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Avian influenza overview February – August 2019

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 August 2019, five HPAI A(H5N8) outbreaks at poultry establishments in Bulgaria, two low pathogenic avian influenza (LPAI) A(H5N1) outbreaks in poultry in Denmark and one in captive birds in Germany, one LPAI A(H7N3) outbreak in poultry in Italy and one LPAI A(H7N7) outbreak in poultry in Denmark were reported in Europe. Genetic characterisation reveals that viruses from Denmark cluster with viruses previously identified in wild birds and poultry in Europe; while the Italian isolate clusters with LPAI viruses circulating in wild birds in Central Asia. No avian influenza outbreaks in wild birds were notified in Europe in the relevant period for this report. A decreased number of outbreaks in poultry and wild birds in Asia, Africa and the Middle East was reported during the time period for this report, particularly during the last three months. Furthermore, only six affected wild birds were reported in the relevant time period of this report. Currently there is no evidence of a new HPAI virus incursion from Asia into Europe. However, passive surveillance systems may not be sensitive for early detection if the prevalence or case fatality in wild birds is very low. Therefore, it is important to encourage and maintain passive surveillance in Europe encouraging a search for carcasses of wild bird species that are in the revised list of target species in order to detect any incursion of HPAI virus early and initiate warning. No human infections due to HPAI viruses - detected in wild birds and poultry outbreaks in Europe - have been reported during the last years and the risk of zoonotic transmission to the general public in Europe is considered very low.

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1. Introduction

This scientific report provides an overview of highly pathogenic avian influenza (HPAI) virus outbreaks detected in poultry, captive and wild birds and significant low pathogenic avian influenza (LPAI) virus outbreaks 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 August 2019. 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 August 2019

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.
- One human case caused by A(H5N1) in Nepal, two cases with A(H9N2) in China and Oman, one human case with A(H7N9) and one with A(H5N6) infection in China have been reported with onset of disease since February 2019.
- In Europe, between 16 February and 15 August 2019 (based on the Animal Disease Notification System (ADNS)):
 - five HPAI A(H5N8) outbreaks were reported in poultry in Bulgaria; phylogenetic analysis revealed that the viruses cluster with A(H5N8) European viruses collected during the 2016–2017 epidemic;
 - five LPAI outbreaks were reported: two A(H5N1) and one A(H7N7) in poultry in Denmark, one A(H7N3) in Italy, and one A(H5N1) in captive birds in Germany. Genetic characterisation of the Danish isolates showed that they cluster with LPAI viruses previously identified in wild birds and poultry in Europe. Phylogenetic analysis of the Italian isolate revealed that the virus clusters with LPAI viruses circulating in wild birds in Central Asia.
- No HPAI cases in wild birds were reported in Europe during this reporting period.
- Taking the half-year period of this report and the dates of notification into account, the number of reported outbreaks in domestic birds for Asia, Africa and the Middle East was lower than in the previous time period, particularly during the last three months. Furthermore, only six infected wild birds were reported in the relevant time period for this report.

2.2. Conclusions

- The risk of zoonotic transmission of AI viruses to the general public in Europe remains very low.
- In the current 2018–2019 season (from October 2018 to August 2019), compared with the previous 2017–2018 season (from October 2017 to September 2018), there is a decreased number of reported outbreaks in poultry in Europe.
- No cases of HPAI virus infection were reported in wild birds from key areas in Mongolia, western China, or Siberia; in previous years, such reports foreshadowed the incursion of HPAI virus in Europe via the autumn migration of wild birds.
- During the period for this report in the EU/EEA, there has been no evidence of any new HPAI virus incursion from Asia. However, passive surveillance systems may not be sensitive for the early detection of new incursion if the case fatality rate in wild birds is very low.

3. Suggestions

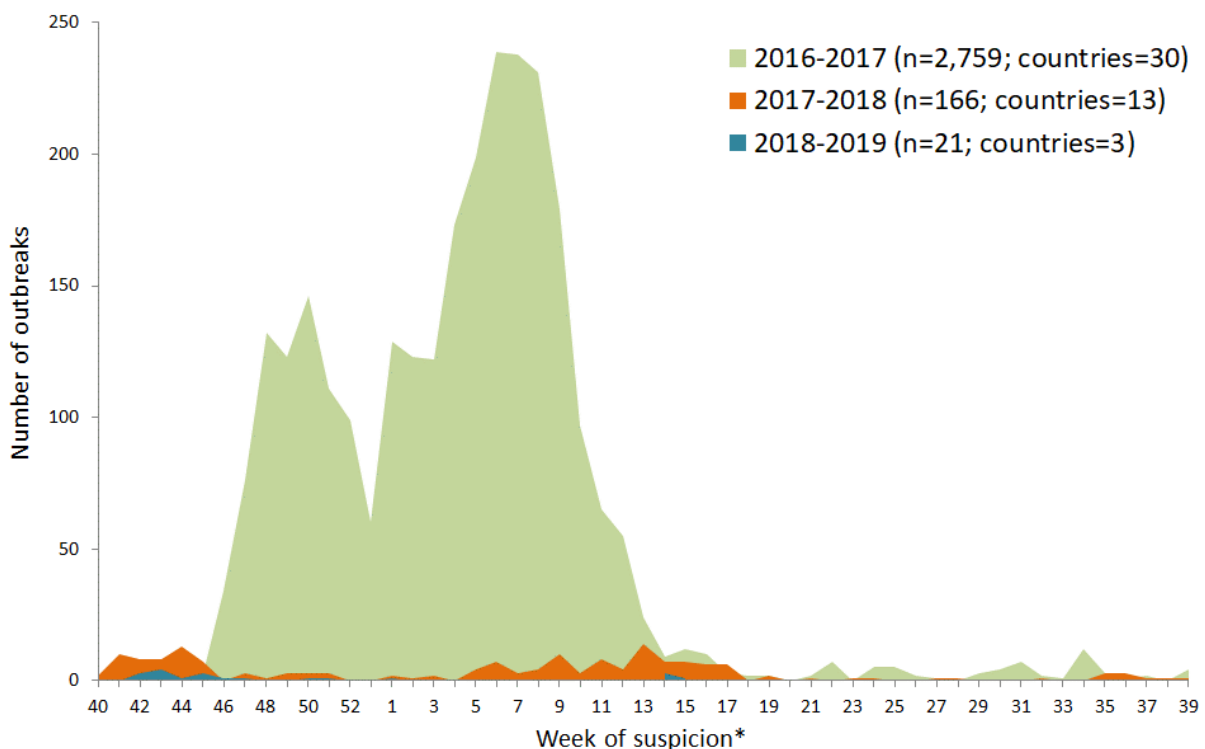
- Continued surveillance for AI virus in wild birds and poultry in Europe and worldwide combined with timely generation of complete viral genome sequences and data sharing among European countries and between animal and human health sectors are crucial to be able to detect and respond promptly to threats that are relevant to animal and public health. 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.
- It is important to maintain passive surveillance in Europe, also encouraging a search for carcasses of wild bird species that are in the revised list of target species (EFSA et al., 2017a) in order to detect HPAI virus early and initiate warning.
- Despite the decrease of AI outbreaks in these last months, it is important to ensure that high standard alert and biosecurity levels are maintained in poultry farms.
- People exposed to birds which 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 and 2018–2019. 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.

The analysis of the characteristics of the previous (2017–2018) and the current AI seasons (2018–2019), from 2 October 2017 to 15 August 2019, are reported in Figures 2–6 by geographical distribution, HPAI virus subtype, affected host population and surveillance stream leading to the outbreak detection. Overall, 187 HPAI outbreaks were detected in Europe and reported via ADNS for the seasons 2017–2018 and 2018–2019. Of those outbreaks, 98 (52%) were of the A(H5N6) virus subtype and 89 (48%) of the A(H5N8) virus subtype. Of the A(H5N6) outbreaks, 90 (92%) were reported in wild birds, 4 (4%) in poultry and 4 (4%) in captive birds whereas of the A(H5N8) outbreaks, 82 (92%) were reported in poultry, 6 (7%) in wild birds and 1 (1%) in captive birds. The vast majority of the A(H5N6) cases in wild birds formed a relatively narrow band along the Baltic and North Sea coasts in a north-east to south-west line, and suggests that these cases occurred along a migratory flyway. The HPAI cases in raptors were reported several weeks later than the first cases in waterfowl; this fits with the concept that raptors become infected by preying or scavenging on infected waterfowl (van den Brand et al., 2015; Krone et al., 2018). In poultry passive surveillance led to the detection of 87% and 76% of the HPAI outbreaks reported in domestic turkey and chicken, respectively. In domestic duck passive surveillance played a smaller role than active surveillance leading to the detection of 31% of the outbreaks; most of the outbreaks (68%) were detected via active and outbreak-related surveillance.



* 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) and reported via ADNS by week of suspicion, 28 September 2015 – 15 August 2019 (n=2,946)

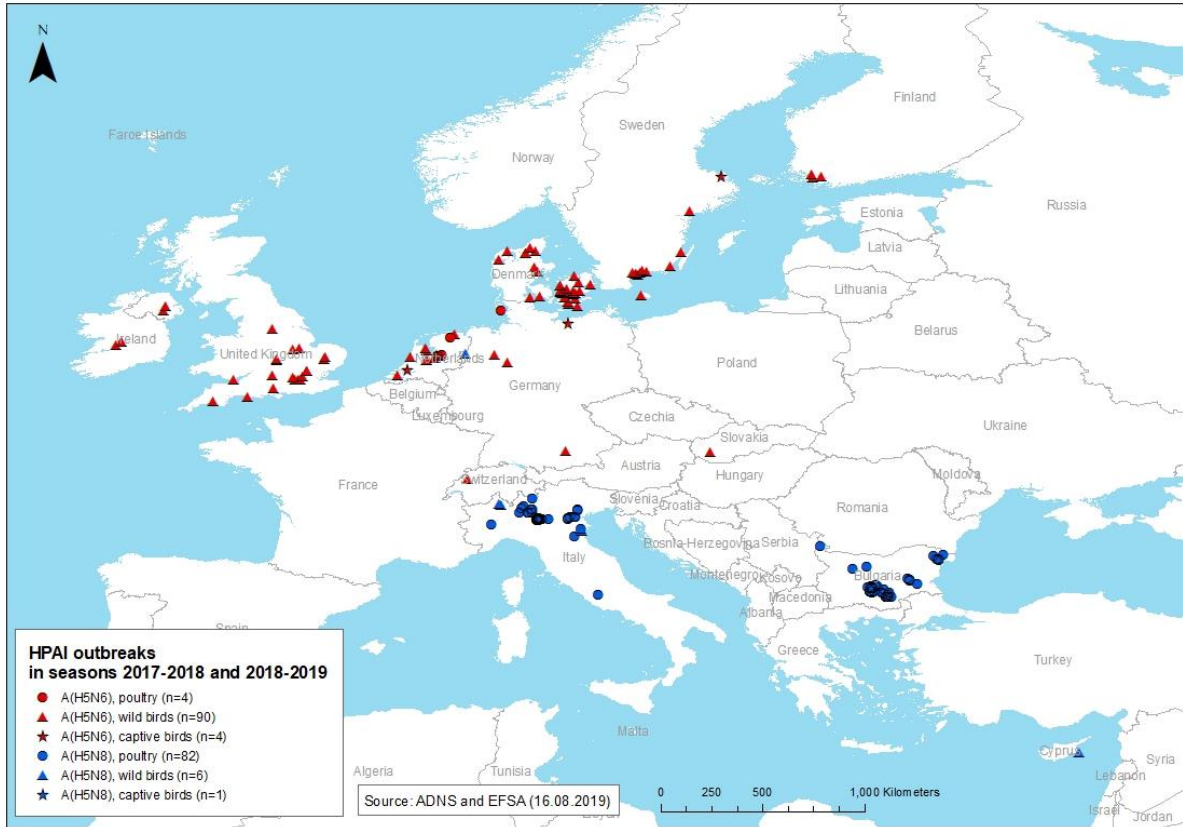
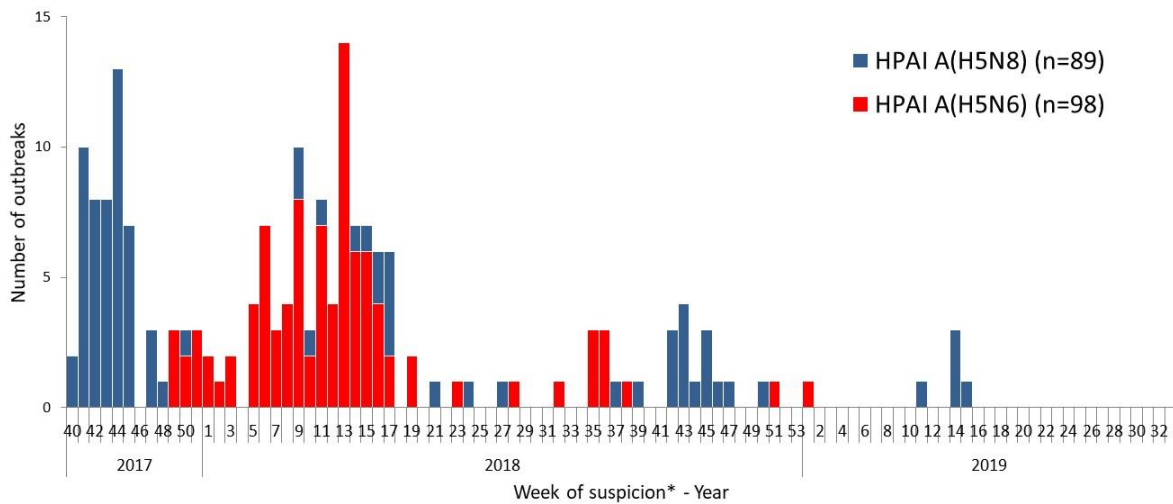
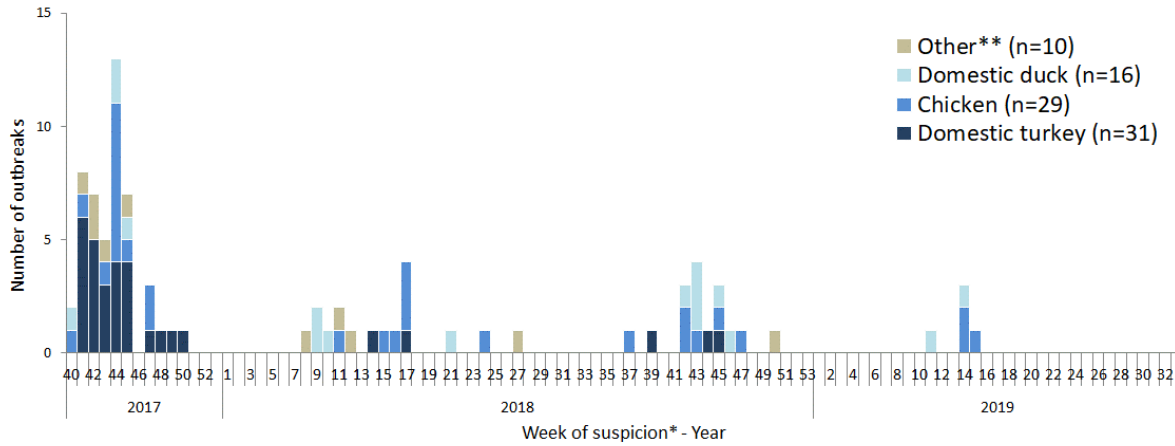


Figure 2: Geographical distribution, based on available geocoordinates, of HPAI outbreaks in Europe by A(H5N6) (red) and A(H5N8) (blue) virus in poultry (circles), wild birds (triangles) and captive birds (stars), in seasons 2017–2018 and 2018–2019 (2 October 2017 – 15 August 2019; n=187)



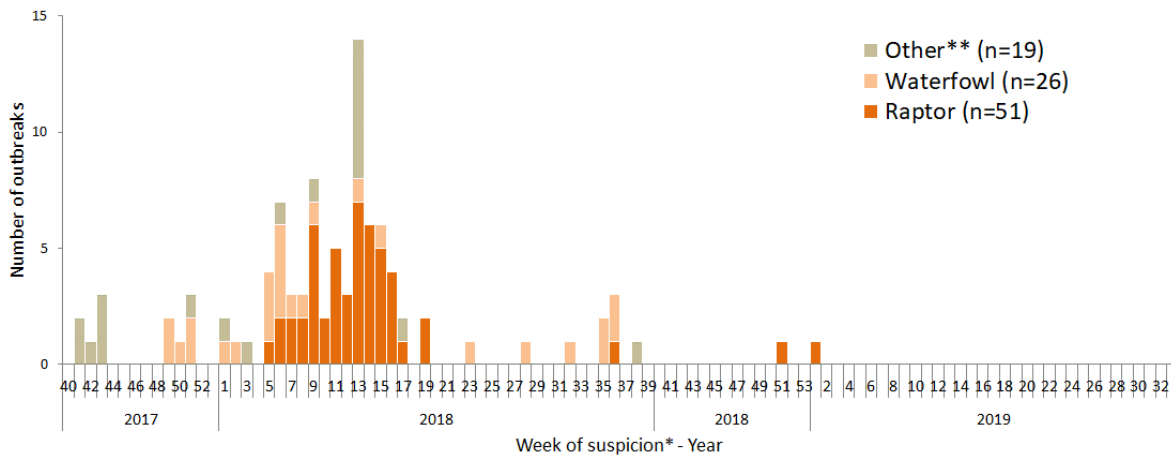
* When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.
Data source: ADNS, EFSA.

Figure 3: Distribution of total number of HPAI A(H5N6) (red) and A(H5N8) (blue) outbreaks in Europe by week of suspicion in seasons 2017–2018 and 2018–2019 (2 October 2017 – 15 August 2019; n=187)



* 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 displayed¹.
 Data source: ADNS, EFSA.

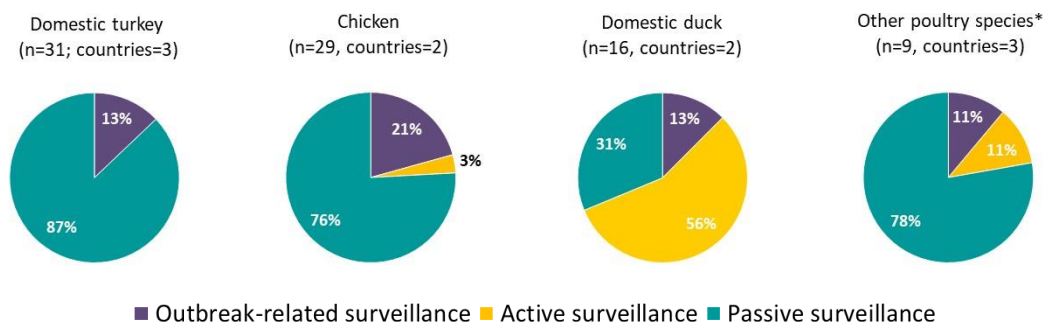
Figure 4: Distribution of total number of HPAI outbreaks in Europe by week of suspicion in seasons 2017–2018 and 2018–2019 by affected poultry species (2 October 2017 – 15 August 2019; n=86)



* 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 displayed².
 Data source: ADNS, EFSA.

Figure 5: Distribution of total number of HPAI outbreaks in Europe by week of suspicion in seasons 2017–2018 and 2018–2019 by affected wild bird category (2 October 2017 – 15 August 2019; n=96)

¹ Pheasant (*Phasianus colchicus*), pigeons (*Columba livia*), partridges (*Perdix perdix*), chukar partridges (*Alectoris chukar*)
² Black-headed gull (*Chroicocephalus ridibundus*), great cormorant (*Phalacrocorax carbo*), herring gull (*Larus argentatus*), hooded crow (*Corvus cornix*), pheasant (*Phasianus colchicus*), white stork (*Ciconia ciconia*)



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

Figure 6: Frequency distribution of HPAI outbreaks in poultry in Europe, by bird species and sampling programme leading to the outbreak detection, in seasons 2017–2018 and 2018–2019 (2 October 2017 – 15 August 2019; n=85)

4.2. HPAI and LPAI outbreaks in Europe, 16 February – 15 August 2019 (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

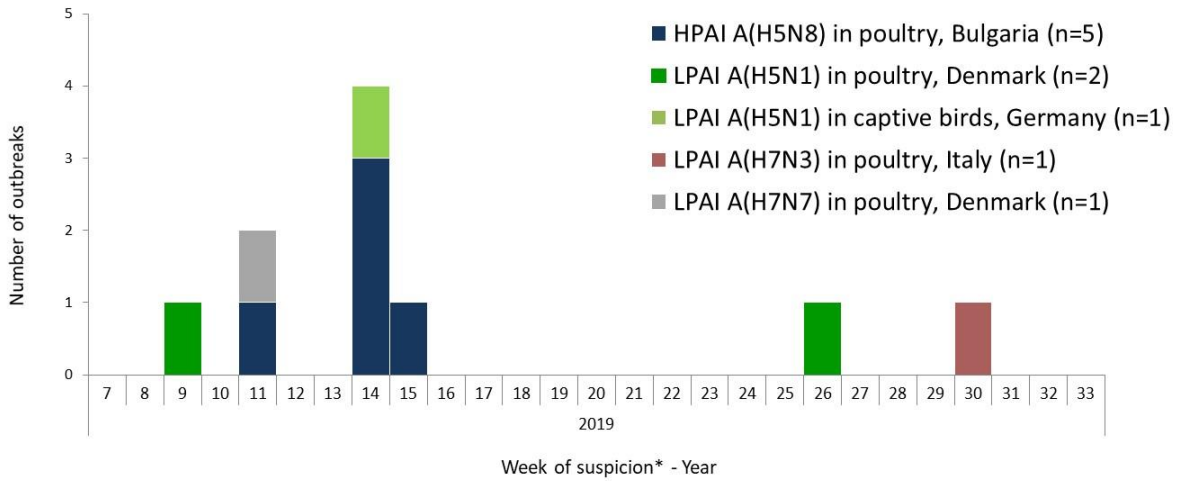
From 16 February to 15 August 2019, five HPAI outbreaks occurred in Europe, all in Bulgaria, and were reported via the ADNS, as presented in **Error! Not a valid bookmark self-reference..** Five LPAI outbreaks, three A(H5N1), one A(H7N3) and one A(H7N7) were also detected during this time period in three European countries: Denmark, Germany, and Italy. The timeline, location and affected subpopulation of the AI outbreaks are shown in Figures 7 and 8. The characterisation of HPAI-affected poultry establishments³ is reported in Section 4.2.2.1. and LPAI outbreaks are described in section 4.2.2.3. No outbreaks were detected in wild birds in Europe during this time period.

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

Country	HPAI outbreaks	LPAI outbreaks			Captive birds A(H5N1)	All AI outbreaks
	Poultry A(H5N8)	Poultry A(H5N1)	A(H7N3)	A(H7N7)		
Bulgaria	5	–	–	–	–	5
Denmark	–	2	–	1	–	3
Germany	–	–	–	–	1 ^(a)	1
Italy	–	–	1	–	–	1
Total (4 countries)	5	2	1	1	1	10

(a) Birds of special breed of ducks, goose and chickens.
Data Source: ADNS (16.09.19)

³ 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).



* When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.
Data source: ADNS (16.09.19).

Figure 7: Distribution of the AI outbreaks in Europe, by week of suspicion, virus subtype, affected subpopulation and country, 16 February – 15 August 2019 (n=10)

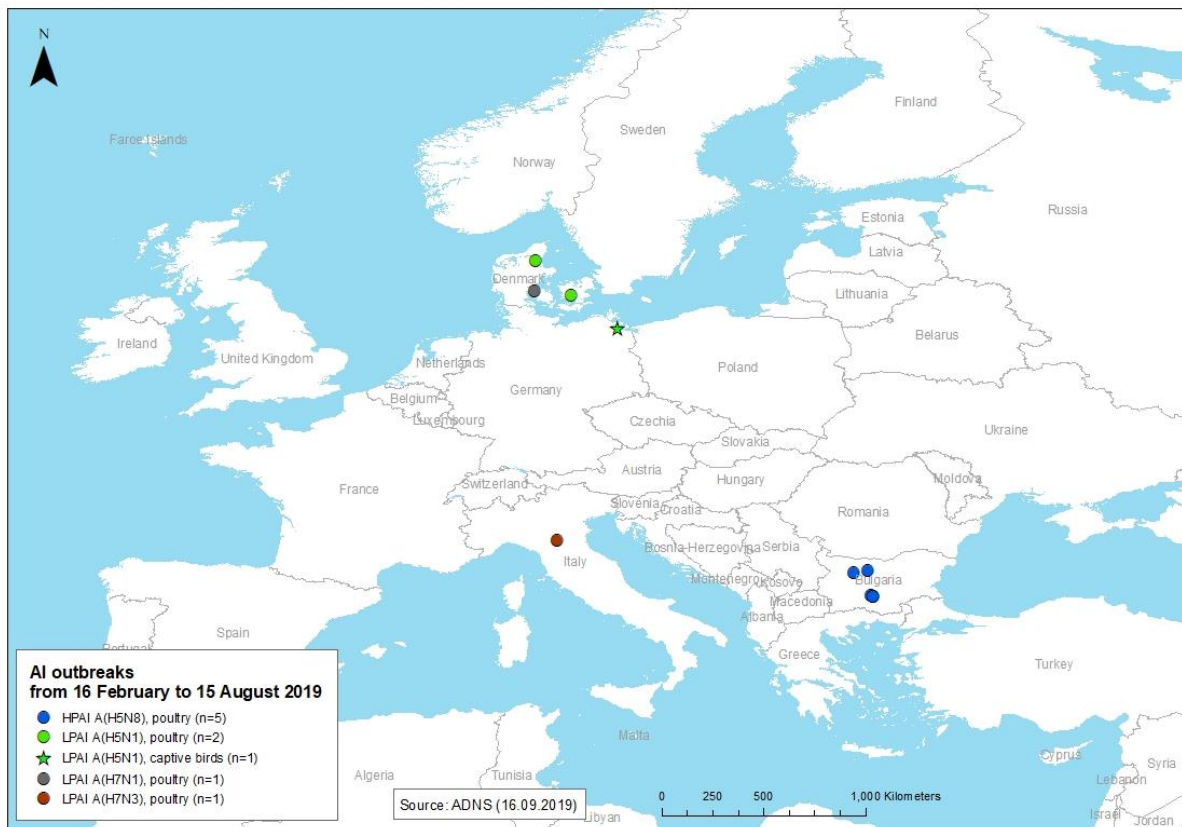


Figure 8: Geographical distribution, based on available geocoordinates, of HPAI outbreaks in Europe, by virus subtype and affected subpopulation, 16 February – 15 August 2019 (n=10)

From 16 February to 15 August 2019, two non-H5/H7 LPAI viruses characterised by an unusual animal and public health impact were detected in poultry in Belgium, France and Italy.

As part of the Belgian AI surveillance programme, LPAI A(H3N1) virus was first isolated on an outdoor laying-hen establishment in January 2019. The affected flock was depopulated. In April 2019, the A(H3N1) virus was detected again on the establishment. Since then, 82 outbreaks in poultry have been reported in Belgium, and more specifically in the Northwest region, during a 16-week period. The outbreaks included various poultry species and establishment types. Only five of the A(H3N1) affected establishments were asymptomatic. The observed clinical picture in the field began with egg discolouration for laying hens and breeders and subsequently increased mortality of up to 40% in layers and 60% in female breeders. A marked decrease in egg yield was noted, up to 100% in some cases. Among the specific lesions found during necroscopy were: petechiae in the proventriculus, trachea and brain; congestion of the kidneys, ovaries and brain; and atrophy of the oviduct resulting in egg yolk leakage and peritonitis. Transmission to humans was not reported. While A(H3N1) virus is classified as LPAI according to official definitions using *in vivo* test (IVPI: 0.13) or molecular criteria, it was more pathogenic and transmissible in poultry, and especially in laying hens under both field and experimental conditions.

In northern France (Nord department), three LPAI A(H3N1) outbreaks were detected in the relevant period for this report, showing epidemiological links with a Belgian company from the affected area (Briand FX et al., 2019). All three detected holdings were breeders for broiler production, located 20 km apart from each other at most and close (around five km) to the Belgian border. Two of these outbreaks were discovered as a result of direct investigations following official declaration of clinical suspicions on 20 May and 12 June 2019, respectively. The other outbreak was a retrospective finding in environmental swab samples taken on 28 May from an empty poultry establishment situated in the 3-km control zone surrounding the first outbreak. The last flock present in this establishment was slaughtered on 2 May, and clinical signs in the birds were observed the week before but were not associated with AI infection at that time, so this may indicate a first introduction of the A(H3N1) virus in French poultry as early as the end of April 2019. A(H3N1) sequences obtained from poultry samples in France were closely related to sequences from the Belgian outbreaks.

On 15 June 2019, an event of likely reverse zoonotic transmission of a human A(H1N1)pdm09 virus was identified in a turkey breeder flock in north-east Italy. The infection led to a significant drop in egg production (approximately 46%) but without mortality. The source of infection was likely a worker with an history of influenza-like illness in charge of artificial insemination on that establishment.

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 August 2019, five HPAI outbreaks A(H5N8) were notified in the poultry sector by Bulgaria (Figure 7). Two outbreaks affected domestic ducks and were detected by active surveillance; three outbreaks were reported in laying hen by means of passive surveillance as the animals reared showed clinical signs of HPAI virus infection. The last outbreak detected in laying hen was a secondary outbreak, and it seems that the virus has spread from the previous outbreak. The source of infection has not been identified for the other four outbreaks. An overview of the characteristics of the affected establishments and species reared is given in Table 2.

Table 2: Characteristics of the A(H5N8) HPAI-affected poultry establishments in Europe, 16 February – 15 August 2019 (n=5)

Country	Poultry species	Production category	Surveillance stream	Presence of signs in the outbreaks	Outdoor access	Date of suspicion ^(a)	Number of susceptible animals ^(b)	Number of people exposed
Bulgaria	Mulard	Fattening	Active	N	N	11/03/2019	12,000	23
	Domestic duck	Fattening	Active	N	N	01/04/2019	1,400	12
	Chicken ^(c)	Egg	Passive	Y	Y	03/04/2019	37	2
	Chicken	Egg	Passive	Y	N	04/04/2019	34,998	18
	Chicken ^(d)	Egg	Passive	Y	N	08/04/2019	168,752	18
Total							217,187	73

(a) Date of confirmation is provided when the date of suspicion is not available.

(b) Based on the number of susceptible domestic birds reported to EFSA.

(c) Non-commercial establishment.

(d) Secondary outbreak.

Data source: ADNS and EFSA.

Information extracted from the scientific literature

No information was found in the scientific literature on the phenotypic characterisation of HPAI viruses circulating in the EU in domestic birds within the reporting period.

4.2.2.2. HPAI in wild birds

Pathogenicity in the affected species

From 16 February to 15 August 2019, no AI outbreaks in wild birds were notified in Europe.

Information extracted from the scientific literature

No information was found in the scientific literature on the phenotypic characterisation of HPAI viruses circulating in the EU in wild birds within the reporting period.

4.2.2.3. LPAI in domestic birds

Characterisation of the LPAI-affected poultry establishments

From 16 February to 15 August 2019, five LPAI outbreaks were notified in the poultry sector and captive birds in Europe. Three LPAI outbreaks, caused by the A(H5N1) and A(H7N7) subtypes, were reported in domestic birds in Denmark. Specifically, the two A(H5N1) cases were identified on a commercial poultry establishment with organic laying hens in the municipality of Rebild and on a mallard establishment in the municipality of Naestved, while the A(H7N7) case was reported in March in a mallard establishment in the municipality of Middelfart (OIE, online-a). In July 2019, an A(H7N3) LPAI virus was identified in the meat chickens of a poultry dealer in northern Italy (Modena province). Information available from the ADNS (European Commission, online-a), from the Standing Committee on Plants, Animals, Food and Feed (SCOPAFF) presentations (European Commission, online-b), from OIE (OIE, online-b) and provided by MS that characterises the LPAI outbreaks is presented in Table 3.

Table 3: Characteristics of the LPAI-affected poultry and captive birds establishments in Europe, 16 February – 15 August 2019 (n=5)

Country	Virus subtype	Poultry species	Surveillance stream	Presence of signs in the outbreaks	Date of suspicion ^(a)	Number of susceptible animals
Denmark	A(H5N1)	Chicken ^(b)	Active surveillance	No	26/02/2019	7,276
	A(H7N7)	Domestic duck ^(c)	Active surveillance	No	12/03/2019	2,828
	A(H5N1)	Domestic duck ^(d)	Active surveillance	No	28/06/2019	5,193
Italy	A(H7N3)	Chicken ^(e)	Active surveillance	Yes ^(f)	26/07/2019	2,167
Germany ^(g)	A(H5N1)	Mixed ^(h)	-	-	01/04/2019	119
Total						17,583

(a) Date of confirmation is provided when the date of suspicion is not available.

(b) Laying hens.

(c) For restocking supplies of game.

(d) For restocking supplies of game and hatching eggs.

(e) Grower.

(f) Unspecified respiratory symptoms.

(g) Captive birds.

(h) 48 geese, 46 ducks and 25 chicken.

Data source: ADNS, OIE, EFSA, SCOPAFF presentations.

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 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(H5N8) viruses spread globally through wild bird migration during 2014–2015 (2.3.4.4.a) and 2016–2017 (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 infected with A(H5N6) of the 2.3.4.4b clade in 2017 with a different gene composition to viruses of the same clade circulating in birds in Europe.

Genetic characterisation of AI viruses of H5 and H7 subtypes circulating in the Europe

Phylogenetic characterization of the complete genomes of Bulgarian HPAI A(H5N8) viruses representative of the five outbreaks that were collected between March and April 2019 from ducks and chickens in the districts of Lovech and Plovdiv revealed that the viruses are closely related to the HPAI A(H5N8) (HA identity of 99.2%-99.8%) described in the EFSA report for August–November 2018 (EFSA et al., 2018c). Specifically, the HA gene segment belongs to clade 2.3.4.4b (Smith et al., 2015; Lee et al., 2017) and clusters with A(H5N8) European viruses collected during the 2016-2017 epidemic. Phylogenies of the remaining gene segments confirm the topology of the HA tree and indicate that the viruses possess the same gene constellation of the previously described A/mute swan/Croatia/70/2016-like genotype (Fusaro et al., 2017).

Genetic characterization of the HA and NA genes of the LPAI A(H5N1) and A(H7N7) viruses reported in domestic birds reported from Denmark, showed that the viruses cluster with LPAI virus genes previously identified in wild birds and poultry in Europe. Phylogenetic analysis of the HA gene of the LPAI A(H7N3) isolated in Italy in July 2019 revealed that the virus clusters with LPAI viruses circulating in wild birds in Central Asia, showing the highest similarity (97.6%) with a 2016 LPAI A(H7N7) strain from Georgia.

Genetic characterisation of AI viruses of A(H1N1) and A(H3N1) subtypes circulating in Europe

In addition to the H5 and H7 subtypes, it is also worth describing the genetic properties of the A(H1N1) and the A(H3N1) viruses identified over the reporting period in Italy and in Belgium, respectively.

Characterisation of the complete genome of the A(H1N1) virus collected in April 2019 in a turkey breeder farm in Italy revealed that it belongs to the human A(H1N1)pdm09 lineage. The high similarity with circulating seasonal H1N1 viruses suggests a human to turkey transmission. Mutations in the HA protein which may be associated with adaptation to the avian host, such as Q226R (Suptawiwat et al., 2013; He et al., 2014) and the loss of a potential glycosylation site at positions 162–164, were identified.

Topology of the phylogenetic trees showed that the eight gene segments of the A(H3N1) viruses circulating in the Belgian poultry flocks since January 2019 cluster with LPAI viruses recovered from wild birds in Eurasia between 2012 and 2017. The acquisition of a 24 aminoacid deletion in the stalk region of the NA protein is indicative of an adaptation of a wild-bird-origin virus to Galliformes (Hossain et al., 2008; Sorrell et al., 2010).

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

No human infection with A(H5N6) or A(H5N8) viruses, as detected in wild birds and poultry in Europe, has been reported during the period for this report and previously (Adlhoch et al., 2018). One study in people exposed to infected or perished birds during the AI outbreaks between November 2016 and March 2017 identified some individuals reactive for antibodies to A(H5N8) clade 2.3.4.4. (Ilyicheva et al., 2018). (Ilyicheva et al., 2018). A study in England in 2018 followed up 69 individuals that have been exposed to AI A(H5N6) in 19 incidents, five developed respiratory symptoms but tested negative (Thornton et al., 2019).

The Bulgarian veterinary authorities reported to EFSA that a total of 73 people were exposed to poultry infected with HPAI A(H5N8) during the outbreaks that occurred in the country from 16 February to 15 August 2019, no additional information is available from the public health authorities (Table 2). A risk assessment on A(H5N8) is available from WHO stating that the likelihood of human infection with A(H5N8) virus is low (WHO, 2016a).

4.3. Applied prevention and control measures in Europe, 16 November 2018 – 15 February 2019 (TOR 3)

4.3.1. Bulgaria

Five HPAI A(H5N8) cases were confirmed in poultry establishments in Bulgaria in the reporting period (Table 1, Figure 7). For the description of the control and prevention measures applied, see Annex A.

4.4. The avian influenza situation in other countries not reporting via ADNS, 16 February – 15 August 2019 (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 August 2019 is presented in Table 1 and Figure 9. 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 1: Number of HPAI outbreaks in other countries not reporting via ADNS by virus subtype and country, 16 February – 15 August 2019 (n=91)

Region	Country	HPAI outbreaks								
		A(H5N1)		A(H5N2)		A(H5N6)	A(H5N8)		A(H7N9)	All HPAI
		Domestic birds	Wild birds	Domestic birds	Wild birds	Domestic birds	Domestic birds	Wild birds	Domestic birds	
Africa	Namibia							3 ^(c)		3
	Nigeria						2			2
	South Africa						3	1 ^(d)		4
Asia	Bhutan	1								1
	Cambodia					1				1
	China	1				2			1	4
	India	1								1
	Iran						3			3
	Iraq						1			1
	Israel						1			1
	Nepal	12	1 ^(a)							13
	Taiwan			53	1 ^(b)					54
	Vietnam	1				2				3
Total	(13 countries)	16	1	53	1	5	10	4	1	91

- (a) House crow (*Corvus splendens*)
- (b) Grey heron (*Ardea cinerea*)
- (c) Jackass penguin (*Spheniscus demersus*)
- (d) Egyptian goose (*Alopochen aegyptiaca*)

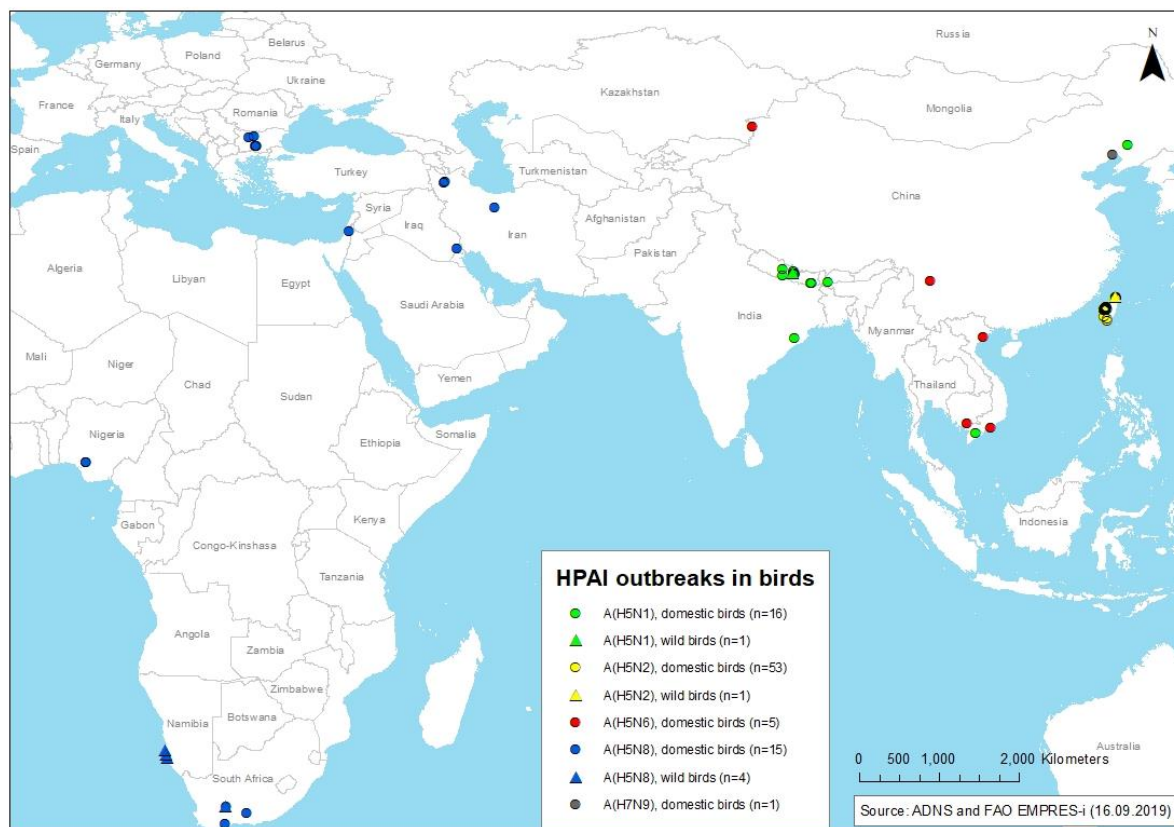


Figure 1: Geographical distribution, based on available geocoordinates, of HPAI outbreaks in Europe, Asia and Africa in domestic birds (circles) and wild birds (triangles), by A(H5N1) (green), A(H5N2) (yellow), A(H5N6) (red), A(H5N8) (blue), A(H7N9) (grey), 16 November 2018 – 15 February 2019 (n=96)

4.4.1. HPAI A(H5N1)

4.4.1.1. Domestic and wild birds

Detections

From 16 February to 15 August 2019 only Asian countries notified the detection of HPAI A(H5N1) in domestic and wild birds. The outbreaks in India and Vietnam continued and new cases were detected on backyard and medium-sized duck and poultry farms in Bhutan, China and Nepal after a period of no reported outbreaks for nearly 10 months. The only wild bird case of the Asian lineage HPAI A(H5N1) was a house crow (*Corvus splendens*) reported by Nepal in the relevant time period (Figure 10).

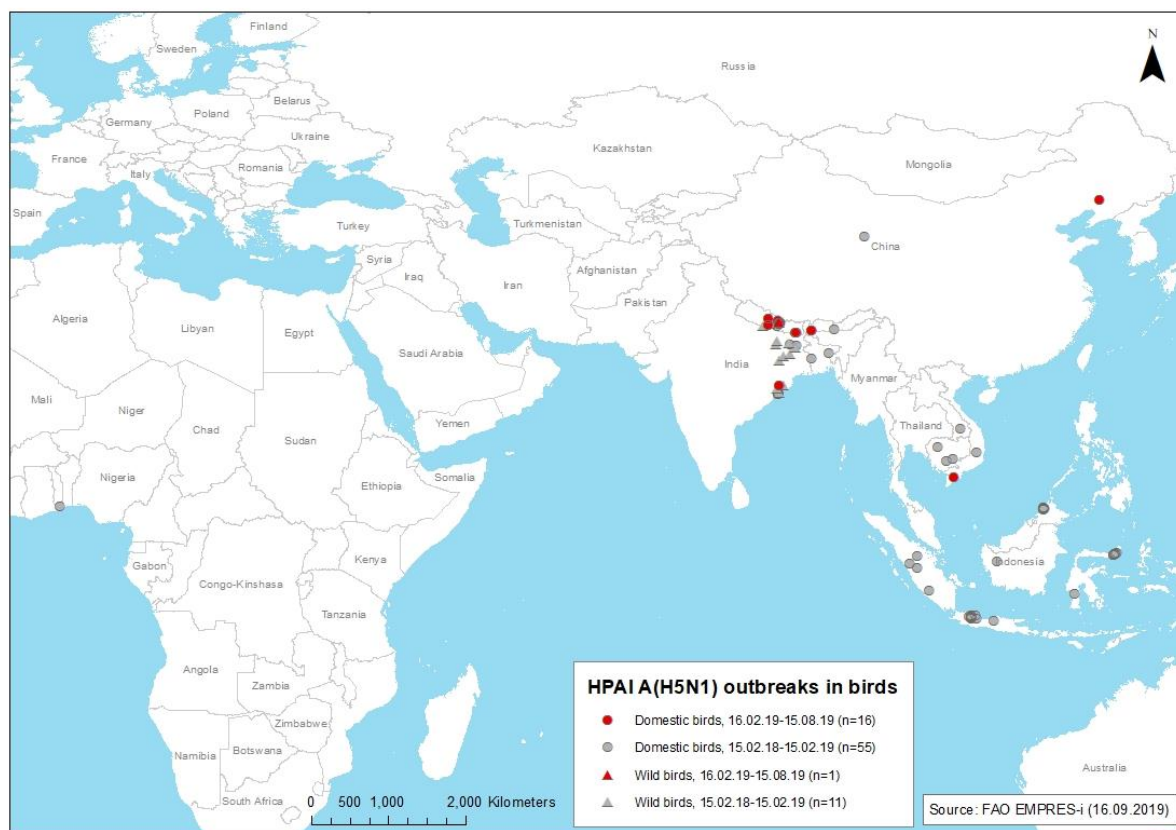


Figure 2: Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N1) outbreaks in domestic birds (circles) and wild birds (triangles); grey symbols indicate outbreaks that occurred from 15 February 2018 to 15 February 2019, red symbols indicate outbreaks that occurred from 16 February to 15 August 2019 (n=83) (FAO, online)

Information extracted from the scientific literature

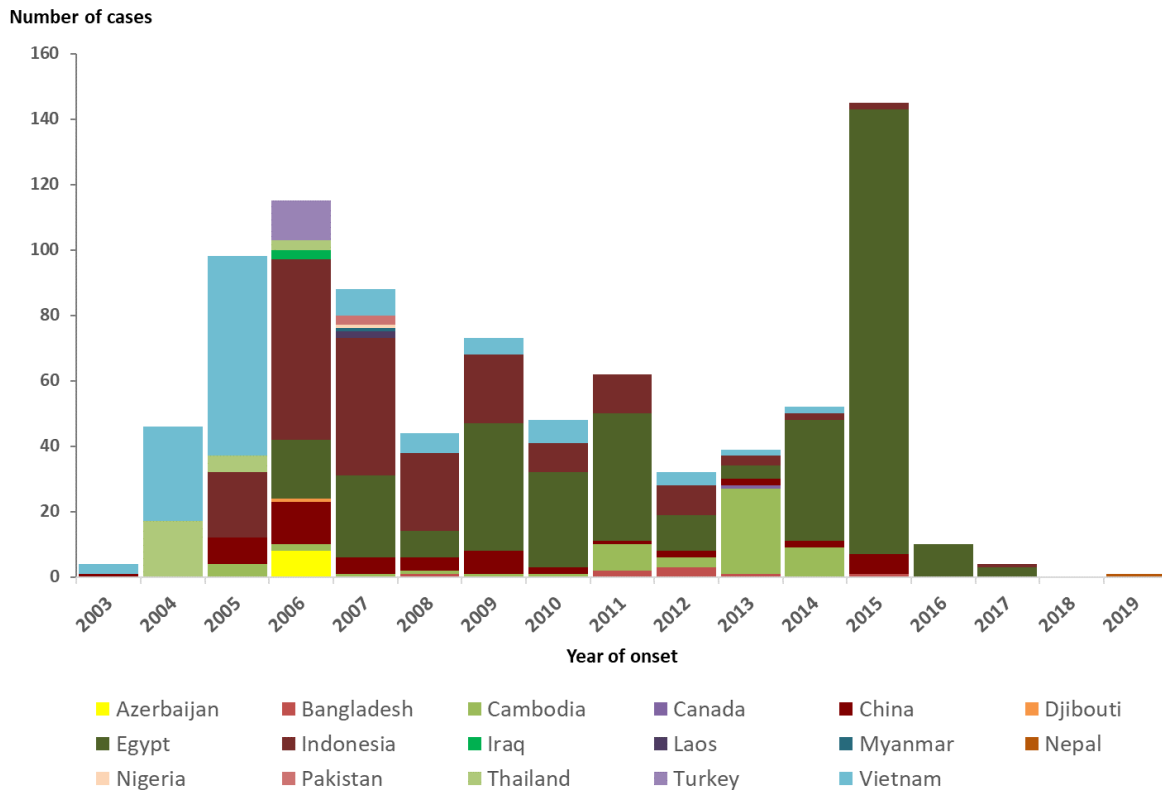
Nooruzzaman et al. (2019) analyzed genomes of A(H5N1) detected in ducks, geese, chickens and turkeys in 2017 in Bangladesh. The viruses were classified in clade 2.3.2.1a, but a number of internal segments originated from LPAI viruses. In another study of Bangladeshi viruses, Barman et al. (2019) performed genetic characterization of A(H5N1) strains from live bird markets. Until 2017, all analysed strains (designated H5N1-R1) belonged to clade 2.3.2.1a. In May 2017, a new variant (H5N1-R2) was identified in which the PA gene segment of H5N1-R1-like virus was replaced with the PA segment from a Eurasian-lineage LPAI virus. Currently there is evidence of co-circulation of both H5N1-R1 and H5N1-R2 in the country.

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

No new relevant information has been published during the reporting period.

4.4.1.3. Human infections due to A(H5N1)

One new human case due to AI A(H5N1) was reported from Nepal in March 2019. This is the first time Nepal reported a human case due to A(H5N1) virus (WHO, 2019b, online-a). The case was a 21-year-old man from Kathmandu with onset of illness on 19 March 2019. He was admitted to hospital and passed away on 29 March 2019. Since 2003, and as of 15 August 2019, 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, a) (Figure 3).



Data source: WHO (WHO, 2019a)

Figure 3: Distribution of confirmed human cases of A(H5N1) by year and country of reporting, 2003 – 15 August 2019 (n=861)

4.4.2. HPAI A(H5N2)

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, but not in wild birds until this reporting period (Lee et al., 2014; Lee et al., 2016). From 16 February to 15 August 2019 Taiwan notified 53 new outbreaks of HPAI A(H5N2) in backyard and mainly medium-sized chicken, duck, goose and turkey establishments to the OIE (Figure 12). Furthermore, the Asian lineage HPAI A(H5N2) was for the first time detected in wild birds; a grey heron (*Ardea cinerea*) found dead in Guandu Park in Taipei City. The Taiwanese lineage of HPAI A(H5N2) differs from the Eurasian HPAI A(H5N2) lineage, belonging to clade 2.3.4.4b, which has been detected in Egypt and Russia as well as in Asian countries in 2016 – 2019 (EFSA et al., 2019).

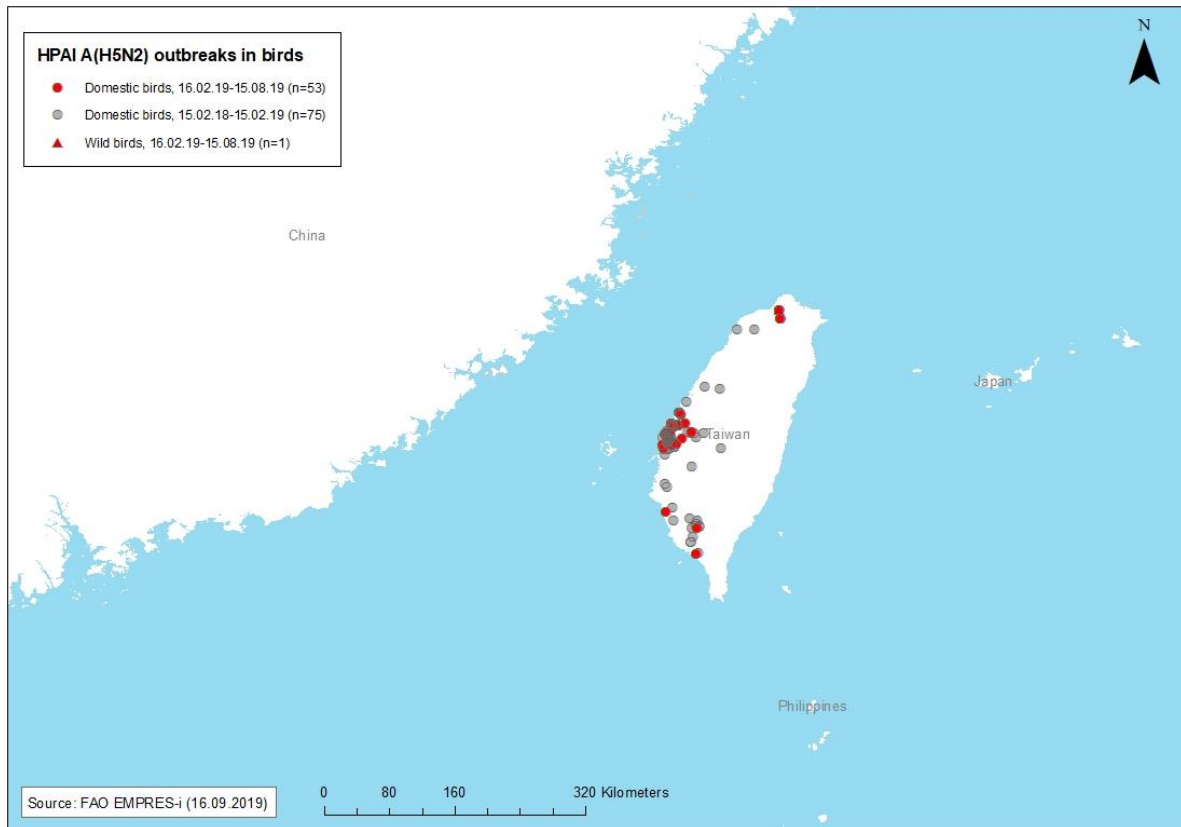


Figure 4: Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N2) outbreaks in domestic birds; grey symbols indicate outbreaks that occurred from 15 February 2017 to 15 February 2019, red symbols indicate outbreaks that occurred from 16 February to 15 August 2019 (n=129) (FAO, online)

Information extracted from scientific literature

At the end of 2018, a new virus subtype A(H5N2) was isolated in Egypt from apparently healthy Muscovy ducks (Hagag et al., 2019). Phylogenetic analysis showed that the virus had emerged as a result of reassortment between A(H5N8) clade 2.3.4.4B and A(H9N2) viruses of the G1 lineage, endemically circulating in the country since 2011. The HA gene segment showed close relatedness to the European 2016–2017 HPAI A(H5N8) clade 2.3.4.4.B viruses and was clearly distinguished from A(H5N8) viruses of the same clade that had caused the previous epidemic in Egypt in 2016 and 2017. The N2 gene was closely related to A(H9N2) G1-like viruses previously isolated in Egypt. All other segments stem from the 2.3.4.b HPAI virus. Additionally, the new virus possessed amino acid substitutions in HA, M1 and NS1 that had been previously described to increase the affinity of H5 subtype viruses to α 2.6 sialic acid receptors or to enhance the virulence for mice.

4.4.3. HPAI A(H5N6)

4.4.3.1. Domestic and wild birds

Detections

In the relevant time period for this report China and Vietnam confirmed further outbreaks of the zoonotic reassortment of HPAI A(H5N6) clade 2.3.4.4c on a backyard and several commercial poultry farms. In April 2019, the first detection of HPAI A(H5N6) was notified to the OIE by Cambodia. The infected chickens were detected at a bird market in the southern province of Takeo (Figure 13).

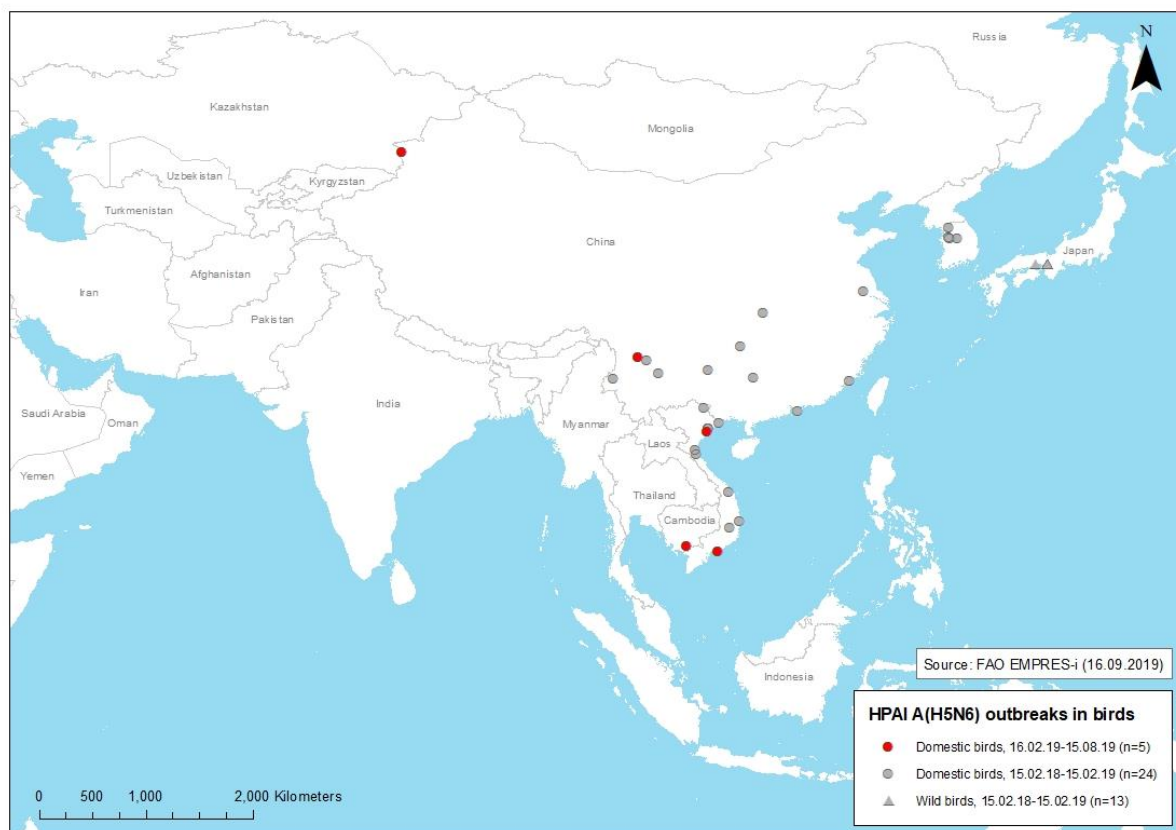


Figure 5: Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N6) outbreaks in domestic birds (circles) and wild birds (triangles); grey symbols indicate outbreaks that occurred from 15 February 2018 to 15 February 2019, red symbols indicate outbreaks that occurred from 16 February to 15 August 2019 (n=42) (FAO, online)

Information extracted from the scientific literature

Molecular characterisation of an HPAI A(H5N6) virus isolated from sick Muscovy ducks in Vietnam in 2018 revealed its similarity to an A(H5N6) strain detected in a common gull (*Larus canus*) in Russia in 2018 as well as to an A(H5N6) strain isolated from a patient in China, also in 2018 (Tsunekuni et al., 2019).

Mine et al. (2019) characterised genetically A(H5N6) clade 2.3.4.4 virus strains isolated from poultry and wild birds in Japan during winter 2017–2018 and concluded that they had been generated through several reassortment events between the European-like 2.3.4.4.B H5N8 HPAI viruses and HxN6 AI virus, possibly in Siberia. The comparative pathogenicity of the strains isolated in 2018 was assessed in four-week-old white leghorn chickens and the lethal infectious dose was higher and transmission efficiency lower for the most recent A(H5N6) strains than the A(H5Nx) HPAI virus responsible for previous epidemics in Japan.

Qu et al. (2019) characterised genetically and phenotypically seven A(H5N6) clade 2.3.4.4 viruses isolated in 2016 in southern China. The viruses were classified to different genotypes and showed high pathogenicity but variable transmissibility in four-week-old chickens.

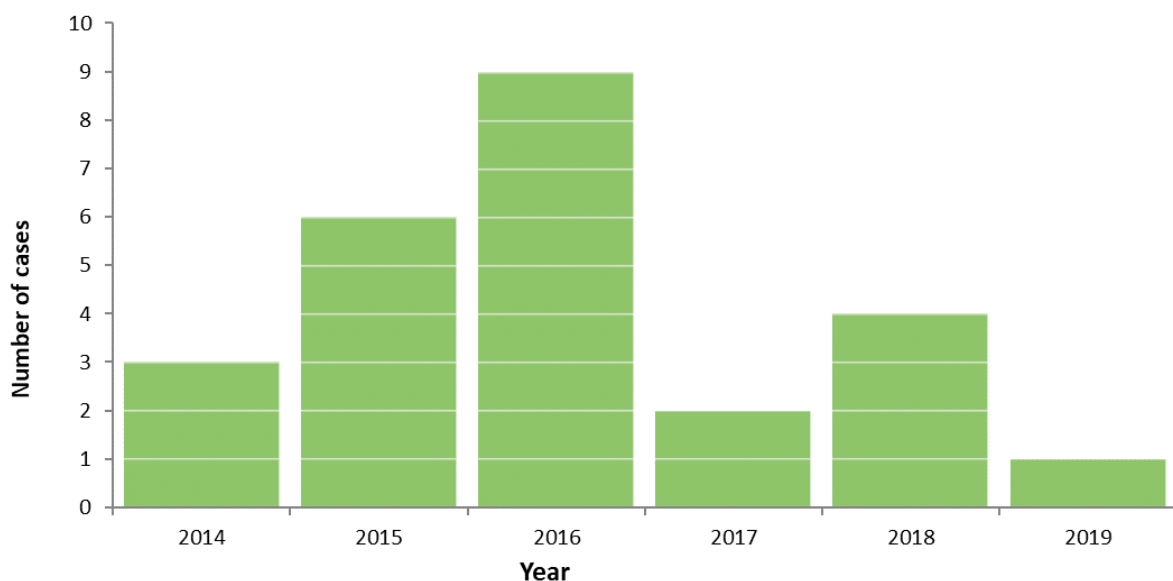
Susceptibility and transmissibility of a Korean A(H5N6) clade 2.3.4.4 virus (2016–17) was determined in three chicken breeds: six-week-old SPF chickens (white leghorn), three-week-old broilers (white line) and eight-week-old Korean native chickens (KNC, brown line) (Park et al., 2019). The values of chicken median lethal dose varied from $10^{3.7}$ (white leghorn) to $10^{4.3}$ (KNC). The KNC also had a longer virus shedding period and longer mean death time than the other examined breeds.

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

No new relevant information was published during the reporting period.

4.4.3.3. Human infections due to A(H5N6)

One new human case due to AI A(H5N6) has been notified since the last EFSA report (EFSA et al., 2019; The Government of the Hong Kong Special Administrative Region Press Releases, 2019; WHO, 2019e). Since 2014, and as of 15 August 2019, 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 6). WHO lists 23 human cases of AI A(H5N6), including 15 with fatal outcomes (WHO, 2019f) and the authorities in Hong Kong list 24 cases including the new case reported on 11 August 2019 (The Government of the Hong Kong Special Administrative Region Press Releases, 2019). 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, 2018c; The Government of the Hong Kong Special Administrative Region Press Releases, 2019).



*If the 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: Data used from ECDC line list (described above).

Figure 6: Number of human cases due to A(H5N6), clade 2.3.4.4, infection by year of onset, China 2014 – 2019 (n=254)

4.4.4. HPAI A(H5N8)

4.4.4.1. Domestic and wild birds

Detections

The outbreaks of clade 2.3.4.4b, HPAI A(H5N8) on ostrich farms in the Eastern and Northern Cape provinces of South Africa as well as on poultry farms in Nigeria continued in the relevant time period for this report. Iran reported further outbreaks of HPAI A(H5N8) on large poultry farms, but the virus was also detected on a chicken farm in Basrah province, Iraq and on a turkey farm in Israel for the first time in 2019. In contrast to the last report Jackass penguins (*Spheniscus demersus*) and Egyptian goose (*Alopochen aegyptiacus*) from the HPAI A(H5N8) outbreaks in Namibia and South Africa were the only reported wild bird species with HPAI A(H5N8) worldwide (Figure 15). In Namibia, by the second half of

February, more than 350 penguin carcasses were found; these findings began in December 2018 and constituted the most severe mortality event on record for this species in Namibia (Molini et al., 2019).

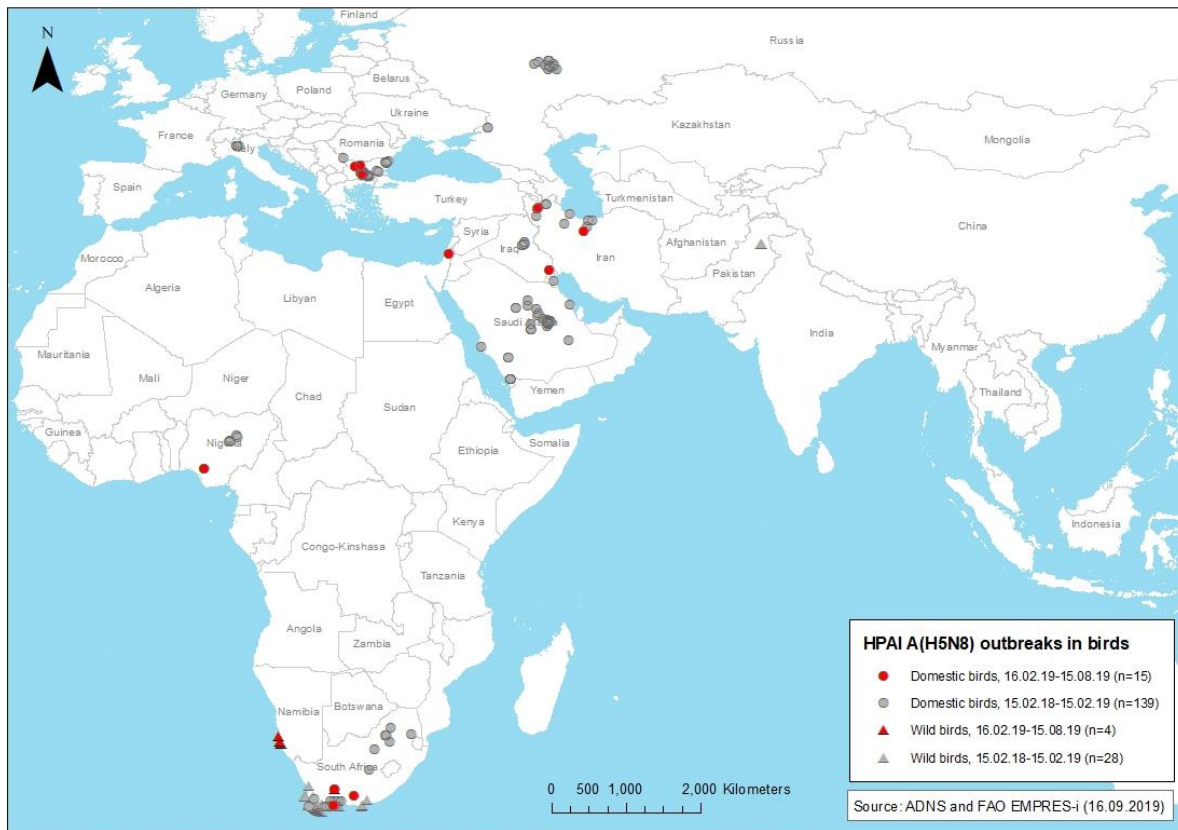


Figure 7: Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N8) outbreaks in domestic birds (circles) and wild birds (triangles); grey symbols indicate outbreaks that occurred from 15 February 2018 to 15 February 2019, red symbols indicate outbreaks that occurred from 16 February to 15 August 2019 (n=186) (FAO, online)

Information extracted from the scientific literature

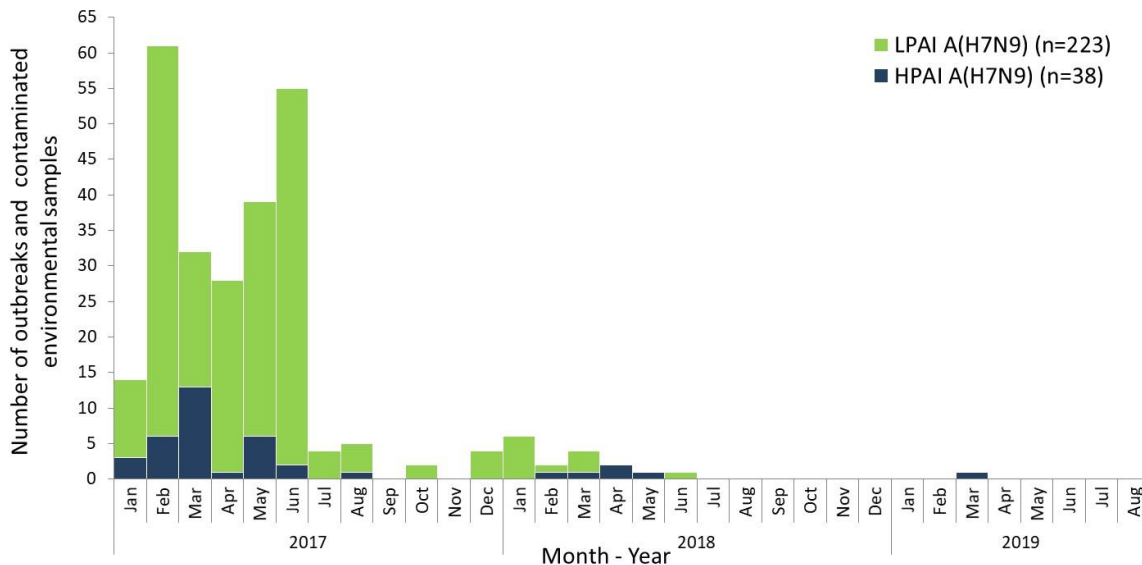
Phylogenetic analyses of the Namibian A(H5N8) viruses demonstrated that the viruses belonged to clade 2.3.4.4b; the viruses were similar (HA:99.5%, NA: 99.3%) but not identical to the A(H5N8) clade 2.3.4.4b viruses that occurred in African penguins between January and October 2018 (Molini et al., 2019). The origin of the Namibian outbreaks remains unclear, but the authors of this publication sustained that virus was probably spread through regional movements of wild birds such as greater crested terns (*Thalasseus bergii*) during the A(H5N8) outbreaks in South Africa in 2017 and 2018. Ghafouri et al. (2019) described the genetic characterization of A(H5N8) virus detected in hooded crow (*Corvus cornix*) in Iran in 2017. The HA gene of the virus belonged to clade 2.3.4.4b but analysis of internal genes showed some distinct features indicative of probable reassortment with East-Asian LPAI viruses. The A(H5N8) clade 2.3.4.4 isolated in October 2016 from the feathers of a sick domestic duck at a commercial farm in Siberia (Russia) showed high lethality, systemic replication and neurotropism in chickens experimentally infected with A(H5N8) (Prokopyeva et al., 2019).

4.4.5. HPAI-LPAI A(H7N9)

4.4.5.1. Domestic and wild birds

Detection

In March 2019 the Chinese authorities reported the outbreak of Chinese lineage HPAI A(H7N9) in Indian peafowls (*Pavo cristatus*) in the zoo of Jinzhou city, Linghe District, Liaoning province. It is the first reported case since June 2018 (Figure 16). No LPAI or HPAI A(H7N9) of the Chinese lineage were detected in wild birds during the relevant time period of this report.



Data source: FAO EMPRES-i (16.09.2019)

Figure 16: Distribution of confirmed LPAI and HPAI A(H7N9) outbreaks among birds and environmental samples in China, by month, 1 January 2017 – 15 August 2019 (n=261)

Information extracted from the scientific literature

A new antigenic variant of A(H7N9) was detected in swabs collected at a live poultry market in China in 2018 (Jia et al., 2019). The virus was highly pathogenic based on the cleavage site sequence of HA protein and phylogenetically belonged to the Yangtze River Delta lineage. The altered antigenic sites included A169T and G186V mutations at the HA protein. Additionally, it possessed the amantadine resistance mutation (S31N) at the M2 protein. A cross-haemagglutination test confirmed that there are significant antigenic differences between the tested strain and the H7N9-Re-1 strain used as a component of the vaccine used in poultry. According to the authors of the article, this is the first antigenic change found after the poultry immunisation programme in China was launched in 2017 with potential implications for the evolution of escape mutants.

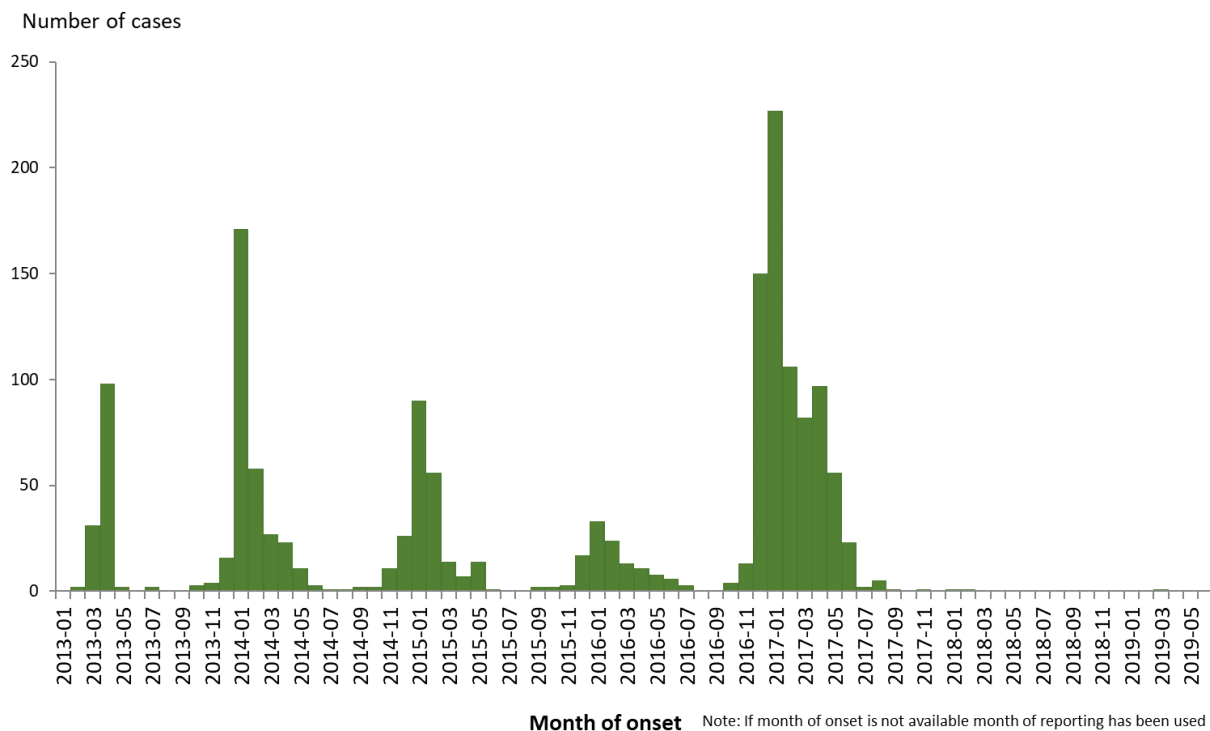
The receptor-binding properties, pathogenicity and transmissibility in ferrets of four A(H7N9) isolates (three HP and one LP) from wave 5 (2016–2017) in China were investigated (Bao et al., 2019). All viruses exhibited preferential recognition of avian-like receptors and a varying degree of binding preference to human-like receptors. Infection of ferrets resulted in different duration of disease and only one isolate was transmitted to ferrets in a neighbouring cage. The authors compared the results to the properties of the virus from the Wave 1 epidemic and concluded that the current public health risk has not significantly increased compared with 2013.

A novel A(H7N3) reassortant strain was detected in a poultry meat product confiscated at the airport in Japan (Nakayama et al., 2019). The virus acquired PB1, PA, HA, NP, M and NS segments from a zoonotic highly pathogenic A(H7N9) virus whereas N3 and PB2 segments were derived from unidentified AIV circulating in wild birds and poultry. The virus showed high lethality in chickens following intranasal

inoculation at the dose 10⁶EID₅₀ (all inoculated chickens died within 3 dpi). In contrast, domestic and mallard ducks remained healthy during the 14-day observation period, but the virus was excreted from the trachea and cloaca and replicated in some internal organs. These findings raise potential implications in terms of possible asymptomatic dissemination of the new variant by wild waterfowl.

4.4.5.2. Human infections due to A(H7N9)

No human cases due to AI A(H7N9) have ever been reported from Europe. One human case has been reported globally since the last EFSA report published in March 2019 (WHO, 2019c, d, b). The latest case was an 82-year-old male with onset of illness on 18 March 2019 reported from Gansu province, but with potential exposure in the Inner Mongolia region of China (WHO, 2019c). Since February 2013, a total of 1,568 human cases have been reported from outside of Europe (Figure 8), including at least 615 deaths (39%) (WHO, 2019c, online-b). Thirty-two human cases, 13 of them fatal, have been due to infection with HPAI virus A(H7N9) according to the Chinese National Influenza Center (Chinese National Influenza Center, 2018).



Source: Data used from ECDC line list (described above).

Figure 8: Number of human cases due to A(H7N9), infection by month and year of onset, 2013 – 2019 (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 viruses in poultry in Asia, the Middle East and North Africa (Bonfante et al., 2018; Chrzastek et al., 2018; Xu et al., 2018; Zhu et al., 2018). The endemic status of these regions continued between 16 February and 15 August 2019.

Information extracted from the scientific literature

In Ghana, the A(H9N2) viruses were isolated in 2017–2018 from the outbreaks in chicken layers, in which a high mortality rate (up to 25%) and significant decrease in egg production were noted (Awuni et al., 2019). Molecular characterization revealed the close relatedness of the isolated A(H9N2) virus strains to the G-1 lineage viruses detected elsewhere in north and west Africa. The IVPI of the isolated strains varied from 0.1 to 0.13. In most of the tested samples, co-infections with infectious bronchitis viruses were found, thus partially explaining the severity of the clinical outcome.

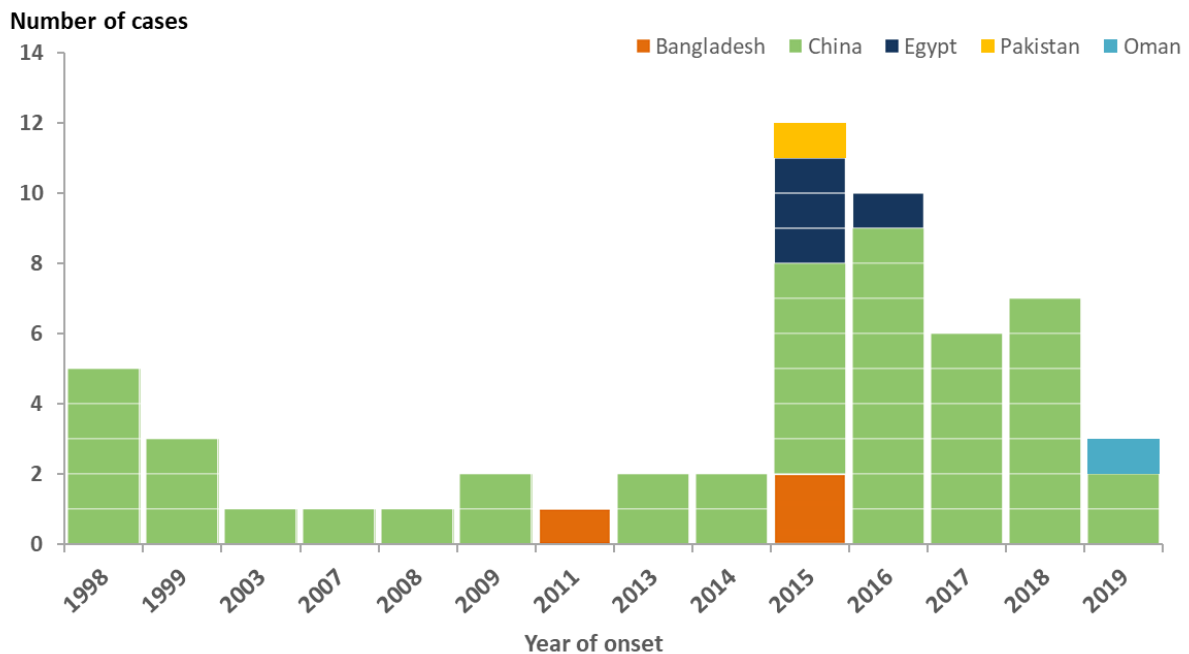
Novianti et al. (2019) provided the first genetic description of A(H9N2) virus in Indonesia. The virus was isolated from an apparently healthy chicken at a live-poultry market in January 2018. Phylogenetic analysis of PB2 and NA genes suggested intra-subtypic reassortment.

Genetic analysis of an A(H9N2) avian influenza virus from Pakistan in 2017 showed that the isolate belongs to the G1-like lineage (Lee et al., 2019).

The infectivity of different genotypes of chicken-derived A(H9N2) viruses was investigated in Pekin, Mallard and Muscovy ducks (Wang et al., 2019). None of the birds exhibited obvious clinical signs and no shedding was demonstrated in Pekin or Mallard ducks. In contrast, Muscovy ducks asymptotically shed the virus. The authors imply that the role of Muscovy ducks in the maintenance and transmission of A(H9N2) deserves attention and further clarifications.

4.4.6.2. Human infections due to A(H9N2)

Two additional human cases have been reported since the last EFSA report (WHO, 2019b, c). The most recent case was reported from Oman with disease onset on 24 April 2019, the first time Oman has reported a human case due to AI infection (WHO, 2019b). Since 1998, and until 15 August 2019, 56 laboratory-confirmed cases of human infection with AI A(H9N2) virus, including one death, have been reported globally. Cases were reported from China (47), Egypt (4), Bangladesh (3), Oman (1) and Pakistan (1) (Figure 9).



Data source: ECDC line list (WHO, 2019b, c)

Figure 9: Distribution of confirmed human cases of A(H9N2) by reporting country, 1998 – 15 August 2019 (n=56)

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., 2018c).

Taking the half-year period from the 16 February to 15 August 2019 and the dates of notification into account, the number of reported outbreaks for Asia, Africa and the Middle East was lower than in the previous time period, in particular for the last three months. Furthermore, more than half of the outbreaks in domestic birds were detected in the context of a long-term epidemic of Asian lineage HPAI A(H5N2), clade 2.3.4.4 in Taiwan. Only six cases in wild birds were reported in the relevant time period for this report from Namibia, Nepal, South Africa and for the first time from the HPAI A(H5N2) outbreak in Taiwan. The reason might be the decreasing environmental stability of AI virus due to the higher temperatures and increased UV radiation during recent months. However, slackening surveillance activities in the wild bird sector likewise can be at the basis of the low number of HPAI wild bird cases. Reported outbreaks of the Asian lineage of HPAI A(H5N1) and the zoonotic reassortment of HPAI A(H5N6) clade 2.3.4.4c are still confined to Asia, but Bhutan, China and Nepal reported the new detection of HPAI A(H5N1) and Cambodia the first detection of HPAI A(H5N6). Beside the outbreaks of HPAI A(H5N8) clade 2.3.4.4b continuously notified by Iran, Nigeria and South Africa, the virus was also detected on poultry farms in Iraq and Israel. Despite the lack of reports on detection of infected wild birds in the key migration areas in northern China, Mongolia and Russia (EFSA AHAW Panel, 2017) during the last six months, uncertainty remains high and close monitoring of the situation is required. There is considerable uncertainty regarding the real geographical distribution of these viruses, particularly in wild birds. Furthermore, autumn migration from breeding sites to wintering sites will start soon, depending on the weather conditions, and the low temperature of autumn and winter may facilitate the environmental survival of AI virus potentially introduced to Europe. Aggregation before and during autumn migration, as well as the mixing of wild birds from different geographic origins during migration, will increase the risk of the infection spreading.

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

4.6.1.1. Surveillance in the EU

As outlined in the EFSA report for November 2017 – February 2018 (EFSA et al., 2018b), human infections with zoonotic and other novel influenza strains are notifiable under EU legislation⁴ and the International Health Regulations (IHR) through the Early Warning and Response System and the IHR notification system, respectively (WHO, 2016b). WHO recently published a 'Protocol to investigate non-seasonal influenza and other emerging acute respiratory diseases', which also covers AI viruses (WHO, 2018a).

4.6.1.2. Diagnosis

Routine laboratory diagnostics were described in the EFSA report covering November 2017 – February 2018 (EFSA et al., 2018b). All influenza A virus isolates or clinical samples that cannot be subtyped are to be submitted to the appropriate national reference laboratory (National Influenza Centres; NICs), and to a WHO Collaborating Centre for Reference and Research on Influenza for characterisation (WHO, 2017). Influenza virus sharing is coordinated by the WHO Global Influenza Surveillance and Response System (GISRS) (WHO). An updated protocol for the molecular diagnosis of influenza viruses has recently been published (WHO, 2018b).

4.6.1.3. Options for public health control measures (in relation to the EU)

Options for public health control measures remain the same as those outlined in the EFSA report for November 2017 – February 2018, and should follow national guidelines and recommendations (EFSA et

⁴ Commission Implementing Decision (EU) 2018/945 of 22 June 2018 on the communicable diseases and related special health issues to be covered by epidemiological surveillance as well as relevant case definitions. OJ L 170/1, 6.7.2018, p. 74

al., 2018b). The public health measures taken in 22 EU/EEA Member States and Israel during the A(H5N8) outbreaks in 2016–2017 have been summarised (Adlhoch et al., 2018). The use of personal protective measures for people exposed to birds that are infected with AI viruses will minimise the risk of transmission to humans.

4.6.1.4. Vaccines

WHO published a status update on the available and recommended vaccines or candidate vaccine viruses (CVVs) for pandemic preparedness in February 2019 following the vaccine composition meeting (WHO, 2019f).

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. Sporadic outbreaks due to AI viruses or detections of infected wild birds continued. Although no transmission of viruses detected in wild birds or poultry to humans has been observed in Europe, zoonotic transmission of viruses related to AI A(H5) clade 2.3.4.4 circulating in wild birds and poultry in Europe cannot be fully excluded, as these viruses reassort readily and new viruses may emerge or be introduced e.g. via migratory birds. AI virus transmission to humans is a rare event overall and the risk is considered very low for viruses with an avian-adapted genetic makeup. The use of personal protective measures for people exposed to AI viruses will minimise any residual risk.

The risk of travel-related importation of human AI cases, particularly from Asia, is very low. Currently, only a few sporadic human cases are reported world-wide. The recent reports from countries reporting the first occurrence of human cases infected with AI, i.e. Nepal and Oman, highlight the risk of transmission whenever people are exposed to infected birds. Therefore, surveillance of AI viruses in wild birds and poultry in the EU/EEA is important for detecting further virus spread among birds and reducing the possible risk of exposure of humans to infected birds. Controlling illegally imported poultry products is also important to prevent the importation of AI viruses relevant for both public and veterinary health.

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Abbreviations

ADNS	Animal Disease Notification System
AI	Avian influenza
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
IHR	International Health Regulations
IVPI	Intravenous pathogenicity index
KNC	Korean native chicken
LPAI	Low pathogenic avian influenza
MS	Member State
OIE	World Organisation for Animal Health
SCOPAFF	Standing Committee on Plants, animals, food and feed
SPF	Specific pathogen free
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, Czech Republic, 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, legislation⁵, 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. 178/2002⁶, EFSA should provide the technical and scientific assistance to the Commission based on the following Terms of Reference:

⁵ 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.

⁶ 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 August 2019 and reported by Member States and neighbouring countries via ADNS. Member States where HPAI 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 an harmonised manner across the EU. Limitations in the performed data collection, reporting and analysis were explained in the first AI overview report (EFSA et al., 2017b).

A description of the applied prevention and control measures (TOR 3) is given in the case report provided by representatives from affected Member States and attached as Annex. The main topics covered are increasing awareness, release and repeal of housing order, strengthening biosecurity, preventive culling, implementation of a regional standstill, ban of 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(H5N6), HPAI A(H5N8), HPAI/LPAI A(H7N9) and LPAI A(H9N2). 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 August 2019 and on information gathered by performing a literature search on papers published in PubMed from 16 February to 15 August 2019. Possible actions for preparedness in the EU are discussed.

The report mainly describes information that became available since the publication of the EFSA report for November 2018 – February 2019 (EFSA et al., 2019) 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 August 2019 submitted by Member States (MSs) to the ADNS (European Commission, online-a) were taken into account for this report. In addition, Bulgaria, Denmark, Germany and Italy were asked to provide more detailed epidemiological data directly to EFSA on the AI outbreaks that occurred in poultry, captive and wild birds during the same period.

The information, which EU MSs 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 MSs to the European Commission, were consulted to extract 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 Bulgarian, the Belgian and the Italian National Reference Laboratories for Avian Influenza and Newcastle Disease were asked to provide the genetic sequences obtained from the AI viruses detected in the respective countries during the reporting period mentioned above. 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 reporting period.

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 August 2019 were searched; the search was run on 19 August 2019.

Relevance criteria Scientific articles added to the database from 16 February to 15 August 2019 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 284 papers. The articles were subsequently screened against the relevance and eligibility criteria. None of the screened paper 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.3453521>.

B.1.2. AI prevention and control measures in Europe (TOR 3)

Bulgaria expressed an interest in supporting the analysis of the HPAI outbreaks occurred from 16 February to 15 August 2019 and submitted the case report on the prevention and control measures that were applied in response of the HPAI outbreaks. The case report provided to EFSA can be consulted in Annex A of this report.

B.1.3. Overview of AI outbreaks on other countries not reporting via ADNS (TOR 4)

Data from FAO EMPRES-i (FAO, online) on HPAI A(H5N1), HPAI A(H5N2), A(H5N6), A(H5N8), HPAI and LPAI A(H7N9) in domestic, captive and wild birds, and environmental samples, were used to describe and to map the geographical distribution of AI cases in domestic and wild birds in Africa, Asia, the Middle East and Europe on the basis of the observation dates. With the purpose of avoiding over-complication of the maps, captive birds and environmental samples have been mapped as domestic birds. Despite the fact that some of these kept animals may be of 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 among the locality, the administrative regions and geocoordinates, and the outbreaks were not officially reported to the OIE, the confirmed outbreaks were not taken into account in the analysis.

B.1.3.1. 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).

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 August 2019 were searched; the search was run on 19 August 2019.

Relevance criteria Scientific articles added to the database between 16 February and 15 August 2019 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 238 papers. The articles were subsequently screened against the relevance and eligibility criteria. Sixteen 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 at <https://doi.org/10.5281/zenodo.3453521>.

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 in Bulgaria

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Scope

This document provides a brief overview of specific prevention and control measures applied in Bulgaria from 16 February to 15 August 2019 in relation to avian influenza outbreaks in poultry. There is only information provided that is relevant to the implementation of measures such as increasing awareness of stakeholders and the general public, housing order, strengthening biosecurity measures (other than poultry confinement), preventive culling, regional stand still, derogations on restriction zone implementation after risk assessment, hunting or any other relevant measures that have been applied. This document is made to support the EFSA working group in generating an overview on the application of the selected measures at EU level. Table A.1 provides timelines for the main events that triggered actions in relation to the selected prevention and control measures in Bulgaria. More information on the actions taken is provided in the sections below the table.

Table A.1: Overview of main actions

Date	Event that triggered action	Type of action taken	Target audience
13.03.2019 2.04.2019 05/04/2019	Confirmation of primary HPAI outbreaks in four commercial establishments	<ul style="list-style-type: none"> Continued the laboratory surveillance as per the Instruction for enhanced surveillance since 2018 (serological testing (every 2 months) and in high risk area (Plovdiv, Stara Zagora and Haskovo region) pre-movement sampling (by PCR) of domestic poultry (all species) for transport to other holdings, and of ducks for force feeding for transport to slaughterhouse. Repopulation of establishments infected or positive for antibodies against HPAI is allowed, as: <ul style="list-style-type: none"> - following the provisions of Article 49 of Directive 2005/94/EC; - after lifting the restriction zones; - repopulation with sentinels 21 days Poultry farm positive for antibodies against HPAI (even if negative for HPAI virus) sent for immediate slaughtering. Six months repopulation ban in the farms where HPAI outbreaks were confirmed more than twice within 12 months. No derogation for trade and poultry movement within the protection and surveillance zones is allowed. 	Official and private veterinarians, poultry farmers

Increasing awareness of the stakeholders and the general public

Regular meetings with representatives of the poultry associations. A number of the measures as increased control and surveillance were proposed by the poultry industry sector itself. The sector is actively engaged and thoroughly cooperate to implement the control and surveillance activities. Close cooperation with public health authority. 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 EFSA 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.