



# OFFLU AVIAN INFLUENZA REPORT

Avian Influenza Events in Animals for the period  
February to September 2017

## Scope

In this document we present a summary of H5, H7, and H9 avian influenza events that occurred between February and September 2017.

# Introduction

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## Data Sources

The H5/H7/H9 epidemiologic summary was generated using data from the Food and Agriculture Organization of the United Nations (FAO) EMPRES Global Animal Disease Information System (EMPRES-i). EMPRES-i is an information system designed to facilitate the compilation of animal disease data from different sources, such as the World Organisation for Animal Health (OIE), government Ministries of Agriculture and veterinary services and partner Non-Governmental Organizations (NGOs). Only data for confirmed reports in wild birds, captive wild birds and domestic birds were used; suspect cases were excluded. Links to the OFFLU files for the interactive data visualization tool 'Microreact' are provided in this document.

## Global H5, H7, and H9 Events in Animals

An overview of H5, H7 and H9 epidemiological data (excluding Chinese H7N9 events) in the last reporting period can be visualized dynamically by following the following link:

<https://microreact.org/project/B1m6XNO5->

An overview of LPAI and HPAI H7N9 outbreaks in China during the 5<sup>th</sup> wave can be visualized dynamically by following the following link:

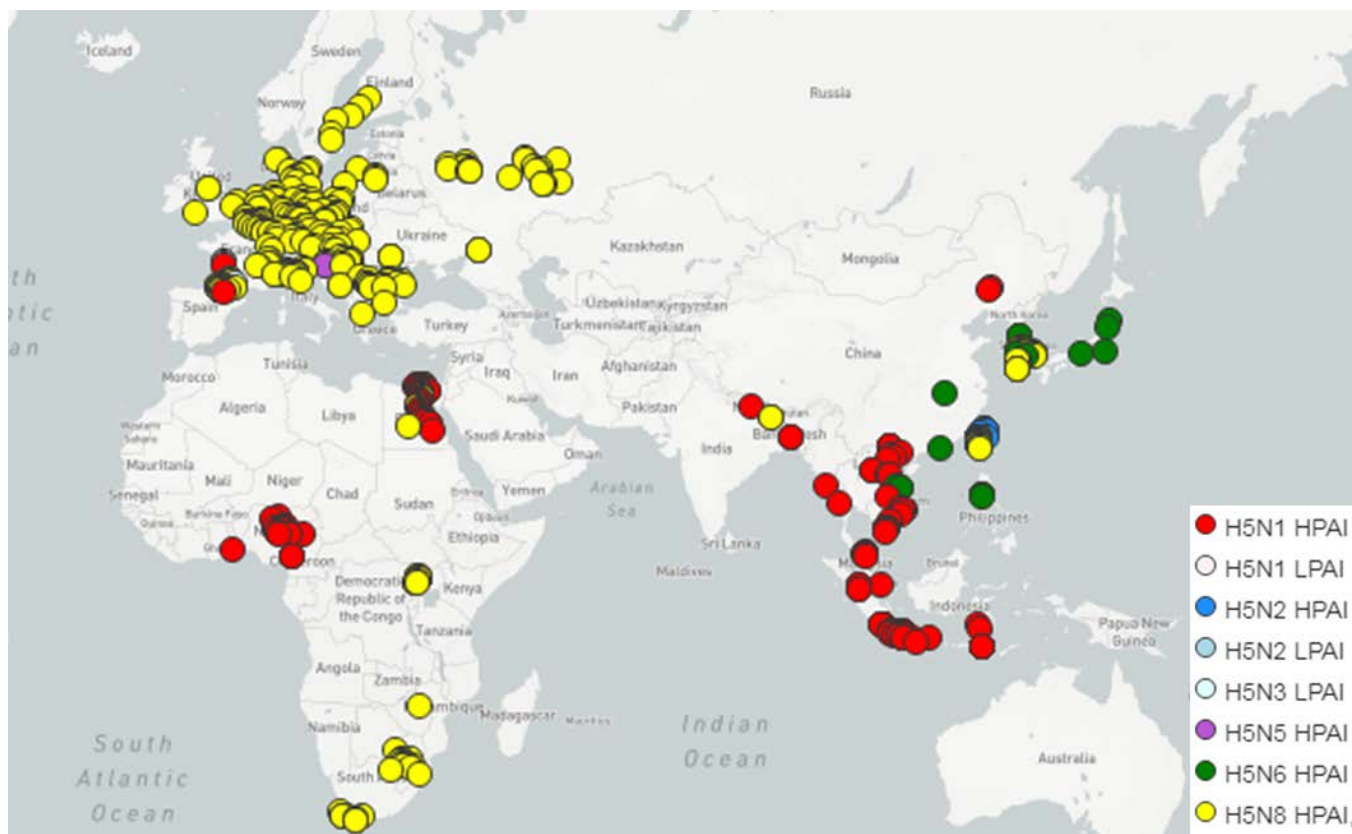
<https://microreact.org/project/HJFveDFqb>

For the period 22 February to 20 September 2017, reports were available from 50 countries/territories representing a total of 1176 H5, H7, and H9 avian influenza (AI) events.

Of these, the majority were due to H5 clade 2.3.4.4 highly pathogenic avian influenza (HPAI) (n=702, 60%: H5N8 HPAI n=539, H5N2 HPAI n=107, H5N6 HPAI n=51, H5N5 HPAI n=5). H5N8 HPAI was detected in 31 countries, affecting predominantly Europe and to a lesser extent Africa and Asia. During the last reporting period, H5N8 HPAI has spread from North to Southern Africa, currently disseminating throughout South Africa. Between February and September 2017, Asian lineage H5N2 clade 2.3.4.4 HPAI caused 107 outbreaks (8%). It is believed to have become endemic in Taiwan and China. H5N6 HPAI was reported in Asia (China, Vietnam, Japan and South Korea), predominantly in March and April, and most recently reported in the Philippines. Although the Philippine strain is most closely related to known sequences isolated from wild birds, the time of detection is not consistent with wild bird dissemination. Reports from China state that H5N6 clade 2.3.4.4 is now the predominant circulating H5 in mainland China.

H5N1 HPAI is endemic in Egypt, Indonesia, Viet Nam, Bangladesh, Cambodia, China and Nigeria and is responsible for repeated epizootics in the Middle East and West Africa. In this reporting period, 264 outbreaks (21%) were reported. In Egypt, clade 2.2.1.2 continues to predominate.

The H5N1 clade 2.3.2.1.c HPAI viruses from Africa are genetically and antigenically distinct from those circulating in Asia. In Indonesia, the predominant clade continues to be 2.3.2.1c, with clade 2.1.3.2a detected only in North Sumatra. Clade 2.3.2.1a continues to circulate in India, Nepal and Bangladesh.



**Map 1.** Map of HPAI H5 reported between 22 February and 20 September 2017.

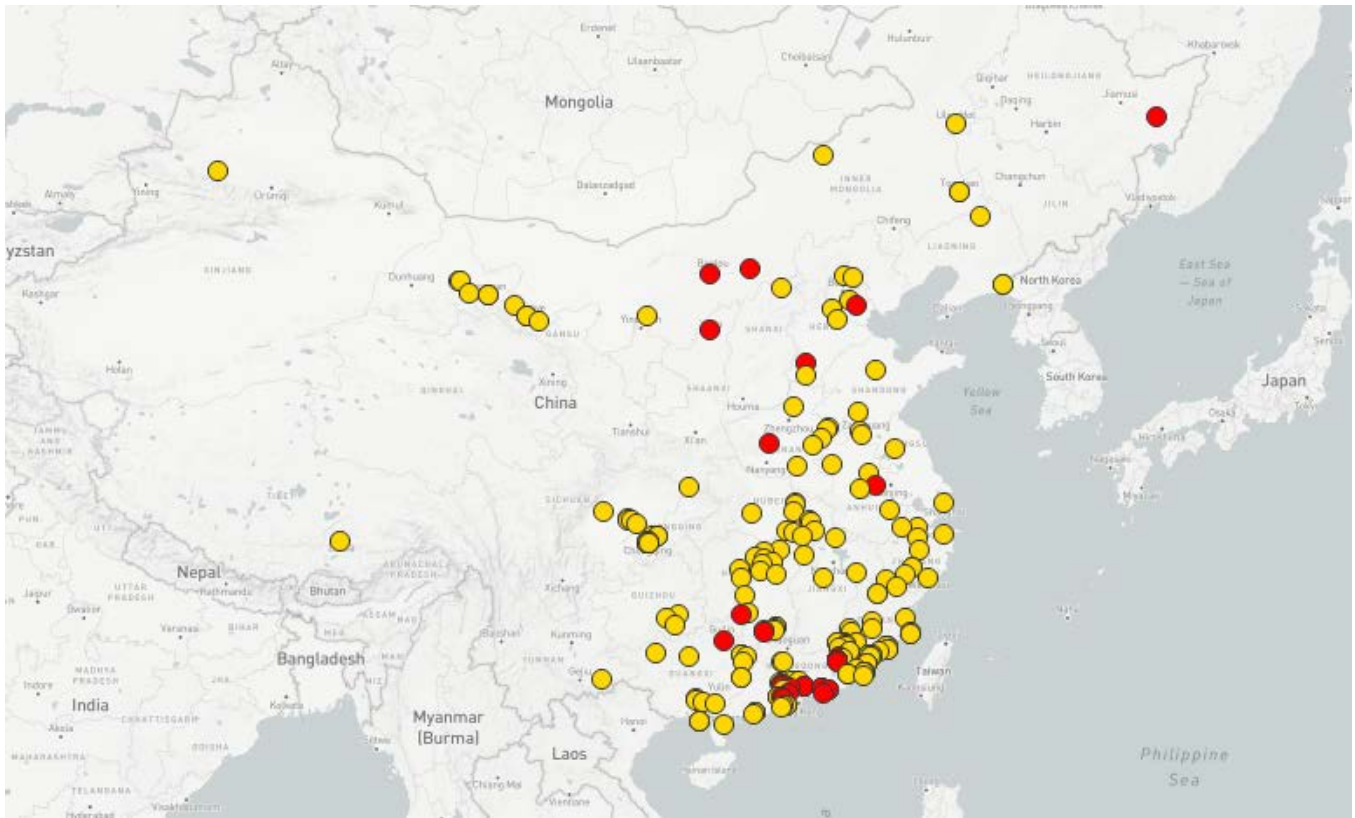
Only a small number of low pathogenic avian influenza (LPAI) H5 events were reported as these are not officially reportable. H5N2 LPAI was reported from Taiwan (Province of China) n=2, the United States of America n=1 and France n=4. France also reported H5N1 LPAI n=2 and LPAI H5N3 n=5.

H7 HPAI was reported in Libya and France, although the Libyan outbreaks were negative upon confirmatory testing in an FAO/OIE reference lab. Mexico reported ongoing issues with H7N3 HPAI, and the USA reported related H7N9 LPAI and HPAI events due to a North American wild bird lineage virus, genetically and antigenically distinct from the H7N9 circulating in China.

The Asian lineage H7N9, first reported in China during 2013, continues to cause issues for animal and public health. The fifth wave is of greater magnitude and has spread farther than previous waves, with 33 provinces or special administrative regions reporting the virus. Data are available for 257 animal detections during the 5<sup>th</sup> wave (176 of which occurred during this reporting period); however, the reported prevalence in animals and the environment is believed to be underestimated.

During the 5<sup>th</sup> wave, an H7N9 HPAI strain emerged and has continued circulate, spreading from Guangdong to Hunan and Guangxi. To date, 37 HPAI outbreaks (34 within this reporting period) have

been reported in animals. Whereas the LPAI virus had reportedly been more associated with yellow-feathered broilers and silkie chickens, the HPAI virus has also impacted commercial layers suggesting a lower infective dose (confirmed by laboratory studies) and the potential for greater impacts to other sectors. Current experimental data and surveillance results suggest that the Asian H7N9 LPAI and HPAI viruses continue to be more adapted to poultry, and present low risk to ducks and other anseriformes. The Ministry of Agriculture of China has intensified animal surveillance and has launched a vaccination campaign of a bivalent vaccine.



**Map 2.** Map of H7N9 HPAI (red) and LPAI (yellow) in China reported between 22 February and 15 September 2017.

Subtype H9N2 was found in reports from Senegal, however does not reflect the true distribution of the poultry-adapted Asian lineage H9N2, which has become endemic in many parts of the world, often co-circulating and reassorting with other influenza subtypes.

## Phylogenetic Analysis

Sequence data for 341 **H5**, **H7**, and **H9** were contributed to OFFLU by animal health laboratories in 36 countries representing Europe, Asia, Africa, and the Americas (**Table 1**). Of these, 146 from 25 countries were collected between February and September 2017 (collection date information not available for all). Sequences from Genbank and GISAID generated by OFFLU reference laboratories were also obtained.

Analysis are provided by subtype and lineage or clade. Phylogenetic trees were generated with a reference dataset using MAFFT alignment followed by maximum likelihood analysis based on the GTRCAT model conducted in RAxML. All positions containing gaps were disregarded in the analysis. Amino acid tables were generated via US-CDC's substitution calculator.

## Antigenic Analysis

Antigenic data generated using the haemagglutination inhibition (HI) assay with WHO-CC provided ferret-origin reagents were contributed by selected OFFLU reference laboratories: Istituto Zooprofilattico Sperimentale delle Venezie in Italy (IZSve), Germany's Friedrich Loeffler institute in Germany (FLI), the Animal and Plant Health Agency in the UK (APHA), and the Australian Animal Health Laboratory (AAHL).

The total number of antigenic submissions was 58 (FLI = 12, APHA = 4, IZSve = 33, AAHL = 10), 48 of which included genetic data (FLI = 6, APHA = 4, IZSve = 28, AAHL = 10). Of the 48 with genetic data, 24 submissions were within the reporting period (FLI = 3, APHA = 3, IZSve = 8, AAHL = 10) and 24 submissions outside the reporting period (FLI = 3, APHA = 1, IZSve = 20).

This period, the H5 antigenic data from the OFFLU partners was visualized by antigenic cartography with special thanks to APHA.

Data received for Sept 2017 but OUTSIDE reporting period			Data received for Sept 2017 WITHIN the reporting period		
Country, area or territory	Host	Genetic clade	Country, area or territory	Host	Genetic clade
Austria	Poultry	2.3.4.4b (H5N8)	Austria	Wild bird	2.3.4.4b (H5N8)
Austria	Wild birds	2.3.4.4b (H5N8)	Bangladesh	Poultry	2.3.2.1a (H5N1)
Bangladesh	Wild birds	2.3.2.1a (H5N1)	Belgium	Wild bird	2.3.4.4b (H5N8)
Bangladesh	Poultry	2.3.2.1a (H5N1)	Belgium	Poultry	2.3.4.4b (H5N8)
Belgium	Wild birds	2.3.4.4b (H5N8)	Bosnia & Herzegovina	Poultry	2.3.4.4b (H5N8)
Belgium	Poultry	2.3.4.4b (H5N8)	Bosnia & Herzegovina	Wild bird	2.3.4.4b (H5N8)
Bhutan	Poultry	2.3.2.1a (H5N1)	Bulgaria	Poultry	2.3.4.4b (H5N8)
Bosnia & Herzegovina	Poultry	2.3.4.4b (H5N8)	Bulgaria	Wild bird	2.3.4.4b (H5N8)
Bulgaria	Poultry	2.3.4.4b (H5N8)	Burkina Faso	Poultry	G1 (H5N2)
Bulgaria	Wild birds	2.3.4.4b (H5N8)	Cameroon	Poultry	presumed 2.3.2.1c (H5N1)
					2.3.2.1c (H5N1), 2.3.4.4 (H5N2/N6/N8), 2.3.4.4 (H5N6), H7N9, H5N2
Cambodia	Poultry	presumed 2.3.2.1c (H5N1)	China	Poultry	2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus
Cameroon	Poultry	2.3.4.4b (H5N8)	Croatia	Poultry	2.3.4.4b (H5N8)
China	Wild birds	2.3.4.4 (H5N6/N8), 2.3.2.1c (H5N1), 2.3.4.4 (H5N2/N6/N8)	Croatia	Wild bird	2.3.4.4b (H5N8)
China	Poultry	2.3.2.1c (H5N1), 2.3.4.4 (H5N2/N6/N8)	Congo (RDC)	Poultry	2.3.4.4 (H5N8)
China	Human (2)†	2.3.4.4 (H5N8)	Côte d'Ivoire	Poultry	G1 (H5N2)
Croatia	Wild birds	2.3.4.4b (H5N8)	Czech Republic	Poultry	2.3.4.4b (H5N8)
Croatia	Poultry	2.3.4.4b (H5N8)	Czech Republic	Wild bird	2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus
Côte d'Ivoire	Poultry	2.3.2.1c (H5N1)	Denmark	Wild bird	2.3.4.4b (H5N8)
Czech Republic	Wild birds	2.3.4.4b (H5N5/N8)	Denmark	Poultry	2.2.1.2 (H5N1), 2.3.4.4b (H5N8), G1 (H5N2)
Czech Republic	Poultry	2.3.4.4b (H5N8)	Finland	Wild bird	2.3.4.4b (H5N8)
Czech Republic	Wild birds	2.3.4.4b (H5N8)	France	Wild bird	2.3.4.4b (H5N8)
Denmark	Poultry	2.3.4.4b (H5N8)	France	Poultry	2.3.4.4b (H5N8), (H5N1 European wild bird lineage)
					2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus
Egypt	Poultry	2.2.1.2 (H5N1), 2.3.4.4b (H5N8)	Georgia	Wild bird	2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus
					2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus
Egypt	Wild birds	2.3.4.4b (H5N8)	Germany	Poultry	2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus
Egypt	Human (2)†	2.2.1.2 (H5N1)	Germany	Wild bird	2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus
					2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus
Finland	Wild birds	2.3.4.4b (H5N8)	Greece	Poultry	2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus
Finland	Poultry	2.3.4.4b (H5N8)	Hong Kong SAR	Wild bird	2.3.4.4 (H5N5)
Former Yug. Rep. of Macedonia	Wild birds	2.3.4.4b (H5N8)	Hungary	Wild bird	2.3.4.4b (H5N8)
Former Yug. Rep. of Macedonia	Poultry	2.3.4.4b (H5N8)	Hungary	Poultry	2.3.4.4b (H5N8)
France	Wild birds	2.3.4.4b (H5N8)	India	Poultry	2.3.2.1a (H5N1)
France	Poultry	2.3.4.4b (H5N8)	India	Poultry	G1 (H5N2)
Georgia	Wild birds	2.3.4.4b (H5N8), 2.3.4.4 (H5N5), 2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus	Indonesia	Poultry	2.3.2.1c (H5N1)
Germany	Wild birds	2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus	Indonesia	Poultry	Y280 (H5N2)
Germany	Poultry	2.3.4.4b (H5N8)	Ireland	Wild bird	2.3.4.4b (H5N8)
Ghana	Poultry	2.3.2.1c (H5N1)	Israel	Poultry	2.3.4.4b (H5N8)
Greece	Wild birds	2.3.4.4b (H5N8)	Italy	Wild bird	2.3.4.4b (H5N8)
Greece	Poultry	2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus	Italy	Poultry	2.3.4.4b (H5N8)
Hong Kong SAR	Wild birds	2.3.4.4 (H5N5)	Japan	Wild bird	2.3.4.4b (H5N8)
Hungary	Wild birds	2.3.4.4b (H5N8)	Japan	Poultry	2.3.4.4 (H5N5)
Hungary	Poultry	2.3.4.4b (H5N8)	Laos	Poultry	presumed 2.3.2.1c (H5N1)
India	Wild birds	2.3.2.1a (H5N1), 2.3.4.4b (H5N8)	Libya	Poultry	H7 LPAI
India	Poultry	2.3.2.1a (H5N1), 2.3.4.4b (H5N8)	Lithuania	Wild bird	2.3.4.4b (H5N8)
Indonesia	Poultry	2.3.2.1c (H5N1), 2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus	Luxembourg	Poultry	2.3.4.4b (H5N8)
Iran	Wild birds	2.3.4.4b (H5N8)	Malaysia	Poultry	presumed 2.3.2.1c (H5N1)
Iran	Poultry	2.3.4.4b (H5N8), 2.3.2.1c (H5N1)	Mexico	Poultry	H7N3 (North American lineage)
Iraq	Poultry	2.3.2.1c (H5N1)	Myanmar	Poultry	2.3.2.1c (H5N1)
Ireland	Wild birds	2.3.4.4b (H5N8)	Nepal	Wild bird	2.3.2.1a (H5N1)
Ireland	Poultry	2.3.4.4b (H5N8)	Nepal	Poultry	2.3.2.1a (H5N1), 2.3.4.4b (H5N8)
Israel	Wild birds	2.3.4.4b (H5N8)	Netherlands	Wild bird	2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus
Israel	Poultry	2.3.4.4b (H5N8)	Niger	Poultry	2.3.2.1c (H5N1)
					2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus
Italy	Wild birds	2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus	Nigeria	Poultry	2.3.2.1c (H5N1)
Italy	Poultry	2.3.4.4b (H5N8)	Philippines	Poultry	2.3.4.4c (H5N6)
Japan	Wild birds	2.3.4.4 (H5N5)	Poland	Wild bird	2.3.4.4b (H5N8)
Japan	Poultry	2.3.4.4 (H5N5)	Poland	Poultry	2.3.4.4b (H5N8)
Kazakhstan	Wild birds	2.3.4.4b (H5N8/NX)	Republic of Korea	Wild bird	2.3.4.4 (H5N5)
Kuwait	Poultry	2.3.4.4b (H5N8)	Republic of Korea	Poultry	2.3.4.4 (H5N6/N8)
Lac P. D.F.	Poultry	2.3.2.1c (H5N1)	Romania	Wild bird	2.3.4.4b (H5N8)
Madagascar	Wild birds	2.3.4.4b (H5N8)	Romania	Poultry	2.3.4.4b (H5N8)
Malaysia	Poultry	2.3.4.4 (H5N5)	Russian Federation	Poultry	2.3.4.4b (H5N8)
					2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus
Netherlands	Wild birds	2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus	Russian Federation	Wild bird	2.3.4.4b (H5N8)
Netherlands	Poultry	2.3.4.4b (H5N8)	Senegal	Poultry	G1 (H5N2)
Niger	Poultry	2.3.2.1c (H5N1), 2.3.4.4b (H5N8)	Serbia	Wild bird	2.3.4.4b (H5N8)
Nigeria	Poultry	2.3.2.1c (H5N1), 2.3.4.4 (H5N8)	Slovakia	Wild bird	2.3.4.4b (H5N8)
					2.3.4.4b (H5N8), H5N5 reassortant with European lineage virus
Poland	Wild birds	2.3.4.4b (H5N8)	Slovakia	Poultry	2.3.4.4b (H5N8)
Poland	Poultry	2.3.4.4b (H5N8)	South Africa	Wild bird	2.3.4.4b (H5N8)
Portugal	Wild birds	2.3.4.4b (H5N8)	South Africa	Poultry	2.3.4.4b (H5N8)
Republic of Korea	Wild birds	2.3.4.4 (H5N6/N8)	Spain	Wild bird	2.3.4.4b (H5N8)
Republic of Korea	Poultry	2.3.4.4 (H5N6)	Sweden	Wild bird	2.3.4.4b (H5N8)
Romania	Wild birds	2.3.4.4b (H5N8)	Sweden	Poultry	2.3.4.4b (H5N8)
Romania	Poultry	2.3.4.4b (H5N8)	Switzerland	Wild bird	2.3.4.4b (H5N8)
					2.3.4.4 (H5N8), H5N6, [presumed] H5N2
Russian Federation	Wild birds	2.3.4.4b (H5N8)	Taiwan	Poultry	2.3.4.4 (H5N8), H5N6, [presumed] H5N2
Russian Federation	Poultry	2.3.4.4b (H5N8)	Togo	Poultry	2.3.2.1c (H5N1)
Serbia	Wild birds	2.3.4.4b (H5N8)	Ukraine	Wild bird	2.3.4.4b (H5N8)
Serbia	Poultry	2.3.4.4b (H5N8)	United Kingdom	Poultry	2.3.4.4b (H5N8)
Slovakia	Wild birds	2.3.4.4b (H5N8)	United Kingdom	Wild bird	2.3.4.4b (H5N8), (H7N9 North American wild bird lineage)
					2.3.2.1c (H5N1), 2.3.4.4 (H5N6)
Slovakia	Poultry	2.3.4.4b (H5N8)	United States of America	Poultry	2.3.4.4b (H5N8)
Slovenia	Wild birds	2.3.4.4b (H5N8)	Vietnam	Poultry	2.3.2.1c (H5N1), 2.3.4.4 (H5N6)
Spain	Wild birds	2.3.4.4b (H5N8)	Zimbabwe	Poultry	2.3.4.4b (H5N8)
Sweden	Wild birds	2.3.4.4b (H5N8)			
Sweden	Poultry	2.3.4.4b (H5N8)			
Switzerland	Wild birds	2.3.4.4b (H5N8)			
Togo	Poultry	2.3.2.1c (H5N1)			
Tunisia	Wild birds	2.3.4.4b (H5N8)			
Uganda	Wild birds	2.3.4.4b (H5N8)			
Uganda	Poultry	2.3.4.4b (H5N8)			
Ukraine	Poultry	2.3.4.4b (H5N8/NX)			
Ukraine	Wild birds	2.3.4.4b (H5N8/NX)			
United Kingdom	Poultry	2.3.4.4b (H5N8)			
United Kingdom	Wild birds	2.3.4.4b (H5N8)			
United States of America	Wild birds	2.3.4.4a (H5N2)			
Vietnam	Poultry	2.3.2.1c (H5N1), 2.3.4.4 (H5N6)			

**Table 1. NOT FOR ONWARD DISTRIBUTION: Avian influenza reports and data within (black font) and outside (blue font) during the current period. Blue highlight indicates genetic data was received.**

	Sep	Oct	Nov	Dec	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	N/A	TOTAL
<b>H5N1 clade 2.1.3.2a</b>														
Indonesia					1									1
<b>H5N1 clade 2.2.1.2</b>														
Egypt					3	1	1							5
<b>H5N1 clade 2.3.2.1a</b>														
Bangladesh													5	5
India						1								1
Nepal						4	1							5
<b>H5N1 clade 2.3.2.1c</b>														
China												1		1
Indonesia						2	5	2						9
Iran					1									1
Ivory Coast	1			1	1					4		1		8
Myanmar (Burma)											4			4
Niger					2									2
Nigeria		1											23	24
Togo													2	2
<b>H5N8/H5N6 clade 2.3.4.4</b>														
Bulgaria				1										1
China							2	1	3			1		7
Congo									4					4
Finland			1											1
Georgia				2										2
Greece													1	1
Iran			2	4	4									10
Ireland				1	1									2
Italy					7	6	4	3	2		10	6		38
Japan			5	47	9	4	1							66
Kuwait													7	7
Lithuania						1								1
Niger					4									4
Nigeria													1	1
Romania			1											1
Russia						1	2	1	1			1		6
Spain													1	1
Taiwan						1								1
Uganda					5									5
Ukraine			3											3
United Kingdom (UK)				7	9	6	1		2	1	1			27
Zimbabwe													1	1
<b>H5N5/H5N8 clade 2.3.4.4b</b>														
Bosnia and Herzegovina													1	1
Egypt					4	4	2	2						12
Germany				2	3	2	7							14
Israel													1	1
Nepal							2							2
<b>H5N6 clade 2.3.4.4c</b>														
Philippines												2		2
<b>H7N9 C</b>														
China					2		5	1	2					10
<b>H9N2 lineage G1</b>														
Burkina Faso						1								1
Egypt					3				4					7
India								1	1					2
Ivory Coast	6	1						3						10
Senegal													3	3
<b>H9N2 lineage Y280</b>														
China							3	3	7					13
Indonesia				2	1	1				1				5
<b>TOTAL</b>	<b>7</b>	<b>2</b>	<b>12</b>	<b>67</b>	<b>60</b>	<b>35</b>	<b>36</b>	<b>17</b>	<b>26</b>	<b>6</b>	<b>15</b>	<b>12</b>	<b>46</b>	<b>341</b>

**Table 2.** Sequence data submitted to OFFLU during the current period by subtype, clade and country.

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- ✓ Friedrich-Loeffler Institut (FLI), Germany
- ✓ Harbin Veterinary Research Institute (HVRI), China
- ✓ Hokkaido University, Japan
- ✓ Istituto Zooprofilattico Sperimentale delle Venezie (IZSve), Italy
- ✓ National Institute of High Security Animal Diseases (ICAR-NIHSAD), Bhopal, India
- ✓ National Laboratory for Veterinary Quality Control on Poultry Production, Egypt
- ✓ Poultry Disease Diagnosis Laboratory, Animal Health Research Institute, Taiwan
- ✓ State Research Center of Virology and Biotechnology Vector, Russian Federation

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