



# OFFLU AVIAN INFLUENZA POST-VCM REPORT

Avian influenza events for the period  
February to September 2018

## Scope

In this document we present a summary of H5, H7, and H9 avian influenza events that occurred February to September 2018.

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## Introduction

The WHO Consultation on the Composition of Influenza Virus Vaccines for the Northern Hemisphere 2017-2018 took place in Atlanta, Georgia on the 24-26 September 2018. The meeting gathered participants from the WHO Collaborating Centres for influenza (CCs), WHO Essential Regulatory Laboratories (ERLs), National Influenza Centres and WHO H5 Reference Laboratories, WHO Collaborating Centre for Modelling, Evolution, and Control of Emerging Infectious Diseases and from OFFLU. The OFFLU contribution on zoonotic influenza viruses was presented by Mia Kim Torchetti from the United States Department of Agriculture National Veterinary Services Laboratory with Cristian DeBattisti from the Food and Agricultural Organization. The OFFLU team would like to give special thanks to Mary Lea Killian, Tod Stuber, Amber Wilson, Yunho Jang, Nicola Lewis, Francesco Bonfante and Frank Wong for their valuable assistance in data collation towards this VCM contribution. The zoonotic report is available [here](#).

## 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 environmental samples, 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.

## Phylogenetic Analysis

Sequence data for 195 **H5**, **H7**, and **H9** were contributed to OFFLU by animal health laboratories in 24 countries representing Europe, Asia, Africa, and the Americas (**Table 1**). Of these, 64 from 15 countries were collected during the current period. Sequences from Genbank and GISAID generated by OFFLU reference laboratories were also obtained.

Analyses 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 by the haemagglutination inhibition (HI) assay using WHO-CC and OFFLU provided ferret-origin reagents was contributed by selected OFFLU reference laboratories: Istituto Zooprofilattico Sperimentale delle Venezie in Italy (IZSVe), Australian Animal Health Laboratory (AAHL) and the Animal and Plant Health Agency in the UK (APHA). For this period 15 viruses and 22 antisera were distributed from WHO-CCs, and IZSVe generated and distributed antigen/antisera for a needed update for the recent H5 clade 2.3.4.4b viruses.

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

H5 and H7 events for the current reporting period, **13 February to 12 September 2018**, can be visualized dynamically using the following link (not accessible with Internet Explorer): [https://microreact.org/project/ry\\_s9xIFm](https://microreact.org/project/ry_s9xIFm)

For the current period, reports were available from 35 countries/territories representing a total of 416 reported H5, H7 or H9 avian influenza (AI) events (**Maps 1, 2 and 3**). Of these, 311 reports were H5 or H7 outbreaks affecting poultry. The majority of reports were due to goose/Guangdong lineage (Gs/GD) H5 clade 2.3.4.4 highly pathogenic avian influenza (HPAI). This period was marked by expansion of the 2.3.4.4 H5N6 virus to the north and northwest of Europe, and re-introduction of 2.3.4.4 H5N6 in Myanmar. There have been ongoing reports of 2.3.4.4 H5N8 from the Middle East (including Egypt), South Africa, and Eastern Europe – with an increase in reports from the western part of the Russian Federation starting from June 2018; however, reports of 2.3.4.4 H5N8 have decreased for Western Europe.

Low pathogenic avian influenza (LPAI) events were also reported in poultry during this period. European lineage viruses in Denmark (H5NX), France (H5N1/N2/N3/N5/NX, and H7N7), Sweden (H5NX); Central American lineage virus in the Dominican Republic (H5N2), and North American wild bird lineage U.S. (H7N1, and unrelated H7N3).

Reports of the highly poultry-adapted Asian H7N9 lineage continue to be low since the fifth wave, with 5 reports each of LPAI and HPAI during live bird market surveillance. An updated FAO qualitative risk assessment for spread of Asian H7N9 within and outside of China is available at: <http://www.fao.org/3/i8705en/I8705EN.PDF>.

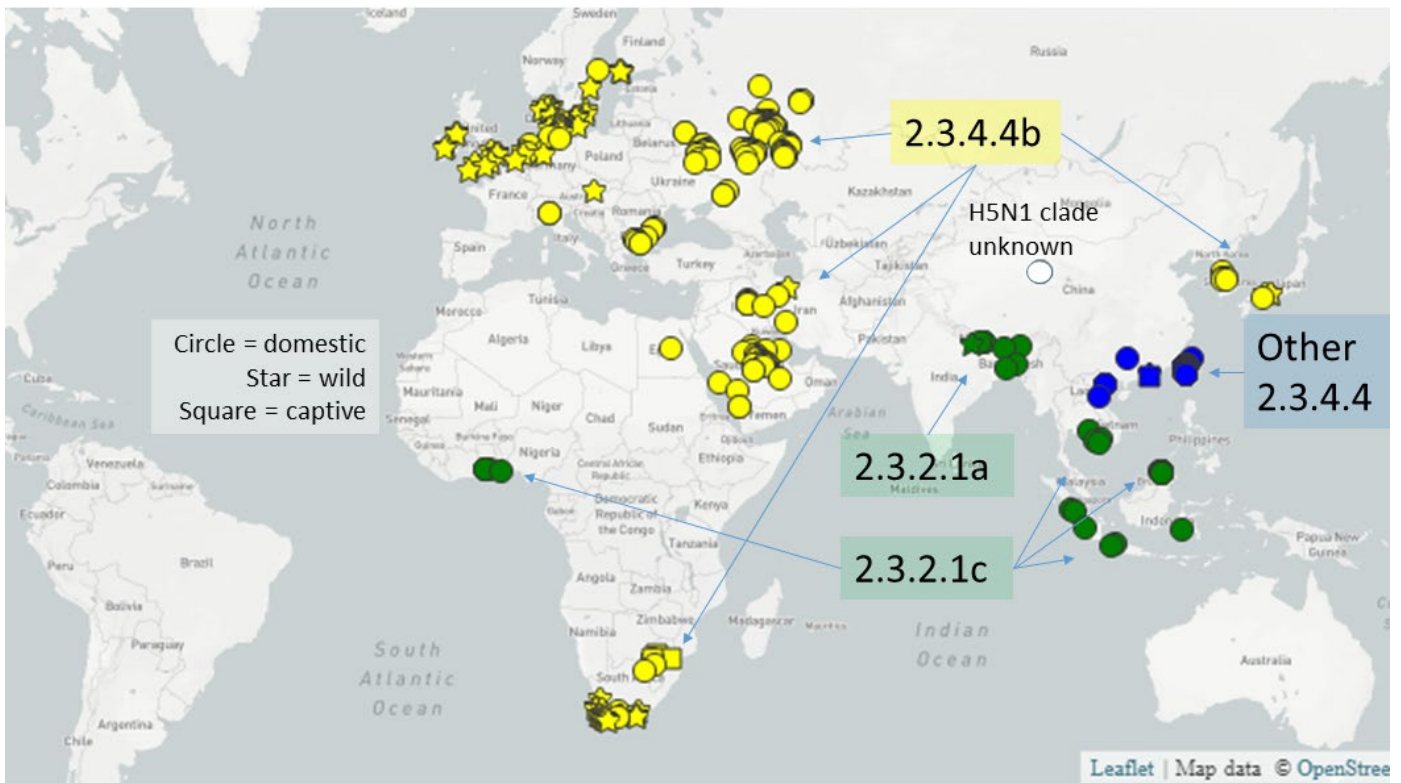
While it is not officially reportable, H9 viruses can significantly impact poultry. A highly poultry-adapted Asian lineage H9N2 continues to cause production losses in many countries in Asia and the Middle East. All reports of the poultry-adapted H9N2 for this period were submitted directly from partner laboratories rather than through official channels, representing 39 viruses from eight countries (Bangladesh [*for previous period*], China, Ghana, India, Myanmar, Nepal, Pakistan [*for previous period*], and Russian Federation).

## *Vaccination*

In some countries, including Viet Nam, Indonesia, Bangladesh, and Egypt, H5 and others vaccination is employed as part of overall control efforts to endemic viruses.

Currently, in China, vaccination of poultry is mandatory in all provinces (including chickens, ducks, geese, quails, pigeons and other rare birds in captivity). From September 2017, a government sponsored campaign using a bivalent H5/H7 vaccine (H5 2.3.4.4 Re-8 based on A/chicken/Guizhou/4/13(H5N1); H7N9 Re-1) has been implemented. Although the backbone HA sequence for the H7 component of the bivalent vaccine is based on A/pigeon/Shanghai/S1069/2013(H7N9), the HA sequence was modified to reflect changes in more contemporary viruses in order to improve the antigenicity and titre of the vaccine stain. Institutions in China also produce various other H5 and H9 vaccines.

Despite the risk of potential incursion of Asian lineage H7N9, H7 vaccination is currently banned in Viet Nam, Lao PDR, Myanmar or Cambodia. Active surveillance for reportable H5 and H7 viruses occurs in poultry along the border in these countries.



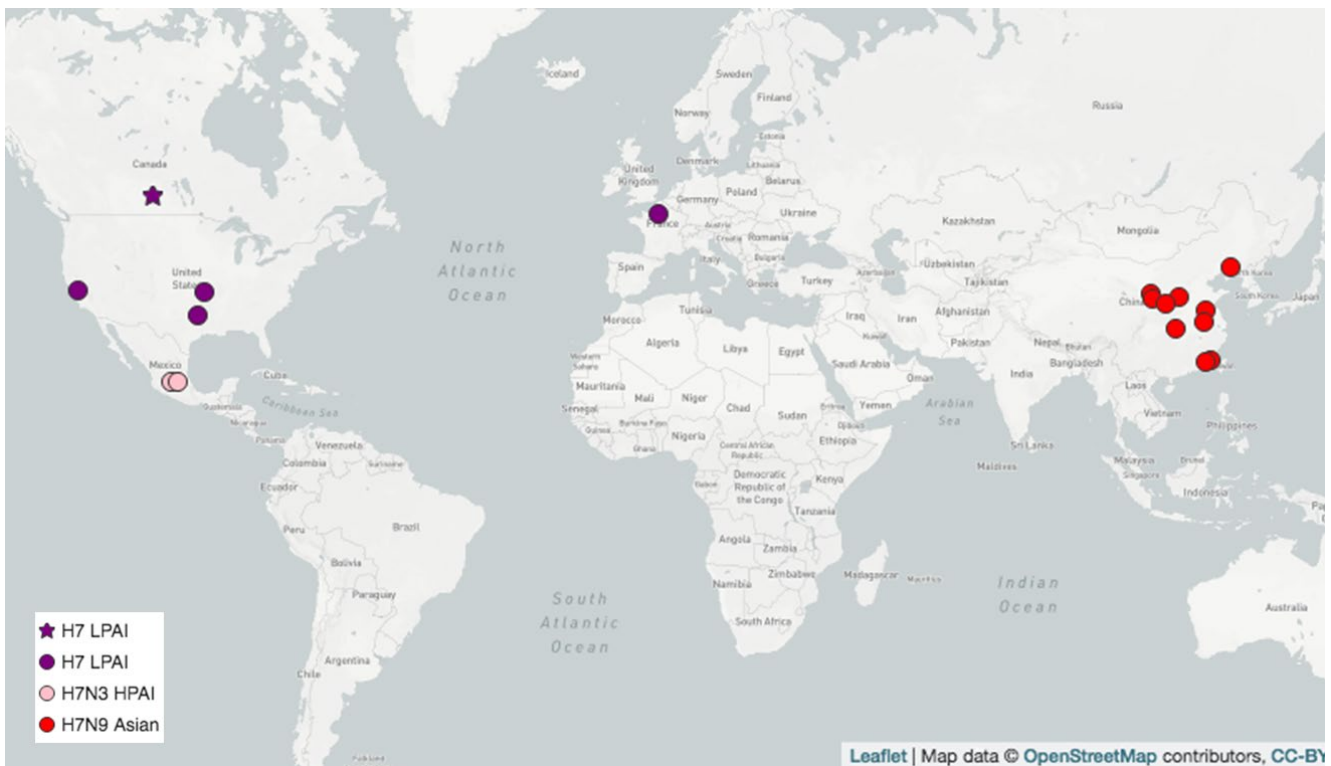
**Map 1.** H5 HPAI reports in birds between 13 February and 12 September 2018.

*Circles represent domestic, star for wild, square for captive wild.*

*Red font indicates change since last period.*

- H5N1 2.3.2.1 (green) **subgroup a** was reported in Bangladesh (domestic), **Bhutan** (domestic), **India** (wild), and **Nepal** (domestic); **subgroup c** was reported in domestic birds (circle) in Cambodia, China (presumed), **Ghana**, Indonesia, **Malaysia**, and **Togo**.
- H5 2.3.4.4<sup>1</sup>
  - **Subgroup b** (yellow) was reported in Bulgaria (N8; domestic), **Denmark** (wild), Egypt (N8; domestic), **Finland** (wild), Germany (N6; domestic and wild), Iran (N8; domestic and wild), Iraq (N8; domestic), Ireland (N6; wild), Italy (N8; domestic), Japan (N6; domestic and wild), Netherlands (N6; domestic and wild), Republic of Korea (N6; domestic), Russia (N8/N2; domestic), **Saudi Arabia** (N8; domestic), **Slovakia** (N6; wild), South Africa (domestic and wild), **Sweden** (N6; domestic and wild), and United Kingdom (N6; wild)
  - Other subgroups (blue) reported in domestic poultry in Taiwan, China, Hong Kong (wild and captive only), Myanmar, and Vietnam.

<sup>1</sup> Informally proposed nomenclature

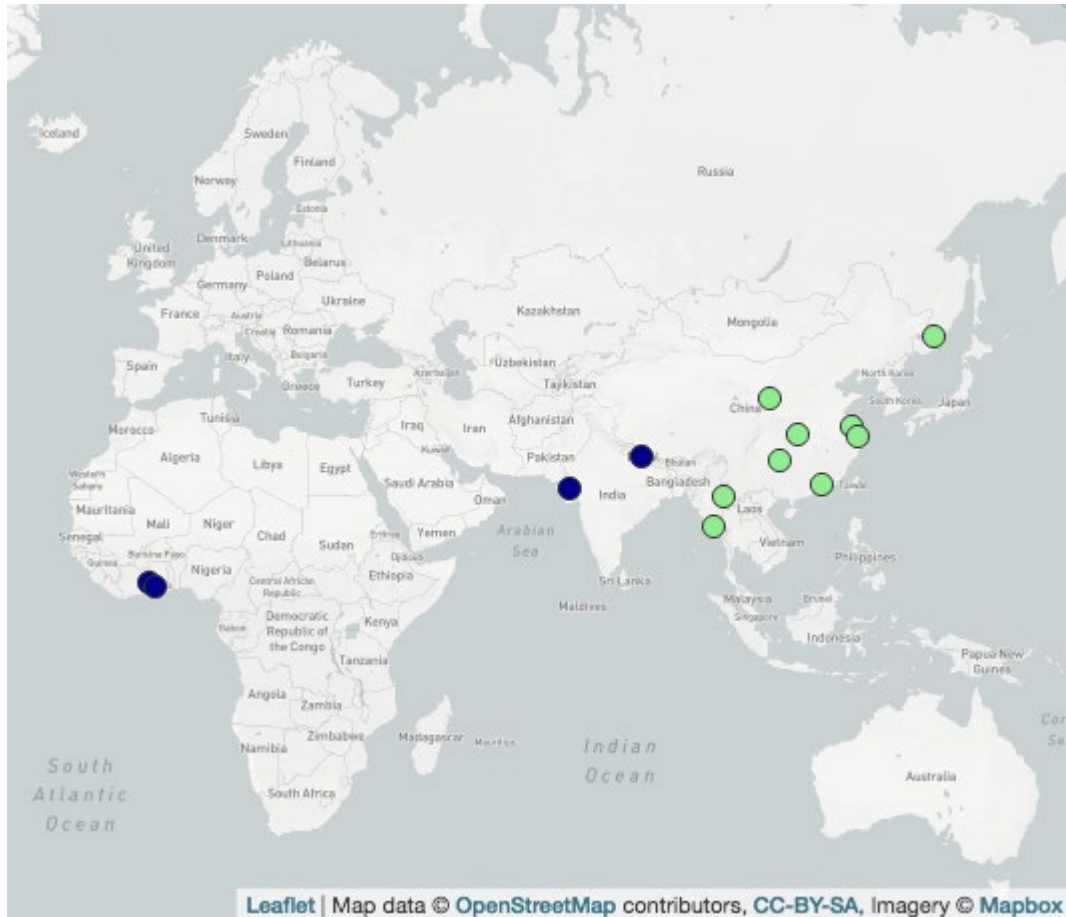


**Map 2.** H7 reports in birds between 13 February and 12 September 2018.

*Circles represent domestic, star for wild, square for captive wild.*

*Red font indicates new emergence since last period.*

- Asian H7N9 (red; domestic) – 5 reports of **HPAI** from layer chicken farms located in Liaoning (1), Shanxi (1), and Shaanxi (1) provinces and Ningxia autonomous region (2), and 5 reports of **LPAI** from the China Ministry of Agriculture.
  - A new reassortment of the Asian H7N9 lineage, **H7N3 HPAI**, was reported by Japan from a smuggled poultry carcass from China.
- One event of **European lineage H7N7 LPAI** (purple; domestic) was reported in northern France in June 2018; the previous report of H7N7 from France was January 2017.
- **North American H7N1 LPAI** (purple; domestic) was reported in Missouri and Texas; although the events were reported within one week, phylogenetic and epidemiologic data suggest independent introductions of wild bird lineage LPAI. Recently, an unrelated **North American H7N3 LPAI** (purple; domestic) was reported in California. Wild bird H7N3 LPAI was shared from Canada (purple; star).
- There were 3 reports of H7N3 **HPAI** (pink; domestic) in Mexico during this period.



**Map 3.** H9 detected in poultry between 13 February and 12 September 2018.

*Circles represent domestic, star for wild, square for captive wild.*

*Red font indicates new emergence since last period.*

No official reports were received; however, virus contributions were received for Asian lineage H9N2

- Y280 (light green; domestic) from China, Myanmar, and **Russian Federation**.
- G1 (navy; domestic and crow in India/Bangladesh) from Bangladesh (previous period), Ghana, India, Pakistan (previous period), and Nepal.



**Table 1.** Recent H5, H7 and H9 activity for the current period.

GREEN font indicates genetic data has been received for this period.

Country	Host	Subtype/clade/lineage
Bhutan	Poultry	H5N1 (2.3.2.1a)
Bulgaria	Poultry	H5NX/N8 (2.3.4.4)
Cambodia	Poultry	H5N1 (previously 2.3.2.1c)
Canada	Wild birds	H5N2, H7N3 (North American LPAI)
China	Poultry	H5N1 (2.3.2.1 presumed from Qinghai), H5N6 (2.3.4.4), H7N9, H9N2 (Y280)
Denmark	Wild birds	H5N6 (2.3.4.4)
	Poultry	H5 (European LPAI)
Dominican Republic	Poultry	H5N2 (Central American LPAI)
Egypt	Poultry	H5N8 (2.3.4.4)
Finland	Wild birds	H5N6 (2.3.4.4)
France	Poultry	H5N1/N2/N3/N5 and H7N7 (all European LPAI)
Germany	Wild birds	H5N6 (2.3.4.4)
	Poultry	H5N6 (2.3.4.4)
Hong Kong, SAR	Wild birds	H5N6 (2.3.4.4)
India	Wild birds (crow)	H5N1 (2.3.2.1a)
	Poultry	H5N1 (2.3.2.1a), H9N2 (G1)
Indonesia	Poultry	H5N1 (previously 2.3.2.1c)
Iran	Wild birds	H5N8 (2.3.4.4)
	Poultry	H5N8/N6 (2.3.4.4)
Iraq	Poultry	H5N8 (2.3.4.4)
Ireland	Wild birds (raptor)	H5N6 (2.3.4.4)
Italy	Poultry	H5N8 (2.3.4.4)
Japan	Wild birds (crow, raptor)	H5N6 (2.3.4.4)
	Poultry	H5N6 (2.3.4.4), H7N9 (smuggled)
Malaysia	Poultry	H5N1 (previously 2.3.2.1c)
Mexico	Poultry	H7N3 (Central American)
Myanmar	Poultry	H5N1 (2.3.2.1c), H5N6 (2.3.4.4), H9N2 (Y280)
Nepal	Poultry	H5N1 (2.3.2.1a), H9N2 (G1)
Nigeria	Poultry	H5N1 (2.3.2.1c)
Netherlands	Wild birds	H5N6 (2.3.4.4)
	Poultry	H5N6 (2.3.4.4)
Republic of Korea	Poultry	H5N6 (previously 2.3.4.4)
Russian Federation	Poultry	H5N2/N8 (2.3.4.4), H9N2 (Y280)
Saudi Arabia	Poultry	H5N8 (previously 2.3.4.4)
Slovakia	Wild birds	H5N6 (2.3.4.4)
South Africa	Wild birds	H5N8 (2.3.4.4)
	Poultry	H5N8 (2.3.4.4)
Sweden	Wild birds	H5N6 (2.3.4.4)
	Poultry	H5N6 (2.3.4.4), H5 (European LPAI)

Taiwan (Prov of China)	Poultry	H5N2 (2.3.4.4)
Togo	Poultry	H5N1 (2.3.2.1c)
UK/Northern Ireland	Wild birds	H5N6 (2.3.4.4)
US	Poultry	H7N1, H7N3 (North American LPAI)
Viet Nam	Poultry	H5N6 (2.3.4.4)

## H5 Highly Pathogenic Avian Influenza (HPAI)

Reports of H5 HPAI during the current period are outlined in **Table 1** and **Map 1**.

### *H5 Clade 2.3.2.1*

H5N1 viruses of Clade 2.3.2.1a were reported from Bangladesh, Bhutan, India (previous reporting period), and Nepal. Clade 2.3.2.1c H5N1 viruses presumably remain endemic in Viet Nam, Cambodia, Nigeria, Iraq and Indonesia with reports from Togo, Ghana, and Myanmar this period. There was a single report from China presumed to be clade 2.3.2.1 (Qinghai Lake area). Based on the current antigenic, genetic and epidemiologic data, a new A/duck/Bangladesh/17D1012/2018-like A(H5N1) CVV was proposed.

### *H5 Clade 2.3.4.4*

Currently, H5 clade 2.3.4.4 predominates globally and contains several phylogenetically distinct subgroups. Ongoing reassortment with native wild bird viruses encountered in migratory birds has been reported. The A/Fujian-Sanyuan/21099/2017-like viruses (subgroup b) have had the greatest global reach outside Asia since 2016. The 2.3.4.4b subgroup continues to evolve and mutate with ongoing opportunities to reassort with native strains. Across the genome, there are fully Asian constellations, as well as H5 2.3.4.4 reassortants with native European strains (N6, N2, as well as reassortments with other internal genes) which have been detected in Europe, Africa, the Middle East and Asia. While N8 and N6 have been reported most frequently, an N2 reassortant has been reported from Russia collected during the last reporting period. The contributors understand that within-period reports from South Africa and South Korea are for viruses similar to previous reports.

## H7

Reports of H7 during the current period are outlined in **Table 1** and **Map 2**.

### *Asian H7N9*

A marked reduction in the number of H7N9 reports has been documented since the fifth wave. There have been five reports each of Asian H7N9 LPAI and HPAI in China from in live poultry markets during the current period. Of note, an H7N3 HPAI (reassortant of H7N9) has been reported by Japan from a smuggled poultry carcass originating in China.

## H9

Reports of H9N2 during the current period are outlined in **Table 1** and **Map 3**.

### *H9N2*

The prevalence of poultry-adapted H9N2 is not well understood as H9 viruses are not reportable. The poultry-adapted Asian lineage H9N2 has become endemic in several countries. Although the epidemiology of the poultry-adapted H9N2 virus differs from that of goose/Guangdong H5 HPAI, any co-circulation represents concerns regarding potential reassortment.

Genetic data for 39 subtype H9N2 viruses was received from China, Ghana, India, Myanmar, Nepal, and Russian Federation. Data from outside the period was also submitted from Australia (Y439), Bangladesh (G1), and Pakistan (G1). Reports of H9N2 viruses reassorting with other viruses encountered in poultry contributes to ongoing diversity.

## Acknowledgements

The OFFLU Network would like to acknowledge and thank the laboratories that provided the data presented in this Report (in alphabetical order):

- Animal and Plant Health Agency (APHA) Weybridge, United Kingdom
- Australian Animal Health Laboratory (AAHL), Australia
- Avian Influenza Research & Diagnostic Division, Animal and Plant Quarantine Agency (APQA), Korea
- China Animal Health and Epidemiology Centre (CAHEC), China
- Erasmus Medical Center
- Federal Centre for Animal Health (FBGI ARRIAH), Russian Federation
- Friedrich-Loeffler Institut (FLI), Germany
- Hokkaido University, Japan
- Istituto Zooprofilattico Sperimentale delle Venezie (IZSve), Italy
- National Centre for Foreign Animal Diseases, Canada
- National Institute of Animal Health, and Animal Quarantine Station, Japan
- National Institute of High Security Animal Diseases (ICAR-NIHSAD), India
- National Veterinary Services Laboratories, USA
- Poultry Disease Diagnosis Laboratory, Animal Health Research Institute, Taiwan
- Southeast Poultry Research Laboratory, USA
- Technical University of Denmark
- Wageningen Bioveterinary Research, Netherlands

We also thank the FAO EMPRES and GLEWS teams for the epidemiological information, and our antigenic partners (Nicola Lewis, Frank Wong, and Francesco Bonfante) for their extra efforts. Finally, we thank the generous contributions of Mary Lea Killian, Tod Stuber, Amber Wilson, Xavier Roche and Yunho Jang for their efforts above and beyond in the analyses presented here.

Annex 1. Sequence data submitted to OFFLU by subtype, clade and country.

	H5N1	H5N2	H5N6	H5N8	H7 LPAI	H9N2	Grand Total
<b>2.3.2.1a</b>	<b>48</b>						<b>48</b>
Bangladesh	36						36
Bhutan	7						7
India	3						3
Nepal	2						2
<b>2.3.2.1c</b>	<b>10</b>						<b>10</b>
Myanmar (Burma)	4						4
Nigeria	1						1
Togo	5						5
<b>2.3.4.4</b>		<b>7</b>	<b>26</b>	<b>28</b>			<b>61</b>
Bulgaria				1			1
China			2				2
Denmark			1				1
Iran			1	13			14
Ireland			1				1
Israel				1			1
Italy				8			8
Japan			6				6
Myanmar (Burma)			6				6
Netherlands			7				7
Russia		5		5			10
Taiwan		2					2
United Kingdom			1				1
Vietnam			1				1
<b>H7N9 Asia</b>							<b>3</b>
Japan (ex-China smuggled)							3
<b>G1</b>						<b>48</b>	<b>48</b>
Bangladesh						30	30
Ghana						7	7
India						1	1
Nepal						9	9
Pakistan						1	1
<b>Y280</b>						<b>21</b>	<b>21</b>
China						11	11
Myanmar (Burma)						9	9
Russia						1	1
<b>North American LPAI</b>		<b>1</b>			<b>3</b>		<b>4</b>
Canada		1			1		2
United States					2		2
<b>Grand Total</b>	<b>22</b>	<b>8</b>	<b>17</b>	<b>23</b>	<b>1</b>	<b>37</b>	<b>195</b>