

Epidemiological situation of HPAI viruses from clade 2.3.4.4 in Europe as of 6th March 2018

For the Epidemic Intelligence team (VSI) (in alphabetical order): Anne Bronner (DGAL), Didier Calavas (Anses), Julien Cauchard (Anses), Sylvain Falala (Inra), Alizé Mercier (Cirad)

For the National Hunting and Wildlife Agency (ONCFS): Anne Van De Wiele

Corresponding author: alize.mercier@cirad.fr

Sources: Data updated on 6th March 2018 (included) ADNS/FAO/OIE, DGAL (General Directorate of Food – French Ministry of Agriculture), ProMED

Since the last situation report on 21st February 2018, the highly pathogenic avian influenza (HPAI) virus of subtype H5N6 has been identified for the first time in Denmark in a white-tailed eagle (*Haliaeetus albicilla*) found dead on 13th February in a forest near Slagelse (ADNS notification 2nd March 2018). The United-Kingdom has notified six new cases of H5N6 in wild birds, and the Netherlands has reported a new case of H5N6 in a greater scaup (*Aythya Marila*) found dead on 20th February and a new outbreak in a poultry farm (species not mentioned) on 28th February.

Also, while the last outbreak of H5N8 in Europe dated back to December 2017, the virus has been identified on 2nd March in Italy in a laying-hen farm in the region of Bergamo, and in Bulgaria in a laying-hen farm in Dobrich (source: ADNS).

From 1st October 2017 to 6th March 2018 (included), a total of 89 outbreaks of HPAI H5 (including 52 outbreaks of H5N8) were notified in ten European countries: Bulgaria, Cyprus, Denmark, Germany, Ireland, Italy, the Netherlands, Sweden, Switzerland, and the United-Kingdom (Table 1, Figure 1). Two serotypes were identified: H5N8 and H5N6.

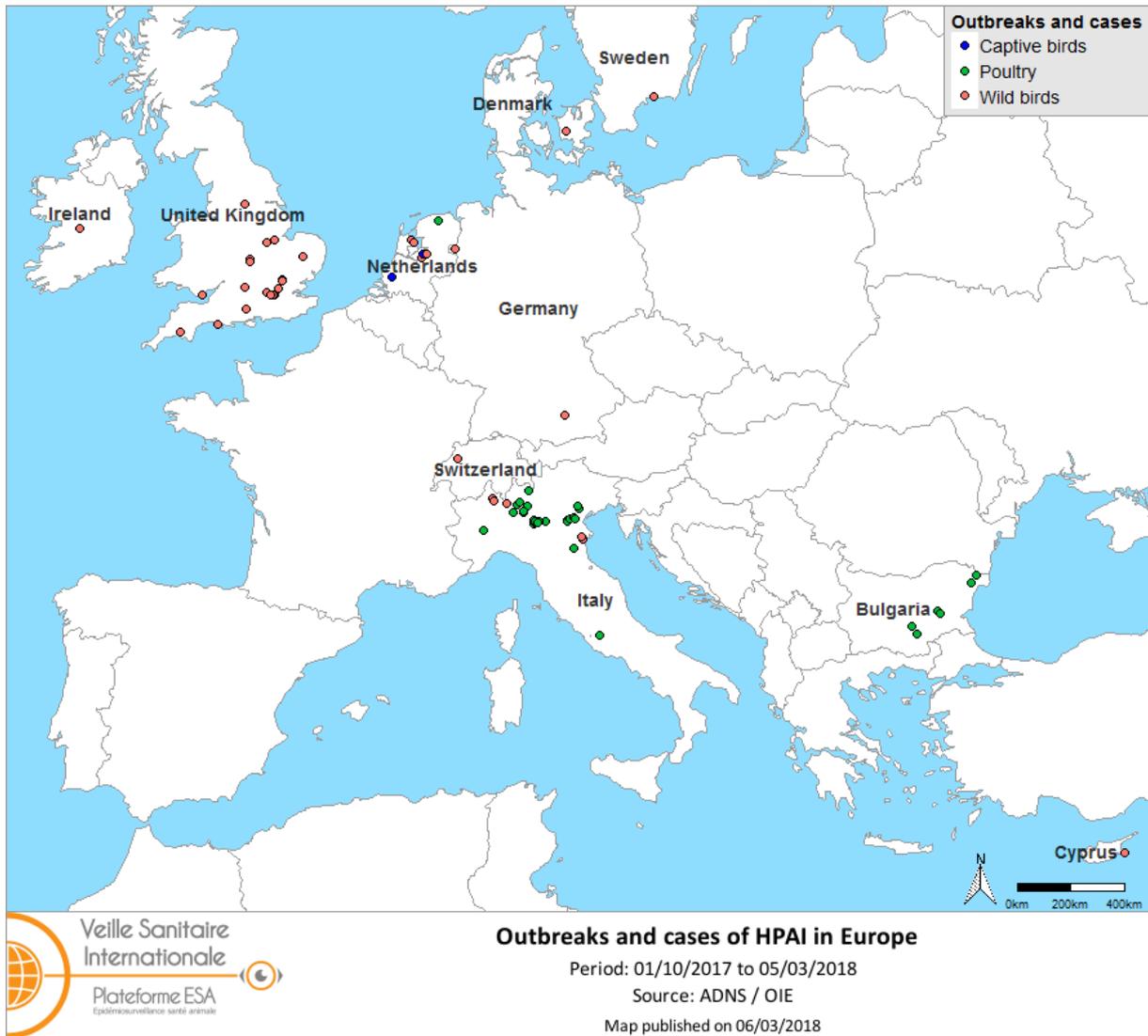


Figure 1. Map of HPAI H5 outbreaks and cases notified in Europe from 1st October 2017 to 6th March 2018 included (source: ADNS/OIE)

Table 1: Number of outbreaks in domestic, wild and captive birds notified in Europe from 1st October 2017 to 6th March 2018 by serotype and type of species (source: ADNS/OIE)

Country	H5N8			H5N6			H5Nx		
	domestic	wild	captive	domestic	wild	captive	domestic	wild	captive
Bulgaria	3	-	-	-	-	-	3	-	-
Cyprus	-	1	-	-	-	-	-	-	-
Denmark	-	-	-	-	1	-	-	-	-
Germany	-	1	-	-	1	-	-	-	-
Ireland	-	-	-	-	1	-	-	-	-
Italy	43	5	-	-	-	-	-	-	-
The Netherlands	-	-	-	2	6	2	-	-	-
Sweden	-	-	-	-	1	-	-	-	-
Switzerland	-	-	-	-	1	-	-	-	-
United-Kingdom	-	-	-	-	18	-	-	-	-
Total	53			33			3		

SEVERAL WILDLIFE SPECIES AND SECTORS OF THE POULTRY INDUSTRY AFFECTED SINCE 1ST OCTOBER 2017

The HPAI H5 outbreaks has affected several sectors of the poultry industry, including fattening turkeys, ducks, geese, laying hens and chickens, in both commercial and backyard farms.

Table 2 lists the affected wild bird species.

Table 2: List of wild bird species affected by HPAI in Europe from 1st October 2017 to 6th March 2017 (source: ADNS) (in yellow: new species/locations since the last update on 21st February 2018)

Family	Latin name	English name	Country where HPAI case was declared
Accipitridae	<i>Buteo buteo</i>	Eurasian buzzard	Cyprus, United-Kingdom
Accipitridae	<i>Haliaeetus albicilla</i>	White-tailed eagle	Ireland, Sweden, Denmark
Accipitridae	<i>Accipiter gentilis</i>	Northern goshawk	United-Kingdom
Anatidae	<i>Anas platyrhynchos</i>	Mallard	United-Kingdom
Anatidae	<i>Anser anser</i>	Greylag goose	United-Kingdom
Anatidae	<i>Aythya ferina</i>	Common pochard	United-Kingdom
Anatidae	<i>Aythya fuligula</i>	Tufted duck	United-Kingdom
Anatidae	<i>Aythya marila</i>	Greater scaup	Netherlands
Anatidae	<i>Branta canadensis</i>	Canada goose	United-Kingdom
Anatidae	<i>Cygnus olor</i>	Mute swan	Netherlands, Switzerland, Italy and United-Kingdom
Anatidae	Species not mentioned	Wild goose	Italy
Anatidae	Species not mentioned	Wild duck	Germany
Colombidae	<i>Columba livia</i>	Rock pigeon	Italy
Falconidae	<i>Falco tinnunculus</i>	Common kestrel	Italy
Laridae	<i>Chroicocephalus ridibundus</i>	Black-headed gull	Netherlands
Laridae	<i>Larus argentus</i>	Herring gull	United-Kingdom
Laridae	<i>Larus canus</i>	Mew gull	United-Kingdom
Laridae	<i>Larus marinus</i>	Great black-headed gull	Netherlands
Phasianidae	<i>Phasianus colchicus</i>	Common pheasant	United-Kingdom
Podicipedidae	<i>Podiceps cristatus</i>	Great-crested grebe	United-Kingdom
Rallidae	<i>Gallinula chloropus</i>	Common moorhen	United-Kingdom

The rock pigeon belongs to the Columbidae family, which is in general though to be less susceptible to avian influenza strains. The only cases of HPAI H5N8 detected in Columbidae in the world were located in the South-West of France (two common wood pigeons and five turtledoves), in direct link with the affected farms, with the hypothesis of a particularly high viral load developed in the affected poultry farms. This hypothesis is also valid for Italy. The list of wild species at risk in Europe has been published in the EFSA journal ([Scientific opinion, adopté le 14 Septembre 2017, doi: 10.2903/j.efsa.2017.4991](#)).

North-South migrations ended several months ago. South-North migrations have now started.

A H5N2 VIRUS DETECTED IN RUSSIA

On 29th December 2017, Russia reported an outbreak of HPAI H5N2 in a poultry farm of more than 660 000 birds, in the region of Kostroma in the Northeast of Moscow (OIE report 29/12/2017). This outbreak was initially notified as H5N8 three days prior.

This is the first report of HPAI H5N2 virus in Russia and the last outbreak of HPAI H5N2 reported in Europe dates back to January 2017 with three outbreaks reported in poultry farms in France.

Regarding the origin of this virus, two hypotheses can be formulated:

- the mutation of a LP H5N2 virus in domestic birds, into a HP virus (as was the case in 2015 with H7N7 in the United Kingdom and Germany, or with H5N1 and H5N2 in France),
- a reassortment between HP H5N8 which circulated in Europe in 2016-2017 with a LP Eurasian strain, as for the H5N6 virus currently circulating in Europe. Indeed, viruses from clade 2.3.4.4 have a strong mutation potential, as illustrated by the emergence of H5N6 and H5N5 viruses following the circulation of H5N8 in Europe in 2016-2017.

Whatever the case may be, further analyses are needed to identify the origin, the link and the genetic composition of these new viruses, and the evolution of the epidemiological situation in Europe should be closely monitored.