SCIENTIFIC REPORT

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Avian influenza overview November 2019 – February 2020

European Food Safety Authority,
European Centre for Disease Prevention and Control and
European Union Reference Laboratory for Avian Influenza

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Abstract

Between 16 November 2019 and 15 February 2020, 36 highly pathogenic avian influenza (HPAI) A(H5N8) virus outbreaks were reported in Europe in poultry (n=34), captive birds (n=1) and wild birds (n=2), in Poland, Hungary, Slovakia, Romania, Germany, Czechia and Ukraine, one HPAI outbreak caused by a simultaneous infection with A(H5N2) and A(H5N8) was reported in poultry in Bulgaria, and two low pathogenic avian influenza (LPAI) A(H5) virus outbreaks were reported in poultry in the United Kingdom and in Denmark. Genomic characterisation of the HPAI A(H5N8) viruses suggests that they are reassortants of HPAI A(H5N8) viruses from Africa and LPAI viruses from Eurasia. It is likely that this reassortment occurred in wild migratory birds in Asia during the summer and then spread to eastern Europe with the autumn migration. This is the first time that wild bird migration from Africa to Eurasia has been implicated in the long-distance spread of HPAI viruses to the EU. Given the late incursion of HPAI A(H5N8) virus into the EU in this winter season (first outbreak reported on 30 December 2019), its overall restriction to eastern Europe, and the approaching spring migration, the risk of the virus spreading further in the west via wild birds is decreasing for the coming months. Genetic analysis of the HPAI A(H5N2) and A(H5N8) viruses detected in the Bulgarian outbreak reveals that these viruses are both related to the 2018–19 Bulgarian HPAI A(H5N8) viruses and not to the HPAI A(H5N8) viruses currently circulating in Europe. An increasing number of HPAI A(H5N1), A(H5N2), A(H5N5) and A(H5N6) virus outbreaks in poultry in Asia were reported during the time period for this report compared with the previous reporting period. Single outbreaks of HPAI A(H5N8) virus were notified by Saudi Arabia and South Africa. Furthermore, in contrast to the last report, HPAI virus-positive wild birds were reported from Israel and one of the key migration areas in northern China. Two human cases due to A(H9N2) virus infection were reported during the reporting period.

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

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1. Introduction

This scientific report provides an overview of highly pathogenic avian influenza (HPAI) virus outbreaks detected in poultry, captive and wild birds and noteworthy outbreaks of low pathogenic avian influenza (LPAI) virus in poultry and captive birds, as well as human cases due to avian influenza (AI) virus, reported in and outside Europe between 16 November 2019 and 15 February 2020. The background, terms of reference and their interpretation are described in Appendix A and the data and methodologies are reported in Appendix B.

2. Conclusions

Avian influenza outbreaks in European countries and in other countries of interest between 16 November 2019 and 15 February 2020

2.1. Main observations

- No human infections with HPAI or LPAI viruses of the same genetic composition as those currently detected in domestic and wild birds in Europe have been reported from the EU/EEA Member States.
- Two human cases with A(H9N2) virus infection have been reported from Hong Kong Special Administrative Region (1) and Senegal (1).
- Since 2005, Europe has experienced six HPAI A(H5) incursions and three of them occurred in the last four years (2016–2017, 2017–2018 and 2019–2020).
- In Europe, between 16 November 2019 and 15 February 2020 (based on the Animal Disease Notification System [ADNS]):
  - thirty-seven HPAI A(H5) outbreaks were reported; of those one outbreak detected in poultry in Bulgaria was caused by a simultaneous infection with A(H5N2) and A(H5N8) and 36 A(H5N8) were reported: 21 in poultry and one in a wild bird in Poland, four in poultry in Hungary, three in poultry and one in captive birds in Slovakia, two in poultry in Romania, one in poultry and one in a wild bird in Germany, one in poultry in the Czechia; one in poultry in Ukraine;
  - two LPAI A(H5) outbreaks were reported in poultry: one A(H5N3) in the United Kingdom and one A(H5N1) in Denmark.
- Genomic characterisation of the HPAI A(H5N8) viruses detected in domestic and wild birds in Europe since December 2019 suggests that they are reassortants of HPAI A(H5N8) viruses from Africa and LPAI viruses from Eurasia. It is likely that this reassortment occurred in wild migratory birds in Asia during the summer and then spread to eastern Europe with the autumn migration.
- Two virus subtypes were detected in the poultry outbreak in Bulgaria, HPAI A(H5N8) and A(H5N2). The analysis of these viruses and of viruses from other two HPAI outbreaks detected in Bulgaria after the end of the reporting period for this report, indicates that A(H5N2) and A(H5N8) viruses are co-circulating in Bulgaria and are not realeted to the HPAI A(H5N8) viruses currently circulating in other European countries; the HA gene of both strains are related to the 2018–19 Bulgarian HPAI A(H5N8) indeed.
- In comparison to the last reporting period, an increasing number of outbreaks of HPAI A(H5N1), HPAI A(H5N2), HPAI A(H5N5) and HPAI A(H5N6) in poultry were notified from Asia. Single outbreaks of HPAI A(H5N8) were notified between 16 November 2019 and 15 February 2020 by Saudi Arabia and South Africa. Furthermore, in contrast to the last report, HPAI virus positive wild birds were reported from north-western China.

2.2. Conclusions

- The risk of zoonotic transmission of AI viruses to the general public in Europe remains very low. No transmission to humans has been observed related to viruses detected in Europe over the last few months, however the evolution of AI viruses and recent reassortment events need to be closely monitored.

- The two cases in wild birds in the EU were notified after outbreaks in poultry had already been reported in the same geographical area; therefore, the direction of transmission between these wild bird cases and poultry is not clear.
- The higher number of outbreaks observed in poultry than in wild birds could be explained by an ineffective passive surveillance of wild birds, by a different host response to virus infection between wild and domestic birds, or by herd immunity of wild birds due to past seasons' exposure to HPAI A(H5).
- Given the late incursion of HPAI A(H5) into the EU in this winter season 2019–2020, its overall restriction to eastern Europe, and the approaching spring migration, the risk of further virus spread in the west via wild birds is decreasing for the coming months.
- This is the first time that wild bird migration from Africa to Eurasia has been implicated in the long-distance spread of HPAI viruses to the EU. It implies that Africa is also a potential source of new virus genes coming to Europe, at least indirectly. However, the low risk of the southern route needs to be reconsidered, as what happened from Africa to Asia might also happen from Africa to Europe.
- The scarcity of data on HPAI infection in wild birds from Africa makes it impossible to identify which areas may be a key source for virus spread and estimate the risk of virus diffusion out of Africa.
- The first European A(H5N8) outbreak was reported on 30 December 2019. Among the possible explanations for this late detection, compared with the previous HPAI (H5) waves, are a) the unusual mild temperatures registered in the moulting areas in Russia in November and December 2019; b) a different route of virus spread; c) an undetected circulation of the virus in wild birds.
- The co-circulation of A(H9N2) viruses belonging to the potentially zoonotic G1 lineage with A(H5N6) and A(H5N8) HPAI viruses in West Africa is a cause of great concern for the possible emergence of reassortant viruses with unknown biological properties, which may present a risk for animal and public health.
- Continued surveillance for AI virus in wild birds and poultry in Europe and worldwide, combined with timely generation of complete viral genome sequences and data sharing among European countries and between animal and human health sectors, are crucial in order to be able to detect and respond promptly to threats that are relevant to animal and public health.
- In recent years, the epidemiology of HPAI viruses in the wild reservoir has changed significantly. Recently, we have seen that passive surveillance has neither been able to detect the circulation of these viruses in wild birds before outbreaks in poultry, nor has provided a real picture of the rate of infection in these populations. This means that it cannot be used as the only tool for an early warning system or for assessing the risk of introducing HPAI viruses into domestic bird populations.

3. Suggestions

- It is particularly important that information on the genetic composition and possible origins of newly detected variants in birds and humans are shared and communicated in a timely manner
- In wild birds a more effective targeted alternative surveillance methods that are sustainable from an economic point of view (e.g. environmental sampling) must be designed and implemented. Furthermore, targeted serological surveillance to assess herd immunity could help to understand some aspects of the host–virus interaction, such as the very low mortality in wild species observed this year.

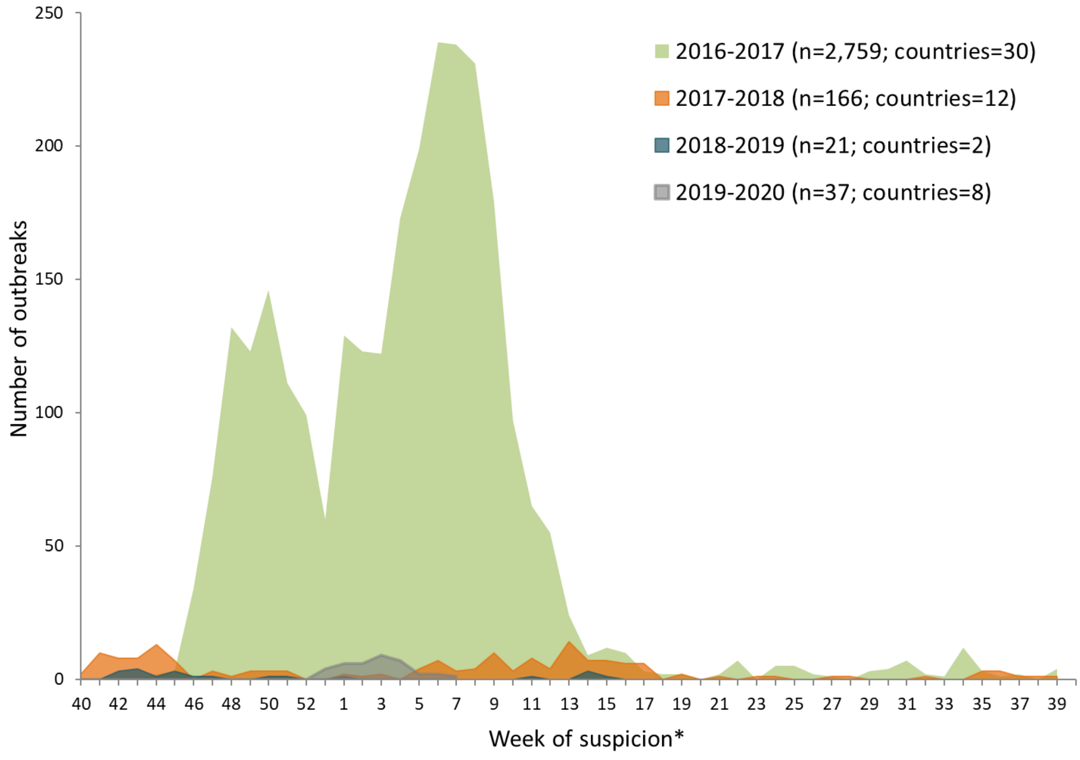
- High standard alert, effective biosecurity measures and the ability of the poultry industry to adapt production systems according to the risk assessment (e.g. free-range birds kept indoors in situations considered to be at high risk) are still the main preventive tools against HPAI in Europe.
- People exposed to birds that may potentially be infected with AI viruses should take appropriate personal protection measures following national guidelines.

4. Results

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

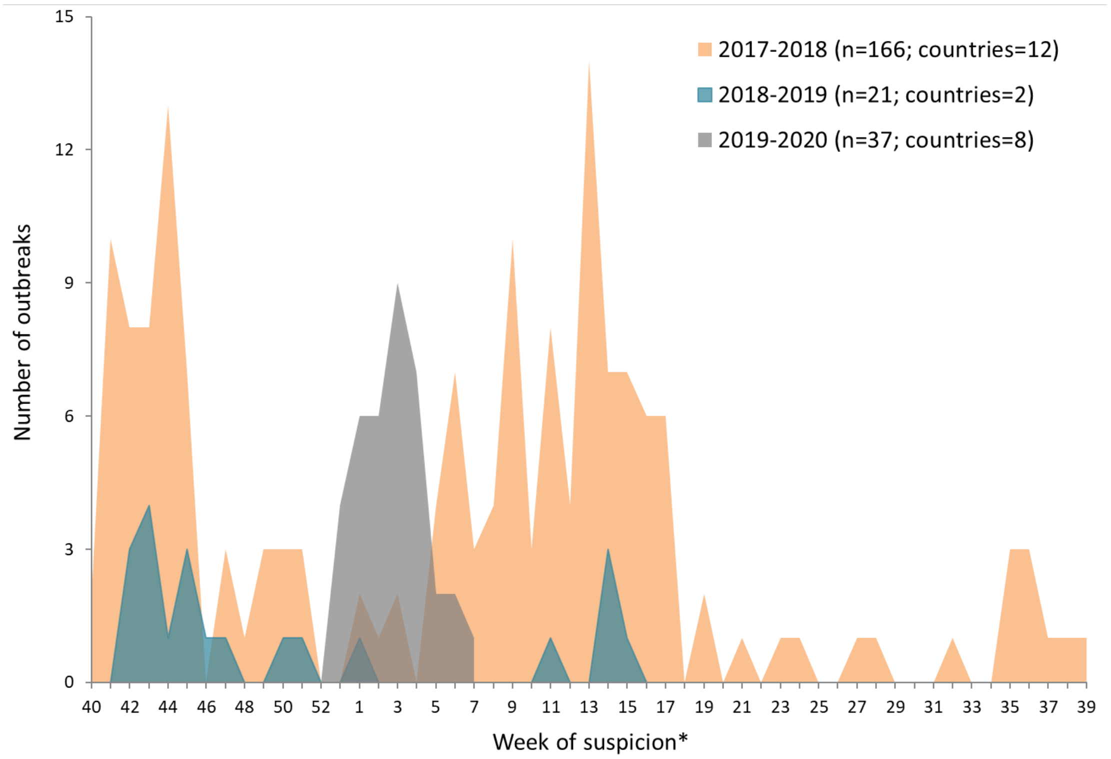
Figure 1 shows the HPAI outbreaks detected in birds (poultry, wild and captive birds) in Europe and reported via ADNS for seasons 2016–2017, 2017–2018, 2018–2019 and 2019–2020. Figure 2 shows the same data only for the last three epidemic seasons. A season is the period that starts in week 40 (the beginning of October) and ends in week 39 (the end of September) of the following year. For the current season 2019–2020, data reported are truncated at the middle of week 7 (on 15 February 2020), as the season is still ongoing.

The analysis of the characteristics of the previous 2017–2018, 2018–2019 and the current 2019–2020 AI seasons, from 2 October 2017 to 15 February 2020, are reported in Figures 3–7 by week of suspicion, geographical distribution, HPAI virus subtype, affected host population and surveillance stream leading to the outbreak detection.



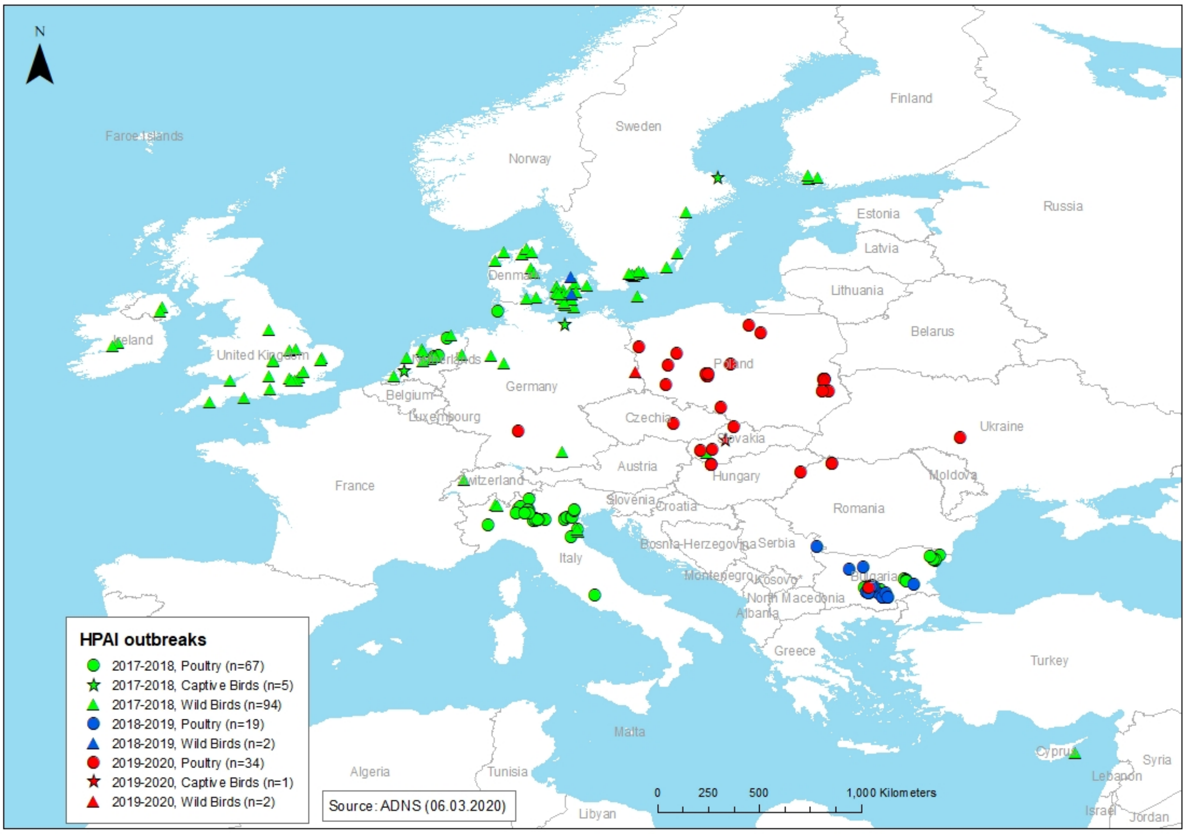
* When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.
Data source: ADNS, EFSA.

Figure 1: Distribution of total number of HPAI outbreaks detected in Europe in seasons 2016–2017 (green), 2017–2018 (orange), 2018–2019 (blue), 2019–2020 (grey) and reported via ADNS by week of suspicion, 28 September 2016 – 15 February 2020 (n=2,983)



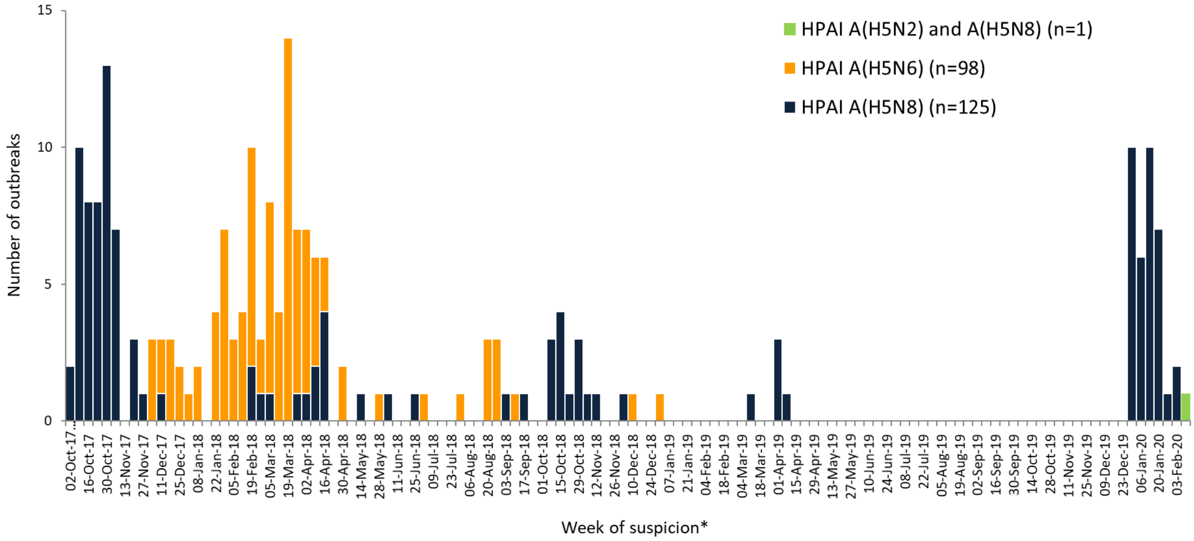
* When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.
Data source: ADNS, EFSA.

Figure 2: Distribution of total number of HPAI outbreaks detected in Europe in seasons, 2017–2018 (orange), 2018–2019 (blue) and 2019–2020 (grey) and reported via ADNS by week of suspicion, 2 October 2017 – 15 February 2020 (n=224)



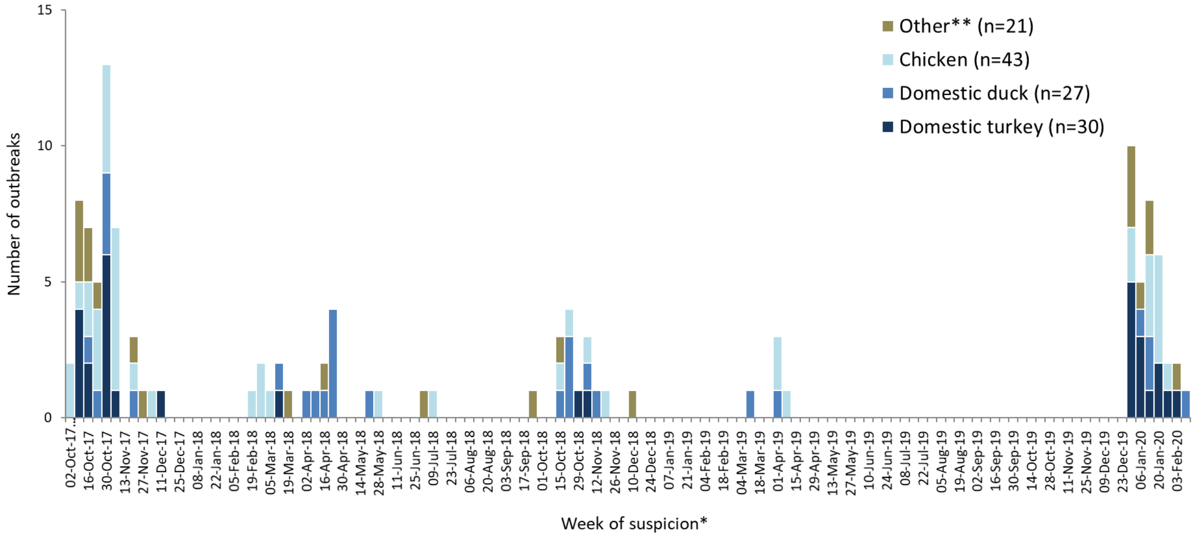
* This designation is without prejudice to positions on status, and is in line with UNSCR 1244 and the ICJ Opinion on the Kosovo Declaration of Independence

Figure 3: Geographical distribution, based on available geocoordinates, of HPAI outbreaks in Europe in seasons 2017–2018 (green), 2018–2019 (blue) and 2019–2020 (red) in poultry (circles), wild birds (triangles) and captive birds (stars) (2 October 2017 – 15 February 2020; n=224)



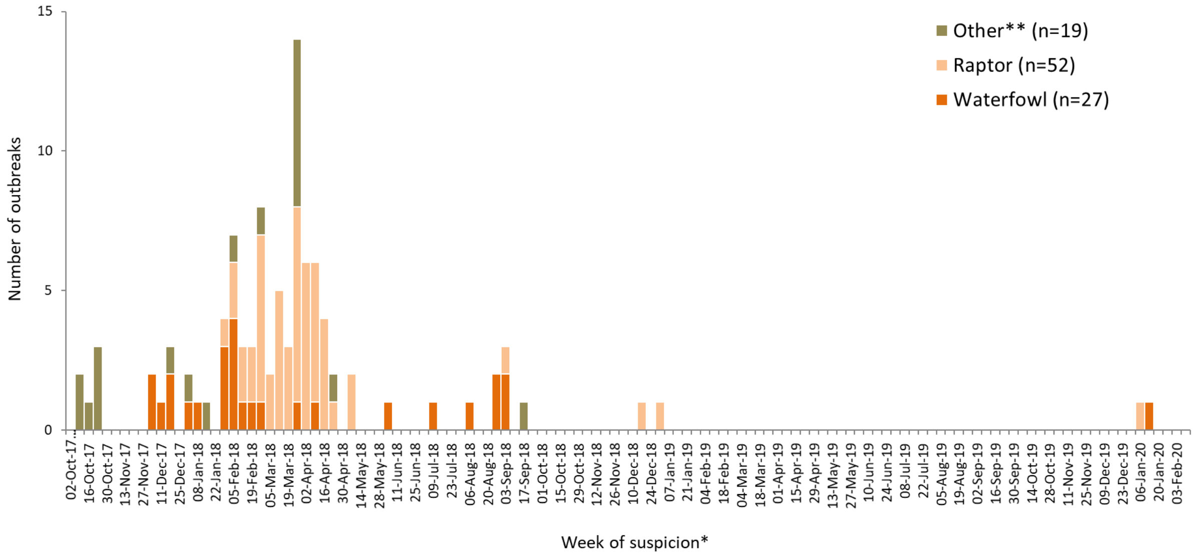
* When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.
Data source: ADNS, EFSA.

Figure 4: Distribution of total number of HPAI A(H5N6) (orange), A(H5N8) (blue) and A(H5N2) and A(H5N8) (green) outbreaks in Europe by week of suspicion (dates indicate the first day of the week) in seasons 2017–2018, 2018–2019 and 2019–2020 (2 October 2017 – 15 February 2020; n=224)



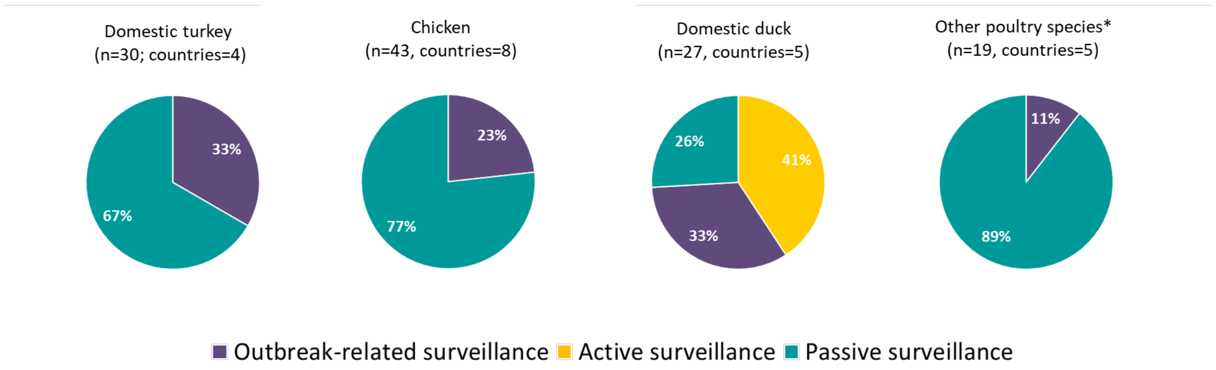
* When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.
** 'Other' category contains mixed, unknown bird species, or categories different from those displayed: pheasant (*Phasianus colchicus*), pigeons (*Columba livia*), partridges (*Perdix perdix*), chukar partridges (*Alectoris chukar*).
Data source: ADNS, EFSA.

Figure 5: Distribution of total number of HPAI outbreaks in Europe by week of suspicion (dates indicate the first day of the week) in seasons 2017–2018, 2018–2019 and 2019–2020 by affected poultry species (2 October 2017 – 15 February 2020; n=121)



* When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.
** 'Other' category contains mixed, unknown bird species, or categories different from those displayed: black-headed gull (*Chroicocephalus ridibundus*), great cormorant (*Phalacrocorax carbo*), herring gull (*Larus argentatus*), hooded crow (*Corvus cornix*), pheasant (*Phasianus colchicus*), white stork (*Ciconia ciconia*).
Data source: ADNS, EFSA.

Figure 6: Distribution of total number of HPAI outbreaks in Europe by week of suspicion (dates indicate the first day of the week) in seasons 2017–2018, 2018–2019 and 2019–2020 by affected wild bird category (2 October 2017 – 15 February 2020; n=98)



* 'Other poultry species' contains mixed, unknown bird species, or species different from those displayed.
Data source: ADNS, EFSA.

Figure 7: Frequency distribution of HPAI outbreaks in poultry in Europe, by bird species and sampling programme leading to the outbreak detection, in seasons 2017–2018, 2018–2019 and 2019–2020 (2 October 2017 – 15 February 2020; n=119)

4.2. HPAI and LPAI outbreaks in Europe, 16 November 2019 – 15 February 2020 (TOR 1 and TOR 2)

4.2.1. Description of the avian influenza detections in time and space

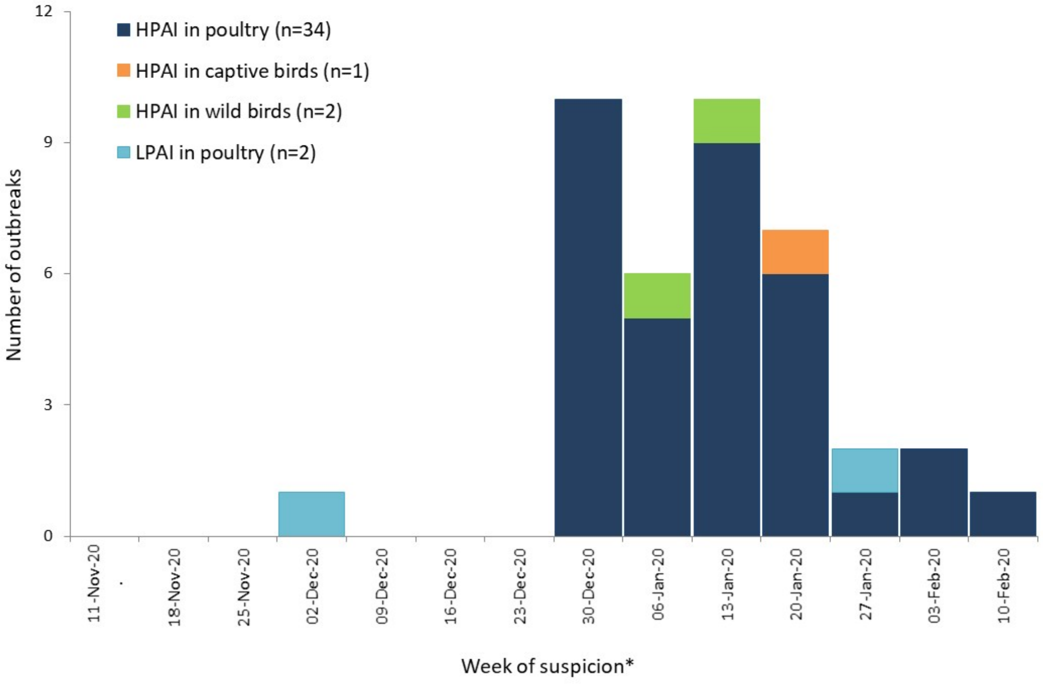
4.2.1.1. HPAI and LPAI in poultry, other captive birds and wild birds

From 16 November 2019 to 15 February 2020, 37 HPAI and 2 LPAI outbreaks were notified in poultry, wild and captive birds in Europe, and were reported via the ADNS, as presented in Table 1. The timeline, location and affected subpopulation of the AI outbreaks are reported Figures 8 and 9. The characterisation of HPAI-affected poultry establishments[1] is reported in Section 4.2.2.1, and LPAI-affected establishments in Section 4.2.2.3. For wild birds, Table 3 displays the number of outbreaks, whereas the description of cases by outbreak is reported in Section 4.2.2.2.

Table 1: Number of AI outbreaks in Europe by virus subtype and country, 16 November 2019 – 15 February 2020

Country	**HPAI outbreaks**				**LPAI outbreaks**		**All avian influenza outbreaks**
	A(H5N8)			**A(H5N2) and A(H5N8)**	**A(H5N1)**	**A(H5N3)**	
	Poultry	**Wild birds**	**Captive birds**	**Poultry**	**Poultry**	**Poultry**	
Bulgaria				1			1
Czechia	1						1
Denmark					1		1
Germany	1	1					2
Hungary	4						4
Poland	21	1					22
Romania	2						2
Slovakia	3		1(a)				4
Ukraine	1						1
United Kingdom						1	1
Total (10 countries)	33	2	1	1	1	1	39

(a) Outbreak recorded in a zoo; affected species: ducks (total n=9); silver teal, *Spatula versicolor* (n=3), Eurasian spoonbill, *Platalea leucorodia* (n=4), Carolina duck, *Aix sponsa* (n=1), Bernier's teal *Anas bernieri* (n=1).
Data Source: ADNS (16.03.20)



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

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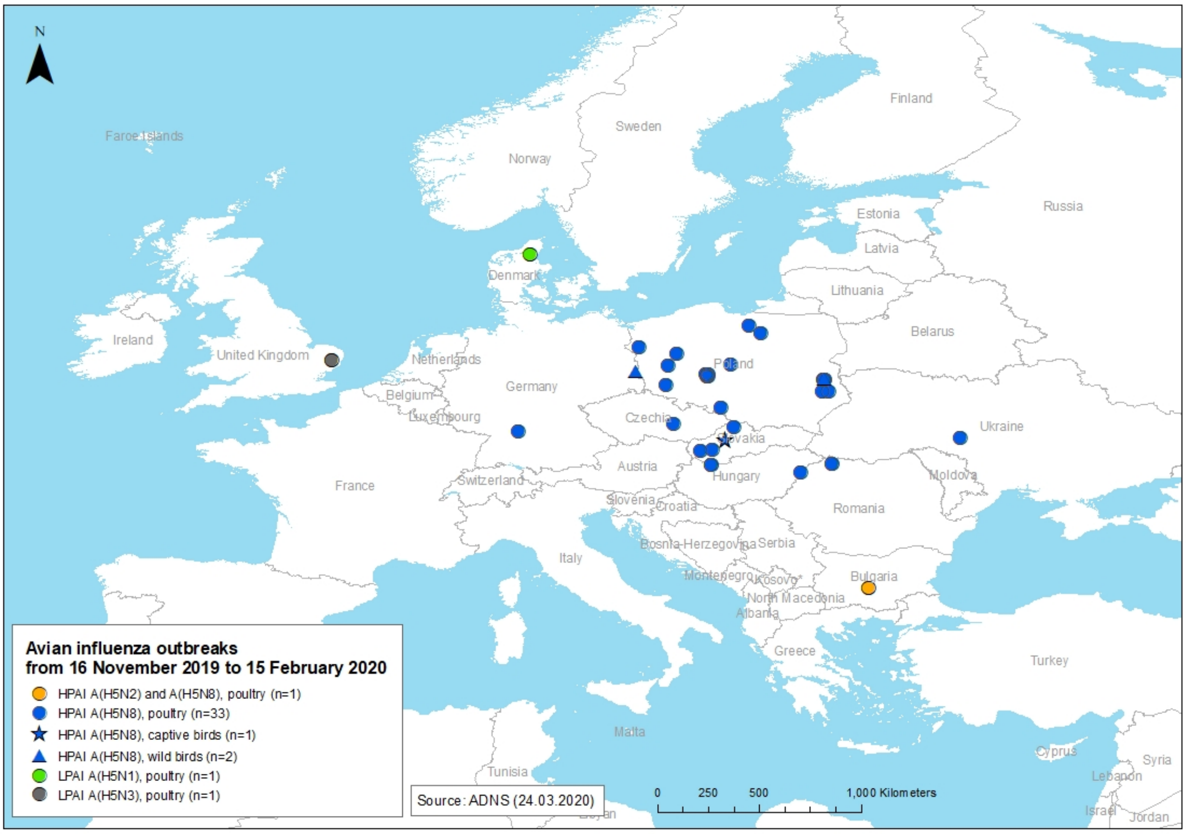
[1] According to Regulation (EU) 2016/429 'establishment' means any premises, structure, or, in the case of open-air farming, any environment or place, where animals or germinal products are kept, on a temporary or permanent basis, except for: (a) households where pet animals are kept; (b) veterinary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

Data source: EFSA and ADNS (16.03.19).

Figure 8: Distribution of the avian influenza outbreaks in Europe, by week of suspicion (dates indicate the first day of the week) and affected subpopulation, 16 November 2019 – 15 February 2020 (n=39)



* This designation is without prejudice to positions on status, and is in line with UNSCR 1244 and the ICJ Opinion on the Kosovo Declaration of Independence

Figure 9: Geographical distribution, based on available geocoordinates, of avian influenza outbreaks in Europe, by virus subtype and affected subpopulation, 16 November 2019 – 15 February 2020 (n=39)

As of 25 March 2020, a number of HPAI A(H5) outbreaks were confirmed in poultry outside the reporting period for this report: one in poultry in Czechia on 16 February 2020, 13 in poultry in Poland, seven in poultry in Bulgaria, one in poultry, one in wild and one in captive birds in Germany.

On 7 January 2020 a swine-origine A(H1N1) was confirmed from a fattening turkey establishment before moving the animals to the slaughterhouse in north-east Italy, in an area characterised by a high density of swine establishments.

4.2.2. Phenotypic characterisation of avian influenza viruses circulating in Europe

4.2.2.1. HPAI in domestic birds

Characterisation of the HPAI-affected poultry establishments

From 16 November 2019 to 15 February 2020, a total of 34 HPAI outbreaks in poultry were notified in Europe (Table 2). All these outbreaks were reported to be A(H5N8) subtype, apart from the Bulgarian outbreak where HPAI A(H5N2) and A(H5N8) viruses were identified. The description of the bird species, the production category, the size of these HPAI affected establishments are shown in Figures 10 and 11.

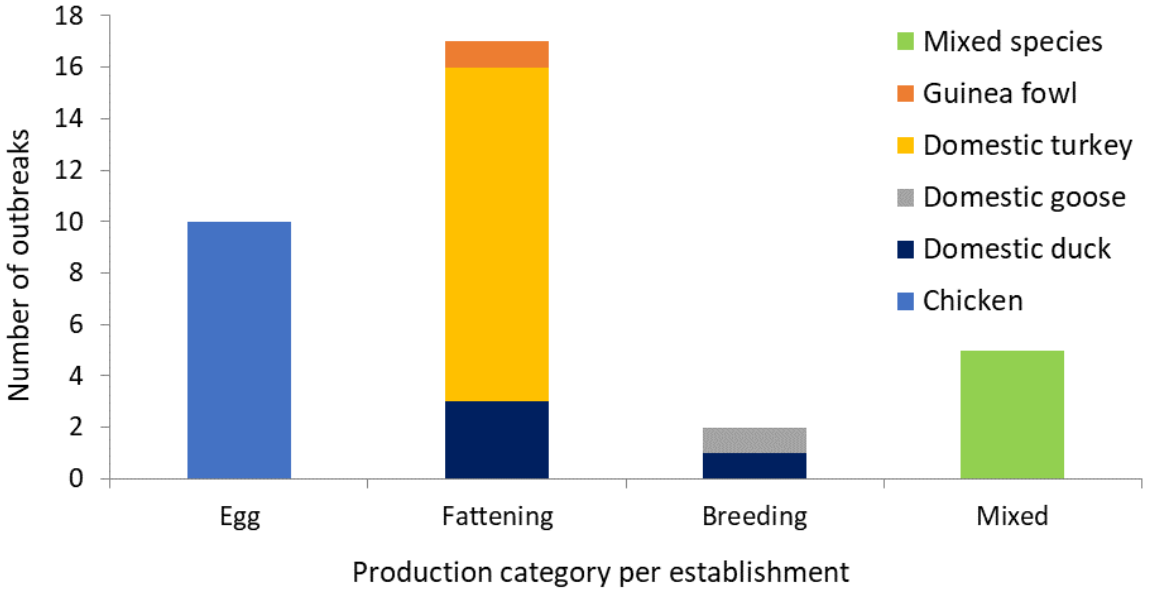


Figure 10: Number of HPAI-affected establishments by poultry species and production category in the EU, 16 November 2019 – 15 February 2020

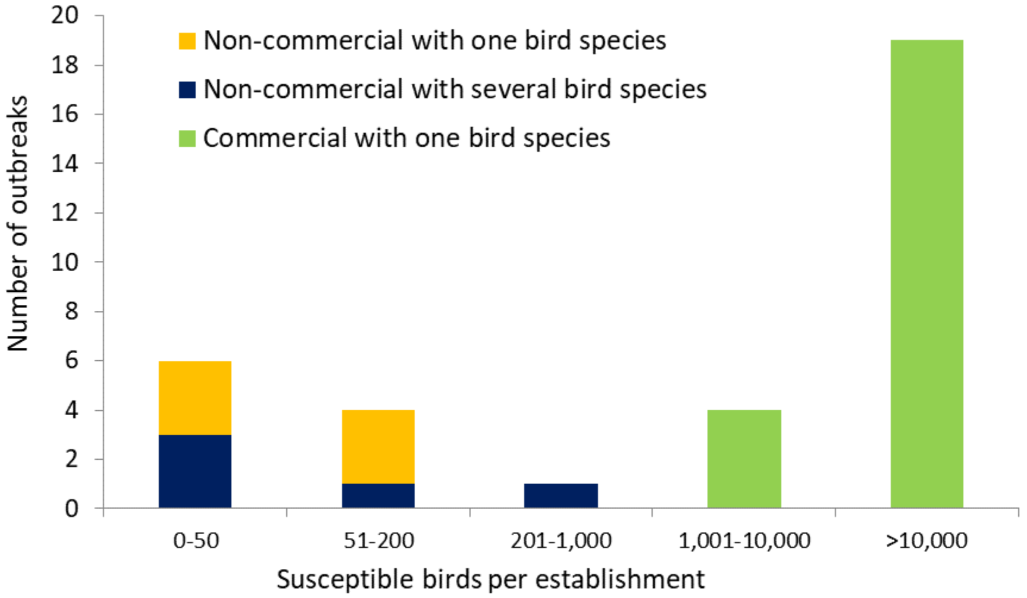


Figure 11: Number of HPAI-affected establishments in the EU from 16 November 2019 – 15 February 2020, according to the commercial type and the number of susceptible bird species bred

Table 2: Characteristics of the HPAI A(H5)-positive poultry establishments by affected EU Member States from 16 November 2019 to 15 February 2020 (n=34). Data source: ADNS and EFSA

Country	Poultry species	Production category	Surveillance stream(a)	Outbreak type	Presence of signs in the outbreaks	Outdoor access	Date of suspicion	Number of susceptible animals
Bulgaria	Domestic duck	Fattening	Passive	Primary	Yes	Yes	12/2/2020	15,729
	Total							**15,729**
Czechia	Mixed(b)(c)	Mixed(b)(c)	Passive	Primary	Yes	Yes	17/1/2020	15
	Total							**15**
Germany	Mixed(d)	Mixed(e)	Passive	Primary	Yes	Yes	6/2/2020	57
	Total							**57**
Hungary	Domestic duck	Fattening	Passive	Primary	Yes	No	13/1/2020	115,548
	Domestic turkey	Fattening	Passive	Primary	Yes	No	9/1/2020	53,500
		Fattening	Outbreak-related	Secondary	Yes	No	10/1/2020	20,000
		Fattening	Outbreak-related	Secondary	Yes	No	15/1/2020	34,000
	Total							**223,048**
Poland	Chicken	Egg	Passive	Primary	Yes	No	31/12/2019	36,069
		Egg(b)	Passive	Primary	Yes	Yes	21/1/2020	161
		Egg(b)	Passive	Primary	Yes	Yes	22/1/2020	165
		Egg(b)	Passive	Primary	Yes	Yes	26/1/2020	63
	Domestic duck	Breeding	Passive	Primary	Yes	No	14/1/2020	19,594
		Fattening	Passive	Primary	Yes	No	15/1/2020	6,621
	Domestic goose	Breeding	Passive	Primary	Yes	Yes	11/1/2020	5,615
	Domestic turkey	Fattening	Passive	Primary	Yes	No	30/12/2019	12,089
		Fattening	Outbreak-related	Secondary	Yes	No	31/12/2019	9,500
		Fattening	Outbreak-related	Secondary	Yes	No	31/12/2019	20,600
		Fattening	Outbreak-related	Secondary	Yes	No	3/1/2020	13,186
		Fattening	Passive	Secondary	Yes	No	4/1/2020	24,000
		Fattening	Passive	Primary	Yes	No	9/1/2020	22,629
		Fattening	Passive	Primary	Yes	No	22/1/2020	37,563
		Fattening	Passive	Primary	Yes	No	24/1/2020	23,351
		Fattening	Passive	Primary	Yes	No	28/1/2020	36,183
		Fattening	Passive	Primary	Yes	No	7/2/2020	3,895
	Guinea fowl	Fattening	Outbreak-related	Secondary	Yes	No	1/1/2020	12,960
	Mixed(b)	Mixed(f)	Passive	Secondary	Yes	Yes	3/1/2020	36
		Mixed(g)	Passive	Primary	Yes	Yes	2/1/2020	43
		Mixed(h)	Passive	Primary	Yes	Yes	17/1/2020	569
	Total							**284,892**
Romania	Chicken	Egg	Passive	Primary	Yes	No	13/1/2020	18,699
		Egg	Outbreak-related	Secondary	Yes	No	17/1/2020	22,762
	Total							**41,461**
Slovakia	Chicken(b)	Egg	Passive	Primary	Yes	Yes	3/1/2020	22
		Egg	Passive	Primary	Yes	Yes	16/1/2020	19
		Egg	Passive	Primary	Yes	Yes	24/1/2020	10
	Total							**51**
Ukraine	Chicken	Egg	Passive	Primary	Yes		18/1/2020	116,544
	Total							**51**
Total for all Countries								**116,544**

(a) 'Outbreak-related', as part of outbreak response, i.e. control zones, tracing; 'passive', notifications of disease suspicion; 'active', screening of apparently healthy populations conducted in accordance with Decision 2010/367/EU.
(b) Non-commercial.
(c) Laying hens (n=12) and domestic ducks (n=3). Production categories: chicken – egg, duck – fattening.
(d) Laying hens (n=49), domestic ducks (n=6) and domestic geese (n=2). In addition, canaries (*Serinus canaria forma domestica*) (n=9) and pheasants (n=3) were kept as non-poultry within the meaning of RL 2005/94 in this population.
(e) Production categories: chicken – egg, geese and ducks – fattening.
(f) Laying hens (n=13), domestic ducks (n=7) and pigeons (n=16). Production category for chicken – egg.
(g) Laying hens (n=19), domestic ducks (n=22) and domestic geese (n=2). Production category for chicken – egg.
(h) Laying hens (n=91), chicken broilers (n=41), domestic geese (n=17), domestic ducks (n=70), pigeons (n=326) and parrots (*Psephotus haematonotus* n=2; *Melopsittacus undulates* n = 24). Production categories: chicken – egg and fattening, goose – breeding, duck – fattening, pigeon and parrot – other (pets).

HPAI A(H5N2) and A(H5N8)-affected poultry establishments in Bulgaria

On 17 February 2020, one outbreak caused by a simultaneous infection with HPAI A(H5N2) and A(H5N8) was detected at a poultry establishment (domestic mule ducks) in Bulgaria. Characteristics of the affected establishment and species reared are presented in Table 2.

HPAI A(H5N8)-affected poultry establishments in Czechia

On 17 January 2020, one HPAI A(H5N8) outbreak was detected in a poultry establishment in Czechia. Characteristics of the affected establishment and species reared are presented in Table 2.

The outbreak was identified in a small non-commercial backyard flock of laying hens and domestic ducks by means of outbreak-related surveillance. The birds were showing mortality and clinical signs. The epidemiological investigation of the affected establishment traced the source of infection to probably be contact with wild birds. The affected establishment is located close to a stream, the backyard is only partly fenced and free-range feeding was not protected.

HPAI A(H5N8)-affected poultry establishments in Germany

On 6 February 2020, one HPAI A(H5N8) outbreak was detected at a poultry establishment in Germany. Characteristics of the affected establishment and of the species reared are presented in Table 2.

The outbreak was identified at a small commercial establishment of laying hens, domestic ducks, and domestic geese by means of passive surveillance. The establishment also had three pheasants and nine canaries (*Serinus canaria forma domestica*) that were kept as non-poultry within the meaning of RL 2005/94 in this population. Preliminary epidemiological investigation lead to the hypothesis that the most likely source of infection was direct or indirect contact with wild birds, this is also supported by genetic analysis (King et al., 2020).

HPAI A(H5N8)-affected poultry establishments in Hungary

Between 9 and 15 January 2020, four HPAI A(H5N8) outbreaks were detected at poultry establishments in two regions of Hungary. Characteristics of the affected establishments and species reared are presented in Table 2.

Two of the outbreaks were detected in the course of passive surveillance activities. In one case that occurred at an establishment for domestic turkeys, mortality and clinical signs were recorded and suspicion was raised. The birds did not have outdoor access. Indirect contact with wild birds was highlighted as the most likely source of infection. In the other case, at a domestic duck establishment, an increased mortality rate was recorded and pathological findings were considered to be suspicious for HPAI. Also, in this case, indirect contact with wild birds was considered to be the most likely source of infection, even considering the fact that the birds did not have outdoor access.

The other two outbreaks were detected in the course of outbreak-related surveillance. Both of these domestic turkey establishments were situated within one kilometre of the first outbreak.

HPAI A(H5N8)-affected poultry establishments in Poland

Between 30 December 2019 and 15 February 2020, 21 HPAI A(H5N8) outbreaks in 11 regions were detected at poultry establishments in Poland. Characteristics of the affected establishments and of the species reared are presented in Table 2.

The first outbreak was detected at a domestic turkey establishment in the course of passive surveillance. The suspicion was raised due to increased mortality rates in the flock. Also, clinical signs and a drop in feed- and water- intake were recorded. The birds did not have outdoor access. The most likely source of infection was considered to be indirect contact with wild birds as there are water reservoirs in the area. The same source of infection was also considered the most likely for five other recorded outbreaks, for two of them it was specified that the establishments are located in close proximity to water reservoirs and one provided outdoor access to their birds. Another affected establishment whose most likely source of infection was indirect contact with wild birds was situated in close proximity to the German border and to the area where one HPAI-affected wild bird was found, this was a non-commercial establishment that provided outdoor access to the poultry.

There were six secondary outbreaks, all related to the first outbreak described above. At all the secondary outbreaks, the signs of infection were the same as for the primary outbreak (mortality, clinical signs and drop in feed and water intake). For five secondary outbreaks the most likely sources of infection were recorded to be the proximity to the primary outbreak establishments, humans or wind. One secondary outbreak recorded the introduction of animal by-products from the first primary outbreak on 27 December 2019, before to the infection. The animal by-products were used for feed for fur animals (foxes) that were kept at the same farm as the poultry.

In total, there were eight establishments involved in primary outbreaks that did not report the possible source of infection or recorded it as unknown.

HPAI A(H5N8)-affected poultry establishments in Romania

Between 13 and 17 January 2020, two HPAI A(H5N8) outbreaks in one region were detected at poultry establishments in Romania. Characteristics of the affected establishments and species reared are presented in Table 2.

The first of the two outbreaks was recorded to be a primary outbreak; the second was a secondary outbreak detected in the course of outbreak-related surveillance. Both establishments were commercial holdings for laying hens, and mortality and clinical signs were present in both. The most likely source of infection for the primary outbreak was recorded to be indirect contact with wild birds. For the secondary outbreak the source was likely to be the manure vehicle ('indirect poultry'). Neither of the establishments provided outdoor access to their birds. In the first outbreak, three people were reported to be exposed to the virus; in the second outbreak five people were reported to be exposed.

HPAI A(H5N8)-affected poultry and captive bird establishments in Slovakia

Between 3 and 24 January 2020, three HPAI A(H5N8) outbreaks in three regions were detected at poultry establishments in Slovakia. Characteristics of the affected establishments and species reared are presented in Table 2.

All three outbreaks were detected in the course of passive surveillance. The establishments were small backyard establishments with outdoor access. In all of them only mortality was present; there were no other signs. The most likely source of infection was recorded to be wild birds. The number of people exposed to the virus is unknown for all three outbreaks.

On 24 January 2020 one HPAI A(H5N8) outbreak was confirmed in a zoo in Slovakia. The suspicion was raised when three birds (one silver teal, *Spatula versicolor*, and two Eurasian spoonbills, *Platalea leucorodia*) suddenly died without previously visible clinical signs. In total, nine birds died during the outbreak; the species were silver teal (n=3), Eurasian spoonbill (n=4), Carolina duck, *Aix sponsa* (n=1), Bernier' s teal, *Anas bernieri* (n=1).

HPAI A(H5N8)-affected poultry establishments in Ukraine

On 18 January 2020, one HPAI A(H5N8) outbreak was detected at a laying hen establishment in Ukraine. Characteristics of the affected establishments and species reared are presented in Table 2.

The outbreak was detected in the course of passive surveillance at an establishment for laying hens. The source of the outbreak is unknown or inconclusive (OIE, online-c).

Information extracted from the scientific literature

No literature has been found on phenotypic characterisation of HPAI viruses circulating in the EU in poultry in the last two years.

4.2.2.2. HPAI in wild birds

Pathogenicity in the affected species

Between 16 November 2019 and 15 February 2020, two HPAI cases in wild birds were notified in Europe (Table 3). This involved a northern goshawk (*Accipiter gentilis*) in Poland and a greater white-fronted goose (*Anser albifrons*) in Germany. The goshawk was found dead in the protection area established in Lubartowski district due to a HPAI poultry outbreak, just 7 days after the detection of the outbreak in poultry, suggesting that the raptor could have acquired the infection from the poultry. In this context, it is noteworthy that goshawks do not commonly feed on dead animals (ref), so it is more likely that this goshawk contracted the infection through contact with live birds, wild or domestic. The goose was found dead on 16 January 2020 in Brandenburg, close to the border with Poland. There were 13 outbreaks of HPAI A(H5N8) in Poland between 30 December 2019 and 16 January 2020. Based on this information, it cannot be ruled out that this goose was infected by spill-over of virus from wild or domestic birds.

Table 3: Cases of HPAI A(H5N8) infection in free-living wild birds in Europe reported to the World Organisation for Animal Health (OIE) by country, outbreak and species, 16 November 2019 – 15 February 2020 (OIE, online-b)

Country	Number of outbreaks by country	Number of cases by outbreak	Number of wild bird species involved in the outbreak	List of wild bird species involved in the country	Total wild bird cases
Poland	1	1	1	Northern goshawk (*Accipiter gentilis*)	1
Germany	1	1	1	Greater white-fronted goose (*Anser albifrons*)	1
Total	**2**	**-**	**-**	**(2)**	**2**

Information extracted from the scientific literature

No literature was found on phenotypic characterisation of HPAI viruses circulating in the EU in wild birds in the last two years.

4.2.2.3. LPAI in domestic birds

Characterisation of the LPAI-affected poultry establishments

Between 16 November 2019 and 15 February 2020, two LPAI outbreaks were notified in the poultry sector in Europe, one A(H5N3) in United Kingdom and one A(H5N1) in Denmark. The A(H5N3) was detected at a broiler breeder establishment located in the county of Suffolk. The A(H5N1) outbreak was identified at an organic laying hen establishment in the municipality of Aalborg. Information available from the ADNS (European Commission, online-a), from the OIE (OIE, online-a) and provided by Member States that characterises the LPAI outbreak is presented in Table 4.

Table 4: Characteristics of the LPAI-affected poultry and captive bird establishments in Europe, 16 November 2019 – 15 February 2020 (n=2)

Country	Virus subtype	Poultry species	Surveillance stream	Presence of signs in the outbreaks	Date of suspicion	Number of susceptible birds
United Kingdom	A(H5N3)	Chicken[(a)]	Passive[(c)]	Yes[(d)]	4/12/2019	27,000
Denmark	A(H5N1)	Chicken[(b)]	Active	No	27/01/2020	48,000
Total						75,000

(a) Broiler breeders laying.
(b) Laying hens.
(c) Testing for exclusion.
(d) Drop of egg production.
Data source: ADNS, OIE, Member States.

For the UK outbreak, the most likely source of infection was considered to be indirect contact with wild birds. Extensive epidemiological investigations did not give rise to any suspicion that disease was likely to have either originated from, or has been spread onwards to, any other premises investigated in connection with the affected establishment. Although the epidemiological investigation concluded that the most likely route of introduction of virus to this establishment was indirect contact with wild birds, an incursion such as this to an individual premises remains a low likelihood event and is influenced by the effectiveness of the biosecurity measures that have been implemented at the particular site (APHA, 2020).

For the Danish outbreak, the epidemiological investigation concluded that the most likely cause of the disease was contact with wild birds.

4.2.3. 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 update of the nomenclature of the A/goose/Guangdong/1/1996-lineage H5Nx virus (Smith et al., 2015). While a revised nomenclature of clade 2.3.4.4 viruses is pending, the genetic clustering described by Lee et al. (2018) is used in this report. The authors recognised four genetic groups (a, b, c, d) within clade 2.3.4.4 that have been identified in China since late 2012. Clades 2.3.4.4a and 2.3.4.4b A(H5) viruses spread globally through wild bird migration during 2014–2015 (2.3.4.4.a) and 2016–2017/2017–2018 (2.3.4.4.b), while clades 2.3.4.4c and 2.3.4.4d A(H5) HPAI viruses have mainly circulated in poultry in Asia (Lee et al., 2018). The latter genetic groups have been sporadically associated with human infections in South-East Asia (Lee et al., 2017). One human case in China was found to be infected with A(H5N6) of the 2.3.4.4b clade in 2017 with a different gene composition from viruses of the same clade circulating in birds in Europe.

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

The complete genome of seven representative HPAI A(H5N8) viruses of clade 2.3.4.4b from the index cases in domestic birds in Poland, Hungary, Romania, Slovakia and Czechia and from the two cases in wild birds in Poland and Germany was characterised. At whole genome level the European viruses cluster together in all the phylogenies and separately from the 2.3.4.4b A(H5N8/H5N6) viruses previously detected in European countries. Specifically, in the PB2, PA, HA, NA, MA and NS phylogenies they are closely related to A(H5N8) viruses collected between April 2018 and June 2019 in South Africa (similarity of 98.1%–99.7%) and in Nigeria (similarity of 98.6%–99.5%), while in the PB1 and NP phylogenies they cluster with LPAI viruses collected in August and October 2018 in wild birds in the Kurgan and Chany regions of Russia (similarity of 99.0%–99.2% for PB1 and 98.3%–98.6% for NP) (Figure 12). The mean time to the most recent common ancestor estimated for the HA, NA, NP and PB1 genes for this novel viral introduction varies from July to September 2019.

These findings suggest that the progenitors of this European strain circulated in the African continent. The virus has emerged from reassortment events between African and Eurasian AI viruses, likely in wild migratory birds in Asia during the summer, and then spread to eastern Europe with the autumn migration. The high genetic relationship between viruses collected from wild and domestic birds supports the hypothesis of the central role of wild birds in the virus spread. This is the first evidence of a possible implication of wild bird migration in the long-distance spread of HPAI viruses from Africa to Eurasia. As more sequencing data becomes available, the origin and spatial dynamics of this strain will be clearer.

On the other hand, analyses of viruses collected from the first three outbreaks in Bulgaria which occurred one within and two outside the reporting period for this report indicate the co-circulations of two virus subtypes, HPAI A(H5N8) and A(H5N2). The two strains were both detected in the first Bulgarian outbreak (domestic duck establishment). The genetic characterzation shows that the HA and N8 genes are related to HPAI A(H5N8) viruses of clade 2.3.4.4b identified in Bulgaria in 2018–2019 and clusters separately from the HPAI A(H5N8) viruses currently circulating in East-Central Europe, while the N2 sequence clusters with LPAI A(H6N2) viruses collected in Bulgaria in 2009–2010 (95.7%–96.6% similarity)

To date, there is no evidence of mutations associated with mammalian adaptation in all the analysed viruses.

Analyses were based on sequence data: a) deposited in GISAID; b) donated by Member States via the EURL (IZSVe); c) produced by the EURL from submitted viruses.

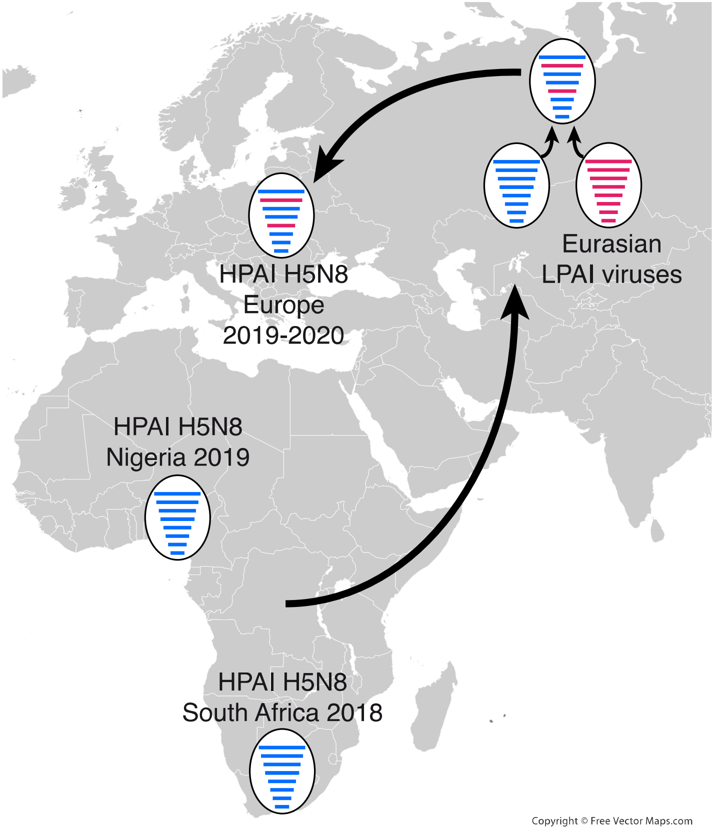


Figure 12. Genesis and proposed geographical spread of the 2019-2020 European A(H5N8) viruses

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

The HA gene of the LPAI A(H5N3) virus identified in December 2019 from a single chicken broiler breeder in the United Kingdom (A/chicken/England/032739/19), shares a common progenitor with the virus derived from an A(H5N1) LPAI chicken case detected in Scotland in January 2016, while the remaining gene segments match closely (nucleotide identities of full gene sequences in the range 98-99%) with those of contemporary viruses from Eurasian wild birds. Such data support the assumption of an indirect/direct introduction from wild birds, rather than the undisclosed maintenance of the virus in poultry populations in the last three years.

The genes of the two surface glycoproteins of the LPAI A(H5N1) virus sampled in January 2020 from a layer establishment in Denmark cluster with LPAI viruses circulating in wild and domestic birds in Europe. Specifically, the HA gene of the Danish virus shows an identity of 97.2% with an A(H5N1) virus identified in poultry in Scotland (2016), while the NA gene possesses a similarity of 99.3% with A(H1N1) viruses collected from wild birds in Italy (2018) and shares a common ancestor with the A(H3N1) viruses responsible for the 2019 epidemic in poultry in Belgium and France.

Genetic characterisation of avian influenza virus of the A(H1) subtype circulating in Europe

In addition to the A(H5) subtype, it is also worth describing the genetic properties of the A(H1N1) virus identified in January 2020 from an Italian domestic turkey flock that showed no clinical signs. HA gene phylogeny of the virus revealed that it belongs to the Eurasian avian-like swine (H1avN1) lineage, clade 1C.2.1 (Anderson et al., 2016). Whole genome sequencing revealed that this virus has a nucleotide identity of 99.9%–100% and a single amino acid difference (PB1 protein) with the A(H1N1) viruses collected from swine farms in proximity to the turkey flock. The high similarity between the swine and turkey A(H1N1) viruses indicates that influenza A virus coming from pigs may be capable of circulating silently in turkeys. Such an event, as well as the infection of turkeys with human influenza viruses, such as the A(H1N1)pdm09 recently reported in a turkey breeder flock (EFSA et al., 2019b), may favour the occurrence of reassortment events with avian influenza viruses and the emergence of viruses with zoonotic potential. These findings, combined with previous evidence of a virus transmission of the H1avN1 lineage to humans (Fraaij et al., 2016; Rovida et al., 2017), highlight the importance of surveillance of turkey premises located in areas with a high density of pig farms.

4.2.4. Human cases due to A(H5N8) or A(H5N6) viruses detected in Europe

Although more than 10,000 people were estimated to have been exposed to HPAI viruses during the events from October 2016 to September 2018 (Adlhoch et al., 2019), no human infection with A(H5N6) or A(H5N8) viruses, as detected in wild birds and poultry in Europe, has been reported during the period covered by this report or previously (Adlhoch et al., 2018; Thornton et al., 2019). Also, a study following up and testing people exposed to infected birds during A(H5N8) outbreaks in South Africa did not report transmission to humans (Valley-Omar et al., 2020). One study of people exposed to infected or perished birds during the AI outbreaks between November 2016 and March 2017 did identify some individuals reactive for antibodies to A(H5N8) cla de 2.3.4.4 (Ilyicheva et al., 2018). A risk assessment on A(H5N8) is available from WHO stating that the likelihood of human infection with A(H5N8) virus is low (WHO, online). A few countries reported that they have followed up people exposed during the recent outbreaks and transmission to humans has not been identified; e.g. in Slovakia, people at possible risk were told by the epidemiologists to be vigilant, keep their contact with other people to a minimum and to monitor their health status. Should symptoms occur, the respective health care staff would inform the regional public health authorities. Laboratory support is performed by the public health authority and the respective regional public health authorities shared relevant information about the situation.

4.3. Applied prevention and control measures in Europe, 16 November 2019– 15 February 2020 (TOR 3)

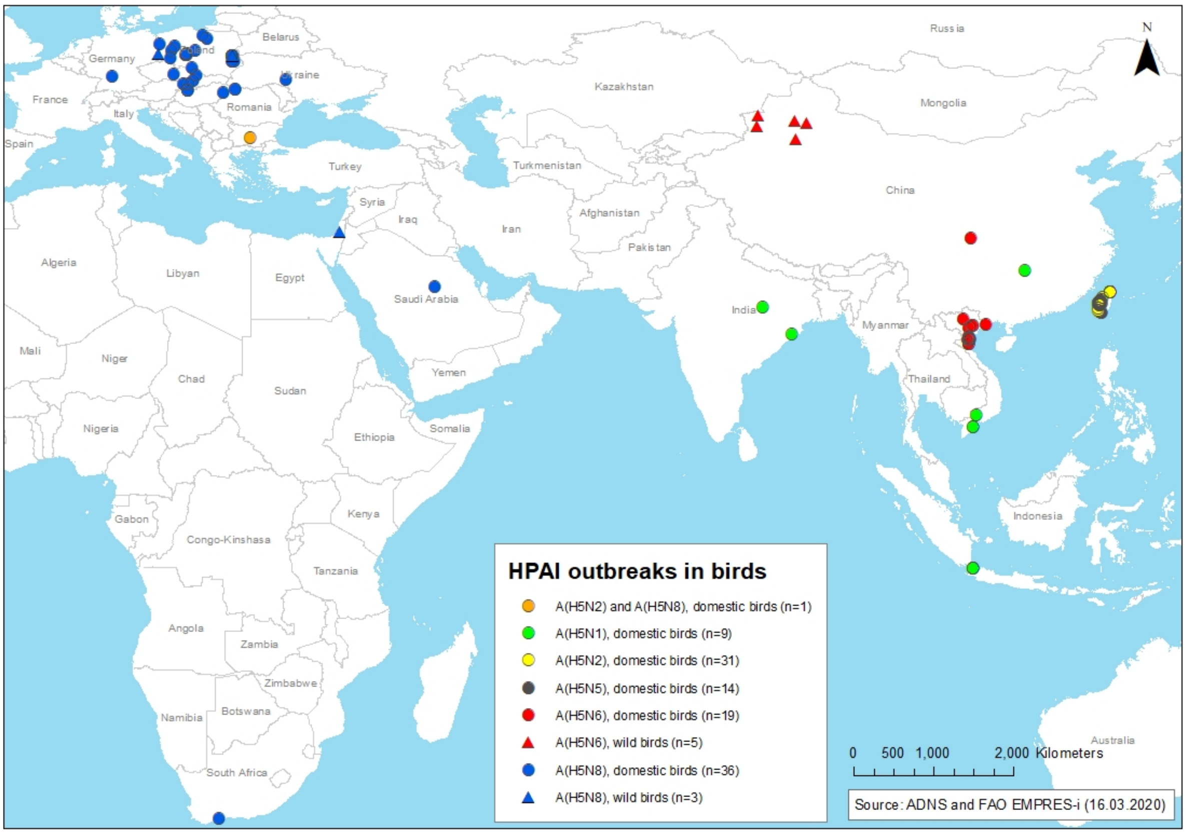
From 16 November 2019 to 15 February 2020, 33 HPAI outbreaks at poultry establishments were notified in Europe. For the description of the control and prevention measures applied in the affected Member States, see Annex A.

4.4. The avian influenza situation in other countries not reporting via ADNS, 16 November 2019 – 15 February 2020 (TOR 4)

An overview of the HPAI outbreaks notified from other countries not reporting via ADNS but via the OIE or national authorities from 16 November 2019 to 15 February 2020 is presented in Table 5 and Figure 13. For the purposes of this report, only findings of AI viruses occurring in countries that are considered to be of epidemiological interest for the EU/EEA or of public health relevance are described.

Table 5: Number of HPAI outbreaks in other countries not reporting via ADNS, by virus subtype and country, 16 November 2019 15 February 2020 (n=81)

Region	Country	HPAI outbreaks							
		Domestic birds					Wild birds		All HPAI
		A(H5N1)	A(H5N2)	A(H5N5)	A(H5N6)	A(H5N8)	A(H5N6)	A(H5N8)	
Africa	South Africa					1			1
Asia	China	1			1		5		7
	India	2							2
	Indonesia	3							3
	Israel							1	1
	Saudi Arabia					1			1
	Taiwan		31	14					45
	Vietnam	3			18				21
Total	**(8 countries)**	9	31	14	19	2	5	1	81



Source: ADNS and FAO EMPRES-i (16.03.2020)

Figure 13: Geographical distribution, based on available geocoordinates, of HPAI outbreaks in Europe, Asia and Africa in domestic birds, by A(H5N1) as green, A(H5N2) as yellow, A(H5N5) as dark grey, A(H5N6) as red, A(H5N8) as blue, A(H5N2) and A(H5N8) as orange, 16 November 2019 to 15 February 2020 (n=118)

4.4.1. HPAI A(H5N1)

4.4.1.1. Domestic and wild birds

Detections

In contrast to the last reporting period, several countries notified cases of the Asian lineage HPAI A(H5N1) in domestic birds. A single outbreak was confirmed on a medium-sized chicken farm in Hunan province, China. Furthermore, HPAI A(H5N1) was detected in quail and chicken kept on a large poultry farm in Chhattisgarh province and on a small poultry farm in Orissa province, India. Several cases of HPAI A(H5N1) were detected in backyard farms keeping chicken and ducks in the village of Kilasah in central Indonesia in November 2019. Vietnam notified three outbreaks at two small and at a medium-sised poultry farm in the relevant reporting period to the OIE. Again, no wild bird cases of HPAI A(H5N1) were reported in the relevant time period (Figure 14).

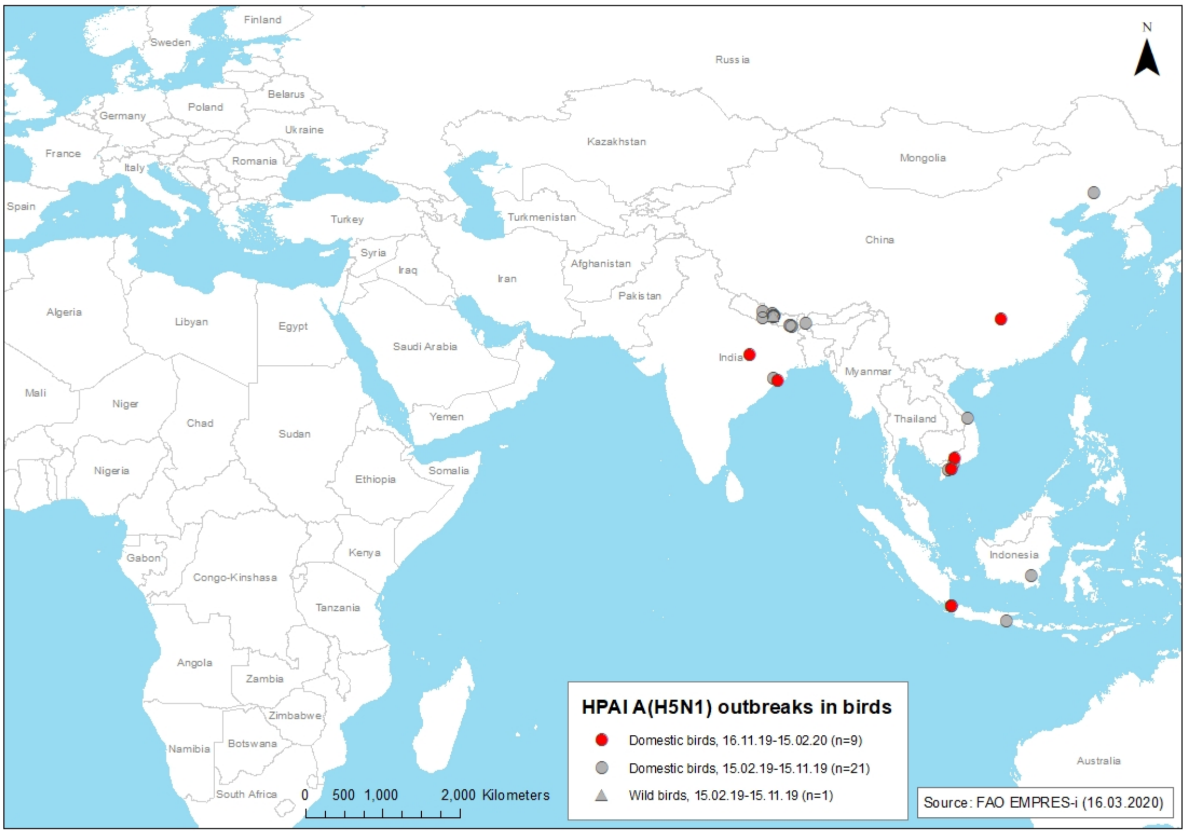


Figure 14: Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N1) outbreaks in domestic birds (circles) and wild birds (triangles) (n=31); grey symbols indicate outbreaks that occurred between 15 February 2019 and 15 November 2019, red symbols indicate outbreaks that occurred between 16 November 2019 and 15 February 2020 (FAO, online-b)

Information extracted from the scientific literature

Full genome sequences were obtained by Hassan et al. (2020) from two clade 2.2.1.2 HPAI A(H5N1) viruses associated with two outbreaks detected in March 2017 in Egypt: the infected poultry species were ducks and laying hens (reported mortality rates were 15% and 30%, respectively). Their genotype was unaltered compared with previously characterised HPAI A(H5N1) viruses in Egypt, belonging to the same clade.

Based on full H5 and N1 gene segment sequences, Fusade-Boyer et al. (2019) characterised a Togolese HPAI A(H5N1) strain isolated from a poultry outbreak in April 2018, associated with high declared mortality rates in chickens and quails (84% and 27%, respectively). This virus was a reassortant between two distinct genetic subgroups of clade 2.3.2.1c HPAI A(H5N1) viruses that have been circulating in western Africa since early 2015. The most closely related sequences belonged to viruses isolated in Nigeria in 2015 and 2016.

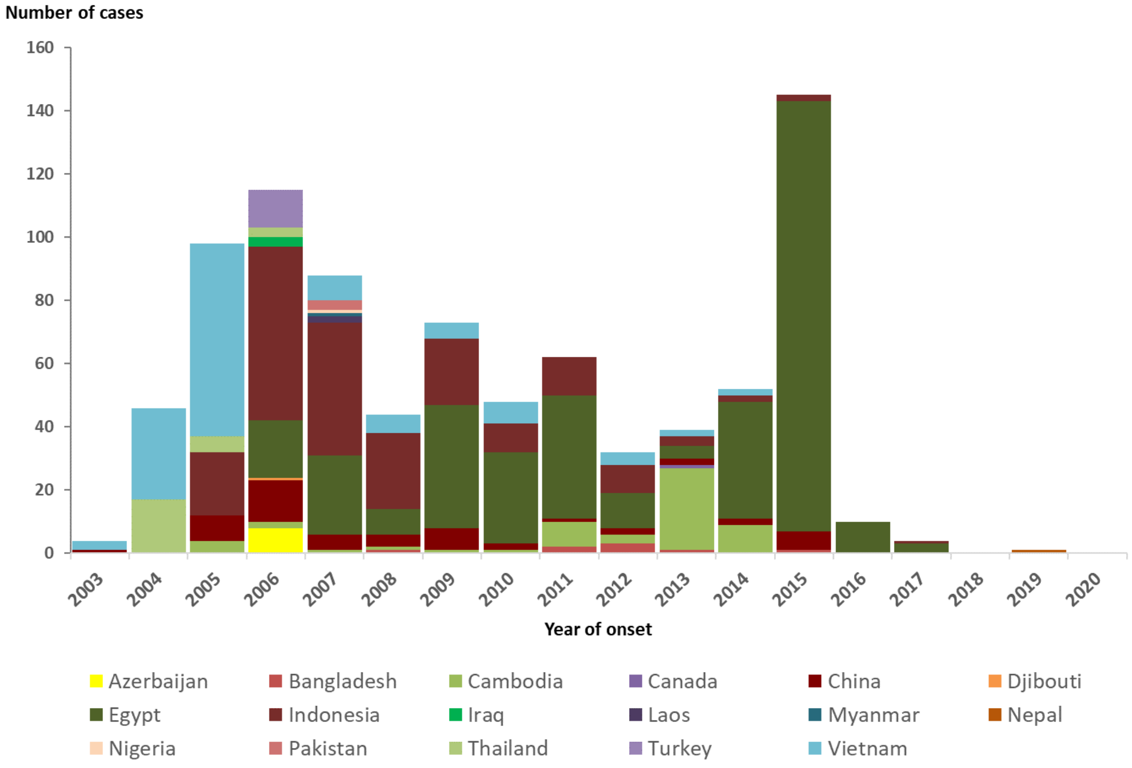
Park et al. (2020) characterised the full genomes of 13 Laotian HPAI A(H5N1) strains involved in poultry outbreaks from late 2015 to 2018: these strains were grouped into two distinct genotypes, discriminated by their NS gene segment. Their common gene constellation background was likely generated by reassortment between two progenitor genotypes (proposed type strains for each of those had been isolated in Vietnam in 2014), leading to the emergence of the first Laotian genotype comprising clade 2.3.2.1c HPAI A(H5N1) strains from early outbreaks, December 2015 to February 2018. A last reassortment step involving only the NS gene segment generated the second Laotian genotype, isolated in October 2018. In all these strains, the only reported mammalian-adapting mutation was the T165A substitution in the H5 segment, resulting in loss of a potential glycosylation site. All viruses also had a 20-amino acid deletion in the stalk domain of their N1 protein, associated with adaptation to terrestrial poultry species, as well as the H274Y mutation related to oseltamivir resistance.

4.4.1.2. A(H5N1) in mammals (excluding humans)

During the reporting period, no new relevant information concerning mammals (humans excluded) has been published on the phenotypic and genetic characterisation of HPAI A(H5N1) viruses circulating in Africa and Asia.

4.4.1.3. Human infections due to A(H5N1)

No new human case due to AI A(H5N1) has been reported since the last report (EFSA et al., 2017). Since 2003, and as of 15 February 2020, 861 laboratory-confirmed cases of human infection with AI A(H5N1) virus, including 455 deaths, have been reported from 17 countries outside the EU/EEA (WHO, 2019c, b) (Figure 15).



Data source: WHO (WHO, 2019c)

Figure 15: Distribution of confirmed human cases of A(H5N1) by year and country of reporting, 2003 – 15 February 2020 (n=861)

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

4.4.2.1. Domestic and wild birds

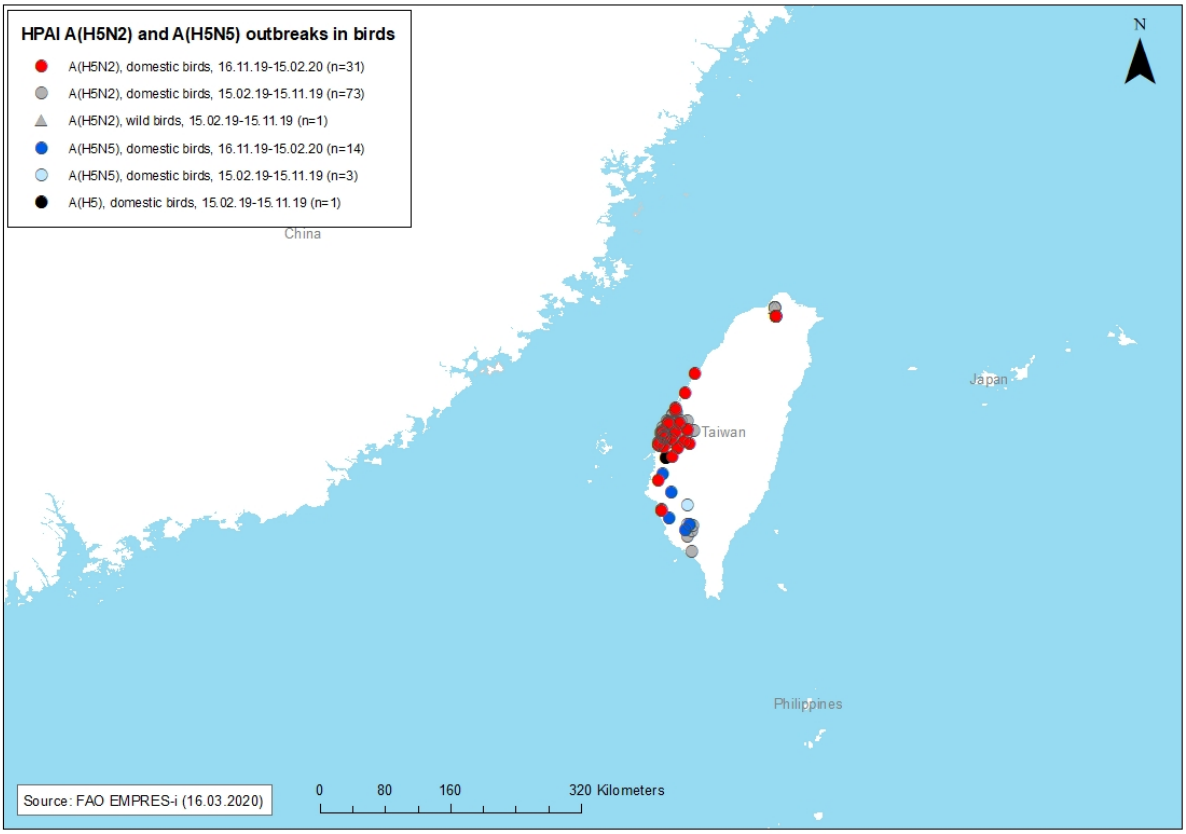
Detections

The Taiwanese lineage HPAI A(H5N2) has been in circulation in Taiwan since 2012 and caused severe outbreaks at chicken, duck, goose and turkey establishments. Between 16 November 2019 and 15 February 2020, Taiwan reported 31 new outbreaks of HPAI A(H5N2) in chicken, ducks, goose and turkey farms. Beside five cases on backyard farms, all other outbreaks were detected on medium-sized poultry holdings (Figure 16). The Taiwanese lineage of HPAI A(H5N2) (clade 2.3.4.4) differs from the Eurasian HPAI A(H5N2) lineage, 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 in 2016–2019 (EFSA et al., 2019a) and in Bulgaria in 2020.

Furthermore, the Taiwanese government reported 14 new outbreaks of HPAI A(H5N5) on backyard and medium-sized chicken farms in southern Taiwan (Figure 16). No sequence data are available at the moment to determine the clade and relationship of this HPAI A(H5N5) virus with other AI viruses.

Information extracted from the scientific literature

Hassan et al. (2020) obtained the full genome of a reassortant clade 2.3.4.4b HPAI A(H5N2) virus identified in Egypt in January 2019, from infected broiler chickens (47% reported mortality rate). The H5 segment was most closely related to viruses identified in 2017 in Egypt. All other seven segments were related to LPAI A(H9N2) viruses circulating in Egypt: PB2, PB1, PA and NS segments derived from novel reassortant A(H9N2) strains that have been first detected in pigeons in 2014; the NP segment was most closely related to A(H9N2) strains circulating in chickens since 2010; the NA and MP segments were similar in both pigeon and chicken A(H9N2) strains, their relationship with the corresponding sequences of the reassortant A(H5N2) virus could not be discriminated. No new mutations have been reported and do not suggest any increased mammalian adaptation.



Source: FAO EMPRES-i (16.03.2020)

Figure 16: Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N2) and A(H5N5) outbreaks in domestic birds (circles) and wild birds (triangle) outside Europe (n=123); grey symbols indicate HPAI A(H5N2) outbreaks that occurred between 15 February 2019 and 15 November 2019, red symbols indicate HPAI A(H5N2) outbreaks that occurred between 16 November 2019 and 15 February 2020, black symbols indicate HPAI A(H5N5) outbreaks that occurred between 16 November 2019 and 15 February 2020 (FAO, online-b)

4.4.3. HPAI A(H5N6)

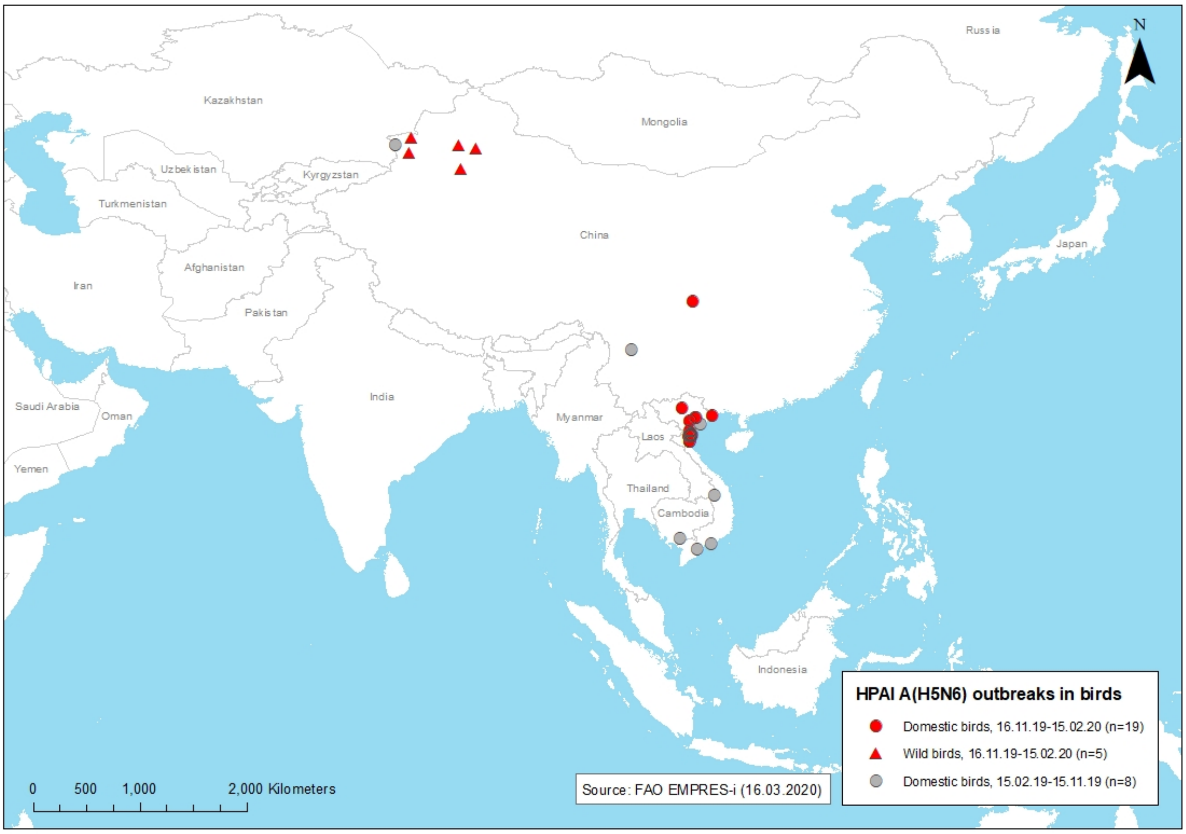
4.4.3.1. Domestic and wild birds

Detections

In the relevant reporting period, Vietnam reported 18 further outbreaks of the zoonotic reassortment of HPAI A(H5N6) clade 2.3.4.4c on backyard and medium-sized commercial poultry farms. Furthermore, HPAI A(H5N6) was detected in poultry on a farm in Sichuan province and in five mute swans (*Cygnus olor*) at several northwestern locations near the Kazakhstan border in Xinjiang Uygur Autonomous Region in January 2020 (Figure 17).

Information extracted from the scientific literature

Li et al. (2019) reported the full genomes of clade 2.3.4.4c HPAI A(H5N6) viruses detected in January 2018 from an outbreak in captive peacocks (*Pavo cristatus*) in Jiangxi, China. All gene segments were closely related to HPAI A(H5N6) virus sequences previously detected in southern China. All reported genomic determinants were consistent with an avian-like α-2,3 receptor specificity and a limited adaptation to mammalian hosts. An 11-amino-acid deletion in the N6 protein stalk region was also present, potentially associated with adaptation and increased virulence in terrestrial poultry species. In vivo experimental studies confirmed these predictions: although the isolates had an intravenous pathogenicity index (IVPI) of 3.0 in chickens (typical of an HPAI polybasic H5 cleavage site sequence), inoculation of 10^6 plaque-forming units induced no mortality in infected 7-week-old BALB/c female mice.



Source: FAO EMPRES-i (16.03.2020)

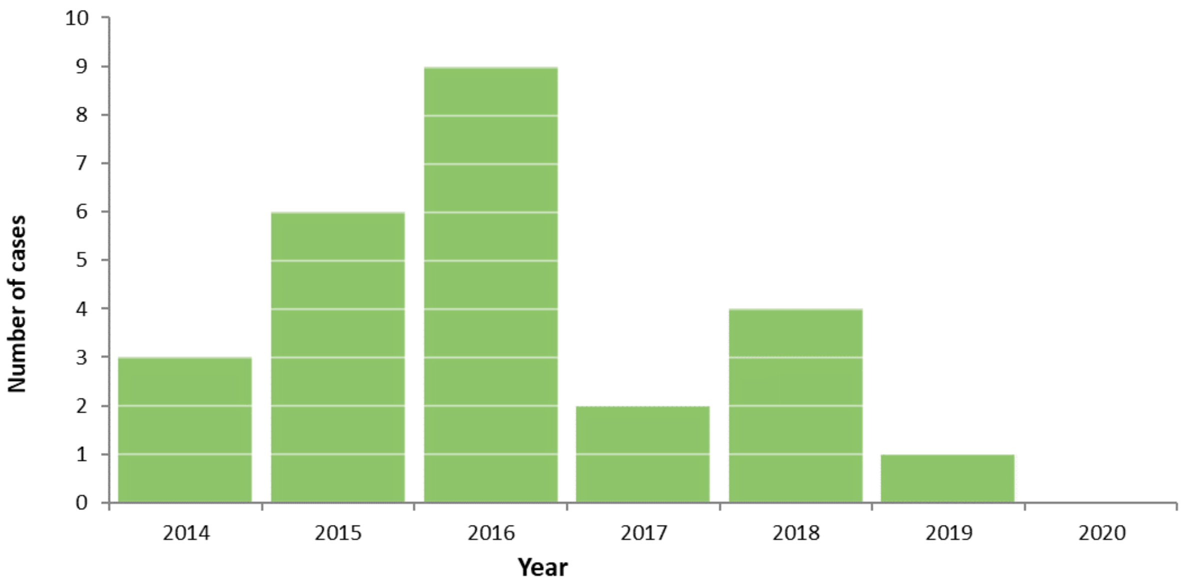
Figure 17: Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N6) outbreaks in domestic birds (circles) and wild birds (triangles) (n=32); grey symbols indicate outbreaks that occurred from 15 February 2019 to 15 November 2019, red symbols indicate outbreaks that occurred from 16 November 2019 to 15 February 2020 (FAO, online-b)

4.4.3.2. A(H5N6) in mammals (excluding humans)

During the reporting period, no new relevant information concerning mammals (humans excluded) has been published on the phenotypic and genetic characterisation of HPAI A(H5N6) viruses circulating in Africa and Asia.

4.4.3.3. Human infections due to A(H5N6)

No new human case due to AI A(H5N6) has been notified since the last EFSA report (EFSA et al., 2019c). Since 2014, and as of 15 February 2020, 25 laboratory-confirmed cases of human infection with AI A(H5N6) viruses of clade 2.3.4.4 circulating in South-East Asia have been reported globally (Figure 18). WHO lists 24 human cases of AI A(H5N6), including 15 with fatal outcomes (WHO, 2019b, d, a). One additional case from 2015 was described by Li et al. (2016). Twelve deaths due to A(H5N6) had been reported between 2014 and 2017 (Jiang et al., 2017). All of the cases were infected and detected in mainland China (WHO, 2019d).



If date of onset is not available, the date of reporting has been used; the epicurve includes one case reported in the literature with year of onset in 2015.
Source: ECDC line list (described above).

Figure 18: Number of human cases due to A(H5N6), clade 2.3.4.4, infection by year of onset, China 2014 – 2020 (n=25)

4.4.4. HPAI A(H5N8)

4.4.4.1. Domestic and wild birds

Detections

In November 2019 South Africa reported the last outbreak of HPAI A(H5N8) virus clade 2.3.4.4b on a commercial ostrich farm in the Western Cape province. Furthermore, Saudi Arabia notified an outbreak on a very large poultry farm near the capital city Riyad. It is the first outbreak of this lineage since July 2018. In contrast to the last report, HPAI A(H5N8) has also been detected in a wild bird. Israel confirmed HPAI A(H5N8) in a Bonelli’s eagle (*Aquila fasciata*) found with neurological symptoms in the Jordan valley (Figure 19).

Information extracted from the scientific literature

Abolnik (2019) described two reassortant HPAI A(H5N8) viruses characterised in northern South Africa, from poultry outbreaks in quails (*Coturnix japonica*), April 2018, and in chickens, June 2018. For their PB1, PA, H5, N8 and MP segments, both viruses shared most recent common ancestors with HPAI A(H5N8) strains detected in South Africa and Zimbabwe in 2017, and had closer phylogenetic relationships with northern cluster South African 2017 viruses than with southern cluster viruses. The most recent common ancestors for the PB2, NP and NS segments were HPAI A(H5N8) strains detected in Cameroon, Democratic Republic of Congo, Uganda and Egypt in 2017.

Hemida et al. (2019) characterised the full genome of 12 HPAI A(H5N8) viruses isolated in Saudi Arabia from outbreaks in backyard flocks, between December 2017 and June 2018: viruses were isolated from ostriches, pigeons and ducks. These clade 2.3.4.4b A(H5N8) viruses were all genetically highly related and formed a closely related monophyletic group, also including A(H5N8) viruses reported previously from various avian species in Riyadh in 2017.

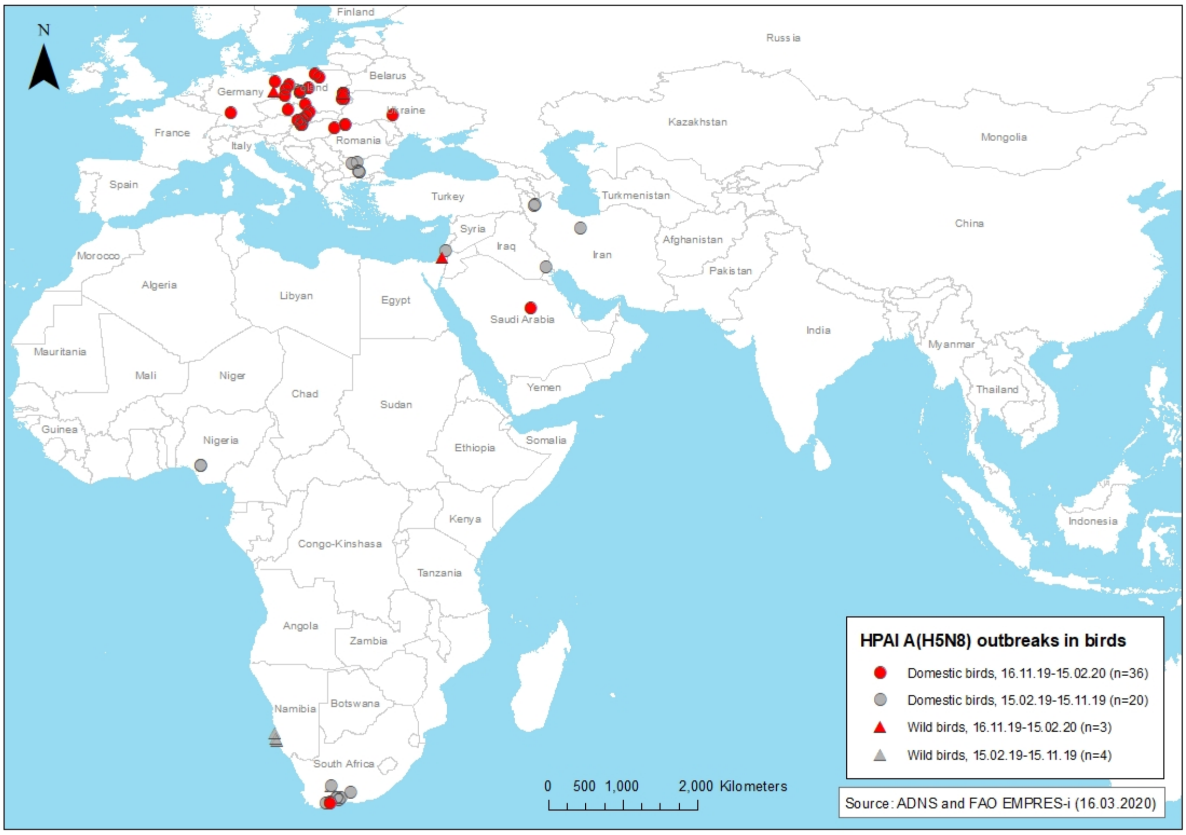


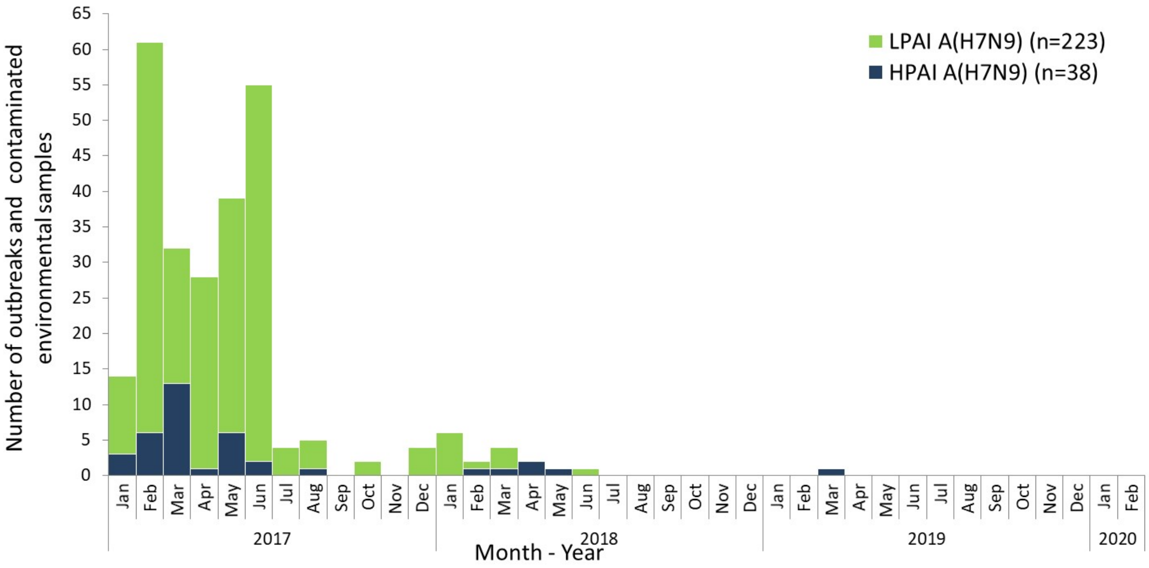
Figure 19: Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N8) outbreaks in domestic birds (circles) and wild birds (triangles) (n=63); grey symbols indicate outbreaks that occurred from 15 February 2019 to 15 November 2019, red symbols indicate outbreaks that occurred between 16 November 2019 and 15 February 2020 (FAO, online-b)

4.4.5. HPAI-LPAI A(H7N9)

4.4.5.1. Domestic and wild birds

Detection

No LPAI or HPAI A(H7N9) cases were notified in poultry or wild birds within the relevant time period for this report. The last case was reported from Liaoning province, China, in March 2019 (Figure 20). The nationwide A(H7N9) vaccination campaigns for poultry, with the exception of poultry in AI-free zones and export farms, started extensively in September 2017 (FAO, online-a).



Data source: FAO EMPRES-i (16.03.2020)

Figure 20: Distribution of confirmed LPAI and HPAI A(H7N9) outbreaks among birds and environmental samples in China, by month, 1 January 2017 – 15 February 2020 (n=261)

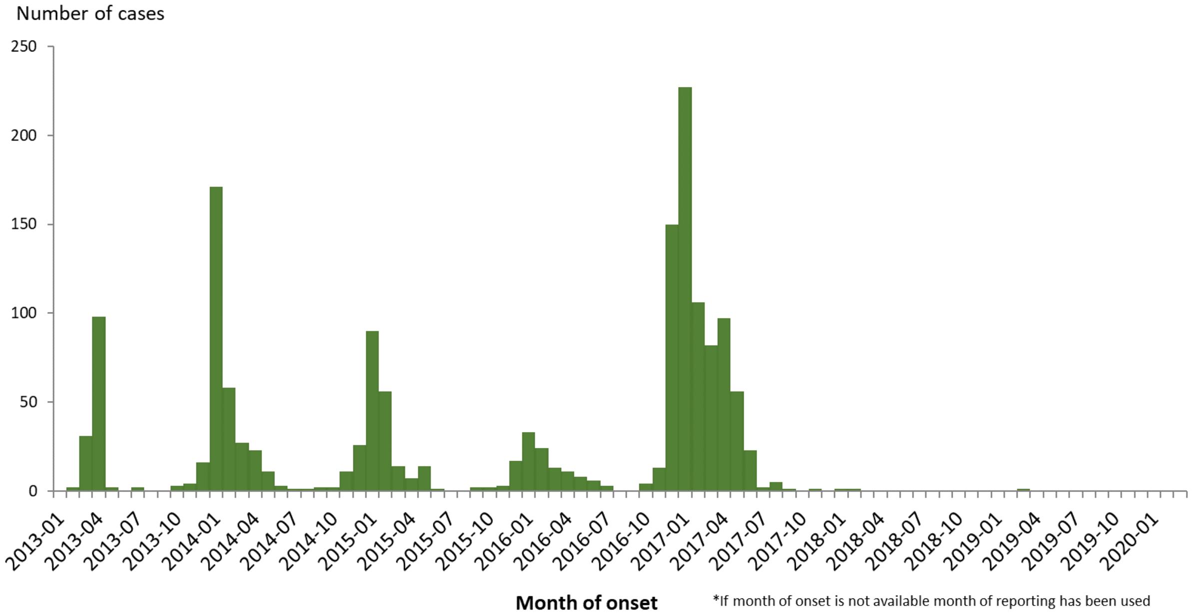
Information extracted from the scientific literature

Seven HPAI A(H7N9) were isolated from infected chickens in 2019 in China, by Jiang et al. (2020). IVPI values in chickens were high (range: 2.18–2.36), however pathogenicity in ducks was low: although the virus replicated in various internal organs and was shed by the oro-pharyngeal and cloacal routes, no mortality or clinical signs of infection were observed within 14 days after inoculation. Full HA sequences from these viruses clustered together and were distinct from sequences of HPAI A(H7N9) viruses isolated in 2017 and 2018. Antigenic drift of these 2019 A(H7N9) strains was observed by serological cross-testing against the H7-Re2 vaccine, and confirmed by lack of protection of this vaccine in chickens challenged with two selected HPAI A(H7N9) strains.

Qu et al. (2020) characterised a reassortant LPAI A(H7N4) identified in 2018 from a human patient and from chickens and ducks raised by the same patient. These viruses derived their segments from multiple progenitor viruses: PB2, PA, H7, NP and NS segments were closely related to LPAI A(H7N7) viruses detected in China and Japan in 2014; N4 and MP segments were related to an A(H8N4) virus characterised in Russia in 2014; whereas the PB1 segment was likely related to an A(H5N1) virus identified in China in 2015. Based on sequence data, the reassortant A(H7N4) had an avian-like receptor binding affinity. The human-origin virus had acquired the major PB2 E627K substitution, and 17 other mutations were identified that may play an unevaluated critical role in human adaptation and increased virulence of the virus.

4.4.5.2. Human infections due to A(H7N9)

No human cases due to AI A(H7N9) have ever been reported from Europe and no human case has been reported globally since the last EFSA report. Since February 2013, a total of 1,568 human cases have been reported from outside of Europe (Figure 21), including at least 615 deaths (39%) (WHO, 2019d, b). Thirty-two human cases, 13 of them fatal, have been infected with HPAI virus A(H7N9) according to the Chinese National Influenza Center (Chinese National Influenza Center et al., 2018).



Source: ECDC line list (described above).

Figure 21: Number of human cases due to A(H7N9), infection by month and year of onset, 2013 – 2020 (n=1,568)

A recent study following hospitalised patients with A(H7N9) infection showed persistent lung damage and long-term pulmonary dysfunction in patients surviving the infection (Wang et al., 2020).

4.4.6. LPAI A(H9N2)

4.4.6.1. Domestic and wild birds

Detection

As mentioned in previous EFSA reports, A(H9N2) is the most commonly detected non-notifiable subtype of influenza virus in poultry in Asia, the Middle East and Africa (Zecchin et al., 2017; Bonfante et al., 2018; Chrzastek et al., 2018; Xu et al., 2018; Zhu et al., 2018; Awuni et al., 2019; Kariithi et al., 2019). The endemic status of these regions continued from 16 November 2019 to 15 February 2020.

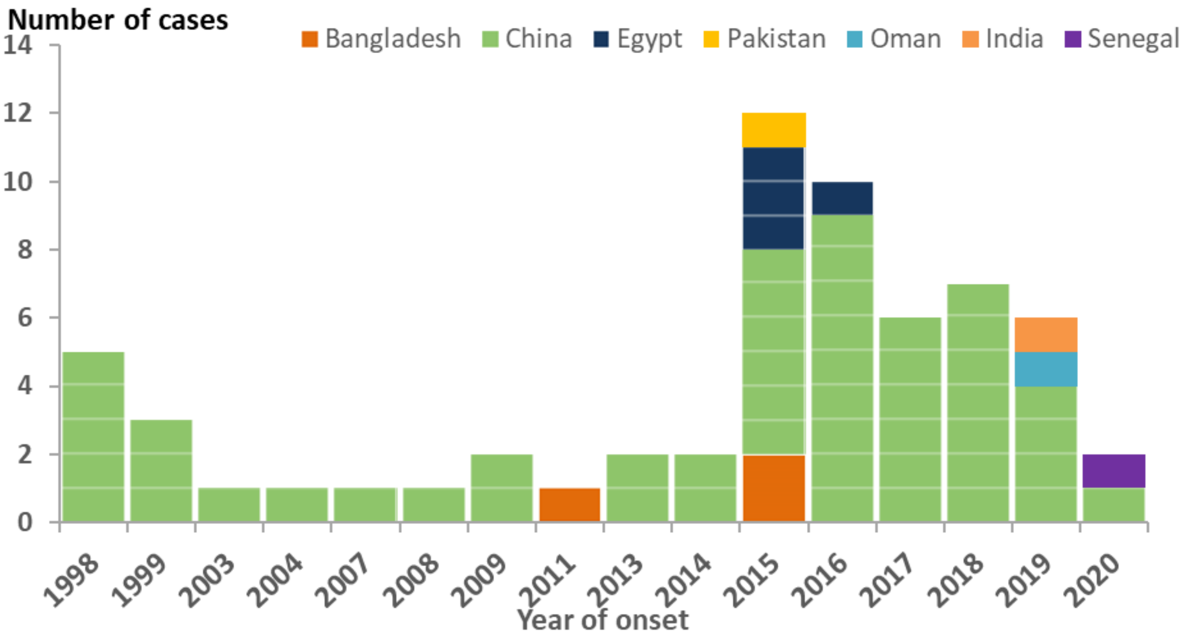
Information extracted from the scientific literature

Alyas et al. (2019) reported isolation in Pakistan, between March and April 2017, of several LPAI A(H9N2) vruses from a healthy duck and a goose in a backyard flock, and from dead chickens in commercial flocks. Based on H9 and N2 sequences, all these isolates belonged to the Middle East B group G1 lineage and were closely related to strains detected in captive zoo birds in Pakistan in 2016. All possessed the Q226L substitution in the H9 gene, associated with increased affinity to mammalian-type receptors.

Lina et al. (2019) compared virulence in mice and transmissibility in guinea pigs of a pair of Y280-like LPAI A(H9N2) viruses: a wild-type virus isolated from chickens in China in 2017, and its mouse-adapted variant following serial in vivo passages. Infections with a 10^6 EID_{50} dose of the wild-type strain did not impair body weight and were not lethal for 6-week-old female BALB/c mice; and infected female guinea pigs did not transmit the wild-type virus to direct or aerosol contact naïve animals. The mouse-adapted variant strain was pathogenic in mice, induced mortality in 5 days, and was transmitted to direct contact and aerosol contact guinea pigs. Although the mouse-adapted virus had acquired 16 amino acid mutations compared with the wild type, introduction of the variant PB2 segment (containing two mutations) in the wild-type virus backbone was necessary and sufficient for efficient aerosol transmission in the guinea pig infection model.

4.4.6.2. Human infections due to A(H9N2)

Two new human cases have been reported from Hong Kong Special Administrative Region, one in a 7-year-old child who visited his grandparents' home in Shenzhen City, Guangdong Province, China, since the last EFSA report (WHO, 2020a, b; The Government of Hong Kong Special Administrative Region Press Release, online) (ref). The boy showed mild symptoms and had disease onset on 4 February 2020. The second case was a child in Senegal with influenza-like illness and reported exposure to backyard poultry. Since 1998, and as of 15 February 2020, 62 laboratory-confirmed cases of human infection with AI A(H9N2) virus, including one death, have been reported globally. Cases were reported from China (51), Egypt (4), Bangladesh (3), India (1), Oman (1), Pakistan (1) and Senegal (1) (ECDC line list) (Figure 22).



Data source: ECDC line list (Peacock et al., 2019; Potdar et al., 2019; WHO, 2019b, 2020a; The Government of Hong Kong Special Administrative Region Press Release, online)

Figure 22: Distribution of confirmed human cases of A(H9N2) by reporting country, 1998 – 15 February 2020 (n=62)

4.5. Scientific analysis of avian influenza spread from non-EU/EEA countries to poultry in the EU/EEA

Possible pathways by which AI viruses can be brought into the EU have been described in previous EFSA reports (EFSA AHAW Panel, 2017; EFSA et al., 2018a; EFSA et al., 2018b).

In comparison to the last report (EFSA et al., 2019c), Section 4.4 showed in the time period of this report from 16 November 2019 to 15 February 2020 there was an increasing number of reported outbreaks in poultry and wild birds, particularly in Asia. The outbreaks of HPAI A(H5N1), clade 2.3.2.1c (China, India, Indonesia and Vietnam), HPAI A(H5N2), clade 2.3.4.4 (Taiwan) and HPAI A(H5N5) (Taiwan) continued in Asia, but no outbreaks were reported in the relevant time period from Africa or the Middle East. By contrast, clade 2.3.4.4b A(H5N8) outbreaks were only notified in Africa (South Africa) and the Middle East (Israel and Saudi Arabia). Moreover, in contrast to previous years, the recent detection of a novel reassortant of HPAI A(H5N8), clade 2.3.4.4b with gene segments closely related to HPAI A(H5N8) viruses collected in Nigeria and South Africa demonstrated that Africa is also a potential source of new virus genes coming to Europe. However, uncertainty regarding the real distribution remains high because information about the virus circulation in some African countries is lacking and close monitoring of the situation is required. Vietnam notified 18 outbreaks in poultry of the novel zoonotic reassortant HPAI A(H5N6) belonging to clade 2.3.4.4c to the OIE during the relevant time period for this report. Besides the detection of HPAI A(H5N6) on a poultry farm in Sichuan province, China reported several cases of HPAI A(H5N6) in mute swans (*Cygnus olor*) in northwestern Xinjiang Uygur Autonomous Region near the Kazakhstan border, one of the key migration areas in northern China. However, there is considerable uncertainty regarding the real geographical distribution of these viruses, particularly in wild birds. Furthermore, spring migration from the wintering to the breeding regions will start in the coming weeks , depending on the climate conditions. Aggregation as well as mixing of wild birds from different geographic origins during migration and spring time, will increase the risk of the infection spreading via this pathway, particulary when the birds will be returning to the wintering sites in autumn.

4.6. Surveillance and diagnosis of human infections and public health measures for prevention and control

4.6.1.1. Surveillance in the EU, diagnosis and options for public health control measures (in relation to the EU)

The measures outlined in the previous EFSA report for November 2017 – February 2018 (EFSA et al., 2018b) remain valid for all different parts.

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

The risk of zoonotic influenza transmission to the general public in EU/EEA countries remains very low, although an increasing number of outbreaks due to AI viruses has been reported in Europe. Transmission to humans of AI viruses, detected in wild birds or poultry in Europe, has not been observed recently.Hhowever, zoonotic transmission of AI viruses cannot be fully excluded in general when AI viruses are present in birds. The use of personal protective measures for people exposed to AI viruses will minimise any residual risk. Overall, AI virus transmission to humans is a rare event and the risk is considered to be very low for viruses adapted to avian species.

The risk of travel-related importation of human AI cases, particularly from Asia, is very low. Currently, only a few sporadic outbreaks in birds and poultry are reported worldwide. Sporadic human cases infected with A(H9N2) LPAI viruses underline the risk of transmission whenever people are exposed to infected birds in countries where A(H9N2) is endemic. Therefore, surveillance of AI viruses in wild birds and poultry in the EU/EEA is important in order to detect newly introduced and circulating viruses and reduce the possible risk of exposure of humans to infected birds.

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Abbreviations

ADNS	Animal Disease Notification System
AI	Avian influenza
CVO	Chief Veterinary Officer
CVV	Candidate vaccine viruses
ECDC	European Centre for Disease Prevention and Control
EFSA	European Food Safety Authority
EEA	European Economic Area
EU	European Union
EURL	European Union Reference Laboratory
FAO	Food and Agriculture Organization
FBO	Food business operator
HPAI	Highly pathogenic avian influenza
IVPI	Intravenous pathogenicity index
LPAI	Low pathogenic avian influenza
NGO	Non-governmental organisation
OIE	World Organisation for Animal Health
PZ	Protection zone
SCOPAFF	Standing Committee on plants, animals, food and feed
SZ	Surveillance zone
TOR	Terms of reference
WHO	World Health Organization

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[2], 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[3], EFSA should provide the technical and scientific assistance to the Commission based on the following Terms of Reference (TOR):

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[2] 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.

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

1. Analyse the epidemiological data on highly pathogenic avian influenza (HPAI) and low pathogenic avian influenza (LPAI), where co-circulating or linked within the same epidemic, from HPAI disease affected Member States.

2. Analyse the temporal and spatial pattern of HPAI and LPAI as appropriate in poultry, captive birds and wild birds, as well the risk factors involved in the occurrence, spread and persistence of the HPAI virus in and at the interface of these avian populations.

3. Based on the findings from the points above, describe the effect of prevention and control measures.

4. Provide for regular quarterly reports updating on the avian influenza situation within the Union and worldwide, in particular with a view to describe the evolution of virus spread from certain regions towards the EU. In case of significant changes in the epidemiology of avian influenza, these reports could be needed more frequently. These reports should in particular closely follow the developments of zoonotic avian influenza viruses (such as HPAI A(H5N6) and LPAI A(H7N9)) in collaboration with the European Centre for Disease Prevention and Control (ECDC).

A.2. Interpretation of the terms of reference

In reply to TOR 1 and TOR 2, this scientific report gives an overview of the HPAI and LPAI outbreaks in poultry, captive and wild birds detected in Europe between 16 November 2019 and 15 February 2020 and reported by Member States and neighbouring countries via ADNS. Member States where AI outbreaks occurred in poultry submitted additional epidemiological data to EFSA, which 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 the performed data collection, reporting and analysis were explained in the first AI overview report (EFSA AHAW Panel, 2017).

If HPAI outbreaks in poultry are detected in the EU, a description of the applied prevention and control measures (TOR 3) is given in the case report provided by representatives from affected Member States and attached as an annex. 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 AI situation in other countries (TOR 4) is based on data submitted via the OIE or reported to the FAO. The description focuses only on findings of AI viruses occurring in countries that are considered to be of epidemiological interest for the EU/EEA or of public health relevance, specifically on HPAI A(H5N1), HPAI A(H5N2), HPAI A(H5N5), HPAI A(H5N6), HPAI A(H5N8), HPAI/LPAI A(H7N9) and LPAI A(H9N2). The background and epidemiology, detections, phenotypic and genetic characterisations are described based on information from confirmed human, poultry and wild bird cases that occurred between 16 November 2019 and 15 February 2020 and on information gathered by performing a literature search on papers published in PubMed from 16 November 2019 to 15 February 2020. Possible actions for preparedness in the EU are discussed.

This report mainly describes information that became available since the publication of the EFSA report for the period August – November 2019 (EFSA et al., 2019c) and that might affect the interpretation of risks related to AI 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 AI outbreaks that occurred in Europe from 16 November 2019 to 15 February 2020 submitted by Member States to the ADNS (European Commission, online-a) were taken into account for this report. In addition, HPAI affected Member States were asked to provide more detailed epidemiological data directly to EFSA on the AI outbreak that occurred in poultry during the same period.

The information, which EU Member States affected by HPAI and LPAI presented to the Standing Committee on Plants, Animals, Food and Feed (SCOPAFF) meetings, and the evidences on HPAI and LPAI outbreaks provided in the info notes from the affected Member States to the European Commission, were consulted to extract the relevant information which is reported in Section 4.2.2. The PDFs of the SCOPAFF presentations are available on the European Commission website (European Commission, online-b).

The public GISAID's EpiFlu™ Database was accessed to download newly released avian influenza sequences.

A descriptive analysis of the data collected is reported in Section 4.2.

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 two years.

Search The PubMed database was searched by using subject index terms and free-text terms combined with the appropriate Boolean operators. Scientific articles added to the database from 16 November 2019 to 15 February 2020 were searched; the search was run on 17 February 2020.

Relevance criteria Scientific articles added to the database from 16 November 2019 to 15 February 2020 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 two 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 123 papers. The articles were subsequently screened against the relevance and eligibility criteria. None of the screened papers was in the end 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.3730481.

B.1.2. Overview of AI outbreaks in other countries not reporting via ADNS (TOR 4)

Data from FAO EMPRES-i (FAO, online-b) on HPAI A(H5N1), HPAI A(H5N2), HPAI A(H5N5), A(H5N6), A(H5N8), HPAI and LPAI A(H7N9) in domestic, captive and wild birds, and environmental samples, were used to describe and to map the geographical distribution of AI cases in domestic and wild birds in Africa, Asia, the Middle East and Europe on the basis of the observation dates. With the purpose of avoiding over-complication of the maps, captive birds and environmental samples have been mapped as domestic birds. Although some of these kept animals may be wild species, in most of the cases captive birds, or, for environmental samples, the birds from which samples have been taken (mainly at live market places) will not move around and not spread the infection by migrating and for this reason have been considered as domestic birds in the maps provided in this report. Only when there was a strong discrepancy between the locality, the administrative regions and geocoordinates, and the outbreaks were not officially reported to the OIE, were the confirmed outbreaks not taken into account in the analysis.

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

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

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

Search The PubMed database was searched by using subject index terms and free-text terms combined with the appropriate Boolean operators. Scientific articles added to the database between 16 November 2019 and 15 February 2020 were searched; the search was run on 17 February 2020.

Relevance criteria Scientific articles added to the database between 16 November 2019 and 15 February 2020 that report information on the presence or absence of clinical signs, pathological changes or mortality or genotypic characterisation (only new information) due to HPAI infection with viruses circulating within the last three years in Asia, Africa or the Middle East in domestic or wild birds or mammals other than humans.

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

Results The search retrieved 109 papers. The articles were subsequently screened against the relevance and eligibility criteria. Ten papers were in the end taken into consideration in the description of phenotypic and genotypic characterisation of HPAI viruses circulating on other continents and in other regions (Africa, Asia, the Middle East) in domestic or wild birds or mammals (excluding humans) in the reporting period.

The search protocol and the results can be consulted at https://doi.org/10.5281/zenodo.3730481.

B.2. Data on humans

The numbers of human cases due to infection with AI viruses have been collected by ECDC. Multiple sources are scanned regularly as part of epidemic intelligence activities at ECDC to collect information about 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.

Annex A – Applied prevention and control measures on avian influenza

Scope

This document provides a brief overview of the specific prevention and control measures applied in Bulgaria, Czechia, Hungary, Poland, Romania and Slovakia between 16 November 2019 and 15 February 2020 in relation to HPAI outbreaks in poultry. Information is only provided if it is considered relevant to the implementation of the following selected measures: increasing the awareness of stakeholders and the general public, housing orders, strengthening biosecurity measures (other than poultry confinement), preventive culling, regional stand still, derogations from restriction zone implementation after risk assessment and hunting ban. This document is made to support the EFSA working group in generating an overview on the application of the selected measures at EU level.

Timing of the applied prevention and control measures

Tables A.1–A.6 provide timelines for the main events that triggered actions in relation to the selected prevention and control measures in Bulgaria, Czechia, Hungary, Poland, Romania and Slovakia. More information on the actions taken is provided in the sections below the tables.

A.1 Bulgaria

Aleksandra Miteva

Animal Health and Welfare, and Feed Control Directorate – Bulgarian Food Safety Agency

Table A.1: Overview of main actions

Date	Event that triggered action	Type of action taken	Target audience
10.01.2020	Epidemiological situation in the EU	Official inspections in poultry holdings for control of biosecurity measures applied by the holdings and self-surveillance programme for control of AI (the programme has been enforced since 2018)	Official veterinarians, private veterinarians poultry farmers .
17.01.2020	Confirmation of HPAI H5N8 outbreak	Measures according to the Directive 2005/94/EC	Official veterinarians, private veterinarians poultry farmers

Increasing awareness of the stakeholders and the general public

1. Regular meetings with representatives of the poultry associations; a number of the measures as increased control and surveillance were proposed by the poultry industry sector itself. The sector is actively engaged and thoroughly cooperates in implementating the control and surveillance activities.

2. Close cooperation with public health authority

3. Publishing information related to the epidemiological situation and prevention and control measures taken:
http://www.babh.government.bg/bg/Page/influentza/index/influentza/%D0%98%D0%BD%D1%84%D0%BB%D1%83%D0%B5%D0%BD%D1%86%D0%B0%20%EF%BF%BD

Housing order

Continuing the enforcement of the measures as described in the previous scientific report.

Strengthening biosecurity measures (other than housing order)

Measures as described in the previous scientific report.

Preventive culling

Not applied.

Regional stand still (beyond the restriction zones specified in the EU Regulation)

Not applied.

Derogations on restriction zone implementation after risk assessment

Not applied.

Hunting.

Not forbidden

A.2 Czechia

Lucie Kalášková, Milada Dubská

Department of Animal Health and Animal Welfare
State Veterinary Administration of the Czech Republic

Information about the first outbreak of highly pathogenic avian influenza (HPAI) in the Czech Republic
On 17 January 2020 the Regional Veterinary Administration of Vysočina Region received information about suspicion of HPAI in a backyard farm in Štěpánov nad Svratkou. In total 15 susceptible birds (12 hens and 3 ducks) were on the farm. Six hens of them died. Dead birds were sent for testing to the State Veterinary Institute in Prague (SVI Prague) – National Reference Laboratory (NRL) for Avian Influenza. NRL in SVI Prague confirmed presence of highly pathogenic avian influenza of subtype H5N8 by PCR method on 18 January 2020. The emergency veterinary measures have been taken according to the Council Directive 2005/94/EC introducing Community measures for the control of avian influenza on 18 January 2020. The emergency veterinary measures included culling of all remaining poultry, disposal of poultry products, feeding stuffs and by-products and preliminary disinfection. The same measures have been ordered for two contact holdings. All these measures were carried out on 18 January 2020. The emergency veterinary measures for the protection and the surveillance zone were taken in line with EU legislation.The final disinfection was carried out on 27 January 2020. The surveillance zone around the outbreak was cancelled on 17 February 2020.

Table A1: Overview of main actions

Date	Event that triggered action	Type of action taken	Target audience (if applicable)
3/1/2020	The poultry outbreak in neighbouring country	Letter to poultry organisations and to Regional Veterinary Administrations Press release about AI situation in neighbouring country and about necessity prevention measures	Poultry organisation and Regional Veterinary Administrations General public, all breeders
6/1/2020	The poultry outbreak in neighbouring country	Letter to Regional Veterinary Administrations - increased control (biosecurity) of poultry holdings in contact with AI affected countries	Regional Veterinary Administrations
From 6/1/2020	New outbreaks in poultry holdings in EU	Regular updating of the website of the State Veterinary Administration about AI situation in Europe	General public, all breeders
From 10/1/2020	New outbreaks in poultry holdings in EU	Regular letters to poultry organisations and to Regional Veterinary Administrations about AI situation in neighbouring countries	Poultry organisation and Regional Veterinary Administrations
17/1/2020	First suspicion in poultry flock (Štěpánov nad Svratkou)	On the spot check, taken measures to prevent spread of the virus, sampling, laboratory testing	
18/1/2020	Confirmation HPAI H5N8 in poultry flock (Štěpánov nad Svratkou))	Publication of emergency veterinary measures for outbreak in Štěpánov nad Svratkou Press release related to first poultry outbreak of AI in the Czech Republic and to emergency veterinary measures taken.	Keeper in the outbreak General public, all breeders
20/1/2020	Confirmation HPAI H5N8 in poultry flock (Štěpánov nad Svratkou)	Publication of emergency veterinary measures for restricted zone	All keepers in the restricted zone
From 20/1/2020	Confirmation HPAI H5N8 in poultry flock (Štěpánov nad Svratkou)	Regular updating of the website of the State Veterinary Administration about AI outbreak in the Czech Republic	General public, all breeders
3/2/2020	New outbreaks in poultry holdings in EU	Letter to Regional Veterinary Administrations - increased control (biosecurity) of poultry holdings in contact with avian influenza countries - continuation	Regional Veterinary Administrations

Increasing awareness of the stakeholders and the general public

On the website of the State veterinary administration was regularly updated the information about avian influenza situation in 2018 - https://www.svscr.cz/zdravi-zvirat/ptaci-chripka-influenza-drubeze/vyskyt-ptaci-chripky-v-evrope-a-ve-svete-2018/

Housing order

Emergency veterinary measures, which are issued by the Regional Veterinary Administration in case of the outbreak and which are binding for a defined restricted area around this outbreak (for protection and surveillance zone), stipulate also for backyard farms in protection zones biosecurity measures which aim is to prevent the contact of poultry with wild birds and their subsequent possible infection.

Strengthening biosecurity measures (other than housing order)

Increased control on biosecuritymeasures applied by poultry holdings in contact with avian influenza affected countries were performed.General public was informed through press on compliance of biosecurity in poultry farms; the current disease situation was available on the website of the State Veterinary Administration: https://www.svscr.cz/zdravi-zvirat/ptaci-chripka-influenza-drubeze/doporuceni-pro-chovatele-drubeze/

Preventive culling

Not applied.

Regional stand still (beyond the restriction zones specified in the EU Regulation)

Not applied.

Derogations on restriction zone implementation after risk assessment

Not applied

Hunting

The releasing of poultry (pheasant, mallard) and other captive birds for the restocking purpose were forbidden in restricted zone (emergency veterinary measure) established around the outbreak.

A.3 Hungary

Georgina Helyes

National Food Chain Safety Office

Table A.3: Overview of main actions

Date	Event that triggered action	Type of action taken	Target audience (if applicable)
12/01/2020	First poultry outbreak	Increasing awareness, release housing order, preventive culling, derogations on restriction zone implementation after risk assessment	

Increasing awareness of the stakeholders and the general public

All information about the avian influenza is available on the website of National Food Chain Safety Office: https://portal.nebih.gov.hu/madarinfluenza

The CVO and head of the National Disease Control Center has communicated the most important information about the epidemic to the national media.

Housing order

On 16 January 2020 the 1/2020 CVO Decision entered into force which ordered the closed keeping of poultry (including backyard) in the whole country: https://portal.nebih.gov.hu/documents/10182/1294174/OFA+hat%C3%A1rozat+1-2020.pdf/df9982e7-8e12-908d-c30a-866902ecb0fc

Strengthening biosecurity measures (other than housing order)

The 3/2017 CVO decision about strengthening biosecurity requirements has been in force since the 2016/2017 HPAI epidemic, no additional measures have been introduced yet.

Preventive culling

In Komárom-Esztergom county after the confirmation of the first outbreak killing of all turkeys within the area of 1 km radius (four holdings including the affected one) was ordered (altogether 167,500 turkeys). Two of these holdings were secondary outbreaks.

Regional stand still (beyond the restriction zones specified in the EU Regulation)

Not applied.

Derogations on restriction zone implementation after risk assessment

Based on risk assessment according to COUNCIL DIRECTIVE 2005/94/EC poultry was transported out of the surveillance zone after laboratory examination to immediate slaughter from Komárom-Esztergom county to Bács-Kiskun county. Transport of day-old chicks and hatching eggs was also authorized out of the surveillance zone from Komárom-Esztergom county to other counties.

Hunting

Not restricted. No special rules apply.

A.4 Poland

Krzysztof Śmietanka and General Veterianary Inspectorate

Table A.4: Overview of main actions

Date	Event that triggered action	Type of action taken	Target audience (if applicable)
30.12.2019.	Samples were taken due to suspicion of HPAI (higher mortality)	Sampling	Local veterinary authority/ farm
31.12.2019	First outbreak was confirmed in commercial farm keeping turkey on the base of test results obtained from NRL in Puławy in relation to samples taken	Notification by ADNS system. Internal notification.	NRL/ local and central level of veterinary authority/EC/general public
3.01.2020	2 other outbreaks confirmed on 31.12.2019 (contact farms to 2019/1 outbreak)	Ordered controls of strengthened biosecurity	Veterinary Inspection/farms
16.01.2020	All current outbreaks, only one case confirmed in wild bird (hawk)	Increasing awareness among hunters	Hunting association

Increasing awareness of the stakeholders and the general public

Information published on the website of the General Veterinary Inspectorate: https://www.wetgiw.gov.pl/nadzor-weterynaryjny/grypa-ptakow

Trainings organized by poultry associations with veterinary services.

Housing order

Orders and prohibitions for poultry breeders in protection and risk zones designated around HPAI outbreaks are set out in the Regulation of the Minister of Agriculture and Rural Development of December 18, 2007 on eradication of avian influenza (implementation of Council Directive 2005/94 / EC).

Requirements in the field of biosecurity applicable to poultry breeders throughout the country are set out in the Regulation of the Minister of Agriculture and Rural Development of April 4, 2017 on the ordinance of measures related to the occurrence of highly pathogenic avian influenza. This regulation imposes the following obligations on breeders:

-an order to keep poultry in a way that limits its contact with wild birds,

- reporting to the District Veterinary Officer places where poultry or other birds are kept, excluding birds kept permanently in living quarters,

- keeping the poultry in a way that excludes its access to water bodies to which wild birds have access,

- storing bird feed in a way that prevents contact with wild birds and their droppings,

- feeding and watering poultry and captive birds in a manner that protects feed and water from access by wild birds and their droppings,

- laying disinfection mats in front of the entrances and exits of livestock buildings in which poultry is kept, in a number ensuring the security of entrances and exits from these buildings - in the case of farms where poultry is kept in a non-running system,

- use by persons entering livestock buildings in which poultry is kept, protective clothing and safety footwear, intended for use only in the given building - in the case of farms where poultry is kept in a non-running system,

- personal hygiene rules applied by persons performing poultry handling operations, including washing hands before entering livestock buildings,

- cleaning and disinfection of equipments and tools used for handling poultry before each use,

- abstentions by persons who have participated in hunting birds in the last 72 hours from carrying out poultry-handling activities,

- carrying out daily inspections of poultry flocks and keeping records containing, in particular, information on the number of dead birds, decrease in feed intake or lay,

- a ban on watering poultry and birds kept by humans with water from tanks to which wild birds have access, and

- a ban on bringing (on foot or by vehicle) to the holding where poultry is kept, corpses of wild birds or carcases of game birds.

Strengthening biosecurity measures (other than housing order)

The Regulation of the Minister of Agriculture and Rural Development of April 4, 2017 regarding the ordinance of measures related to the occurrence of highly pathogenic avian influenza introduces into the territory of the Republic of Poland, among others, issues an order to keep the poultry in a way that limits its contact with wild birds or to store feed for birds in a way that prevents contact with wild birds and their droppings. The measures specified in the provisions of this Regulation are also applied during outbreaks of highly pathogenic avian influenza in the territory of the Republic of Poland.

The Chief Veterinary Officer in messages informing about outbreaks reminds poultry farmers about the necessity to follow biosecurity principles when handling poultry: https://www.wetgiw.gov.pl/main/grypa-ptakow

In addition, information on avian influenza is available on the website of the Chief Veterinary Officer (https://www.wetgiw.gov.pl/nadzor-weterynaryjny/grypa-ptakow), including a description of biosecurity rules (https://www.wetgiw.gov.pl/nadzor-weterynaryjny/zasady-ochrony-drobiu-przed-grypa-ptakow).

Preventive culling

Pursuant to the Regulation of the Minister of Agriculture and Rural Development of December 18, 2007 on eradication of avian influenza, slaughter / preventive killing of poultry may be implemented in a protection zone, i.e. 3 km around the HPAI outbreak. The competent authority to make a decision in this matter is the District Veterinary Officer. Decisions regarding the slaughter / preventive killing of poultry, related to the occurrence of HPAI in a given protection zone, are taken on the basis of a risk assessment, which takes into account, inter alia, the following areas: the specificity of poultry production in a given district together with the number of commercial / non-commercial farms, possible pathways of the pathogen spread in the environment and potential ways of entering the farm, among others the manner of its protection, as well as topographic conditions of the area, infrastructure and all other circumstances affecting decision taking in the matter in question.

Regional stand still (beyond the restriction zones specified in the EU Regulation)

The National Reference Laboratory for Avian Influenza, i.e. NVI-NRI Puławy, in the 2016/2017 season has developed a map of HPAI risk area in the Country. The last updated map was prepared by NVI-NRI Puławy on 10 February 2020 (Figure A.4). The map was forwarded to local units of the Veterinary

Inspection. In the near future, the guidelines for proceedings in these areas of increased risk will be developed and forwarded to the Veterinary Inspection field units.

Derogations on restriction zone implementation after risk assessment

Not applied.

Hunting

The Chief Veterinary Officer sent a letter on 16 January 2020 to the Polish Hunting Association of hunters in Poland, informing about the need to exercise extreme caution when hunting birds, and in the event of finding unusual changes in the carcass of a bird shot - to report this case to the appropriate District Veterinary Officer in order to send samples for testing for avian influenza. In addition, the letter contained a request to refrain from hunting in restricted areas designated in connection with HPAI outbreaks.

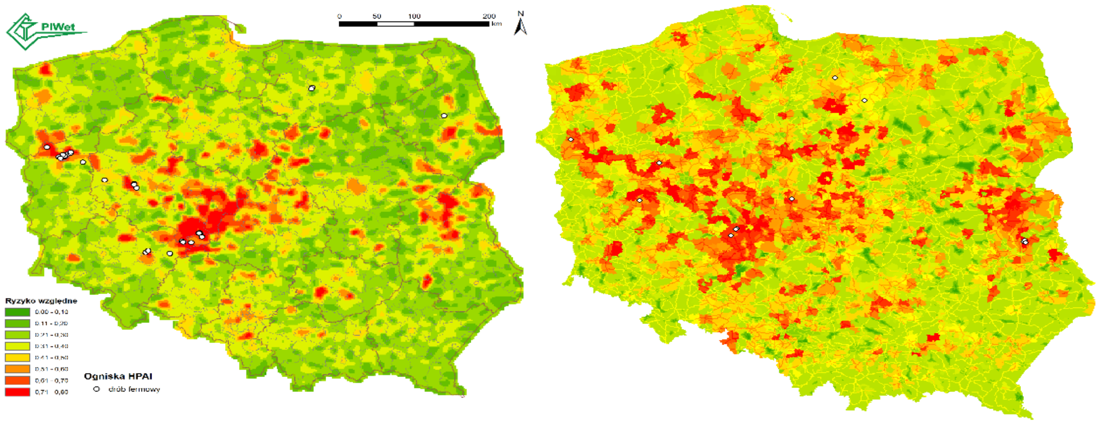

Figure A.4: Risk maps of HPAI occurrence in Poland developed by the Department of Epidemiology and Risk Assessment and Reference Laboratory for Avian Influenza (NVRI, Puławy) for season 2016 – 2017 on the left and last update on 10 February 2020 on the right.

A.5 Romania

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National Sanitary Veterinary and Food Safety Authority in Romania

Table A.5: Overview of main communication actions

Date	Event that triggered action	Type of action taken	Target audience
In January 2020, before the first case of HPAI was confirmed in Romania.	The appearance of HPAI cases (H5N8 outbreaks) in Europe (Poland, Slovakia and Hungary).	Following the notification from EU bodies of the evolution of HPAI outbreaks, the NSVFSA notified the counties (administrative regions of Romania) of this situation and requested an increase in the degree of awareness for all sanitary veterinary personnel. In detail, a more drastic monitoring of trade was enforced (referring to MSs having AI outbreaks), a revision of the biosecurity programs in place for FBO's of avian profile was decided and also a full review of the available resources for veterinary	Poultry industry, backyard keepers, veterinary profession, gamekeepers, pigeon fanciers. Livestock auctioneers.

		official laboratories, in order to meet any challenges posed by an eventual outbreak of HPAI. The same analysis was performed for all necessary equipment (protection, disinfection, neutralization) for an eventual enforcement of specific measures. Also official veterinarians gave housing instructions for backyards, so that all birds need to be sheltered and prevented from having access to open spaces, in order to prevent all forms of contact with wild birds. Notifying other competent authorities from the public health field of the evolution of HPAI in Europe in wild, domestic and captive birds and establishing the future working frame for the fight against HPAI. Notifying Food Business Operators of the situation and assisting them with instructions of compulsory and additional bio security measures for prevention and fight against Highly Pathogenic Avian Influenza. In the case of hunting grounds, it was decided to enhance the active surveillance for wild bird populations. All national movements of birds and hatchery eggs is only performed with an inter-county approval and with a minimum of 48 hours prior notification. Collecting data on the migratory and domestic wild bird populations (areas, census, migration routes, etc.). Alerting the counties neighbouring MS where HPAI was evolving of the situation and intensifying surveillance for those areas.	Other public institutions involved in public health; Non-Governmental Organizations and professional organizations of avian profile (e.g. hunters, breeders, etc.). Poultry industry, veterinary profession, pigeon fanciers. Zoological Gardens. General Public. Targeted public (control and surveillance areas) and/or NGOs and professional organizations of avian profile (e.g. hunters, breeders, etc.).
14/01/2020	First commercial outbreak, Maramureș county, Seini locality	Enforcing the 3 km and 10 km PZ and SZ; notifying all competent central and local authorities of the evolution of the outbreak; notifying local FBO of the evolution of the disease; issuing housing orders for the backyards and FBOs in the 3 km and 10 km PZ and SZ; prohibiting bird movements in the 3 km and 10 km PZ and SZ, based on a risk assessment; PZ and SZ surveillance and monitoring of avian profile FBOs; PZ and SZ birds census (backyards and FBOs); monitoring all mortalities in the FBOs from the PZ and SZ; notifying all official and free practice veterinarians to instruct the population to immediately announce any suspicious clinical signs of their poultry and all suspicious mortalities; notifying the public of the current situation and providing general and specific prophylactic measures for safeguard; notifying all competent authorities in the public health domain. After the suspicion diagnosis, all the remaining domestic birds were culled by a team of representatives from the Maramureș CSVFSD and the Local Centre for Fight Against Diseases	

		(Inter-Agency local public health organism). All provisions of EU Directive 94/2005 were complied with (disinfections, sampling, neutralisation, restrictions, etc.)	
18.01.2020	Second outbreak (commercial), Maramureș county, Seini locality	This outbreak was at just about 300m distance from the previous one, so the above mentioned measures were already in place.	

Bouth outbreaks generated a linear reaction from the National Sanitary Veterinary and Food Safety Authority (NSVFSA) in Romania, namely respecting the following actions:

1. Event notification by animal owners and/or food business operators.
2. On-site official inspection by the official veterinarians.
3. Implementation of primary sanitary veterinary measures.
4. Activation of the Local Centres for Disease Fight (teams of representatives from all official institutions that hold responsibilities in public health, coordinated by the Prefect of the respective county), entities that would draw up, approve and enforce all public health measures in relation to HPAI.
5. Collecting samples from diseased/dead birds and sending them for specific laboratory assays (disease suspicion – the County Sanitary Veterinary and Food Safety Laboratories).
6. Following the positive disease suspicion, most of the culling actions were scheduled at farm level.
7. Notification of all stakeholders (e.g. official institutions, FBOs, animal owners, etc.) of the presence of HPAI suspicion/confirmation in Romania.
8. Elaborating and creating the framework for the official enforcement of the necessary sanitary veterinary and food safety measures for the prevention and fight against HPAI; in some cases, where it was justified by an epidemiologic assessment and a risk evaluation, the local Competent Authority took action in order to prevent the dissemination of the disease, prior to having the official confirmation of the disease by the National Reference Laboratory for Avian Influenza.
9. Sending the samples to the National Reference Laboratory for Avian Influenza (the Institute for Diagnosis and Animal Health).
10. Following the official confirmation of the disease, the implementation of the entire set of sanitary veterinary and food safety measures for the prevention and fight against HPAI was enforced.
11. Enforcing the provisions of the European and national legislation (Operational Manual for Avian Influenza and Newcastle Disease), until the moment when the Central Competent Authority considers appropriate to lift the restrictions and confirms the absence of the virus in the respective affected areas.

Increasing awareness of the stakeholders and the general public

The NSVFSA in Romania adopted three lines of strategy when it came to communication plans and activities in relation to Highly Pathogenic Avian Influenza:

a) Communicating with stakeholders and relevant authorities in the field of public health and veterinary public health:

- Stakeholders: the NSVFSA, as a critically important actor for public health, has implemented a series of collaboration protocols with numerous institutions and legal representatives that also provide for securing public health in Romania (e.g. the Ministry of Health, the Ministry of Internal Affairs, etc.); these protocols serve to provide multidisciplinary contingency plans for high risk situations, when one competent authority cannot provide sufficient human resources, logistics or scientific input to efficiently address such a situation; thus, the NSVFSA issued a series of notifications to these institutions in respect to the evolution of HPAI in Romania, as well as on-point requests for collaboration (e.g. support in monitoring the effectiveness of the ban on poultry markets/fairs, compliance with the restrictions of birds movement, etc.); these notification provisions were also applied in the case of NGO's, associations, professional organisations and other legally established stakeholders;

- General public: the NSVFSA, obliged under the national legislation for release of information of public importance and free data access, namely Law no. 544/2001, has constantly informed the general public of the evolution of Highly Pathogenic Avian Influenza (H5N8) in Romania, through press releases and by using its own website (http://www.ansvsa.ro/), as well as media partners (e.g. newspapers, TV channels, social media, etc.) (Figure A.5);

- Local public: where localities and/or commercial establishments were included in the protection/surveillance areas following the confirmation of a wild birds case or an outbreak, the NSVFSA, through its territorial representatives, namely the County Sanitary Veterinary and Food Safety Directorates, and with the help of other public institutions, issued and disseminated targeted advice for the economic operators and the people living in these areas, in respect to sanitary veterinary measures concerning:

1. restrictions for the animals in the backyards;
2. the ban on animal movements;
3. the movement of objects/materials/feed that could act as vectors for the disease;
4. specific rules for consuming poultry and the risks that HPAI poses for human health;
5. the mandatory notification of the empowered free practice veterinarians or the official veterinarian when noticing any change in the health status and/or other health criteria (a drop in the intake of feed, water and any other abnormal behaviour) in backyard birds. However, the latter have not been reported in any of the notifications made by animal owners, rendering them of little statistical significance in the case of backyards;
6. basic food safety and hygiene rules.

The abovementioned were disseminated via leaflets, broadcasts on public radios and TV stations and by door-to-door verbal communications done by official teams.

Figure A.5: Example of a public warning of the evolution of HPAI in Romania

Housing orders

Concerning the housing orders, it is imperative to acknowledge the fact that the backyards husbandry system has several particularities that require a special set of measures in order to prevent and combat infectious diseases. In detail, the legal, social and economic aspects are primordial:

- The legal aspect: backyards do not possess a legal personality and the vast majority of the national and international regulations are inapplicable to them; thus, it is difficult to enforce strict sanitary veterinary measures and even more problematic to supervise the enforcement of these actions, due to reasons as is the necessary high input of human resources; however, specific parts of the national legislation have been specially adapted to address the particular issue of backyards (e.g. sanctions and fines, animal movement, transport, welfare, etc.);

- The social and economic aspects: the foremost important aspect is that animal husbandry is a vital part of the subsistence for these backyards, the animal owners being totally dependent on the products of animal origin obtained from these animals; thus, the backyard animals cannot be regarded as hobby, sport or companionship animals from the view of animal owners.

Considering the abovementioned, issuing house confinement orders is an extremely difficult decision to implement. Since the moment of the first HPAI outbreak, housing orders apply for both the 3 km protection zone, as well as for the 10 km surveillance zone. No bird movements from backyards are permitted until the ending of the outbreaks, as well as the obligation of housing the animals in enclosed and sheltered premises within the backyards in order to prevent direct and indirect contact with wild birds. The enforcement of these measures is performed by official veterinary personnel, assisted by other public establishments involved in public health. Regular visits and inspections are carried on to check for compliance with the sanitary veterinary measures. Based on the evolution of the disease in Romania, on the courses for migration of wild birds, of the evolution of the seasons (from cold to warm), on the compliance of the FBOs and non-professional backyards to the sanitary veterinary and food safety enforced measures, on the cross-border evolution of outbreaks in Europe and not only, on the efficiency of the measures quantified in negative laboratory assays and no mortality in birds (wild, domestic and captive birds), for each individual outbreak we conducted a risk assessment procedure to determine if lifting the restrictions at the minimum waiting period (21 days for the control zone and 30 days for the surveillance zone) is the best option, and concluded that no prolongations of the enforced measures are needed.

Strengthening biosecurity measures (other than housing order)

<u>For commercial establishments</u>

The veterinary officials verified the comercial establishments in the PZ to have no breaches in the three levels risk biosecurity system:

a) Administrative zone: offices and administrative spaces

- Restricting access to these spaces and installing a sign that clearly informs of these restrictions;
- Ensuring that allowed personnel has clean clothing and footwear (no organic materials that could contaminate the area).

b) Professional zone: the area that separates the production zone from the administrative zone

- Preventing the access of mammals (rodents control and other companionship animals);
- Providing cover for storage spaces;
- Clean clothing and footwear when passing through the sanitary filter;
- Creating an environment less propitious for wild birds (cleaning adjacent spaces, cutting the grass, trimming the trees, collecting fallen leaves and installing devices destined to scare off wild birds);
- Draining existing water surfaces, as well as preventing their accumulation following rain;
- Eliminating all spaces destined for non-commercial birds (e.g. companionship birds or those used for various hobbies);
- Training all personnel in complying with the specifics of the disease and redefining their roles and responsibilities within the commercial establishments;
- Contracted personnel and visitors would only be allowed inside this area an in the production zone if 72 hours have passed since their last contact with any domestic or captive birds, with products of avian origin or avian by-products (including manure);
- Exaggerating the disinfection of all transport means and their annexes, as well as all types of equipment and by-products not destined for human consumption;
- Where it is possible, the transport of birds, hatchery eggs and manure should avoid passing through this zone; if it is not possible, cleaning procedures must be in place.

c) Production zone: halls for animal husbandry, physically separated from the two aforementioned zones:

- Limiting the production to a single category, without mixing several categories (e.g. broilers with laying hens);
- Preventing the access of mammals (rodents control and other companionship animals);
- Restricting the access of visitors and of any other personnel that do not work in these premises;
- Using strictly single-use footwear and clothing, hand washing and an adequate hair grip under a bonnet, both for personnel as well as for visitors;
- Clothing and footwear would be specific for each individual hall and at the entrance of every hall there would be filter destined for change of clothes and footwear;
- Using strictly potable water in the halls and restricting access to surface waters;
- Farm production management based on the all full / all empty principle;
- Cleaning and disinfecting mobile equipment following each use (entry-exit);
- Transport means carrying feed and different materials are banned from entering this area, all necessary actions being done through reloading;
- Carcasses disposal will be done at a significant distance from the production halls and close to a public road (accessible from outside the commercial establishment); freezing is recommended, because it facilitates long term storage and a low frequency transport rate that involves a significantly lower risk;
- In the case of web-footed birds (e.g. ducks, geese, etc.), in addition to the specific biosecurity measures, all contact of the birds with any type of water surface will be prohibited.

For backyards

The veterinary officials verified in the PZ the following:

- Preventing any direct or indirect contact between wild birds and domestic or captive birds;
- Prohibiting the access to any type of water surfaces for domestic or captive birds;
- Separating, within the same backyard, laying hens/broilers from web-footed birds;
- Prohibiting the keeping birds in backyards in open spaces;
- Prohibiting using water surfaces as water reservoirs for domestic and captive birds;
- Limiting human circulation inside the backyard only to the owner and family members;
- Preventing contact with other domestic animals;
- Using different clothing and footwear when entering the premises where the birds are kept;
- Prohibiting the use of Anseriformes and Charadriiformes as decoy birds;
- Prohibiting the organisation and participation of animal owners to public manifestations as exhibits, markets, exhibitions of domestic and captive birds.

At least one official inspection and census were performed in every commercial establishment and every backyard in the surveillance and protection areas, while conducting a bird census and verifying biosecurity measures all together. Also, from 14 of January 2020 – present (February 2020), the sanitary veterinary officials monitored the mortality for every avian farm in the affected counties and neighbouring counties, on a daily basis.

Preventive culling

Preventive culling following these outbreaks was not enforced yet in Romania, as the epidemiological investigation did not conclude any direct risk towards other commercial farms or backyards.

Regional stand still (beyond the restriction zones specified in the EU Regulation)

Regional stand still was not applied, mainly by considering the fact that the outbreaks were isolated both in terms of region, number of affected animals as well as the spread of the disease.

Derogations on restriction zone implementation after risk assessment

Derogations for one FBOs in the restriction zone was granted in the 3 km protection zone enforced by the competent sanitary veterinary services that included a commercial poultry farms, respectively a broiler farm.

In this particular case, the National Sanitary Veterinary and Food Safety Authority, through its county representative – the Maramureș County Sanitary Veterinary and Food Safety Directorate, implemented derogations for this Food Business Operator in terms of:

- Transport of live birds (broilers) for slaughtering in a designated slaughterhouse – in the neighbouring county of Satu Mare according to the provisions of art.23 (1) of the Directive 2005/94/CE;
- Transport of eggs destined for human consumption;

Derogation was given for the slaughter of a total number of 280.000 broilers within the protection period of 21 days, while complying with the specifics of the legislation for serologic and virus sample testing. The tests were performed in order to prove that all transports under the derogations are free of the virus and all were negative for the presence of Avian Influenza viruses.

Hunting

The only enforced restriction in relation to hunting was to prohibit the use of Anseriformes and Charadriiformes as decoy birds.

A.6 Slovakia

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Table A.6: Overview of main actions

Date	**Event that triggered action**	**Type of action taken**	**Target audience (if applicable)**
09.01.2020	1st poultry outbreak	All relevant measures ordered by DVFA in accordance with 2005/94/EC and Slovak national legislation for outbreak, protection zone and surveillance zone	stakeholders, general public, private vets
17.01.2020	2nd poultry outbreak	ditto	stakeholders, general public, private vets
27.01.2020	3rd poultry outbreak	ditto	stakeholders, general public, private vets

Increasing awareness of the stakeholders and the general public

Information in relation to avian influenza via to relevant website: https://www.svps.sk/zvierata/choroby_chripka.asp

Other ways of providing information are through the media, municipalities, etc.

Housing order

Special emergency veterinary measures of the Chief Veterinary Officer of The Slovak republic due to HPAI avian influenza are published on the website:

https://www.svps.sk/zvierata/mno_4373_05.asp

Strengthening biosecurity measures (other than housing order)

Checks on poultry health regarding avian influenza (including compliance with biosecurity measures) have been ordered by SVFA to DVFAs in relation to commercial poultry farms, not for backyard holdings. It started in December 2013.

Preventive culling

Nnot applied.

Regional stand still (beyond the restriction zones specified in the EU Regulation)

Not applied.

Derogations on restriction zone implementation after risk assessment

Not applied.

Hunting

Not prohibited.