



OFFLU ANIMAL INFLUENZA REPORT

September 2019 to February 2020

Scope

In this document, we present a summary of H5, H7, and H9 avian influenza A virus events that were reported from September 2019 to February 2020, as well as a summary of H1 and H3 swine influenza A virus evolution from 2012 to present.

Global avian influenza virus events in animals

Introduction

Data sources and acknowledgements

Avian influenza A viruses

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, which for this reporting period included H5 HPAI from South Africa, as results were based solely on serology. Sequence data and viruses were shared by the OFFLU network and OIE/FAO partner countries and we are very grateful for their collaboration. We acknowledge and thank the OIE Reference laboratory and diagnostic laboratory teams at APHA, IZSVe, AAHL, FLI and NVSL for their expertise in data analyses and compiling the report.

Avian influenza A virus haemagglutination inhibition (HI) assay antigenic data was generated by the Animal and Plant Health Agency (APHA), UK, by IZSVe, by AAHL, Australia using WHO-CC and OFFLU provided ferret-origin reagents and harmonised protocols.

Avian influenza A virus 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.

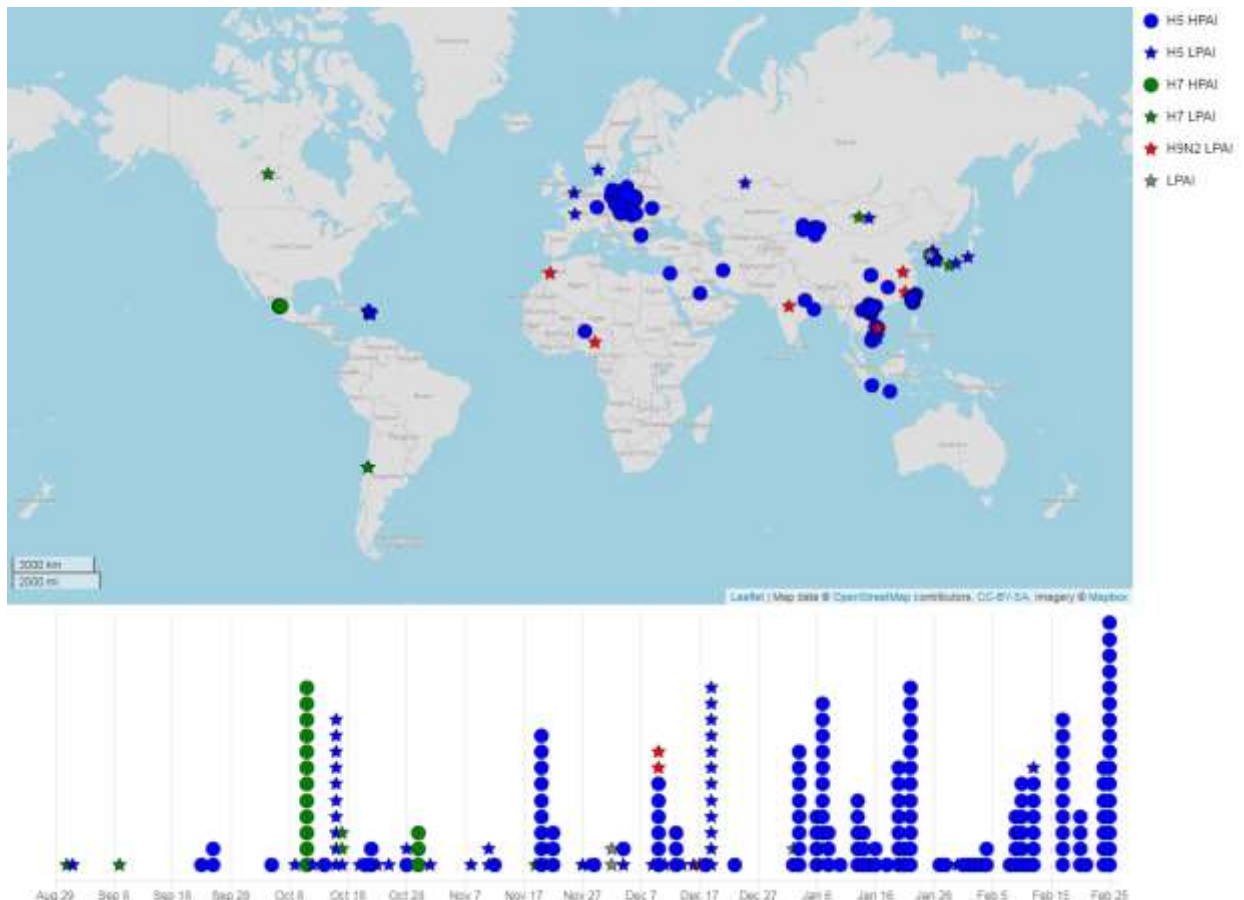
Currently, in China, vaccination of poultry is mandatory in all provinces (including chickens, ducks, geese, quails, pigeons and other rare birds in captivity). From

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. Current understanding is that RE-13 is the H5 vaccine representative and RE-2 is the H7 component.

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.

Global H5, H7, and H9 Events in Animals

Map 1. H5, H7 and H9 events for the current reporting period, 21 September 2019 to 25 February 2020. Points are scaled by number of reports, and colored by subtype. Shape denotes low pathogenic (star) or highly pathogenic (circle) avian influenza viruses. *Note: geographic centroid coordinates were used for reports with no precise geolocation available.*



Overall, there was an increase in reports compared to the previous period with a total of 235 H5, H7 or H9 avian influenza (AI) events reported from 30 countries/territories (see **Map 1.**).

Of these, 194 reports were in domestic birds with 27 reports attributed to H5 LPAI and 150 reports to H5 HPAI. The majority of H5 events were due to goose/Guangdong lineage (Gs/GD) H5 clade highly pathogenic avian influenza (HPAI) viruses. This period was marked by a decrease of **2.3.4.4b H5N8** HPAI virus activity in Africa and Middle East while, since early January 2020, there have been increasing reports of **2.3.4.4b H5N8**

HPAI in Europe including Bulgaria (n=3), Czech Republic (n=2), Germany (n=2), Hungary (n=4), Poland (n=27), Romania (n=2), Slovakia (n=4), and Ukraine (n=1). Israel and Saudi Arabia each reported one event of H5N8 HPAI in February 2020. Nigeria reported a **2.3.4.4b H5N6** HPAI virus, being the first report of H5N6 HPAI from Africa.

2.3.4.4h H5N6 HPAI was detected in wild birds in January 2020 in China, while H5N1 HPAI was reported early February. **2.3.4.4c H5N2** HPAI is well established in Taiwan, China, while a new **2.3.4.4c H5N5** HPAI was first reported in the territory in September 2019. **2.3.2.1c H5N1** HPAI and **2.3.4.4g H5N6** HPAI are continuously reported in Viet Nam. India reported **2.3.2.1a H5N1** HPAI during this time period.

During this period, 47 H5 LPAI events were reported in Denmark (n=1), France (n=1), the United Kingdom (n=1), the Russian Federation (n=1), the Dominican Republic (n=22), Japan (n=2), the Republic of Korea (n=16), Russian Federation (n=1), and Taiwan, China (n=2). Additional sequence data from EA-nonGsGd H5 LPAI viruses circulating in Mongolia was also contributed in the reporting period. See Annex for summary table of subtypes (H5N1, H5N3, H5N6, H7N7, H9N2), date of isolation and location of sampling from Vietnam and Mongolia contributed by University of Hokkaido, Japan.

H7N3 HPAI virus continues to circulate in Mexico with 15 outbreaks reported. Reports of the highly poultry-adapted Asian H7N9 lineage continue to be low since the fifth wave, with no reports of LPAI nor HPAI during the covered period. The most recent positive virological samples were detected in April 2019 according to the veterinary bulletin of the Ministry of Agriculture, China. An updated FAO qualitative risk assessment for spread of Asian H7N9 within and outside of China is available at:

<http://www.fao.org/3/CA3206EN/ca3206en.pdf>.

H7N6 LPAI was reported in Chile (n=2) in poultry while H7N7 LPAI virus was found in a wild bird in Japan.

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 Africa, Asia, and in the Middle East. The majority of the poultry-adapted H9N2 virus reports for this period were submitted directly from partner laboratories rather than through official channels, representing viruses from six countries (China, India, Morocco, Nigeria, Republic of Korea, and Viet Nam).

Sequence data for 89 H5, 3 H7, and 139 H9 were contributed to OFFLU by animal health laboratories in countries representing Europe, Asia, Africa, Oceania, and the Americas (Table 1) to which was added sequences from Genbank and GISAID.

A geographic summary of circulating subtypes and clade designations for outbreaks for which we have sequence data is shown in Table 1.

Table 1: Summarised outbreak report data from EMPRES-i for this reporting period.
Bold - sequence data available and lineage confirmed.

Pathotype and subtype	H5/H7/H9 CVV lineage	Country	Year (unless 2019)
H5 HPAI		Taiwan, China	
H5N1 HPAI		China	
	2.3.2.1a	India	
		Indonesia	
	2.3.2.1c	Viet Nam	
H5N2 HPAI	2.3.4.4c	Taiwan, China	
H5N3 HPAI	2.3.4.4b	Iran	
H5N5 HPAI	2.3.4.4c	Taiwan, China	
H5N6 HPAI	2.3.4.4h	China	2020
		Lao PDR	
	2.3.4.4b	Nigeria	
	2.3.4.4g	Viet Nam	
H5N8 HPAI	2.3.4.4b	Bulgaria	2020
		Czech Republic	2020
	2.3.4.4b	Egypt	
		Germany	2020
		Hungary	2020
		Israel	2020
	2.3.4.4b	Nigeria	
	2.3.4.4b	Poland	
	2.3.4.4b	Romania	2020
		Saudi Arabia	2020
	2.3.4.4b	Slovakia	2020
	2.3.4.4b	South Africa	
2.3.4.4b	Ukraine	2020	
H5 LPAI		Denmark	
		Dominican Republic	
		France	
		Iran (Islamic Republic of)	
		Japan	
		Mongolia	

		Netherlands	
		Republic of Korea	
		Russian Federation	
		United Kingdom	
		Viet Nam	
H7N3 HPAI		Mexico	
H7 LPAI		Canada	
		Chile	
		Japan	
		Mongolia	
H9N2 LPAI		China	
		India	
	G1	Morocco	
	G1	Nigeria	
		Republic of Korea	
		Viet Nam	