SCIENTIFIC REPORT

European Union Reference Laboratory for Avian Influenza

APPROVED: 24 September 2018

doi:10.2903/j.efsa.2018.5430

Avian influenza overview May – August 2018

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

Cornelia Adlhoch, Thijs Kuiken, Paolo Mulatti, Krzysztof Smietanka, Christoph Staubach,
Irene Muñoz Guajardo, Laura Amato and Francesca Baldinelli

Abstract

Between 16 May and 15 August 2018, three highly pathogenic avian influenza (HPAI) A(H5N8) outbreaks in poultry establishments and three HPAI A(H5N6) outbreaks in wild birds were reported in Europe. Three low pathogenic avian influenza (LPAI) outbreaks were reported in three Member States. Few HPAI and LPAI bird cases have been detected in this period of the year, in accordance with the seasonal expected pattern of LPAI and HPAI. There is no evidence to date that HPAI A(H5N8) and A(H5N6) viruses circulating in Europe have caused any human infections. The risk of zoonotic transmission to the general public in Europe is considered to be very low. Several HPAI outbreaks in poultry were reported during this period from Russia. The presence of the A(H5N2) and A(H5N8) viruses in parts of Russia connected with fall migration routes of wild birds is of concern for possible introduction and spread with wild birds migrating to the EU. Although few AI outbreaks were observed in Africa, Asia and the Middle East during the reporting period, the probability of AI virus introductions from non-EU countries via wild birds particularly via the north-eastern route from Russia is increasing, as the fall migration of wild birds will start in the coming weeks. Further, the lower temperatures in autumn and winter may facilitate the environmental survival of avian influenza viruses potentially introduced to Europe.

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

Requestor: European Commission

Question number: EFSA-Q-2018-00504

Correspondence: ALPHA@efsa.europa.eu

Acknowledgements: in addition to the listed authors, EFSA, ECDC and the EURL wish to thank the following: Member State representatives that provided data on avian influenza outbreaks, animal populations or wrote case reports for this scientific output: Bulgaria (Aleksandra Miteva), Denmark (Pernille Dahl Nielsen), United Kingdom (Helen Roberts; Adam Brower); Dominique Bicout, Jan Arend Stegeman and Preben Willeberg for reviewing the document; Timm Harder and Daisy Duncan 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, Kuiken T, Mulatti P, Smietanka K, Staubach C, Munoz Guajardo I, Amato L and Baldinelli F, 2018. Scientific report: Avian influenza overview May - August 2018. EFSA Journal 2018;16(9):5430, 43 pp. doi:10.2903/j.efsa.2018.5430

ISSN: 1831-4732

The EFSA Journal is a publication of the European Food Safety Authority, an agency of the European Union.

Table of contents

1. Introduction....4
2. Conclusions....4
3. Suggestions....5
4. Results....6
4.1. Overview of HPAI and LPAI outbreaks in Europe between 16 May and 15 August 2018 (TOR 1 and TOR 2)....6
4.1.1. Description of the AI detections in time and space....6
4.2. Phenotypic characterisation of AI viruses circulating in the EU....7
4.2.1. HPAI in domestic birds....7
4.2.2. HPAI in wild birds....9
4.2.3. LPAI in domestic birds....10
4.2.4. Human cases due to A(H5N8) or A(H5N6) viruses detected in Europe....10
4.3. Genetic characterisation of AI viruses circulating in the EU....10
4.4. Applied prevention and control measures (TOR3)....11
4.4.1. Bulgaria....11
4.4.2. Denmark....11
4.4.3. United Kingdom....11
4.5. The AI situation on other continents between 16 May and 15 August 2018 (TOR 4)....11
4.5.1. HPAI A(H5N1)....11
4.5.2. HPAI A(H5N6)....14
4.5.3. HPAI A(H5N8)....16
4.5.4. Human infection due to A(H7N4)....18
4.5.5. HPAI-LPAI A(H7N9)....18
4.5.6. LPAI A(H9N2)....22
4.5.7. Scientific analysis of AI spread from non-EU countries to poultry in the EU....23
4.5.8. Surveillance and diagnosis of human infections and public health measures for prevention and control....24
4.5.9. ECDC risk assessment for the general public in the EU....25
References....26
Abbreviations....31
Appendix A – Terms of reference....32
Appendix B – Data and methodologies....34
Appendix C – Literature search on phenotypic and genetic characterisation of AI viruses....36
Annex A – Applied prevention and control measures on avian influenza....39
A.1 Bulgaria....39
A.2 Denmark....41
A.3 United Kingdom....42

1. Introduction

The present document gives an overview of highly pathogenic avian influenza (HPAI) outbreaks detected in poultry, captive and wild birds and low pathogenic avian influenza (LPAI) outbreaks in poultry and captive birds, as well as human cases due to avian influenza (AI) reported in and outside Europe between 16 May and 15 August 2018. The background, terms of reference (TORs) and their interpretation are reported in Appendix A; data and methodologies are reported in Appendix B and C.

2. Conclusions

HPAI and LPAI outbreaks in Europe between 16 May and 15 August 2018 (TOR 1 and TOR 2)

Main observations

- No human infections with HPAI or related LPAI viruses of the same genetic composition as those currently detected in European domestic and wild birds have been reported so far.
- In the EU, between 16 May and 15 August 2018 (based on the Animal Disease Notification System (ADNS)):
  – three HPAI A(H5N8) outbreaks were reported in poultry in Bulgaria;

  – three HPAI A(H5N6) outbreaks were reported in wild birds: two in Denmark and one in the United Kingdom;

  – three LPAI outbreaks were reported in poultry: one A(H5N2) in Denmark, one A(H5Nx) in Sweden and, one A(H7N7) in France.
- Mortality in wild birds from HPAI virus A(H5N6) was reported in Denmark and in the United Kingdom and involved species were listed in the revised list of target species for passive surveillance. The number of cases in the outbreaks, three, was a marked drop compared with the previous three-month period, when 68 cases were reported. This fits with the anticipated seasonal pattern for LPAI and HPAI in free-living wild birds during the summer period.

Conclusions

- The risk of zoonotic transmission of AI viruses to the general public in EU/EEA countries is considered to be very low.
- Occurrence of HPAI and LPAI in this time period was very low, which fits with the seasonal pattern of LPAI and HPAI.

Applied prevention and control measures between 16 May and 15 August 2018 (TOR 3)

Main observations

- After the detection of HPAI virus in wild birds in Denmark and United Kingdom, risk assessments were performed that took into account the ecology of the wild bird species involved in the period of interest, and no preventive and control measures were applied to poultry.

Conclusions

- The continued presence of the virus in the environment indicates that biosecurity measures on poultry establishments remain important to prevent incursion from wild birds and further spread within the poultry population.

Avian influenza situation on other continents between 16 May and 15 August 2018 (TOR 4)

Main observations

- In the reporting period, a decreasing number of AI outbreaks were observed in Africa, Asia and the Middle East, and no new outbreaks were reported from some previously affected areas.

- A HPAI A(H5N2) and several HPAI A(H5N8) outbreaks were reported in poultry in this time period from Russia.

Conclusions

- The continued presence of A(H5N8) in parts of Russia spatially associated with fall migration routes of wild waterbirds is of concern for the possible spread of the virus via wild birds migrating to the EU.
- The probability of AI virus being introduced from non-EU countries via wild birds is increasing as the fall migration of wild birds from breeding sites to the wintering sites will start in the coming weeks.
- The environmental survival of AI viruses potentially introduced to Europe can be facilitated by the low temperatures of autumn and winter.

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 Member States and between animal and human health sectors is crucial to be able to detect and respond early to threats that are relevant to animal and public health. It is particularly important that information on the genetic composition and possible origins of recently detected new subtype combinations, e.g. A(H5N2), are shared and communicated in a timely fashion.
- In relation to the HPAI cases in domestic and wild birds over the reporting period, due to the fall migration and to the expected higher environmental stability of the virus (exposure to lower temperature and lower ultraviolet radiation), the probability of new cases among poultry and wild birds will increase in Europe in the coming weeks. Therefore, enhanced surveillance is recommended in Europe, also including outbreaks involving single sick or dead birds of the target species, for comprehensive passive surveillance of HPAI A(H5).
- People exposed to birds that may potentially be infected with AI should consider taking appropriate personal protection measures following national guidelines.

4. Results

4.1. Overview of HPAI and LPAI outbreaks in Europe between 16 May and 15 August 2018 (TOR 1 and TOR 2)

4.1.1. Description of the AI detections in time and space

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

From 16 May to 15 August 2018, a total of nine outbreaks of AI, six A(H5) HPAI, two A(H5) LPAI and one A(H7) LPAI, occurred in the EU, as presented in Table 1. The timeline, location and affected sub-population of the AI outbreaks are reported in Figure 1 and 2. The characterisation of HPAI-affected poultry establishments[1] is reported in Section 4.2.1. For wild birds, Table 1 displays the number of outbreaks, whereas the description of cases by outbreak is reported in Section 4.2.2.

Table 1: Number of HPAI and LPAI outbreaks in Europe by virus subtype and country, 16 May-15 August 2018

Country	**HPAI**		**LPAI**			**All AI**
	A(H5N6) in wild birds	**A(H5N8) in poultry**	**A(H5N2)**	**A(H5Nx)**	**A(H7N7)**	
Bulgaria		3				3
Denmark	2		1			3
France					1	1
Sweden				1		1
United Kingdom	1					1
Total (5 countries)	3	3	1	1	1	9

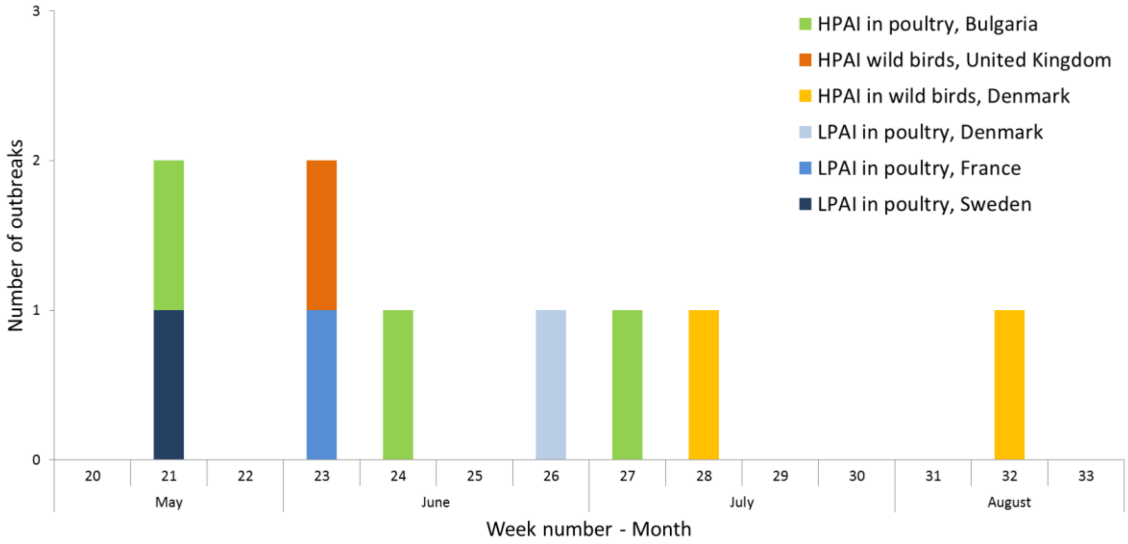
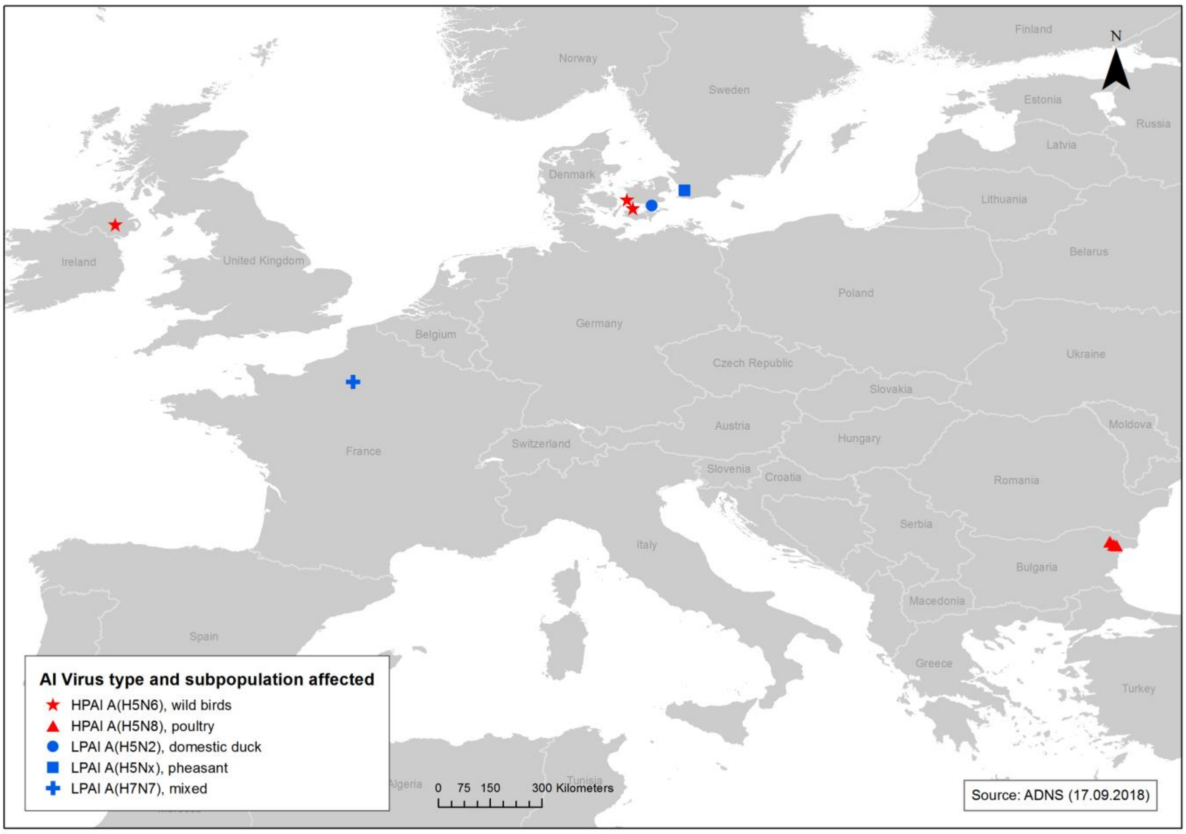


Figure 1: Distribution of the HPAI and LPAI outbreaks in Europe by week, sub-population and affected country, 16 May-15 August 2018 (n=9)

---

[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.



Source: ADNS (17.09.2018)

Figure 2: Geographical distribution of HPAI and LPAI outbreaks in Europe by virus subtype and affected sub-population, 16 May-15 August 2018 (n=9)

4.2. Phenotypic characterisation of AI viruses circulating in the EU

4.2.1. HPAI in domestic birds

4.2.1.1. Characterisation of the HPAI-affected poultry establishments

From 16 May to 15 August 2018, three HPAI outbreaks were notified in the poultry sector in the EU, all three caused by A(H5N8) viruses. The three outbreaks were recorded in Bulgaria. Two of them occurred in commercial establishments, while one outbreak was identified in a non-commercial establishment. All the outbreaks were primary and identified by means of passive surveillance. Characteristics of the affected establishments are reported in Table 2.

Table 2: Characteristics of the A(H5N8) HPAI affected poultry establishments in Europe, 16 May-15 August 2018 (n=3)

Country	Poultry species	Production category	Date of suspicion	Presence of signs due to HPAI infection	Number of susceptible animals[(a)]
Bulgaria	Domestic duck	Mixed	23/05/2018	Yes	21 071
	Chicken	Egg	12/06/2018	Yes	323 800
	Chicken, pigeon[(b)]	Mixed	05/07/2018	Yes	62
Total					**344 933**

(a) Based on the number of susceptible domestic birds reported to EFSA
(b) Non-commercial establishment

Two HPAI outbreaks were detected outside the reporting period for this report in the course of the AI surveillance and control programme: one A(H5N6) outbreak was suspected on 31 August in a captive bird establishment in Germany where chicken, domestic ducks and domestic geese were kept for private, non-commercial purposes; one HPAI A(H5) outbreak was identified on 19 September in a commercial establishment of laying hens in Bulgaria, Plovdiv region (Trilistnik village).

HPAI A(H5N8)-affected poultry establishments in Bulgaria

From 16 May to 15 August 2018, three HPAI A(H5N8) outbreaks were detected at poultry establishments in Bulgaria. The characteristics of the affected establishments and species reared are reported in Table 2.

All the outbreaks detected in the referring period were primary outbreaks, and all were identified by passive surveillance activities.

One outbreak occurred at a commercial duck establishment in which mortality of around 25% and clinical signs were reported by the owner. The birds had had no outdoor access in the 21 days before the outbreak. The most likely source of introduction was direct contact with wild birds, as significant biosecurity breakthroughs were noted on the establishment (access of wild birds to the premises and the presence of nests under the roofs). The same establishment had been affected by another HPAI outbreak in October 2017.

One outbreak was detected at a commercial laying hen establishment. Mortality, clinical signs and drop in egg production raised the suspicion in one out of six units of the establishment. During the controls performed in the other units after the confirmation of the outbreak, another premise was found to be positive for HPAI A(H5N8), without mortality or morbidity. The birds had had no outdoor access in the 21 days before the outbreak. Indirect contact with wild birds was identified as the most likely source of introduction: a forest surrounded the establishment, and nearby there was a dam with high density of wild migratory birds.

The third Bulgarian outbreak occurred in a non-commercial establishment, rearing chickens and pigeons. The suspicion was raised by the notification of increased mortality in chickens and pigeons and clinical signs in chickens by the owner. The birds were kept outdoors in the 21 days before the identification of the outbreak. The most likely source of introduction was direct contact with wild birds.

4.2.1.2. Information extracted from the scientific literature

Mutational events from LPAI to HPAI A(H7)

Seekings et al. (2018) provided evidence of A(H7N7) LPAI virus mutation to HPAI virus at a single poultry premise during an outbreak that occurred in June 2008 in free range laying hens in Oxfordshire, United Kingdom. Observation of increased mortality prompted a veterinary investigation for a notifiable disease. Other clinical signs included a drop in egg production, lethargy, pyrexia, swollen combs and wattles (some cyanotic), watery white diarrhoea, sticky mucus in the mouth, and subcutaneous haemorrhages on the legs. Based on virological, clinical, and epidemiological analyses, a wild-bird origin A(H7N7) LPAIV precursor likely entered the premises, and subsequently changed to a HP pathotype due to mutation at the haemagglutinin cleavage site.

Dietze et al. (2018) reported two spatiotemporally linked outbreaks caused by LPAI virus, and subsequently, HPAI virus A(H7N7), in two-layer establishments in Germany in 2015. LPAI virus infection was characterised by a drop in egg production of 16% over a 3-day period, but clinical inspection of the flock did not reveal further clinical signs. HPAI virus infection was first suspected based on mortality, with 1.85% mortality overnight, compared wiht 0.69% over the previous three weeks. In addition, a drop in egg production became evident. Results of virological and epidemiological analyses suggested an initial introduction of the LPAI virus progenitor and a subsequent switch to HPAI virus A(H7N7) after the incursion.

4.2.2. HPAI in wild birds

Pathogenicity in the affected species

From 16 May to 15 August 2018, the only HPAI virus subtype that was identified in carcasses of wild birds submitted for AI virus testing was A(H5N6) (three cases in two countries) (Table 3). This is a marked drop in the number of cases compared wiht the previous 3-month period (EFSA, 2018a), when 68 cases were reported in eight countries. This decline in the number of cases in spring and summer fits with the overall seasonal pattern of LPAI in wild birds (Olsen et al., 2006). However, it does underline the potential for HPAI virus A(H5N6) to remain present in free-living wild birds until at least July, necessitating continued vigilance regarding incursion into poultry establishments.

Table 3: Cases of HPAI A(H5N6) infection in free-living wild birds in Europe reported to the World Organisation for Animal Health (OIE) by country, outbreak and species, 16 May-15 August 2018 (OIE, online-b)

OIE report no.	Country	No. of outbreaks by country	No. of cases by outbreak	No. of wild bird species involved by outbreak	List of wild birds species involved in the country	Total wild bird cases by country
27587	Denmark	2	1, 1	1, 1	Common eider, mute swan	2
26949	United Kingdom	1	1	1	Greylag goose	1
Total	**(2)**	**3**	**-**	**-**	**(3)**	**3**

A HPAI A(H5N6) outbreak was detected outside the reporting period in the Netherlands; it involved a mallard (*Anas platyrhynchos*) reported on 30 August and a marsh harrier (*Circus aeruginosus*) reported on 3 September found dead in Eemmeer (Eem Lake), near Blaricum.

Three HPAI (H5N6) outbreaks were detected outside the reporting period in Denmark; one involved two mallards (*Anas platyrhynchos*) and two pheasants (*Phasianus colchicus*) from the island Asgersø that were found dead on 27 August; one was identified in the municipality of Guldborgsund, where one mute swan (*Cygnus olor*) and one common eider (*Somateria mollissima*) were found dead on 3 September; onle involved a greylag goose (*Anser anser*) found dead on 3 September in the municipality of Lolland.

4.2.2.1. Information extracted from the scientific literature

HPAI A(H5N8) characterisation (virulence, replication)

Grund et al. (2018) investigated the biological properties of recent A(H5N8) virus isolates collected during the epidemics in Germany in 2014 and 2016 (DE14-H5N8A and DE16-H5N8B), whose HA genes represented groups 2.3.4.4a and b, respectively, in chickens, Pekin ducks, and domestic geese. Their data indicated that the 2016 HPAIV H5N8B was avian-adapted with augmented virulence for waterfowl. The clinical correlate of the increased virulence for ducks of DE16-H5N8B compared to DE14-H5N8A was pronounced neuro- and hepatotropism inducing necrotizing and inflammatory processes in these organs. Furthermore, the striking lack of lymphohistiocytic perivascular infiltrations in these lesions suggested a direct or indirect lymphocytotoxic effect of DE16-H5N8B which could subsequently result in immunosuppression.

For both viruses, oro-pharyngeal shedding superseded cloacal excretion by a factor of up to 100 and lasted up to 7 dpi. High level oropharyngeal shedding indicates the importance of virus replication in the epithelium of the upper respiratory tract, including the infraorbital sinuses. This conclusion is in agreement with an observed strong antigen signal in the sinuses, but rare antigen detection in the intestine. However, this opposes the paradigm of preferential replication in the gastrointestinal tract of (low pathogenic) influenza viruses in aquatic birds. Apparently, this reflects the differences in biological properties of the long circulating gs/GD-like HPAI A(H5) viruses.

4.2.3. LPAI in domestic birds

From 16 May to 15 August 2018, three LPAI outbreaks were notified in the poultry sector in the EU, one in Denmark, one in France and one in Sweden. Information available from the ADNS (European Commission, online-a) and in the Standing Committee on Plants, Animals, Food and Feed (SCOPAFF) presentations (European Commission, online-b) to characterise the LPAI affected establishments is presented in Table 4.

Table 4: Characteristics of the LPAI affected poultry establishments in Europe, 16 May-15 August 2018 (n=3)

Country	Poultry species	Outbreak type	Surveillance programme	Date of suspicion or sampling	Presence of signs due to LPAI infection	Number of susceptible animals
Denmark	Domestic duck	Primary	Active surveillance	25/06/2018	No	2 679*
France	Pheasant and domestic duck	Primary	Active surveillance	06/06/2018	No	10 000
Sweden	Pheasant	Primary	Active surveillance	23/05/2018	No	14 704
Total						**27 383**

* In the establishment, 2 667 ducklings of 1-4 weeks old and 12 laying hens of 2 years old were present; the laying hens did not show any clinical symptoms and they were not tested

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

No human infection related to A(H5N6) or A(H5N8) viruses detected in wild birds and poultry in Europe has been reported so far (Adlhoch et al., 2018). Four genetic groups (a, b, c, d) of clade 2.3.4.4 have been proposed by Lee et al. (2018) based on the HA sequences. A(H5N8) and A(H5N6) viruses detected in birds and poultry in Europe cluster in clade 2.3.4.4.b. One human case in China was infected with A(H5N6) of the 2.3.4.4.b clade in 2017. According to the World Health Organization (WHO), this case was a three year old girl with reported exposure to live poultry before the onset of symptoms in December 2017 (WHO, 2018b). The girl was not hospitalised but treated as an outpatient and recovered. Although all viruses circulating and causing outbreaks in European domestic and wild birds since 2016 also cluster within this clade 2.3.4.4.b (Globig et al., 2017; Pohlmann et al., 2018), there is a high variability within the gene segments within the A(H5N6) viruses world-wide and the overall gene composition of the European viruses in birds differs from the human case detected in China (DEFRA, 2018; GISAID, online).

A recent study found that HPAI A(H5N8) group b viruses showed increased virulence causing severe disease and mortality in Peking ducks. The virulence differed across mammalian hosts: it was high for Balb/c mice and reduced in ferrets. No transmission between ferrets and a marginal replication in human lung cultures was observed (Grund et al., 2018). The virus was considered avian-adapted with low zoonotic potential.

4.3. Genetic characterisation of AI viruses circulating in the EU

The latest European 2.3.4.4 viruses are all group b, including A(H5N6). These strains do not cluster with the A(H5N6) that is associated with human infections and is predominantly circulating in poultry in China and with sporadic detections in both wild birds and poultry in South-East Asia (clade 2.3.4.4c). The 2.3.4.4b A(H5N6) European viruses cluster together and separate from the 2.3.4.4b A(H5N8) viruses that have been isolated from domestic birds in Bulgaria and Italy. At the whole genome level, there is no evidence to date of any reassortment that has resulted in the inclusion of A(H5N6) genes from clades that have been associated with human infections and there has been no detection of mammalian adaptation.

4.4. Applied prevention and control measures (TOR3)

4.4.1. Bulgaria

Due to the evolution of the epidemiological situation in Bulgaria, measures already described in the Avian Infuenza overview February – May 2018 (EFSA, 2018a) were also applied in the period of reference (May – August 2018).

Following the confirmation of a primary outbreak on 25 May 2018, restriction measures were applied at the country-level, including housing orders, a ban on live-bird markets, the improvement of active surveillance in poultry (with a special focus on non-commercial establishments), the enhancement of passive surveillance for wild birds, strengthene biosecurity, and a ban on restocking of game birds in the protection and surveillance zones.

Active surveillance measures were further enhanced in chicken breeders, laying hens, and waterfowl starting on 9 May, based on the epidemiological situation in the country. Samples were indicated to be taken on a 3-weekly basis for a period of three months, and then at 50-60 days of age, according to sampling protocols indicated by EU Council Directive 2005/94.

Information campaigns were carried out to increase awareness, through regular meetings with poultry company representatives, collaboration with public health authorities, and the publication of information on the epidemiological situation and measures applied.

Details on the control measures applied in Bulgaria are given in Annex A.1.

4.4.2. Denmark

The detection of an A(H5N6) HPAI virus in a common eider found dead on 8 July indicated that the virus was still present in wild birds in Denmark at that time. Because it occurred after a prolonged period with no cases in wild birds or poultry, it was considered to be a sporadic event by the competent authorities, taking account of the opinion of ornithologists on the behaviour of eiders in mid-summer.

The competent authorities did not apply any restrictive measures; however, an information campaign was conducted that included communication with producers and press releases to suggest both enhancing of biosecurity measures at poultry establishments and encourage the public to report any suspect findings.

Details on the control measures applied in Denmark are given in Annex A.2.

4.4.3. United Kingdom

After the reduction in the rate of reporting of A(H5N6) HPAI viruses in wild birds in the first months of 2018, risk assessments conducted by the competent authorities led to reduce the risk of spread of AI to poultry from High to Low, also accounting for migratory wild waterfowl leaving the United Kingdom. Furthermore, restriction and biosecurity measures in the prevention zones located in England and Wales were lifted as of 1 May 2018.

The identification of A(H5N6) in a single greylag goose (*Anser anser*) in Northern Ireland on 15 June was not considered sufficient to change the level of risk, and no further actions were taken.

Details on the control measures applied in United Kingdom are given in Annex A.3.

4.5. The AI situation on other continents between 16 May and 15 August 2018 (TOR 4)

4.5.1. HPAI A(H5N1)

4.5.1.1. Domestic and wild birds

Detections

In the relevant time period for this report outbreaks of the Asian lineage HPAI A(H5N1) in poultry have been observed in commercial chicken establishments in China, Malaysia and Nepal. The Nepalese authorities notified that a large duck establishment in the same region was also affected by the disease. Furthermore, the Asian lineage HPAI A(H5N1) was also detected in a captive flock of pheasants in Bangladesh. From 16 May to 15 August 2018 no outbreaks of the Asian lineage HPAI A(H5N1) in poultry or wild birds were reported from African countries or from the Middle East (see Figure 3).

Since November 2015, the European avian lineage of HPAI A(H5) with three different subtypes (A(H5N1), A(H5N2) and A(H5N9)) emerged in southwestern France and caused severe outbreaks in domestic ducks and domestic geese. In the country a virus similar to this A(H5N1) was detected upon pre-movement control in a duck establishment in March 2017. Unfortunately, due to the low viral load of samples, no further analyses to characterise the virus were possible (Briand et al., 2017; Briand et al., 2018).

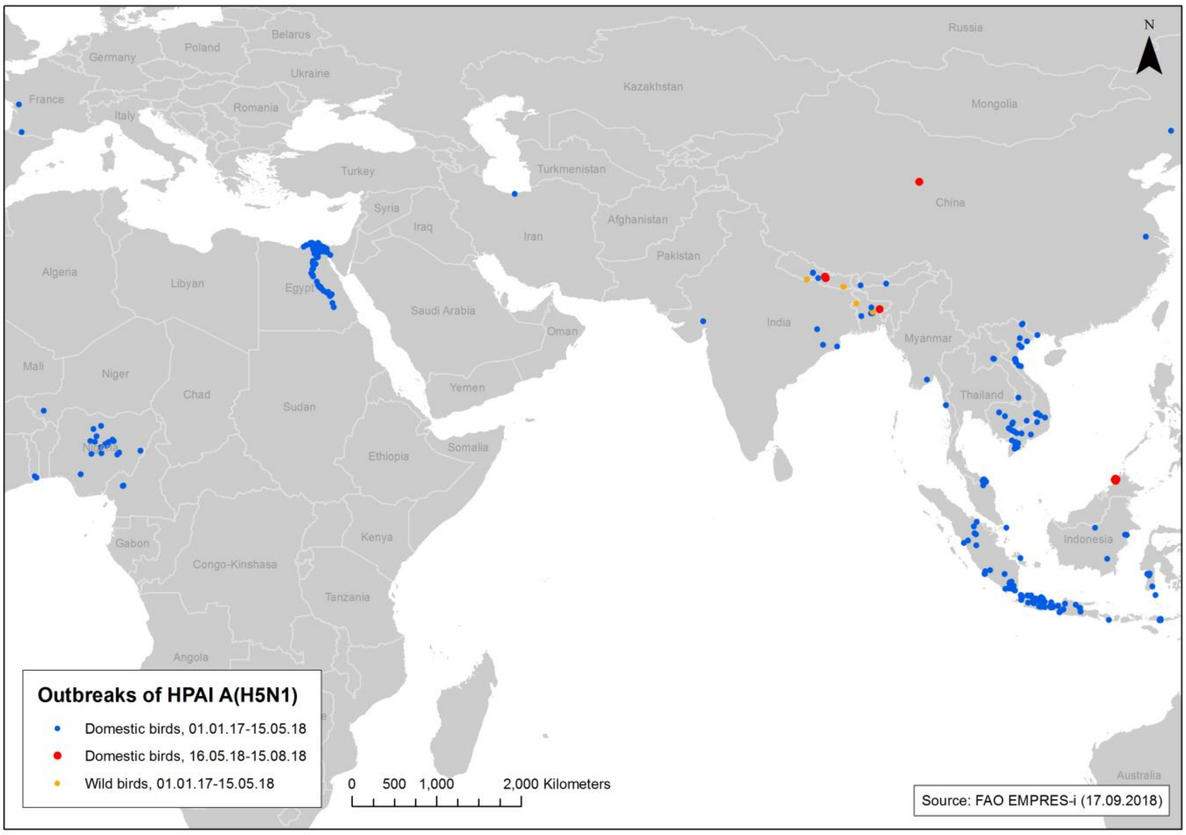


Figure 3: Distribution of confirmed HPAI A(H5N1) outbreaks in birds by place of origin, 1 January 2017-15 August 2018 (FAO, online-a)

Genetic information

There is evidence of continuous reassortment between A(H5N1) and A(H9N2) viruses in Asia: two HPAI viruses isolated from live bird markets in Cambodia in 2015 possessed seven genome segments derived from the A(H5N1) clade 2.3.2.1 and single genes (PB1 and M) from the A(H9N2) virus (Suttie et al., 2018).

Parvin et al. (2018) performed a genetic analysis of all A(H5N1) sequences from Bangladesh available at GenBank and found that they belonged to three clades: 2.2.2, 2.3.2.1 and 2.3.4.2. Only clade 2.3.2.1a is still present in the country.

Wade et al. (2018b) characterised the A(H5N1) viruses responsible for outbreaks of HPAI in 2016-2017 in Cameroon and found that they clustered within the genetic clade 2.3.2.1c. Moreover, the authors provided evidence of H5N1/H9N2 reassortment.

Phenotypic characterisation

No new relevant information was published during the reporting period.

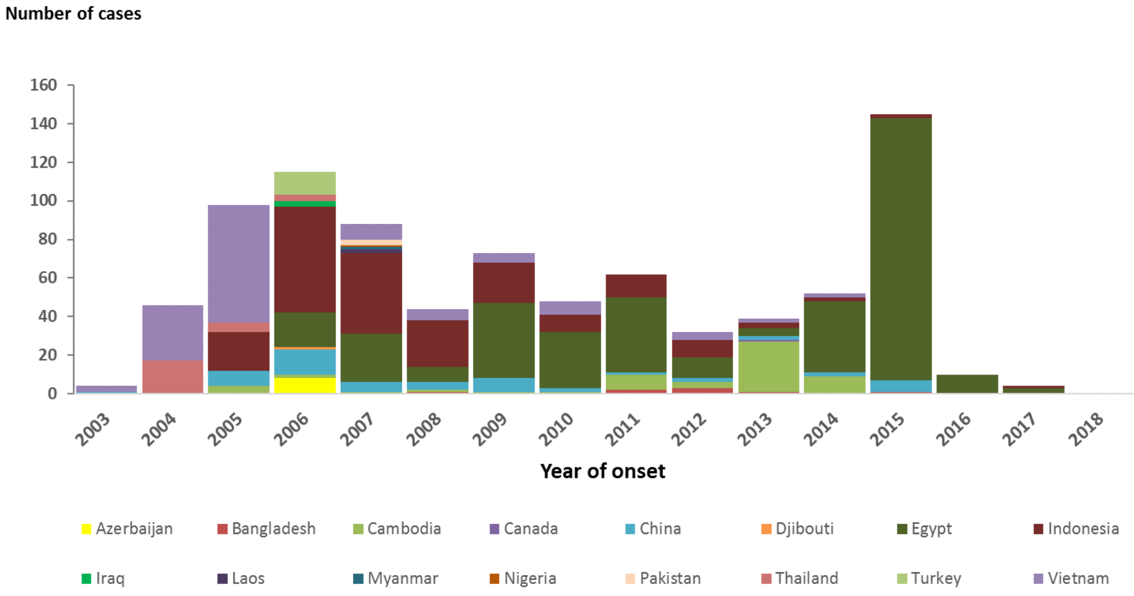
4.5.1.2. A(H5N1) in mammals (excluding humans)

No new relevant information was published during the reporting period.

4.5.1.3. Human infections due to A(H5N1)

No new human cases due to AI A(H5N1) have been reported in 2018 worldwide (CHP, 2018; EFSA, 2018b).

Since 2003 and as of 15 August 2018, 860 laboratory-confirmed cases of human infection with AI A(H5N1) virus, including 454 deaths, have been reported from 16 countries outside the EU/EEA. The latest case was reported in September 2017 by Indonesia (Figure 4).



Source: Data from CPH and WHO (CHP, 2018; WHO, 2018a).

Figure 4: Distribution of confirmed human cases of A(H5N1) by year and country of reporting, 2003–15 August 2018 (n=860)

Recent research showed that combinations between clade 2.3.4 HA and N1 or between clade 2.3.4.4 HA and Nx, promoted viral growth, NA activity, thermostability, low-pH stability and pathogenicity in chicken and mice (Qin et al., 2018). These viral characteristics were less promoted in combinations between clade 2.3.4.4 HA and N1, or between clade 2.3.4 HA and Nx. This indicates that N1 is not a good match with the HA of clades 2.3.4.4 but viruses of this clade might have better viral fitness if another N-type is included. This helps to explain a higher prevalence of 2.3.4. HA/N1 viruses than of 2.3.4.4 HA/N1 and why a higher variability of different N-types is detected in the currently circulating viruses.

4.5.2. HPAI A(H5N6)

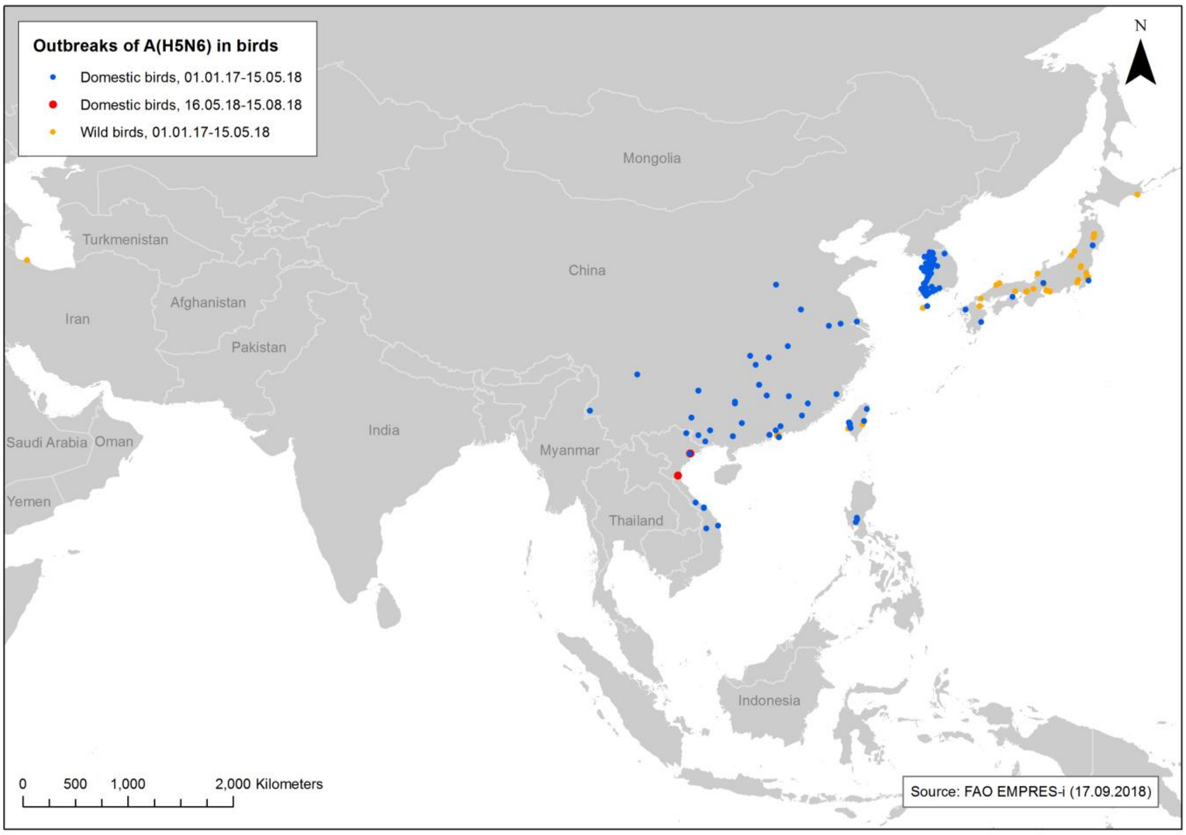
4.5.2.1. Domestic and wild birds

Detections

The four genetic groups (a, b, c, d) of clade 2.3.4.4 introduced by Lee et al. (2018) are used in this section to give a better insight onto the characteristics of the HPAI A(H5N6) viruses detected in domestic and wild birds.

As mentioned in the EFSA report for November 2017 – February 2018 (EFSA, 2018b), two novel HPAI A(H5N6) reassortants are co-circulating in Asia: (1) the zoonotic reassortant belonging to clade 2.3.4.4c that was detected in domestic and wild birds in China, Japan, Myanmar, the Philippines, South Korea, Taiwan and Vietnam, and (2) a reassortant closely associated with clade 2.3.4.4b that is mainly circulating in Eurasia (Kwon HI et al., 2018; Lee et al., 2018).

Between 16 May and 15 August 2018, Vietnam reported three outbreaks to the OIE of A(H5N6) HPAI virus on medium-sized poultry establishments from two different provinces Hai Phong and Nghe An, all confirmed at the end of July. In the relevant time period for this report, no cases of A(H5N6) HPAI virus were detected in wild birds in Asia (Figure 5).



Source: FAO EMPRES-i (17.09.2018)

Figure 5: Distribution of confirmed HPAI A(H5N6) outbreaks in birds by place of origin, 1 January 2017-15 August 2018 (FAO, online-a)

Genetic characterisation

Sun et al. (2018) carried out genetic characterization of the internal genes of A(H5N6) viruses downloaded from the Influenza Research Database, GISAID or generated in the study and divided them into four genotypes depending on the origin of the genome segments. The receptor-binding of four isolates detected in 2016 at a live poultry market demonstrated their ability to bind to both α-2,3-linked ('avian like') and α-2,6-linked ('human like') sialic acid receptors.

The genetic characterisation of an A(H5N6) virus isolated from a meat-type duck in Taiwan in February 2017 revealed that the virus belonged to clade 2.3.4.4c and is similar to viruses found in China, South Korea, and Japan during the epidemic in 2016–2017 (Chen et al., 2018).

Phenotypic characterisation

Four A(H5N6) viruses isolated from live poultry markets in China in 2016 were highly pathogenic for chickens (intravenous pathogenicity index (IVPI) range 2.9-3.0) but only two of them had high IVPI values in ducks (1.67-2.61), while the other two did not induce noticeable clinical signs in ducks (Sun et al., 2018). The viruses showed different replication potential in chickens inoculated oculo-nasally with a dose of 10^6EID$_{50}$/bird as well as varying degrees of histological lesions.

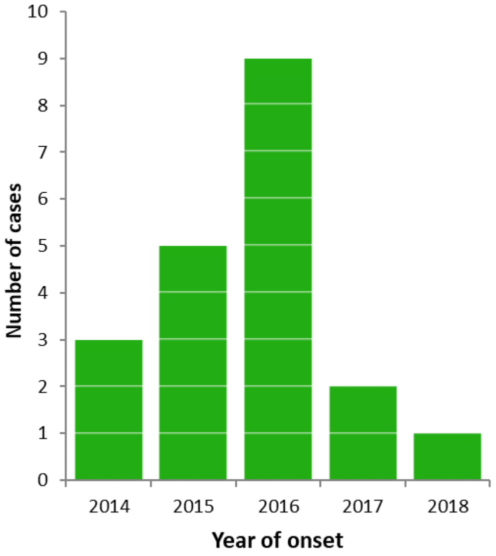
4.5.2.2. A(H5N6) in mammals (excluding humans)

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

4.5.2.3. Human infections due to A(H5N6)

One new human case due to AI A(H5N6) has been reported since the last EFSA report and within the reporting period (EFSA, 2018b; The Government of the Hong Kong Special Administrative Region, online). The patient, a 42-year-old man from Guanxi Province, China, was hospitalised with a critical illness. He reported contact with live poultry before symptom onset. The clade of this virus is not yet available. Since 2016, all reassortant A(H5N6) viruses circulating and causing outbreaks in Europe have clustered within clade 2.3.4.4.b. An A(H5N6) virus of this clade caused one single human infection in China; however, the overall viral gene composition of the European viruses in birds differs from the human case detected in China (GISAID, online). The assigment to a clade is based on the H5 sequence only and does not include the characteristics of the other virus segments, which are also relevant for transmission to humans and pathogenicity.

Since 2014 and as of 15 August 2018, 20 laboratory-confirmed cases of human infection with AI A(H5N6) virus of clade 2.3.4.4 circulating in South-east Asia, including six deaths, have been reported globally (Figure 6). All the cases occurred in mainland China (CHP, 2018). According to an article in 2017, 12 deaths due to A(H5N6) have been reported since 2014 (Jiang et al., 2017).



Source: Data used from WHO, the Hong Kong Centre for Health Protection of the Department of Health of the Government of Hong Kong SAR and Jiang et al. 2017 (Jiang et al., 2017; CHP, 2018; WHO, 2018b)

Figure 6: Number of human cases due to A(H5N6), clade 2.3.4.4, infection by year of onset, 2014–2018 (n=20)

The virus characteristics and composition of the A(H5N6) viruses within clade 2.3.4.4 causing human infections have been described (Sun et al., 2018). Four main gene types within these reassortments were identified that showed a high variabilty in the origin and composition of the different gene segments. This underlines a constant reassortment and evolution of viruses within this clade.

A descriptive study among 870 poultry farmers was performed in the Republic of Korea during the outbreaks of HPAI A(H5N6) virus of clade 2.3.4.4 in 2016-2017 (Ryu et al., 2018). Serological testing was performed in 523 of the exposed farmers the same day an outbreak was confirmed at the establishment and four weeks later. The investigators assumed contact with infected poultry, but all sera tested were negative and no transmission to humans exposed was identified.

High proportions of avian-isolated A(H5N6) HPAI viruses showed a series of genotypic markers associated with cross-species transmission from birds to humans. These markers are related to amino acid changes D94N, S123P, 129Del & I151T, S133A, and T156A (H5 numbering) in HA, which increase virus binding to α-2,6 receptors (Guo et al., 2018). The proportions of two mutations increased over time: a single amino acid change S123P that increases viruses binding to human receptors, and a double mutation of deletion of residue 129 and substitution of I151T that increases attachment to and infectivity in humans. A(H5N6) viruses may exhibit enhanced and increasing affinity for human type receptors, which may help to explain sporadic human infections.

Patients infected with A(H5N6) showed some clinical differences compared with patients with A(H5N1), A(H7N9) or the seasonal A(H1N1)pdm09, including higher levels of elevated alanine aminotransferase, lactate dehydrogenase, hypercytokinaemia and higher incidence of lymphopenia (Bi et al., 2018). Early cellular immunity and lower levels of cytokines might contribute to the survival of infected patients.

4.5.3. HPAI A(H5N8)

4.5.3.1. Domestic and wild birds

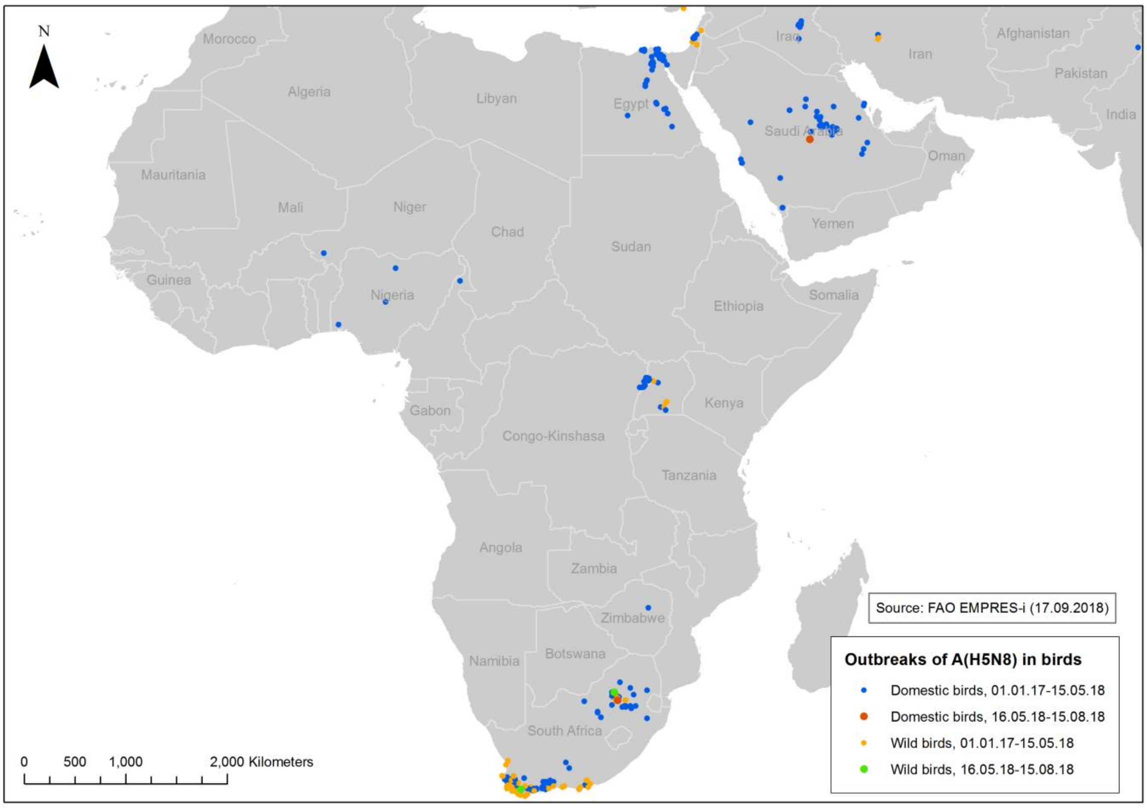
Detections

The four genetic groups (a, b, c, d) of clade 2.3.4.4 introduced by Lee et al. (2018) are used in this section to give a better insight on the characteristics of the HPAI A(H5N8) viruses detected in domestic and wild birds.

In June 2018 the national authorities in South Africa notified an outbreak of HPAI A(H5N8) clade 2.3.4.4b in poultry establishment in the Gauteng province. Furthermore, HPAI A(H5N8) was also detected in African sacred ibis (*Threskiornis aethiopicus*) and blue crane (*Grus paradisea*) in North West and Western Cape province, respectively. In the relevant time period for this report Saudi Arabia reported an outbreak on a medium-sized duck establishment, but underreporting is suspected, since Saudi Arabia has been hit by a wave of outbreaks of HPAI A(H5N8) in medium-sized to very large poultry establishments since November 2017 (see Figure 7).

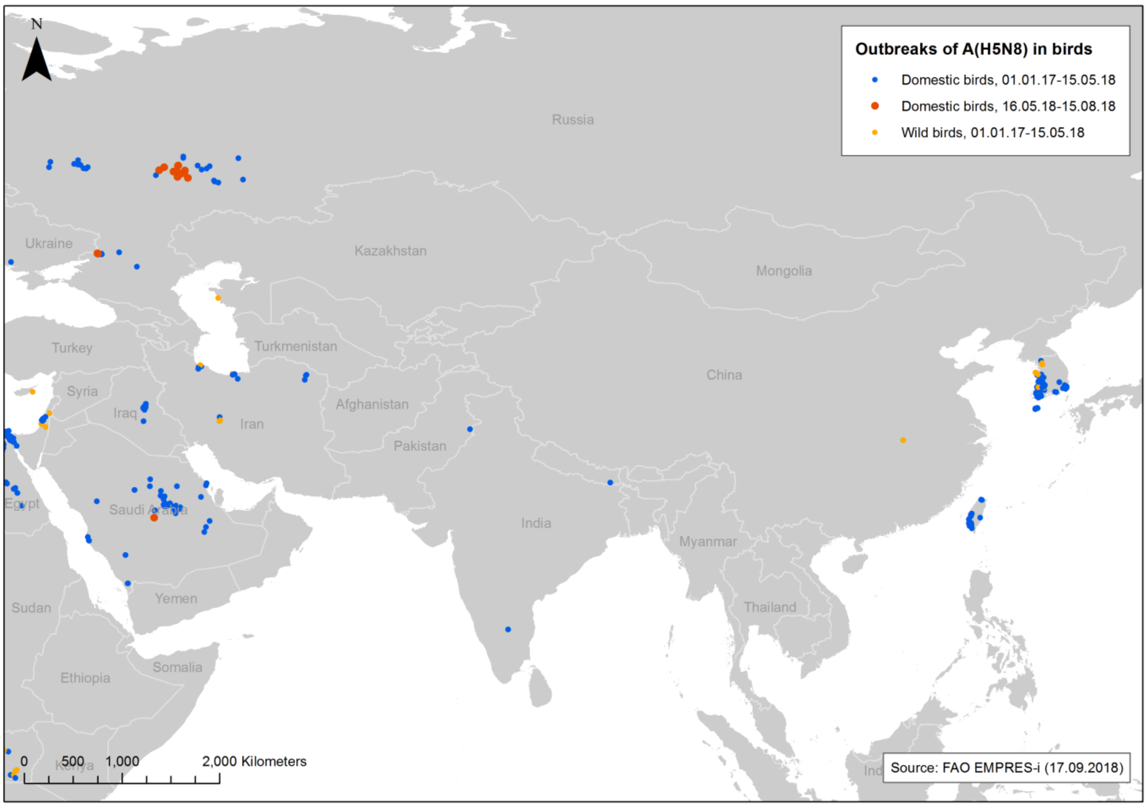
Between 16 May and 15 August 2018 the national authorities of Russia reported 13 outbreaks of HPAI A(H5N8) in domestic birds on two large establishments in the Rostovskaya Oblast, and in several backyard establishment mainly in Chuvashiya Republic, but also in Tatarstan Republic and Nizhegorodskaya Oblast. Furthermore, Russia reported to the OIE an outbreak of HPAI A(H5N2) in the Kostromskaya Oblast in August 2018 on the same establishment as the HPAI A(H5N2) outbreak in December 2017 (Harder, 2018, pers. communication). The isolate belongs to clade 2.3.4.4b, which has been spreading in Russia as well as in Asian, European, Middle Eastern and African countries in 2016-2018 (OIE, online-a).

No outbreaks of HPAI A(H5N8) in poultry or wild birds were reported from China, Japan, the Korean Peninsula or South-east Asia (see Figure 8).



Source: FAO EMPRES-i (17.09.2018)

Figure 7: Distribution of confirmed HPAI A(H5N8) outbreaks in birds by place of origin in Africa and the Middle East,1 January 2017-15 August 2018 (FAO, online-a)



Source: FAO EMPRES-i (17.09.2018)

Figure 8: Distribution of confirmed HPAI A(H5N8) outbreaks in birds by place of origin in Asia and the Middle East,1 January 2017-15 August 2018 (FAO, online-a)

Genetic characterisation

Genetic characterisation of the complete genome of A(H5N8) viruses detected in chickens, ducks, pigeons and Indian peafowl in poultry markets in Cameroon in January 2017 suggested at least two separate introductions of clade 2.3.4.4b A(H5) viruses (Wade et al., 2018a).

Whole-genome sequences of four A(H5N8) viruses detected in domestic ducks in four HPAI-affected areas of the Democratic Republic of the Congo showed that they also clustered with clade 2.3.4.4b (Twabela et al., 2018).

Phenotypic characterisation

During the outbreak of HPAI A(H5N8) in domestic ducks and chickens in the Democratic Republic of the Congo (April 2017) generalized weakness, prostration, dyspnea, yellowish diarrhea, torticollis were observed. At necropsy, haemorrhages in all organs, soft livers, and empty gizzards were observed (Twabela et al., 2018).

4.5.3.2. A(H5N8) in mammals (excluding humans)

The A(H5N8) clade 2.3.4.4a virus from North America produced asymptomatic infection in cottontail rabbits, accompanied by a low level of shedding following experimental inoculation with $10^{5.9}$ plaque-forming units (Root et al., 2018).

4.5.4. Human infection due to A(H7N4)

No human cases have been recorded during the reporting period. One human case was detected in China in February 2018 as described by WHO and in the EFSA report November 2017 – February 2018 (EFSA, 2018b; WHO, 2018d, c). Additional clinical information about the case was published, and contract tracing of 28 close contacts did not reveal any transmission between humans (Tong et al., 2018).

Another report describes outbreaks and detections of AI A(H7N4) in birds worldwide and speculates that A(H7N4) might have been present in bird populations in China since 1993, but did not spread widely within the country (Gao et al., 2018).

4.5.5. HPAI-LPAI A(H7N9)

4.5.5.1. Domestic and wild birds

Detection

In June 2018 the Chinese authorities reported the outbreak of HPAI A(H7N9) in a layer chicken establishment with 17 000 birds in Liaozhong District, Shenyang City. Furthermore, LPAI A(H7N9) was detected in one sample from a chicken in a live bird market in Anhui Province during the routine virological surveillance conducted in 25 provinces between 16 May and 15 August 2018 (see Figure 9, Figure 10 and Figure 11) (FAO, online-a; MoA, online). No LPAI or HPAI A(H7N9) were detected in wild birds during the relevant time period for this report. The results of the surveillance campaigns are published monthly by the Chinese Ministry of Agriculture (MoA, online) and are also available on the EMPRES-i website of the Food and Agriculture Organization (FAO) (FAO, online-a). Furthermore, at the end of June 2018, the Chinese Ministry of Agriculture reported that 92.14% of poultry samples, taken after the vaccination campaigns in 29 provinces, achieved the required immunity level (MoA, online). The nationwide campaigns for A(H7N9) vaccination of poultry, with the exception of poultry in AI-free zones and export establishments, started extensively in September 2017 (FAO, online-b).

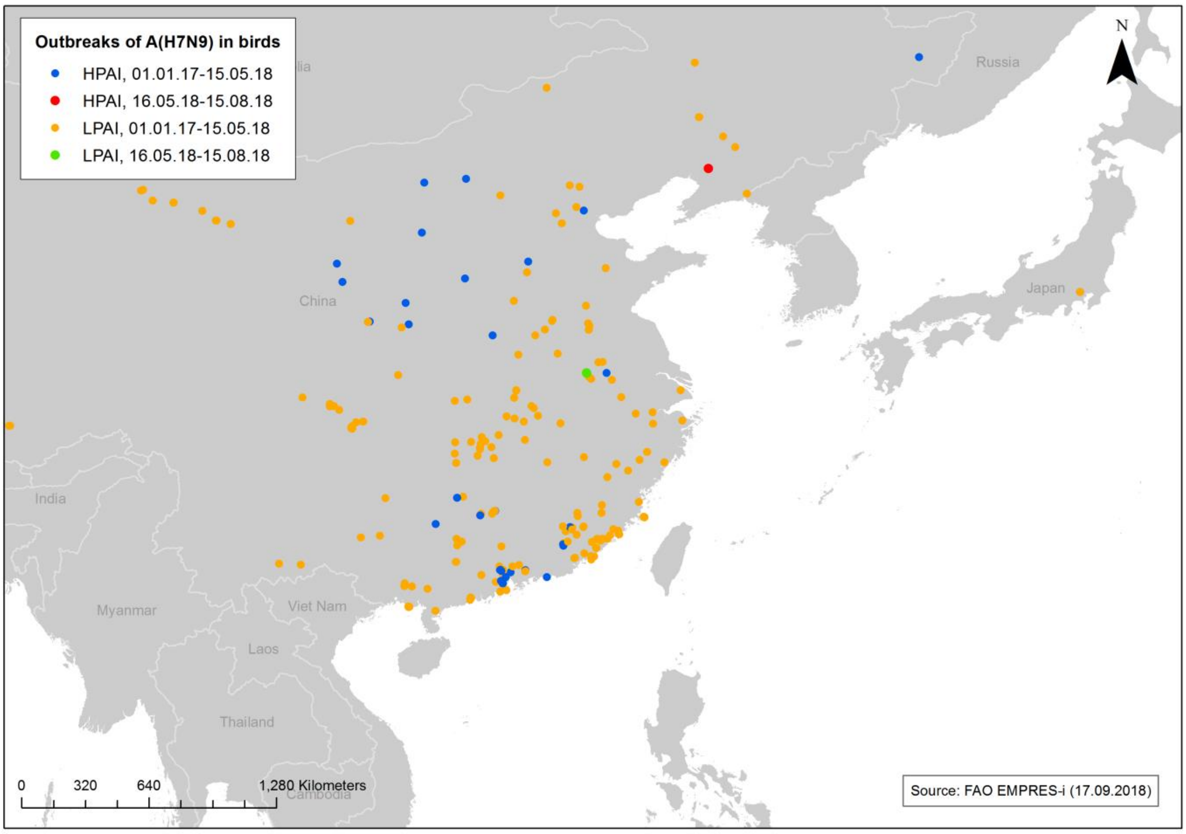


Figure 9: Distribution of confirmed LPAIV and HPAIV A(H7N9) in birds and environmental samples by place of origin, 1 January 2017-15 August 2018 (FAO, online-a)

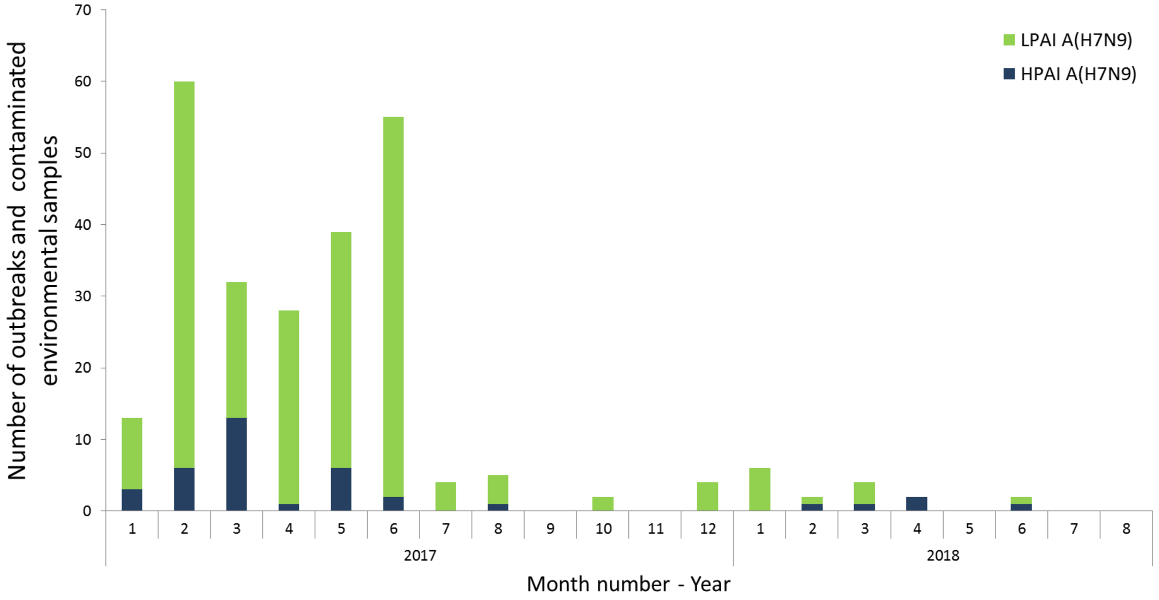


Figure 10: Distribution of confirmed LPAI and HPAI A(H7N9) outbreaks in birds and of contaminated environmental samples in China by month, 1 January 2017-15 August 2018 (Source: FAO EMPRES-i (17.09.2018))

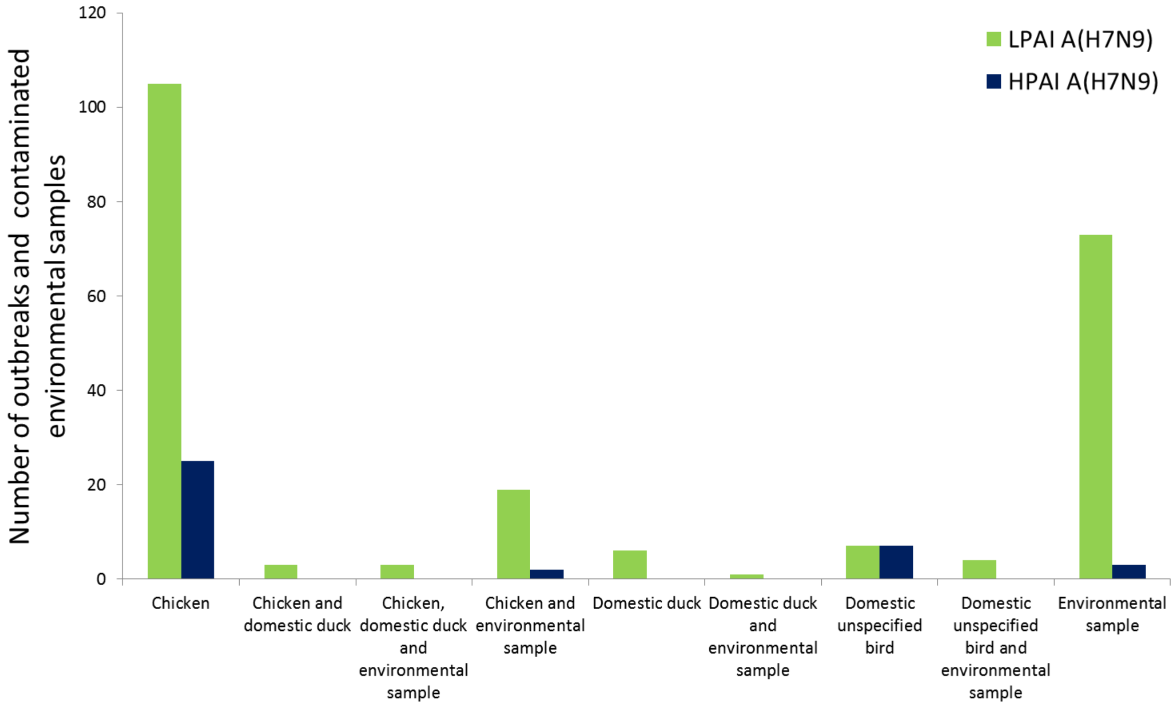


Figure 11: Distribution of confirmed LPAI and HPAI A(H7N9) outbreaks by bird species and of contaminated environmental samples in China, 1 January 2017-15 August 2018 (Source: FAO EMPRES-i (17.09.2018))

Phenotypic characterisation

The pathogenicity of chicken-derived highly pathogenic A(H7N9) (n=6) and low pathogenic A(H7N9) (n=6) viruses isolated in 2017 was tested in 6-week-old BALB/c mice inoculated with doses from 10^3 to $10^{6.5}$ EID_{50}. None of the LPAIV induced mortality in mice, but the viruses caused weight loss and replicated efficiently in the lungs and spread to non-respiratory organs (brain, kidney and spleen). One third of the tested HPAIV A(H7N9) strains caused weight loss and death in infected mice (He et al., 2018).

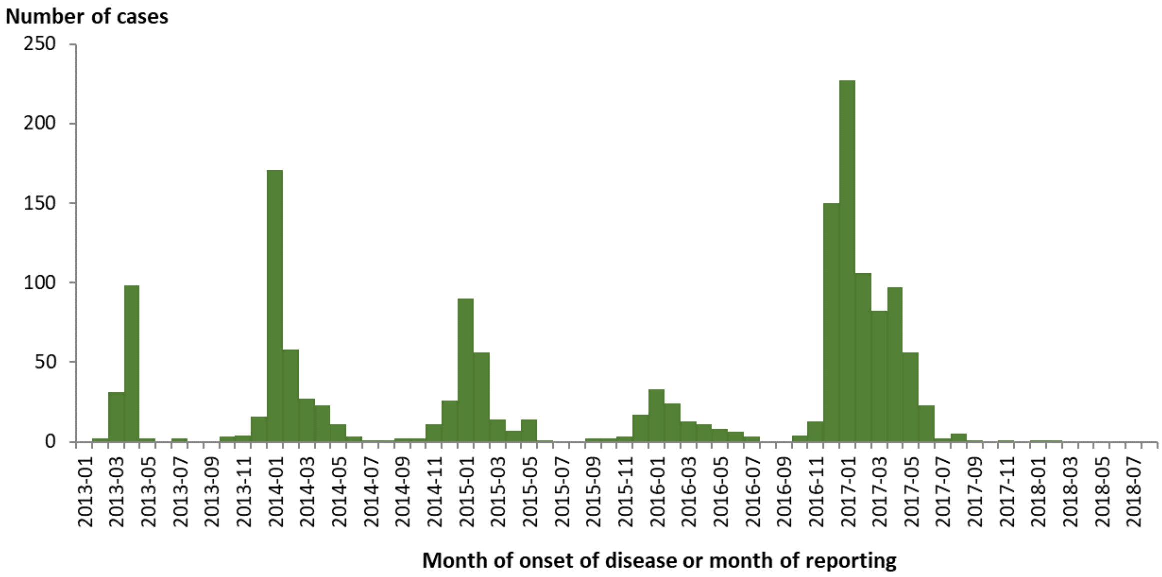
Genetic characterisation

He et al. (2018) compared six highly pathogenic A(H7N9) and six low pathogenic A(H7N9) viruses recovered from chickens in China in 2017 and found no differences in terms of molecular markers associated with the HA receptor binding capacity, but showed higher thermal stability of HP isolates (a possible factor contributing to better transmissibility of some HP viruses in ferrets). Phylogenetic analyses proved that the isolates belong to the ‘Yangtze Delta River’ clade, but were placed in two separate branches consistent with the pathotype.

4.5.5.2. Human infections due to A(H7N9)

No human cases due to AI A(H7N9) have ever been reported from Europe. No human cases infected with AI A(H7N9) have been reported globally since the last EFSA report in June 2018 (CHP, 2018; EFSA, 2018b; WHO, 2018c). The latest case was reported from China in February 2018.

Since February 2013 a total of 1 567 human cases have been reported from outside of Europe, including 569 with fatal outcome (CHP, 2018; WHO, 2018c, online-a); see Figure 12 and Table 5). According to the Chinese National Influenza Center (2018), 32 people have been infected with HPAI A(H7N9) in China.



Source: Data from WHO (CHP, 2018; WHO, online-a).

Figure 12: Distribution of confirmed human cases of A(H7N9) by month of disease onset or month of reporting, February 2013–15 August 2018 (n= 1 567)

Table 5: Number of reported human cases and fatalities due to A(H7N9) infection up to 15 August 2018

	First wave (02/2013–09/2013)	**Second wave (10/2013–09/2014)**	**Third wave (10/2014–09/2015)**	**Fourth wave (09/2015–10/2016)**	**Fifth wave (10/2016-10/2017)**	**Sixth wave (10/2017-05/2018)**	**Cumulative number of cases**
Cases	135	320	223	120	766	3	1 567
Deaths	43	134	98	45	248	1	569
CFR (%)	32%	42%	44%	38%	32%	33%	36%

Source: Data from WHO (WHO, 2018c, online-a).

The virological characteristics of the HPAI and LPAI A(H7N9) viruses of the fifth wave were investigated and a higher thermostability as well as a slightly higher pathogenicity in mice of HPAI virus compared to LPAI virus were identified (He et al., 2018). Genetic changes of molecular markers in LPAI but also in HPAI viruses within the HA gene were described to possibly affect receptor binding properties. Both, LPAI and HPAI viruses bound to alpha-2.3 and alpha-2.6 receptors while LPAI virus had an increased preference for alpha-2.6. The gene composition of the viruses showed some variation indicating different virus evolution and reassortment events.

Another study (Changwen et al., 2018) found that, over time, mutations in HA gene were related to sites relevant for receptor recognition or antigenicity. Evolution processes related to adaptation were described for highly pathogenic viruses. In addition, it was possible to identify separate antigenic clusters of different lineages.

LPAI virus and HPAI virus A(H7N9) were repeatedly detected in raw duck meat transported illegally in hand luggage by flight passengers from China to Japan between 2016 and 2018 (Shibata et al., 2018).

4.5.6. LPAI A(H9N2)

4.5.6.1. Domestic and wild birds

Detection

As mentioned in the previous reports (EFSA, 2018b, a), A(H9N2) is the most commonly detected non-notifiable subtype of influenza viruses in poultry in Asia, the Middle East and North Africa. The endemic status of these regions continued between 16 May 2018 and 15 August 2018.

Phenotypic characterisation

Recently published studies reported on the reduced replication of A(H9N2) during simultaneous infection with infectious bronchitis virus (Aouini et al., 2018), but also enhanced clinical signs and mortality rates in chickens infected with A(H9N2) virus and vaccinated against infectious laryngotracheitis (Arafat et al., 2018) or co-infected with A(H9N2) virus and *Escherichia coli* (Jaleel et al., 2017).

Pathogenicity and transmission studies of A(H9N2) BJ/94-like isolates from 2011-2014 in 3-week-old specific-pathogen-free chickens revealed better virus replication in the upper respiratory tract than in the lower respiratory tract, and showed distinct airborne transmission among isolates possibly correlated with differences in viral shedding from the trachea and cloaca (Zhu et al., 2018a).

Experimental infection of chukars with A(H9N2) of duck origin resulted in inflammatory lesions in the trachea, bronchus and parabronchus combined with the presence of viral antigen in the upper respiratory tract. The virus could be isolated from oropharyngeal swabs and lungs. The birds seroconverted 14 days post infection (Zhu et al., 2018b).

Genetic characterisation

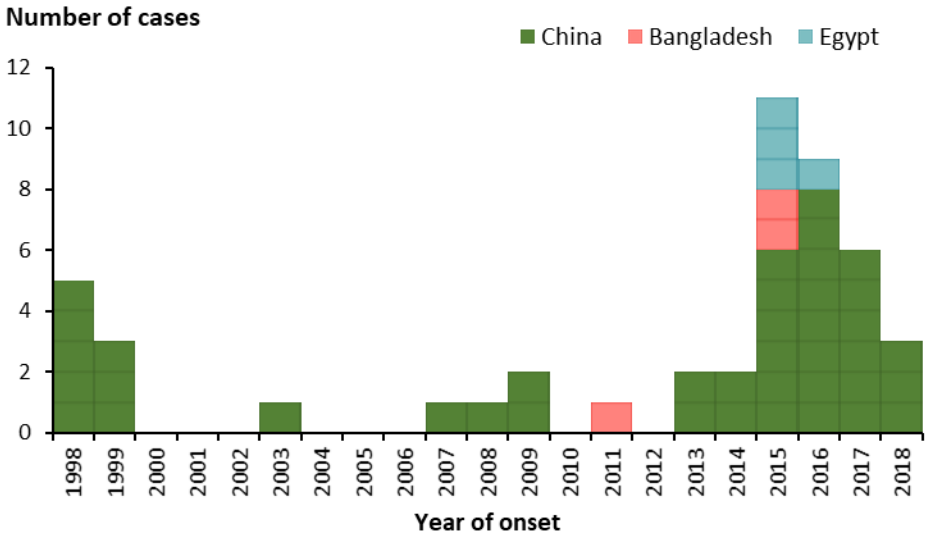
Phylogenetic analysis of 28 A(H9N2) strains isolated in China in 2011-2014 showed that they belong to BJ/94-like lineage but clustered in two independent branches (Zhu et al., 2018a). The authors reported 16 amino acid alterations in the antigenic sites and one amino acid change in the receptor binding site of HA. In another study performed in 13 provinces of China during 2012-2016, a total of 23 A(H9N2) strains were detected and the vast majority fell into lineage h9.4.2.5 (Xu et al., 2018).

Eight A(H9N2) viruses from wild birds sampled in Anhui Province in China (2014-2015) were genetically characterized by Ge et al. (2018). The authors described reassortment events between viruses representing North American and Eurasian lineages. Notably, two viruses from fecal samples collected from a pigeon and an unspecified species of wild anseriform had the mutation E627K in the PB2 protein, a feature associated with the adaptation of influenza viruses to mammalian species.

4.5.6.2. Human infections due to A(H9N2)

One new human case due to AI A(H9N2) has been reported from China since the last EFSA report (Government Information Bureau, online; Outbreak News Today, online). The case was a 24-year-old woman from Guangdong Province, China with onset of mild ilness on 21 July 2018. Exposure to a contaminated environment was assumed as the most likely source of infection. Close contacts tested negative (Government Information Bureau, online; Outbreak News Today, online).

Since 1998 and as of 15 August 2018, 47 laboratory-confirmed cases of human infection with AI A(H9N2) virus, including one death, have been reported globally. Cases occurred in China (40), Egypt (4) and Bangladesh (3) (Figure 13).



Source: WHO (WHO, 2018c)

Figure 13: Distribution of confirmed human cases of A(H9N2) by repoting country, 1998–15 August 2018 (n=47)

A(H9N2) viruses were detected in raw chicken or duck meat transported illegally in hand luggage by air passengers from China to Japan (Shibata et al., 2018).

4.5.7. Scientific analysis of AI spread from non-EU countries to poultry in the EU

In contrast to the last report (EFSA, 2018a), in the time period of this report from 16 May to 15 August 2018 a decreasing number of reported outbreaks in poultry and wild birds in Asia, Africa and the Middle East (sections 4.5.1–4.5.6). The reason might be the decreasing environmental stability of AI virus due to the higher temperatures and increased ultraviolet radiation during the recent months, as well as decreasing proportions of susceptible individuals in wild bird populations as a result of increased population immunity. Nevertheless, possible incursion into poultry establishments cannot be excluded due to the presence of HPAI virus in wild and domestic bird populations. Several outbreaks of clade 2.3.2.1c, A(H5N1) were reported from Asia, but no further outbreaks were reported in the relevant time period from Africa or the Middle East. Between 16 May and 15 August 2018 only two outbreaks of clade 2.3.4.4b, A(H5N8) were notified in poultry from South Africa and Saudi Arabia respectively, but several outbreaks in large commercial establishments and backyards were reported from Russia in July 2018. The introduction via the north-eastern and eastern route from Russia has been associated with a high risk of A(H5) HPAI virus-infected wild birds entering the EU in contrast to the southern route associated with the Middle East and Africa (EFSA AHAW Panel, 2017). However, uncertainty remains high and close monitoring of the situation is required. Furthermore, fall migration from breeding sites to wintering sites will start soon depending on the weather conditions and the low temperature of autumn and winter may facilitate the environmental survival of AI virus potentially introduced to Europe. Aggregation before and during fall migration, as well as the mixing of wild birds from different geographic origins during migration, will increase the risk of the infection spreading.Outbreaks of novel zoonotic reassortant HPAI A(H5N6) belonging to clade 2.3.4.4c and HPAI A(H5N6) closely associated with clade 2.3.4.4b in poultry and wild birds are still confined to Asia. However, the reassortant closely associated with clade 2.3.4.4b was also detected in migratory wild birds in the first half of the year and demonstrates that the continued circulation of this lineage in multiple geographical regions is likely mediated by wild bird spread. There is considerable uncertainty regarding the real geographical distribution of these viruses. Furthermore, during the relevant period for this report, A(H7N9) and A(H5N1) viruses have not been detected in wild waterfowl. Constant monitoring is warranted, despite the low risk associated with the incursion of these subtypes into poultry establishments by means of wild birds due not only to the absence of detections of the viruses in wild birds in the breeding areas for the European free-living populations, but also to the high degree of adaptation of A(H7N9) to gallinaceous poultry species.

As mentioned in the last reports, there are several possible pathways through which AI viruses can be brought into the EU, including legal and illegal trade of poultry and poultry products, contaminated fomites and wild birds. Nevertheless, the risk of AI viruses being transported to Europe through poultry trade is negligible as live poultry, day-old chicks and semen have been identified as the only non-wild bird pathways via which AI virus introduction is non-negligible and as suitable risk management measures are in place, such as testing and quarantine (EFSA AHAW Panel, 2017). EU legislation (Regulation (EC) No 798/2008[2]) prohibits the importation of live poultry, day-old chicks and hatching eggs and Regulation (EU) No 139/2013[3] of other birds (captive birds such as parrots, finches and other ornamental birds for trade) from countries which cannot provide suitable health guarantees to comply with the required certification. The list of approved countries is therefore limited (for reference see Table F5 of Appendix F in EFSA AHAW Panel (2017)). Furthermore, the illegal movement of captive birds (passerines in particular) is a viable pathway for the spread of the viruses, notably A(H5Nx), but the risk is difficult to assess due to the paucity of data.

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

4.5.8.1. Surveillance in the EU

As outlined in the EFSA report for November 2017 – February 2018 (EFSA, 2018b), human infections with zoonotic and other novel influenza strains are notifiable under EU legislation[4] and the International Health Regulations (IHR) through the Early Warning and Response System and the IHR notification system, respectively (WHO, 2016).

4.5.8.2. Diagnosis

Routine laboratory diagnostics were described in the EFSA report November 2017 – February 2018 (EFSA, 2018b). All influenza A virus isolates or clinical samples that cannot be subtyped are to be submitted to the appropriate national reference laboratory (National Influenza Centres; NICs), and to a WHO Collaborating Centre for Reference and Research on Influenza for characterisation (WHO, 2017). Influenza virus sharing is coordinated by the WHO Global Influenza Surveillance and Response System (GISRS) (WHO, online-b).

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

Options for public health control measures remain the same as outlined in the EFSA report for November 2017 – February 2018 and should follow national guidelines and recommendations (EFSA, 2018b). A new publication summarises the public health measures taken in 22 EU/EEA Member States and Israel during the A(H5N8) outbreaks in 2016-17 (Adlhoch et al., 2018).

The use of personal protective measures for people exposed to birds that are infected with AI viruses will minimise the risk of transmission to humans.

4.5.8.4. Vaccines

Available and recommended vaccines or candidate vaccine viruses (CVVs) for humans were described in the EFSA report for November 2017 – February 2018 (EFSA, 2018b). Representative virus A/Fujian-Sanyuan/21099/2017 of the 2.3.4.4b HA lineage reacted less well with postinfection ferret antiserum raised against the available CVVs and the developemnt of a new CVV was proposed (WHO, 2018d).

---

[2] Commission Regulation (EC) No 798/2008 of 8 August 2008 laying down a list of third countries, territories, zones or compartments from which poultry and poultry products may be imported into and transit through the Community and the veterinary certification requirements. OJ L 226, 23.8.2008, p. 1–94.

[3] Commission Implementing Regulation (EU) No 139/2013 of 7 January 2013 laying down animal health conditions for imports of certain birds into the Union and the quarantine conditions thereof . OJ L 47/1, 20.02.2013, p. 1-17.

[4] Decision No 1082/2013/EU of the European Parliament and of the Council of 22 October 2013 on serious cross-border threats to health and repealing Decision No 2119/98/EC. OJ L 293, 5.11.2013, p. 1–15.

WHO published a status update on avian influenza A(H7N9) CVV development and availability (WHO, online-c).

4.5.9. ECDC risk assessment for the general public in the EU

The risk of zoonotic influenza transmission to the general public in EU countries remains very low. Viruses detected in wild birds or poultry in Europe have not been shown to transmit to humans and have been considered as avian adapted viruses. Outbreaks due to AI viruses or detections of infected wild birds continued at a very low level during the summer months. Surveillance of avian influenza viruses in wild birds and poultry in the EU is important for detecting further virus spread among birds and reducing the possible risk of exposure of humans to infected birds. Controlling illegally imported poultry products is also important in order to prevent the importation of AI viruses relevant for both public and veterinary health.

Zoonotic transmission of viruses related to AI A(H5) clade 2.3.4.4 that are circulating in wild birds and poultry in Europe cannot be fully excluded as these viruses are able to reassort and new viruses may emerge or be introduced e.g. via migratory birds. So far, however, no transmission to any person exposed to an infected bird has been described in Europe. Avian influenza virus transmission to humans is a rare event overall and the risk is considered very low for viruses with an avian-adapted genetic makeup. The use of personal protective measures for people exposed to avian influenza viruses will minimise any residual risk.

The risk of travel-related importation of human AI cases particularly from Asia is low. Currently, a very low number of human cases are reported from China and other countries in South-east Asia. This indicates a low level of virus circulation, e.g. of A(H7N9) viruses in poultry markets and the environment.

References

Adlhoch C, Dabrera G, Penttinen P, Pebody R and Country E, 2018. Protective Measures for Humans against Avian Influenza A(H5N8) Outbreaks in 22 European Union/European Economic Area Countries and Israel, 2016-17. Emerging Infectious Diseases, 2018 Oct 17;24(10). doi:10.3201/eid2410.180269

Aouini R, Laamiri N and Ghram A, 2018. Viral interference between low pathogenic avian influenza H9N2 and avian infectious bronchitis viruses in vitro and in ovo. Journal of Virological Methods, 259, 92-99. doi:10.1016/j.jviromet.2018.06.011

Arafat N, Eladl AH, Marghani BH, Saif MA and El-shafei RA, 2018. Enhanced infection of avian influenza virus H9N2 with infectious laryngeotracheitis vaccination in chickens. Veterinary Microbiology, 219, 8-16. doi:10.1016/j.vetmic.2018.04.009

Bi Y, Tan S, Yang Y, Wong G, Zhao M, Zhang Q, Wang Q, Zhao X, Li L, Yuan J, Li H, Li H, Xu W, Shi W, Quan C, Zou R, Li J, Zheng H, Yang L, Liu WJ, Liu D, Wang H, Qin Y, Liu L, Jiang C, Liu W, Lu L, Gao GF and Liu Y, 2018. Clinical and immunological characteristics of human infections with H5N6 avian influenza virus. Clinical Infectious Diseases, ciy681-ciy681. doi:10.1093/cid/ciy681

Briand FX, Niqueux E, Schmitz A, Hirchaud E, Quenault H, Allee C, Le Prioux A, Guillou-Cloarec C, Ogor K, Le Bras MO, Gares H, Daniel P, Fediaevsky A, Martenot C, Massin P, Le Bouquin S, Blanchard Y and Eterradossi N, 2018. Emergence and multiple reassortments of French 2015-2016 highly pathogenic H5 avian influenza viruses. Infect Genet Evol, 61, 208-214. doi:10.1016/j.meegid.2018.04.007

Briand FX, Schmitz A, Ogor K, Le Prioux A, Guillou-Cloarec C, Guillemoto C, Allée C, Le Bras MO, Hirchaud E, Quenault H, Touzain F, Cherbonnel-Pansart M, Lemaitre E, Courtillon C, Gares H, Daniel P, Fediaevsky A, Massin P, Blanchard Y, Eterradossi N, van der Werf S, Jestin V and Niqueux E, 2017. Emerging highly pathogenic H5 avian influenza viruses in France during winter 2015/16: phylogenetic analyses and markers for zoonotic potential. Eurosurveillance, 22(9):pii=30473. doi:10.2807/1560-7917.ES.2017.22.9.30473

Changwen K, Jayna R, Rhys P, Thomas AB, Julien T, Shanqian H, Yingchao S, Lirong Z, Lijun L, Ru B, Yi J, Pingping Z, Min K, Lina Y, Jie W and Oliver GP, 2018. Molecular Evolution, Diversity, and Adaptation of Influenza A(H7N9) Viruses in China. Emerging Infectious Disease journal, 24, 1795. doi:10.3201/eid2410.171063

Chen L-H, Lee D-H, Liu Y-P, Li W-C, Swayne DE, Chang J-C, Chen Y-P, Lee F, Tu W-J and Lin Y-J, 2018. Reassortant Clade 2.3.4.4 of Highly Pathogenic Avian Influenza A(H5N6) Virus, Taiwan, 2017. Emerging Infectious Diseases, 24, 1147-1149. doi:10.3201/eid2406.172071

CHP (Centre for Health Protection of the Department of Health), 2018. Avian Influenza Report August 12 - August 18, 2018 (Week 33). Avian Influenza Report, 14, 33, 8 pp., Available online: https://www.chp.gov.hk/files/pdf/2018_avian_influenza_report_vol14_wk33.pdf

DEFRA (Department for Environment Food & Rural Affairs), 2018. Rapid Risk Assessment on the finding of H5N6 HPAI in wild birds in Dorset. Available online: https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/673851/rra-avian-flu-h5n6.pdf [Accessed: 14 September 2018]

Dietze K, Graaf A, Homeier-Bachmann T, Grund C, Forth L, Pohlmann A, Jeske C, Wintermann M, Beer M, Conraths FJ and Harder T, 2018. From low to high pathogenicity—Characterization of H7N7 avian influenza viruses in two epidemiologically linked outbreaks. Transboundary and Emerging Diseases, 2018 May 23. doi:10.1111/tbed.12906

EFSA (European Food Safety Authority), ECDC (European Centre for Disease Prevention and Control), EURL (EU Reference Laboratory for Avian Influenza), Adlhoch C, Brouwer A, Kuiken T, Mulatti P, Smietanka K, Staubach C, Willeberg P, Barrucci F, Verdonck F, Amato L and Baldinelli F, 2018a. Scientific Report: Avian influenza overview February – May 2018. EFSA Journal 2018;16(6):5358, 50 pp., doi: 10.2903/j.efsa.2018.5358

EFSA (European Food Safety Authority), ECDC (European Centre for Disease Prevention and Control), EURL (EU Reference Laboratory for Avian Influenza), Adlhoch C, Brouwer A, Kuiken T, Mulatti P, Smietanka K, Staubach C, Willeberg P, Barrucci F, Verdonck F, Amato L and Baldinelli F, 2018b. Scientific Report: Avian influenza overview November 2017 - February 2018. EFSA Journal 2018;16(3):5240, 55 pp. doi: 10.2903/j.efsa.2018.5240

EFSA (European Food Safety Authority), ECDC (European Centre for Disease Prevention and Control), EURL (EU Reference Laboratory for Avian Influenza), Brown I, Kuiken T, Mulatti P, Smietanka

K, Staubach C, Stroud D, Therkildsen OR, Willeberg P, Baldinelli F, Verdonck F and Adlhoch C, 2017a. Scientific Report: Avian influenza overview September - November 2017. EFSA Journal 2017;15(12):5141, 70 pp. doi: 10.2903/j.efsa.2017.5141

EFSA (European Food Safety Authority), ECDC (European Centre for Disease Prevention and Control), EURL (EU Reference Laboratory for Avian Influenza), Brown I, Mulatti P, Smietanka K, Staubach C, Willeberg P, Adlhoch C, Candiani D, Fabris C, Zancanaro G, Morgado J and Verdonck F, 2017b. Scientific report on the avian influenza overview October 2016 – August 2017. EFSA Journal 2017;15(10):5018, 101 pp. doi: 10.2903/j.efsa.2017.5018

EFSA AHAW Panel (EFSA Panel on Animal Health and Animal Welfare), Breed A, Brouwer A, Guillemain M, Harder T, Monne I, Roberts H, Baldinelli F, Barrucci F, Fabris C, Martino L, Mosbach-Schulz O, Verdonck F, Morgado J and Stegeman JA, 2017. Scientific opinion on avian influenza. EFSA Journal 2017;15(10):4991, 233 pp. doi: 10.2903/j.efsa.2017.4991

European Commission, online-a. Animal Disease Notification System (ADNS). Available online: https://ec.europa.eu/food/animals/animal-diseases/not-system_en [Accessed: 4 September 2018]

European Commission, online-b. Animal Health - Regulatory Committee presentations. Available online: https://ec.europa.eu/food/animals/health/regulatory_committee/presentations_en [Accessed: 4 September 2018]

FAO (Food and Agriculture Organization), online-a. EMPRES-i - Global Animal Disease Information System. Available online: http://empres-i.fao.org/eipws3g/ [Accessed: 4 September 2018]

FAO (Food and Agriculture Organization), online-b. H7N9 situation update - 24 November 2017. Available online: http://www.fao.org/ag/againfo/programmes/en/empres/h7n9/wave_6/Situation_update_2017_11_24.html [Accessed: 4 September 2018]

Gao P, Du H, Fan L, Chen L, Liao M, Xu C, Xiang B and Ren T, 2018. Human infection with an avian-origin influenza A (H7N4) virus in Jiangsu: A potential threat to China. Journal of infection, 77, 249-257. doi:https://doi.org/10.1016/j.jinf.2018.07.005

Ge Y, Yao Q, Chai H, Hua Y, Deng G and Hualan C, 2018. A 627K variant in the PB2 protein of H9 subtype influenza virus in wild birds. Influenza and Other Respiratory Viruses, 2018 Jul 12. doi:10.1111/irv.12592

GISAID, online. GISAID - Homepage. Available online: https://www.gisaid.org/ [Accessed: 4 September 2018]

Globig A, Staubach C, Sauter-Louis C, Dietze K, Homeier-Bachmann T, Probst C, Gethmann J, Depner KR, Grund C, Harder TC, Starick E, Pohlmann A, Hoper D, Beer M, Mettenleiter TC and Conraths FJ, 2017. Highly Pathogenic Avian Influenza H5N8 Clade 2.3.4.4b in Germany in 2016/2017. Frontiers in Veterinary Science 2017, 4, 240. doi:10.3389/fvets.2017.00240

Government Information Bureau online. Guangdong confirmed a case of human infection with H9N2 avian influenza Health Bureau. Available online: https://www.gcs.gov.mo/showNews.php?DataUcn=128061&PageLang=C [Accessed: 18 September 2018]

Grund C, Hoffmann D, Ulrich R, Naguib M, Schinkothe J, Hoffmann B, Harder T, Saenger S, Zscheppang K, Tonnies M, Hippenstiel S, Hocke A, Wolff T and Beer M, 2018. A novel European H5N8 influenza A virus has increased virulence in ducks but low zoonotic potential. Emerging Microbes & Infections, 7, 132. doi:10.1038/s41426-018-0130-1

Guo F, Luo T, Pu Z, Xiang D, Shen X, Irwin DM, Liao M and Shen Y, 2018. Increasing the potential ability of human infections in H5N6 avian influenza A viruses. Journal of infection, 2018 Aug 2. doi:https://doi.org/10.1016/j.jinf.2018.07.015

Harder T, 2018, pers. communication. Reported by C. Staubach via email on 06 Sept 2018. Friedrich-Loeffler-Institut (FLI), e-mail.

He L, Liu D, Hu J, Sun W, Gao R, Shi L, He D, Li B, Wang X, Gu M, Hu S, Liu X, Hu Z, Chen S, Peng D and Liu X, 2018. A comprehensive comparison of the fifth-wave highly pathogenic and low-pathogenic H7N9 avian influenza viruses reveals potential threat posed by both types of viruses in mammals. Transboundary and Emerging Diseases, 2018 Jul 17. doi:http://doi.org/10.1111/tbed.12954

Jaleel S, Younus M, Idrees A, Arshad M, Khan AU, Ehtisham-ul-Haque S, Zaheer MI, Tanweer M, Towakal F, Tipu MY, Sohail ML and Umar S, 2017. Pathological alterations in respiratory system during co-infection with low pathogenic avian influenza virus (H9N2) and Escherichia coli in broiler chickens. Journal of Veterinary Research, 61, 253-258. doi:https://doi.org/10.1515/jvetres-2017-0035

Jiang H, Wu P, Uyeki TM, He J, Deng Z, Xu W, Lv Q, Zhang J, Wu Y, Tsang TK, Kang M, Zheng J, Wang L, Yang B, Qin Y, Feng L, Fang VJ, Gao GF, Leung GM, Yu H and Cowling BJ, 2017. Preliminary Epidemiologic Assessment of Human Infections With Highly Pathogenic Avian Influenza A(H5N6) Virus, China. Clinical Infectious Diseases, 65, 383-388. doi:https://doi.org/10.1093/cid/cix334

Kwon HI, Kim EH, Kim YI, Park SJ, Si YJ, Lee IW, Nguyen HD, Yu KM, Yu MA, Jung JH, Choi WS, Kwon JJ, Ahn SJ, Baek YH, Van Lai D, Lee OJ, Kim SW, Song MS, Yoon SW, Kim CJ, Webby RJ, Mo IP and Choi YK, 2018. Comparison of the pathogenic potential of highly pathogenic avian influenza (HPAI) H5N6, and H5N8 viruses isolated in South Korea during the 2016-2017 winter season. Emerging Microbes & Infection, 7, 29. doi:https://doi.org/10.1038/s41426-018-0029-x

Lee EK, Lee YN, Kye SJ, Lewis NS, Brown IH, Sagong M, Heo GB, Kang YM, Cho HK, Kang HM, Cheon SH, Lee M, Park BK, Kim YJ and Lee YJ, 2018. Characterization of a novel reassortant H5N6 highly pathogenic avian influenza virus clade 2.3.4.4 in Korea, 2017. Emerging Microbes & Infection, 2018 Jun 13;7(1):103. doi:https://doi.org/10.1038/s41426-018-0104-3

MoA (Ministry of Agriculture of the People's republic of China), online. H7N9 situation update. Available online: http://english.agri.gov.cn/ [Accessed: 4 September 2018]

OIE (World Organisation for Animal Health), online-a. H5N2 HPAI poultry in Russia - WAHIS Disease Information. 3 pp., Available online: http://www.oie.int/wahis_2/temp/reports/en_imm_0000027576_20180817_120856.pdf

OIE (World Organisation for Animal Health), online-b. WAHIS Interface disease information. Available online: http://www.oie.int/wahis_2/public/wahid.php/Diseaseinformation/Diseasehome [Accessed: 4 September 2018]

Olsen B, Munster VJ, Wallensten A, Waldenstrom J, Osterhaus AD and Fouchier RA, 2006. Global patterns of influenza A virus in wild birds. Science, 312, 384-388. doi:https://doi.org/10.1126/science.1122438

Outbreak News Today online. H9N2 avian influenza case reported in Guangdong Province, China. Available online: http://outbreaknewstoday.com/h9n2-avian-influenza-case-reported-guangdong-province-china-78738/ [Accessed: 18 September 2018]

Parvin R, Begum JA, Nooruzzaman M, Chowdhury EH, Islam MR and Vahlenkamp TW, 2018. Review analysis and impact of co-circulating H5N1 and H9N2 avian influenza viruses in Bangladesh. Epidemiology and Infection, 146, 1259-1266. doi:https://doi.org/10.1017/s0950268818001292

Pohlmann A, Starick E, Grund C, Hoper D, Strebelow G, Globig A, Staubach C, Conraths FJ, Mettenleiter TC, Harder T and Beer M, 2018. Swarm incursions of reassortants of highly pathogenic avian influenza virus strains H5N8 and H5N5, clade 2.3.4.4b, Germany, winter 2016/17. Scientific Reports, 2018 Jan 8;8(1):15, doi:10.1038/s41598-017-16936-8

Qin T, Zhu J, Ma R, Yin Y, Chen S, Peng D and Liu X, 2018. Compatibility between haemagglutinin and neuraminidase drives the recent emergence of novel clade 2.3.4.4 H5Nx avian influenza viruses in China. Transboundary and Emerging Diseases, 2018 Jul 12. doi:https://doi.org/10.1111/tbed.12949

Root JJ, Bosco-Lauth AM, Marlenee NL and Bowen RA, 2018. Cottontail rabbits shed clade 2.3.4.4 H5 highly pathogenic avian influenza A viruses. Archives of Virology, 2018 Oct;163(10):2823-2827. doi:https://doi.org/10.1007/s00705-018-3907-6

Ryu S, Kim CK, Kim K, Woo SH and Chun BC, 2018. Serosurveillance of avian influenza (H5N6) virus infection in poultry farmers, Gyeonggi Province, Republic of Korea, 2016-2017. International Journal of Infectious Diseases, 2018 Aug 7;75:49-51. doi:https://doi.org/10.1016/j.ijid.2018.08.002

Seekings AH, Slomka MJ, Russell C, Howard WA, Choudhury B, Nuñéz A, Löndt BZ, Cox W, Ceeraz V, Thorén P, Irvine RM, Manvell RJ, Banks J and Brown IH, 2018. Direct evidence of H7N7 avian influenza virus mutation from low to high virulence on a single poultry premises during an outbreak in free range chickens in the UK, 2008. Infection, genetics and evolution, 64, 13-31. doi:https://doi.org/10.1016/j.meegid.2018.06.005

Shibata A, Okamatsu M, Sumiyoshi R, Matsuno K, Wang Z-J, Kida H, Osaka H and Sakoda Y, 2018. Repeated detection of H7N9 avian influenza viruses in raw poultry meat illegally brought to

Japan by international flight passengers. Virology, 524, 10-17. doi:https://doi.org/10.1016/j.virol.2018.08.001

Sun W, Li J, Hu J, Jiang D, Xing C, Zhan T and Liu X, 2018. Genetic analysis and biological characteristics of different internal gene origin H5N6 reassortment avian influenza virus in China in 2016. Veterinary Microbiology, 219, 200-211. doi:https://doi.org/10.1016/j.vetmic.2018.04.023

Suttie A, Karlsson EA, Deng Y-M, Horm SV, Yann S, Tok S, Sorn S, Holl D, Tum S, Hurt AC, Greenhill AR, Barr IG, Horwood PF and Dussart P, 2018. Influenza A(H5N1) viruses with A(H9N2) single gene (matrix or PB1) reassortment isolated from Cambodian live bird markets. Virology, 523, 22-26. doi:https://doi.org/10.1016/j.virol.2018.07.028

The Government of the Hong Kong Special Administrative Region, online. CHP notified of human case of avian influenza A(H5N6) in Guangxi [Press release]. Available online: http://www.info.gov.hk/gia/general/201808/20/P2018082000427.htm [Accessed: 23 August 2018]

Tong X-C, Weng S-S, Xue F, Wu X, Xu T-M and Zhang W-H, 2018. First human infection by a novel avian influenza A(H7N4) virus. Journal of infection, 77, 249-257. doi:https://doi.org/10.1016/j.jinf.2018.06.002

Twabela AT, Tshilenge GM, Sakoda Y, Okamatsu M, Bushu E, Kone P, Wiersma L, Zamperin G, Drago A, Zecchin B and Monne I, 2018. Highly Pathogenic Avian Influenza A(H5N8) Virus, Democratic Republic of the Congo, 2017. Emerging Infectious Diseases, 24, 1371-1374. doi:https://doi.org/10.3201/eid2407.172123

Wade A, Jumbo SD, Zecchin B, Fusaro A, Taiga T, Bianco A, Rodrigue PN, Salomoni A, Kameni JMF, Zamperin G, Nenkam R, Foupouapouognigni Y, Abdoulkadiri S, Aboubakar Y, Wiersma L, Cattoli G and Monne I, 2018a. Highly Pathogenic Avian Influenza A(H5N8) Virus, Cameroon, 2017. Emerging Infectious Diseases, 24, 1367-1370. doi:https://doi.org/10.3201/eid2407.172120

Wade A, Taïga, Fouda MA, MaiMoussa A, Jean Marc FK, Njouom R, Vernet M-A, Djonwe G, Mballa E, Kazi JP, Nenkam R, Poueme Namegni R, Bamanga H, Casimir NKM, Lebreton M, Nwobegahay J, Fusaro A, Zecchin B, Milani A, Gaston M, Chepnda VR, Dickmu Jumbo S, Souley A, Aboubakar Y, Fotso Kamnga Z, Couo K, Atkam H, Dauphin G, Wiersma L, Bebay C, Nzietchueng S, Vincent T, Biaou C, Mbacham W, Monne I and Cattoli G, 2018b. Highly pathogenic avian influenza A/H5N1 Clade 2.3.2.1c virus in poultry in Cameroon, 2016-2017. Avian Pathology, 1-51. doi:https://doi.org/10.1080/03079457.2018.1492087

Wageningen University and Research online. Bird flu in Emmer. Available online: https://www.wur.nl/nl/nieuws/Vogelgriep-in-Eemmeer.htm [Accessed: 25 September 2018]

WHO (World Health Organization), 2016. International Health Regulations (2005) - Third edition. Available online: http://www.who.int/ihr/publications/9789241580496/en/ [Accessed: 4 September 2017]

WHO (World Health Organization), 2017. Operational Guidance on Sharing Influenza Viruses with Human Pandemic Potential (IVPP) under the Pandemic Influenza Preparedness (PIP) Framework. Available online: http://apps.who.int/iris/bitstream/handle/10665/259402/WHO-WHE-IHM-GIP-2017.3-eng.pdf;jsessionid=FF66316FB599ADA38D34499AA56765FA?sequence=1 [Accessed: 4 September 2018]

WHO (World Health Organization), 2018a. Cumulative number of confirmed human cases of avian influenza A(H5N1) reported to WHO, 2013-2017. WHO, Geneva. 3 pp., Available online: http://www.who.int/influenza/human_animal_interface/2017_09_27_tableH5N1.pdf?ua=1

WHO (World Health Organization), 2018b. Influenza at the human-animal interface; Summary and assessment, 8 December 2017 to 25 January 2018., 5 pp., Available online: http://www.who.int/influenza/human_animal_interface/Influenza_Summary_IRA_HA_interface_25_01_2018_FINAL.pdf?ua=1

WHO (World Health Organization), 2018c. Influenza at the human-animal interface - Summary and assessment, 26 January to 2 March 2018. Available online: http://www.who.int/influenza/human_animal_interface/Influenza_Summary_IRA_HA_interface_02_03_2018.pdf?ua=1 [Accessed: 4 September 2018]

WHO (World Health Organization), 2018d. Antigenic and genetic characteristics of zoonotic influenza viruses and development of candidate vaccine viruses for pandemic preparedness. WHO, Geneva. 10 pp., Available online: http://www.who.int/influenza/vaccines/virus/201802_zoonotic_vaccinevirusupdate.pdf?ua=1

WHO (World Health Organization), online-a. Human infection with avian influenza A(H7N4) virus – China: Update. Available online: http://www.who.int/csr/don/05-september-2018-ah7n9-china/en/ [Accessed: 18 September 2018]

WHO (World Health Organization), online-b. Influenza - Virus Sharing. Available online: http://www.who.int/influenza/pip/virus_sharing/en/ [Accessed: 4 September 2018]

WHO (World Health Organization), online-c. Summary of status of development and availability of avian influenza A(H7N9) candidate vaccine viruses and potency testing reagents. Available online: http://www.who.int/influenza/vaccines/virus/candidates_reagents/summary_a_h7n9_cvv_20180808.pdf?ua=1&ua=1 [Accessed: 18 September 2018]

Xu C, Ye H, Qiu W, Lin H, Chen Y, Zhang H and Liao M, 2018. Phylogenetic classification of hemagglutinin gene of H9N2 avian influenza viruses isolated in China during 2012–2016 and evaluation of selected candidate vaccine strains. Poultry Science, 97, 3023-3030. doi:https://doi.org/10.3382/ps/pey154

Zhu R, Xu D, Yang X, Zhang J, Wang S, Shi H and Liu X, 2018a. Genetic and biological characterization of H9N2 avian influenza viruses isolated in China from 2011 to 2014. Plos One, 13, e0199260. doi:https://doi.org/10.1371/journal.pone.0199260

Zhu YC, Zhang B, Sun ZH, Wang XJ, Fan XH, Gao LX, Liang Y, Chen XY and Zhang ZF, 2018b. Replication and Pathology of Duck Influenza Virus Subtype H9N2 in Chukar. Biomedical and environmental sciences : BES, 31, 306-310. doi:https://doi.org/10.3967/bes2018.039

Abbreviations

ADNS	Animal Disease Notification System
AI	Avian Influenza
CVV	Candidate vaccine virus
ECDC	European Centre for Disease Prevention and Control
EFSA	European Food Safety Authority
FAO	Food and Agriculture Organization
HPAI	Highly pathogenic avian influenza
IHR	International Health Regulations
IVPI	Intravenous pathogenicity index
LPAI	Low pathogenic avian influenza
MS	Member State
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, 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[5], 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[6], EFSA should provide the technical and scientific assistance to the Commission based on the following Terms of Reference:

---

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

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

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

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

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

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

A.2. Interpretation of the terms of reference

In reply to TOR 1 and 2, this scientific report gives an overview of the HPAI and LPAI outbreaks in poultry and captive birds as well as the HPAI outbreaks in wild birds detected in Europe between 16 May and 15 August 2018, mainly based on data submitted by Member States and neighbouring countries via ADNS. Member States where HPAI outbreaks occurred in poultry submitted additional epidemiological data to EFSA, which have been used to analyse the characteristics of poultry establishments affected between 16 May and 15 August 2018.

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, etc.), which should be collected in a harmonised manner across the EU. Limitations in the performed data collection, reporting and analysis were exlained in the first avian influenza overview report (EFSA, 2017b).

A description of the applied prevention and control measures (TOR3) is given based on case reports provided by representatives from Bulgaria, Denmark and the United Kingdom and attached as Annex A to this report. The main topics covered are increasing awareness, release and repeal of housing order, strengthening biosecurity, preventive culling, and implementation of a regional stand still, hunting and derogations from restriction zone implementation after a risk assessment.

The monitoring of the avian influenza situation on other continents (TOR 4) focuses on HPAI A(H5N1), HPAI A(H5N6), HPAI A(H5N8), A(H7N4), HPAI/LPAI A(H7N9) and LPAI A(H9N2). Background and epidemiology, detections, phenotypic and genetic characterisations are described based on information from confirmed human, poultry and wild bird cases that occurred between 16 May and 15 August 2018. Possible actions for preparedness in the EU are discussed.

The report mainly describes information that became available since the publication of the EFSA report for February– May 2018 (EFSA, 2018b) and that might affect the interpretation of risks related to avian influenza 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)

The data on the avian influenza outbreaks that occurred from 16 May to 15 August 2018 submitted by Member States (MSs) to the ADNS (European Commission, online-a) were taken into account for this report. In addition, Bulgaria was asked to provide more detailed epidemiological data (see Table A.1, Appendix A in EFSA (EFSA, 2018b)) directly to EFSA on the HPAI outbreaks that occurred in poultry during the same period.

The slide presentations, which EU Member States affected by HPAI and LPAI presented to the SCOPAFF meeting, and the information on HPAI and LPAI outbreaks provided in the INFO NOTEs by the affected MSs to the European Commission, were consulted to extract relevant information reported in Sections 4.2.1, 4.2.2 and 4.2.3. The PDFs of the SCOPAFF presentations are available on the European Commission website (European Commission, online-b). Information from the website of Wageningen Bioveterinary Research (Wageningen University and Research, online) was used to complement data on HPAI in wild birds occurred outside the reporting period in the Netherlands.

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

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

Review question Update on the phenotypic characterisation of HPAI viruses circulating in the EU in domestic and wild birds within the reporting period.

Search The PubMed database was searched by using subject index terms and free text terms combined with the appropriate Boolean operators. Scientific articles added to the database from 16 May to 15 August were searched; the search was run on 20 August 2018. Information regarding the search strategy (terms and search string) is provided in Appendix C.1.

Relevance criteria Scientific articles added to the database from 16 May 2018 to 15 August 2018 and reporting information on the presence or absence of clinical signs or pathological changes or mortality due to HPAI infection with viruses circulating 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; -only for experimental studies the age of the infected animals should be reported (at least as juvenile/adult).

Results The search retrieved 120 papers. After de-duplication against previous searches, 118 papers remained. The articles were subsequently screened against the relevance and eligibility criteria. Three papers were 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.

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

Bulgaria, Denmark and the United Kingdom expressed an interest in supporting the analysis of the AI outbreaks from 16 May to 15 August 2018 and submitted case reports on their AI prevention and control measures based on the template that was generated for previous reports (EFSA, 2017a; EFSA, 2018b). The case reports provided to EFSA can be consulted in Annex A.

B.1.3. Overview of AI outbreaks on other continents (TOR 4)

Data from FAO EMPRES-i (FAO, online-a) on HPAI A(H5N1), A(H5N6), A(H5N8), HPAI and LPAI A(H7N9) in domestic, captive and wild birds, and environmental samples, were used to map the 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 overcomplication of the maps, captive birds and environmental samples have been mapped as domestic birds. Despite the fact that some of these kept animals may be of wild species, in most of the cases captive birds, or, for environmental samples, the birds from which samples have been taken (mainly at live market places) will not move around and not spread the infection by migrating and for this reason have been reported as domestic birds. Only when there was a strong discrepancy among the locality, the administrative regions and geo-coordinates, and the outbreaks were not officially reported to the OIE (e.g. national authorities), were confirmed outbreaks not taken into account in the analysis.

B.1.3.1. Literature review on phenotypic and genetic characterisation of HPAI viruses circulating on other continents

Information on phenotypic and genotypic characterisation of HPAI viruses circulating on other continents and 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 in other continents and regions (Africa, Asia, the Middle East) in domestic or wild birds or mammals (excluding humans).

Search The PubMed database was searched by using subject index terms and free-text terms combined with the appropriate Boolean operators. Scientific articles added to the database from 16 May to 15 August were searched; the search was run on 20 August 2018. Information regarding the search strategy (terms and search string) is provided in Appendix C.2.

Relevance criteria Scientific articles added to the database from 16 May 2018 to 15 August 2018 and reporting information on the presence or absence of clinical signs, pathological changes or mortality or genotypic characterisation due to HPAI infection with viruses circulating 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; -only for experimental studies the age of the infected animals should be reported (at least as juvenile/adult).

Results The search retrieved 123 papers. After de-duplication against previous searches, 122 papers remained. The articles were subsequently screened against the relevance and eligibility criteria. Sixteen papers were in the end taken into consideration in the description of phenotypic and genotypic characterisation of HPAI viruses circulating on other continents and regions (Africa, Asia, the Middle East) in domestic or wild birds or mammals (excluding humans) in the reporting period.

B.2. Data on humans

The collection of numbers of human cases due to infection with AI viruses has been performed 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 are laboratory-confirmed cases. Data are continuously checked for double entries and validity. The data on human cases covers 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 new human cases during the reporting period.

Literature searches were performed until 24 August 2018 in the PubMed database with the key words: 'humans' and 'A(H5N1)'; 'A(H5N6)'; 'A(H5N8)'; 'A(H7N4); 'A(H7N9)'; A(H9N2)'; and narrowed to the most recent available publications as well as using specific search parameters such as 'seroprevalence'; 'risk factors'; 'transmission'; 'humans'; 'mammals'. The literature search was not systematic or comprehensive.

Appendix C – Literature search on phenotypic and genetic characterisation of AI viruses

C.1. Phenotypic characterisation of HPAI viruses circulating in the EU in domestic and wild birds in the reporting period

Terms

Concept	Terms
Avian influenza	Avian influenza, avian flu, influenza in birds, influenza in bird, bird flu, birds flu, bird influenza, birds influenza, influenza virus A, influenza viruses A, flu virus A, flu viruses A, influenzavirusA, influenza A, influenza A virus, Influenza A viruses, flu A, flu A virus, flu A viruses, fluvirus A, high pathogenic avian influenza, high pathogenic avian influenza virus, HPAI, HPAIV, HPAIVs, low pathogenic avian influenza, high pathogenic avian influenza virus, LPAI, LPAIV, LPAIVs, AIV, AIVs, H5N*, AH5N*, H7N*, AH7N*, H9N*, AH9N*, A(H5N*), A(H7N*), A(H9N*)
Birds	Bird, birds, aves, avian population, avian populations, poultry, poultries, fowl, fowls, chicken, chickens, gallus gallus, g. gallus, waterfowl, waterfowls, water fowl, water fowls, duck, ducks, swan, swans, anatidae, mallard, mallards, Anas platyrhynchos, A platyrhynchos, geese, goose, anser, turkey, turkeys, meleagris, quail, quails, coturnix, patridge, patridges, phasianidae, guineafowl, guineafowls, numida, numidae, ostrich, ostriches, struthio

Search strings (PubMed)

Search	Query	Items found
#4	**Search** #3 AND ("2018/05/15"[Date - Entrez] : "2018/08/15"[Date - Entrez])	120
#3	Search (#1 AND #2)	11 113
#2	**Search** "Influenza in Birds"[Mesh] OR "Influenzavirus A"[Mesh] OR (avian[tiab] AND (influenza*[tiab]OR flu[tiab])) OR "influenza in bird"[tiab] OR "influenza in birds"[tiab] OR "bird flu"[tiab] OR "birds flu"[tiab] OR bird influenza*[tiab] OR "birds influenza"[tiab] OR ((influenza*[tiab] OR flu[tiab]) AND ("virus A" OR "viruses A")) OR "influenza A"[tiab] OR "flu A"[tiab] OR "influenzavirus A"[tiab] OR "fluvirus A"[tiab] OR HPAI[tiab] OR HPAIV[tiab] OR HPAIVs[tiab] OR LPAI [tiab] OR lPAIV[tiab] OR AIV[tiab] OR AIVs[tiab] OR H5N*[tiab] OR H7N*[tiab] OR H9N*[tiab] OR AH5N*[tiab] OR AH7N*[tiab] OR AH9N*[tiab]	51 253
#1	**Search** "Birds"[Mesh] OR bird[tiab] OR birds[tiab] OR aves[tiab] OR "avian population"[tiab] OR "avian populations"[tiab] OR poultr*[tiab] OR fowl[tiab] OR fowls[tiab] OR chicken*[tiab] OR "gallus gallus"[tiab] OR "g gallus"[tiab] OR waterfowl*[tiab] OR duck[tiab] OR ducks[tiab] OR anatidae[tiab] OR mallard[tiab] OR mallards[tiab] OR swan[tiab] OR swans[tiab] OR "Anas platyrhynchos"[tiab] OR "A platyrhynchos"[tiab] OR geese[tiab] OR goose[tiab] OR anser[tiab] OR turkey[tiab] OR turkeys[tiab] OR meleagris[tiab] OR quail[tiab] OR quails[tiab] OR coturnix[tiab] OR partridge*[tiab] OR phasianidae[tiab] OR guineafowl*[tiab] OR numida*[tiab] OR ostrich*[tiab] OR struthio[tiab]	298 415

C.2. Phenotypic and genetic characterisation of HPAI viruses circulating on other continents in domestic or wild birds or mammals (excluding humans)

Terms

Concept	Terms
Highly pathogenic avian influenza	High/highly pathogen* avian influenza, high/highly pathogen* avian flu, high/highly pathogen* influenza in birds, high/highly pathogen* influenza in bird, high/highly pathogen* bird flu, high/highly pathogen* birds flu, high/highly pathogen* bird influenza , high/highly pathogen* birds influenza , high/highly pathogen* influenza virus A, high/highly pathogen* influenza viruses

	A, high/highly pathogen* flu virus A, high/highly pathogen* flu viruses A, high/highly pathogen* infuenzavirusA, influenza A, high/highly pathogen* influenza A virus, high/highly pathogen* influenza A viruses, high/highly pathogen* flu A, high/highly pathogen* flu A virus, high/highly pathogen* flu A viruses, high/highly pathogen* fluvirus A, high/highly pathogen* AIV, high/highly pathogen* AIVs, HPAI, HPAIV, HPAIVs, H5N*, AH5N*, H7N*, AH7N*, H9N*, AH9N*, A(H5N*), A(H7N*), A(H9N*)
Animals	In order to simplify the retrieval of studies in animals, the search filter referenced below was used and adapted to include a better coverage of terms related to birds: Hooijmans CR, Tillema A, Leenaars M and Ritskes-Hoitinga M, 2010. Enhancing search efficiency by means of a search filter for finding all studies on animal experimentation in PubMed. Lab Anim, 44, 170-175. doi:10.1258/la.2010.009117 The search string is designed to retrieve studies in animal experimentation, but it also can be used to retrieve all type of studies in animals. It contains names of animals not relevant for avian influenza; these terms will not affect the results. However, the use of the already made filter simplifies the construction of the search string.

Search strings (PubMed)

Search	Query	Items found
#4	**Search** (#3) AND ("2018/05/15"[Date - Entrez] : "2018/08/15"[Date - Entrez])	123
#3	**Search** (#2 AND #1)	8 037
#2	**Search** ((high pathogen*[tiab] OR highly pathogen*[tiab]) AND ("Influenza in Birds"[Mesh] OR "Influenzavirus A"[Mesh] OR (avian[tiab] AND (influenza*[tiab]OR flu[tiab])) OR "influenza in bird"[tiab] OR "influenza in birds"[tiab] OR "bird flu"[tiab] OR "birds flu"[tiab] OR bird influenza*[tiab] OR "birds influenza"[tiab] OR "influenza virus A"[tiab] OR "influenza viruses A"[tiab] OR "influenza A"[tiab] OR "flu virus A"[tiab] OR "flu A"[tiab] OR "influenzavirus A"[tiab] OR "fluvirus A"[tiab] OR AIV[tiab] OR AIVs[tiab])) OR HPAI[tiab] OR HPAIV[tiab] OR HPAIVs[tiab] OR H5N*[tiab] OR H7N*[tiab] OR H9N*[tiab] OR AH5N*[tiab] OR AH7N*[tiab] OR AH9N*[tiab]	10 187
#1[7]	**Search** "animal experimentation"[MeSH Terms] OR "models, animal"[MeSH Terms] OR "invertebrates"[MeSH Terms] OR "Animals"[Mesh:noexp] OR "animal population groups"[MeSH Terms] OR "chordata"[MeSH Terms:noexp] OR "chordata, nonvertebrate"[MeSH Terms] OR "vertebrates"[MeSH Terms:noexp] OR "mammals"[MeSH Terms:noexp] OR "primates"[MeSH Terms:noexp] OR "artiodactyla"[MeSH Terms] OR "carnivora"[MeSH Terms] OR "cetacea"[MeSH Terms] OR "chiroptera"[MeSH Terms] OR "elephants"[MeSH Terms] OR "hyraxes"[MeSH Terms] OR "insectivora"[MeSH Terms] OR "lagomorpha"[MeSH Terms] OR "marsupialia"[MeSH Terms] OR "monotremata"[MeSH Terms] OR "perissodactyla"[MeSH Terms] OR "rodentia"[MeSH Terms] OR "scandentia"[MeSH Terms] OR "sirenia"[MeSH Terms] OR "xenarthra"[MeSH Terms] OR "haplorhini"[MeSH Terms:noexp] OR "strepsirhini"[MeSH Terms] OR "platyrrhini"[MeSH Terms] OR "tarsii"[MeSH Terms] OR "catarrhini"[MeSH Terms:noexp] OR "cercopithecidae"[MeSH Terms] OR "hylobatidae"[MeSH Terms] OR "hominidae"[MeSH Terms:noexp] OR "gorilla gorilla"[MeSH Terms] OR "pan paniscus"[MeSH Terms] OR "pan troglodytes"[MeSH Terms] OR "pongo pygmaeus"[MeSH Terms] OR ((animals[tiab] OR animal[tiab] OR mice[Tiab] OR mus[Tiab] OR mouse[Tiab] OR murine[Tiab] OR woodmouse[tiab] OR rats[Tiab] OR rat[Tiab] OR murinae[Tiab] OR muridae[Tiab] OR cottonrat[tiab] OR cottonrats[tiab] OR hamster[tiab] OR hamsters[tiab] OR cricetinae[tiab] OR rodentia[Tiab] OR rodent[Tiab] OR rodents[Tiab] OR pigs[Tiab] OR pig[Tiab] OR swine[tiab] OR swines[tiab] OR piglets[tiab] OR piglet[tiab] OR boar[tiab] OR boars[tiab] OR "sus scrofa"[tiab] OR ferrets[tiab] OR ferret[tiab] OR polecat[tiab] OR polecats[tiab] OR "mustela putorius"[tiab] OR "guinea pigs"[Tiab] OR "guinea pig"[Tiab] OR cavia[Tiab] OR callithrix[Tiab] OR marmoset[Tiab] OR marmosets[Tiab] OR cebuella[Tiab] OR hapale[Tiab] OR octodon[Tiab] OR chinchilla[Tiab] OR chinchillas[Tiab] OR gerbillinae[Tiab] OR gerbil[Tiab] OR gerbils[Tiab] OR jird[Tiab] OR jirds[Tiab] OR merione[Tiab] OR meriones[Tiab] OR rabbits[Tiab] OR rabbit[Tiab] OR hares[Tiab] OR hare[Tiab] OR diptera[Tiab] OR flies[Tiab] OR fly[Tiab] OR dipteral[Tiab] OR	6 673 045

---

[7] Animals search string adapted from: Hooijmans CR, Tillema A, Leenaars M and Ritskes-Hoitinga M, 2010. Enhancing search efficiency by means of a search filter for finding all studies on animal experimentation in PubMed. Lab Anim, 44, 170-175. doi:10.1258/la.2010.009117

drosphila[Tiab] OR drosophilidae[Tiab] OR cats[Tiab] OR cat[Tiab] OR carus[Tiab] OR felis[Tiab] OR nematoda[Tiab] OR nematode[Tiab] OR nematoda[Tiab] OR nematode[Tiab] OR nematodes[Tiab] OR sipunculida[Tiab] OR dogs[Tiab] OR dog[Tiab] OR canine[Tiab] OR canines[Tiab] OR canis[Tiab] OR sheep[Tiab] OR sheeps[Tiab] OR mouflon[Tiab] OR mouflons[Tiab] OR ovis[Tiab] OR goats[Tiab] OR goat[Tiab] OR capra[Tiab] OR capras[Tiab] OR rupicapra[Tiab] OR chamois[Tiab] OR haplorhini[Tiab] OR monkey[Tiab] OR monkeys[Tiab] OR anthropoidea[Tiab] OR anthropoids[Tiab] OR saguinus[Tiab] OR tamarin[Tiab] OR tamarins[Tiab] OR leontopithecus[Tiab] OR hominidae[Tiab] OR ape[Tiab] OR apes[Tiab] OR pan[Tiab] OR paniscus[Tiab] OR "pan paniscus"[Tiab] OR bonobo[Tiab] OR bonobos[Tiab] OR troglodytes[Tiab] OR "pan troglodytes"[Tiab] OR gibbon[Tiab] OR gibbons[Tiab] OR siamang[Tiab] OR siamangs[Tiab] OR nomascus[Tiab] OR symphalangus[Tiab] OR chimpanzee[Tiab] OR chimpanzees[Tiab] OR prosimians[Tiab] OR "bush baby"[Tiab] OR prosimian[Tiab] OR bush babies[Tiab] OR galagos[Tiab] OR galago[Tiab] OR pongidae[Tiab] OR gorilla[Tiab] OR gorillas[Tiab] OR pongo[Tiab] OR pygmaeus[Tiab] OR "pongo pygmaeus"[Tiab] OR orangutans[Tiab] OR pygmaeus[Tiab] OR lemur[Tiab] OR lemurs[Tiab] OR lemuridae[Tiab] OR horse[Tiab] OR horses[Tiab] OR pongo[Tiab] OR equus[Tiab] OR cow[Tiab] OR calf[Tiab] OR bull[Tiab] OR reptile[Tiab] OR reptilia[Tiab] OR reptiles[Tiab] OR snakes[Tiab] OR snake[Tiab] OR lizard[Tiab] OR lizards[Tiab] OR alligator[Tiab] OR alligators[Tiab] OR crocodile[Tiab] OR crocodiles[Tiab] OR turtle[Tiab] OR turtles[Tiab] OR amphibian[Tiab] OR amphibians[Tiab] OR amphibia[Tiab] OR frog[Tiab] OR frogs[Tiab] OR bombina[Tiab] OR salientia[Tiab] OR toad[Tiab] OR toads[Tiab] OR "epidalea calamita"[Tiab] OR salamander[Tiab] OR salamanders[Tiab] OR eel[Tiab] OR eels[Tiab] OR fish[Tiab] OR fishes[Tiab] OR pisces[Tiab] OR catfish[Tiab] OR catfishes[Tiab] OR siluriformes[Tiab] OR arius[Tiab] OR heteropneustes[Tiab] OR sheatfish[Tiab] OR perch[Tiab] OR perches[Tiab] OR percidae[Tiab] OR perca[Tiab] OR trout[Tiab] OR trouts[Tiab] OR char[Tiab] OR chars[Tiab] OR salvelinus[Tiab] OR "fathead minnow"[Tiab] OR minnow[Tiab] OR cyprinidae[Tiab] OR carps[Tiab] OR carp[Tiab] OR zebrafish[Tiab] OR zebrafishes[Tiab] OR goldfish[Tiab] OR goldfishes[Tiab] OR guppy[Tiab] OR guppies[Tiab] OR chub[Tiab] OR chubs[Tiab] OR tinca[Tiab] OR barbels[Tiab] OR barbus[Tiab] OR pimephales[Tiab] OR promelas[Tiab] OR "poecilia reticulata"[Tiab] OR mullet[Tiab] OR mullets[Tiab] OR seahorse[Tiab] OR seahorses[Tiab] OR mugil curema[Tiab] OR atlantic cod[Tiab] OR shark[Tiab] OR sharks[Tiab] OR catshark[Tiab] OR anguilla[Tiab] OR salmonid[Tiab] OR salmonids[Tiab] OR whitefish[Tiab] OR whitefishes[Tiab] OR salmon[Tiab] OR salmons[Tiab] OR sole[Tiab] OR solea[Tiab] OR "sea lamprey"[Tiab] OR lamprey[Tiab] OR lampreys[Tiab] OR pumpkinseed[Tiab] OR sunfish[Tiab] OR sunfishes[Tiab] OR tilapia[Tiab] OR tilapias[Tiab] OR turbot[Tiab] OR turbots[Tiab] OR flatfish[Tiab] OR flatfishes[Tiab] OR sciuridae[Tiab] OR squirrel[Tiab] OR squirrels[Tiab] OR chipmunk[Tiab] OR chipmunks[Tiab] OR suslik[Tiab] OR susliks[Tiab] OR vole[Tiab] OR voles[Tiab] OR lemming[Tiab] OR lemmings[Tiab] OR muskrat[Tiab] OR muskrats[Tiab] OR lemmus[Tiab] OR otter[Tiab] OR otters[Tiab] OR marten[Tiab] OR martens[Tiab] OR martes[Tiab] OR weasel[Tiab] OR badger[Tiab] OR badgers[Tiab] OR ermine[Tiab] OR mink[Tiab] OR minks[Tiab] OR sable[Tiab] OR sables[Tiab] OR gulo[Tiab] OR gulos[Tiab] OR wolverine[Tiab] OR wolverines[Tiab] OR minks[Tiab] OR mustela[Tiab] OR llama[Tiab] OR llamas[Tiab] OR alpaca[Tiab] OR alpacas[Tiab] OR camelid[Tiab] OR camelids[Tiab] OR guanaco[Tiab] OR guanacos[Tiab] OR chiroptera[Tiab] OR chiropteras[Tiab] OR bat[Tiab] OR bats[Tiab] OR fox[Tiab] OR foxes[Tiab] OR iguana[Tiab] OR iguanas[Tiab] OR xenopus laevis[Tiab] OR parakeet[Tiab] OR parakeets[Tiab] OR parrot[Tiab] OR parrots[Tiab] OR donkey[Tiab] OR donkeys[Tiab] OR mule[Tiab] OR mules[Tiab] OR zebra[Tiab] OR zebras[Tiab] OR shrew[Tiab] OR shrews[Tiab] OR bison[Tiab] OR bisons[Tiab] OR buffalo[Tiab] OR buffaloes[Tiab] OR deer[Tiab] OR deers[Tiab] OR bear[Tiab] OR bears[Tiab] OR panda[Tiab] OR pandas[Tiab] OR "wild hog"[Tiab] OR "wild boar"[Tiab] OR fitchew[Tiab] OR fitch[Tiab] OR beaver[Tiab] OR beavers[Tiab] OR jerboa[Tiab] OR jerboas[Tiab] OR capybara[Tiab] OR capybaras[Tiab] OR mammal*[tiab]) NOT medline[subset]) OR "Birds"[Mesh] OR bird[tiab] OR birds[tiab] OR aves[tiab] OR "avian population"[tiab] OR "avian populations"[tiab] OR poultr*[tiab] OR fowl[tiab] OR fowls[tiab] OR chicken*[tiab] OR "gallus gallus"[tiab] OR "g gallus"[tiab] OR waterfowl*[tiab] OR duck[tiab] OR ducks[tiab] OR anatidae[tiab] OR mallard[tiab] OR mallards[tiab] OR swan[tiab] OR swans[tiab] OR "Anas platyrhynchos"[tiab] OR "A platyrhynchos"[tiab] OR geese[tiab] OR goose[tiab] OR anser[tiab] OR turkey[tiab] OR turkeys[tiab] OR meleagris[tiab] OR quail[tiab] OR quails[tiab] OR coturnix[tiab] OR partridge*[tiab] OR phasianidae[tiab] OR guineafowl*[tiab] OR numida*[tiab] OR ostrich*[tiab] OR struthio[tiab]

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 Denmark and the United Kingdom between 16 May and 15 August 2018 in relation to avian influenza outbreaks in poultry and wild birds. Information is only provided if it is considered relevant to the implementation of the following selected measures: increasing awareness of stakeholders and the general public, housing order, strengthening biosecurity measures (other than poultry confinement), preventive culling, regional stand-still, derogations from restriction zone implementation after risk assessment and hunting ban. This document is made to support the EFSA working group in generating an overview on the application of the selected measures at EU level.

Timing of the applied prevention and control measures

Tables A.1, A.2 and A.3 provide timelines for the main events that triggered actions in relation to the selected prevention and control measures in Bulgaria, Denmark and the United Kingdom, respectively. More information on the actions taken is provided in the sections below the tables.

A.1 Bulgaria

Aleksandra Miteva

Animal Health and Welfare, and Feed Control Directorate

Bulgarian Food Safety Agency

Table A.1: Overview of main communication actions

Date	Event that triggered action	Type of action taken	Target audience (if applicable)
09.05.2018	Epidemiological situation in the country	• Enhanced active surveillance in poultry farms (Galliformes (breeders and laying hens) and waterfowl (duck farms)), as follows: Frequency of sampling- Every 21 days for period of 3 months and then 50-60 days of age. Sampling protocol - in accordance with Directive 2005/94 • Objectives: 1)surveillance and screening of the reared population and poultry farms; 2) enhanced control and engagement by the operators.	Official vets, poultry associations, farmers
25.05.2018	Confirmation of primary outbreak of HPAI in poultry (in duck farm) (ADNS 2018/10)	• Housing of poultry across whole territory of the country. • Ban on live poultry markets and exhibitions of birds across whole territory of the country. • Enhancing the active surveillance in poultry – clinical examination on poultry farms (special focus on backyards). • Conducting epidemiological investigation, establishing restrictive zones, enforcing all restrictive measures according to Council Directive 2005/94/EC on Community measures for the control of avian influenza and the National contingency plan for AI. • Enhancing the passive surveillance in wild birds. • Strengthening biosecurity on poultry farms and regularly inspection to control it. • Ban for restocking of wild-feathered game was forbidden across the entire territory of the country, including gathering and restocking of game in 3 and 10 km restriction zones.	

13.06.2018	Confirmation of primary outbreak of HPAI in poultry (laying hen farm) (ADNS 2018/11)	Please refer to measures related to outbreaks ADNS 2018/10.	
06.07.3018	Confirmation of primary outbreak of HPAI in poultry (in backyard) (ADNS 2018/12)	Please refer to measures related to outbreaks ADNS 2018/10.	

Increasing awareness of the stakeholders and the general public

- Regular meetings with representatives of the poultry associations;
- Close cooperation with public health authority;
- Publishing information related to the epidemiological situation and prevention and control measures taken

http://www.babh.government.bg/bg/Page/influentza/index/influentza/%D0%98%D0%BD%D1%84%D0%BB%D1%83%D0%B5%D0%BD%D1%86%D0%B0%20%EF%BF%BD

Housing order

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

Precautionary measures such as keeping poultry indoors, taking steps to separate them from wild birds and ensuring feed and water is not accessible to wild birds were also required. There was a special focus on backyards, due to lack of biosecurity measures.

Strengthening biosecurity measures (other than housing orders)

The national legislation related to minimum requirements for farm animals and poultry was amended resulting in strengthening the biosecurity in waterfowl (white/black zones; density, capacity to keep the poultry indoor if necessary etc.

Preventive culling

Not applied.

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

Not applied.

Derogations on restriction zone implementation after risk assessment

Not applied.

Hunting

Hunting was not forbidden.

A.2 Denmark

Pernille Dahl Nielsen

Division of Animal Health, The Danish Veterinary and Food Administration

Table A.2: Overview of main actions

Date	Event that triggered action	Type of action taken	Target audience
16/07/2018	Confirmation of HPAI A(H5N6) in a wild bird (common eider, *Somateria mollissima*)	17/07/2018 a. Contact with an ornithologist from the AI expert group to get information about seasonal behaviour of common eiders etc. b. Information to the AI expert group and poultry industry about the finding 18/07/2018 c. Press release about the finding with information about biosecurity	Poultry industry and general public - especially owners of hobby poultry/backyard flocks
15/08/2018	Confirmation of HPAI A(H5N6) in a wild bird (mute swan, *Cygnus olor*)	16/08/2018 d. Information to the AI expert group and update on the DVFA homepage 24/08/2018 e. News feed on DVFA homepage and Facebook with information about how to notify DVFA about dead wild birds – focus on using the app 'Fugleinfluenza Tip'	General public

Action taken

On 8 July, a common eider (*Somateria mollissima*) was found dead on the island of Vejrø, municipality of Lolland. The bird was found among several other dead wild birds of different species, but mostly eiders. On 16 July, the National Veterinary Institute confirmed HPAI A(H5N6) in the s amples from one eider; the other birds were unsuitable for testing.

The confirmation of HPAI A(H5N6) in a wild bird on 16 July was the 30th case in Denmark in 2018 and was detected after a longer period with no cases. The bird was found together with several other dead birds mostly common eiders. The finding of HPAI in a wild bird in the middle of the summer is not, what is normally expected, so it was considered as a sporadic event. Nevertheless the poultry industry was contacted and warned about the finding, and a press release was sent out to sharpen the public attention on biosecurity measures, especially among owners of hobby poultry. The public were also asked to report findings of dead wild birds.

On 9 August, a mute swan (*Cygnus olor*) was found dead on a beach near the city Korsør in the municipality of Slagelse. The bird was found together with three other dead mute swans. On 15 August, the National Veterinary Institute confirmed HPAI A(H5N6) in the samples from the one of mute swans. The other swans were not sampled.

The confirmation of HPAI A(H5N6) in a wild bird on 15 August was the 31st case in Denmark in 2018 and was detected a month after the former case on the island of Vejrø.

A.3 United Kingdom

Helen Roberts[1], Adam Brouwer[2]

[1]Exotic Disease Control team, Defra, London, UK

[2]Avian Influenza Reference laboratory, Animal and Plant Health Agency, Weybridge, UK

Table A.3: Overview of main actions

Date	Event that triggered action	Type of action taken	Target audience (if applicable)
08/01/2018	H5N6 HPAI identified in mute swans (Cygnus olor) at a site on the south coast of England (Dorset) where AI is frequently reported in the wild waterfowl migration season.	Risk assessment undertaken (Defra, 2018a) concluded that the overall risk to poultry (LOW to MEDIUM depending on biosecurity) had not increased as a result of these cases. No action taken.	Industry and general public
22/01/2018	Large wild bird die off in central England, involving gulls and waterfowl	Risk assessment undertaken (Defra, 2018b) concluded that the overall risk of further incursions in wild birds had now increased to HIGH as a result of these cases. Avian Influenza Prevention Zones in place in England and Wales (across the whole country) where enhanced biosecurity is required, but no housing requirements.	Industry and general public
04/04/2018	Additional cases including raptors across England, Wales and Northern Ireland in the previous few weeks	Risk level maintained as HIGH, although migratory wild waterfowl will be leaving the UK but the presence in raptors suggests there is circulating virus in resident wild birds (Defra, 2018c). Prevention Zones remain in place.	Industry and general public
01/05/2018	Reduction in rate of reporting positive cases and end of migration season so the population of waterfowl is at its lowest	Risk lowered from High to Low (Defra 2018d). Additional biosecurity measures in the AI Prevention Zones in England and Wales are lifted. OIE report closed	Industry and general public
15/06/2018	Single case in a resident Greylag goose (*Anser anser*) in Northern Ireland	No change in risk, OIE report initiated and closed on the same day.	N/A
15/08/2018	No further cases	No action since the lifting of biosecurity measures.	N/A

Action taken

In the UK Avian Influenza Prevention Zones are in place all year round, but the measures required within them change according to the risk level. During wild bird HIGH risk periods, there is no requirement for the housing of poultry, commercial or otherwise, but this might be required if we considered the avian influenza virus was spreading to poultry and the risk was HIGH for poultry. In the case of H5N6 HPAI virus, there was no indication that poultry in Europe were becoming infected as readily as with H5N8 HPAI in the previous season. The last wild bird case reported in Great Britain was on 23 April and the last case in Northern Ireland on 15 June 2018, when the OIE reports were closed.

References (if relevant)

Defra (2018a) Rapid Risk Assessment on the finding of H5N6 HPAI in wild birds in Dorset. Available from: https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/673851/rra-avian-flu-h5n6.pdf

Defra (2018b) Rapid Risk Assessment on the finding of H5N6 HPAI in wild birds in England and Wales. Available from: https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/675425/rapid-risk-assessment-avian-flu-wild-birds-H5N6-180121.pdf

Defra (2018c) Update on H5N6 HPAI in UK/Europe and H5N8 HPAI in Europe. Available from: https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/698979/avian-flu-wild-birds-H5N6-180410.pdf

Defra (2018d) Updated Rapid Risk Assessment on the finding of H5N6 HPAI in wild birds in England, Scotland and Wales. Available from: https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/708535/avian-flu-rra-may2018.pdf