

APPROVED: 24 September 2020

doi:10.2903/j.efsa.2020.6270

Avian influenza overview May – August 2020

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

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Abstract

Between 16 May and 15 August 2020, seven highly pathogenic avian influenza (HPAI) A(H5N8) virus outbreaks were reported in Europe in poultry, with one outbreak reported in Bulgaria (n=1) and six in Hungary (n=6) and one low pathogenic avian influenza (LPAI) A(H5N3) virus outbreak was reported in poultry in Italy. All six outbreaks detected in Hungary were secondary outbreaks and seem to be the tail end of the HPAI A(H5N8) epidemic that was observed in poultry over the winter and spring in central Europe from December 2019 (n=334). Genetic analysis of the HPAI A(H5N8) viruses isolated during this reporting period from Bulgaria and Hungary did not identify any major changes compared to the viruses collected in the respective countries during the first months of 2020. This suggests a persistence of the virus in the two countries rather than new introductions via infected wild birds. HPAI A(H5N8) virus has been detected in poultry and wild birds in western Russia within the reporting period, and as of the middle of September also in Kazakhstan. The presence of HPAI virus in western Russia and in north Kazakhstan, spatially associated with autumn migration routes of wild waterbirds, is of concern due to the possible spread of the virus via wild birds migrating to the EU. It is highly recommended that Member States take appropriate measures to promptly detect suspected cases of HPAI, including increasing biosecurity measures. According to past experiences (2005-2006 and 2016-2017 epidemic waves), the northern and eastern European areas might be at higher risk of virus introduction in the coming autumn-winter season and should be the key regions where prompt response measures to early detect the virus should be set up. One human case due to A(H9N2) avian influenza virus infection was reported during the reporting period.

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

Requestor: European Commission

Question number: EFSA-Q-2020-00460

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Acknowledgements: In addition to the listed authors, EFSA, ECDC and the EURL wish to thank the following: Member State representatives who provided data on avian influenza outbreaks, or wrote case reports for this scientific output: Aleksandra Miteva and Gabriela Goujgoulova (Bulgaria); Georgina Helyes, Adam Balint and Malik Peter (Hungary); Paolo Mulatti (Italy); Dominique Bicout, Jan Arend Stegeman and Preben Willeberg for reviewing the document; Bianca Zecchin from IZSVE for her support with the genetic analyses of European A(H5N8); Victor Irza from Federal Center for Animal Health (FGBI 'ARRIAH', Russia), Timm Harder from Friedrich Loeffler Institut, Inmaculada Aznar and Elisabeth Dorbek-Kolin from EFSA for the support provided to this scientific output.

Suggested citation: EFSA (European Food Safety Authority), ECDC (European Centre for Disease Prevention and Control), EURL (European Reference Laboratory for Avian Influenza), Adlhoch C, Fusaro A, Kuiken T, Niqueux É, Terregino C, Staubach C, Muñoz Guajardo I and Baldinelli F, 2020. Scientific report: Avian influenza overview February – May 2020. *EFSA Journal* 2020;18(9):6270, 40 pp. doi:10.2903/j.efsa.2020.6270

ISSN: 1831-4732

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Table of contents

1.	Introduction.....	4
2.	Conclusions	4
2.1.	Main observations	4
2.2.	Conclusions	4
3.	Suggestions.....	5
4.1.	Overview of HPAI outbreaks in Europe during the previous and current seasons.....	6
4.2.	HPAI and LPAI outbreaks in Europe, 16 May – 15 August 2020 (TOR 1 and TOR 2).....	10
4.2.1.	Description of the avian influenza detections in time and space	10
4.2.2.	Phenotypic characterisation of avian influenza viruses circulating in Europe	12
4.2.3.	Genetic characterisation of avian influenza viruses	14
4.2.4.	Human cases due to A(H5N8) viruses detected in Europe.....	14
4.3.	Prevention and control measures applied in Europe, 16 May – 15 August 2020 (TOR 3).....	15
4.4.	The avian influenza situation in other countries not reporting via ADNS, 16 May – 15 August 2020 (TOR 4)	15
4.4.1.	HPAI A(H5N1).....	16
4.4.2.	HPAI A(H5N2) and A(H5N5)	18
4.4.3.	HPAI A(H5N6).....	20
4.4.4.	HPAI A(H5N8).....	21
4.4.5.	HPAI-LPAI A(H7N9).....	23
4.4.6.	LPAI A(H9N2)	24
4.5.	Scientific analysis of avian influenza spread from non-EU/EEA countries to poultry in the EU/EEA	26
4.6.	Surveillance and diagnosis of human infections and public health measures for prevention and control	27
4.6.1.	Surveillance in the EU, diagnosis and options for public health control measures (in relation to the EU)	27
4.6.2.	Candidate vaccine viruses.....	27
4.7.	ECDC risk assessment for the general public in the EU/EEA	27
	References.....	28
	Abbreviations	33
	Appendix A – Terms of reference	34
	Appendix B – Data and methodologies	36
	Annex A – Applied prevention and control measures on avian influenza	38
A.1	Bulgaria.....	38
A.2	Hungary	40

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 virus, reported in and outside Europe between 16 May and 15 August 2020. The background, terms of reference and their interpretation are described in Appendix A and the data and methodologies are reported in Appendix B.

2. Conclusions

Avian influenza outbreaks in European countries and in other countries of interest between 16 May and 15 August 2020

2.1. Main observations

- One human infection due to A(H9N2) avian influenza virus has been reported from China during the period of the report.
- Since 2005, Europe has experienced six HPAI A(H5) incursions, three of which occurred in the last four years (2016–2017, 2017–2018 and 2019–2020).
- In Europe, between 16 May and 15 August 2020 (based on the Animal Disease Notification System (ADNS)):
 - seven HPAI A(H5N8) outbreaks were reported in poultry: one in Bulgaria and six in Hungary;
 - one LPAI A(H5N3) outbreak was reported in poultry in Italy.
- The genomic characterisation of the HPAI A(H5N8) viruses detected in domestic birds in Europe indicates the persistent circulation of two distinct A(H5N8) genotypes of clade 2.3.4.4b in Hungary and Bulgaria.
- Between 16 May and 15 August 2020, HPAI A(H5N8) has been reported in poultry and in two wild waterbirds in Russia, near the eastern border with Kazakhstan. In Russia, outside the reporting period for this report and as of 22 September 2020, HPAI A(H5N8) were detected in 37 poultry outbreaks, four mute swans (*Cygnus olor*), four anatids of unknown species, and one tufted duck (*Aythya fuligula*), all cases were detected near the eastern and western border with Kazakhstan; in North Kazakhstan HPAI A(H5) was detected in seven poultry backyards as well as in 86 corvids and two wild waterbirds of unknown species (all wild birds were found dead). The areas where these birds were found are important staging sites for several migratory bird species before moving to wintering areas.
- The low number of avian influenza outbreaks reported outside the EU in the previous report decreased further in the time period for this report. Outbreaks of HPAI A(H5N1), A(H5N2), A(H5N5), A(H5N6) and A(H5N8) in domestic birds were reported from Russia, South-east Asia (Philippines, Taiwan and Vietnam) and South Africa.
- HPAI A(H5N6) viruses found in wild birds in China in January 2020 share 97.4%–98.1% nucleotide identity with A(H5N6) viruses that were responsible for human cases in China in 2018.

2.2. Conclusions

- The risk of zoonotic transmission of avian influenza viruses to the general public in Europe remains very low. The evolution of the viruses and recent reassortment events need to be closely monitored to assess the future risk for human transmission.
- All six poultry outbreaks detected in Hungary were secondary outbreaks due to poultry-to-poultry virus spread and seem to be the tail end of the HPAI A(H5N8) epidemic that was observed over the winter and spring in central Europe from December 2019.

- The situation between March and May 2020 in Hungary was reminiscent of the large number of secondary HPAI outbreaks previously observed in the domestic waterfowl production sector in France, Hungary and Bulgaria in 2016–2017. Initial epidemiological investigations (Bronner et al., 2017) and retrospective studies in France (Guinat et al., 2020a; Guinat et al., 2020b; Huneau-Salaun et al., 2020) pointed out the prominent role of the movement of infected animals, human beings and shared equipment and commodities, these acting as vectors of virus transmission between poultry holdings. Subsequently, a comprehensive set of enhanced biosecurity measures was implemented in the establishments and during the transport of the animals.
- No major genetic changes have been identified in the HPAI A(H5N8) viruses isolated during this reporting period in Hungary and Bulgaria compared to the viruses collected in the two countries during the first months of 2020. This suggests a persistence of the virus in the two countries rather than new introductions via infected wild birds.
- The repeated detection of HPAI A(H5N8) or A(H5) in domestic and wild birds in western Russia and north Kazakhstan between July and September 2020 indicates either ongoing local circulation of HPAI viruses or new virus introductions by infected wild birds. The mortality observed in corvids in North Kazakhstan (which probably were exposed by feeding on infected carcasses) is indicative of a significant virus circulation in the area.
- The presence of HPAI virus in western Russia and north Kazakhstan, spatially associated with autumn migration routes of wild waterbirds and the previous detection of HPAI virus in mute swans in northern China (EFSA et al., 2020a), also linked to key migration areas, is of concern due to the possible spread of the virus via wild birds migrating to the EU.
- The scarce information on the wild birds species found dead makes difficult to identify the most probable migratory flyways that might lead to the introduction of the virus in the EU and therefore to identify the area in the EU that are at higher risk of virus introduction. Nonetheless, during the 2005–2006 and 2016–2017 epidemic waves, HPAI virus detection in the same area of Russia between July and September (OIE, 2005; Lipatov et al., 2007; FAO, 2016) led to northern and eastern Europe being detected as first places of virus introduction (Cattoli et al., 2009; EFSA et al., 2017b), and they will likely be the first areas where HPAI viruses might be detected in the coming autumn-winter season.
- Sudden and persistent drop in the temperatures in Russia and Kazakhstan may favour a westward/southward spread of the virus. Several studies demonstrated that cold weather conditions might have triggered the rapid westward expansion of the HPAI A(H5) virus by infected migratory birds during the 2005–2006 and 2016–17 epidemic waves (Ottaviani et al., 2010; Fusaro et al., 2017; Napp et al., 2018).
- Despite the decreasing number of HPAI A(H5)-affected countries and outbreaks outside Europe, there is considerable uncertainty about the real geographical distribution of these viruses; the low number of HPAI outbreaks notified from outside Europe might be also due to the COVID-19 situation.
- Continued surveillance for avian influenza virus in wild birds and poultry in Europe and worldwide, combined with timely generation of complete viral genome sequences and data sharing among European countries and between animal and human health sectors, are crucial in order to be able to detect and respond promptly to threats that are relevant to animal and public health.

3. Suggestions

- It is particularly important that information on the genetic composition and possible origins (e.g. to distinguish between local circulation and long-distance transport from wild bird migration or human activities) of newly detected variants in birds and humans are shared and communicated in a timely manner.

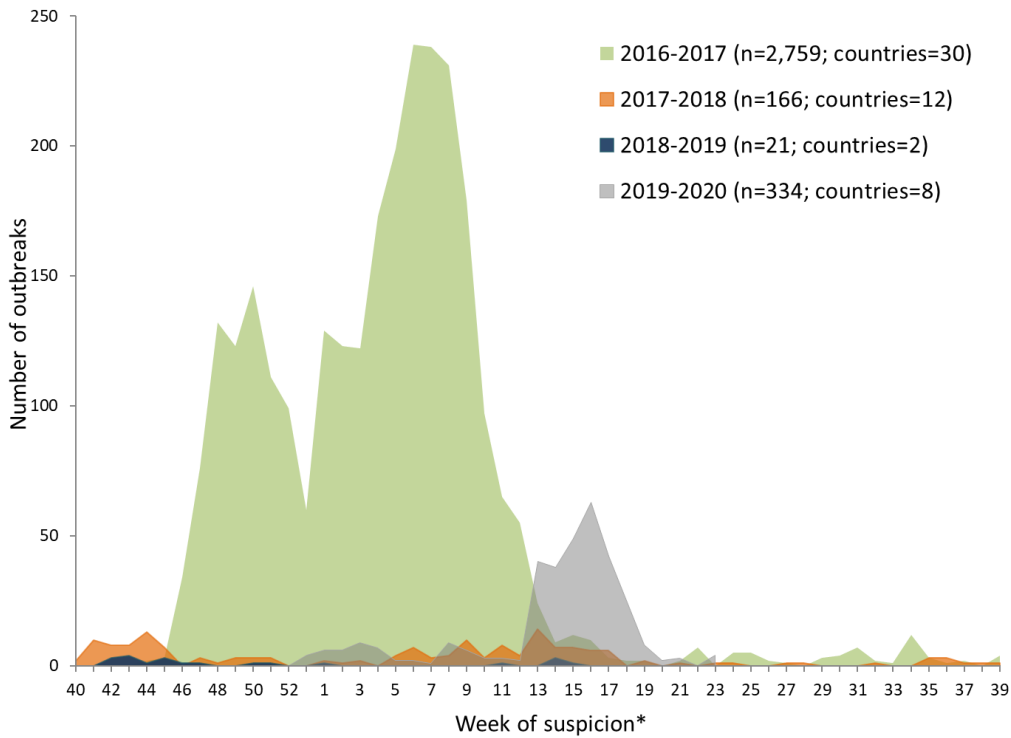
- The high number of secondary outbreaks recorded in duck and goose establishments in some countries, such as Hungary, since December 2019, indicates that these categories of poultry need to be better regulated to increase biosecurity and to prevent uncontrolled spread of infection. Given the apparent similarity of this situation with the previous 2016–2017 HPAI A(H5N8) epidemic, some actions such as i) the poultry production sector to limit the risk of virus spread from already contaminated establishments to in-contact production units and to prevent introduction from infected wild birds (e.g. strict physical separation of poultry production units and prevention of contact with wild birds, poultry densities adapted to allow lockdown of the animals) and ii) the animal transport sector to prevent further spread on a larger scale (e.g. equipment should be designed and facilities should be made available for easy cleaning and disinfection procedures), should be jointly implemented.
- The presence of HPAI A(H5) outbreaks in Russia and Kazakhstan in wild and domestic birds should lead Member States to take appropriate measures to promptly detect suspected cases of HPAI, and to stimulate poultry industries to increase biosecurity measures intended to avoid a possible involvement of poultry. Increasing the level of alert is highly recommended: Member States should warn veterinary and wildlife health authorities of the likely risk of HPAI introduction in the EU due to the recent detection of HPAI viruses in Russia and Kazakhstan, and they should inform about the possibility of finding dead or sick wild birds to be promptly tested for HPAI.
- In the absence of complete information on the species of infected wild birds detected in Russia and Kazakhstan, passive surveillance should still focus on sick or dead birds of the target species (EFSA et al., 2017a); in case of low or absence of wild birds mortality, active surveillance should be implemented. In addition to testing captured and hunted wild birds, collection of faecal droppings and swabs on plumage might be performed in target areas.
- According to past experience (2005-2006 and 2016-2017 epidemic waves), the northern and eastern European areas might be at higher risk of virus introduction in this autumn-winter season and should be the key regions where prompt response measures to early detect the virus should be set up. A subsequent involvement of the more southern and western areas cannot be excluded.
- People who are exposed to birds that may potentially be infected with avian influenza viruses should take appropriate personal protection measures following national guidelines.

4. Results

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

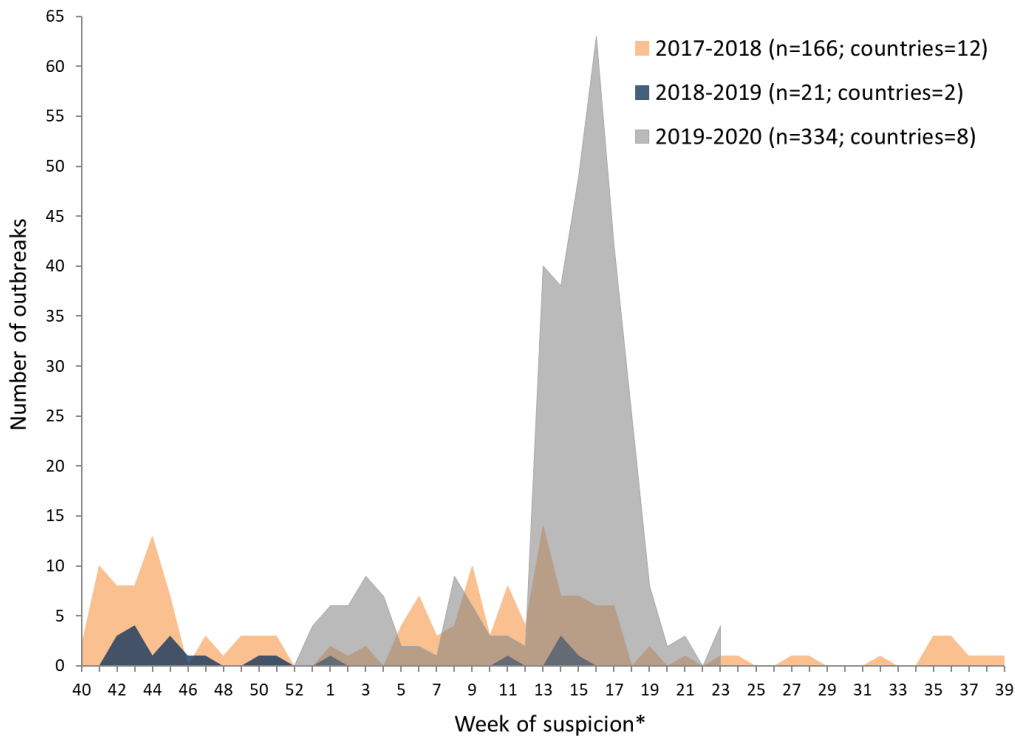
Figure 1 shows the HPAI outbreaks detected in birds (poultry, wild and captive birds) in Europe and reported via ADNS for seasons 2016–2017, 2017–2018, 2018–2019 and 2019–2020. Figure 2 shows the same data only for the last three epidemic seasons. A season is the period that starts in week 40 (the beginning of October) and ends in week 39 (the end of September) of the following year. For the current season, 2019–2020, data reported are truncated at the middle of week 33 (on 15 August 2020), as the season is still ongoing.

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



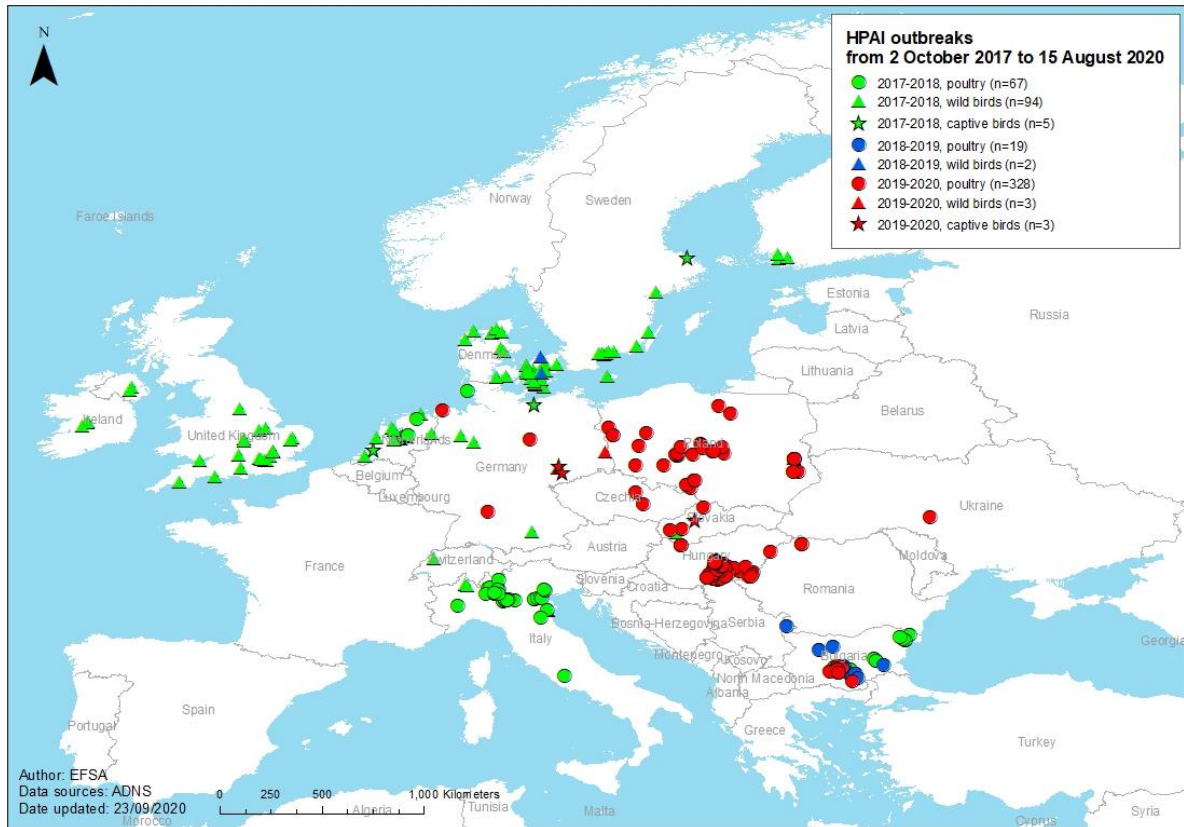
* When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.
 Data source: ADNS, EFSA.

Figure 1: Distribution of total number of HPAI outbreaks detected in Europe in seasons 2016–2017 (green), 2017–2018 (orange), 2018–2019 (blue), 2019–2020 (grey) and reported via ADNS by week of suspicion, 28 September 2016 – 15 August 2020 (n=3,280)



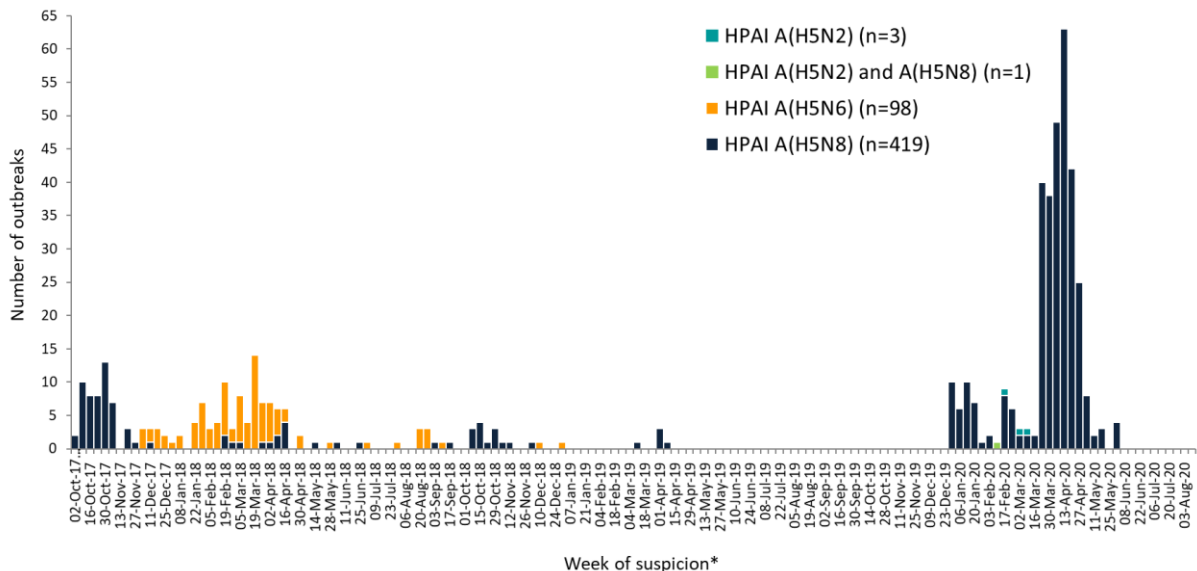
* When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.
 Data source: ADNS, EFSA.

Figure 2: Distribution of total number of HPAI outbreaks detected in Europe in seasons, 2017–2018 (orange), 2018–2019 (blue) and 2019–2020 (grey) and reported via ADNS by week of suspicion, 2 October 2017 – 15 August 2020 (n=521)



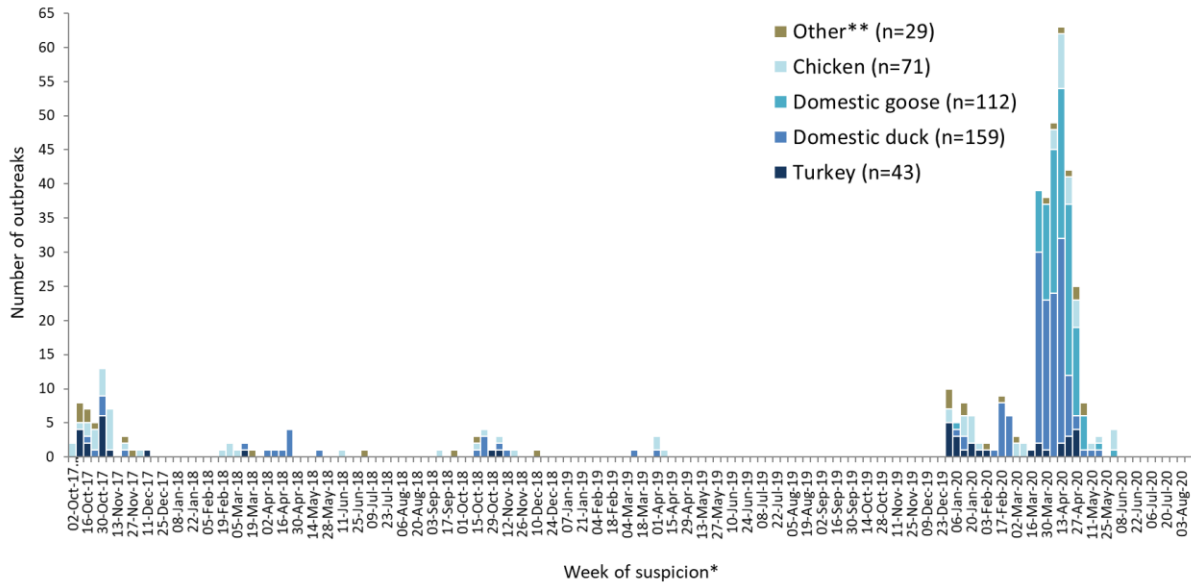
* This designation is without prejudice to positions on status and is in line with United Nations Security Council Resolution 1244 and the International Court of Justice Opinion on the Kosovo Declaration of Independence.

Figure 3: Geographical distribution, based on available geocoordinates, of HPAI outbreaks in Europe in seasons 2017–2018 (green), 2018–2019 (blue) and 2019–2020 (red) in poultry (circles), wild birds (triangles) and captive birds (stars) (2 October 2017 – 15 August 2020; n=521)



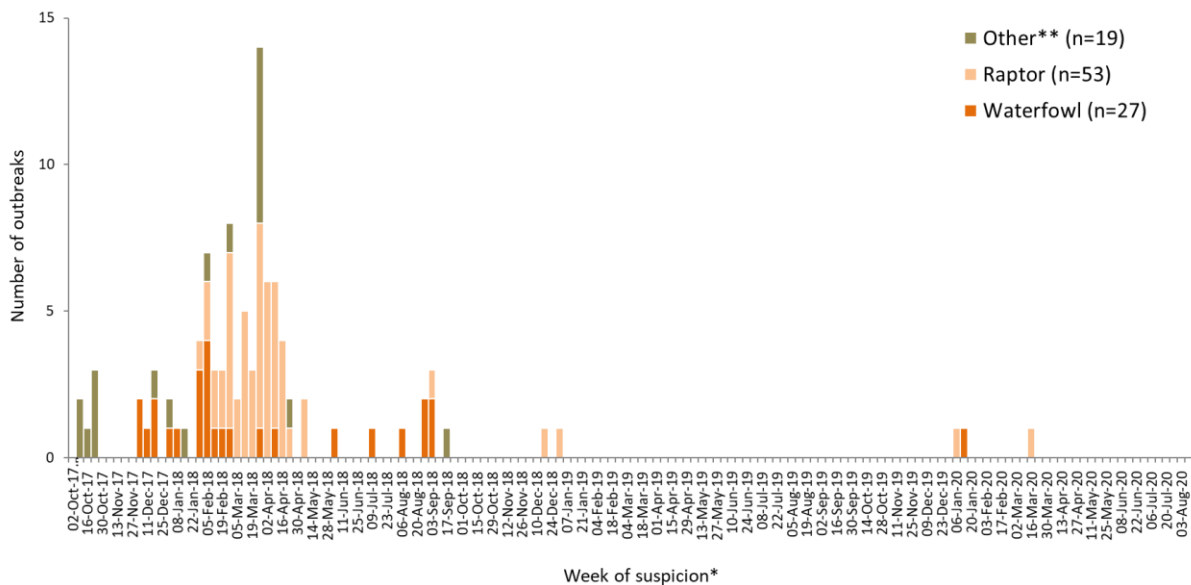
* When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.
Data source: ADNS, EFSA.

Figure 4: Distribution of total number of HPAI A(H5N6) (orange), A(H5N8) (blue), A(H5N2) (light blue) and A(H5N2) A(H5N8) (green) outbreaks in Europe by week of suspicion (dates indicate the first day of the week) in seasons 2017–2018, 2018–2019 and 2019–2020 (2 October 2017 – 15 August 2020; n=521)



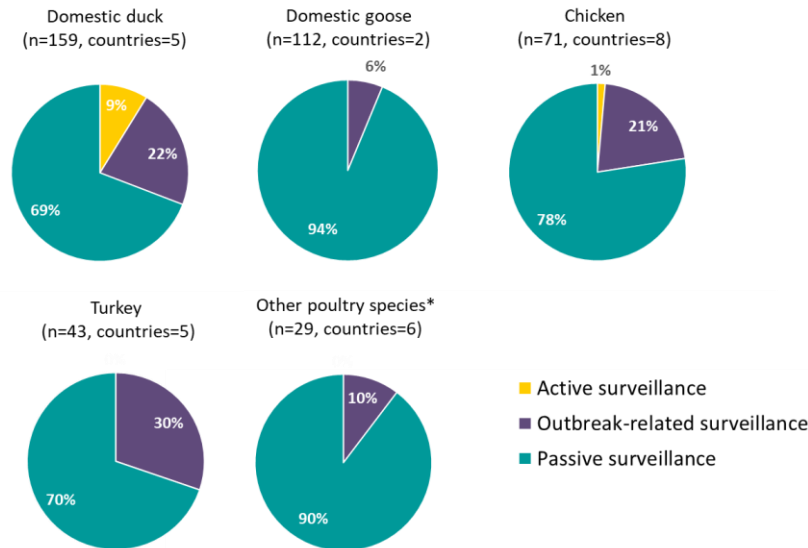
* When the date of suspicion is not available then the date of confirmation is used to assign the week of suspicion.
 ** 'Other' category contains mixed, unknown bird species, or categories different from those displayed: pheasant (*Phasianus colchicus*), pigeon (*Columba livia*), partridge (*Perdix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

Figure 5: Distribution of total number of HPAI outbreaks in Europe by week of suspicion (dates indicate the first day of the week) in seasons 2017–2018, 2018–2019 and 2019–2020 by affected poultry species (2 October 2017 – 15 August 2020; n=414)



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

Figure 6: Distribution of total number of HPAI outbreaks in Europe by week of suspicion (dates indicate the first day of the week) in seasons 2017–2018, 2018–2019 and 2019–2020 by affected wild bird category (2 October 2017 – 15 August 2020; n=99)



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

Figure 7: Frequency distribution of HPAI outbreaks in poultry in Europe, by bird species (domestic goose, domestic duck, chicken, turkey and mixed species) and sampling programme leading to the outbreak detection, in seasons 2017–2018, 2018–2019 and 2019–2020 (2 October 2017 – 15 August 2020; n=414)

4.2. HPAI and LPAI outbreaks in Europe, 16 May – 15 August 2020 (TOR 1 and TOR 2)

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

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

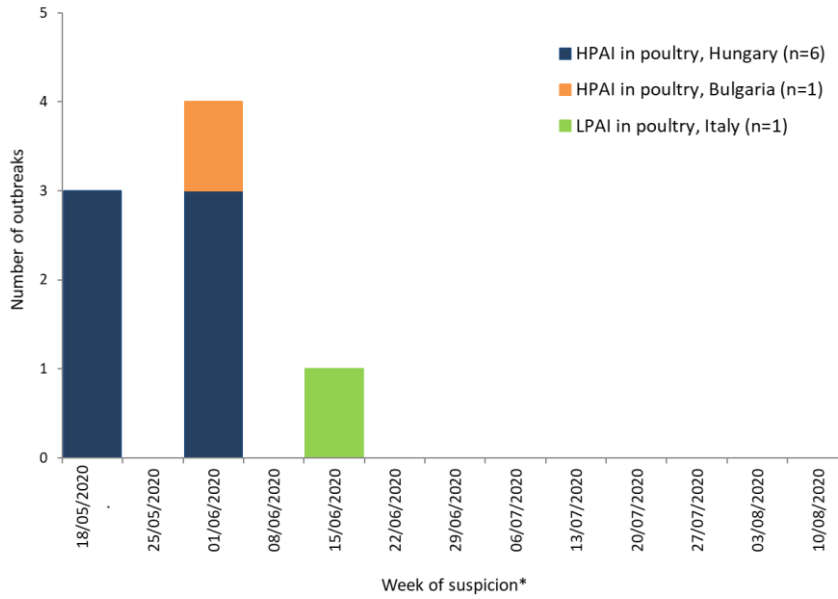
From 16 May to 15 August 2020, seven HPAI outbreaks and one LPAI outbreak were notified in poultry in Europe, and were reported via the ADNS, as presented in Table 1. The timeline, location and affected subpopulation of the avian influenza outbreaks are presented in Figures 8 and 9. The characterisation of HPAI-affected poultry establishments¹ is reported in Section 4.2.2.1, and LPAI-affected establishments in Section 4.2.2.3.

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

Country	HPAI outbreaks	LPAI outbreaks	All avian influenza outbreaks
	A(H5N8) Poultry	A(H5N3) Poultry	
Bulgaria	1		1
Hungary	6		6
Italy		1	1
Total (3 countries)	7	1	8

Data source: ADNS (23.09.20).

¹ According to Regulation (EU) 2016/429 'establishment' means any premises, structure, or, in the case of open-air farming, any environment or place, where animals or germinal products are kept, on a temporary or permanent basis, except for: (a) households where pet animals are kept; (b) veterinary practices or clinics. 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: EFSA and ADNS (23.09.20).

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



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

Figure 9: Geographical distribution, based on available geocoordinates, of avian influenza outbreaks in Europe, by virus subtype and affected subpopulation, 16 May – 15 August 2020 (n=8)

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 May to 15 August 2020, a total of seven HPAI outbreaks in poultry were notified in Europe (Table 2): one in Bulgaria and six in Hungary. All these outbreaks were reported to be the A(H5N8) subtype. The description of the bird species and the production category of these HPAI-affected establishments are shown in Figure 10. All the establishments rearing chickens were housing >10,000 birds each; all the other infected establishments were rearing 1,001–10,000 birds.

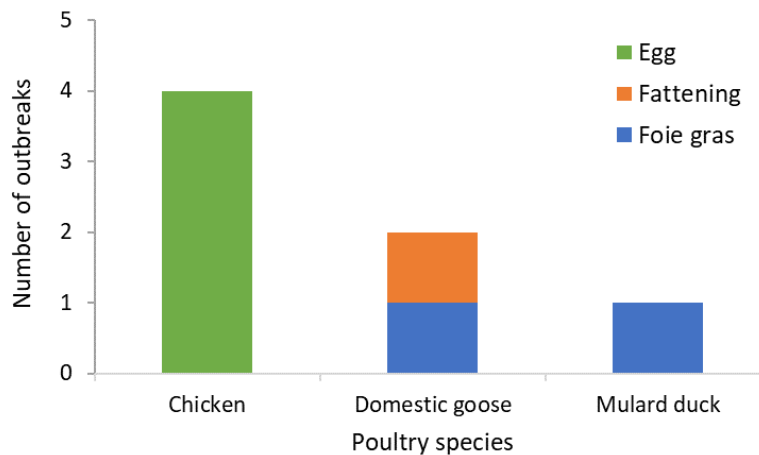


Figure 10: Number of HPAI-affected establishments by poultry species and production category in the EU, 16 May – 15 August 2020 (n=7)

A(H5N8)-affected poultry establishments in Bulgaria

On 4 June 2020, one HPAI A(H5N8) primary outbreak was detected at poultry establishment in the Plovdiv region in Bulgaria. The suspicion of the infection was raised on 3 June due to highly increased mortality (increase of 75%). Epidemiological investigations found that the main pathways for introducing the virus were likely to be breaks in biosecurity and human factors. The characteristics of the affected establishments and species reared are presented in Table 2.

HPAI A(H5N8)-affected poultry establishments in Hungary

Between 18 May and 4 June 2020, six HPAI A(H5N8) secondary outbreaks were detected at poultry establishments in the Bács-Kiskun region in Hungary. The outbreaks were reported to be secondary outbreaks with five of these secondary outbreaks related to the first secondary outbreak in this reporting period. All affected establishments were commercial ones, housing only one species of poultry each. Signs of infection were reported at all six establishments (all reported mortality, five reported other clinical signs and one reported a drop in egg production and in feed/water intake). None of them had provided outdoor access for poultry, and all establishments reported the source of infection to be indirect contact with poultry. In some cases, aerogenic spread of the virus in the direction of the prevailing winds was reported; in other cases, it was noted that ducks or geese were transported for gavage within the incubation period from establishments which later became positive. Movements of feed and other transport probably also played a role in the spread of the virus. The characteristics of the affected establishments and species reared are presented in Table 2.

Table 2: Characteristics of the HPAI A(H5N8)-positive poultry establishments by affected EU Member State, from 16 May to 15 August 2020 (n=7). Data source: ADNS and EFSA

Country	Poultry species	Production category	Surveillance stream ^(a)	Presence of signs in the outbreaks	Outdoor access	Date of suspicion	Number of susceptible animals	Number of people exposed
Bulgaria	Chicken	Egg	Passive	Yes	No	3/6/2020	252,861	28
Hungary	Chicken ^(b)	Egg	Outbreak related	Yes	No	18/5/2020	24,920	-
	Domestic duck ^{(b) (c)}	Foie gras	Outbreak related	Yes	No	20/5/2020	6,200	-
	Domestic goose ^(b)	Foie gras	Outbreak related	Yes	No	22/5/2020	3,736	-
	Domestic goose ^(b)	Fattening	Outbreak related	Yes	No	31/5/2020	6,300	-
	Chicken ^(b)	Egg	Outbreak related	Yes	No	2/6/2020	52,800	-
	Chicken ^(b)	Egg	Outbreak related	Yes	No	4/6/2020	80,000	-
Total for all countries							426,817	28

(a) 'Outbreak-related', as part of outbreak response, i.e. control zones, tracing; 'passive', notifications of disease suspicion; 'active', screening of apparently healthy populations conducted in accordance with Decision 2010/367/EU.

(b) Secondary outbreak.

(c) Mulard ducks.

Information extracted from the scientific literature

Schreuder et al. (2020) analysed data on daily mortality and clinical signs from nine egg-producing chicken and seven Pekin duck establishments infected with HPAI H5N8 (2014 and 2016) and H5N6 (2017–2018) in the Netherlands. In 12 out of 15 outbreaks for which a mortality ratio (MR) was available, MR increase preceded or coincided with the first observation of clinical signs by the farmer (MR was defined as the ratio between current daily mortality and the average weekly mortality of the previous week for that particular flock, with a threshold of 2.9). In one chicken and two Pekin duck outbreaks, clinical signs were observed before the MR increase. This case series suggests that a MR with a set threshold could be an objective parameter to detect HPAI infection on chicken and Pekin duck farms at an early stage. Observation of clinical signs may provide additional indications for farmers and veterinarians to notify a clinical suspicion of HPAI infection.

4.2.2.2. HPAI in wild birds

Pathogenicity in the affected species

No HPAI viruses were detected in wild birds in Europe within the relevant time period for this report.

Information extracted from the scientific literature

During the reporting period, no new relevant information concerning wild birds has been published on phenotypic characterisation of HPAI viruses circulating in the EU.

4.2.2.3. LPAI in domestic birds

Characterisation of the LPAI-affected poultry establishments

Between 16 May and 15 August 2020, one LPAI A(H5N3) outbreak was notified in the poultry sector in Europe in Mantua province (Lombardy region) in Italy. Information available from the ADNS (European Commission, online-a), from the OIE (OIE, online-b) and provided by Member State, characterising the LPAI outbreak, is presented in Table 3. At the time of confirmation, the affected establishment was housing 120 fattening ostriches and 12 breeders. The suspicion was raised on 15 June, following a serological positivity in five samples taken at the slaughterhouse in the context of the national surveillance plan. On 19 June 2020, the virus responsible for seroconversion in the outbreak was

characterised by the Italian Reference Centre as an A(H5N3) subtype by detection of specific antibodies against the virus. No active circulation of live virus was found through virological tests performed on swabs and faces. On 20 June, culling of birds, disposal of carcasses and cleansing and disinfection procedures were concluded.

No symptoms were observed in the animals. The establishment, which is a free-range/open air, is located in proximity to the river Po and the presence of wild ducks has been observed.

Table 3: Characteristics of the LPAI-affected poultry and captive bird establishments in Europe, 16 May – 15 August 2020 (n=1)

Country	Virus subtype	Poultry species	Surveillance stream	Presence of signs in the outbreaks	Date of suspicion	Number of susceptible birds
Italy	A(H5N3)	Ostrich	Active	No	15/6/2020	132
Total						132

Data source: ADNS, OIE, Member States.

4.2.3. Genetic characterisation of avian influenza viruses

Description of the nomenclature of the HPAI A(H5) viruses used in the document

The HA gene of clade 2.3.4.4 A(H5) viruses has rapidly evolved since the most recent official update of the nomenclature of the A/goose/Guangdong/1/1996-lineage H5Nx virus (Smith et al., 2015). This clade emerged in China in 2008 and since then it has acquired various neuraminidase subtypes, including N1, N2, N5, N6 and N8, by reassortments with other enzootic avian influenza viruses from different regions, and evolved into several subgroups. While a revised nomenclature of clade 2.3.4.4 viruses is pending, in the previous reports (EFSA et al., 2017a; EFSA et al., 2018a, 2019a; EFSA et al., 2019b; EFSA et al., 2019c; EFSA et al., 2020a, b) we used the genetic clustering described in 2018 by Lee and co-authors, who recognised four groups (a to d) within clade 2.3.4.4 (Lee et al., 2018). Recently, an update to the unified nomenclature for clade 2.3.4.4 A(H5) viruses has been proposed by WHO (WHO, 2020d) and eight genetic groups (a to h) have been recognised. In order to align the nomenclature system between international organisations this classification has been adopted for this report. Based on this proposed clustering, A(H5) viruses of clades 2.3.4.4a and d–h have mainly been circulating in poultry in Asia, while clades 2.3.4.4b and 2.3.4.4c have spread globally through wild bird migrations during 2014–2015 (2.3.4.4c) and 2016–2017 (2.3.4.4b)

Genetic characterisation of HPAI viruses of the A(H5N8) subtype circulating in Europe

The HPAI A(H5N8) virus collected in June in Bulgaria belongs to clade 2.3.4.4b and clusters with A(H5N8) viruses that have been circulating in the country since 2017. In particular, the eight gene segments are highly related to the genes of a A(H5N8) virus identified in March 2020 in layer hens in the Plovdiv region.

The HA and NA gene segments of one HPAI A(H5N8) virus collected from layer hens in Hungary in May 2020 were characterised. The virus clusters with A(H5N8) viruses of clade 2.3.4.4b which have been identified in east-central Europe since December 2019, showing the highest identity with A(H5N8) viruses detected in poultry in Hungary during the period March–May 2020.

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

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

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

(Adlhoch et al., 2019)(Adlhoch et al., 2019)(Adlhoch et al., 2019)(Adlhoch et al., 2019)(Adlhoch et al., 2019)(Adlhoch et al., 2019)(Adlhoch et al., 2019)(Adlhoch et al., 2019)(Adlhoch et al., 2019)No human infection with avian influenza viruses, as detected in wild birds and poultry in Europe, has been reported during the period covered by this report or been previously reported (EFSA et al., 2020a). 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. Prevention and control measures applied in Europe, 16 May – 15 August 2020 (TOR 3)

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

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

An overview of the HPAI outbreaks notified from other countries not reporting via ADNS but via the OIE or national authorities from 16 May to 15 August 2020 is presented in Table 4 and Figure 11. For the purposes of this report, only findings of avian influenza viruses occurring in countries that are considered to be of epidemiological interest for the EU/EEA or of public health relevance are described.

Table 4: Number of HPAI outbreaks in other countries not reporting via ADNS, by virus subtype and country, 16 May – 15 August 2020 (n=29)

Region	Country	HPAI outbreaks						
		Domestic birds					Wild birds	All HPAI
		A(H5N1)	A(H5N2)	A(H5N5)	A(H5N6)	A(H5N8)	A(H5N8)	
Africa	South Africa					1		1
Asia	Philippines				1			1
	Taiwan		1	12				13
	Vietnam	1			4			35
Europe	Russia					7	2	9
Total	(5 countries)	1	1	12	5	8	2	29

Outside the reporting period for this report and as of 22 September 2020, Russia reported to OIE the detection of HPAI A(H5N8) in 37 poultry outbreaks in Omskaya, Kurganskaya, Chelyabinskaya, Tyumenskaya and Saratovskaya Oblast (OIE, online-a); four mute swans (*Cygnus olor*) found dead in Tyumenskaya Oblast on 28 August; four anatids of unknown species in Omskaya Oblast; and one tufted duck (*Aythya fuligula*) in Kurganskaya Oblast (OIE, 2020b). Furthermore, seven HPAI A(H5) poultry outbreaks and 86 HPAI A(H5) infected corvids were found dead in Kazakhstan at the border with Russia (OIE, 2020c, a).

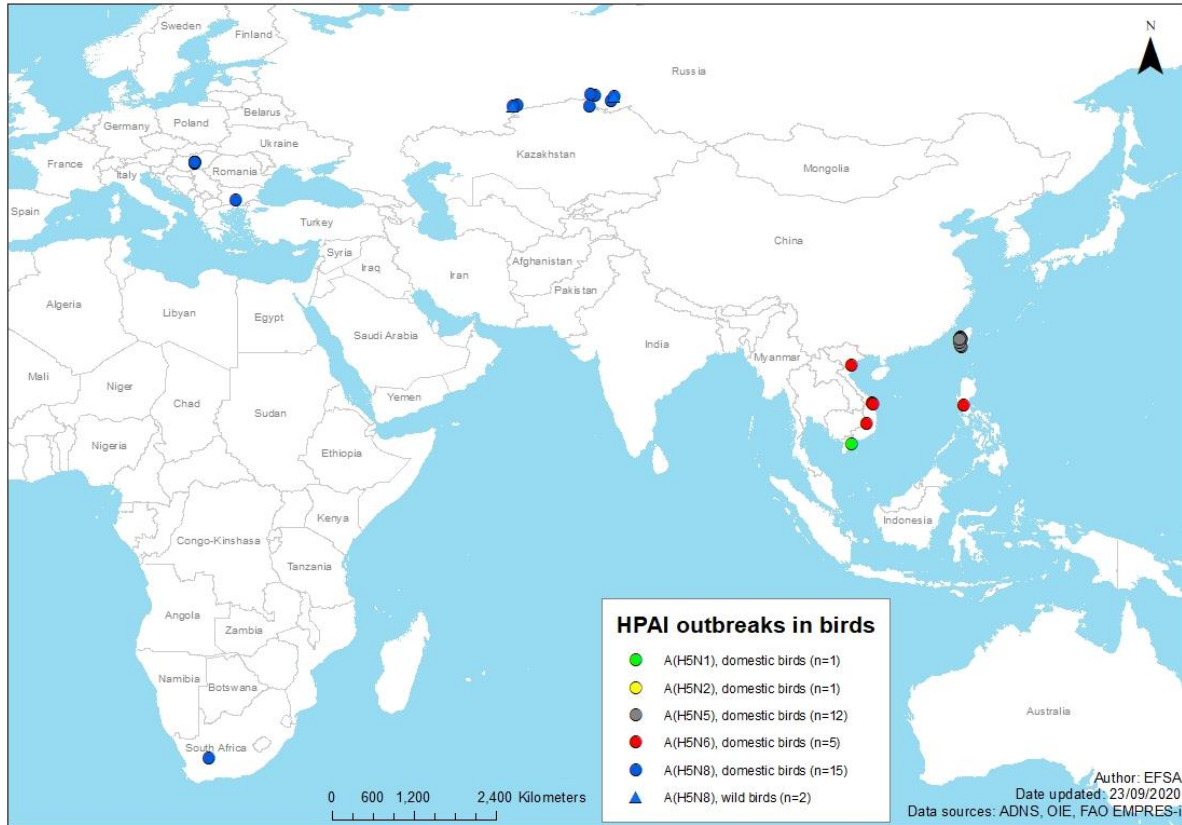


Figure 11: Geographical distribution, based on available geocoordinates, of HPAI outbreaks in Europe, Asia and Africa in domestic birds, by A(H5N1) as green, A(H5N5) as grey, A(H5N6) as red, A(H5N8) as blue, 16 May – 15 August 2020 (n=36)

4.4.1. HPAI A(H5N1)

4.4.1.1. Domestic and wild birds in previously affected regions

Detections

In the relevant time period of the report, only Vietnam notified a detection of HPAI A(H5N1), on one medium-sized poultry farm in a previously infected province on 23 July 2020. In contrast to the last report, no wild bird cases of HPAI A(H5N1) were reported in the relevant time period (Figure 12).

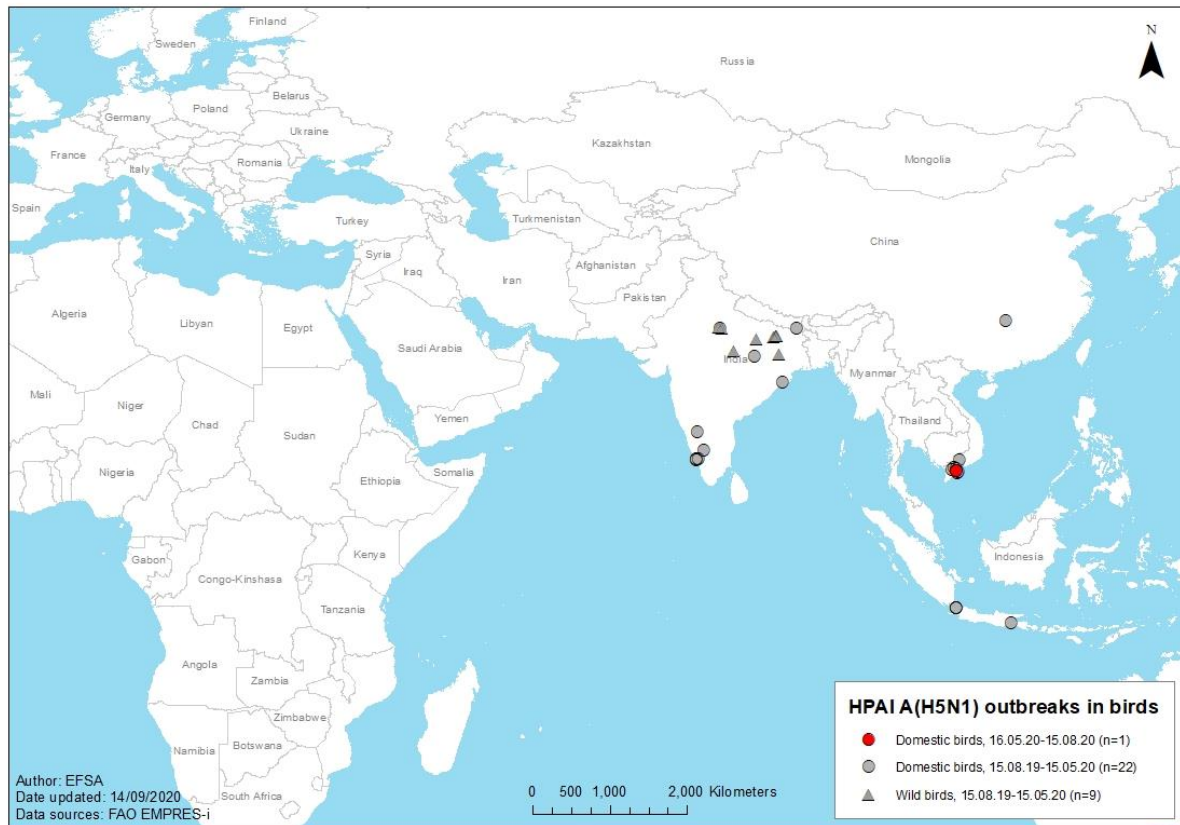


Figure 12: Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N1) outbreaks in domestic birds (circles) and wild birds (triangles) (n=32); red symbols indicate outbreaks that occurred between 16 May and 15 August 2020, grey symbols indicate outbreaks that occurred between 15 August 2019 and 15 May 2020 (FAO, online-a)

Information extracted from the scientific literature

Annand et al. (2020) described two A(H5N1) viruses isolated from infected chickens collected during an HPAI outbreak that took place in October 2018, in a backyard flock in south-eastern Laos. Their H5 sequences belonged to clade 2.3.2.1c and were related to other HPAI A(H5N1) viruses detected in Laos, Myanmar and Vietnam during the previous years.

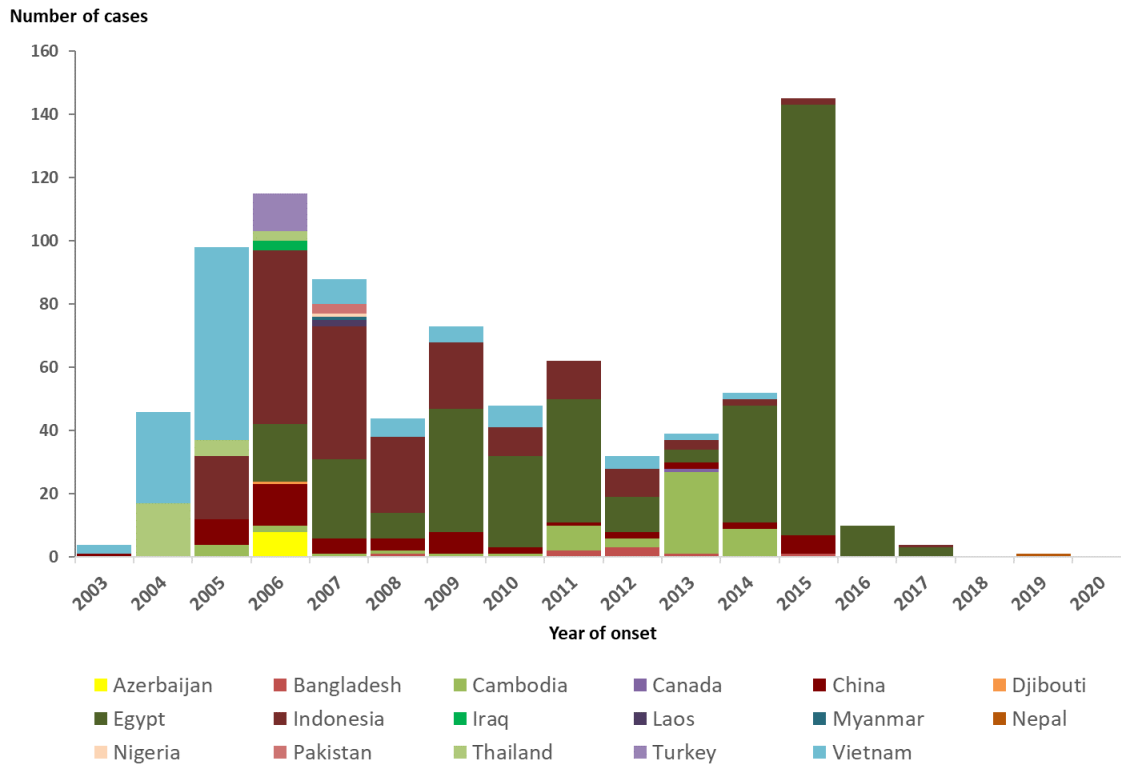
Following a surveillance programme from environment and poultry samples collected at live bird markets in Indonesia between 2014 and 2019, Dharmayanti et al. (2020a) reported detection of HPAI A(H5N1) viruses belonging to clades 2.1.3.2a and 2.3.2.1c. Between 2017 and 2019, three clade 2.3.2.1c viruses were identified (one in 2017, from duck swab samples, and two in 2019, from Muscovy duck and chicken samples) as well as one clade 2.1.2.3a A(H5N1) virus (the latter characterised in 2018, from chicken swab samples). Based on the available full genome sequences, the 2018 and 2019 viruses were reassortant viruses. All their gene segments were derived from clade 2.3.2.1c A(H5N1) viruses, except a clade 2.1.2.3a-derived H5 gene segment for A/chicken/West Java/CIA.77/2018 (H5N1) and a clade 2.3.2.1a-derived matrix gene segment for A/Muscovy duck/Central Java/BBS96/2019 (H5N1) and A/chicken/Central Java/Abr1/2019 (H5N1), with a PB2 gene segment of unresolved origin for this last virus. The major molecular markers presented for the viruses in this study did not show mammalian virulence or human adaptation signatures.

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

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

4.4.1.3. Human infections due to A(H5N1)

No new human case due to avian influenza A(H5N1) has been reported in 2020. Since 2003, and as of 15 August 2020, 861 laboratory-confirmed cases of human infection with avian influenza A(H5N1) virus, including 455 deaths, have been reported from 17 countries outside the EU/EEA (WHO, 2019c, a, 2020a) (Figure 13).



Data source: WHO (WHO, 2019c).

Figure 13: Distribution of confirmed human cases of A(H5N1) by year and country of reporting, 2003 – 15 August 2020 (n=861)

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

4.4.2.1. Domestic and wild birds

Detections

The Taiwanese lineage HPAI A(H5N2) has been in circulation in Taiwan since 2012 and caused severe outbreaks at chicken, duck, goose and turkey establishments. In contrast to the last report, only one case of HPAI A(H5N2) on a medium-sized poultry farm was reported to the OIE between 16 May and 15 August. The Taiwanese lineages of HPAI A(H5N2) (clade 2.3.4.4) differ from the Eurasian HPAI A(H5N2) lineage (Li et al., 2020); the latter belonging to clade 2.3.4.4b, which has been detected, with different genotypes, in Egypt and Russia as well as in Asian countries between 2016 and 2019 (EFSA et al., 2019a) and in Bulgaria in 2020.

Taiwan notified twelve new outbreaks of HPAI A(H5N5) on one backyard and several medium-sized and large poultry farms in western Taiwan (Figure 14). No sequence data are currently available to determine the clade and relationship of this HPAI A(H5N5) virus to other avian influenza viruses.

Information extracted from the scientific literature

Following an active surveillance programme implemented in Taiwan during the first quarter of 2019, two chicken farms were detected with A(H5) viruses from faecal swabs collected in February and March 2019. From these viruses, Li et al. (2020) characterised two distinct novel reassortant genotypes of HPAI A(H5N2) A/goose/Guangdong/1/1996-lineage viruses, one on each farm. For both genotypes, the HA and NA genes were most closely related to those of a clade 2.3.4.4c HPAI A(H5N2) virus identified in 2016 in Taiwan, and their M gene segments were related to those of earlier isolates of clade 2.3.4.4 A(H5Nx) viruses.

The genotype identified from the February 2019 case also derived its NP and NS gene segments from the previously mentioned clade 2.3.4.4c A(H5N2) detected in 2016. For this same genotype, the polymerase gene segments were derived from a Eurasian LPAI virus gene pool for PB2 and PA, and from a north American LPAI virus gene pool for PB1. Whereas, for the genotype detected in March 2019, all internal gene segments (except M) were distinct from known A(H5) virus sequences detected in Taiwan, but clustered with other Eurasian LPAI viruses.

In the same study, Li et al. (2020) also reported codetection in March 2019 of another A(H5N2) virus on the same farm as one of the above described novel reassortant HPAI A(H5N2) viruses. This virus belonged for all its gene segments to the Mexican-like LPAI A(H5N2) virus lineage, recurrently detected in Taiwan since 2003 and responsible for the emergence in 2012 of a directly related HPAI virus. The cleavage site of the H5 protein from the A(H5N2) virus identified in 2019 had an unusual dibasic amino acid sequence, but direct *in vivo* assessment of its associated pathotype was not possible. However, the closely related A(H5N2) viruses isolated in Taiwan in 2015 (which also possessed a slightly different dibasic cleavage site) had been shown to be low pathogenicity viruses by inoculation in chickens.

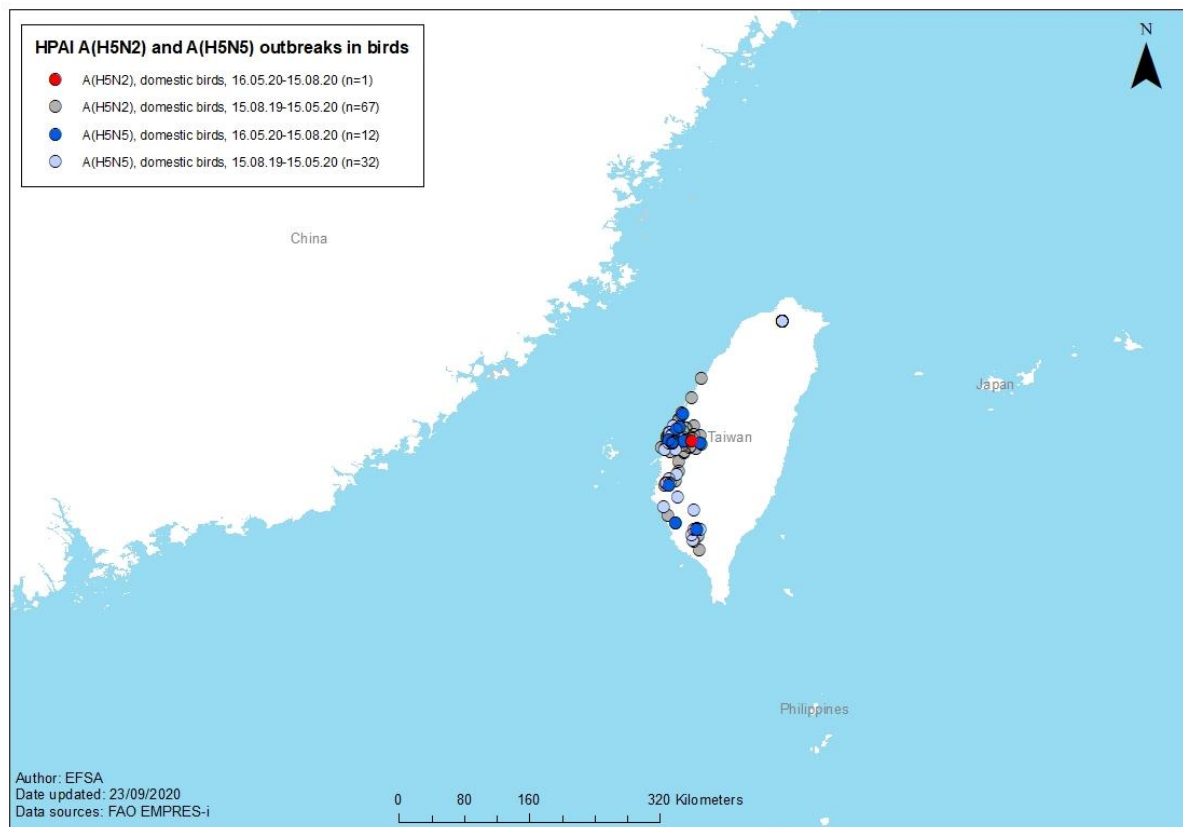


Figure 14: Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N2) and A(H5N5) outbreaks in domestic birds outside Europe (n=101); red symbols indicate HPAI A(H5N2) outbreaks that occurred between 16 May and 15 August 2020, grey symbols indicate HPAI A(H5N2) outbreaks that occurred between 15 August 2019 and 15 May 2020, dark blue symbols indicate HPAI A(H5N5) outbreaks that occurred between 16 May and 15 August 2020, light blue indicate HPAI A(H5N5) outbreaks that occurred between 15 August 2019 and 15 May 2020, (FAO, online-a)

4.4.3. HPAI A(H5N6)

4.4.3.1. Domestic and wild birds

Detections

The outbreak of the zoonotic reassortment of HPAI A(H5N6) clade 2.3.4.4a continued in Vietnam. Four new cases were detected on medium-sized poultry farms in also newly affected provinces Dak Lak and Quang Ngai in June and August 2020. The Philippines confirmed the second case of HPAI A(H5N6) in 2020 during the relevant time period for this report. The disease was detected on a large chicken farm in Central Luzon province. No wild bird cases of HPAI A(H5N6) were reported in the relevant time period (Figure 15).

The complete genome of 13 A(H5N6) viruses collected in January 2020 from whooper swans (*Cygnus cygnus*) and mute swans (*Cygnus olor*) from several northwestern locations near the Kazakhstan border in Xinjiang Uygur Autonomous Region in the Saratov region, were recently released by GISAID. The HA gene of these viruses clusters together within the zoonotic clade 2.3.4.4h. They show the highest similarity (98.8–99%) to A(H5N6) viruses collected from environmental samples and from minks in China in 2017–2018 and possess a nucleotide identity of 97.4–98.1% with A(H5N6), which was responsible for human cases reported in China in 2018. Analyses of the remaining gene segments confirm this clustering.

Unlike the Chinese strains associated with human infections, the 2020 viruses do not contain mutation E627K in the PB2, which is associated with the adaptation of avian influenza viruses to mammalian species (Subbarao et al., 1993).

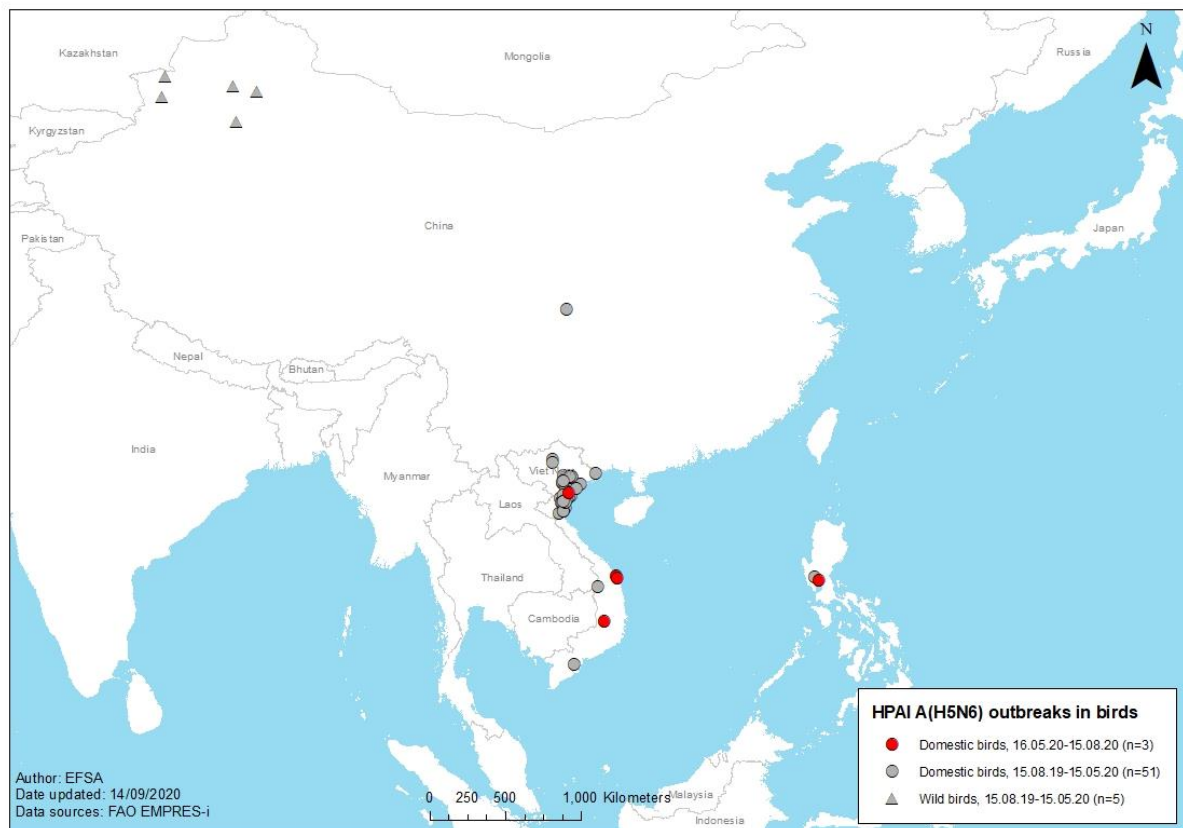


Figure 15: Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N6) outbreaks in domestic birds (circles) and wild birds (triangles) (n=59); red symbols indicate outbreaks that occurred from 16 May to 15 August 2020, grey symbols indicate outbreaks that occurred from 15 August 2019 to 15 May 2020, (FAO, online-a)

Information extracted from the scientific literature

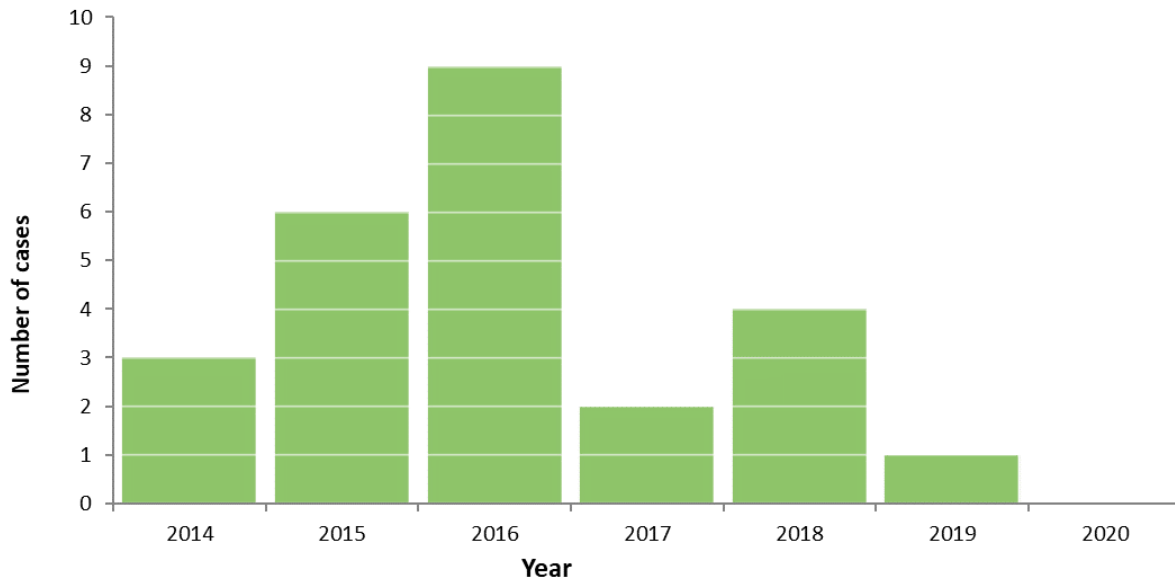
During the reporting period, no new relevant information concerning domestic and wild birds has been published on the phenotypic and genetic characterisation of HPAI A(H5N6) viruses circulating in countries outside the EU/EEA.

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

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

4.4.3.3. Human infections due to A(H5N6)

No new human case due to avian influenza A(H5N6) has been notified since the last EFSA report (EFSA et al., 2020a; WHO, 2020f, c). Since 2014, and as of 15 August 2020, 25 laboratory-confirmed cases of human infection with avian influenza A(H5N6) viruses of clade 2.3.4.4 circulating in South-East Asia have been reported globally (Figure 16). WHO lists 24 human cases of avian influenza A(H5N6), including 15 with fatal outcomes (WHO, 2020b). 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 (see Appendix B.2).

Figure 16: Number of human cases due to A(H5N6), clade 2.3.4.4, infection by year of onset, China 2014–2020 (n=25)

4.4.4. HPAI A(H5N8)

4.4.4.1. Domestic and wild birds

Detections

The outbreak of clade 2.3.4.4b, HPAI A(H5N8) on ostrich farms in the Northern Cape province of South Africa continued in the relevant time period of this report. One medium-sized ostrich farm was affected in June 2020, but no wild bird cases were reported from this region. Between 16 May and 15 August 2020, the national authorities in Russia notified the detection of HPAI A(H5N8) in chickens, ducks and geese, one in a backyard holding in the village of Maloe Shumakovo and one in the village of Peschanoe, Chelyabinskaya Oblast during the same time period as in 2018. Furthermore, Russia reported to the

OIE that HPAI A(H5N8) was also confirmed in a wild duck carcass, which was found on the lake near the village of Peschanoe just before the outbreak started at the end of July (Figure 17). HPAI A(H5N8) was also detected in a wild duck of unknown species on 14 August in Omskaya Oblast (OIE, online-a). Outside the reporting period for this report, the national authorities of Russia notified to OIE, 37 HPAI A(H5N8) outbreaks in backyard, medium-sized and large poultry farms in Omskaya, Kurganskaya, Chelyabinskaya, Tyumenskaya and Saratovskaya Oblast, with the latter area being on western border with Kazakhstan. Furthermore, Russia reported the detection of HPAI A(H5N8) in four mute swans (*Cygnus olor*) found dead in Tyumenskaya Oblast on 28 August 2020, in four anatids of unknown species in Omskaya Oblast and in one tufted duck (*Aythya fuligula*) in Kurganskaya Oblast found dead between August and September 2020. In Kazakhstan, near the border with Russia, HPAI A(H5) virus was found in seven poultry outbreaks and in 86 corvids that were found dead.

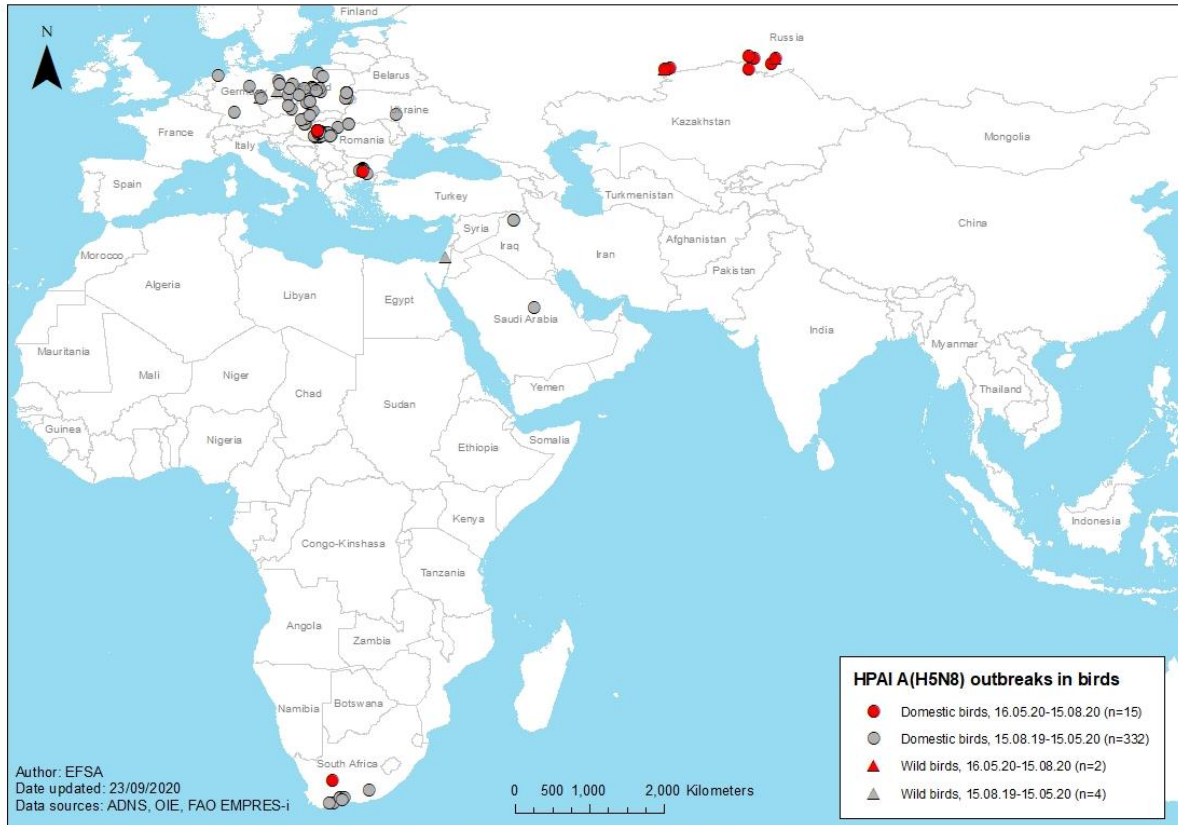


Figure 17: Geographical distribution, based on available geocoordinates, of confirmed HPAI A(H5N8) outbreaks in domestic birds (circles) and wild birds (triangles) (n=353); red symbols indicate outbreaks that occurred between 16 May and 15 August 2020, grey symbols indicate outbreaks that occurred from 15 August 2019 to 15 May 2020, (FAO, online-a)

Information extracted from the scientific literature

Hassan et al. (2020) reported investigations performed on oropharyngeal and cloacal swab samples collected in Egypt between April 2018 and April 2019, from 37 poultry flocks (duck, broiler chicken and turkey) with mild to severe signs of respiratory disease, observed mortality rates of at least 50% and for the ducks, obvious central nervous symptoms. Twenty-one flocks (16 duck, 4 chicken and 1 turkey flock) were positive for HPAI A(H5N8) viruses and 2 of these (1 duck and 1 chicken flock) were also positive for A(H9N2) viruses. Ten samples (from all three species of poultry) were selected for full H5 gene sequencing: all belonged to clade 2.3.4.4b and the major amino acid sequence markers of the receptor-binding site indicated an α -2,3 sialic acid avian-type receptor affinity. However, several mutations were also present that could increase binding to human-type α -2,6 receptors, while reducing binding to α -2,3 sialic acid receptors, and that affected the same antigenic sites as previously described Egyptian clade 2.3.4.4b A(H5N8) strains from 2018.

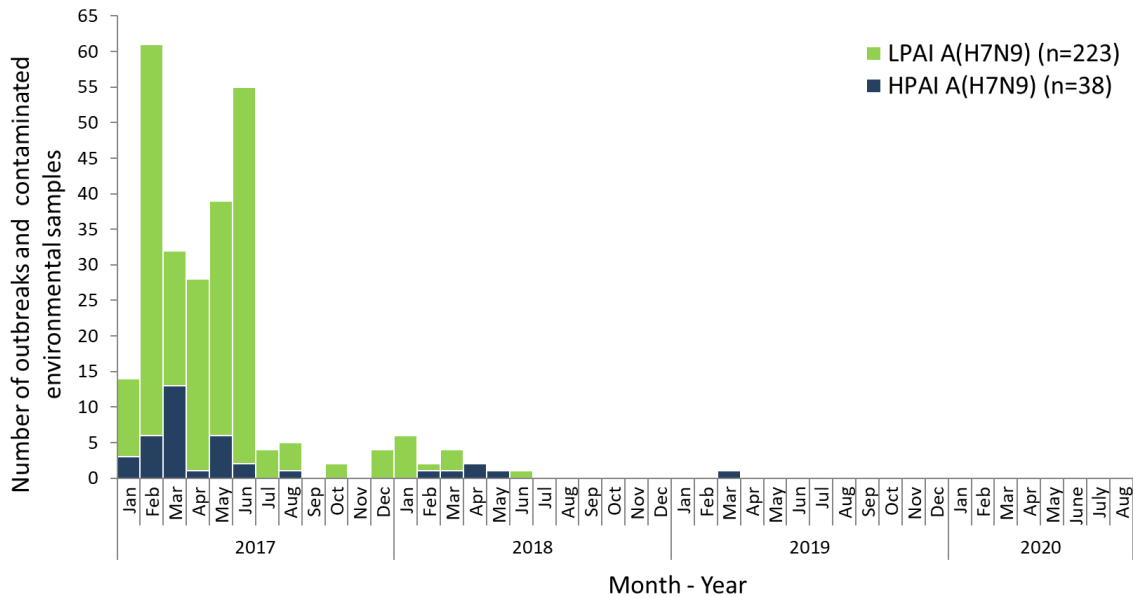
Of the strains described above, three HPAI A(H5N8) viruses characterised from chicken and turkey flocks were sequenced for their full genome. All three strains belonged to the same genotype, which has been detected in poultry only and has become dominant in Egypt since 2018. Several amino acid mutations were present in the M2 and N8 proteins that are known to increase resistance to amantadine and neuraminidase inhibitors, respectively. Other mutations in the NS-1 and PA proteins were also described, associated with increased virulence in A(H5N1) viruses.

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 18). The nationwide A(H7N9) vaccination campaigns for poultry, with the exception of poultry in AI-free zones and export farms, started extensively in September 2017 (FAO, online-b).



Data source: FAO EMPRES-i (14.09.2020)

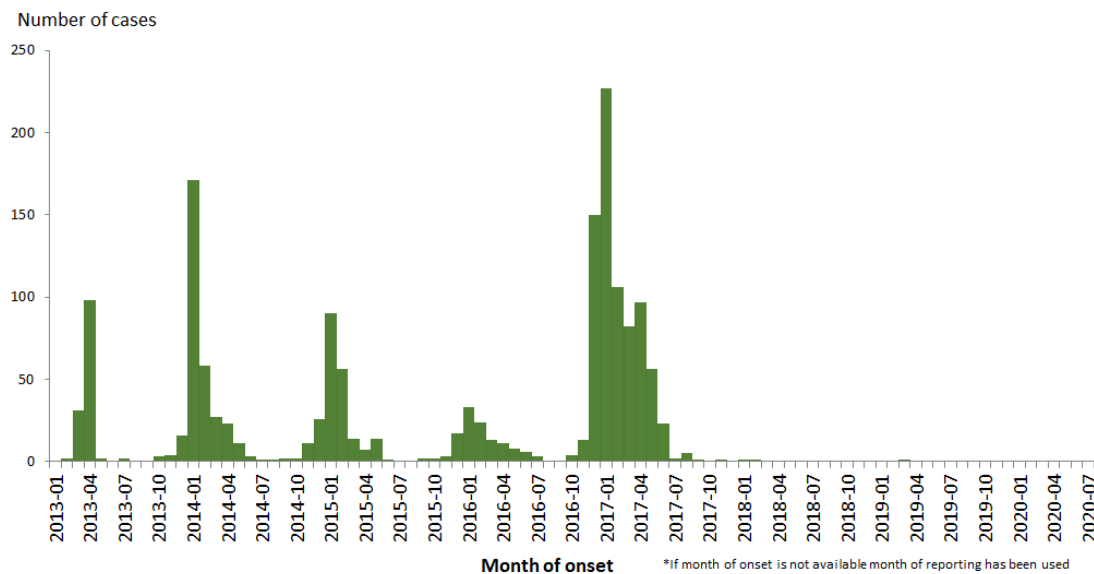
Figure 18: Distribution of confirmed LPAI and HPAI A(H7N9) outbreaks among birds and environmental samples in China, by month, 1 January 2017 – 15 August 2020 (n=261)

Information extracted from the scientific literature

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

4.4.5.2. Human infections due to A(H7N9)

No human cases due to avian influenza A(H7N9) have ever been reported from Europe and no human case has been reported globally since 2019 (WHO, 2020f, c). Since February 2013, a total of 1,568 human cases have been reported from outside of Europe (Figure 19), including at least 615 deaths (39%) (WHO, 2019b, a). Of all human cases, 32, 13 of them fatal, have been infected with HPAI virus A(H7N9) according to the Chinese National Influenza Center (Chinese National Influenza Center et al., 2018).



Source: ECDC line list (see Appendix B.2).

Figure 19: Number of human cases due to A(H7N9), infection by month and year of onset, 2013 – 2020 (n=1,568)

4.4.6. LPAI A(H9N2)

4.4.6.1. Domestic and wild birds

Detection

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

Information extracted from the scientific literature

Dharmayanti et al. (2020b) described two A(H9N2) viruses isolated in Indonesia in 2018: one of these from a chicken flock with respiratory disease, decrease in egg production and an observed mortality rate of more than 10%; the other strain was obtained from a live bird market surveillance programme of chickens. Both viruses were reassortants deriving their PB2 gene segment from clade 2.3.2.1c HPAI A(H5N1) viruses and the rest of their segments from A(H9N2) strains circulating in Indonesia and Vietnam (H9 gene belonging to the Y280/G9 lineage).

Pathogenicity of the A(H9N2) strain isolated from the 2018 clinical case was assessed by intranasal instillation of a 10^6 EID₅₀ dose to 10 23-week-old specific pathogen-free chickens. Clinical signs in all inoculated chickens (conjunctivitis, decreased activity and decreased egg production, down to 23% at two weeks after inoculation) began at 4 days post-infection and one chicken out of 10 died at 6 days post-infection. Gross and microscopic pathology for the dead bird included congestion and haemorrhages of the lungs and ovarian follicles with oedema and mononuclear cell infiltration, hypertrophy of the liver with necrosis and mononuclear cell infiltration, and spleen atrophy with necrosis and lymphocyte infiltration.

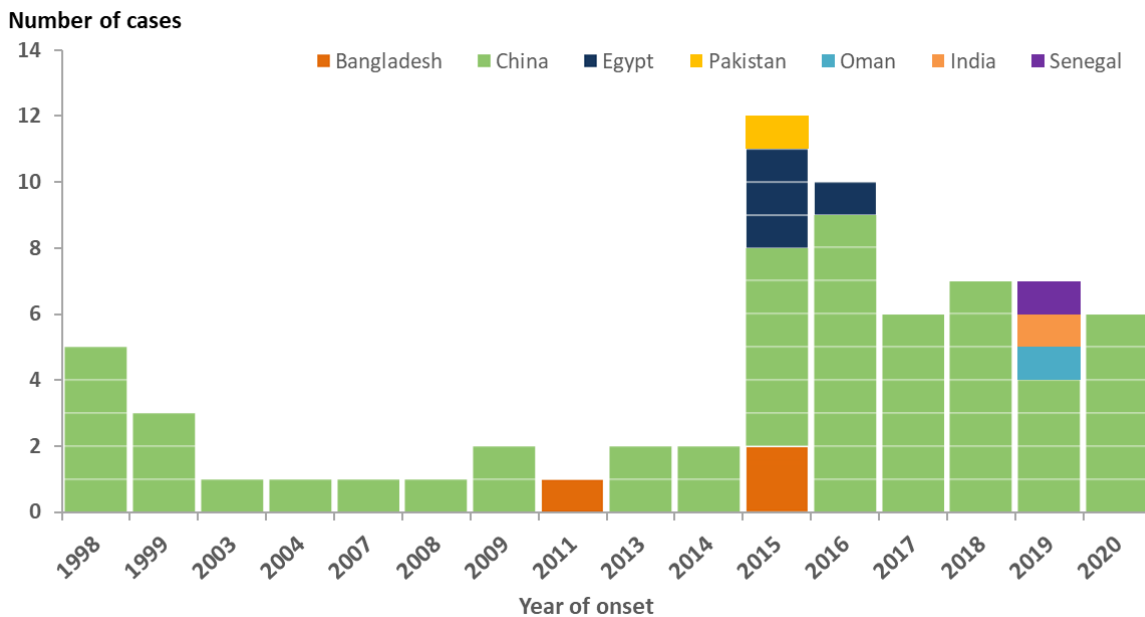
Belser et al. (2020) reported the detection of 163 A(H9N2) positive oropharyngeal swabs and environmental (feces and water) samples collected between September 2018 and September 2019 in live poultry markets in Vietnam. 55 complete genome sequences were obtained: all clustered with Y280/G9 lineage A(H9N2) viruses and were grouped in two large sublineages named A and B in this study, and respectively related to candidate vaccine viruses A/chicken/Hong Kong/G9/1997 and A/Hong Kong/308/2014 or A/Anhui-Lujiang/39/2018.

From the above described 2018-2019 viruses, four A(H9N2) isolates (two belonging to each A and B Y280/G9 sublineage) were selected for further phenotypic testing. All viruses had identical amino acid residues in their H9 proteins at major positions associated with receptor specificity and indicated potential for a dual-receptor specificity. However, the A(H9N2) viruses belonging to sublineage A had a T180A substitution in H9 compared to sublineage B: both A and B sublineage A(H9N2) viruses bound to α -2,6 resialylated turkey red blood cells (RBC), whereas only B sublineage viruses bound to α -2,3 resialylated turkey RBC. In a glycan microarray binding assay, the same four viruses only bound to a limited number of α -2,3 sialosides and to none of the other glycans including those with α -2,6 links.

All four viruses had a pH threshold for fusion ability equal or lower than 5.5, characteristic of the acid stability for human seasonal influenza viruses. All four viruses also grew to similar mean peak titers (within a 1 log₁₀ variation) in human bronchial epithelial Calu-3 cell line at both 33°C and 37°C: however, growth kinetics were reduced and delayed by at least 24 hours, at 33°C compared to 37°C (as typically observed for avian adapted AI viruses). Following inoculation of one A(H9N2) virus from each Y280/G9 sublineage in 6-week-old female BALB/c mice (intranasal inoculation of a 10⁶ EID₅₀ dose), there was no weight loss recorded and virus replication was detected only for sublineage B, in nose and lung tissue on day 3 after inoculation (no virus replication was detected on day 6).

4.4.6.2. Human infections due to A(H9N2)

Since the last EFSA report, one human case infection in a four year old girl has been reported from China (CHP, 2020). Since 1998, and as of 15 August 2020, 67 laboratory-confirmed cases of human infection with avian influenza A(H9N2) virus, including one death, have been reported globally. Cases were reported from China (56), Egypt (4), Bangladesh (3), India (1), Oman (1), Pakistan (1) and Senegal (1) (ECDC line list; see Appendix B.2) (Figure 20). Exposure to live or slaughtered poultry or contaminated environment has been reported. The age group most affected by A(H9N2) infections in humans is children under 10 years of age (Figure 21).



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

Figure 20: Distribution of confirmed human cases of A(H9N2) by reporting country, 1998 – 15 August 2020 (n=67)

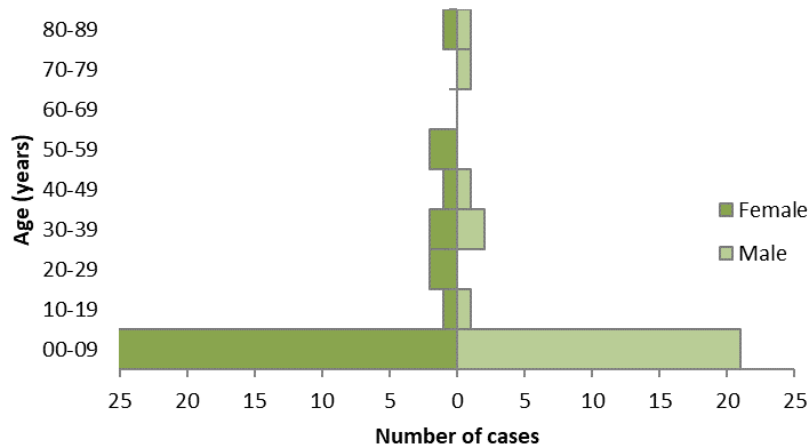


Figure 21: Distribution of confirmed human cases of A(H9N2) by age group, 1998 – 15 August 2020 (n=67)

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

Possible pathways by which avian influenza 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 low number of avian influenza outbreaks reported in the last report (EFSA et al., 2020b) decreased further from 16 May to 15 August 2020, the time period for this report. Outbreaks in domestic birds were reported from countries in Europe (Russia), Asia (Philippines, Taiwan and Vietnam) and southern Africa (South Africa), but no further cases were notified from the Middle East. The reason might be the decreasing environmental stability of avian influenza virus due to the higher temperatures and increased ultraviolet radiation in recent months. Between 16 May and 15 August 2020, the outbreaks of HPAI A(H5N1), clade 2.3.2.1c and of the novel zoonotic reassortant HPAI A(H5N6) belonging to clade 2.3.4.4a continued in Vietnam. The latter clade was also detected in a single case in the Philippines. Taiwan notified an outbreaks of HPAI A(H5N2) and twelve further outbreaks of the Taiwanese lineage of HPAI A(H5N5), clade 2.3.4.4, and South Africa reported an outbreak of HPAI A(H5N8) on an ostrich farm in a previously affected area. Furthermore, HPAI A(H5N8) was detected again in backyard poultry, six wild waterbirds, one tufted duck (*Aythya fuligula*) and four mute swans (*Cygnus olor*) in Russia, during the same time period as in 2018 (EFSA et al., 2018b). The circulation of HPAI virus was assured by the notification of further HPAI A(H5N8) and A(H5) outbreaks in poultry and in wild waterbirds in Russia, near the eastern and western border with Kazakhstan, and in north Kazakhstan outside the reporting period. The presence of HPAI virus in western Russia and northern Kazakhstan spatially associated with autumn migration routes of wild water birds and the previous detection in mute swans in northern China (EFSA et al., 2020a), also linked to key migration areas, is of concern for the possible spread of the virus via wild birds migrating to the EU (EFSA AHAW Panel et al., 2017). Autumn migration from breeding sites to wintering sites will start soon depending on the weather conditions, and sudden and persistent drop of the temperatures in central Russia and Kazakhstan may favour a westward/southward spread of the virus. Several studies demonstrated that cold weather conditions might have triggered the rapid westward expansion of the HPAI A(H5) virus by infected migratory birds during the 2005-2006 and 2016-17 epidemic waves (Ottaviani et al., 2010; Fusaro et al., 2017; Napp et al., 2018).

Furthermore, the low temperatures of autumn and winter may facilitate the environmental survival of avian influenza 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. There is considerable uncertainty about the real geographical distribution of these viruses and constant monitoring is warranted. The scarce information on the wild birds species found dead in Russia makes difficult to identify the most probable migratory flyways that might lead to

the introduction of the virus in the EU and therefore to identify the area in the EU that are at higher risk of virus introduction. Nonetheless, during the 2005-2006 and 2016-2017 epidemic waves, HPAI virus detection in the same area of Russia between July and September (OIE, 2005; Lipatov et al., 2007; FAO, 2016) lead to the involvement of northern and eastern Europe as first places of virus introduction (Cattoli et al., 2009; EFSA et al., 2017b), and they will likely be the first areas where HPAI viruses might be detected in this autumn-winter season.

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

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

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

4.6.2. Candidate vaccine viruses

Candidate vaccine viruses developed, under development or proposed are listed in a report from WHO (WHO, 2020d).

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. Transmission to humans of avian influenza viruses, detected in wild birds or poultry in Europe, has not been observed over the last few years. However, zoonotic transmission of avian influenza viruses cannot be fully excluded in general when the viruses are present in birds. The use of personal protective measures for people exposed to avian influenza viruses will minimise any residual risk. Overall, avian influenza 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 avian influenza cases from countries where the viruses are detected in poultry or wild birds is very low. Currently, only a few sporadic outbreaks in birds and poultry are reported worldwide. Sporadic human cases infected with A(H9N2) LPAI or A(H5N6) highly pathogenic viruses as reported in 2020 underline the risk of transmission whenever people are exposed to infected birds. Therefore, surveillance of avian influenza viruses in wild birds and poultry in the EU/EEA is important in order to detect newly introduced and circulating viruses and reduce the possible risk of exposure of humans to infected birds.

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Abbreviations

ADNS	Animal Disease Notification System
AI	Avian influenza
CVO	Chief Veterinary Officer
ECDC	European Centre for Disease Prevention and Control
EFSA	European Food Safety Authority
EEA	European Economic Area
EU	European Union
EURL	European Union Reference Laboratory
FAO	Food and Agriculture Organization
HPAI	Highly pathogenic avian influenza
LPAI	Low pathogenic avian influenza
MR	Mortality ratio
OIE	World Organisation for Animal Health
SCOPAFF	Standing Committee on plants, animals, food and feed
TOR	Terms of reference
WHO	World Health Organization

Appendix A – Terms of reference

A.1. Background and terms of reference as provided by the requestor

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

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

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

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

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

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

There is knowledge, legislation², 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. 178/2002³, EFSA should provide the technical and scientific assistance to the Commission based on the following Terms of Reference (TOR):

² Council Directive 2005/94/EC of 20 December 2005 on Community measures for the control of avian influenza and repealing Directive 92/40/EEC. OJ L 10, 14.1.2006, p. 16.

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

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

A.2. Interpretation of the terms of reference

In reply to TOR 1 and TOR 2, this scientific report gives an overview of the HPAI and LPAI outbreaks in poultry, captive and wild birds detected in Europe between 16 May and 15 August 2020 and reported by Member States and neighbouring countries via ADNS. Member States, where avian influenza (AI) outbreaks occurred in poultry, submitted additional epidemiological data to EFSA, which have been used to analyse the characteristics of the affected poultry establishments.

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

If HPAI outbreaks in poultry are detected in the EU, a description of the applied prevention and control measures (TOR 3) is given in the case report provided by representatives from the affected Member States and attached as an annex. The main topics covered are increasing awareness, release and repeal of housing orders, strengthening biosecurity, preventive culling, implementation of a regional standstill, bans on hunting and derogations from restriction zone implementation after a risk assessment.

Monitoring of the AI situation in other countries (TOR 4) is based on data submitted via the OIE or reported to the FAO. The description focuses only on findings of AI viruses occurring in countries that are considered to be of epidemiological interest for the EU/EEA or of public health relevance, specifically on HPAI A(H5N1), HPAI A(H5N2), HPAI A(H5N5), HPAI A(H5N6), HPAI A(H5N8), HPAI/LPAI A(H7N9) and LPAI A(H9N2). The background and epidemiology, detections, phenotypic and genetic characterisations are described based on information from confirmed human, poultry and wild bird cases that occurred between 16 May and 15 August 2020 and on information gathered by performing a literature search on papers published in PubMed from 16 May to 15 August 2020. Possible actions for preparedness in the EU are discussed.

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

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

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

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

B.1.1.1. Literature review on phenotypic characterisation of HPAI viruses circulating in the EU

Information on the phenotypic characterisation of AI viruses circulating in the EU was extracted from the scientific literature by performing a literature review.

Review question Update on the phenotypic characterisation of HPAI viruses circulating in the EU in domestic and wild birds within the last two years.

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

Relevance criteria Scientific articles added to the database from 16 May to 15 August 2020 and reporting information on the presence or absence of clinical signs or pathological changes or mortality due to HPAI infection with viruses circulating within the last two years in the EU in domestic or wild birds.

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

Results The search retrieved 138 papers. The articles were subsequently screened against the relevance and eligibility criteria. One of the screened papers was in the end taken into consideration in the description of the phenotypic characterisation of HPAI viruses circulating in the EU in domestic and wild birds in the reporting period.

The search protocol and the results can be consulted at <https://doi.org/10.5281/zenodo.4054976>.

B.1.2. Overview of avian influenza outbreaks in 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 and Europe on the basis of the observation dates. Data were extracted on 23 September 2020. Also, OIE WHAIS (OIE, online-b) was consulted on 23 September to complement the information reported by FAO. With the purpose of avoiding over-complication of the maps, captive birds and environmental samples have been mapped as domestic birds. Although some of these kept animals may be wild species, in most of the cases captive birds, or, for environmental samples, the birds from which

samples have been taken (mainly at live market-places) will not move around and not spread the infection by migrating and for this reason have been considered as domestic birds in the maps provided in this report. Only when there was a strong discrepancy between the locality, the administrative regions and geocoordinates, and the outbreaks were not officially reported to the OIE, the outbreaks were 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 May and 15 August 2020 were searched; the search was run on 17 August 2020.

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

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

Results The search retrieved 121 papers. The articles were subsequently screened against the relevance and eligibility criteria. Seven papers were in the end taken into consideration in the description of phenotypic and genotypic characterisation of HPAI viruses circulating on other continents and in other regions (Africa, Asia, the Middle East) in domestic or wild birds or mammals (excluding humans) in the reporting period.

The search protocol and the results can be consulted at <https://doi.org/10.5281/zenodo.4054976>.

B.2. Data on humans

The numbers of human cases due to infection with AI viruses have been collected by ECDC. Multiple sources are scanned regularly as part of epidemic intelligence activities at ECDC to collect information about laboratory-confirmed human cases. Data were extracted and line lists developed to collect case-based information on virus type, date of disease onset, country of reporting, country of exposure, sex, age, exposure, clinical information (hospitalisation, severity) and outcome. All cases included in the line list and mentioned in the document have been laboratory-confirmed. Data are continuously checked for double entries and validity. The data on human cases cover the full period of time since the first human case was reported. Therefore, data on human cases refer to different time periods and are included irrespective of whether there have been any new human cases during the reporting period.

Annex A – Applied prevention and control measures on avian influenza

Scope

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

Timing of the applied prevention and control measures

Tables A.1–A.2 provide timelines for the main events that triggered actions in relation to the selected prevention and control measures in Bulgaria and Hungary. More information on the actions taken is provided in the sections below the tables.

A.1 Bulgaria

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Table A.1: Overview of main actions

Date	Event that triggered action	Type of action taken	Target audience
Second half of February 2020	Screening in the duck farms located in the risk areas	The one-off sampling on waterfowl holdings was decided as a screening for detection/or exclusion of presence of AI virus in the farms. The regions were defined considering the following factors: Distribution of the waterfowl holdings in the country Technology cycle and technology links between waterfowl holdings in the country (hatcheries, holdings, slaughterhouses) No positive results of presence of AI virus were detected. The surveillance supplements the surveillance in the restriction zones around the outbreaks.	Official veterinarians, poultry farmers
02.03.2020	Enlarged restriction zone	Having confirmed three outbreaks (ADNS 2020/3-5) within the active surveillance in the surveillance zone of ADNS 2020/1, the surveillance zone around outbreaks ADNS 2020/3-5 was enlarged covering more than 85% of the duck population in the region concerned. The measures implemented in the zone were as those related to surveillance zone (Art 30 , Dir 2005/94)	Official and private veterinarians, poultry farmers
Last week of March, 2020		One-off serology sampling in backyard poultry holdings, with samples taken in high-risk areas and in 10 km zones around the outbreaks. The village was defined as one epidemiological unit, at least 60 blood samples per village were taken (it was organized as a representative sampling covering all poultry spp. located in the village). Sampling was carried out by the official or private veterinarians under official control. All results were negative	Official veterinarians, poultry farmers
05.05-13.05.2020	Reorganization of the duck sector and implementation of sanitary period at least 21 days; (please refer to Report XI)	Official inspections in the duck farms; State of play of the compliance with biosecurity and implementation of the sanitary periods in the duck farms	Official veterinarians, poultry farmers
04.06.2020	Confirmation of HPAI H5N8 outbreak	Measures according to the Directive 2005/94/EC	Official veterinarians,

			private veterinarians poultry farmers
12.06.2020	Confirmation of HPAI H5N8 outbreak on 04.06.2020	A contact laying hens farm was located within the same enclosure with the outbreak confirmed on 04.06.2020 (ADNS 2020/9) and owned by the same company. HPAI H5N8 was confirmed in these holdings in April 2019 (ADNS 4-5/2019). The infection was spread from the first affected farm to the second contact farm. Having considered the findings of the epidemiological investigation and based on the scenario in 2019, the CA decided a preventive culling to be implemented in the second contact farm. The findings of the epidemiological investigation suggest crossing of many epidemiological ways that could transmit/spreads the infection (inside transport, stuff/personnel, services). As a result, the CA decided the flocks in the contact holding to be culled	Official veterinarians, private veterinarians poultry farmer
17.06-30.07.2020	Reorganization of the duck sector and implementation of sanitary period at least 21 days; (please refer to Report XI)	Official inspections in the duck farms after the sanitary periods and permission for restocking. The poultry farmers are required to draw up an individual plan for biosecurity and contingency plan for emergency disease (measures laid down into the national legislation)	Official veterinarians, poultry farmers

Increasing awareness of the stakeholders and the general public

1. Regular meetings with representatives of the poultry associations; a number of the measures such as increased control, surveillance strategy, reorganization of the duck sector, sanitary periods, were enforced in close cooperation and contribution with the poultry industry sector.
2. Close cooperation with the public health authority.
3. Publishing information related to the epidemiological situation and prevention and control measures taken:
<http://www.babh.government.bg/bg/Page/influentza/index/influentza/%D0%98%D0%BD%D1%84%D0%BB%D1%83%D0%B5%D0%BD%D1%86%D0%B0%20%EF%BF%BD>

Housing order

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

Strengthening biosecurity measures (other than housing order)

Measures as described in the previous scientific report.

Preventive culling

Please refer to the table A.1.

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

Not applied.

Derogations on restriction zone implementation after risk assessment

In accordance with Directive 2005/94.

Hunting

Not forbidden.

A.2 Hungary

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National Food Chain Safety Office

Table A.2: Overview of main actions

Date	Event that triggered action	Type of action taken	Target audience (if applicable)
25/03/2020	First poultry outbreak in Bács-Kiskun County in 2020	Increasing awareness, release housing order, preventive culling, regional stand still, derogations on restriction zone implementation after risk assessment	-
20/05/2020	First secondary poultry outbreak in Bács-Kiskun county in this period		-

Increasing awareness of the stakeholders and the general public

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

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

Housing order

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

On 15 July 2020 the 3/2020 CVO Decision entered into force which withdrew the 1/2020 CVO Decision, thereby lifting the compulsory closed keeping of poultry.

https://portal.nebih.gov.hu/documents/10182/1281409/3_2020_OFA+hatarozat.pdf/686e57c6-4312-4232-4c58-818484e30a9d?t=1594985641820

Strengthening biosecurity measures (other than housing order)

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

Preventive culling

Preventive killing/slaughter has been carried out based on a risk assessment.

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

In the whole territory of the affected counties: transport of poultry can only take place after a negative PCR result. No stocking can take place in the restricted zones. As additional measures to control the HPAI spread, the radius of the surveillance zones have been enlarged based on the density of poultry establishments and of the administrative boundaries in some areas. The last HPAI outbreak was on 5 June 2020. In accordance with European Union regulations, restricted areas due to the disease were lifted on 10 July 2020. International (OIE) country freedom expected on 8 September 2020.

Derogations on restriction zone implementation after risk assessment

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

Hunting

Not restricted. No special rules apply.