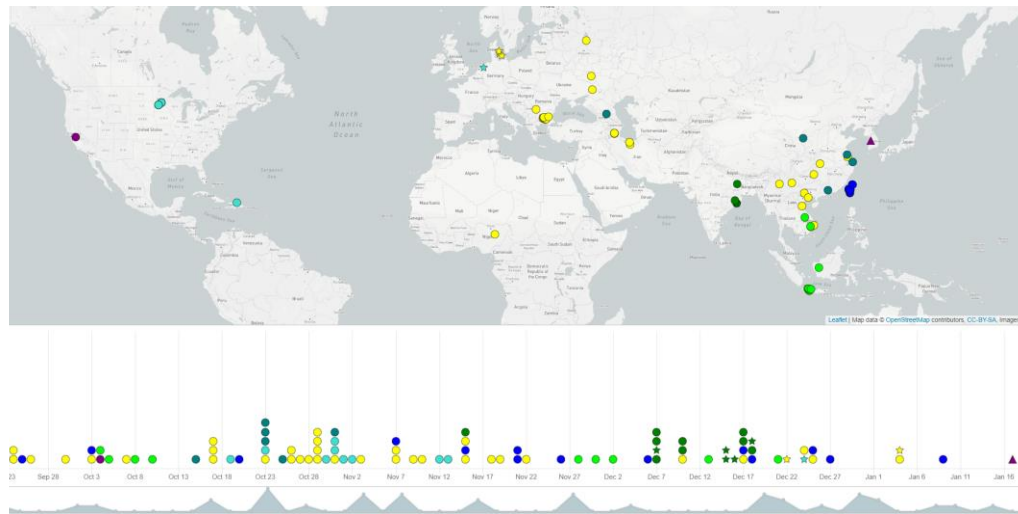




OFFLU AVIAN INFLUENZA POST-VCM REPORT

Events for the period September 2018 to February 2019



Scope

In this document we present a summary of H5, H7, and H9 avian influenza events that occurred September 2018 to February 2019.

Table of Contents

Introduction.....	3
Global H5, H7, and H9 Events in Animals.....	3
Map 1. H5 reported in birds during the current period.	5
Map 2. H7 reported in birds during the current period.	6
Map 3. H9 reported in poultry during the current period.	6
Table 1. Recent H5, H7 and H9 activity from reports and shared data.....	7
Acknowledgements	8
Annex 1. Sequence data submitted to OFFLU by subtype, clade and country.	9

Introduction

The WHO Consultation on the Composition of Influenza Virus Vaccines for the Northern Hemisphere 2019-2020 took place in Beijing, China on 17-20 February 2019. 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, Nicola Lewis, Francesco Bonfante, Timm Harder 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.

Sequence data for **94 H5, H7, and H9** were contributed to OFFLU by animal health laboratories in **25** countries representing Europe, Asia, Africa, Oceania, and the Americas (**Table 1**). Of these, **28** from **9** countries were collected during the current period. Sequences from Genbank and GISAID generated by OFFLU reference laboratories were also obtained.

Antigenic data generated by the haemagglutination inhibition (HI) assay using WHO-CC and OFFLU ferret-origin reagents was contributed by the Animal and Plant Health Agency in the UK (APHA) and the Australian Animal Health Laboratory (AAHL) in Australia.

Global H5, H7, and H9 Events in Animals

H5, H7 and H9 events for the current reporting period, **13 September 2018 to 12 February 2019**, can be visualized dynamically using the following link (not accessible with Internet Explorer): https://microreact.org/project/xTmSDSr_1

Overall, there was a decrease in reports compared to the previous period with **16** countries/territories reporting a total of **94** reported H5, H7 or H9 avian influenza (AI) events (**Maps 1, 2 and 3**). Of these, **84** reports were H5 or H7 outbreaks affecting poultry. The majority of events continue to be caused by

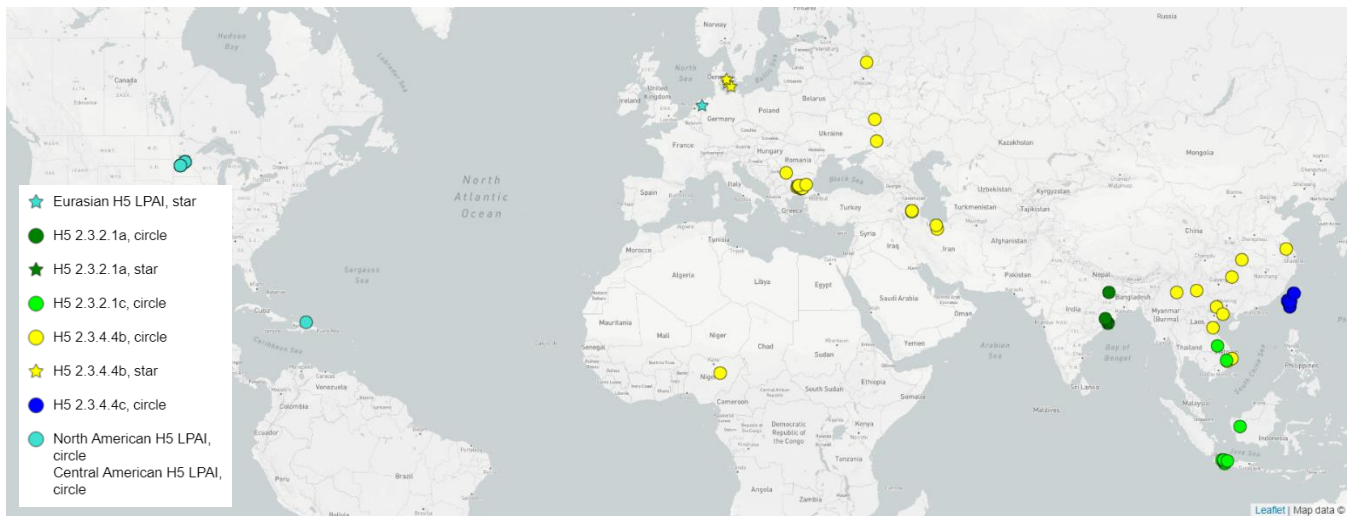
goose/Guangdong lineage (Gs/GD) H5 clade 2.3.4.4 highly pathogenic avian influenza (HPAI). Outside Asia, there were fewer reports of 2.3.4.4 H5N6 and ongoing reports of 2.3.4.4 H5N8.

H5 HPAI clade 2.3.4.4 continues to predominate globally and contains several phylogenetically distinct subgroups. Reassortment with native wild bird viruses encountered in migratory birds has been reported. The A/Fujian-Sanyuan/21099/2017-like viruses 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.

There were no reports of the highly poultry-adapted A/Anhui/1/2013 H7N9 lineage (AH/13) in China during this period.

For H5 and H7 low pathogenic avian influenza (LPAI), wild bird lineage viruses were reported in poultry from the United States (North American H5N2) and the Dominican Republic (Central American H5N2). There were also reports of LPAI in wild birds from the United States and Canada (North American H5 and H7), and the Netherlands (European H5), and from an environmental sample in the Republic of Korea (Eurasian H7N9).

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. 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 reassortment. There was one report of the poultry-adapted H9N2 (Russia) for this period, and OFFLU received sequence data directly from partner laboratories representing 27 viruses from three countries: China in the current period, and from Egypt and Ghana and Nepal outside the current period.



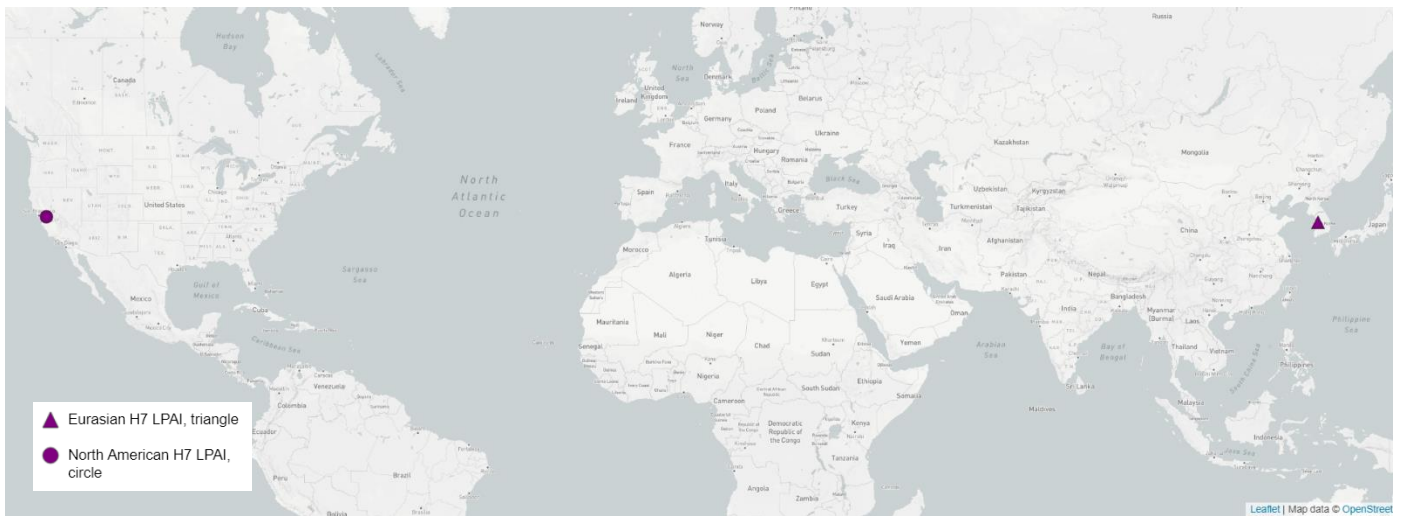
Map 1. H5 reported in birds during the current period.

Circles represents domestic and star for wild.

Red font indicates change since last period.

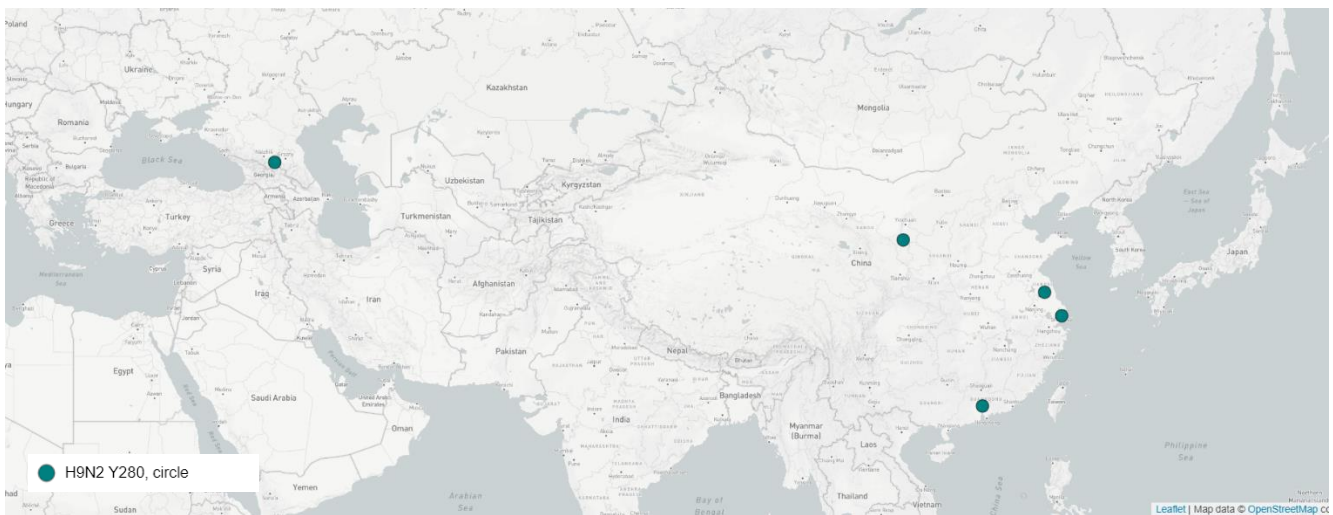
- H5N1 **2.3.2.1a** (green) was reported in India (domestic and wild); **2.3.2.1c** (light green) was reported in domestic birds (circle) in Indonesia, **Laos**, and **Viet Nam**.
- H5 2.3.4.4¹
 - **2.3.4.4b** (yellow) was reported in Bulgaria (N8; domestic), Denmark (N6; wild), Iran (N8; domestic), Russia (N8; domestic), South Africa (domestic and wild)
 - Other subgroups (blue) reported in Taiwan (2.3.4.4c; domestic), China (2.3.4.4d; domestic), and Vietnam (domestic).
- H5 LPAI (turquoise) of **European lineage** was reported in the **Netherlands (captive wild)**, and of **Mexican lineage** in the Dominican Republic (N2; domestic), and of **North American lineage** in the **United States** (N2; domestic).

¹ Informally proposed nomenclature



Map 2. H7 reported in birds during the current period.
Circles represent domestic, triangle represent environmental.

- North American H7N3 LPAI (purple; domestic) was reported in California.
- Eurasian wild bird lineage H7N9 LPAI was detected from an environmental sample in the Republic of Korea.



Map 3. H9 reported in poultry during the current period.
Circle represents domestic.

One official report was received and virus contributions were received for Asian lineage H9N2.

- Y280 (teal green; domestic) from China and the Russian Federation.

Table 1. Recent H5, H7 and H9 activity from reports and shared data.

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

2.3.4.4 subgroups from proposed nomenclature.

	Country list	Host	Subtype/clade/lineage
Goose Guangdong H5 HP AI	Bulgaria	Poultry	H5NX/N8 (2.3.4.4b)
	China	Poultry	H5N6 2.3.4.4d and H9N2 Y280
	Denmark	Wild birds	H5N6 (2.3.4.4b)
	<i>Egypt (previous period)</i>	Poultry	H5 (2.3.4.4b) and H9N2 (G1)
	<i>Ghana (previous period)</i>	Poultry	H5N1 (2.3.2.1c) and H9N2 (G1)
	India	Wild birds (crow)	H5N1 (2.3.2.1a)
		Poultry	H5N1 (2.3.2.1a)
	Indonesia	Poultry	H5N1 (previously 2.3.2.1c)
	Iran	Poultry	H5N8 (2.3.4.4b)
	Lao People's Democratic Republic	Poultry	H5N1 (previously 2.3.2.1c)
	<i>Nepal (previous period)</i>	Poultry	H5N1 (2.3.2.1a) and H9N2 (G1)
	Nigeria	Poultry	H5N8 (2.3.4.4b)
	Russian Federation	Poultry	H5N8 (2.3.4.4b) and H9N2 (Y280)
	South Africa	Poultry	H5N8 (2.3.4.4b)
	Taiwan (Prov of China)	Poultry	H5N2 (2.3.4.4c)
Viet Nam	Poultry	H5N6 (2.3.4.4)	
H5/H7 LPAI	Canada	Wild birds	H5N2, H7N3 (North American LPAI)
	Dominican Republic	Poultry	H5N2 (Mexican LPAI)
	<i>France (previous period)</i>	Domestic waterfowl	H5/H7 (European LPAI)
	Netherlands	Wild birds	H5 (European LPAI)
	Papua New Guinea	Wild birds	H7N7 (Australasian LPAI)
	Republic of Korea	Environment	H7N9 (Eurasian LPAI)
	United States of America	Poultry	H7N3 and H5N2 (North American LPAI)

Acknowledgements

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

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- Avian Influenza Research & Diagnostic Division, Animal and Plant Quarantine Agency (APQA), Korea
- China Animal Health and Epidemiology Centre (CAHEC), China
- Federal Centre for Animal Health (FBGI ARRIAH), Russian Federation
- French Reference Laboratory for avian influenza and Newcastle disease, Ploufragan, France
- Friedrich-Loeffler Institut (FLI), Germany
- National Centre for Foreign Animal Diseases, Canada
- National Institute of High Security Animal Diseases (ICAR-NIHSAD), India
- National Veterinary Services Laboratories, USA
- Poultry Disease Diagnosis Laboratory, Animal Health Research Institute, Taiwan
- State Research Center of Virology and Biotechnology Vector, Russian Federation
- Wageningen Bioveterinary Research, Netherlands

We also thank the FAO EMPRES and GLEWS teams for the epidemiological information, and our core antigenic team (APHA, AAHL, IZSve, and FLI) for their extra efforts. Finally, we thank the generous contributions of Mary Lea Killian, Tod Stuber, Lidewij Wiersma, and Xavier Roche for their efforts above and beyond in the analyses presented here.

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

	H5	H5N1	H5N2	H5N3	H5N6	H5N8	H7N7	H9N2	Total
2.2.1.2		3							3
Egypt		3							3
2.3.2.1a		4							9
India		4							4
Nepal		5							5
2.3.2.1c		3							3
Ghana		3							3
2.3.4.4b					3	29			32
Bulgaria						3			3
Egypt						21			21
Netherlands					1				1
Russia						5			5
South Korea					2				2
2.3.4.4c			4						4
Taiwan			4						4
2.3.4.4d					3				3
China					3				3
H9N2 G1								21	21
Egypt								18	18
Ghana								2	2
Nepal								1	1
H9N2 Y280								6	6
China								6	6
Americas LPAI	1		5						6
Canada	1		2						3
Dominican Republic			1						1
US			2						2
European LPAI			1	2			1	1	5
France			1	2			1	1	3
Australasian LPAI							2		2
Papua New Guinea							2		2
Grand Total	1	10	10	2	6	29	2	28	94