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## Avian influenza overview February – May 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 February and 15 May 2020, 290 highly pathogenic avian influenza (HPAI) A(H5) virus outbreaks were reported in Europe in poultry (n=287), captive birds (n=2) and wild birds (n=1) in Bulgaria, Czechia, Germany, Hungary and Poland and two low pathogenic avian influenza (LPAI) A(H7N1) virus outbreaks were reported in poultry in Italy. 258 of 287 poultry outbreaks detected in Europe were secondary outbreaks, suggesting that in the large majority of cases the spread of the virus was not due to wild birds. All the HPAI outbreaks were A(H5N8) apart from three, which were reported as A(H5N2) from Bulgaria. Genetic analysis of the HPAI A(H5N8) viruses isolated from the eastern and central European countries indicates that this is a reassortant between HPAI A(H5N8) viruses from Africa and LPAI viruses from Eurasia. Two distinct subtypes were identified in Bulgaria, a novel reassortant A(H5N2) and A(H5N8) that is persisting in the country since 2016. There could be several reasons why only very few HPAI cases were detected in wild birds in this 2019–2020 epidemic season and a better knowledge of wild bird movements and virus–host interaction (e.g. susceptibility of the hosts to this virus) could help to understand the reasons for poor detection of HPAI infected wild birds. In comparison with the last reporting period, a decreasing number of HPAI A(H5)-affected countries and outbreaks were reported from outside Europe. However, there is considerable uncertainty regarding the current epidemiological situation in many countries out of Europe. Four human cases due to A(H9N2) virus infection were reported during the reporting period from China.

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## Table of contents

1.	Introduction.....	4
2.	Conclusions .....	4
2.1.	Main observations .....	4
2.2.	Conclusions .....	4
3.	Suggestions.....	5
4.1.	Overview of HPAI outbreaks in Europe during the previous and current seasons.....	6
4.2.	HPAI and LPAI outbreaks in Europe, 16 February – 15 May 2020 (TOR 1 and TOR 2) .....	10
4.2.1.	Description of the avian influenza detections in time and space .....	10
4.2.2.	Phenotypic characterisation of avian influenza viruses circulating in Europe .....	12
4.2.3.	Genetic characterisation of avian influenza viruses .....	18
4.2.4.	Human cases due to A(H5N8) or A(H5N2) viruses detected in Europe .....	19
4.3.	Prevention and control measures applied in Europe, 16 February – 15 May 2020 (TOR 3) .....	19
4.4.	The avian influenza situation in other countries not reporting via ADNS, 16 February – 15 May 2020 (TOR 4) .....	20
4.4.1.	HPAI A(H5N1).....	21
4.4.2.	HPAI A(H5N2) and A(H5N5) .....	23
4.4.3.	HPAI A(H5N6).....	24
4.4.4.	HPAI A(H5N8).....	26
4.4.5.	HPAI-LPAI A(H7N9).....	27
4.4.6.	LPAI A(H9N2) .....	29
4.5.	Scientific analysis of avian influenza spread from non-EU/EEA countries to poultry in the EU/EEA .....	31
4.6.	Surveillance and diagnosis of human infections and public health measures for prevention and control .....	31
4.6.1.	Surveillance in the EU, diagnosis and options for public health control measures (in relation to the EU) .....	31
4.6.2.	Candidate vaccine viruses.....	31
4.7.	ECDC risk assessment for the general public in the EU/EEA .....	31
	References.....	32
	Abbreviations .....	36
	Appendix A – Terms of reference .....	37
	Appendix B – Data and methodologies .....	39
	Annex A – Applied prevention and control measures on avian influenza .....	41
A.1	Bulgaria.....	41
A.2	Czechia .....	42
A.3	Hungary .....	44
A.4	Poland.....	45

## 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 February and 15 May 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 February and 15 May 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.
- Four infections of children with A(H9N2) virus have been reported from China.
- 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 February and 15 May 2020 (based on the Animal Disease Notification System (ADNS)):
  - 287 HPAI A(H5N8) outbreaks were reported: 263 in poultry in Hungary, 14 in poultry in Poland, 2 in poultry, 2 in captive birds and 1 in a wild bird in Germany, 4 in poultry in Bulgaria, 1 in poultry in Czechia; 3 HPAI A(H5N2) outbreaks were reported in poultry in Bulgaria;
  - two LPAI A(H7N1) outbreaks were reported in poultry in Italy.
- The genomic characterisation of the HPAI A(H5) viruses detected in domestic and wild birds in Europe indicates the circulation of three genotypes of clade 2.3.4.4b. Specifically, a reassortant HPAI A(H5N8) between HPAI A(H5N8) viruses from Africa and LPAI viruses from Eurasia has been identified in six eastern and central European countries (Poland, Germany, Czechia, Hungary, Romania and Slovakia) since the end of December 2019. In the same period, two subtypes with different genetic characteristics were reported in Bulgaria: i) an HPAI A(H5N8) descendant of the A(H5N8) strain introduced into Europe in 2016 and ii) a reassortant HPAI A(H5N2) between the Bulgarian A(H5N8) and Eurasian LPAI viruses.
- In contrast to the last reporting period, no HPAI outbreaks were notified from Africa and a decreasing number of outbreaks of HPAI A(H5N1), A(H5N2), A(H5N5), A(H5N6) and A(H5N8) in poultry and wild birds were notified from Asia and the Middle East.

#### 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 first European A(H5N8) outbreak was reported in poultry on 30 December 2019 and remained confined to a few countries in eastern and central Europe. Some of the possible explanations for this localised epidemic wave are i) the late virus introduction; ii) a different route of virus spread; iii) a mild winter; and iv) the spring migration.

- Only five of the 263 poultry outbreaks detected in Hungary were primary, suggesting that the spread of the virus was mainly due to secondary spread and not to multiple introductions from wild birds.
- The genetic analysis of the HPAI A(H5N8) viruses that have been isolated from Poland, Czechia, Germany, Hungary, Romania and Slovakia since December 2019 indicates that the virus is a reassortant between HPAI A(H5N8) viruses from Africa and LPAI viruses from Eurasia.
- The genetic analysis conducted on the HPAI A(H5N2) and A(H5N8) viruses isolated in Bulgaria suggest a persistence of the virus in the country since 2016 rather than a new introduction via migratory wild birds.
- The long persistence of the virus in a few countries may pose a risk for the emergence of new reassortant viruses and be a source of virus spread to wild or domestic birds in the EU/EEA Member States.
- There were a low number of HPAI cases identified in wild birds in this 2019–2020 epidemic season in Europe. There may be several explanations for this low numbers: i) the relatively high temperatures may have determined changes in westward and southward movement of migratory birds coming from Asiatic countries; ii) the effort of passive surveillance activities might not be enough to detect infected wild birds if the prevalence of the infection is low as it might have been this year; iii) a reduction of surveillance activities due to the COVID-19 epidemic; iv) an increased resistance against the disease due to a herd immunity of wild birds following past seasonal exposures to AI A(H5); v) difficulty of the current surveillance system to identify infected migratory birds coming through unusual migratory flyways. At present, data are not sufficient to confirm what is being assumed. More time and further studies are needed to confirm these hypotheses.
- Despite the decreasing number of HPAI A(H5)-affected countries and outbreaks outside Europe, there is considerable uncertainty regarding the real geographical distribution of these viruses.
- 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.

### 3. Suggestions

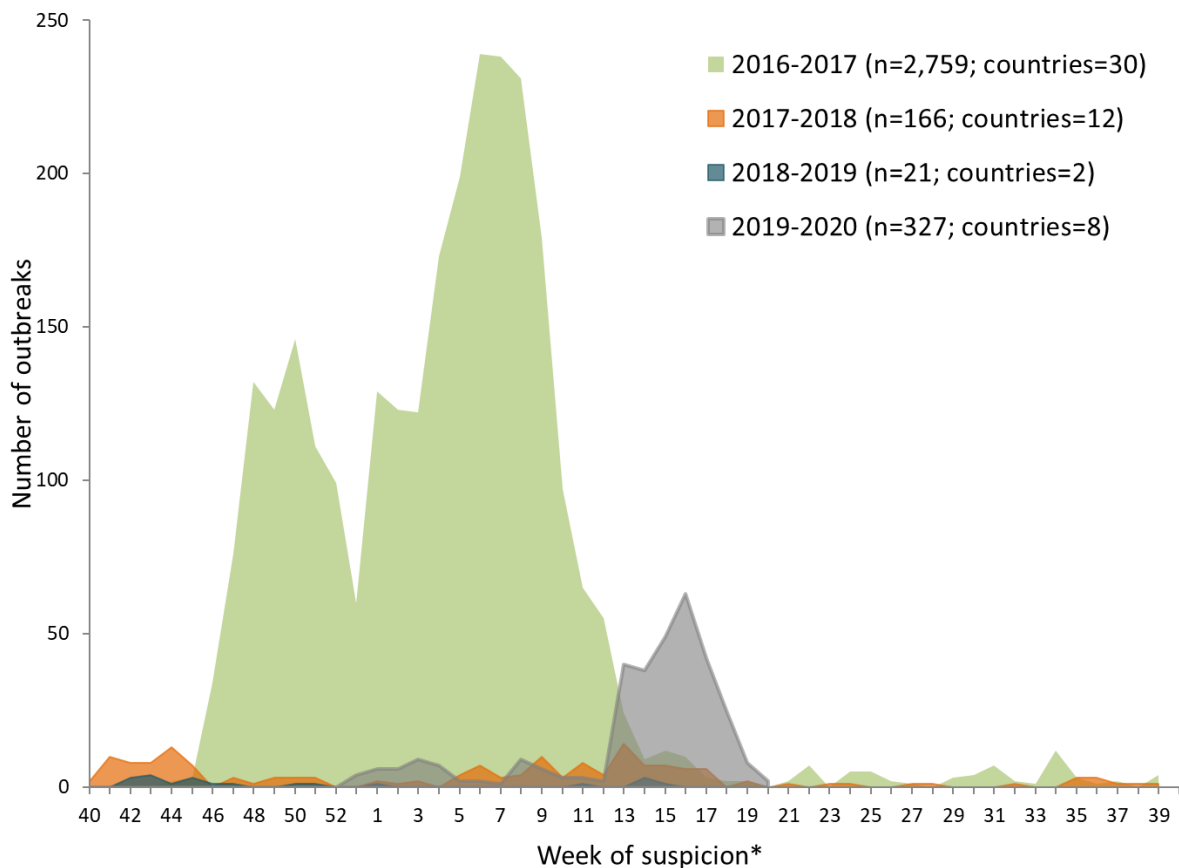
- It is particularly important that information on the genetic composition and possible origins of newly detected variants in birds and humans are shared and communicated in a timely manner.
- The high number of secondary spreads recorded in duck and goose establishments in some countries, such as Hungary, indicates that these types of poultry category need to be better regulated to increase biosecurity and to prevent uncontrolled spread of infection.
- A better understanding of the factors regulating wild bird migration is of the utmost importance to improve our ability to detect the virus early and monitor its spread.
- A more effective surveillance (economically sustainable) that considers the new epidemiological scenarios of HPAI viruses in wild birds should be designed and implemented.
- Due to the difficulty of predicting and identifying the spread of HPAI viruses in their natural reservoirs, high standard alert, effective biosecurity measures particularly during high risk periods such as the winter season, 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 who are 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

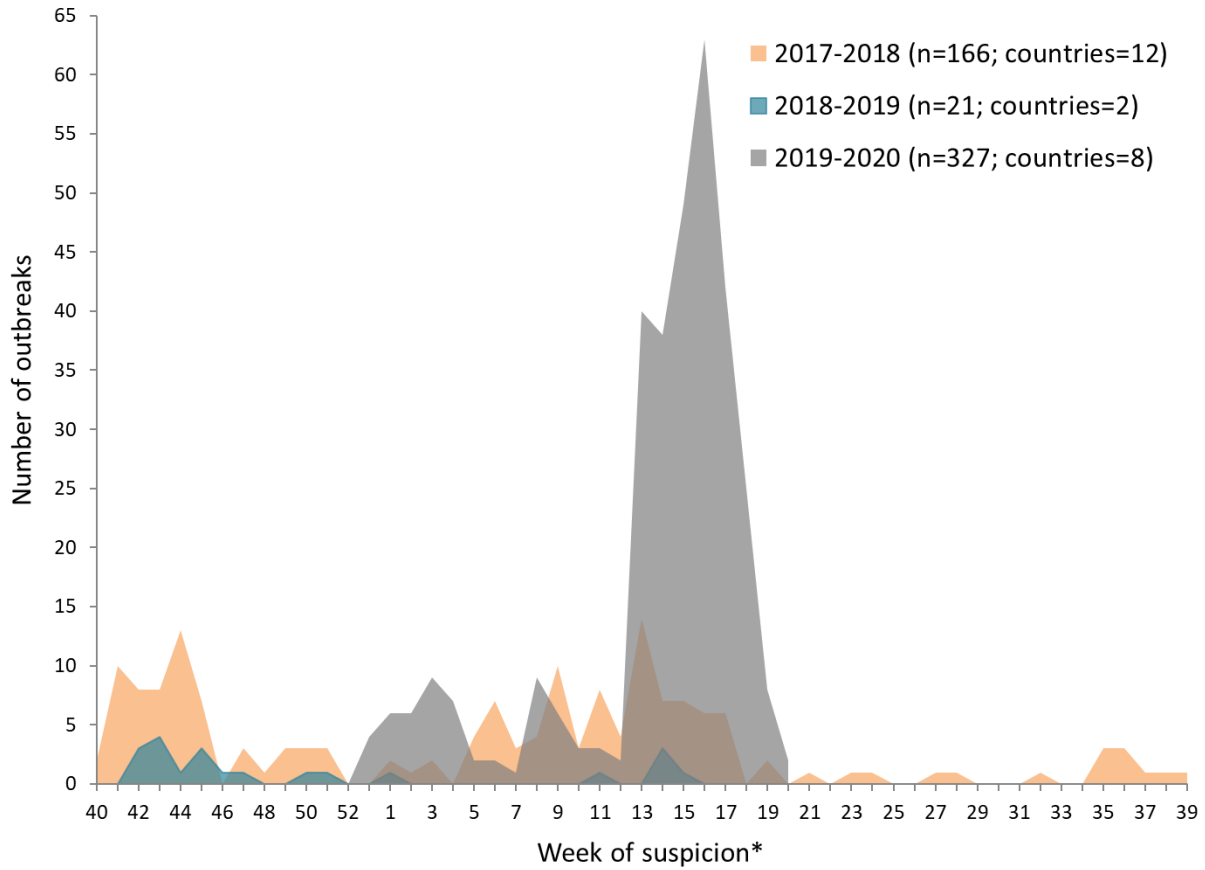
Figure 1 shows the HPAI outbreaks detected in birds (poultry, wild and captive birds) in Europe and reported via ADNS for seasons 2016–2017, 2017–2018, 2018–2019 and 2019–2020. Figure 2 shows the same data only for the last three epidemic seasons. A season is the period that starts in week 40 (the beginning 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 20 (on 15 May 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 May 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.



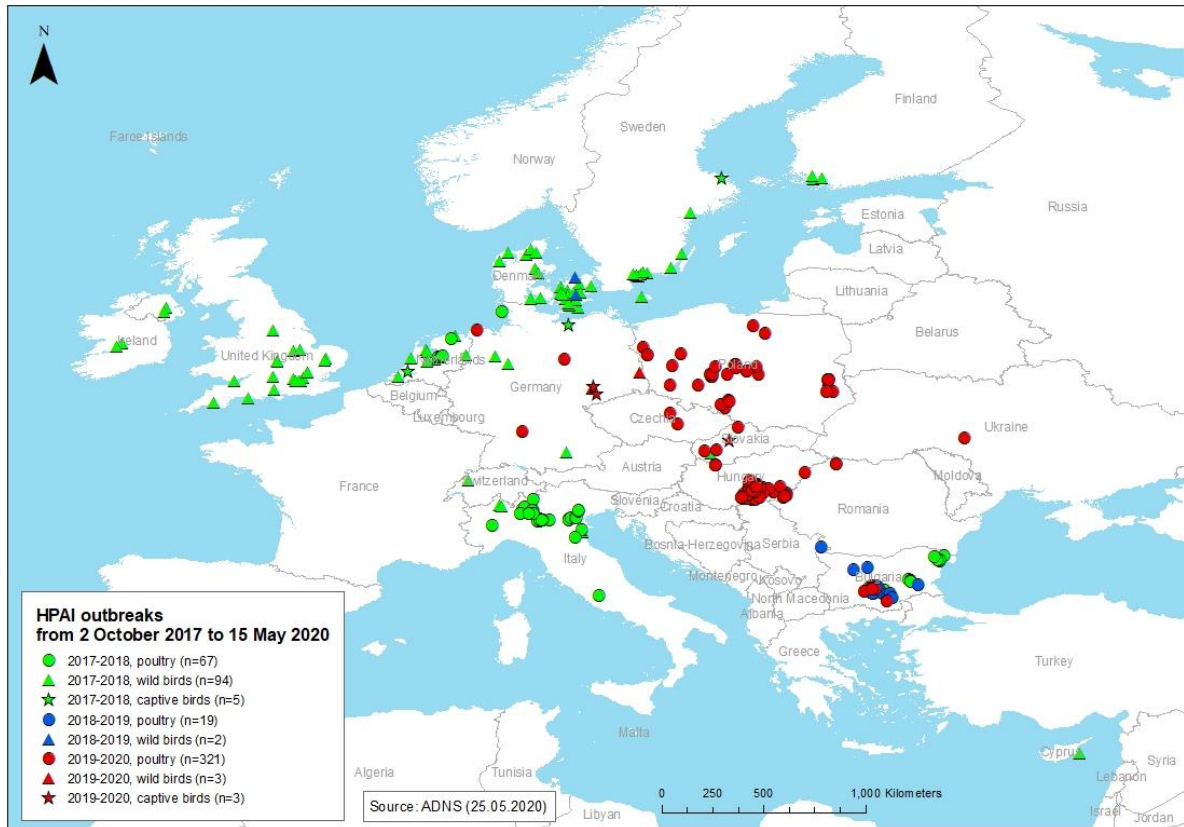
\* When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.  
Data source: ADNS, EFSA.

**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 May 2020 (n=3,273)



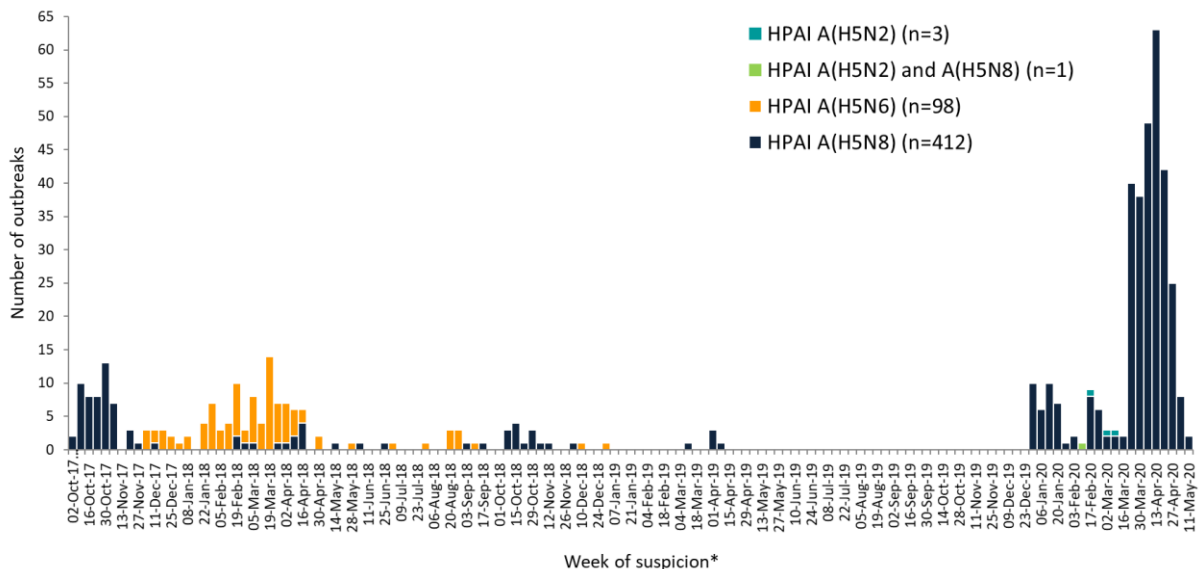
\* When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.  
Data source: ADNS, EFSA.

**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 May 2020 (n=514)



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

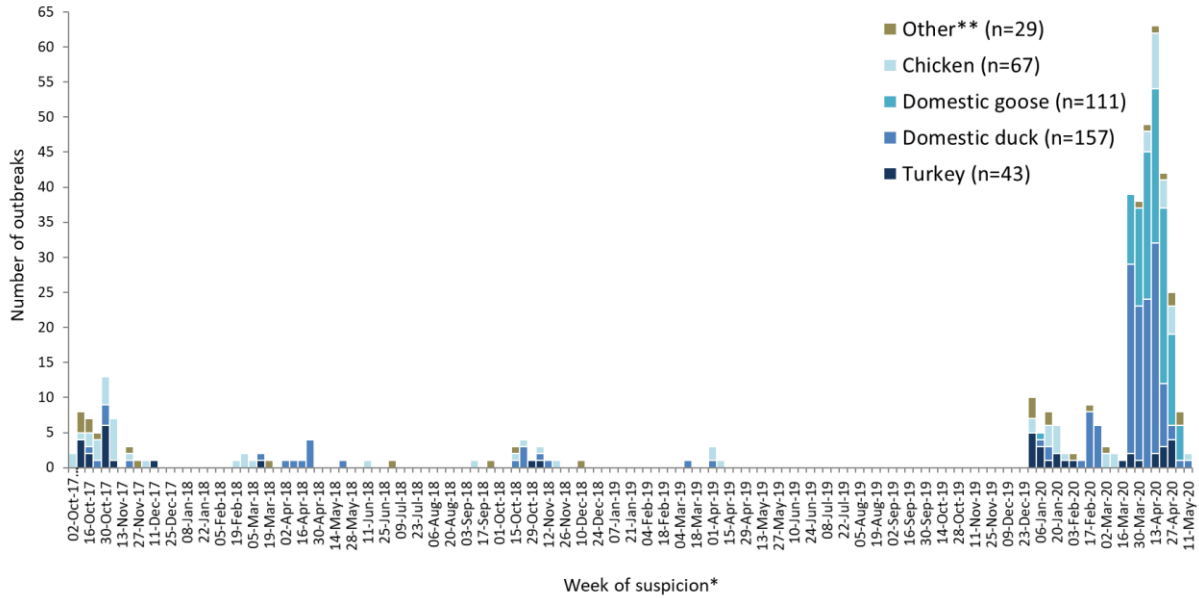
**Figure 3:** Geographical distribution, based on available geocoordinates, of HPAI outbreaks in Europe in seasons 2017–2018 (green), 2018–2019 (blue) and 2019–2020 (red) in poultry (circles), wild birds (triangles) and captive birds (stars) (2 October 2017 – 15 May 2020; n=514)



\* 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.

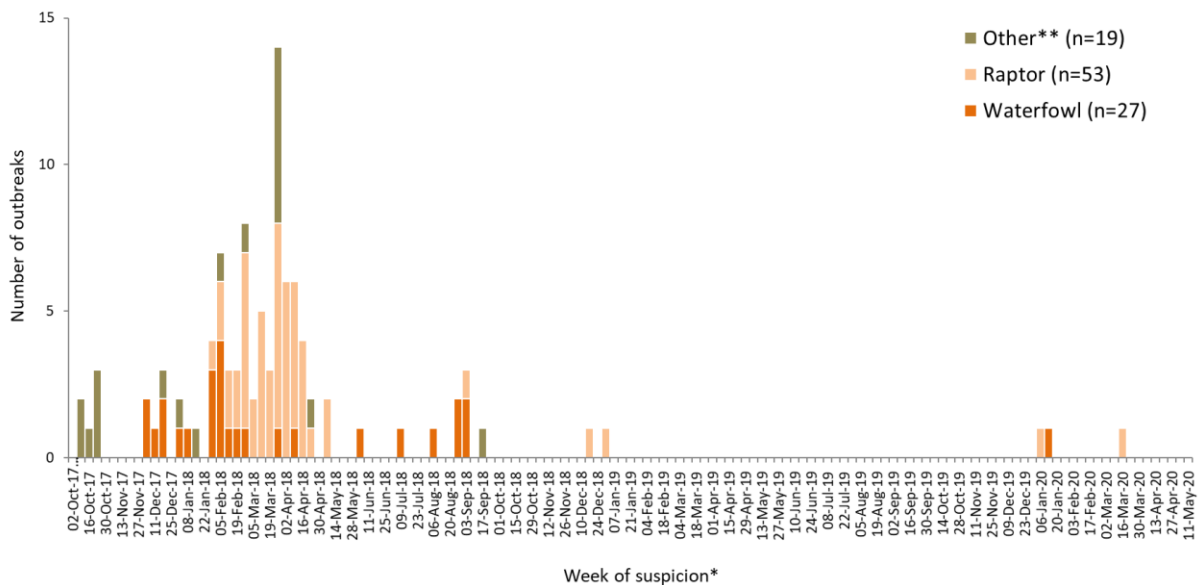
**Figure 4:** Distribution of total number of HPAI A(H5N6) (orange), A(H5N8) (blue), A(H5N2) (light blue) and A(H5N2) A(H5N8) (green) outbreaks in Europe by week of suspicion (dates indicate the first day of the week) in seasons 2017–2018, 2018–2019 and 2019–2020 (2 October 2017 – 15 May 2020; n=514)





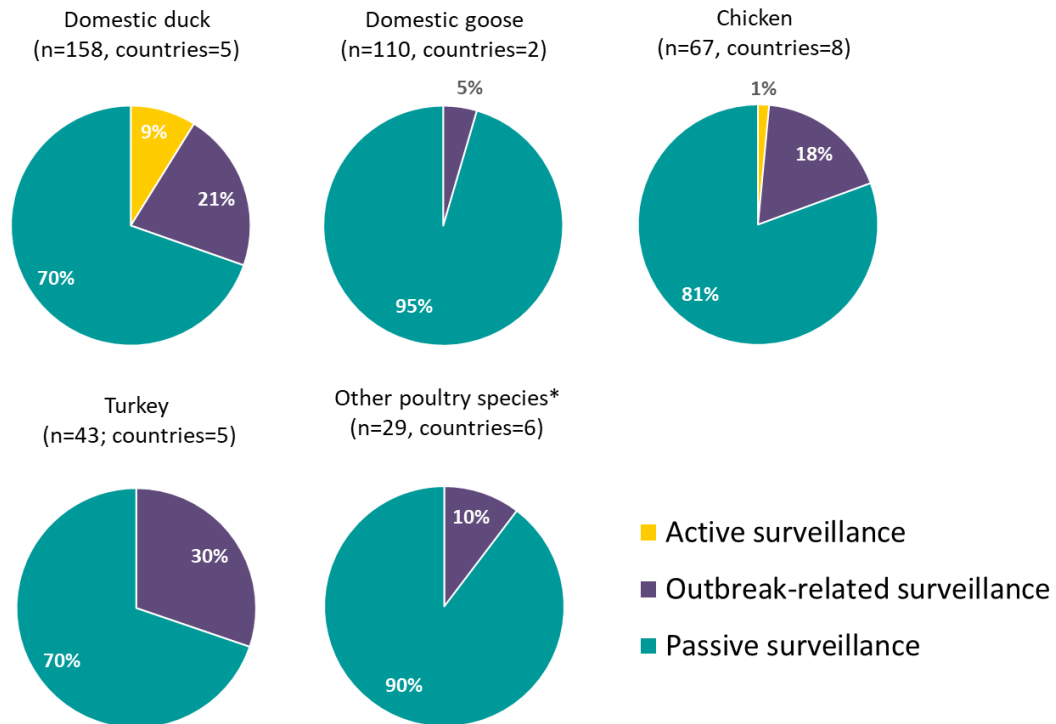
\* When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.  
 \*\* 'Other' category contains mixed, unknown bird species, or categories different from those displayed: pheasant (*Phasianus colchicus*), pigeon (*Columba livia*), partridge (*Perdix perdix*), chukar partridge (*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 May 2020; n=407)



\* 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 May 2020; n=99)



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

**Figure 7:** Frequency distribution of HPAI outbreaks in poultry in Europe, by bird species (domestic goose, domestic duck, chicken, turkey and mixed species) and sampling programme leading to the outbreak detection, in seasons 2017–2018, 2018–2019 and 2019–2020 (2 October 2017 – 15 May 2020; n=407)

## 4.2. HPAI and LPAI outbreaks in Europe, 16 February – 15 May 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 February to 15 May 2020, 290 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<sup>1</sup> 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.

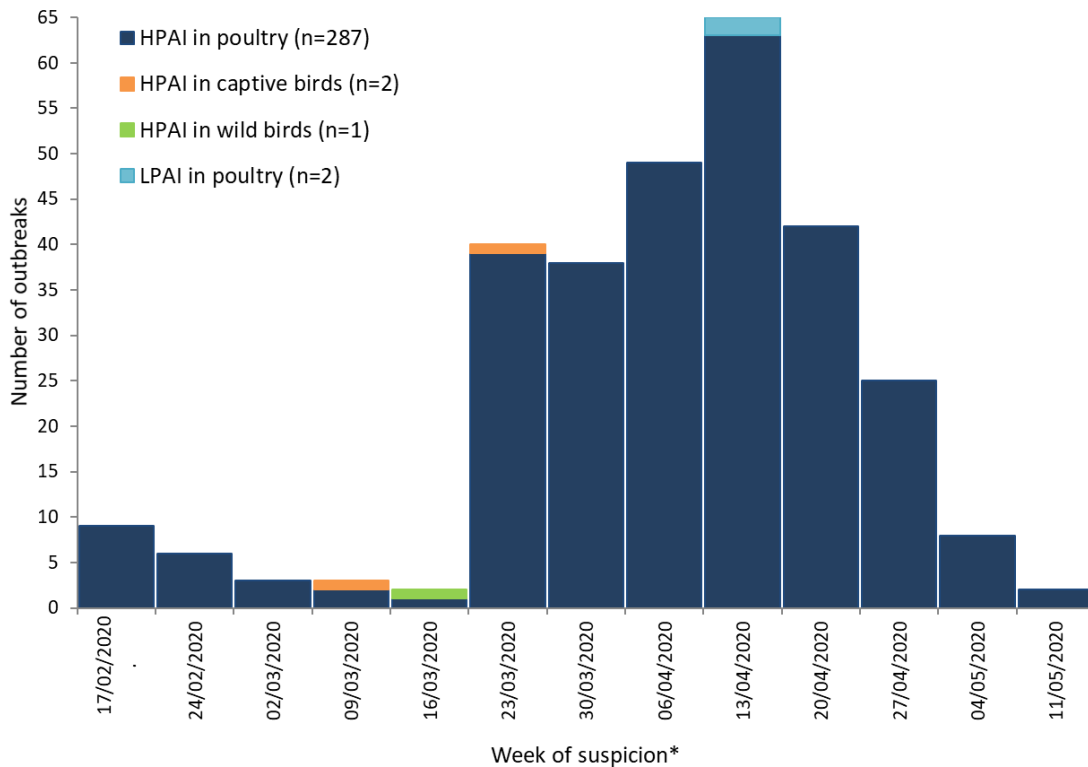
<sup>1</sup> According to Regulation (EU) 2016/429 'establishment' means any premises, structure, or, in the case of open-air farming, any environment or place, where animals or germinal products are kept, on a temporary or permanent basis, except for: (a) households where pet animals are kept; (b) veterinary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

**Table 1:** Number of avian influenza outbreaks in Europe, by virus subtype and country, 16 February – 15 May 2020

Country	HPAI outbreaks				LPAI outbreaks	All avian influenza outbreaks
	A(H5N2)	A(H5N8)	Wild birds	Captive birds	A(H7N1)	
	Poultry	Poultry			Poultry	
<b>Bulgaria</b>	3	4				7
<b>Czechia</b>		1				1
<b>Germany</b>		2	1	2 <sup>(a)</sup>		5
<b>Hungary</b>		263				263
<b>Italy</b>					2	2
<b>Poland</b>		14				14
<b>Total (6 countries)</b>	3	284	1	2	2	292

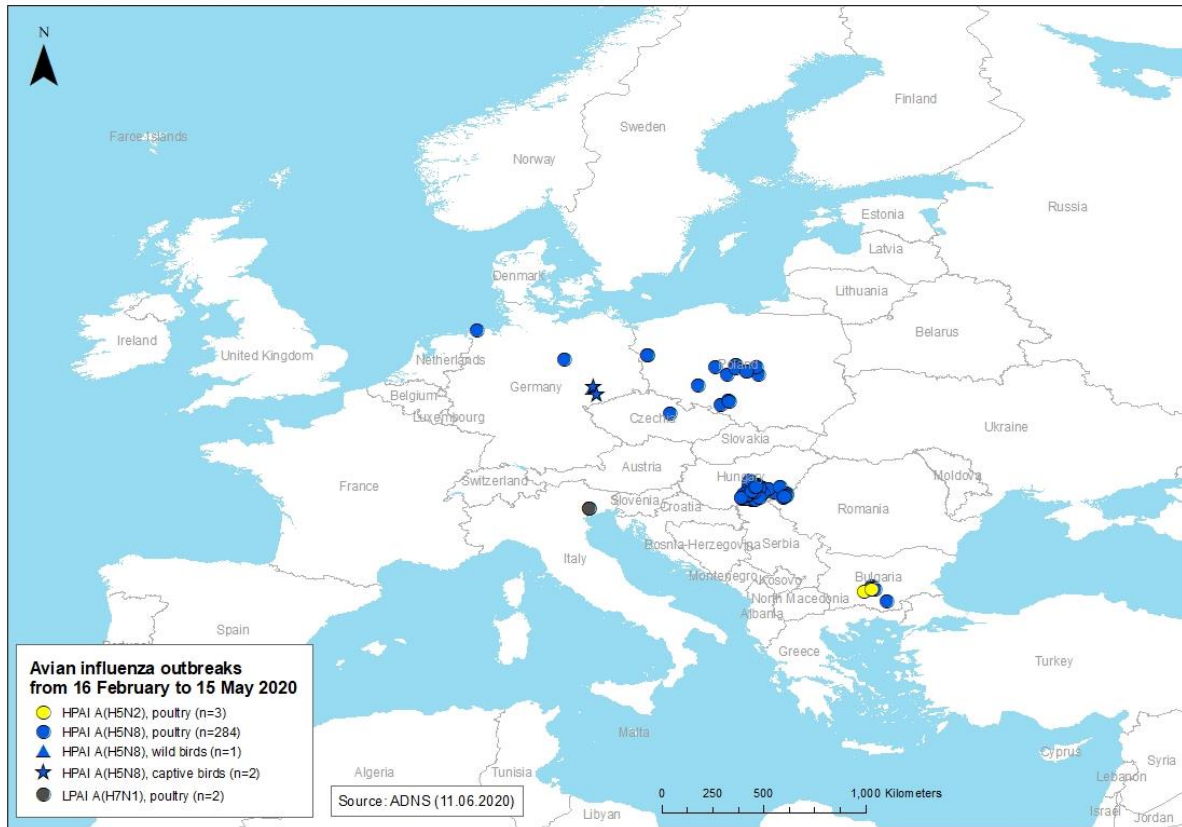
(a) One outbreak recorded in a zoo; affected species: of 89 ducks tested, one single steamer duck (*Tachyeres sp.*) tested positive.

Data source: ADNS (11.06.20).



\* When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion. Data source: EFSA and ADNS (11.06.20).

**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 February – 15 May 2020 (n=292)



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

**Figure 9:** Geographical distribution, based on available geocoordinates, of avian influenza outbreaks in Europe, by virus subtype and affected subpopulation, 16 February – 15 May 2020 (n=292)

As of 22 June 2020, a number of HPAI outbreaks have been confirmed in poultry outside the reporting period for this report: one in Bulgaria on 4 June 2020 and six in Hungary between 18 May and 4 June 2020.

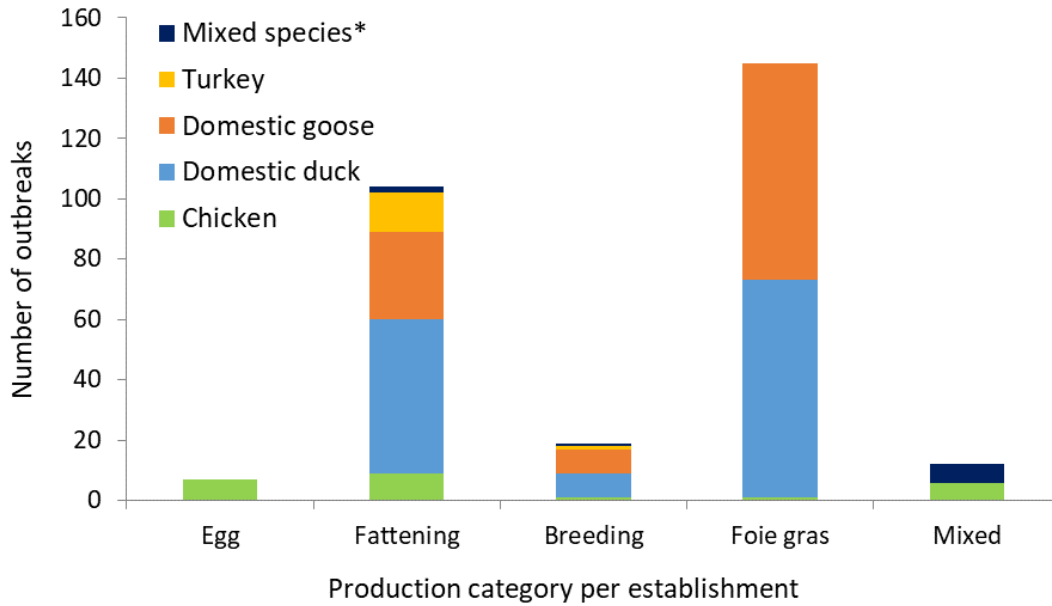
An LPAI A(H5N3) outbreak was confirmed outside the reporting period for this report, on 16 June 2020, in an ostrich establishment located in Mantova province, Italy.

#### 4.2.2. Phenotypic characterisation of avian influenza viruses circulating in Europe

##### 4.2.2.1. HPAI in domestic birds

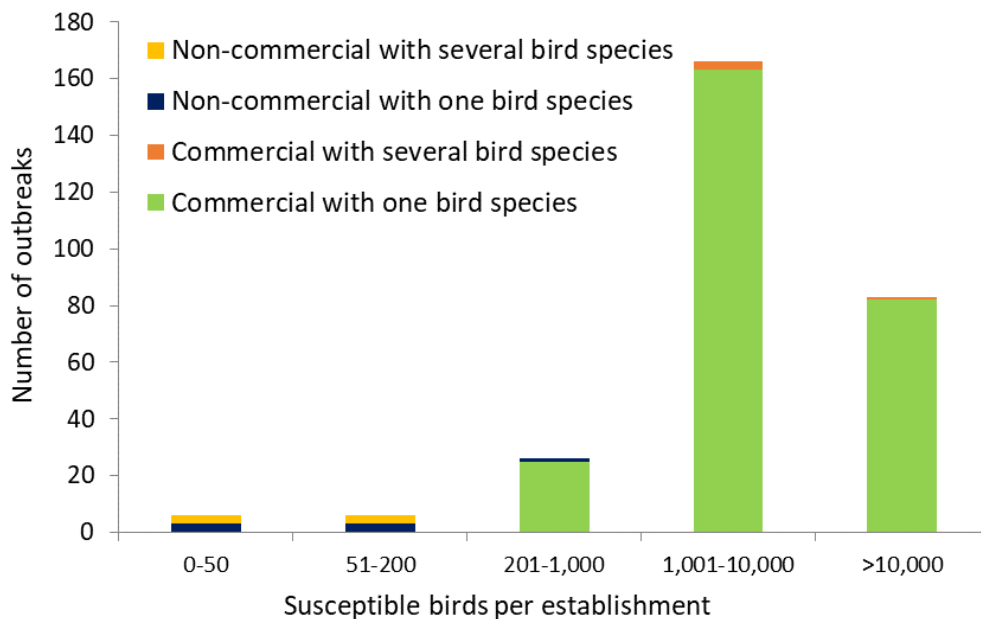
###### *Characterisation of the HPAI-affected poultry establishments*

From 16 February to 15 May 2020, a total of 287 HPAI outbreaks in poultry were notified in Europe (Table 2): 263 in Hungary, 14 in Poland, 7 in Bulgaria, 2 in Germany and 1 in Chechia. All these outbreaks were reported to be the A(H5N8) subtype, apart from three of the Bulgarian outbreaks where HPAI A(H5N2) virus was identified. The description of the bird species, the production category and the size of these HPAI affected establishments are shown in Figures 10 and 11.



\*'Mixed species' category indicates establishments where more than one of the following bird species were reared: chicken, turkey, domestic duck and domestic goose, guinea fowl (*Numida meleagris*), partridge (*Perdix perdix*), peacock (*Pavo cristatus*) and pheasant (*Phasianus colchucus*).

**Figure 10:** Number of HPAI-affected establishments by poultry species and production category in the EU, 16 February – 15 May 2020 (n=287).



**Figure 11:** Number of HPAI-affected establishments in the EU from 16 February – 15 May 2020, according to the commercial type and the number of susceptible bird species bred (n=287)

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

Between 20 February and 3 March 2020, three HPAI A(H5N2) and four HPAI A(H5N8) outbreaks were detected at poultry establishments in two regions in Bulgaria. Six of those were detected in Plovdiv Region and only one in Kardjali. The last outbreak detected in Plovdiv was a secondary outbreak. The characteristics of the affected establishments and species reared are presented in Table 2.

### *HPAI A(H5N8)-affected poultry establishments in Czechia*

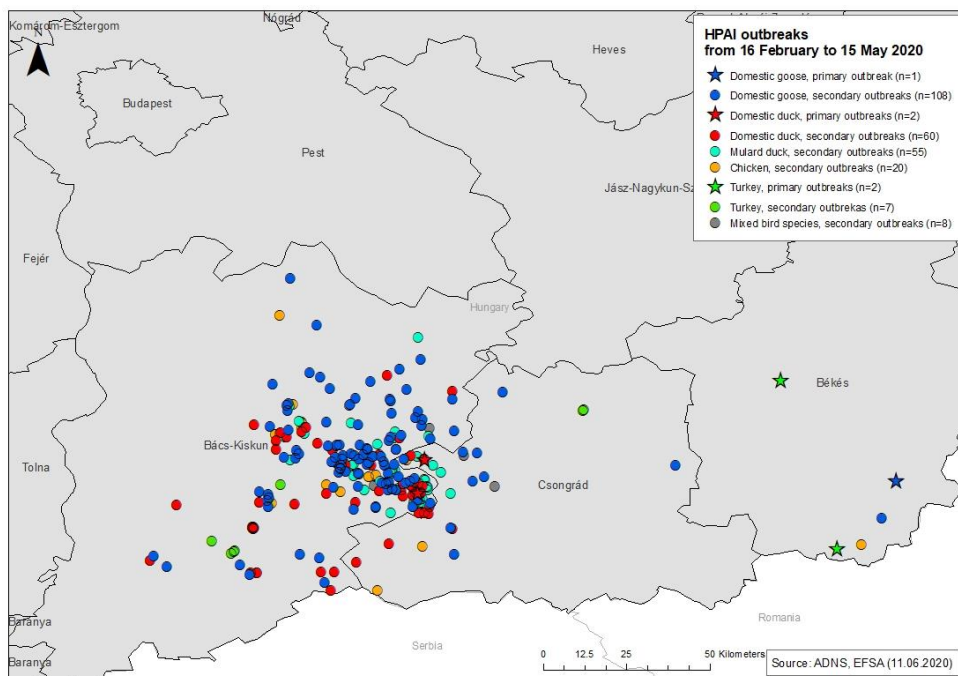
On 17 February, one HPAI A(H5N8) outbreak was detected at a mixed poultry establishment in Pardubice Region in Czechia. Mortality, clinical signs and a drop in feed/water intake were detected in turkeys; no signs of AI infections were reported in the broilers. Indirect contact with wild birds was mentioned as the most likely source of infection. The characteristics of the affected establishment and species reared are presented in Table 2.

### *HPAI A(H5N8)-affected poultry establishments in Germany*

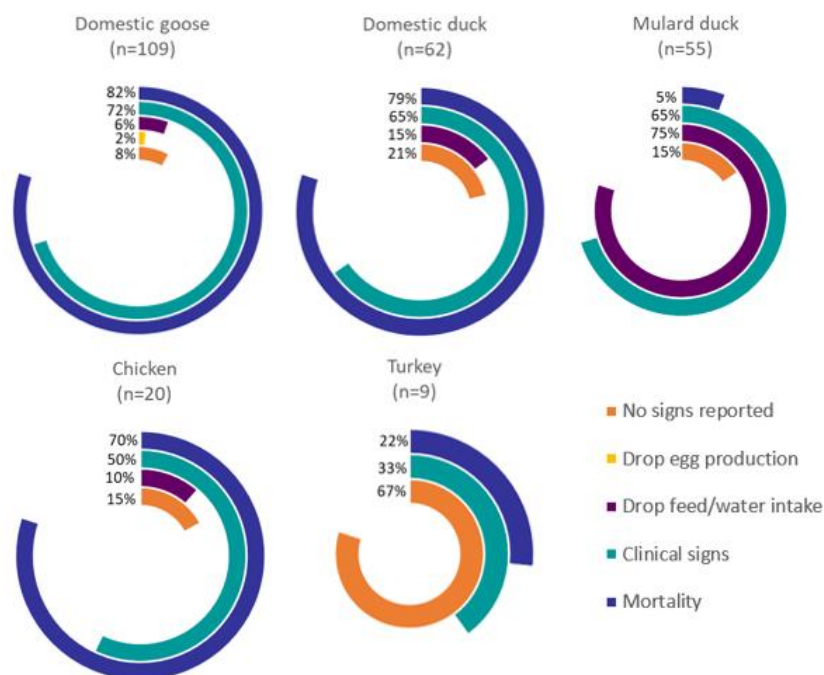
On 20 and 27 February 2020, two HPAI A(H5N8) outbreaks were detected at poultry establishments in Aurich and Börde regions, respectively, in Germany. The outbreak in Aurich was identified in a breeding turkey establishment in an area close to a wild bird resting place; the one in Börde in a fattening turkey establishment in the direct neighbourhood of a large river. The epidemiological investigations of both outbreaks identified indirect contact with wild birds as the most likely source of infection. Characteristics of the affected establishments and species reared are presented in Table 2.

### *HPAI A(H5N8)-affected poultry establishments in Hungary*

Between 22 March and 12 May 2020, 263 HPAI A(H5N8) outbreaks were detected at poultry establishments in Bács-Kiskun, Békés and Csongrád regions in Hungary (Figure 12). Five of the outbreaks were reported to be primary outbreaks, and the rest were secondary outbreaks with some of these secondary outbreaks related to other secondary outbreaks. There were eight mixed species establishments and the rest all house only one species. In total, 31 establishments did not record any signs of infections, while the other 232 establishments did (figure 12). One establishment reported the source of infection to be unknown, two establishments reported it to be indirect contact with wild birds, and all the rest reported the source of infection to be indirect contact with poultry. None of the establishments reported having outdoor access. Of all the establishments, only 12 were reported as non-commercial; the rest were commercial. The characteristics of the primary affected establishment and species reared are presented in Table 2.



**Figure 12.** Geographical distribution, based on available geocoordinates, of primary and secondary avian influenza outbreaks in Hungary, by virus affected subpopulation, 16 February – 15 May 2020 (n=263).



**Figure 13.** Signs of HPAI A(H5N8) infection in poultry species between 22 March and 12 May 2020 in Hungary (n=263).

*HPAI A(H5N8)-affected poultry establishments in Poland*

Between 20 February and 30 March 2020, 14 HPAI A(H5N8) outbreaks were detected at poultry establishments in 12 regions in Poland. Of those, one establishment reared mixed bird species (domestic duck, domestic goose and chicken); it was detected via outbreak-related surveillance as secondary to an outbreak reported in the previous EFSA report (EFSA et al., 2020) with the most likely source of infection being indirect contact with poultry. For all the other outbreaks identified by means of outbreak-related surveillance, the same transport company which delivered duckings was involved in the spread of the virus among those establishments. Indirect contact with wild birds was reported as the most likely source of infection for a duck establishment and the chicken establishment, in the latter the animals had access to an outdoor river. For the two turkey establishments the most likely source of infection was unknown. Characteristics of the affected establishments and species reared are presented in Table 2.

**Table 2:** Characteristics of the HPAI A(H5)-positive poultry establishments by affected EU Member State, from 16 February to 15 May 2020 excluding secondary putbreaks in Hungary (n=29). Data source: ADNS and EFSA

Country	Poultry species	Production category	Surveillance stream <sup>(a)</sup>	Presence of signs in the outbreaks	Outdoor access	Date of suspicion	Number of susceptible animals	Number of people exposed
<b>Bulgaria</b>	Domestic duck <sup>(b)</sup>	Foie gras	Active	No	Yes	20/2/2020	11,650	4
	Domestic duck <sup>(b)(c)</sup>	Foie gras	Passive	Yes	Yes	20/2/2020	55,437	6
	Domestic duck <sup>(b)</sup>	Foie gras	Active	No	Yes	28/2/2020	5,000	5
	Domestic duck <sup>(b)</sup>	Foie gras	Active	No	Yes	27/2/2020	3,620	5
	Chicken <sup>(c)</sup>	Egg	Active	Yes	Yes	3/3/2020	31,322	12
	Chicken	Egg	Passive	Yes	Yes	9/3/2020	16,800	10
	Chicken <sup>(c)</sup>	Egg	Passive <sup>(d)</sup>	Yes	Yes	9/3/2020	39,120	6
<b>Czechia</b>	Mixed <sup>(e)</sup>	Fattening	Passive	Yes	No	16/2/2020	140,495	82

<b>Germany</b>	Turkey	Breeding	Passive	Yes	No	20/3/2020	10,313	-
	Turkey	Fattening	Passive	Yes	No	27/3/2020	20,087	-
<b>Hungary</b>	Domestic duck	Fattening	Passive	Yes	No	22/3/2020	15,547	-
	Domestic duck	Fattening	Outbreak related	No	No	29/3/2020	141,652	-
	Domestic turkey	Breeding	Outbreak related	No	No	26/4/2020	23,532	-
	Domestic goose	Fattening	Passive	No	No	27/4/2020	9,872	-
	Domestic turkey	Fattening	Outbreak related	Yes	No	2/5/2020	11,138	-
<b>Poland</b>	Domestic duck	Fattening	Passive	Yes	No	20/2/2020	6,960	20
	Domestic duck	Breeding	Passive	Yes	No	20/2/2020	19,437	12
	Domestic duck	Fattening	Outbreak related	Yes	No	20/2/2020	49,321	34
	Domestic duck	Fattening	Outbreak related	Yes	No	22/2/2020	13,000	6
	Domestic duck	Fattening	Outbreak related	Yes	No	21/2/2020	56,503	7
	Domestic duck	Fattening	Outbreak related	Yes	No	22/2/2020	9,046	12
	Domestic duck	Fattening	Outbreak related	Yes	No	24/2/2020	4,895	7
	Domestic duck	Fattening	Outbreak related	Yes	No	26/2/2020	15,220	6
	Domestic duck	Fattening	Outbreak related	Yes	No	27/2/2020	30,183	27
	Mixed <sup>(f)</sup>	Mixed	Outbreak related <sup>(d)</sup>	Yes	Yes	1/3/2020	4,372	30
	Domestic duck	Fattening	Outbreak related	Yes	No	26/2/2020	10,338	7
	Chicken <sup>(g)</sup>	Egg	Passive	Yes	Yes	5/3/2020	74	2
	Turkey	Fattening	Passive	Yes	No	23/3/2020	94,206	55
	Turkey	Fattening	Outbreak related <sup>(d)</sup>	Yes	No	30/3/2020	28,938	55
	<b>Total for all countries</b>							<b>878,078</b>

(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) Mulard ducks.

(c) A(H5N2) outbreaks.

(d) Secondary outbreaks.

(e) Turkeys (n=7,206) and domestic broilers (n=133,289).

(f) Domestic duck, domestic goose, broiler and laying hens.

(g) Non-commercial establishment.

#### Information extracted from the scientific literature

A HPAI A(H5N8) virus infection (Ger-01-20) was detected in chickens in Baden-Wuerttemberg, Germany on 6 February 2020. It was a reassortant with six gene segments closely related to the 2.3.4.4b clade of the gs/Gd lineage of HPAI (H5), and the gene segments coding for PB1 and NP closely related to a LPAI A(H3N8) virus circulating in wild waterbirds in central Russia. At gross autopsy, the birds showed moderate mucous discharge in the upper respiratory tract and diarrhea. By histopathology, they had a severe acute diffuse necrotizing lymphohistiocytic enteritis and a moderate necrotizing encephalitis with perivascular cuffing and gliosis (King et al., 2020).



#### 4.2.2.2. HPAI in wild birds

##### *Pathogenicity in the affected species*

Between 16 February and 15 May 2020, one HPAI case in wild birds was notified in Europe (Table 3). It was HPAI A(H5N8) virus in a common buzzard (*Buteo buteo*) found dead near Leipzig, Germany, on 21 March, a few days after HPAI A(H5N8) virus was detected on 12 March in a non-commercial establishment of chickens in the same area.

**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 February – 15 May 2020 (OIE, online)

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
Germany	1	1	1	Common buzzard ( <i>Buteo buteo</i> )	1
<b>Total</b>	<b>1</b>	-	-	<b>1</b>	<b>1</b>

##### *Information extracted from the scientific literature*

The same Ger-01-20 reassortant that was detected in chickens (see 4.2.2.1) was detected in a greater white-fronted goose (*Anser albifrons*) that was found dead close to the Polish border in the federal state of Brandenburg, Germany on 16 January 2020. Although the proximate cause of death was trauma, the ultimate cause of death was considered to be a severe necrotizing poliomyelitis associated with the virus infection, which most likely causing disorientation and predisposed the goose to the traumatic event (King et al., 2020).

#### 4.2.2.3. LPAI in domestic birds

##### *Characterisation of the LPAI-affected poultry establishments*

Between 16 February and 15 May 2020, two LPAI outbreaks were notified in the poultry sector in Europe; two A(H7N1) in Italy. Information available from the ADNS (European Commission, online-a), from the OIE (OIE, online) and provided by Member States characterising the LPAI outbreak is presented in Table 4. The two affected establishments were located adjacent to each other. LPAI infected animals showed only very mild respiratory symptoms. The most likely source of virus entrance was identified as indirect contact with wild birds; the establishments were in proximity to wetlands where wild birds (e.g. herons, ducks) were present.

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

Country	Virus subtype	Poultry species	Surveillance stream	Presence of signs in the outbreaks	Date of suspicion	Number of susceptible birds
<b>Italy</b>	A(H7N1)	Domestic turkey	Passive	Yes	16/4/2020	7,096
	A(H7N1)	Domestic turkey	Outbreak-related	Yes	16/4/2020	7,161
<b>Total</b>						<b>14,257</b>

Data source: ADNS, OIE, Member States.

### 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 HPAI viruses of the A(H5) subtype circulating in Europe*

The complete genome of 40 HPAI A(H5N8) and 4 HPAI A(H5N2) viruses of clade 2.3.4.4b circulating in eastern and central Europe since December 2019 was characterised together with the partial genome (HA and NA) of 35 recent HPAI A(H5N8) viruses from Hungary.

Phylogenetic analyses identified the circulation of viral genotypes showing three distinct gene constellations (Figure 14).

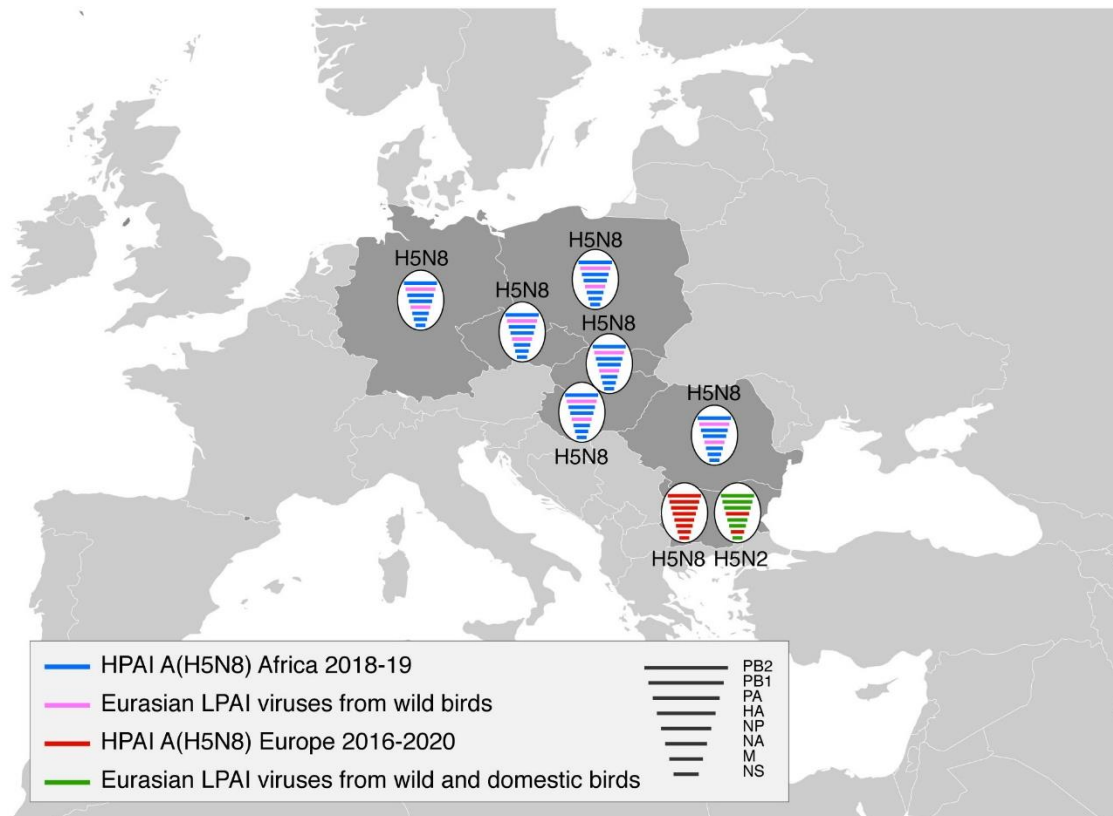
Specifically, HPAI A(H5N8) viruses from Poland, Czechia, Germany, Hungary, Romania and Slovakia cluster together for all the eight gene segments. This genotype was generated through reassortment events between HPAI A(H5N8) viruses from Africa and LPAI viruses from Eurasia, as described in the previous report (EFSA et al., 2020; King et al., 2020; Świętoń et al., 2020).

The HPAI A(H5N8) viruses from Bulgaria cluster separately from the A(H5N8) viruses currently circulating in eastern and central Europe. They belong to the previously defined A/mute swan/Croatia/70/2016-like genotype (Fusaro et al., 2017) and show the highest genetic identity with HPAI A(H5N8) identified in the country in 2018–2019 (EFSA et al., 2019b), which indicates a persistent circulation of this strain since 2017.

Four out of the eight HPAI outbreaks identified in Bulgaria from February 2020 were caused by an A(H5N2) subtype arising from reassortment events between the HPAI A(H5N8) from Bulgaria and the LPAI viruses identified in wild and domestic birds in Eurasia.

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

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



**Figure 14.** Distribution of the three distinct viral genotypes detected in Europe between December 2019 and May 2020

*Genetic characterisation of LPAI viruses of the A(H7) subtype circulating in Europe*

The genomes of the two LPAI A(H7N1) viruses identified in two contiguous turkey farms (same epidemiological unit) in Italy are highly related. The HA gene of the two viruses shares a common progenitor with a LPAI A(H7N3) virus identified in chicken of a poultry dealer in Italy in July 2019, while the remaining gene segments cluster with those of contemporary viruses from Eurasian wild birds. Such data suggest the occurrence of a single introduction from wild birds rather than the undisclosed maintenance of the virus in poultry populations.

**4.2.4. Human cases due to A(H5N8) or A(H5N2) viruses detected in Europe**

No human infection with A(H5N2) or A(H5N8) viruses, as detected in wild birds and poultry in Europe, has been reported during the period covered by this report or been previously reported (EFSA et al., 2020). 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). Of the 410 people (Table 2) exposed during the recent outbreaks, no transmission of avian influenza has been reported.

**4.3. Prevention and control measures applied in Europe, 16 February – 15 May 2020 (TOR 3)**

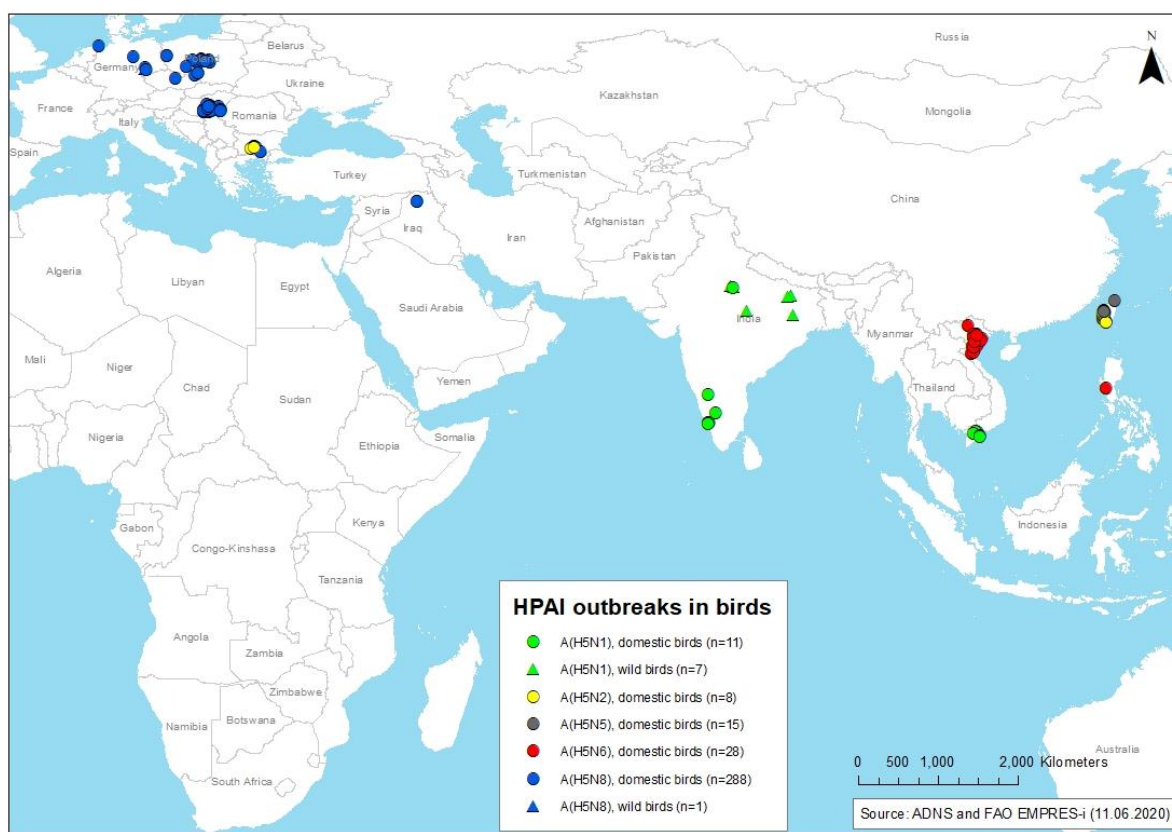
From 16 February to 15 May 2020, 287 HPAI outbreaks at poultry establishments were notified in Europe. For the description of the control and prevention measures applied in the affected Member States, see Annex A.

#### 4.4. The avian influenza situation in other countries not reporting via ADNS, 16 February – 15 May 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 February to 15 May 2020 is presented in Table 5 and Figure 15. 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 February – 15 May 2020 (n=54)

Region	Country	HPAI outbreaks							
		Domestic birds					Wild birds	All HPAI	
		A(H5N1)	A(H5N2)	A(H5N5)	A(H5N6)	A(H5N8)	A(H5N1)		
Asia	India	6						7	13
	Iraq					2			2
	Philippines				1				1
	Taiwan		5	15					20
	Vietnam	5			27				32
<b>Total</b>	<b>(5 countries)</b>	<b>11</b>	<b>5</b>	<b>15</b>	<b>28</b>	<b>2</b>	<b>7</b>	<b>68</b>	



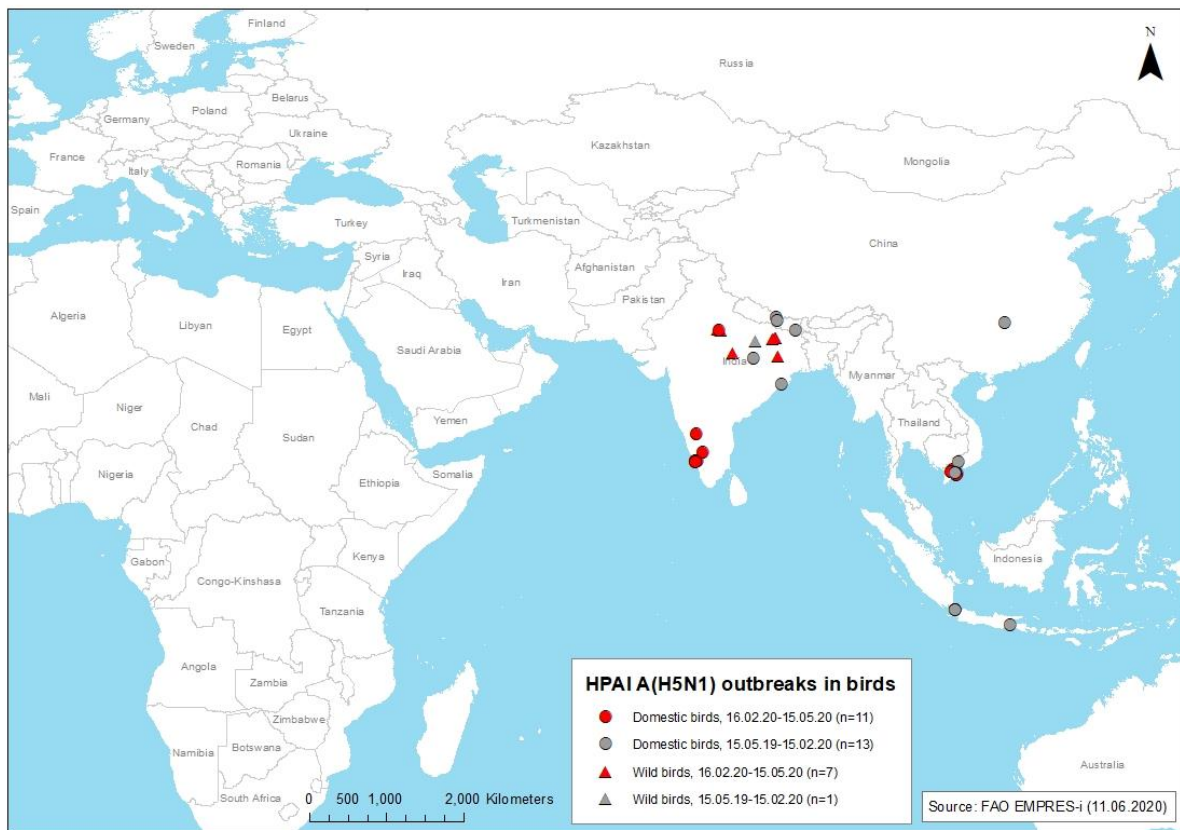
**Figure 15:** Geographical distribution, based on available geocoordinates, of HPAI outbreaks in Europe, Asia and Africa in domestic birds, by A(H5N1) as green, A(H5N2) as yellow, A(H5N5) as dark grey, A(H5N6) as red, A(H5N8) as blue, 16 February – 15 May 2020 (n=358)

#### 4.4.1. HPAI A(H5N1)

##### 4.4.1.1. Domestic and wild birds in previously affected regions

###### Detections

From 16 February to 15 May 2020 only two Asian countries notified the detection of HPAI A(H5N1) in domestic birds. The outbreak in Vietnam continued and new cases were detected on small and medium-sized poultry farms in the same region of southern Vietnam. India reported six outbreaks of HPAI A(H5N1) on backyard and medium-sized poultry farms; some in previously unaffected provinces Karnataka and Kerala. Furthermore, India detected several cases of HPAI A(H5N1) in several house crows (*Corvus splendens*) in previously affected regions and in Bhagawan Birsa Biological Park in Jharkhand Province affecting lesser adjutant (*Leptoptilos javanicus*), black-headed ibis (*Threskiornis melanocephalus*) and eastern grass owl (*Tyto longimembris*) during the relevant time period (Figure 16).



**Figure 16:** Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N1) outbreaks in domestic birds (circles) and wild birds (triangles) (n=32); grey symbols indicate outbreaks that occurred between 15 May 2019 and 15 February 2020, red symbols indicate outbreaks that occurred between 16 February and 15 May 2020 (FAO, online-b)

###### Information extracted from the scientific literature

Thurain et al. (2020) described the full genome sequences of four 2.3.2.1c HPAI A(H5N1) viruses detected from swab samples collected in December 2017 from layer chickens, at a live bird market in Myanmar. All segments were closely related to sequences obtained from clade 2.3.2.1c A(H5N1) viruses characterised in China and Vietnam in 2014-2015. Reported sequence determinants in the H5 protein were consistent with a conserved avian-like  $\alpha$ -2,3 receptor specificity. All viruses also had a 20-amino acid deletion in the stalk domain of their N1 protein, associated with adaptation to terrestrial poultry species, and no oseltamivir resistance markers. Some mammalian virulence and human adaptation

sequence signatures were also reported in the PB1, PA, NP and NS segments, but not for the PB2-627E and -335R positions.

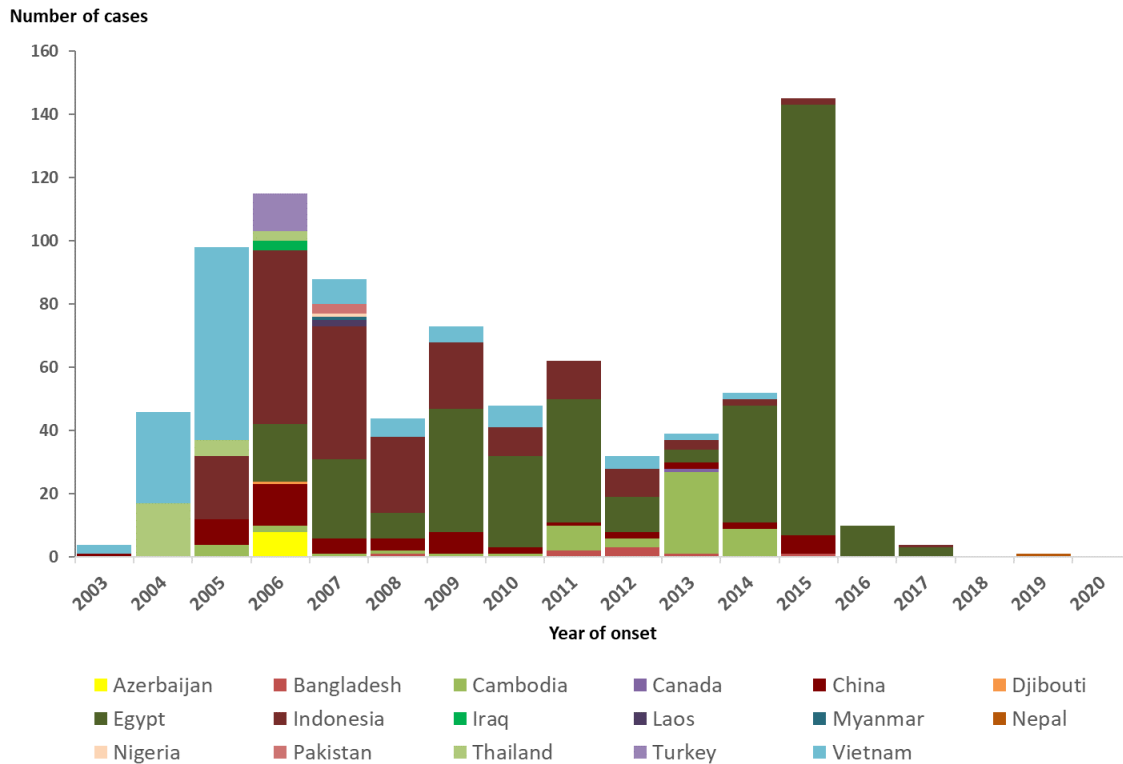
An original clade 2.3.2.1c HPAI A(H5N1) reassortant virus was reported by Abdollahi et al. (2020), collected in 2017 from a domestic duck commercial farm in Iran. This strain inherited its PB2, PA and NS segments from Eurasian LPAI viruses; the remaining segments being related to the previously characterised clade 2.3.2.1c A(H5N1) that was isolated in 2015 in the same country.

**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 countries outside the EU/EEA.

**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., 2020). Since 2003, and as of 15 May 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, 2019b, d, 2020d) (Figure 17).



Data source: WHO (WHO, 2019b).

**Figure 17:** Distribution of confirmed human cases of A(H5N1) by year and country of reporting, 2003 – 15 May 2020 (n=861)

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

##### 4.4.2.1. Domestic and wild birds

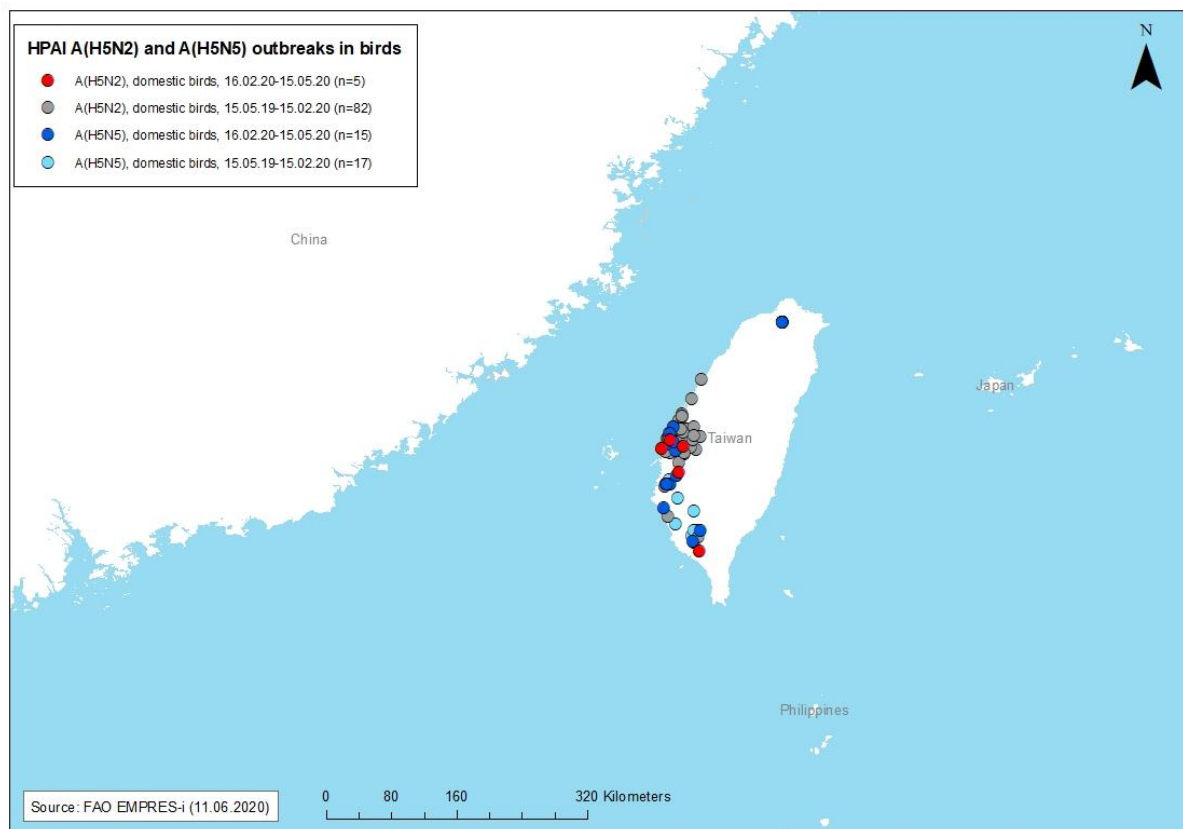
###### *Detections*

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. In the relevant time period for this report Taiwan detected four new outbreaks of HPAI A(H5N2) on medium-sized poultry farms and one case was confirmed on a large chicken farm (Figure 18). 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 between 2016 and 2019 (EFSA et al., 2019a) and in Bulgaria in 2020.

Furthermore, the Taiwanese government reported a case of HPAI A(H5N5) on a backyard chicken farm in northern Taiwan for the first time. The outbreak of HPAI A(H5N5) in southern Taiwan continued with 15 new cases on medium-sized and large poultry farms (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*

During the reporting period, no new relevant information concerning domestic and wild birds has been published on the phenotypic and genetic characterisation of HPAI A(H5N2) and A(H5N5) viruses circulating in countries outside the EU/EEA.



**Figure 18:** 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=119); grey symbols indicate HPAI A(H5N2) outbreaks that occurred between 15 May 2019 and 15 February 2020, red symbols indicate HPAI A(H5N2) outbreaks that occurred between 16 February and 15 May 2020, light-blue symbols indicate HPAI A(H5N5) outbreaks that occurred between 15 May 2019 and 15

February 2020, blue symbols indicate HPAI A(H5N5) outbreaks that occurred between 16 February and 15 May 2020, (FAO, online-b)

#### 4.4.3. HPAI A(H5N6)

##### 4.4.3.1. Domestic and wild birds

###### *Detections*

From 16 February to 15 May 2020, Vietnam reported 27 further outbreaks of the zoonotic reassortment of HPAI A(H5N6) clade 2.3.4.4c on one backyard farm and medium- to large-sized poultry farms in previously affected provinces of northern Vietnam. Furthermore, Philippines has notified the first case of HPAI A(H5N6) since September 2017. The disease was confirmed in a flock of 15,000 quails, around 3,000 of which died. In contrast to the last report, no wild bird cases of HPAI A(H5N6) were reported in the relevant time period (Figure 19).

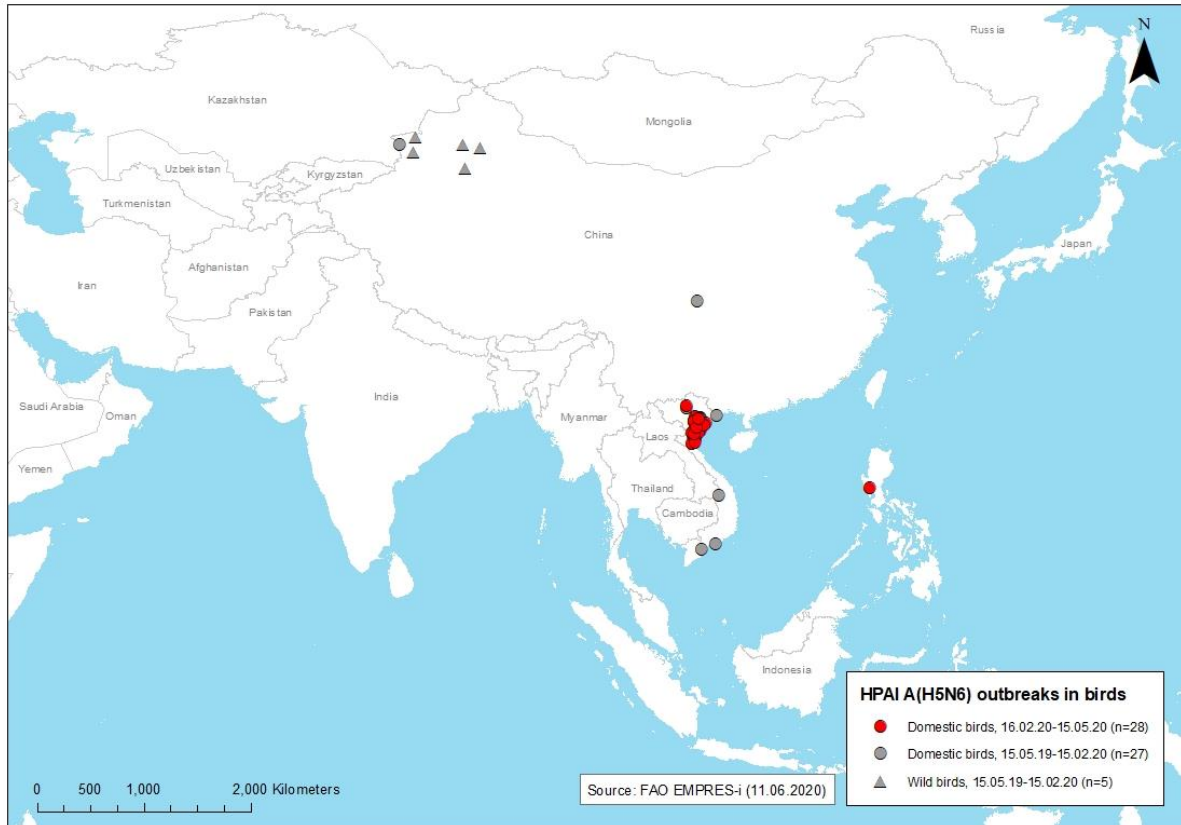
###### *Information extracted from the scientific literature*

Shin et al. (2020) described the full genome sequences of 12 HPAI A(H5N6) viruses detected in wild birds in South Korea, from December 2017 to August 2019. HPAI A(H5N6) strains characterised in 2017 (n=5) and 2019 (n=5) all belonged to clade 2.3.4.4c and were closely related for all their gene segments with HPAI A/environment/Korea/ W544/2016(H5N6)-like viruses, a reassortant genotype incorporating PB1 and PA segments from other subtypes of Eurasian viruses. These strains possessed genomic features associated with enhanced pathogenicity in poultry host species: an N6 stalk domain deletion and a 4-amino acid deletion in the NS1 gene. The major H5 sequence determinants corresponding to the receptor-binding domain indicated an avian-like  $\alpha$ -2,3 receptor specificity, but a deletion at position 133 (commonly found in A(H5N6) viruses infecting humans) was present. These viruses also harboured a 20 amino acid deletion in the stalk domain of their N6 stalk domain (associated with poultry adaptation) and several sequence determinants in their NS1 gene involved in increased virulence in mammalian and bird species. In contrast, HPAI A(H5N6) virus strains isolated in 2018 (n=2) were closely related to clade 2.3.4.4b A/mallard/Korea/612/2017-like reassortant viruses, clustering with other European and Korean A(H5N6) viruses. These viruses did not possess any of the sequence determinants mentioned above for the A(H5N6) characterised in 2017 and 2019.

Abdollahi et al. (2020) characterised the first full genotype of an HPAI A(H5N6) virus collected in 2018 from wild birds (gadwall, *Mareca strepera*) in Iran: all segments were related to A/mallard/Republic of Georgia/1/2018 (H5N6)-like European clade 2.3.4.4b viruses identified in wild birds and poultry in 2017–2018.

The full genome of the first HPAI A(H5N6) virus detected in Africa was described by Shittu et al. (2020). This virus isolated in June 2019 in Nigeria, from a duck sampled in a live bird market, is closely similar for all its segments to the same European clade 2.3.4.4b A(H5N6) viruses mentioned above. High pathogenicity of the virus was confirmed by its intravenous pathogenicity index (IVPI) test result of 2.89. Haemagglutination inhibition assays with ferret antisera raised against one clade 2.3.4.4d A(H5N6) and two clade 2.3.4.4b A(H5N8) viruses revealed no antigenic drift of the Nigerian virus.





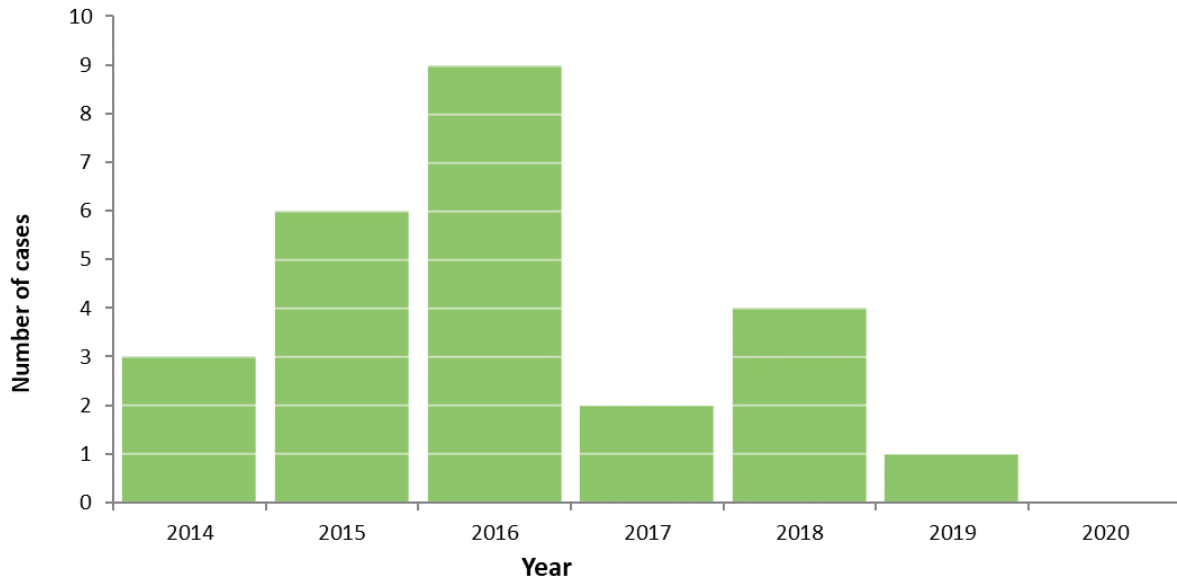
**Figure 19:** Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N6) outbreaks in domestic birds (circles) and wild birds (triangles) (n=60); grey symbols indicate outbreaks that occurred from 15 May 2019 to 15 February 2020, red symbols indicate outbreaks that occurred from 16 February to 15 May 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 countries outside the EU/EEA.

#### 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., 2020; WHO, 2020c, a). Since 2014, and as of 15 May 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 20). WHO lists 24 human cases of AI A(H5N6), including 15 with fatal outcomes (WHO, 2019d, a, c). 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, 2019a).



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 (Appendix B.2).

**Figure 20:** 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)

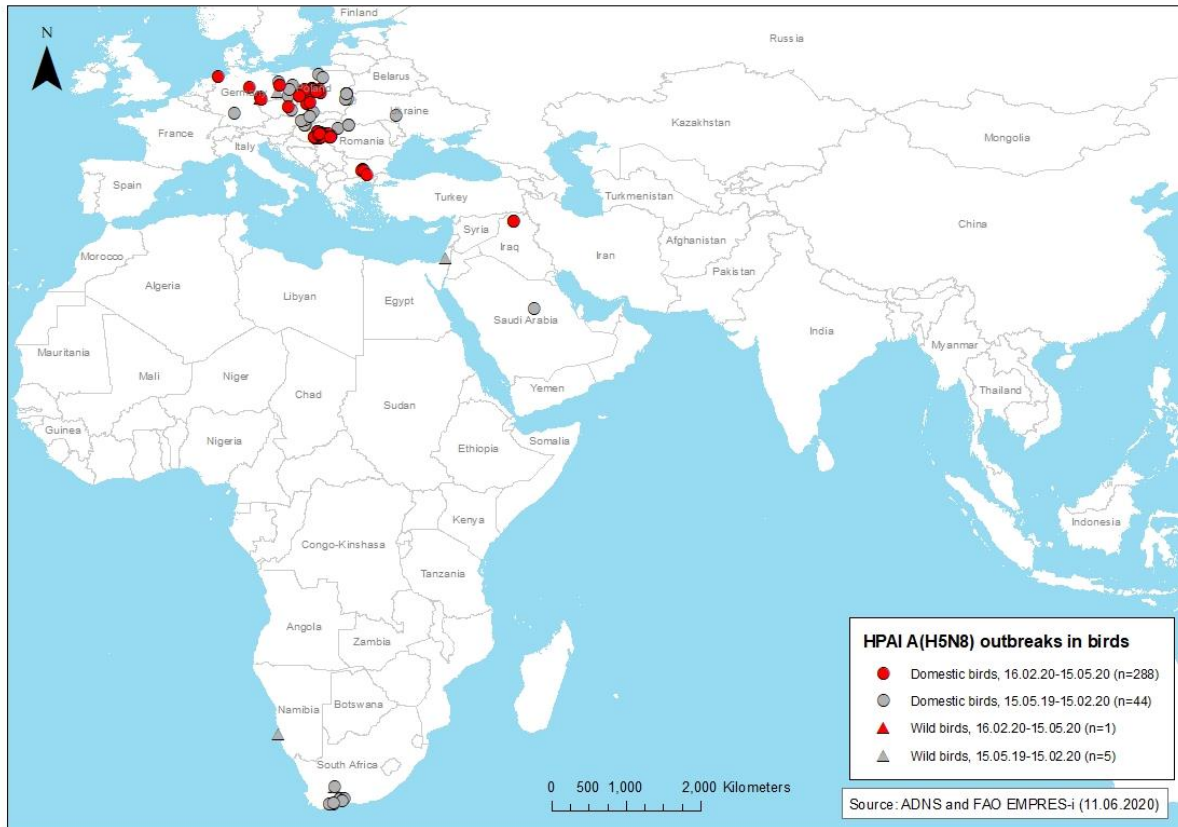
##### 4.4.4.1. Domestic and wild birds

###### *Detections*

Iraq reported two outbreaks of HPAI A(H5N8) at large poultry farms in Ninewa, located on the outskirts of Mosul. But no wild bird cases have been reported from Africa, Asia or the Middle East since the last EFSA report (EFSA et al., 2020) (Figure 21).

###### *Information extracted from the scientific literature*

Full genome sequences of 14 HPAI clade 2.3.4.4b A(H5N8) viruses, collected during 2016–2017 from wild birds (n=4) and chickens (n=10) in Iran, were described by Abdollahi et al. (2020) and grouped into eight distinct genotypes. Two of these were similar to previously identified genotypes, including A(H5N8) viruses present in 2016 in Europe and Asia: they probably correspond to different viral introductions in Iran. However, all other genotypes were novel reassortants combining segments from different clade 2.3.4.4b A(H5N8) viruses and Eurasian LPAI viruses: some of these may have been generated locally.



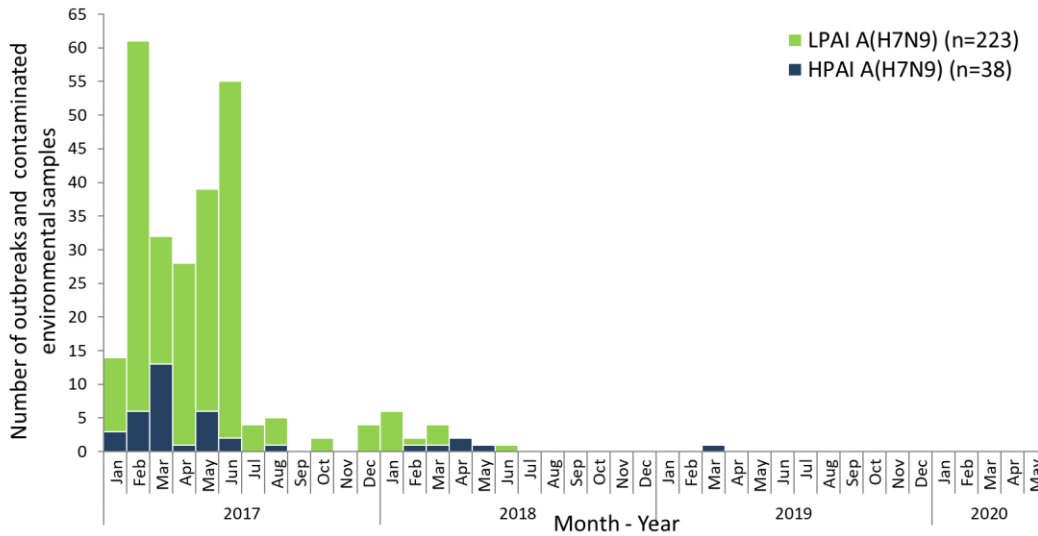
**Figure 21:** Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N8) outbreaks in domestic birds (circles) and wild birds (triangles) (n=338); grey symbols indicate outbreaks that occurred from 15 May 2019 to 15 February 2020, red symbols indicate outbreaks that occurred between 16 February and 15 May 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 22). 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 (25.05.2020)

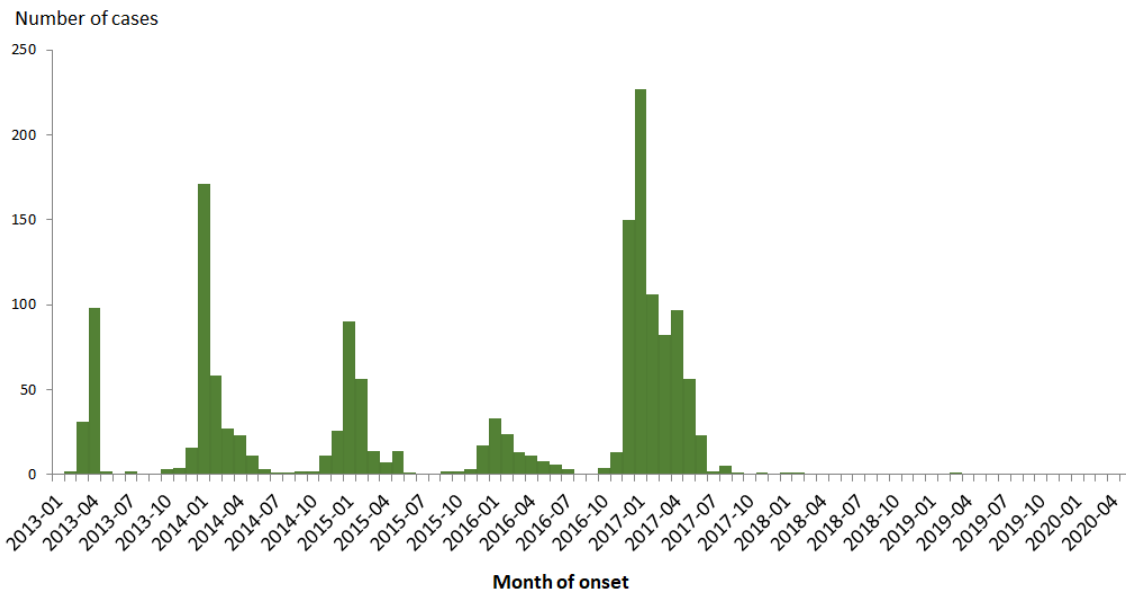
**Figure 22:** Distribution of confirmed LPAI and HPAI A(H7N9) outbreaks among birds and environmental samples in China, by month, 1 January 2017 – 15 May 2020 (n=261)

*Information extracted from the scientific literature*

During the reporting period, no new relevant information concerning domestic and wild birds has been published on the phenotypic and genetic characterisation of HPAI or LPAI A(H7N9) viruses circulating in countries outside the EU/EEA.

**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 (WHO, 2020c, a). Since February 2013, a total of 1,568 human cases have been reported from outside of Europe (Figure 23), including at least 615 deaths (39%) (WHO, 2019a, d). Of all cases, 32 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 (Appendix B.2).

**Figure 23:** Number of human cases due to A(H7N9), infection by month and year of onset, 2013 – 2020 (n=1,568)

#### 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 February to 15 May 2020.

###### *Information extracted from the scientific literature*

Li et al. (2020) characterised an LPAI A(H9N2) virus isolated in December 2017 in China, from an unidentified migratory wild waterbird species. This virus was a reassortant carrying PB1, HA and NA gene segments closely related to North American lineage wild-bird-origin LPAI viruses, while the other gene segments were related to various LPAI viruses isolated in China or Japan. Haemagglutination tests against different types of red blood cells indicated that this strain possessed an avian-like  $\alpha$ -2,3-linked sialic acid receptor specificity. The H9 sequence had a monobasic cleavage site sequence characteristic of avian influenza viruses with low pathogenicity in chickens, and the PB2 sequence did not possess previously described major substitutions associated with adaptation to mammalian hosts. Although mutations in the M1 and NS1 sequences were observed that suggested an enhanced virulence in mice, *in vivo* intranasal inoculation in 6-week-old female BALB/c mice with doses varying from 10 to 106 EID<sub>50</sub> only induced a transient loss of weight at 3 days post-inoculation, which was compensated for at 14 days post-inoculation when compared with uninfected control mice. At 3 days post-inoculation, virus was not detected from brain, spleen, kidney, lung or the nasal turbinate tissues of mice inoculated with the highest 106 EID<sub>50</sub> dose. *In vivo* studies therefore indicated low pathogenicity of this A(H9N2) in mice.

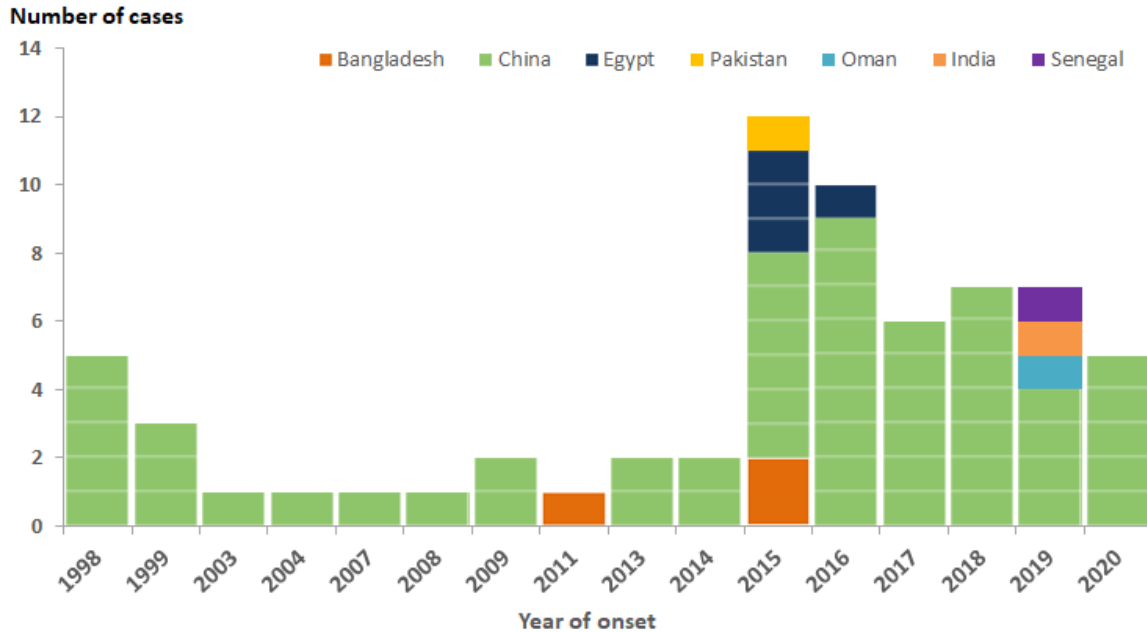
Parvin et al. (2020) tested a panel of LPAI A(H9Nx) viruses, including a majority of LPAI A(H9N2) belonging to the G1 lineage and isolated in chickens or turkeys from 2006 to 2018, in order to investigate the relationship between the monobasic, dibasic or tribasic nature of the H9 cleavage sites and their *in vitro* cleavability as well as their *in ovo* and *in vivo* pathogenicity. The tribasic motifs were here observed in A(H9N2) G1-like viruses isolated in Bangladesh and India in 2016–2018. Although the H9 tribasic and some of the H9 dibasic motifs were cleaved *in vitro* by endoproteases more easily than all H9 monobasic motifs, *in vitro* growth of all these viruses in MDCK-II cells remained trypsin-dependent. *In ovo* infectivity testing also indicated that A(H9N2) viruses expressing tribasic motifs or some dibasic motifs showed extended replication in various tissues and organs of infected chicken embryos, in addition to the virus replication consistently observed in the chorio-allantoic membrane for all viruses tested. These observations could indicate enhanced pathogenicity for the polybasic A(H9N2) viruses. However, there was no endothelial replication observed in infected embryos and *in vivo* testing in 6-week-old chickens resulted in minimal IVPI values of 0 for all A(H9Nx) viruses tested, demonstrating their low pathogenicity in chickens.

Chen et al. (2020) studied 21 LPAI A(H9N2) viruses belonging to the same genotype within the G1 lineage: strains had been isolated from chickens and domestic ducks in China between February 2016 and June 2019. The *in vitro* infectivity in MDCK cells and *in vivo* pathogenicity in 6-week-old BALB/c mice, following intranasal inoculation of a 106 EID<sub>50</sub> viral dose, were variable. Only some of the tested A(H9N2) strains were able to replicate in mouse lung tissues and to induce alveolar tissue damage and body weight loss after inoculation. In this last case, weight loss was, at most, slightly more than 10% and was compensated for by the end of the 13-day observation period: for all tested A(H9N2) viruses, no mortality was observed and final body weights were equivalent to the control group. Although nine amino acid substitutions in five genome segments are here described as correlating with enhanced replication or pathogenicity in mice, their contribution remains to be elucidated.

##### 4.4.6.2. Human infections due to A(H9N2)

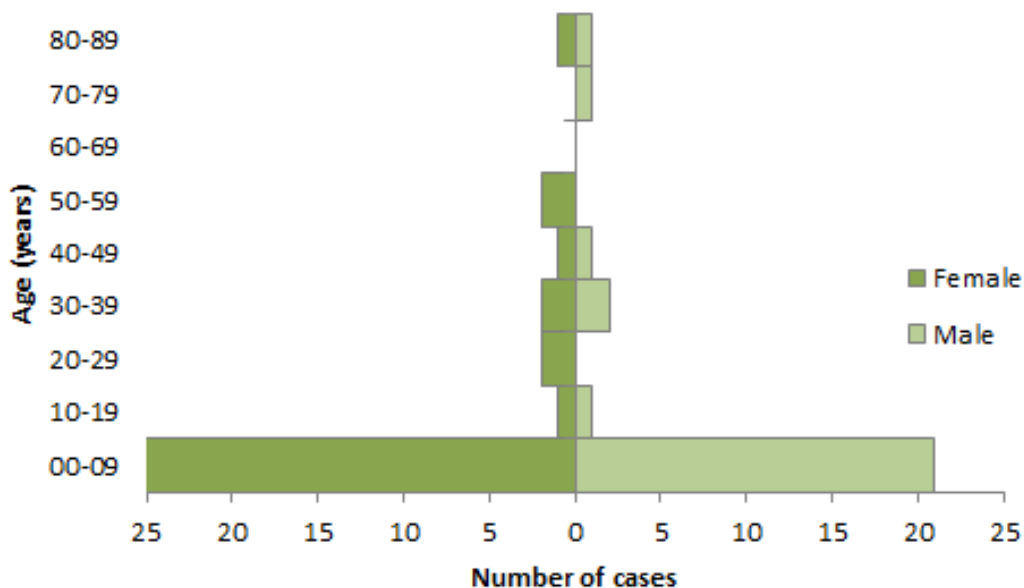
Since the last EFSA report, four new human cases have been reported from China: one in a 3-year-old girl with onset of symptoms on 22 March 2020 in Guangdong Province, China; a second in a 5-year-old girl from Hunan Province with onset of symptoms on 20 April 2020; a third on 4 May 2020 in a 10-

month-old boy in Xiamen, Fujian Province and a fourth case in a 6-year-boy from Weihai, Shandong Shen (WHO, 2020a; Taiwan Centers for Disease Control Press Releases, online). The recent slight increase in reported human cases due to A(H9N2) could be related to an intensified testing of all people with respiratory symptoms due to the ongoing COVID-19 pandemic. All cases reported exposure to domestic poultry or slaughtered poultry. Since 1998, and as of 15 May 2020, 66 laboratory-confirmed cases of human infection with AI A(H9N2) virus, including one death, have been reported globally. Cases were reported from China (55), Egypt (4), Bangladesh (3), India (1), Oman (1), Pakistan (1) and Senegal (1) (ECDC line list in Appendix B.2) (Figure 24). The age-group most affected by A(H9N2) infections in humans are children under 10 years of age (Figure 25).



Data source: Appendix B.2; (Peacock et al., 2019; Potdar et al., 2019; WHO, 2019d, 2020b, a; Taiwan Centers for Disease Control Press Releases, online; The Government of Hong Kong Special Administrative Region Press Release, online)

**Figure 24:** Distribution of confirmed human cases of A(H9N2) by reporting country, 1998 – 15 May 2020 (n=66)



**Figure 25:** Distribution of confirmed human cases of A(H9N2) by age group, 1998 – 15 May 2020 (n=66)

#### **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 contrast to the last report (EFSA et al., 2020), outbreaks of HPAI in non-EU/EEA countries were only notified by Asian and Middle Eastern countries during the time period of this report from 16 February to 15 May 2020. The number of affected countries and outbreaks decreased by one quarter compared with the previous reporting period. Moreover, cases in wild birds were only detected outside the EU in India during the relevant time period. Furthermore, India reported several outbreaks of HPAI A(H5N1), clade 2.3.2.1c in poultry and several cases of this clade were notified by Vietnam. However, no outbreaks were reported again in the relevant time period from Africa or the Middle East. The outbreaks of HPAI A(H5N2), clade 2.3.4.4 and HPAI A(H5N5) continued in Taiwan as well as the outbreaks of the novel zoonotic reassortant HPAI A(H5N6) belonging to clade 2.3.4.4c in Vietnam. Furthermore, the Philippines have notified the first case of HPAI A(H5N6), on a commercial quail farm, since September 2017. In contrast to the previous report, outbreaks of HPAI A(H5N8) reassortants were only detected outside the EU/EEA in Iraq. Despite the lack of reports on detection of wild birds outside Europe and India there is considerable uncertainty regarding the real geographical distribution of these viruses. The environmental stability of avian influenza viruses will likely decrease with the higher temperatures and increased ultraviolet radiation in spring and summer, but constant monitoring is warranted due to the presence of HPAI virus in wild birds worldwide, including key migration areas, during the previous reporting period (EFSA et al., 2020).

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

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

The measures outlined in the EFSA report for November 2017 – February 2018 (EFSA et al., 2018c) remain valid.

##### **4.6.2. Candidate vaccine viruses**

In February 2020, a new candidate vaccine virus for A(H9N2) (WHO, 2020e) based available antigenic, genetic and epidemiologic data, A/Oman/2747/2019-like A(H9N2), was proposed.

#### **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. However, 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
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
HPAI	Highly pathogenic avian influenza
IVPI	Intravenous pathogenicity index
LPAI	Low pathogenic avian influenza
OIE	World Organisation for Animal Health
SCOPAFF	Standing Committee on plants, animals, food and feed
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<sup>2</sup>, 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<sup>3</sup>, EFSA should provide the technical and scientific assistance to the Commission based on the following Terms of Reference (TOR):

<sup>2</sup> 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.

<sup>3</sup> 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 February and 15 May 2020 and reported by Member States and neighbouring countries via ADNS. Member States where avian influenza (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 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 the 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 February and 15 May 2020 and on information gathered by performing a literature search on papers published in PubMed from 16 February to 15 May 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 November 2019 – February 2020 (EFSA et al., 2020) 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 February to 15 May 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 February to 15 May 2020 were searched; the search was run on 17 February 2020.

*Relevance criteria* Scientific articles added to the database from 16 February to 15 May 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 140 papers. The articles were subsequently screened against the relevance and eligibility criteria. One 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.3908523>.

#### B.1.2. Overview of avian influenza 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. Data were extracted on 11 June 2020. 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 February and 15 May 2020 were searched; the search was run on 17 February 2020.

*Relevance criteria* Scientific articles added to the database between 16 February and 15 May 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 118 papers. The articles were subsequently screened against the relevance and eligibility criteria. Seven 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.3908523>.

## **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 and Poland between 16 February and 15 May 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 prepared 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.4 provide timelines for the main events that triggered actions in relation to the selected prevention and control measures in Bulgaria, Czechia, Hungary and Poland. 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 (if applicable)
24.02-12.03.2020	Confirmation of HPAI H5N8 outbreak	Measures according to Directive 2005/94/EC	Official veterinarians, poultry farmers
20.03.2020	Epidemiological situation in Bulgaria	<ol style="list-style-type: none"> <li>1. Reorganisation of the duck sector – the whole technology cycle/life to be in one holding or different but technologically linked and belonging to the same owner/company/operator. This measure aims at decreasing the movement of ducks from farm to farm and avoiding one farm (gavage) to be used by different owners/companies.</li> <li>2. Transport of ducks – separate transport means to be used for ducks and Galliformes. GPS equipment for all poultry transport in order to allow the traceability of poultry movement.</li> <li>3. Established a sanitary period of at least 21 days (one incubation period) - a ban on restocking of all duck farms in Bulgaria (2.05.2020 - 28.05.2020) and on slaughtering ducks (24.07.2020 - 23.08.2020). During the sanitary periods, cleaning and disinfection of all premises will be carried out. The duck farms will be inspected for compliance with biosecurity rules by an Expert Commission requiring positive results before restocking. This sanitary period shall be implemented every year as the period to be fixed additionally.</li> <li>4. Enhanced laboratory surveillance, as follows:                         <ul style="list-style-type: none"> <li>- official control and serology/virology sampling of poultry in backyards located in risk areas (areas with high density of poultry holdings and areas with high population of migratory wild birds)</li> <li>- routine official control four times per year at least in duck farms and serology sampling of all flocks at 45-65 days old present in the farm at the time of the visit. The official control will replace the current self-control.</li> </ul> </li> <li>5. Increased official inspections ensuring the implementation of the biosecurity measures in poultry farms - twice per year in the risk areas mentioned above (in the duck sector these checks to be part of the inspections related to the laboratory surveillance).</li> </ol>	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 such as increased control and surveillance, were proposed by the poultry industry sector itself. The sector is actively engaged and thoroughly cooperates in implementing the control and surveillance activities.

2. Close cooperation with the 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 second outbreak of highly pathogenic avian influenza (HPAI) in Czechia

On 16 February 2020 the State Veterinary Administration in Pardubice Region received information about higher mortality among turkeys on a commercial farm with turkeys, broilers (*Gallus Gallus*) and pigs. At the same time, the official vets visited this holding and took samples from dead birds for laboratory testing. The samples were sent to the State Veterinary Institute in Prague (SVI Prague) – National Reference Laboratory (NRL) for Avian Influenza, which confirmed the presence of HPAI subtype H5N8 by PCR on 17 February 2020.

On 17 February 2020 the emergency veterinary measures were in place in accordance to the Council Directive 2005/94/EC introducing Community measures for the control of avian influenza. The emergency veterinary measures included culling of all remaining poultry, safe disposal of poultry products, feed stuffs and by-products and preliminary cleaning and disinfection. The emergency veterinary measures for the protection and the surveillance zone were taken in line with EU legislation.

The final cleaning and disinfection was carried out on 12 March 2020. The surveillance zone around the outbreak was lifted on 23 March 2020.

**Table A1:** Overview of main actions

Date	Event that triggered action	Type of action taken	Target audience (if applicable)
Still continuing	New outbreaks in poultry holdings in the EU	Regular updating of the website of the State Veterinary Administration about the AI situation in Europe: <a href="https://www.svscr.cz/zdravi-zvirat/ptaci-chripka-influenza-drubeze/vysocepatogenni-aviarni-influenza/">https://www.svscr.cz/zdravi-zvirat/ptaci-chripka-influenza-drubeze/vysocepatogenni-aviarni-influenza/</a>	General public, all breeders
		Increased control (biosecurity) of poultry holdings in contact with avian influenza affected countries  Regular information about the AI situation in neighbouring countries	Regional Veterinary Administrations
16/2/2020	Second suspicion of AI in a commercial poultry farm (Slepotice)	Spot checks, measures taken to prevent spread of the virus, sampling, laboratory testing	
17/2/2020	Confirmation of HPAI H5N8 in a commercial poultry farm (Slepotice)	Publication of emergency veterinary measures for the second outbreak in Slepotice	Keeper of the outbreak poultry farm
		Press release related to the second outbreak of AI in Czechia and to emergency veterinary measures taken	General public, all breeders
		Publication of emergency veterinary measures for the restricted zone	All keepers in the restricted zone
23/3/2020	Lifting of emergency veterinary measures in the surveillance zone around second the HPAI outbreak	Press release related to lifting of the emergency veterinary measures in the surveillance zone around the second HPAI outbreak	General public, all breeders

### Increasing awareness of the stakeholders and the general public

On the website of the State veterinary administration was regularly updated with 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 the event of an outbreak and which are binding within a defined restricted area around the outbreak (the protection and surveillance zone), also stipulate biosecurity measures for backyard farms in protection zones with the aim preventing the contact of poultry with wild birds and their subsequent possible infection.

### Strengthening biosecurity measures (other than housing order)

Increased control (biosecurity) of poultry holdings in contact with avian influenza affected countries was put in place.

Additional national emergency veterinary measures to control the spread of HPAI in connection with the second outbreak of HPAI were not applied in Czechia.

The general public was informed through the press on compliance with biosecurity in poultry farms, and the current disease situation was published 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 release of poultry (pheasant, mallard) and other captive birds for restocking purpose was forbidden inside the 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)
25/03/2020	First poultry outbreak in Bács-Kiskun County in 2020	Increasing awareness, release housing order, preventive culling, regional stand still, derogations on restriction zone implementation after risk assessment	-
31/03/2020	First poultry outbreak in Csongrád County in 2020		-
30/04/2020	First poultry outbreak in Békés County in 2020		-

### Increasing awareness of the stakeholders and the general public

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

The Chief Veterinary Officer (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

Preventive killing/slaughter has been carried out – based on a risk assessment – in protection zones and also in certain parts of the surveillance zones.

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

In the whole territory of the affected counties: transport of poultry can only take place after a negative PCR result. No stocking can take place in the restricted zones. As additional measures to control the HPAI spread, the radius of the surveillance zones have been enlarged based on the density of poultry establishments and of the administrative boundaries in some areas. This was the case in Bács-Kiskun and Csongrád-Csanád county (where most of the outbreaks were) and in Békés county (Figure A.3.1)

### Derogations on restriction zone implementation after risk assessment

Based on risk assessment in accordance with to Council Directive 2005/94/EC, poultry was transported out of the surveillance zone after laboratory examination to immediate slaughter.

## Hunting

Not restricted. No special rules apply.

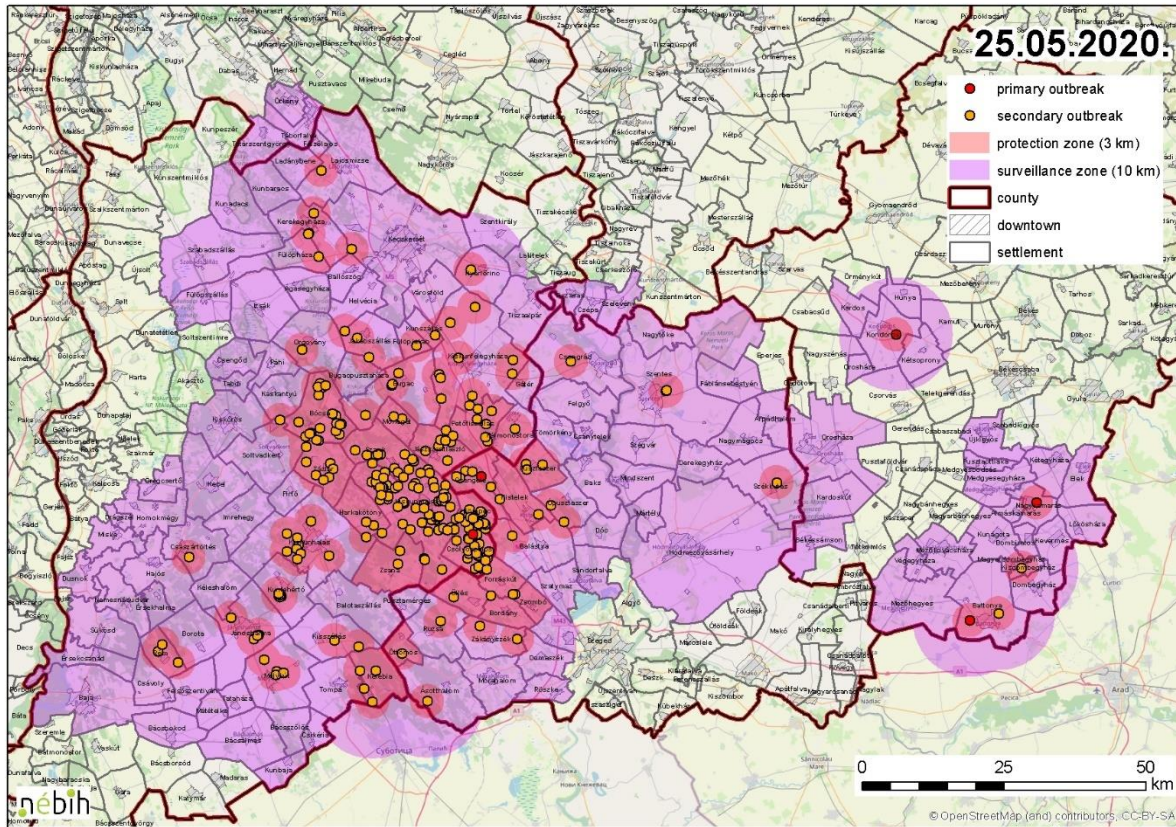


Figure A.3.1 Primary and secondary outbreaks with related protection and surveillance zones in Hungary by County

## A.4 Poland

Magdalena Gawędzka

General Veterinary Inspectorate

Table A.4: Overview of main actions

Date	Event that triggered action	Type of action taken	Target audience (if applicable)
16.02-23.03.2020		Continuation of intensified farm inspections keeping poultry as in Letter of CVO dated 3.01.2020 and continuation of awareness campaigns for poultry keepers and poultry associations	Veterinary Inspectorate, poultry keepers/ poultry associations
20.03.2020	Imposition of the epidemic state in Poland in connection with COVID-19		
23.03.2020		Lifting of intensified biosecurity controls in poultry farms. Performing actions to confirm or exclude avian influenza on farms and in wild birds based on	Veterinary Inspection,

		suspicious and the national control programme in relation to AI	
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### Increasing awareness of the stakeholders and the general public

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

### 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 18 December 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 4 April, 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 their 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 are 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 of protective clothing and safety footwear by persons entering livestock buildings in which poultry are held, intended for use only in the given building - in the case of farms where poultry are 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 equipment and tools used for handling poultry before each use,
- abstentions by persons who have participated in the hunting of 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 carcasses of game birds.

### Strengthening biosecurity measures (other than housing order)

The Regulation of the Minister of Agriculture and Rural Development of 4 April, 2017 regarding the ordinance of measures related to the occurrence of HPAI introduced 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 HPAI in the territory of the Republic of Poland.

The Chief Veterinary Officer in messages about outbreaks reminds poultry farmers about the necessity of following 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 18 December, 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 on 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.

In the period covered by the report, preventive culling was carried out on three farms associated with outbreaks 2020/31 and 2020/32.

### **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**

On 4 April, 2020 the Ministry of the Environment announced a ban on entry to forests from 3 to 11 April, 2020 because of the epidemic of COVID-19, which resulted in no hunting during that period.