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## Avian influenza overview August – November 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 August and 15 November 2019, one low pathogenic avian influenza (LPAI) A(H5) outbreak in poultry in France was reported in Europe. Genetic characterisation reveals that the virus clusters with Eurasian LPAI viruses. No highly pathogenic avian influenza (HPAI) outbreaks in birds were notified in Europe in the relevant period for this report. HPAI A(H5N6) virus was identified in chickens in Nigeria, this is the first report of HPAI A(H5N6) from the African continent. Fewer HPAI outbreaks in Asia and Africa were reported during the time period for this report compared with the previous reporting period. Apart from the long-term epidemic of HPAI A(H5N2) in Taiwan, only six HPAI outbreaks were reported in domestic birds from Nepal, South Africa and Taiwan. Furthermore, no HPAI detections from wild birds were reported worldwide in the relevant time period for this report. Even if the risk of incursion of HPAI from wild birds into poultry establishments in Europe is currently assessed as low, it is important to maintain passive surveillance activities. The focus should be on wild bird species that are in the revised list of target species in order to detect any incursion of HPAI virus early and initiate a warning. Despite the decrease in the number of avian influenza outbreaks over recent months, it is important to maintain a high alert level and high standard of biosecurity on poultry establishments. In Europe, no human infections due to HPAI viruses detected in wild bird or poultry outbreaks, have been reported. The risk of zoonotic transmission to the general public in Europe is considered to be 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 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 August and 15 November 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 August and 15 November 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.
- Three human cases with A(H9N2) infection have been reported from India (1) and China (2).
- In Europe, between 16 August and 15 November 2019 (based on the Animal Disease Notification System (ADNS)):
  - one LPAI A(H5) outbreak was reported in poultry by France; phylogenetic analysis revealed that the virus clusters with Eurasian LPAI viruses.
- No HPAI detections were reported in birds in Europe during this reporting period.
- A HPAI A(H5N6) virus has been recently identified in chickens at a live-bird market in Nigeria. This virus showed high genetic identity with the A(H5N6) viruses of clade 2.3.4.4b obtained from wild and domestic birds in Europe in 2016–2017. It is the first report of an HPAI A(H5N6) on the African continent.
- The number of reported outbreaks for Asia and Africa was again lower than in the previous time period and apart from the long-term epidemic of HPAI A(H5N2), clade 2.3.4.4 in Taiwan, only six outbreaks in domestic birds were reported between 16 August and 15 November from Nepal, South Africa and Taiwan. Furthermore, no HPAI cases in wild birds were reported worldwide 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.
- No cases of HPAI virus infection were reported in wild birds from Asian key areas such as Mongolia, western China or Siberia; in previous years, such reports foreshadowed the incursion of HPAI virus into Europe via the autumn migration of wild birds.
- Since no HPAI outbreaks in wild birds were reported worldwide in this reporting period, the risk of incursion of HPAI viruses from wild birds into the poultry population in Europe is currently low.
- 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 enough for the early detection of new incursions if the case–fatality rate for 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 an effective passive surveillance in wild birds in Europe, also encouraging a search for carcasses of birds that are on the revised list of target species (EFSA et al., 2017) in order to detect HPAI virus early and initiate a warning.
- Despite the decrease in the number of AI outbreaks in these last months, it is important to maintain a high alert level and high standard of biosecurity on poultry establishments.
- 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

No new HPAI outbreaks have been notified in Europe since the publication of the last EFSA report in September 2019 (EFSA et al., 2019b).

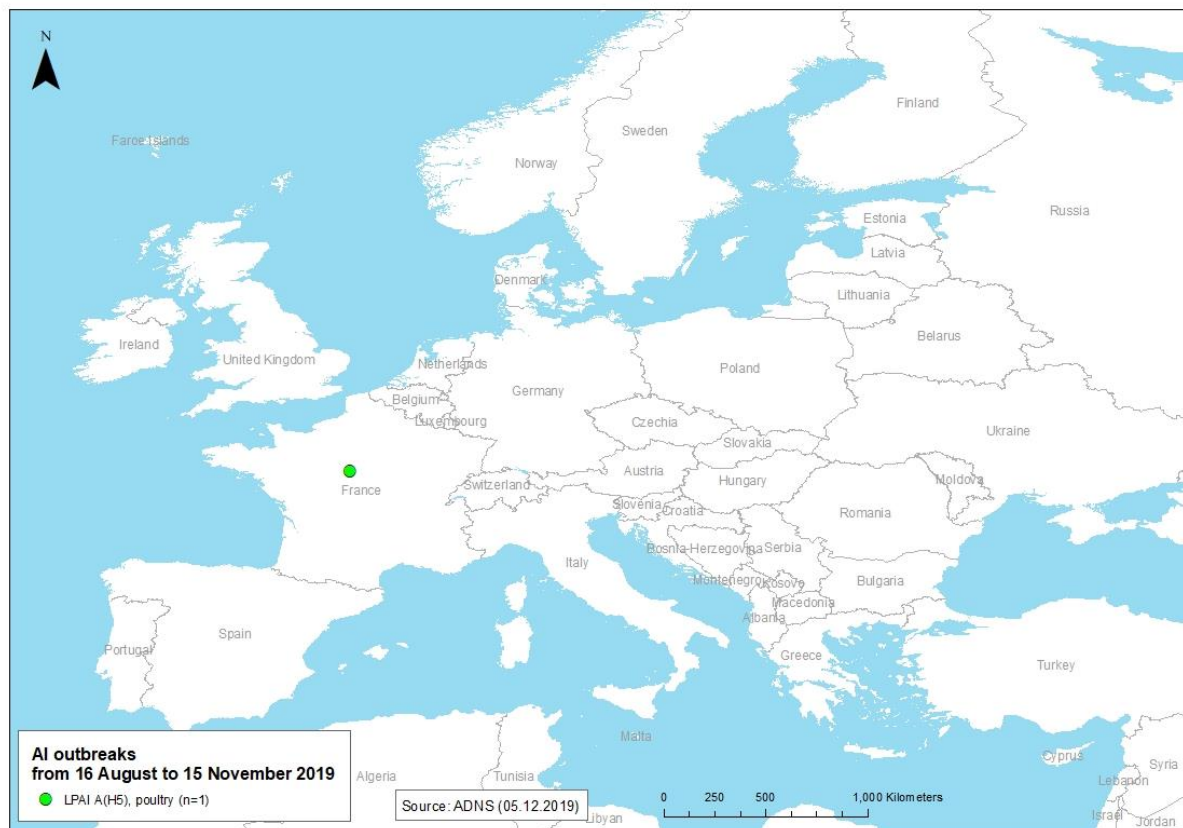
The analyses of the characteristics of the HPAI outbreaks detected in birds (poultry, wild and captive birds) in Europe and reported via the ADNS, from 2 October 2017 to 15 November 2019, are reported in [Figures 2–6 in the previous EFSA report](#) (EFSA et al., 2019b) by geographical distribution, HPAI virus subtype, affected host population and surveillance stream leading to outbreak detection.

### 4.2. HPAI and LPAI outbreaks in Europe, 16 August – 15 November 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 August to 15 November 2019, one LPAI outbreak occurred in poultry in Europe, in France, and was reported via the ADNS, as presented in Figure 1. The timeline, location and affected subpopulation of the AI outbreak are described in Table 1. No HPAI outbreaks were detected in poultry, wild or captive birds in Europe during this time period.



**Figure 1:** Geographical distribution, based on available geocoordinates, of avian influenza (AI) outbreaks in Europe, by virus subtype and affected subpopulation, 16 August – 15 November 2019 (n=1)

An LPAI (H5N3) outbreak was confirmed outside the reporting period for this report, on 10 December 2019, in a broiler breeder chickens establishment located in county Suffolk, United Kingdom.

#### 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 August to 15 November 2019, no HPAI outbreaks in poultry were notified in Europe.

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

No new relevant information has been published on the phenotypic characterisation of HPAI viruses circulating in the EU in domestic birds during the reporting period.

##### 4.2.2.2. HPAI in wild birds

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

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

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

No new relevant information has been published on the phenotypic characterisation of HPAI viruses circulating in the EU in wild birds during the reporting period.

##### 4.2.2.3. LPAI in domestic birds

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

From 16 August to 15 November 2019, one LPAI outbreak was notified in the poultry sector in Europe. This A(H5) case was identified at a free-range mallard (*Anas platyrhynchos*) establishment in the Loir-et-Cher Departement. The mallards were reared to restock supplies of game birds and were divided into four different batches: ducks ready to be released, breeders and two batches of future breeders. The virus was detected as part of the official planned active surveillance and the animals did not show clinical signs of AI. Information available from the ADNS (European Commission, online-a), from the OIE (OIE, online) and provided by Member States that characterises the LPAI outbreak is presented in Table 1.

**Table 1:** Characteristics of the LPAI-affected poultry and captive bird establishments in Europe, 16 August – 15 November 2019 (n=1)

Country	Virus subtype	Poultry species	Surveillance stream	Presence of signs in the outbreaks	Date of suspicion	Number of susceptible birds
France	A(H5)	Domestic duck	Active surveillance	No	03/10/2019	2,600
<b>Total</b>						<b>2,600</b>

Data source: ADNS, OIE, Member State.

#### 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(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 avian influenza virus of H5 subtype circulating in Europe*

The A(H5) virus from France showed a HA cleavage site (PQRETRGLF) typical of A(H5) LPAI viruses. Preliminary genetic analysis of a short partial H5 sequence indicates that the virus clusters with Eurasian LPAI viruses.

Shin et al. (2019) described the finding of two grey seals (*Halichoerus grypus*), found dead on the Baltic coast of Poland in 2016 and 2017, infected by a HPAI A(H5N8) virus. Both animals were infected by the same A(H5N8) virus and phylogenetic analysis revealed that the isolate belonged to the clade 2.3.4.4b with 99%–100% identity to the avian strains that were circulating in aquatic wild bird species in Europe during 2016–2017. There is no evidence that this virus is highly pathogenic for seals.

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

Although more than 10,000 people were estimated to have been exposed to HPAI viruses during the events from October 2016 until September 2018 (Adlhoch et al., 2019), no human infection with A(H5N6) or A(H5N8) viruses, as detected in wild birds and poultry in Europe, has been reported during the period for this report or previously (Adlhoch et al., 2018; Thornton et al., 2019). 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). 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).

#### **4.3. Applied prevention and control measures in Europe, 16 August–15 November 2019 (TOR 3)**

From 16 August to 15 November 2019, no HPAI outbreaks on poultry establishments were notified in Europe.

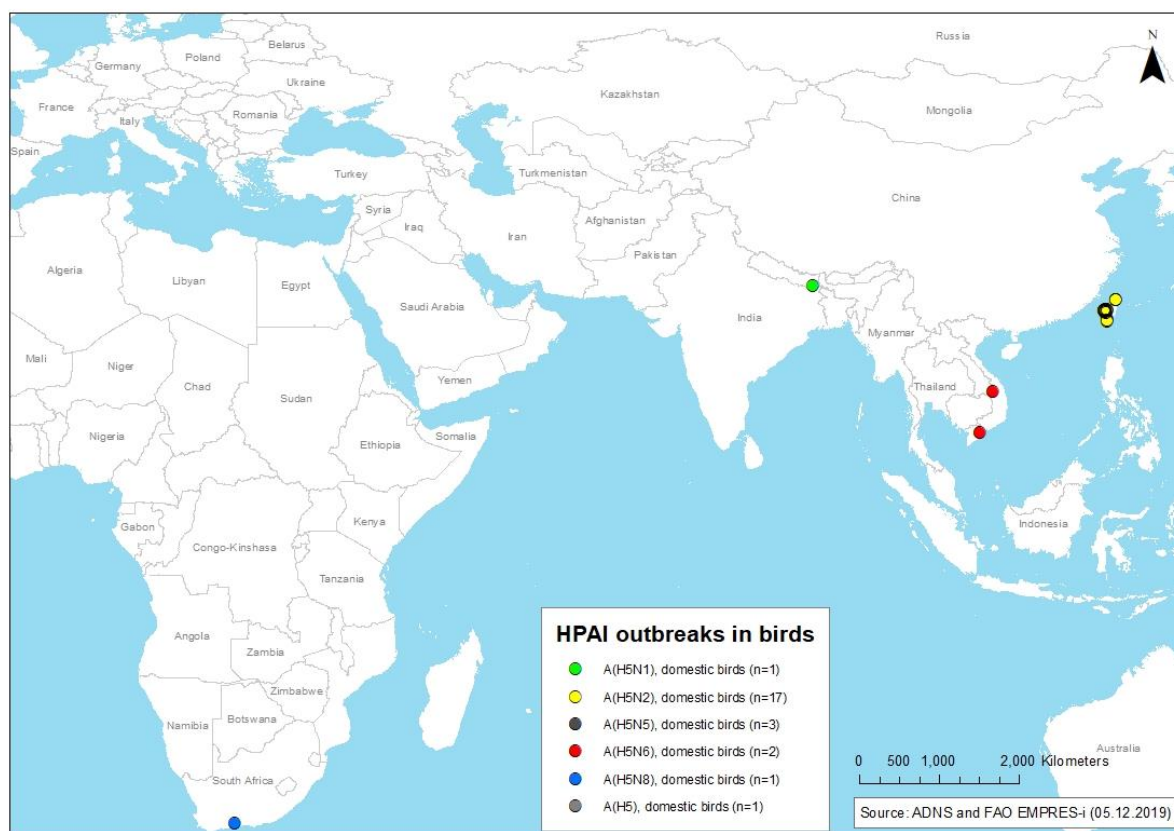
#### **4.4. The avian influenza situation in other countries not reporting via ADNS, 16 August – 15 November 2019 (TOR 4)**

An overview of the HPAI outbreaks notified from other countries not reporting via ADNS but via the OIE or national authorities from 16 August to 15 November 2019 is presented in Table 2 and Figure 2. 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 2:** Number of HPAI outbreaks in other countries not reporting via ADNS, by virus subtype and country, 16 August to 15 November 2019 (n=25)

Region	Country	HPAI outbreaks						
		A(H5N1) Domestic birds	A(H5N2) Domestic birds	A(H5N5) Domestic birds	A(H5N6) Domestic birds	A(H5N8) Domestic birds	A(H5) Domestic birds	All HPAI
<b>Africa</b>	South Africa					1		1
<b>Asia</b>	Nepal	1						1
	Taiwan		17	3			1	21
	Vietnam				2			2
<b>Total</b>	<b>(4 countries)</b>	<b>1</b>	<b>17</b>	<b>3</b>	<b>2</b>	<b>1</b>	<b>1</b>	<b>25</b>



**Figure 2:** Geographical distribution, based on available geocoordinates, of HPAI outbreaks in Europe, Asia and Africa in domestic birds, by A(H5N1) as green, A(H5N2) as yellow, A(H5N5) as dark grey, A(H5N6) as red, A(H5N8) as blue, A(H5) as light grey, 16 August – 15 November 2019 (n=25)

#### 4.4.1. HPAI A(H5N1)

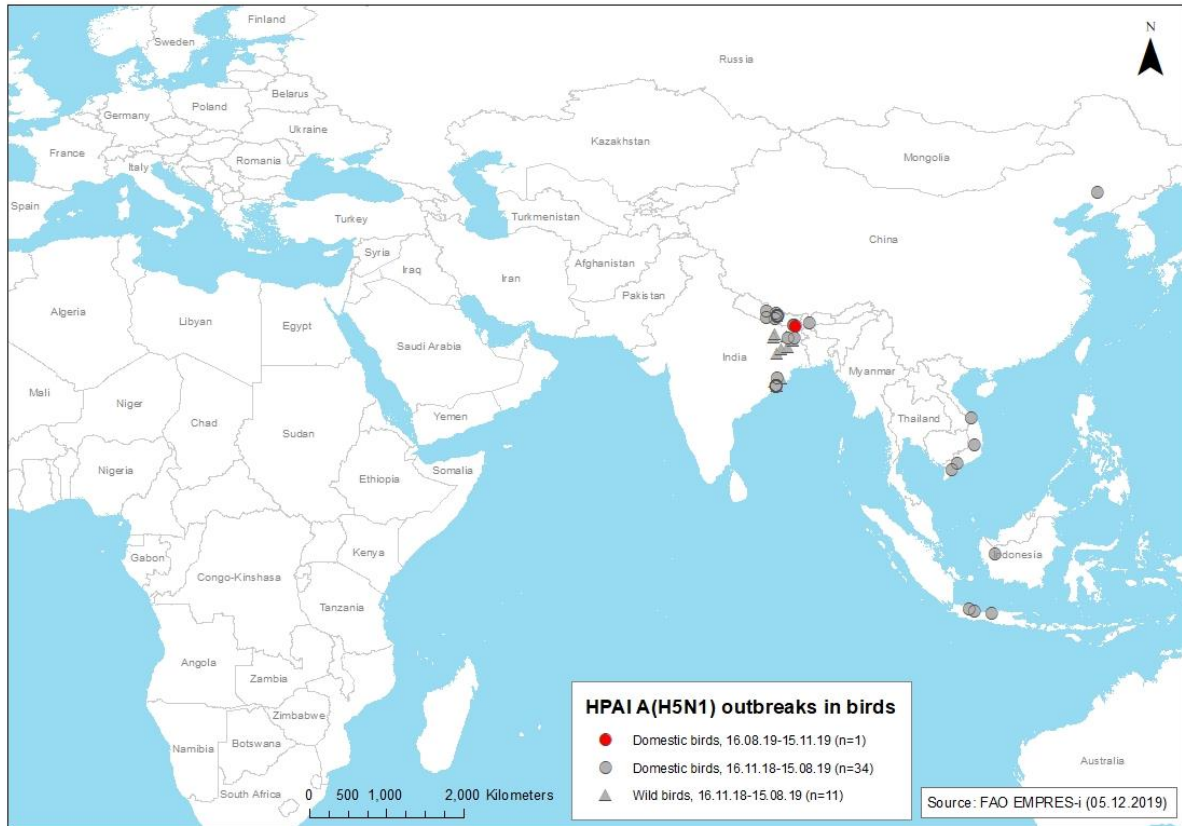
##### 4.4.1.1. Domestic and wild birds

###### *Detections*

In the relevant reporting period, only Nepal notified the detection of HPAI A(H5N1), in domestic birds. The outbreak was confirmed on a medium-sized poultry establishment in the village of Kanepokhari in the Eastern province in August 2019. In contrast to the last report, no wild bird cases of the Asian lineage HPAI A(H5N1) were reported in the relevant time period (Figure 3).

### Information extracted from the scientific literature

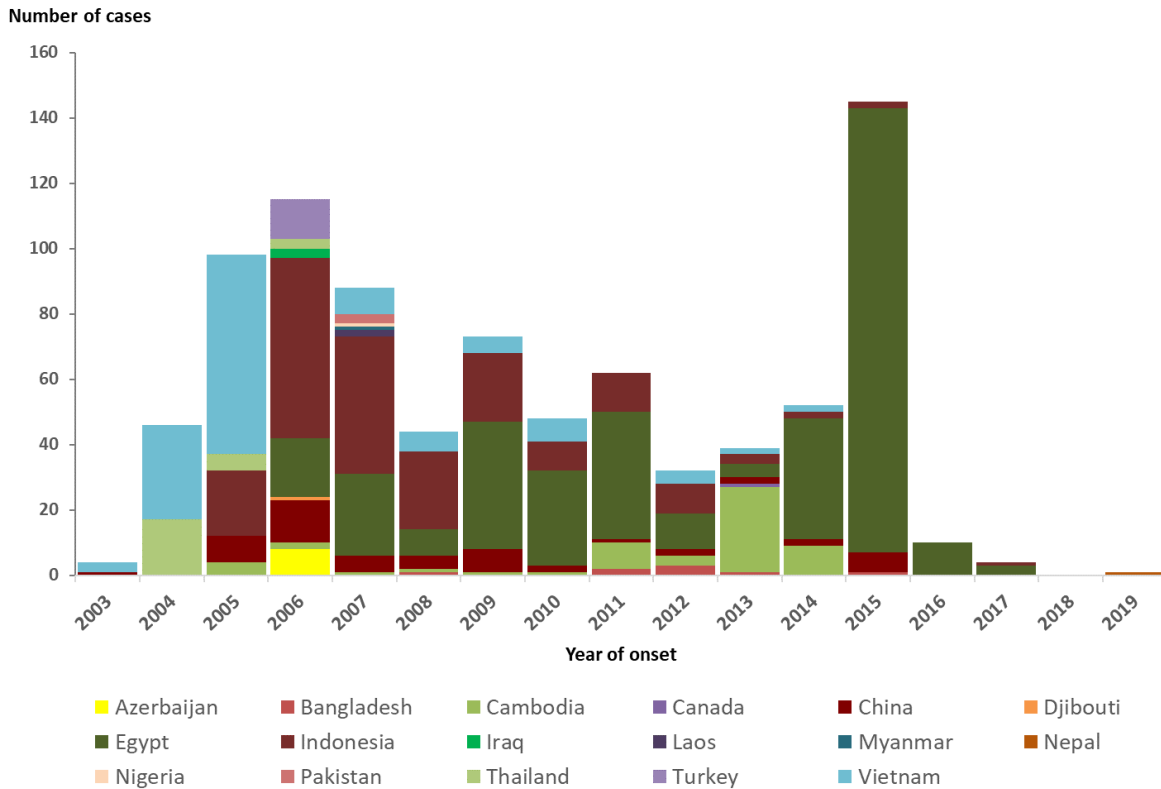
No new relevant information has been published on the phenotypic and genetic characterisation of HPAI viruses circulating in Africa and Asia in birds during the reporting period.



**Figure 3:** Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N1) outbreaks in domestic birds (circles) and wild birds (triangles) (n=46); grey symbols indicate outbreaks that occurred from 15 November 2018 to 15 August 2019, red symbols indicate outbreaks that occurred from 16 August to 15 November 2019 (FAO, online-a)

#### 4.4.1.2. Human infections due to A(H5N1)

No new human case due to AI A(H5N1) was reported since the last report (EFSA et al., 2019b). Since 2003, and as of 15 November 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, 2019d, c) (Figure 4).



Data source: WHO (WHO, 2019d)

**Figure 4:** Distribution of confirmed human cases of A(H5N1) by year and country of reporting, 2003 – 15 November 2019 (n=861)

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

##### 4.4.2.1. Domestic and wild birds

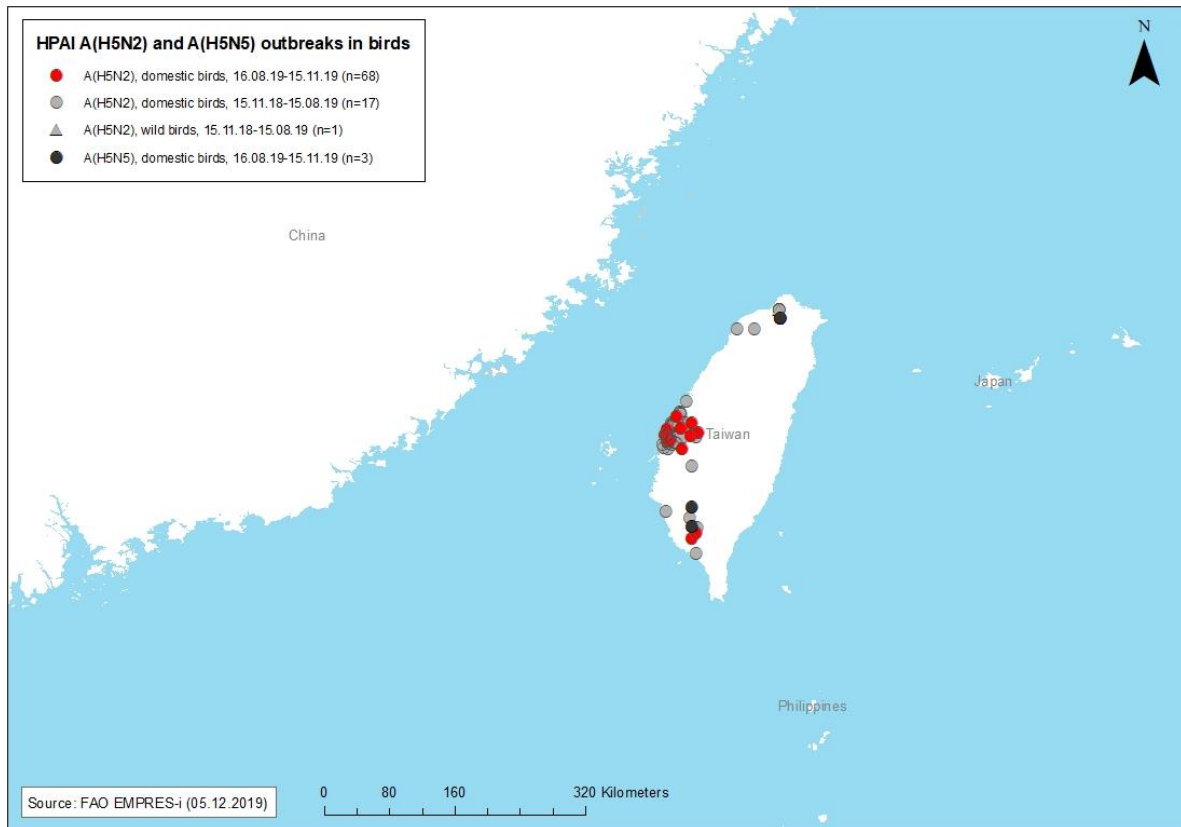
###### *Detections*

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 reporting period, Taiwan notified 17 new outbreaks of HPAI A(H5N2) in three backyard flocks, on two large chicken farms and on several medium-sized poultry and duck farms to the OIE (Figure 5). In contrast to the last report, no further wild bird cases of the Taiwanese lineage HPAI A(H5N2) were reported from 16 August to 15 November 2019. The Taiwanese lineage of HPAI A(H5N2) differs from the Eurasian HPAI A(H5N2) lineage, the latter belonging to clade 2.3.4.4b, which has been detected, with different genotypes, in Egypt and Russia as well as in Asian countries in 2016–2019 (EFSA et al., 2019a).

Furthermore, Taiwan has confirmed the first cases of HPAI A(H5N5) on a small duck farm and two medium-sized chicken farms in southern Taiwan and Taipei city (Figure 5). 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*

No new relevant information has been published on the phenotypic and genetic characterisation of HPAI viruses circulating in Africa and Asia in birds during the reporting period.



**Figure 5:** Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N2) and A(H5N5) outbreaks in domestic birds (circles) and wild birds (triangle) (n=89); grey symbols indicate HPAI A(H5N2) outbreaks that occurred from 15 November 2018 to 15 August 2019, red symbols indicate HPAI A(H5N2) outbreaks that occurred from 16 August to 15 November 2019, black symbols indicate HPAI A(H5N5) outbreaks that occurred from 16 August to 15 November 2019 (FAO, online-a)

#### 4.4.3. HPAI A(H5N6)

##### 4.4.3.1. Domestic and wild birds

###### *Detections*

From 16 August to 15 November 2019, Vietnam reported two further outbreaks of the zoonotic reassortment of HPAI A(H5N6) clade 2.3.4.4c on medium-sized commercial poultry farms in previously affected provinces (Figure 6).

In November 2019, Nigeria notified the first detection of HPAI A(H5N6) virus in chickens at a live-bird market in Sokoto in June 2019. The genetic characterisation of the HA and NA gene sequences shows that the virus possesses a high genetic identity with the A(H5N6) viruses of clade 2.3.4.4b identified in wild birds in Europe in 2016–2017 ( Dr A Fusaro, EURL on AI at IZSVe, 2019; ProMed, online).

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

Baek et al. (2019) described a novel reassortant of A(H5N6) clade 2.3.4.4 virus detected at the beginning of 2018 in chickens and a spot-billed duck (*Anas poecilorhyncha*) in South Korea. The new variant possessed PB2, PA, and NP gene segments of the Eurasian LPAI viruses and the remaining gene segments from A(H5N6) genotype H35-like viruses.

The novel reassortants A(H5N6) clade 2.3.4.4 viruses were detected in November 2017 in migratory wild birds (spot-billed ducks, a mallard and a gadwall (*Mareca strepera*)) in Ningxia in China (Sun et al.,

2019b). The genetic analysis revealed that they were the products of reassortment between A(H5N8) clade 2.3.4.4b viruses and LPAI viruses.

Zhang et al. (2019) reported the first detection of a novel A(H5N6) virus that resulted from the reassortment between A(H5N1) clade 2.3.2.1c (gene segments HA, PB2, PB1, NS) and A(H5N6) clade 2.3.4.4 (gene segments NA, PA, NP and M). The virus was isolated from a Eurasian collard dove (*Streptopelia decaocto*) in the Jiangxi province in China, in 2016.

Bai et al. (2019) analysed A(H5N6) strains from Guangdong Province in China and demonstrated antigenic drift in comparison with a vaccine strain, resulting in decreased protection of vaccinated chickens against circulating clade 2.3.4.4 A(H5) viruses.

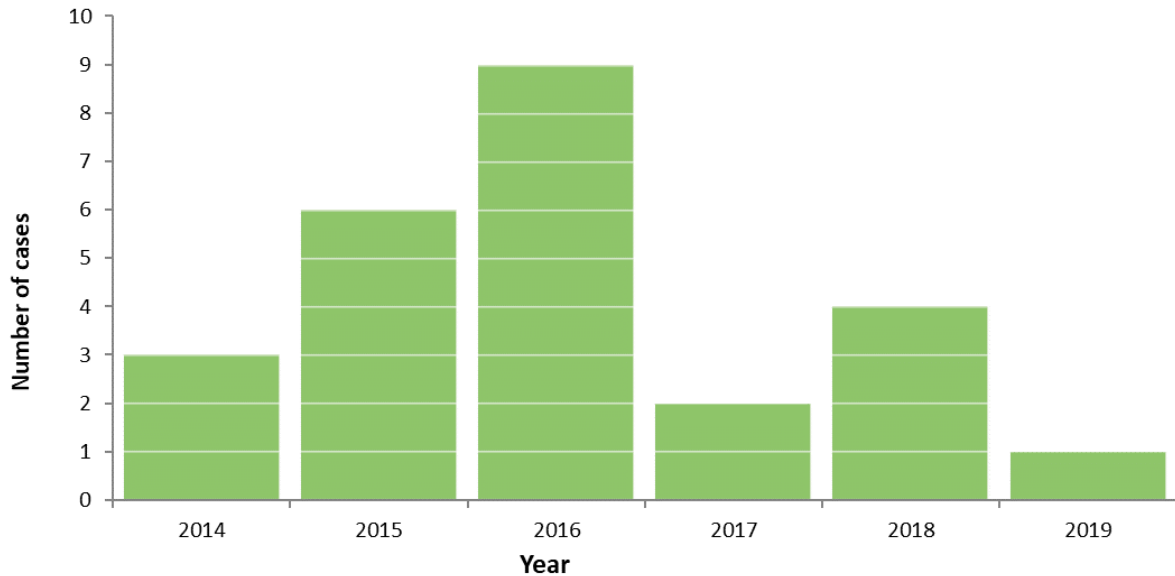


**Figure 6:** Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N6) outbreaks in domestic birds (circles) and wild birds (triangles) (n=10); grey symbols indicate outbreaks that occurred from 15 November 2018 to 15 August 2019, red symbols indicate outbreaks that occurred from 16 August to 15 November 2019 (FAO, online-a)

#### 4.4.3.2. 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., 2019b). Since 2014, and as of 15 November 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 7). WHO lists 24 human cases of AI A(H5N6), including 15 with fatal outcomes (WHO, 2019c, b, a). One additional case from 2015 was described by Li et al. (2016). Twelve deaths due to A(H5N6) had been reported between 2014 and 2017 (Jiang et al., 2017). All of the cases were infected and detected in mainland China (WHO, 2019b).





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

**Figure 7:** Number of human cases due to A(H5N6), clade 2.3.4.4, infection by year of onset, China 2014 – 2019 (n=25)

#### 4.4.4. HPAI A(H5N8)

##### 4.4.4.1. Domestic and wild birds

###### *Detections*

In the relevant reporting period, South Africa reported one further outbreak of clade 2.3.4.4b, HPAI A(H5N8) virus on a commercial ostrich farm in the Western Cape province (Figure 8). No further infections with HPAI A(H5N8) virus of Jackass penguins (*Spheniscus demersus*) from Namibia (Umberto et al., 2019) or other wild birds were reported from Africa or worldwide.

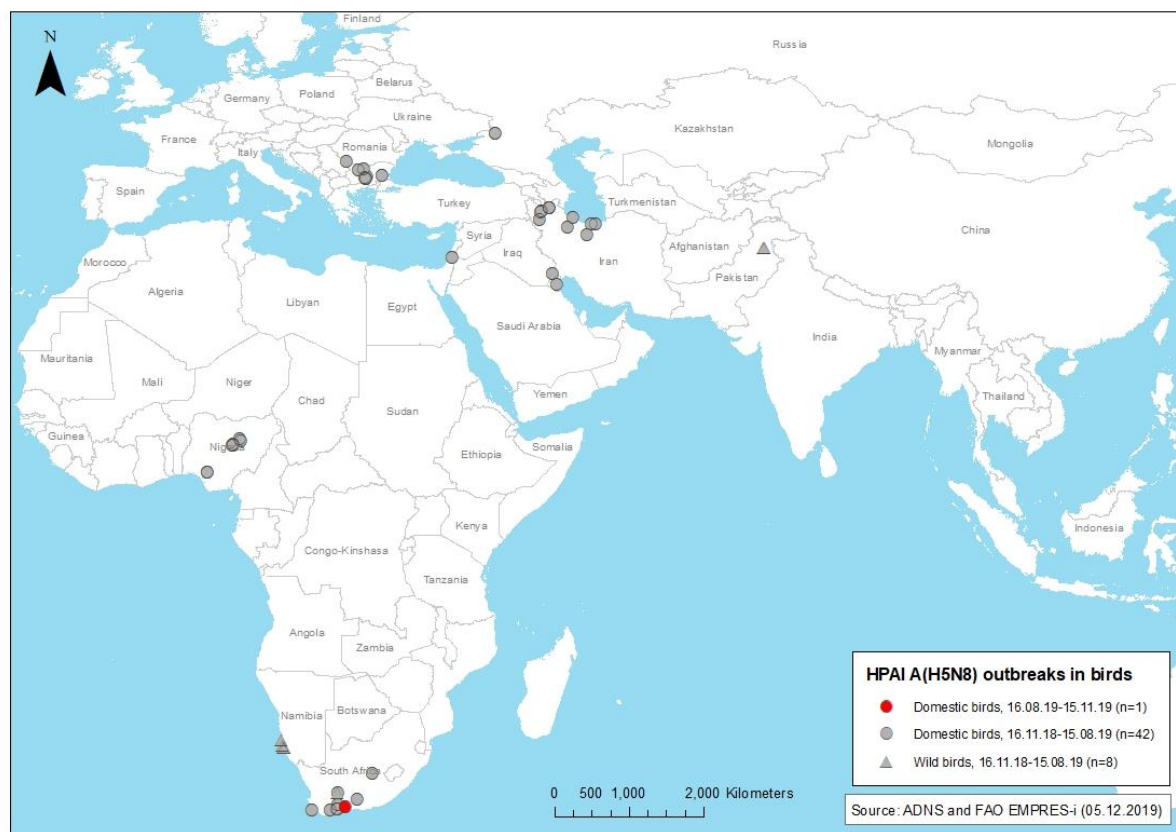
###### *Information extracted from the scientific literature*

Experimental studies on the infectivity and transmissibility of a European A(H5N8) clade 2.3.4.4b virus strain performed on chickens (3 weeks old) and mallards (3 weeks old) revealed that the virus was less adapted to chickens than mallards. High mortality (but no transmission) was observed only in chickens infected with the highest dose ( $6 \log_{10} \text{EID}_{50}$ ) while mallards showed high mortality (at least 80%) and transmission to contact birds when infected with the doses  $4 \log_{10} \text{EID}_{50}$  and  $6 \log_{10} \text{EID}_{50}$  (Leyson et al., 2019).

Three A(H5N8) clade 2.3.4.4b viruses that were detected in Egypt in the winter of 2016–2017 were shown to replicate well in mice without prior adaptation but induced varied mortality rates (20–80%). Three weeks old Pekin ducks infected with a dose  $10^6 \text{EID}_{50}$  of each virus showed mortality from 0% to 28%. The following clinical signs were observed in sick ducks: haemorrhagic feet, discolouration of beak, incoordination, loss of balance, locomotoric problems and secretions from the eyes. Four weeks old SPF chickens died between 48 to 96 hours post infection and the clinical symptoms included ocular and nasal discharge, swelling of the head, listlessness, cyanosis of the unfeathered skin, wattles and comb, and diarrhoea (Moatasim et al., 2019).

The whole genome analysis performed on 12 A(H5N8) strains detected in May 2017 in Muscovy ducks in the Democratic Republic of Congo demonstrated that they clustered in clade 2.3.4.4b (Twabela et al., 2019). A representative strain was used to test its pathogenicity in 6 weeks old chickens, 4 weeks old Muscovy ducks and 4 weeks old Pekin ducks (dose  $10^6 \text{EID}_{50}/\text{bird}$ ). The virus induced high mortality

in chickens and Muscovy ducks (all birds died within 4 dpi), but no mortality in Pekin ducks was seen (one bird showed transient neurological signs and lack of appetite).



**Figure 8:** Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N8) outbreaks in domestic birds (circles) and wild birds (triangles) (n=51); grey symbols indicate outbreaks that occurred from 15 November 2018 to 15 August 2019, red symbols indicate outbreaks that occurred from 16 August to 15 November 2019 (FAO, online-a)

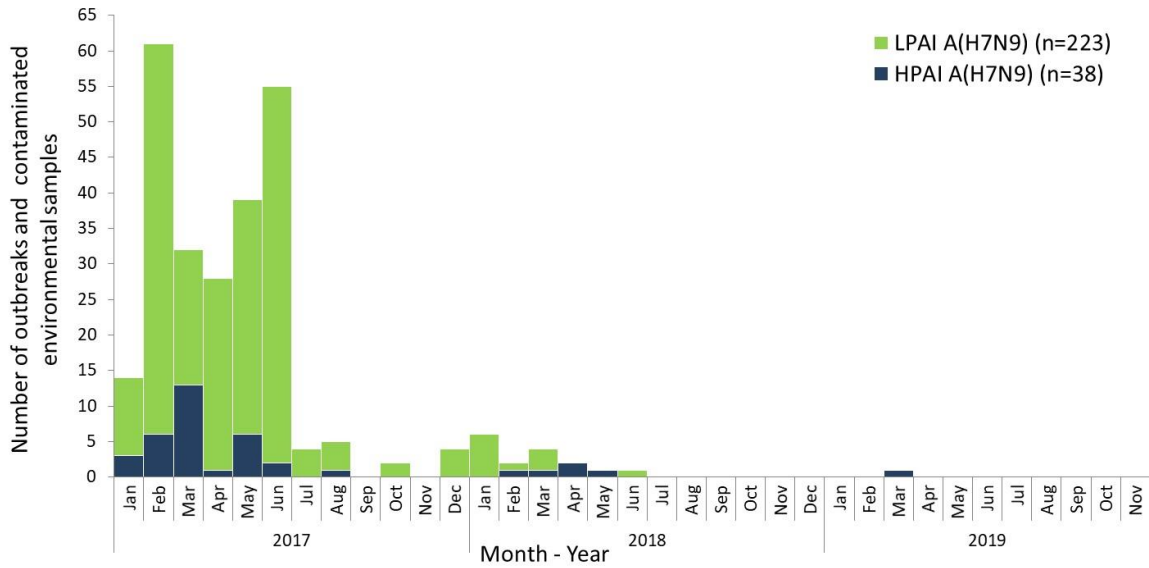
#### 4.4.5. HPAI-LPAI A(H7N9)

##### 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 9). The results of the surveillance campaigns in China are published monthly by the Chinese Ministry of Agriculture (Ministry of Agriculture and Rural Affairs of People's Republic of China, 2019) and are also available on the EMPRES-i website of the Food and Agriculture Organization (FAO) (FAO, online-a). The results show that 96.07% of the 100,529 serum poultry samples, taken after vaccination campaigns from 3,421 locations in 29 provinces in August 2019, achieved the required immunity level (Ministry of Agriculture and Rural Affairs of People's Republic of China, 2019). Furthermore, 16,525 virological samples were collected from poultry and the environment in August 2019. The nationwide A(H7N9) vaccination campaigns of poultry, with the exception of poultry in AI-free zones and export farms, started extensively in September 2017 (FAO, online-b).





Data source: FAO EMPRES-i (05.12.2019)

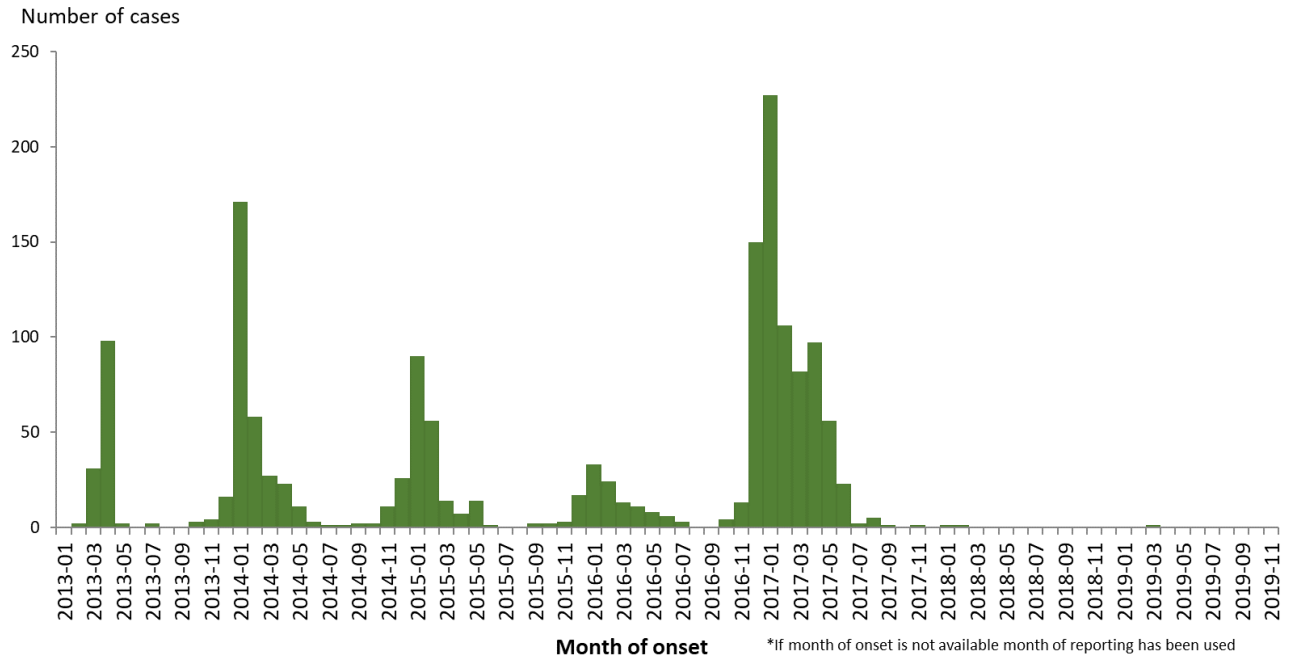
**Figure 9:** Distribution of confirmed LPAI and HPAI A(H7N9) outbreaks among birds and environmental samples in China, by month, 1 January 2017 – 15 November 2019 (n=261)

*Information extracted from the scientific literature*

A novel reassortant A(H7N2) was isolated in May 2019 in China from a vaccinated layer flock and genetic analysis revealed that it was a reassortant that had most likely derived its genome segments from A(H7N9) subtype virus (PB2, PB1, PA, HA, M and NS gens) and A(H9N2) virus (NP and NA genes). The virus contained multiple basic amino acids at the cleavage site and had an intravenous pathogenicity index value of 2.26, indicating a high pathogenicity. Inoculated ducks showed no mortality but multi-organ replication. The virus strain exhibited distinct antigenicity relative to the H7-Re2 vaccine strain indicative of rapid antigenic drift (Qiu et al., 2019).

**4.4.5.2. Human infections due to A(H7N9)**

No human cases due to AI A(H7N9) have ever been reported from Europe and no human case has been reported globally since the last EFSA report. Since February 2013, a total of 1,568 human cases have been reported from outside of Europe (Figure 10), including at least 615 deaths (39%) (WHO, 2019b, c). 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 et al., 2018).



Source: ECDC line list (described above).

**Figure 10:** 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 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 between 16 August and 15 November 2019.

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

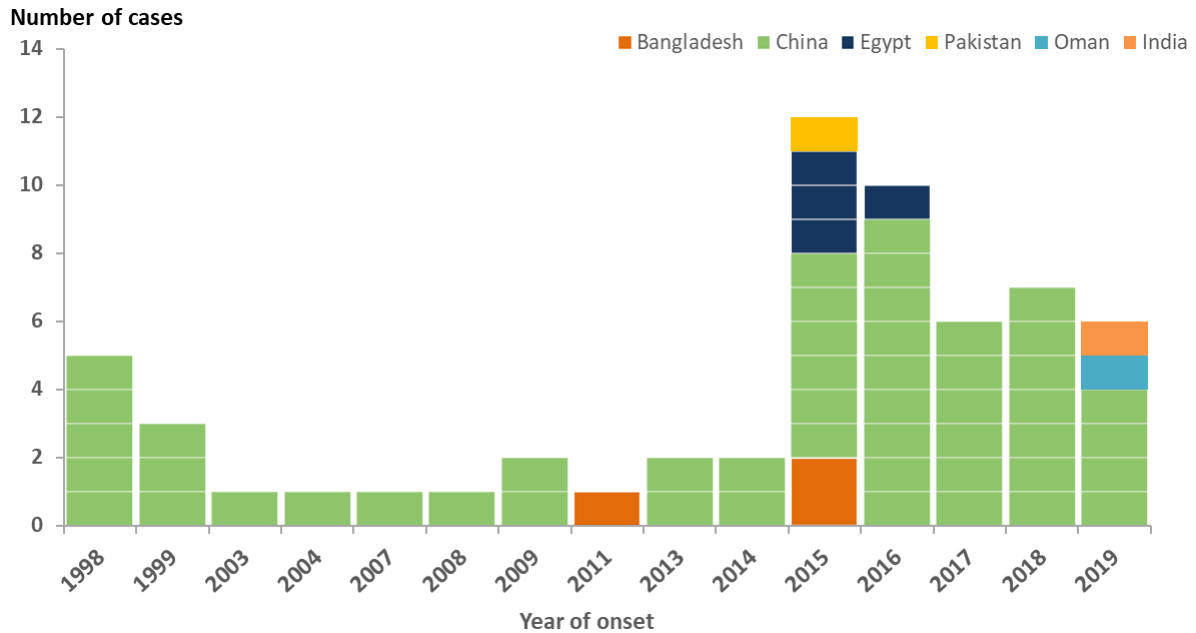
The first report of the A(H9N2) subtype in Kenyan poultry was provided by Kariithi et al. (2019). The virus belonged to the G1 lineage and was genetically similar to an A(H9N2) strain isolated in 2017 in Uganda.

The analysis of A(H9N2) virus strains isolated from poultry in southern China during 2017–2018 indicated that the viruses belong to the Y280-like lineage (genotype G57) with internal genes similar to A(H7N9) viruses recently circulating in China. The viruses preferentially bound to the human receptors and acquired multiple mutations adaptive to mammals (Sun et al., 2019a).

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

Three new human cases have been reported since the last EFSA report (EFSA et al., 2019b; Potdar et al., 2019; Ministry of Health and Welfare Taiwan, online) and one case from 2004 newly identified from literature search has been added to the ECDC line list (Peacock et al., 2019). The most recent cases were reported from India (1) and China (2). The first Indian human A(H9N2) case had disease onset on 12 February 2019, the two cases from China were reported with onset of disease on 26 October and 12 November 2019. Since 1998, and until 15 November 2019, 60 laboratory-confirmed cases of human infection with AI A(H9N2) virus, including one death, have been reported globally. Cases were reported

from China (50), Egypt (4), Bangladesh (3), India (1), Oman (1) and Pakistan (1) (ECDC line list) (Figure 11).



Data source: ECDC line list (Peacock et al., 2019; Potdar et al., 2019; WHO, 2019c)

**Figure 11:** Distribution of confirmed human cases of A(H9N2) by reporting country, 1998 – 15 November 2019 (n=60)

#### 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).

The number of reported outbreaks for Asia and Africa was again lower than in the previous time period. Apart from cases during the long-term epidemic of Taiwanese lineage HPAI A(H5N2), clade 2.3.4.4 in Taiwan, only six outbreaks in domestic birds were reported from 16 August to 15 November 2019 from Nepal, South Africa and Taiwan. For the first time, HPAI A(H5N5) outbreaks in duck and chicken farms were notified by the Taiwanese Government. Reported outbreaks of the Asian lineage of HPAI A(H5N1), the zoonotic reassortment of HPAI A(H5N6) clade 2.3.4.4c are still confined to Asia and HPAI A(H5N8) to Africa.

No cases in wild birds were reported worldwide in the relevant time period for this report. Despite the lack of reports on the 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, there is still uncertainty and close monitoring of the situation is required. Furthermore, the autumn migration from breeding sites to wintering sites is still ongoing, depending on the weather conditions and bird species.

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

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

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

### 4.6.1.2. Vaccines

WHO published a status update on the available and recommended vaccines or candidate vaccine viruses (CVVs) for pandemic preparedness in September 2019 following the vaccine composition meeting and proposed a new A/Gansu/23277/2019-like A(H7) CVV to be developed (WHO, 2019e).

## 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. No outbreaks due to AI viruses have been reported in Europe. Transmission to humans of AI viruses detected in wild birds or poultry recently has not been observed in Europe, 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. The reports from countries reporting the first occurrence of human cases infected with A(H9N2) LPAI viruses in 2019, i.e. India and Oman, highlight 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
CVV	Candidate vaccine viruses
ECDC	European Centre for Disease Prevention and Control
EFSA	European Food Safety Authority
EEA	European Economic Area
EU	European Union
EURL	European Union Reference Laboratory
FAO	Food and Agriculture Organization
HPAI	Highly pathogenic avian influenza
LPAI	Low pathogenic avian influenza
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, legislation<sup>1</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>2</sup>, EFSA should provide the technical and scientific assistance to the Commission based on the following Terms of Reference (TOR):

<sup>1</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>2</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 August and 15 November 2019 and reported by Member States and neighbouring countries via ADNS. Member States where AI outbreaks occurred in poultry submitted additional epidemiological data to EFSA, which have been used to analyse the characteristics of the affected poultry establishments.

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

In case of detection of HPAI outbreaks in poultry in the EU, a description of the applied prevention and control measures (TOR 3) is given in the case report provided by representatives from affected Member States and attached as an Annex. The main topics covered are increasing awareness, release and repeal of housing orders, strengthening biosecurity, preventive culling, implementation of a regional standstill, bans on hunting and derogations from restriction zone implementation after a risk assessment. As there were no HPAI outbreaks in the EU in the relevant period for this report, no annex is attached to this report.

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 August and 15 November 2019 and on information gathered by performing a literature search on papers published in PubMed from 16 August to 15 November 2019. Possible actions for preparedness in the EU are discussed.

This report mainly describes information that became available since the publication of the EFSA report for the period August – November 2019 (EFSA et al., 2019a) 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 August to 15 November 2019 submitted by Member States to the ADNS (European Commission, online-a) were taken into account for this report. In addition, France was 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 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 August to 15 November 2019 were searched; the search was run on 18 November 2019.

*Relevance criteria* Scientific articles added to the database from 16 August to 15 November 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 135 papers. The articles were subsequently screened against the relevance and eligibility criteria. None of the screened papers was in the end taken into consideration in the description of the phenotypic characterisation of HPAI viruses circulating in the EU in domestic and wild birds in the reporting period.

The search protocol and the results can be consulted at <https://doi.org/10.5281/zenodo.3453860>.

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

Data from FAO EMPRES-i (FAO, online-a) on HPAI A(H5N1), HPAI A(H5N2), HPAI A(H5N5), A(H5N6), A(H5N8), HPAI and LPAI A(H7N9) in domestic, captive and wild birds, and environmental samples, were used to describe and to map the geographical distribution of AI cases in domestic and wild birds in Africa, Asia, the Middle East and Europe on the basis of the observation dates. With the purpose of avoiding over-complication of the maps, captive birds and environmental samples have been mapped as domestic birds. Although some of these kept animals may be wild species, in most of the cases captive birds, or, for environmental samples, the birds from which samples have been taken (mainly at

live market places) will not move around and not spread the infection by migrating and for this reason have been considered as domestic birds in the maps provided in this report. Only when there was a strong discrepancy among 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 August and 15 November 2019 were searched; the search was run on 18 November 2019.

*Relevance criteria* Scientific articles added to the database between 16 August and 15 November 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 115 papers. The articles were subsequently screened against the relevance and eligibility criteria. Ten papers were in the end taken into consideration in the description of phenotypic and genotypic characterisation of HPAI viruses circulating on other continents and in other regions (Africa, Asia, the Middle East) in domestic or wild birds or mammals (excluding humans) in the reporting period.

The search protocol and the results can be consulted at at <https://doi.org/10.5281/zenodo.3453860>.

## **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.