The avian influenza situation in other countries not reporting via ADIS, 10 September to 2 December 2022 (ToR 4)

An overview of the HPAI detections notified from other countries not reporting via ADIS but via the WOAH or national authorities from 10 September to 2 December 2022 is presented in Table 6 and Figure 12. 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 6: Number of HPAI detections in non-European countries, by virus subtype and country, from 10 September to 2 December 2022

Region	**Country**	**Domestic birds (344)**				**Wild birds (50)**			**Total**
		A(H5N1)	**A(H5N2)**	**A(H5N4)**	**A(Not typed)**	**A(H5N1)**	**A(H5N2)**	**A(Not typed)**	
Africa (14)	Algeria	1							1
	Nigeria	7							7
	Reunion	2							2
	South Africa	3	1						4
Americas (320)	Canada	93							93
	Colombia	18				1			19
	Ecuador				1				1
	Mexico	4				2			6
	Peru							1	1
	United States of America	188		1		10			199
	Venezuela	1							1
Asia (55)	Chinese Taipei		1						1
	Hong Kong					2			2
	India	2							2
	Israel	2							2
	Japan	12				31	1		44
	Korea (Rep. of)	3							3
	Vietnam	1							1
Europe (5)	Russia	3				2			5
Total		340	2	1	1	48	1	1	394

Source: WOAH-WAHIS (data extraction carried out on 2 December 2022).



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 02/12/2022

Figure 12: Geographical distribution, based on available geocoordinates, of highly pathogenic avian influenza virus detections reported in domestic birds (893) and wild birds (663) by virus type, from 10 September to 2 December 2022

4.5.1. Avian influenza A(H3N8)

4.5.1.1. Human infections with A(H3N8)

No new cases have been reported due to infection with A(H3N8) since the last report (EFSA et al., 2022a). Two human infections with avian influenza A(H3N8) reassortant virus were reported for the first time in a 4-year-old child with critical conditions in April 2022 (WHO, 2022b) and a 5-year-old child in May 2022, both in China (The Government of the Hong Kong Special Administrative Region Press Releases, 2022b). Both children had been exposed to live poultry before the onset of symptoms. A preliminary FAO/WOAH/WHO Joint Rapid Risk Assessment ranks the risk for A(H3N8) as low for human health (FAO, 2022).

4.5.2. HPAI A(H5)

4.5.2.1. Human infections with A(H5)

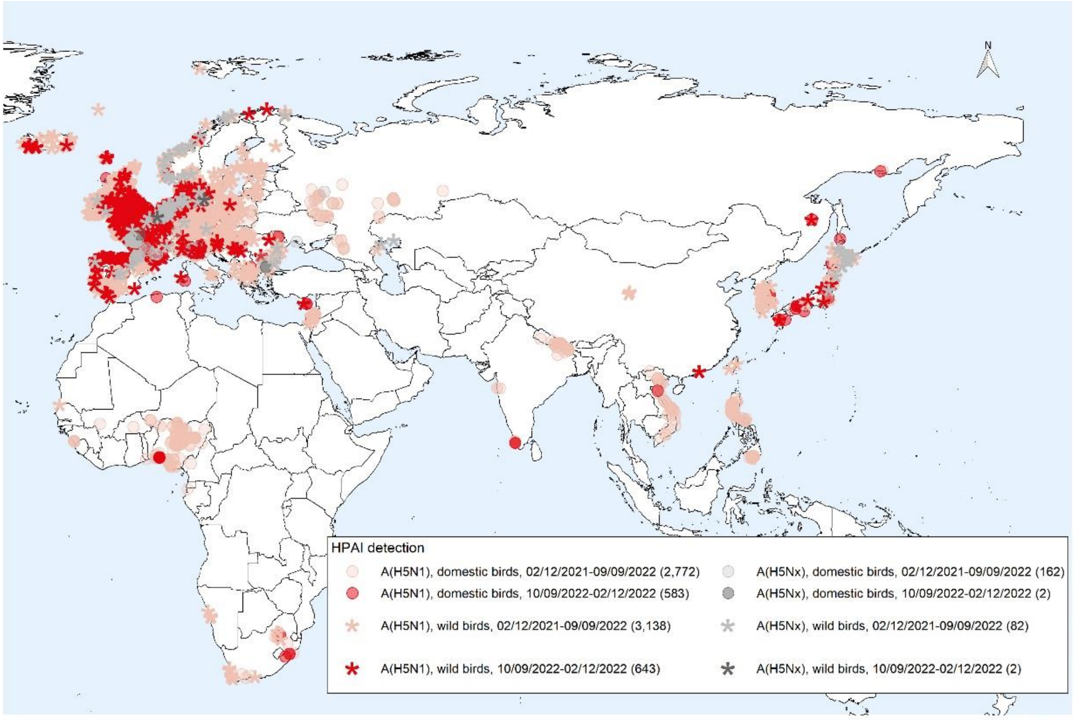
In October 2022, a human infection with avian influenza A(H5) without NA-type was reported in Vietnam in a five-year-old girl from Phu Tho, the first case of avian influenza in Vietnam since 2014 (WHO, 2022a; VNExpress, online). The girl developed symptoms on 5 October 2022 and was hospitalised in critical condition on 7 October 2022. Prior to symptoms' onset she had exposure to sick poultry and other domestic birds. All of the 65 identified contacts tested negative for influenza A(H5).

4.5.3. HPAI A(H5N1)

4.5.3.1. Domestic birds and wild animals

Detections

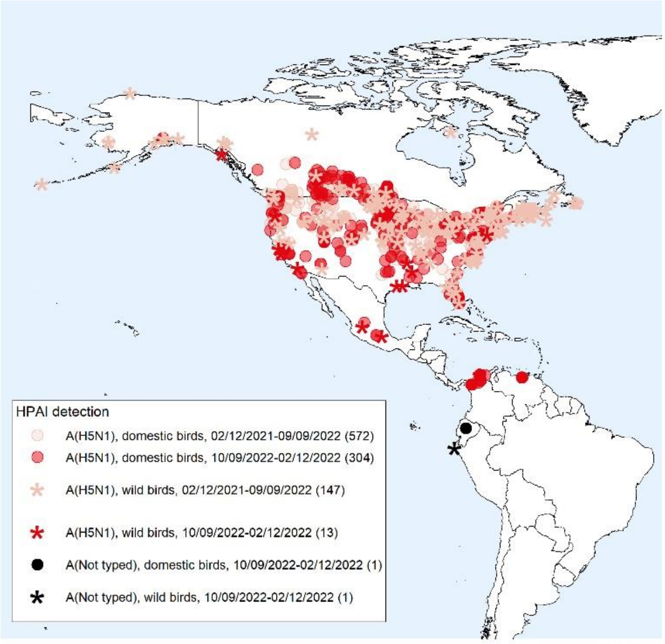
Outbreaks of HPAI A(H5N1) in Africa were detected on poultry farms in previously affected regions (Nigeria, South Africa), but also the first time ever on the island Reunion in the Indian Ocean and returned to Algeria after 18 months of absence (Figure 13). Furthermore, South Africa detected the Eurasian lineage serotype HPAI A(H5N2) on a medium-sized poultry farm in the long-time affected province KwaZulu-Natal. Contrary to the last report, no wild bird cases from Africa were reported to the WOAH. Although the number of outbreaks in Asia has slightly decreased compared to the last report (68 vs 55), the number of countries has doubled (6 vs 3). India, Israel, Korea and Vietnam detected HPAI A(H5N1) on several poultry farms of medium size during the current reporting period. Japan notified several cases in wild birds of various species (e.g., northern pintail, greater white-fronted goose, hooded crane, white-naped crane, peregrine falcon) to the WOAH in addition to outbreaks in poultry farms of all sizes. Furthermore, a black-faced spoonbill and an undetermined wild bird were tested positive for HPAI A(H5N1) in Hongkong. Russia reported outbreaks of HPAI A(H5N1) and HPAI A(H5Nx) in poultry farms and in wild birds (e.g., rock dove, corvids) from eastern provinces neighbouring the Pacific Ocean (Figure 13). The outbreak in Canada and the USA continues with a large number of HPAI A(H5N1) cases on farms of all sizes and one HPAI A(H5N4) case in previously affected regions (Figure 14). Furthermore, several wild bird species were affected, for example blue-winged teal, Canada goose, cackling goose, Forster's tern, black-crowned night heron, glossy ibisn and western gull. In addition, the USA detected HPAI A(H5N1) virus in several mammal species, the red fox (*Vulpes vulpes*), striped skunk (*Mephitis mephitis*), Virginia opossum (*Didelphis virginiana*) and American black bear (*Ursus americanus*) (Table 5). For the first time ever, the Eurasian lineage of HPAI A(H5N1) spread to Central and South America. First reports from Colombia of outbreaks in backyard poultry farms and wild birds (e.g. helmeted guineafowl, yellow-crowned amazon, scarlet macaw) in a wildlife reserve were reported to WOAH in October 2022. In the following month Mexico detected HPAI A(H5N1) in captive birds (e.g. mallards, snow goose, northern goshawk, Cooper's hawk) and several wild waterfowl (mallards and lesser scaup). In Ecuador, an outbreak with HPAI A(H5Nx) was reported in a commercial laying hen farm on 28 November 2022. On the coasts of Venezuela, Peru, and Chile thousands of Peruvian pelicans, in which HPAI A(H5N1) was detectable, have died since the beginning of November (ProMed, online-a, b; Tribune, online) (Figure 14).



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 02/12/2022

Red and dark grey symbols indicate outbreaks that occurred between 10 September and 2 December 2022, light red and light grey symbols indicate outbreaks that occurred between 2 December 2021 and 9 September 2022.

Figure 13: Geographical distribution, based on available geocoordinates, of HPAI A(H5N1) and A(H5Nx) virus detections reported in domestic birds (circles) and wild birds (stars) (7,384)



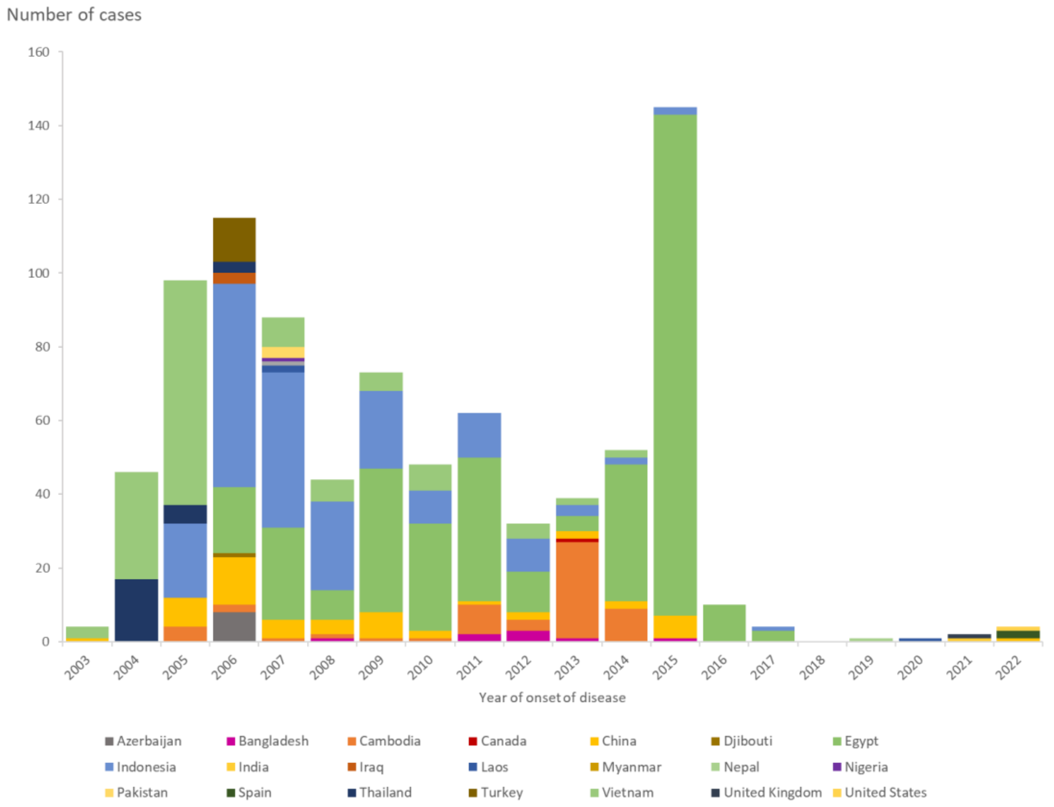
Author: EFSA
Data sources: ADIS, WOAH
Date updated: 02/12/2022

Red symbols indicate outbreaks that occurred between 10 September and 2 December 2022, light red symbols indicate outbreaks that occurred between 2 December 2021 and 9 September 2022.

Figure 14: Geographical distribution, based on available geocoordinates, of HPAI A(H5N1) and A(H5Nx) virus detections reported in domestic birds (circles) and wild birds (stars) (1,038)

4.5.3.2. Human infections due to A(H5N1)

Three new detections of avian influenza A(H5N1) have been reported in two poultry workers in Spain and one lethal case in China over the reporting period (ECDC, 2022b, a; Sanidad, 2022; WHO, 2022a, online-a). In 2022, two detections in people involved in culling operations were reported in September and October from Spain, both people were asymptomatic and were tested as routine surveillance following a confirmation of an influenza A(H5N1) outbreak in one commercial poultry facility. One lethal case was reported from China in October with severe pneumonia and exposure history to culling sick chicken (WHO, 2022a; CHP, online). Since 2003, and as of 17 November 2022, 867 laboratory-confirmed cases of human infection with avian influenza A(H5N1) virus, including 456 deaths, have been reported from 21 countries, including one EU country (Spain) (ECDC, 2022b, a; WHO, 2022a) (WHO, 2022b) (Figure 15).



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

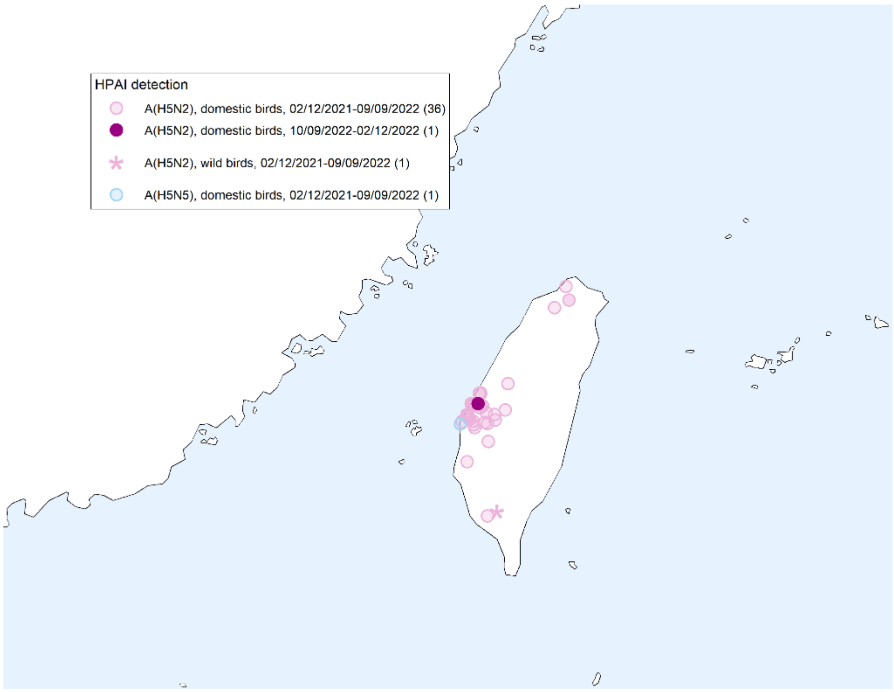
Figure 15: Distribution of confirmed human cases of A(H5N1) by year and country of reporting, 2003 to 28 November 2022 (868)

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

4.5.4.1. Domestic and wild birds

Detections

In the current reporting period, Taiwan reported no new outbreaks of the Taiwanese lineage HPAI A(H5N5) to the WOAH. However, one outbreak of the Taiwanese lineage HPAI A(H5N2) in a backyard poultry farm were detected in October 2022. 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. As in the previous reporting period, no wild bird cases were reported between 10 September and 2 December 2022 (Figure 16).



Author: EFSA
Data sources: ADIS, WOAH
Date updated: 02/12/2022

Purple symbols indicate HPAI A(H5N2) virus detections between 10 September and 2 December 2022, light purple symbols indicate HPAI A(H5N2) virus detections between 2 December 2021 and 9 September 2022, light blue symbols indicate HPAI A(H5N5) virus detections between 2 December 2021 and 9 September 2022.

Figure 16: Geographical distribution, based on available geocoordinates, of HPAI A(H5N2) and HPAI A(H5N5) virus detections reported in domestic birds (circles) and wild birds (stars) in Taiwan (38)

4.5.5. HPAI A(H5N6)

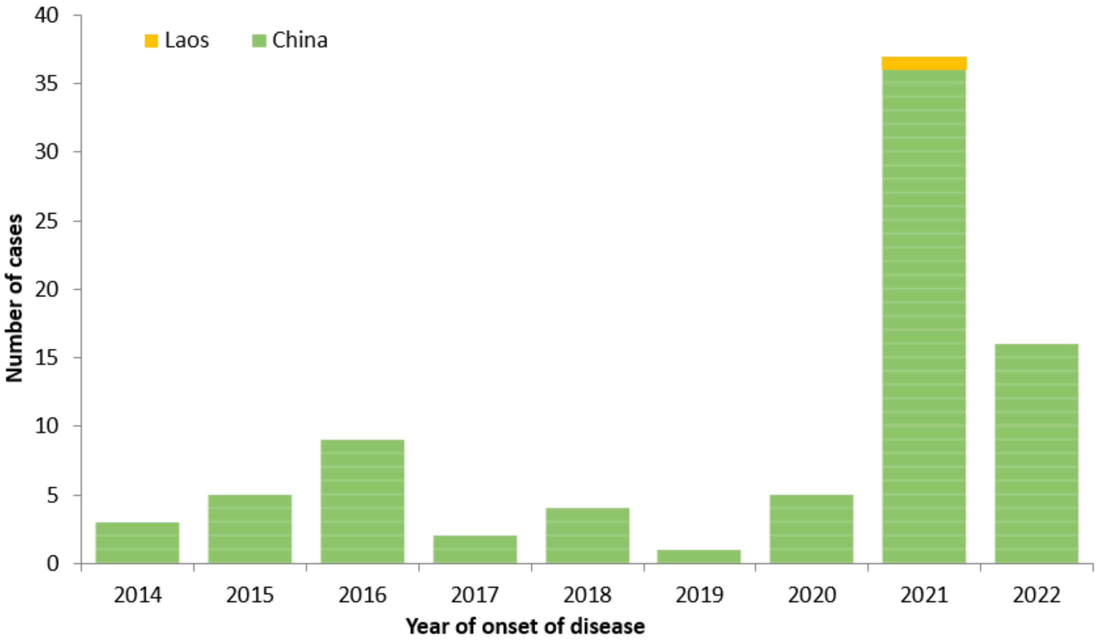
4.5.5.1. Domestic and wild birds

Detections

No new outbreaks of the zoonotic reassortment of HPAI A(H5N6) clade 2.3.4.4c were detected within the relevant time period for this report. New human cases of A(H5N6) from China in the current reporting period might suggest underreporting of poultry outbreaks in the Asian region.

4.5.5.2. Human infections due to A(H5N6)

One new patient infected with avian influenza A(H5N6) and hospitalised with severe pneumonia following exposure to backyard poultry has been reported from China since the last EFSA report (WHO, 2022a, c). Since 2014, and as of 17 November 2022, 82 laboratory-confirmed human infections with avian influenza A(H5N6) viruses have been reported from China (81 cases) and Laos (1), 33 of the patients died (CHP, 2022a) (Figure 17). Twelve of these 33 deaths due to A(H5N6) had been reported between 2014 and 2017 (Jiang et al., 2017) and at least 17 deaths occurred in the most recent period 2018–2021 (ECDC line list; please refer to Appendix B.2). A household cluster with two infections was observed in a couple preparing a duck purchased from a live-bird market for meal (The Government of the Hong Kong Special Administrative Region Press Releases, 2022a; BNO, online; GovMO, online). The overall case fatality ratio of A(H5N6) in humans is estimated to be 42% (limitation: case reports might not have been a complete or lacking updated information).



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

Figure 17: Number of human cases due to A(H5N6) infection by year of onset, 2014 to 28 November 2022 (N = 82)

4.5.6. HPAI A(H5N8)

4.5.6.1. Domestic and wild birds

Detections

No outbreaks of HPAI A(H5N8) in poultry or wild birds were notified outside Europe between 10 September and 2 December 2022.

4.5.7. HPAI–LPAI A(H7N9)

4.5.7.1. Domestic and wild birds

Detection

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

4.5.7.2. Human infections due to A(H7N9)

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

4.5.8. LPAI A(H9N2)

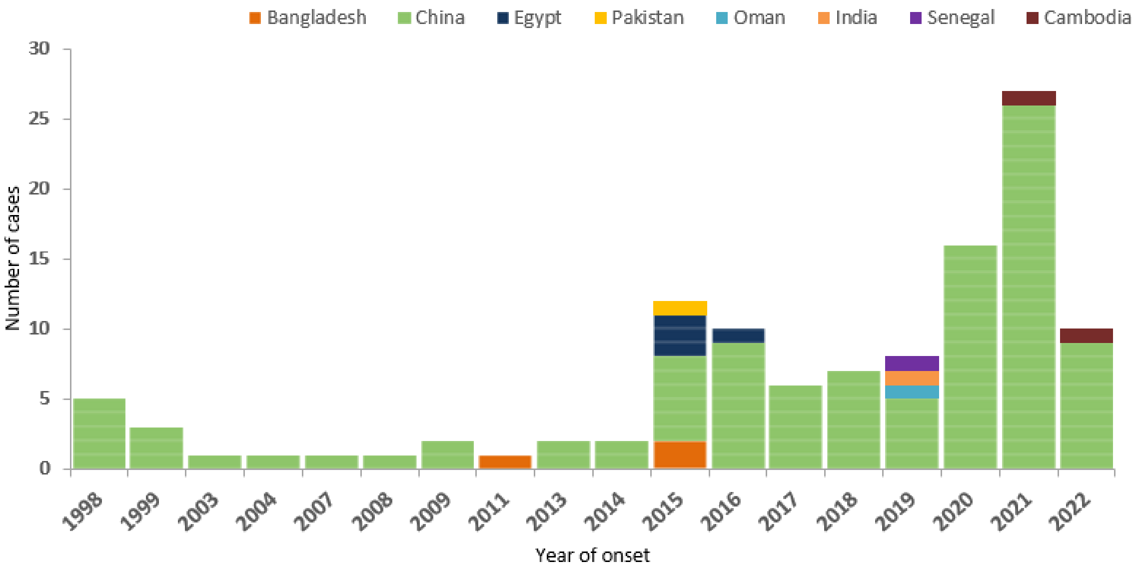
4.5.8.1. Domestic and wild birds

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 2 December 2022.

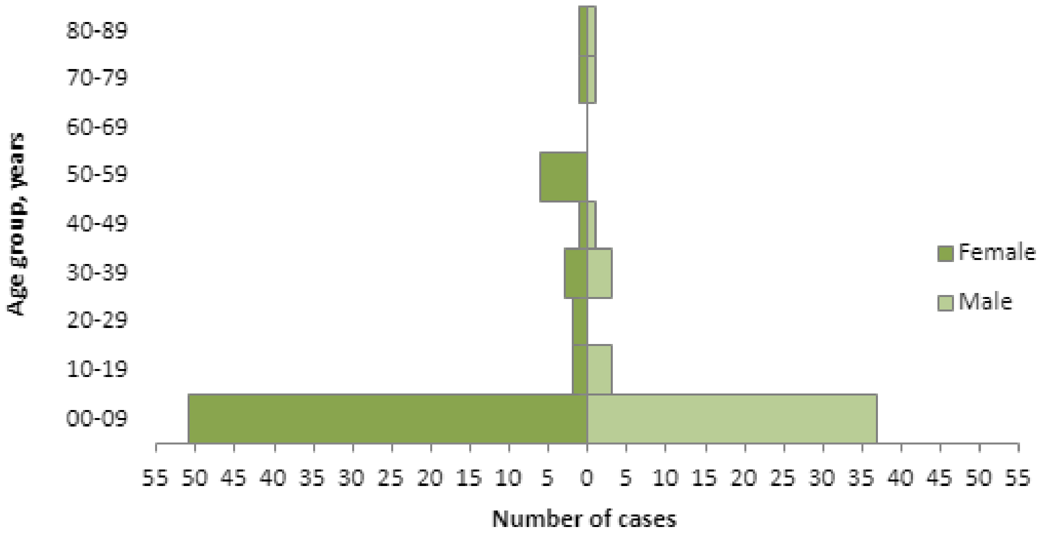
4.5.8.2. Human infections due to A(H9N2)

One new case of human infection with avian influenza A(H9N2) has been reported in China since the previous report (CHP, 2022b; WHO, 2022a). Since 1998, and as of 17 November 2022, 115 laboratory-confirmed human infections with avian influenza A(H9N2) virus, including two deaths, have been reported globally. Infections were reported from China (101), Egypt (4), Bangladesh (3), Cambodia (2), India (1), Oman (1), Pakistan (1) and Senegal (1) (ECDC line list; please refer to Appendix B.2) (Figure 18). Exposure to live or slaughtered poultry or contaminated environment has been reported. The age group mostly affected by A(H9N2) infections in humans was children under 10 years of age, who developed mild symptoms (WHO, 2020c; CHP, 2021b; ECDC, 2021a) (ECDC line list; please refer to Appendix B.2) (Figure 19).



Source: ECDC line list.

Figure 18: Distribution of confirmed human cases of A(H9N2) by reporting country, 1998 to 28 November 2022 (115)



Source: ECDC line list.

Figure 19: and sex distribution of confirmed human cases of A(H9N2) by age group, 1998 to 28 November 2022 (115)

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

No new detections of any avian influenza A(H10) virus in humans have been reported during this reporting period. In June 2021, the first human case of A(H10N3) was detected in China (NHCGovCN, online). China reported a second infection in 2022. Both patients were adults between 30 to 45 years of age with unknown exposure to birds or poultry. To date, there were three people infected with influenza A(H10N8) between November 2013 and February 2014, two of whom died (Parry, 2014; GovHK, online). Both adults were above 55 years of age in China and reported exposure to live poultry/poultry market before onset of symptoms.

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

Since Autumn 2021, HPAI A(H5N1) virus subtype has been circulating in wild birds in Europe, indicating a persistent circulation of this virus in Europe. In the 2021–2022 epidemiological year, the high infection pressure due to the sustained circulation of the virus in the wild reservoir resulted in frequent introductions of the virus into domestic bird populations across Europe. In several countries (e.g., France, Italy, Hungary), devastating epidemics occurred in areas with high poultry densities due to the rapid spread of the infection between poultry establishments.

The epidemic observed in the 2021–2022 HPAI epidemiological year in Europe was the largest in history, involving 37 countries and with a total of 2,520 HPAI outbreaks in poultry and 50 million birds culled in the affected establishments, 227 detections in captive birds, and 3,867 detections in wild birds. The overall number of detections was 1.7 times higher than in the 2020–2021 epidemiological year, and 2.4 times higher than in the 2016–2017 epidemiological year.

A novel aspect of the 2021—2022 epidemic was the extensive spread of HPAI to colony-breeding seabirds (Figure 5C). This has resulted in high mortality rates and purported population-level effects in some species (Wille et al. 2022) documented confirmed or probable cases of HPAI affecting seabirds inhabiting geographic areas extending latitudinally from Alaska to South Africa, including approximately 19 seabird species in the EU and 16 in Canada. Reports include high mortality among breeding colonies of Caspian Terns in the US, Great Skuas in Scotland, Sandwich Terns in the Netherlands and Northern Gannets and Common Murres in Canada and in the UK. Regarding the link between wild birds and poultry, it is pertinent that the shape of the epidemic curve in poultry in 2021–2022 resembled that in waterfowl, but not that in seabirds (Figure 5C). This suggests that waterfowl are more involved than seabirds in the incursion of HPAI virus into poultry establishments, likely because the habitat of waterfowl is more likely to overlap with the location of poultry establishments than seabird colony sites.

In the current reporting period, from 10 September to 2 December 2022, primary HPAI outbreaks due to direct or indirect contact with infected wild birds frequently occurred in poultry in several European countries (e.g., France, Germany, Italy, The Netherlands) without an extensive secondary spread of the virus. Indeed, these countries reported, until now, only a limited number of secondary infections, whereas various secondary HPAI outbreaks were detected in commercial poultry in Hungary. Primary outbreaks were often identified in farms without outdoor access and poultry production systems (e.g., breeders) with high biosecurity standards were also affected.

The biosecurity measures implemented along the poultry production chain did not seem effective in preventing all introductions of the HPAI A(H5N1) virus into poultry farms, especially in some poultry production systems (e.g., ducks, turkeys, and layers). In this situation, there is a high risk of serious epidemics in densely populated poultry areas. To mitigate the risk of further spread of the infection, adequate early detection and rapid control of HPAI outbreaks should be ensured.

The patterns of HPAI virus introduction into the different poultry production systems should be investigated and identified. Appropriate risk mitigation measures should be rapidly defined and implemented. The overall structure and organization of the affected poultry production systems should also be scrutinised, especially in countries where severe epidemics have repeatedly occurred in recent years. Based on a risk assessment, competent authorities and poultry producers should identify the stages of the poultry production process where: biosecurity standards need to be improved; poultry production systems need to be reorganized.

Taking into account the epidemiology of the disease, critical points for HPAI control should be identified, and appropriate corrective actions should be implemented to mitigate the HPAI risk.

In the coming months, the sustained and increasing infection pressure on poultry establishments will challenge the effectiveness of applied biosecurity measures. Stringent biosecurity must constantly be in place to reduce the HPAI risk posed by infected wild birds.

Based on the available genetic data, to date no new virus incursions seem to have occurred in Europe with the wild bird fall migration. Most of the genetically characterized A(H5N1) viruses collected since September 2022 belong to three genotypes that have been circulating in Europe in the summer months. The virus retains a high propensity to reassort with LPAI viruses, likely as a consequence of its extensive circulation in wild birds, and eight new reassortant viruses have been detected in Europe in the last three months. All the new genotypes seem to have originated through local reassortment events with viruses circulating in the European wild bird population, and each of them has been identified in one or few viruses, in a single European country or at most in two European countries, rather than having emerged in other geographic areas and introduced in Europe through migratory birds. The low number of sequences of the latest A(H5N1) viruses deposited in public sequence repository from non-European countries (e.g. Asiatic countries) does not allow to confirm this hypothesis.

Since October 2020, 13 European countries have reported infections of HPAI A(H5) viruses of clade 2.3.4.4b in multiple mammalian species, including red foxes, harbour seals, grey seals, a Eurasian otter, a lynx, a harbour porpoise, domestic pigs, a European badger, a European polecat, a ferret, farmed mink. The last reported infection in a wild mammal (red fox) was detected in Ireland in the month of September. In October, Spain reported an A(H5N1) outbreak in a large mink farm, which represents the first identification in Europe of a A(H5N1) virus infection in farmed American mink (*Neovison vison*). Increased mortality among the animals and mink-to-mink transmission with spread across the farm through animal contact but also likely through aerosol after possible introduction of the virus through infected wild birds to the open-housed farm were observed. The characterized viruses from mink belong to a genotype that has been circulating mainly in sea birds in northern Europe during the summer; however, compared to the viruses detected in birds, the mink A(H5N1) virus contains a mutation in the polymerase protein that favours virus replication in mammals.

As well as in Europe, several HPAI A(H5N1) mammalian cases have recently been reported also in an American black bear, striped skunks, red foxes, a Virginia opossum and an Amur leopard in the USA.

The continuous detection of HPAI viruses in wild and domestic mammals, the rapid acquisition of viral mutations associated with mammalian adaptation after transmission to mammals, as well as the sporadic human infections with HPAI A(H5Nx) viruses of clade 2.3.4.4b, including the two human cases recently reported in Spain, are all factors that highlight the need to intensify surveillance in mammals and humans, particularly in high-risk areas with an intensive viral circulation.

Worldwide, HPAI A(H5) virus continues to be reported in poultry and wild birds in Russia, Asia and North America, and since October 2022 has been increasingly reported from Central and South America. For the first time ever, the Eurasian lineage of HPAI A(H5N1) and A(H5Nx) were detected in poultry, captive and wild birds in Mexico, Colombia, Ecuador, Peru and Venezuela. The spread in Central and South America seems to continue from north to south with unforeseeable consequences.

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

There is an extensive set of regulations to protect workers from health and safety risks and in accordance with occupational health and safety legislation, employers have responsibilities[8]. Employers' responsibilities include the implementation of appropriate preventive measures after a workplace risk assessment, taking into account all risks, including the risks from unintentional exposure to biological agents, in agreement with the health or safety committee or with workers’ representatives. This includes prioritising technical and organisational measures over personal measures, the obligation to consult, inform and train workers and the need to provide appropriate health surveillance. Employers should periodically revise their workplace risk assessment and ensure that all necessary technical, organisational, maintenance and hygiene measures are taken to prevent the infection of workers.

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 by the employer and appropriate measures should be taken. 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 the above-mentioned collective 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. The employer should provide the possibility for storing work clothing and street clothing separately. 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 (e.g. establishments, slaughterhouses), for example when directly exposed to birds, their products or droppings, which may potentially be infected or contaminated with avian influenza viruses, stricter measures should be applied. To reduce the risk of infection with zoonotic influenza viruses, workers should be protected from direct physical contact with sick or dead animals or their remains (e.g. sick birds, poultry carcasses, poultry faeces or litter, surfaces and water that might be contaminated with excretions in the case of infected or dead birds). At poultry farms, it should be ensured that living areas are not contaminated, and working and living areas should be strictly separated. Good hand hygiene practice (proper use of gloves, hand-washing, and use of waterless hand sanitisers) is important and helps prevent infections and keep the virus from spreading. Showering at the worksite or at a nearby decontamination station at the end of the work shift and leaving all contaminated clothing and equipment at work should be facilitated by the employer. Workers must receive training and instructions on appropriate working practices, the application of the technical, organisational and decontamination measures, the use of PPE, and how to

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[8] 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.

put on, use, take off, and dispose of it. Employers should ensure that there are proper waste storage and disposal facilities in closed containers. Workers should be informed of any emergency measures and know to whom they should report any incident that could cause the spread of the virus.

In the event of an outbreak, the occupational safety and health authorities may be consulted on the appropriate preventive measures to take. Ideally, occupational safety and health authorities should be notified of any such outbreaks – e.g. by the public health authorities.

Employers must keep a record of any workers that may have been exposed to the viruses and offer health surveillance as appropriate, according to national requirements. If self-isolation is advised, employers should set out clear procedures clarifying how workers should self-isolate, the duration of isolation and any health surveillance they should undergo. Employers should seek advice from the occupational health services and/or occupational physician on any measures and also recommend health surveillance for any other potentially infected workers The confidentiality of sensitive medical data should however be respected and maintained. Workers should be able to return to work safely and clear procedures should be developed by employers to ensure this.

4.7.2. Monitoring and options for public health measures

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

4.7.3. Diagnosis

People in the EU presenting with severe acute respiratory or influenza-like infection and a history of exposure to poultry or wild birds will require careful investigation, management and infection control. Neurological symptoms have also been observed in mammals infected with avian influenza viruses. Should transmission to humans occur, also other non-respiratory symptoms might possibly occur, and clinicians should consider testing for influenza severely ill patients 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 10-14 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.

If testing of asymptomatic workers is conducted, also follow-up investigations should be in place if exposed people are testing positive to monitor the case and close contacts, to confirm the infection or to identify a contamination or amplification of low-level virus material.

The confirmation of a true avian influenza infection in a person following a positive PCR should include repeated testing to exclude a false-positive signal, subsequent virus sequencing to produce full-length genomes for further analysis, virus cultivation, and material should be shared with reference laboratories and WHO-CCs for virus characterisation as outlined in the guidance document about testing and detection of zoonotic influenza virus infections in humans in the EU/EEA, and occupationally safety and health measures for those exposed at work (ECDC, 2022c). Also, serological investigations are needed to identify seroconversion for case ascertainment. However, for some virus positivity findings it might be challenging to confirm or rule out a true infection. More work needs to be performed globally to develop criteria how to address such inconclusive results. Reference viruses and sera against these reference viruses need to be developed, constantly updated and provided to the countries to investigate transmission events and confirm infections serologically. This is also needed to conduct larger studies in population groups exposed to avian influenza viruses and also potentially infected birds such as poultry workers, cullers but also slaughterhouse workers, to support risk assessments.

ECDC jointly with EFSA, EU-OSHA and the EURL published a separate document that provides guidance for the testing of humans for zoonotic influenza viruses. The document describes different exposed groups at risk and raises awareness about the possibility of atypical presentations in humans similar to what has been recently observed in other mammals with severe infection of the brain, i.e. encephalitis or meningoencephalitis (ECDC, 2022c).

4.7.4. Reporting

Human infections with avian influenza viruses are notifiable under EU legislation within 24 hours through the Early Warning and Response System (EWRS) according to EU Decision 1082/2013/EU[9]. Reporting is also required through the International Health Regulations (IHR) notification system (WHO, 2017): 'Each State Party shall notify WHO, by the most efficient means of communication available, by way of the National IHR Focal Point, and within 24 hours of assessment of public health information, of all events that may constitute a public health emergency of international concern within its territory according to the decision instrument, and any health measure implemented in response to those events.'

Information should also be shared with local OSH authorities.

4.7.5. Sharing of sequences

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

4.7.6. Candidate vaccine viruses

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

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

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

During this reporting period, Spain reported the first detections of avian influenza A(H5N1) virus in two workers exposed to infected poultry before and during culling activities during an outbreak in a farm (ECDC, 2022a, b; Sanidad, 2022; WHO, online-a). Virus load in the sample was low and the full virus could not be sequenced suggesting a contamination rather than an active infection with virus replication in the person (ECDC, 2022a; Sanidad, 2022). Spanish authorities are routinely testing all workers involved in culling and cleaning activities during avian influenza virus outbreaks in poultry farms and workers are required to wear personal protective equipment including FFP2 masks during these activities. None of the workers had experienced any symptom. Preliminary results from serological investigation showed no evidence of seroconversion of at least one of the workers indicating no systemic infection but rather exposure and amplification of low-level viral RNA. Similar reports of avian influenza detections in workers exposed to avian influenza infected birds or the environment during culling operations without any clinical symptoms and with limited information and evidence of a systemic viral infection add challenges to the situational and overall risk assessment.

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 very mild in human infected with recent A(H5N1) or A(H5N8) viruses circulating in Europe related to different detections in humans involved in culling activities (see Table 4), therefore the impact based on severity has been considered low but with high uncertainty due to the high diversity of circulating avian influenza viruses. The recent human A(H5N1) infection and infections with A(H5N6) in China have shown a high level of

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

severity, which has not been observed elsewhere related to clade 2.3.4.4b viruses and further analyses e.g. sequence and virus characterisation data are needed to better understand differences and similarities of the viruses causing severe or no illness globally. There are no indications so far that viruses differ antigenically from developed candidate vaccine viruses of previously circulating A(H5) viruses in Europe.

The risk of human transmission due to avian influenza viruses of the currently circulating clade 2.3.4.4b in Europe is assessed as *low* for the general population and *low to moderate* for people occupationally or otherwise HPAI virus exposed*.* The recent detection of A(H5N1) in asymptomatic workers in Spain does not alter this assessment. Further information about the severe A(H5N1) case in China is needed for the assessment.

Sporadic transmission of uncommon avian influenza viruses such as A(H3N8) and A(H10N3) reported in 2022 have been observed before e.g. for A(H6N1), A(H7N4), A(H10N8) and is therefore not an unexpected event. This does not alter the assessment that avian influenza virus transmission to humans is a rare event and the risk is considered very low for viruses adapted to avian species. Viruses currently circulating in bird populations in Europe are considered to be avian-adapted viruses. However, the detection of viruses carrying markers for mammalian adaptation, and correlated with increased replication and virulence in mammals, is of concern. The additional reports of transmission events to and between mammals, e.g. mink, seals, foxes and other carnivores as well as seroepidemiological evidence of transmission to wild boar and domestic pigs, associated with evolutionary processes including mammalian adaptation are of concern and need to be closely followed up. People involved and exposed to these animals need to be followed up to identify early any transmission between humans. Also outbreaks in mink farms showing adaptation processes to mammals with mutations associated with enhanced polymerase activity need to be carefully monitored and workers exposed during such outbreaks monitored for at least 10-14 days actively or passively and immediately tested and isolated should they develop symptoms e.g. fever, conjunctivitis, diarrhoea, respiratory, neurological, or other atypical symptoms.

Direct and unprotected exposure to possibly infected poultry or wild birds and their products including blood, remains limited to mostly occupationally exposed groups of people in the EU/EEA countries. Also, other groups of people such as backyard farmers or wild bird hunters with possible exposure to infected poultry or wild birds should be made aware of the potential risk of transmission and appropriately protected. Such unprotected exposure to infected backyard birds was the source of infection in the recent human A(H5N1) infection in the United Kingdom (GovUK, online-a; WHO, online-d). Workers in close contact to potentially infected mammals such as mink, foxes or other wildlife e.g. at rehabilitation centres or in areas with high level of avian influenza outbreaks in wild birds, should also be informed about possible avian influenza infections and should be appropriately protected when having to handle such animals. If they develop symptoms after exposure, they should consult a practitioner, inform about the exposure and get tested for avian influenza virus.

The use of antiviral pre-and postexposure should be considered for exposed people and in particular for possible cases of avian influenza infection according to national guidelines.

The uncertainty of this risk assessment is high due to the high variability of the avian influenza viruses of clade 2.3.4.4 with many reassorted subtypes and genetic lineages co-circulating in Europe and globally. Reassortment events will continue and zoonotic transmission of avian influenza viruses cannot be fully excluded in general when avian influenza viruses are present in birds. People should avoid touching sick or dead birds or their droppings and should wear PPE when in direct contact. Workers should be protected following an updated workplace risk assessment and preventive measures should be set accordingly[10]. Additionally the use of personal protective equipment and 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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[10] Council Directive 2005/94/EC of 20 December 2005 on Community measures for the control of avian influenza and repealing Directive 92/40/EEC. OJ L 10, 14.1.2006, p. 16-65.

References

Adlhoch C, Baldinelli F, Fusaro A and Terregino C, 2021. Avian influenza, a new threat to public health in Europe? Clin Microbiol Infect. doi: 10.1016/j.cmi.2021.11.005

Alkie TN, Lopes S, Hisanaga T, Xu W, Suderman M, Koziuk J, Fisher M, Redford T, Lung O, Joseph T, Himsworth CG, Brown IH, Bowes V, Lewis NS and Berhane Y, 2022. A threat from both sides: Multiple introductions of genetically distinct H5 HPAI viruses into Canada via both East Asia-Australasia/Pacific and Atlantic flyways. Virus Evol, 8:veac077. doi: 10.1093/ve/veac077

Ärzteblatt D, online. Bird flu virus detected in dead seals.

Avian Flu Diary, online. Canada Reports (Fatal) H5N1 Infection In A White-Sided Dolphin.

Avian Flu Diary, online. Two Reports On HPAI H5N8 Infecting Marine Mammals (Denmark & Germany).

Awuni JA, Bianco A, Dogbey OJ, Fusaro A, Yingar DT, Salviato A, Ababio PT, Milani A, Bonfante F and Monne I, 2019. Avian influenza H9N2 subtype in Ghana: virus characterization and evidence of co-infection. Avian Pathology, 48:470-476. doi: 10.1080/03079457.2019.1624687

BBC, online. Peru bird flu: Thousands of pelicans found dead.

BNO, online. China reports 2 new human cases of H5N6 bird flu.

Bonfante F, Mazzetto E, Zanardello C, Fortin A, Gobbo F, Maniero S, Bigolaro M, Davidson I, Haddas R, Cattoli G and Terregino C, 2018. A G1-lineage H9N2 virus with oviduct tropism causes chronic pathological changes in the infundibulum and a long-lasting drop in egg production. Veterinary Research, 49:83. doi: 10.1186/s13567-018-0575-1

Bussey KA, Bousse TL, Desmet EA, Kim B, Takimoto T. PB2 residue 271 plays a key role in enhanced polymerase activity of influenza A viruses in mammalian host cells. J Virol. 2010 May;84(9):4395-406. doi: 10.1128/JVI.02642-09. Epub 2010 Feb 24. PMID: 20181719; PMCID: PMC2863787.

Zhang Y, Zhang Q, Gao Y, He X, Kong H, Jiang Y, et al. Key molecular factors in hemagglutinin and PB2 contribute to efficient transmission of the 2009 H1N1 pandemic influenza virus. J Virol. 2012 Sep;86(18):9666-74. doi: 10.1128/JVI.00958-12

Caliendo V, Leijten L, van de Bildt MWG, Poen MJ, Kok A, Bestebroer T, Richard M, Fouchier RAM and Kuiken T, 2022. Long-Term Protective Effect of Serial Infections with H5N8 Highly Pathogenic Avian Influenza Virus in Wild Ducks. J Virol, 96:e0123322. doi: 10.1128/jvi.01233-22

CDC (Centers for Disease Control and Prevention), online. Highly Pathogenic Avian Influenza A(H5N1) Virus: Recommendations for Human Health Investigations and Response.

CDC (Centers for Disease Control and Prevention), online. March 7, 2022 Update: H5N1 Bird Flu Poses Low Risk to the Public.

CDC (Centers for Disease Control and Prevention), online. Past Reported Global Human Cases with Highly Pathogenic Avian Influenza A(H5N1) (HPAI H5N1) by Country, 1997-2022.

CDC (Centers for Disease Control and Prevention), online. U.S. Case of Human Avian Influenza A(H5) Virus Reported.

CDC (Centers for Disease Control and Prevention), online. Update on A(H5N6) Bird Flu: How is the U.S. CDC Monitoring A(H5N6) Infections and Contributing to Global Pandemic Preparedness?

Chinese National Influenza Center, WHO Collaborating Center for Reference and Research on Influenza and National Institute for Viral Disease Control and Prevention China, 2018. Chinese Influenza Weekly Report week 44, 2018. 6 pp.

CHP (Center for Health Protection Hong Kong), 2021a. Avian Influenza Report, Reporting period: Apr 18, 2021 – Apr 24, 2021 (Week 17). Hong Kong, CHP. 12 pp.

CHP (Center for Health Protection Hong Kong), 2021b. Avian Influenza Report, Reporting period: Nov 14 – Nov 20, 2021 (Week 47). Hong Kong, CHP. 13 pp.

CHP (Center for Health Protection Hong Kong), 2022a. Avian Influenza Report, Reporting period: May 15 – May 21, 2022 (Week 21). Hong Kong, CHP. 13 pp.

CHP (Center for Health Protection Hong Kong), 2022b. Avian Influenza Report, Reporting period: Nov 20 – Nov 26, 2022 (Week 48). Hong Kong, CHP. 13 pp.

CHP (The Governmentof the Hong King Special Administrative Region), online. CHP closely monitors human case of avian influenza A(H5N1) in Mainland.

Chrzastek K, Lee DH, Gharaibeh S, Zsak A and Kapczynski DR, 2018. Characterization of H9N2 avian influenza viruses from the Middle East demonstrates heterogeneity at amino acid position 226 in the hemagglutinin and potential for transmission to mammals. Virology, 518:195-201. doi: 10.1016/j.virol.2018.02.016

CTV News, online. Bird flu found in Alberta skunks for first time.

ECDC (European Centre for Disease Prevention and Control), 2021a. Communicable Disease Threats Report - Week 46, 14-20 November 2021. ECDC: Stockholm. 14 pp.

ECDC (European Centre for Disease Prevention and Control), 2021b. Threat Assessment Brief: First identification of human cases of avian influenza A(H5N8) infection. ECDC: Stockholm, 24 February 2021. 9 pp.

ECDC (European Centre for Disease Prevention and Control), 2022a. Communicable Disease Threats Report - Week 40, 2-8 October 2022. ECDC: Stockholm. 13 pp.

ECDC (European Centre for Disease Prevention and Control), 2022b. Communicable Disease Threats Report - Week 45, 6-12 November 2022. ECDC: Stockholm. 18 pp.

ECDC (European Centre for Disease Prevention and Control), 2022c. Testing and detection of zoonotic influenza virus infections in humans in the EU/EEA, and occupational safety and health measures for those exposed at work. ECDC: Stockholm, . 32 pp. doi: 10.2900/852604.

EFSA AHAW Panel (EFSA Panel on Animal Health and Welfare), 2017. Scientific opinion on avian influenza. 4991. EFSA Journal 2017;15(10):4991. 233 pp. doi: 10.2903/j.efsa.2017.4991

EFSA ECDC, EURL (European Food Safety Authority, European Centre for Disease Prevention and Control, European Reference Laboratory), Adlhoch C, Brouwer A, Kuiken T, Miteva A, Mulatti P, Smietanka K, Staubach C, Gogin A, Munoz Guajardo I and Baldinelli F, 2019. Scientific Report: Avian influenza overview November 2018 – February 2019. EFSA Journal 2019;17(3):5664. 35 pp. doi: 10.2903/j.efsa.2019.5664

EFSA ECDC, EURL (European Food Safety Authority, European Centre for Disease Prevention and Control, European Reference Laboratory), Adlhoch C, Fusaro A, Gozales JL, Kuiken T, Marangon S, Niqueux E, Staubach C, Terregino C, Aznar I, Munoz Guajardo I and Baldinelli F, 2021. Scientific Report: Avian influenza overview September – December 2021. EFSA Journal 2021;19(12):7108. 94 pp. doi: 10.2903/j.efsa.2021.7108.

EFSA ECDC, EURL (European Food Safety Authority, European Centre for Disease Prevention and Control, European Reference Laboratory), Adlhoch C, Fusaro A, Gozales JL, Kuiken T, Marangon S, Niqueux E, Staubach C, Terregino C, Aznar I, Munoz Guajardo I and Baldinelli F, 2022a. Scientific Report: Avian influenza overview March – June 2022. EFSA Journal 2022;20(8):7415. 67 pp. doi: 10.2903/j.efsa.2022.7415.

EFSA ECDC, EURL (European Food Safety Authority, European Centre for Disease Prevention and Control, European Reference Laboratory), Adlhoch C, Fusaro A, Gozales JL, Kuiken T, Marangon S, Niqueux E, Staubach C, Terregino C, Chuzhakina K, Munoz Guajardo I and Baldinelli F, 2022b. Scientific Report: Avian influenza overview June – September 2022. EFSA Journal 2022;20(10):7597. 58 pp. doi: 10.2903/j.efsa.2022.7597.

Elsayed HS, Adel A, Alshaya DS, Safhi FA, Jalal AS, Elmasry DMA, Selim K, Erfan AA, Eid S, Selim S, El-Saadony MT and Shahein M, 2022. First isolation of influenza a subtype H5N8 in ostrich: pathological and genetic characterization. Poult Sci, 101:102156. doi: 10.1016/j.psj.2022.102156

European Commission, online. Animal Health - Regulatory Committee presentations.

FAO (Preliminary FAO/OIE/WHO Joint Rapid Risk Assessment), 2022. Human infection with Influenza A(H3N8), China. 5 pp.

FAO (Food and Agriculture Organization), online. Avian Influenza A(H7N9) virus situation update.

FFA (Finnish Food Authority), online. Avian influenza cases in Finland.

Floyd T, Banyard AC, Lean FZX, Byrne AMP, Fullick E, Whittard E, Mollett BC, Bexton S, Swinson V, Macrelli M, Lewis NS, Reid SM, Núñez A, Duff JP, Hansen R and Brown IH, 2021. Systemic infection with highly pathogenic H5N8 of avian origin produces encephalitis and mortality in wild mammals at a UK rehabilitation centre. bioRxiv:2021.2005.2026.445666. doi: 10.1101/2021.05.26.445666

Fujimoto Y, Ogasawara K, Isoda N, Hatai H, Okuya K, Watanabe Y, Takada A, Sakoda Y, Saito K and Ozawa M, 2022. Experimental and natural infections of white-tailed sea eagles (Haliaeetus albicilla) with high pathogenicity avian influenza virus of H5 subtype. Front Microbiol, 13:1007350. doi: 10.3389/fmicb.2022.1007350

Galicia Xd, online. La Xunta detecta un foco de influenza aviar en una explotación de visones en la provincia de A Coruña.

GovHK (The Government of Hong Kong Special Administrative News), online. 75-year-old man in Jiangxi dies of H10N8 infection.

GovUK (UK Health Security Agency), online. Human case of avian flu detected in UK.

GovUK (UK Health Security Agency), online. Influenza of avian origin in UK seal populations: qualitative assessment of the risk to the UK human population.

GovUK (UK Health Security Agency), online. Technical risk assessment for avian influenza (human health): influenza A H5N1 2.3.4.4b.

GSAID, online. GISAID EpiFlu™ Database.

Hayama Y, Sawai K, Yoshinori M, Yamaguchi E and Yamamoto T, 2022. Estimation of introduction time window of highly pathogenic avian influenza virus into broiler chicken farms during the 2020 - 2021 winter season outbreak in Japan. Prev Vet Med, 208:105768. doi: 10.1016/j.prevetmed.2022.105768

Healthy Wildlife (Canadan Wildlife Health Cooperative), online. First case of highly pathogenic H5N1 avian influenza virus infection in a black bear.

Herve S, Schmitz A, Briand FX, Gorin S, Queguiner S, Niqueux E, Paboeuf F, Scoizec A, Le Bouquin-Leneveu S, Eterradossi N and Simon G, 2021. Serological Evidence of Backyard Pig Exposure to Highly Pathogenic Avian Influenza H5N8 Virus during 2016-2017 Epizootic in France. Pathogens, 10. doi: 10.3390/pathogens10050621

Isoda N, Onuma M, Hiono T, Sobolev I, Lim HY, Nabeshima K, Honjyo H, Yokoyama M, Shestopalov A and Sakoda Y, 2022. Detection of New H5N1 High Pathogenicity Avian Influenza Viruses in Winter 2021-2022 in the Far East, Which Are Genetically Close to Those in Europe. Viruses, 14. doi: 10.3390/v14102168

Jiang H, Wu P, Uyeki TM, He J, Deng Z, Xu W, Lv Q, Zhang J, Wu Y, Tsang TK, Kang M, Zheng J, Wang L, Yang B, Qin Y, Feng L, Fang VJ, Gao GF, Leung GM, Yu H and Cowling BJ, 2017. Preliminary Epidemiologic Assessment of Human Infections With Highly Pathogenic Avian Influenza A(H5N6) Virus, China. Clinical Infectious Diseases, 65:383-388. doi: 10.1093/cid/cix334

Kariithi HM, Welch CN, Ferreira HL, Pusch EA, Ateya LO, Binepal YS, Apopo AA, Dulu TD, Afonso CL and Suarez DL, 2019. Genetic characterization and pathogenesis of the first H9N2 low pathogenic avian influenza viruses isolated from chickens in Kenyan live bird markets. Infection, Genetics and Evolution:104074. doi: 10.1016/j.meegid.2019.104074

Kiniradio, online. Brown Bear Cub in Alaska tests positive for Avian Influenza.

KTOO, online. First bear with bird flu in US was cub in Glacier Bay.

Lee EK, Lee YN, Kye SJ, Lewis NS, Brown IH, Sagong M, Heo GB, Kang YM, Cho HK, Kang HM, Cheon SH, Lee M, Park BK, Kim YJ and Lee YJ, 2018. Characterization of a novel reassortant H5N6 highly pathogenic avian influenza virus clade 2.3.4.4 in Korea, 2017. Emerging Microbes & Infections, 7:103. doi: 10.1038/s41426-018-0104-3

Li YT, Chen CC, Chang AM, Chao DY and Smith GJD, 2020. Co-circulation of both low and highly pathogenic avian influenza H5 viruses in current poultry epidemics in Taiwan. Virus Evol, 6:veaa037. doi: 10.1093/ve/veaa037

Liang Y, Hjulsager CK, Seekings AH, Warren CJ, Lean FZX, Nunez A, James J, Thomas SS, Banyard AC, Slomka MJ, Brown IH and Larsen LE, 2022. Pathogenesis and infection dynamics of high pathogenicity avian influenza virus (HPAIV) H5N6 (clade 2.3.4.4b) in pheasants and onward transmission to chickens. Virology, 577:138-148. doi: 10.1016/j.virol.2022.10.009

NHCGovCN (National Health Commission of the People's Republic of China), online. One case of human infection with H10N3 avian influenza was detected in Jiangsu Province.

Outbreak News, online. Denmark reports 1st highly pathogenic avian influenza case in harbor seal.

Parry J, 2014. H10N8 avian flu virus claims its first known human casualty. BMJ, 348:g1360. doi: 10.1136/bmj.g1360

ProMed, online. Avian influenza (226): Americas (Peru) pelican, HPAI H5N1, Archive Number: 20221202.8707032.

ProMed, online. Avian influenza (231): Americas (Chile) wild bird, HPAI H5N1, Archive Number: 20221209.8707163.

Pulit-Penaloza J, Belser J, Brock N, Thakur PB, Tumpey T and Maines T, 2022. Pathogenesis and Transmissibility of North American Highly Pathogenic Avian Influenza A(H5N1) Virus in Ferrets. Emerging Infectious Disease journal, 28:1913. doi: 10.3201/eid2809.220879

Puryear W, Sawatzki K, Hill N, Foss A, Stone JJ, Doughty L, Walk D, Gilbert K, Murray M, Cox E, Patel P, Mertz Z, Ellis S, Taylor J, Fauquier D, Smith A, DiGiovanni RA, van de Guchte A, Gonzalez-Reiche AS, Khalil Z, van Bakel H, Torchetti MK, Lenoch JB, Lantz K and Runstadler J, 2022. Outbreak of Highly Pathogenic Avian Influenza H5N1 in New England Seals. bioRxiv:2022.2007.2029.501155. doi: 10.1101/2022.07.29.501155

Pyankova OG, Susloparov IM, Moiseeva AA, Kolosova NP, Onkhonova GS, Danilenko AV, Vakalova EV, Shendo GL, Nekeshina NN, Noskova LN, Demina JV, Frolova NV, Gavrilova EV, Maksyutov RA and Ryzhikov AB, 2021. Isolation of clade 2.3.4.4b A(H5N8), a highly pathogenic avian influenza virus, from a worker during an outbreak on a poultry farm, Russia, December 2020. Eurosurveillance, 26:2100439.

Rijks JM, Leopold MF, Kuhn S, In 't Veld R, Schenk F, Brenninkmeijer A, Lilipaly SJ, Ballmann MZ, Kelder L, de Jong JW, Courtens W, Slaterus R, Kleyheeg E, Vreman S, Kik MJL, Grone A, Fouchier RAM, Engelsma M, de Jong MCM, Kuiken T and Beerens N, 2022. Mass Mortality Caused by Highly Pathogenic Influenza A(H5N1) Virus in Sandwich Terns, the Netherlands, 2022. Emerg Infect Dis, 28:2538-2542. doi: 10.3201/eid2812.221292

Sanidad Md, 2022. Primera detección de gripe aviar A(H5N1) en humanos en España. 13 pp.

Schülein A, Ritzmann M, Christian J, Schneider K and Neubauer-Juric A, 2021. Exposure of wild boar to Influenza A viruses in Bavaria: Analysis of seroprevalences and antibody subtype specificity before and after the panzootic of highly pathogenic avian influenza viruses A (H5N8). Zoonoses and Public Health, n/a.

Shin D, Siebert U, Lakemeyer J, Grilo M, Pawliczka I, Wu N, Valentin-Weigand P, Haas L and Herrler G, 2019. Highly Pathogenic Avian Influenza A(H5N8) Virus in Gray Seals, Baltic Sea. Emerging Infectious Diseases, 25:2295-2298. doi: 10.3201/eid2512.181472

Smith GJ, Donis RO, World Health Organization/World Organisation for Animal HF and Agriculture Organization HEWG, 2015. Nomenclature updates resulting from the evolution of avian influenza A(H5) virus clades 2.1.3.2a, 2.2.1, and 2.3.4 during 2013-2014. Influenza Other Respir Viruses, 9:271-276. doi: 10.1111/irv.12324

SSI (Staten Serum Insitut), online. Bird flu in Danish seals.

SVA (National Veterinary Institute Sweden), online. First case of bird flu confirmed in porpoises.

SVA (National Veterinary Institute Sweden), online. Highly pathogenic bird flu - the past season and the infection situation for the coming season.

The Government of the Hong Kong Special Administrative Region Press Releases, online. CHP closely monitors human case of avian influenza A(H5N6) in Mainland.

The Government of the Hong Kong Special Administrative Region Press Releases, online. CHP notified of human case of avian influenza A(H3N8) in Mainland.

Tribune O, online. Bird Flu Virus Detected in Pelicans in Eastern Venezuela.

UFHealth (University of Florida Helath), online. A first: Avian influenza detected in American dolphin.

USDA (U.S. Department of Agriculture), online. 2022 Detections of Highly Pathogenic Avian Influenza in Mammals.

VNExpress, online. Vietnam records first human case of bird flu in 8 years.

Wille M, Avery-Gomm S, Caliendo V, Camphuysen K, Humphreys E, Lang A, Philip E, Ramey A, Rijks J, Robertson G, Roberts L, 2022. High pathogenicity avian influenza represents an unprecedented conservation challenge for globally declining seabird populations. Response to: Editorial, Protect wildlife from livestock diseases (Thijs Kuiken & Ruth Cromie), Science 6 Oct 2022, Vol 378, Issue 6615, p. 5 DOI: 10.1126/science.adf0956

WHO (World Health Organization), 2017. Operational Guidance on Sharing Influenza Viruses with Human Pandemic Potential (IVPP) under the Pandemic Influenza Preparedness (PIP) Framework. Geneva, WHO. 20 pp.

WHO (World Health Organization), 2019a. Avian Influenza Weekly Update Number 713. Geneva, WHO. 3 pp.

WHO (World Health Organization), 2019b. Influenza at the human-animal interface - Summary and assessment, from 25 June 2019 to 27 September 2019. Geneva, WHO. 3 pp.

WHO (World Health Organization), 2020a. Antigenic and genetic characteristics of zoonotic influenza A viruses and development of candidate vaccine viruses for pandemic preparedness. Geneva, WHO. 15 pp.

WHO (World Health Organization), 2020b. Influenza at the human-animal interface - Summary and assessment, from 21 January to 28 February 2020. Geneva. 4 pp.

WHO (World Health Organization), 2020c. Influenza at the human-animal interface; Summary and assessment, from 9 August to 1 October 2021. Geneva. 7 pp.

WHO (World Health Organization), 2020d. Influenza at the human-animal interface; Summary and assessment, from 28 February to 8 May 2020. Geneva. 3 pp.

WHO (World Health Organization), 2021a. Antigenic and genetic characteristics of zoonotic influenza A viruses and development of candidate vaccine viruses for pandemic preparedness. Geneva. 15 pp.

WHO (World Health Organization), 2021b. Cumulative number of confirmed human cases for avian influenza A(H5N1) reported to WHO, 2003-2021 (22 June 2021). Geneva, WHO. 4 pp.

WHO (World Health Organization), 2021c. Influenza at the human-animal interface; Summary and assessment, from 22 May to 22 June 2021. Geneva. 7 pp.

WHO (World Health Organization), 2021d. Influenza at the human-animal interface; Summary and assessment, from 23 June to 8 August 2021. Geneva. 13 pp.

WHO (World Health Organization), 2021e. Influenza at the human-animal interface; Summary and assessment, from 30 Jannuary to 15 April 2021. Geneva. 7 pp.

WHO (World Health Organization), 2022a. Influenza at the human-animal interface; Summary and assessment, from 6 October to 11 November 2022. Geneva. 6 pp.

WHO (World Health Organization), 2022b. Influenza at the human-animal interface; Summary and assessment, from 8 April to 13 May 2022. Geneva. 6 pp.

WHO (World Health Organization), 2022c. Influenza at the human-animal interface; Summary and assessment, from 30 August to 5 October 2022. Geneva. 5 pp.

WHO (World Health Organization), online. Avian Influenza A (H5N1) - Spain.

WHO (World Health Organization), online. Global Influenza Surveillance and Response System (GISRS).

WHO (World Health Organization), online. Human infection with avian influenza A (H5N8) - Russian Federation.

WHO (World Health Organization), online. Human infection with avian influenza A(H5) virus.

WHO (World Health Organization), online. Human infection with avian influenza A(H5N1) – India.

WHO (World Health Organization), online. Influenza A (H5) - United Kingdom of Great Britain and Northern Ireland.

WOAH (World Organization for Animal Health), 2022. High pathogenicity avian influneza (HPAI) - Situation report 15/11/2022. Paris. 5 pp.

WUR (Wageningen University Research), online. Bird flu (H5N1) detected in a fox with neurological symptoms.

Xu C, Ye H, Qiu W, Lin H, Chen Y, Zhang H and Liao M, 2018. Phylogenetic classification of hemagglutinin gene of H9N2 avian influenza viruses isolated in China during 2012–2016 and evaluation of selected candidate vaccine strains. Poultry Science, 97:3023-3030. doi: 10.3382/ps/pey154

Yang ZY, Wei CJ, Kong WP, Wu L, Xu L, Smith DF and Nabel GJ, 2007. Immunization by avian H5 influenza hemagglutinin mutants with altered receptor binding specificity. Science, 317:825-828. doi: 10.1126/science.1135165

Zecchin B, Minoungou G, Fusaro A, Moctar S, Ouedraogo-Kabore A, Schivo A, Salviato A, Marciano S and Monne I, 2017. Influenza A(H9N2) Virus, Burkina Faso. Emerging Infectious Diseases, 23:2118-2119. doi: 10.3201/eid2312.171294

Zhu C, Hu C, Gui B, Chen Q, Zhang S and He G, 2018. Genetic characteristics of H9N2 avian influenza viruses isolated from free-range poultry in Eastern China, in 2014-2015. Poultry Science, 97:3793-3800. doi: 10.3382/ps/pey187

Abbreviations

ADIS	Animal Disease Information System
ADNS	Animal Disease Notification System
ECDC	European Centre for Disease Prevention and Control
EEA	European Economic Area
EFSA	European Food Safety Authority
EU	European Union
EURL	European Union Reference Laboratory
EWRS	Early Warning and Response System
FAO	Food and Agriculture Organization
GISRS	Global Influenza Surveillance and Response System
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
NRL	National Reference Laboratory
OSH	Occupational safety and health
PCR	Polymerase chain reaction
PIP	Pandemic Influenza Preparedness
PPE	Personal protective equipment
RA	Risk assessment
SSI	Statens Serum Institut
ToR	Term of Reference
WAHIS	World Animal Health System
WOAH	World Organisation for Animal Health
WHO	World Health Organization
WUR	Wageningen University Research

Appendix A – Terms of Reference

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

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

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

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

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

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

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

There is knowledge, legislation[11], 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[12], 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.

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

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

A.2. Interpretation of the Terms of Reference

In reply to ToR 1 and ToR 2, this scientific report gives an overview of the HPAI and LPAI outbreaks in poultry, captive and wild birds detected in Europe from 10 September to 2 December 2022 and reported by Member States and neighbouring countries to the ADIS or WOAH-WAHIS. Member States where avian influenza outbreaks have occurred in poultry have submitted additional epidemiological data to EFSA, that have been used to analyse the characteristics of the affected poultry establishments.

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

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

Monitoring of the avian influenza situation in other countries (ToR 4) is based on data reported to WOAH-WAHIS. The description focuses only on findings of avian influenza viruses occurring in countries that are considered to be of epidemiological interest for the EU/EEA and the 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 from 10 September and 2 December 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 June to September 2022 (EFSA et al., 2022a) 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 10 September and 2 December 2022 submitted by Member States to the ADIS (European Commission, online) were taken into account for this report. Data extraction was carried on 5 December 2022. The WOAH's World Animal Health Information Database (WOAH, online-c) was consulted to complement the information for European countries not reporting HPAI notifications to ADIS. In addition, HPAI-affected European countries were asked to provide more detailed epidemiological data directly to EFSA on the avian influenza outbreaks that occurred in poultry during the same period. Wild bird species have been categorised according to Table B1, and the common and scientific name of wild bird species described in this report in relation to Europe is reported in Table B2. The public GISAID's EpiFlu Database was accessed to download newly released avian influenza sequences. A descriptive analysis of the data collected is reported in Section 4.1 and 4.2. The PDFs of the SCOPAFF presentations are available on the European Commission website (European Commission, online)

Table B1. Categorisation of the wild bird species detected as HPAI virus-positive between 1 October 2016 and 2 December 2022

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

Tawny owl	Nene	Sulidae	European greenfinch
True owls	Northern shoveler	Western gull	Finches
Ural owl	Pink-footed goose	Yellow-legged gull	Great Blue heron
Western marsh-harrier	Tufted duck		Great crested grebe
White-tailed sea-eagle	Whooper swan		Great white egret
			Green sandpiper
			Grey heron
			Grey plover
			Guineafowl
			Haematopodidae
			Hooded crow
			House sparrow
			Little egret
			Little grebe
			Northern bald ibis
			Northern lapwing
			Passeridae
			Pheasants and allies
			Pied avocet
			Rallidae
			Red knot
			Rock dove
			Rook
			Ruddy turnstone
			Sanderling
			Semipalmated sandpiper
			Snipe
			Song thrush
			Turdidae
			Western grebe
			Western sandpiper
			Western water rail
			Whimbrel
			White stork
			White-rumped sandpiper

Table B2. Common and scientific name of the wild bird species detected as HPAI virus-positive between 1 October 2016 and 2 December 2022

Common name	**Scientific name**	**Common name**	**Scientific name**
Anambra waxbill	*Estrilda poliopareia*	Common goldeneye	*Bucephala clangula*
Arctic tern	*Sterna paradisaea*	Common kestrel	*Falco tinnunculus*
Atlantic puffin	*Fratercula arctica*	Common moorhen	*Gallinula chloropus*
Bald eagle	*Haliaeetus leucocephalus*	Common murre	*Uria aalge*
Barnacle goose	*Branta leucopsis*	common pheasant	*Phasianus colchicus*
Bean goose	*Anser fabalis*	Common pochard	*Aythya ferina*
Bearded vulture	*Gypaetus barbatus*	Common raven	*Corvus corax*
Black guillemot	*Cepphus grylle*	Common redshank	*Tringa totanus*
		Common ringed plover	*(Charadrius hiaticula)*
Black swan	*Cygnus atratus*	Common shelduck	*Tadorna tadorna*

Common name	Scientific name	Common name	Scientific name
Black-headed gull	*Larus ridibundus*	Common starling	*Sturnus vulgaris*
Brent goose	*Branta bernicla*	Common teal	*Anas crecca*
Bufflehead	*Bucephala albeola*	Common tern	*Sterna hirundo*
Calidris	*Calidris spp.*	Common woodpigeon	*Columba palumbus*
Canada goose	*Branta canadensis*	Crowned cormorant	*Microcarbo coronatus*
Carrion crow	*Corvus corone*	Curlew sandpiper	*Calidris ferruginea*
Caspian gull	*Larus cachinnans*	Dalmatian pelican	*Pelecanus crispus*
Common barn-owl	*Tyto alba*	Dunlin	*Calidris alpina*
Common coot	*Fulica atra*	Egyptian goose	*Alopochen aegyptiaca*
Common crane	*Grus grus*	Eurasian blackbird	*Turdus merula*
Common eider	*Somateria mollissima*	Mew gull	*Larus canus*
Eurasian bullfinch	*Pyrrhula pyrrhula*	Mediterranean gull	*Larus melanocephalus*
Eurasian buzzard	*Buteo buteo*	Merlin	*Falco columbarius*
Eurasian collared-dove	*Streptopelia decaocto*	Montagu's harrier	*Circus pygargus*
Eurasian curlew	*Numenius arquata*	Muscovy duck	*Cairina moschata*
Eurasian eagle-owl	*Bubo bubo*	Mute swan	*Cygnus olor*
Eurasian jackdaw	*Corvus monedula*	Nene	*Branta bernicla*
Eurasian jay	*Garrulus glandarius*	Northern bald ibis	*Geronticus eremita*
Eurasian magpie	*Pica pica*	Northern fulmar	*Fulmarus glacialis*
Eurasian oystercatcher	*Haematopus ostralegus*	Northern gannet	*Morus bassanus*
Eurasian sparrowhawk	*Accipiter nisus*	Northern goshawk	*Accipiter gentilis*
Eurasian spoonbill	*Platalea leucorodia*	Northern lapwing	*Vanellus vanellus*
Eurasian wigeon	*Mareca penelope*	Northern long-eared Owl	*Asio otus*
Eurasian woodcock	*Scolopax rusticola*	Northern Pintail	*Anas acuta*
European greenfinch	*Chloris chloris*	Northern shoveler	*Spatula clypeata*
European herring gull	*Larus argentatus*	Osprey	*Pandion haliaetus*
Ferruginous duck	*Aythya nyroca*	Peregrine falcon	*Falco peregrinus*
Finches	*Fringillidae*	Pied avocet	*Recurvirostra avosetta*
Gadwall	*Mareca strepera*	Pink-footed goose	*Anser brachyrhynchus*
Garganey	*Spatula querquedula*	Razorbill	*Alca torda*
Glaucous gull	*Larus hyperboreus*	Red-breasted goose	*Branta ruficollis*
Golden eagle	*Aquila chrysaetos*	Red kite	*Milvus milvus*
Goosander	*Mergus merganser*	Red knot	*Calidris canutus*
Great black-backed gull	*Larus marinus*	Red-legged partridge	*Alectoris rufa*
Great blue heron	*Ardea herodias*	Ring-billed gull	*Larus delawarensis*
Great cormorant	*Phalacrocorax carbo*	Rock dove	*Columba livia*
Great crested grebe	*Podiceps cristatus*	Rook	*Corvus frugilegus*
Great skua	*Catharacta skua*	Rough-legged buzzard	*Buteo lagopus*
Greater Flamingo	*Phoenicopterus roseus*	Ruddy turnstone	*Arenaria interpres*
Great white egret	*Ardea alba*	Sanderling	*Calidris alba*
Greater scaup	*Aythya marila*	Sandwich tern	*Thalasseus sandvicensis*
Great spotted woodpecker	*Dendrocopos major*	Semipalmated sandpiper	*Calidris pusilla*
Greater white-fronted goose	*Anser albifrons*	Short-eared owl	*Asio flammeus*
Green sandpiper	*Tringa ochropus*	Silver gull	*Chroicocephalus novaehollandiae*

Common name	Scientific name	Common name	Scientific name
Grey heron	*Ardea cinerea*	Song thrush	*Turdus philomelos*
Grey plover	*Pluvialis squatarola*	Spotted harrier	*Circus assimilis*
Grey-headed gull	*Larus cirrocephalus*	Tawny owl	*Strix aluco*
Greylag goose	*Anser anser*	Tufted duck	*Aythya fuligula*
Griffon vulture	*Gyps fulvus*	Ural owl	*Strix uralensis*
Guineafowl	*Numididae*	western grebe	*Aechmophorus occidentalis*
Gyrfalcon	*Falco rusticolus*	Western gull	*Larus occidentalis*
Hen harrier	*Crcus cyaneus*	Western marsh-harrier	*Circus aeruginosus*
Hooded crow	*Corvus coronus*	Western sandpiper	*Calidris mauri*
House sparrow	*Passer domesticus*	Western water Rail	*Rallus aquaticus*
Lanner falcon	*Falco biarmicus*	Whimbrel	*Numenius phaeopus*
Lesser black-backed gull	*Larus fuscus*	White stork	*Ciconia ciconia*
Lesser white-fronted goose	*Anser erythropus*	White-rumped sandpiper	*Calidris fuscicollis*
Little auk	*Alle alle*	White-tailed eagle	*Haliaeetus albicilla*
Little egret	*Egretta garzetta*	Whooper swan	*Cygnus cygnus*
Little grebe	*Tachybaptus ruficollis*	Yellow-legged gull	*Larus michahellis*
Little owl	*Athene noctua*		
Mallard	*Anas platyrhynchos*		
Manx shearwater	*Puffinus puffinus*		

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 6 September to 1 December 2022 were searched; the search was run on 14 November and 2 December 2022.

Relevance criteria Scientific articles added to the database from 6 September to 1 December 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 135 papers. The articles were subsequently screened against the relevance and eligibility criteria. Seven of the screened papers were finally taken into consideration in the description of the phenotypic characterisation of HPAI viruses circulating in the EU in domestic and wild birds in the reporting period.

The search protocol and the results can be consulted at https://doi.org/10.5281/zenodo.7446257.

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

Data from WOAH-WAHIS (WOAH, online-c) on HPAI A(H5N1), HPAI A(H5N2), HPAI A(H5N5), A(H5N6), A(H5N8), HPAI and LPAI A(H7N9) in domestic and wild birds were used to describe and to map the geographical distribution of avian influenza detections in domestic and wild birds in Africa, the Americas, Asia and Europe based on the observation dates. Data were retrieved on 5 December 2022 and extracted by EFSA. Reproduced with permission. WOAH bears no responsibility for the integrity or accuracy of the data contained herein, but not limited to, any deletion, manipulation, or reformatting of data that may have occurred beyond its control

B.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.7426549

The annexes contain the following information:

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

The Annex contains a table with the characteristics of the HPAI A(H5Nx)-positive poultry establishments by affected EU Member State from 3 September to 18 November 2022. In addition, the Netherlands reported on the characteristics of the HPAI A(H5Nx)-positive poultry establishments affected before 3 September that were not included in the previous published report; those information are also included in Annex A.

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, Denmark, France, Germany, Hungary, Ireland, Italy, Moldova, Norway, the Netherlands, Poland, Portugal and Spain, from 3 September to 18 November 2022 in relation to HPAI outbreaks in poultry.

Annex C – Data on wild birds

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