OFFLU Animal Influenza Report

February 2019-September 2019

Scope:
In this document we present a summary of H5, H7, and H9 avian influenza A virus events that primarily occurred February 2019 to September 2019, as well as a summary of H1 and H3 swine influenza A virus evolution from the last 6 months in the USA and 2016-present for all other countries.

Global avian influenza virus events in animals

Introduction

The WHO Consultation on the Composition of Influenza Virus Vaccines for the Southern Hemisphere 2020 influenza season took place in Geneva, Switzerland on 23 – 27 September 2019. The meeting gathered participants from the WHO Collaborating Centres for influenza (CCs), WHO Essential Regulatory Laboratories (ERLs), National Influenza Centres, WHO H5 Reference Laboratories and from OFFLU. The OFFLU contribution on animal influenza (avian influenza and swine influenza) was presented by Dr Nicola Lewis from the Royal Veterinary College/Animal Plant Health Agency, UK. The OFFLU team would like to give special thanks to all Reference Laboratories and national laboratories who have contributed data and provided assistance towards this VCM contribution.

Data sources and acknowledgements

Avian influenza A viruses

The H3/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

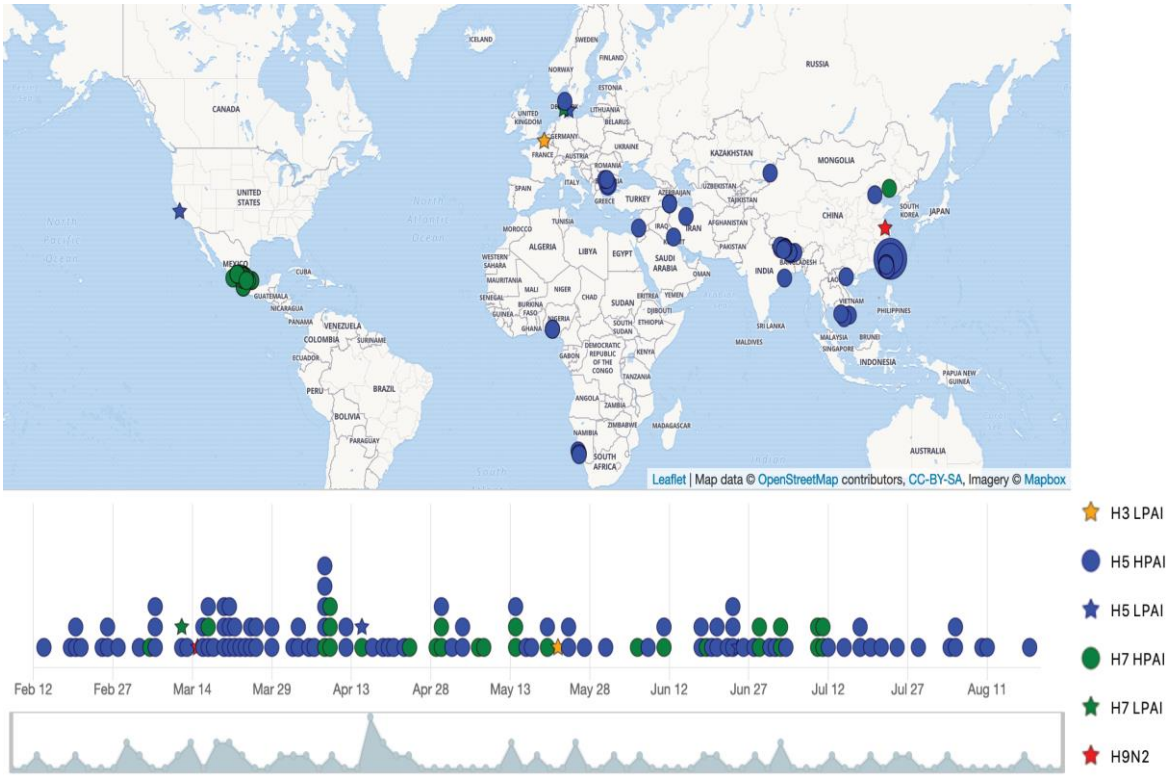
In some countries, including Viet Nam, Indonesia, Bangladesh, and Egypt, H5 and others vaccination is employed as part of overall control efforts to endemic viruses.

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

H5, H7 and H9 events for the current reporting period, ***13 February 2019 to 20 September 2019***. Points are scaled by number of reports, and coloured by subtype. Shape denotes LPAI (star) or HPAI (circle).



Overall, there was an increase in reports compared to the previous period with 17 countries/territories reporting a total of 115 reported H5, H7 or H9 avian influenza (AI) events.

Of these, 5 reports were H5 LPAI in domestic birds, and 86 reports were H5 viruses in domestic birds and penguins. The majority of H5 events continue to be caused by A/Goose/Guangdong lineage (Gs/GD) H5 clade highly pathogenic avian influenza (HPAI) viruses. Of note, The report contains 2.3.2.1 a viruses related to the zoonotic 2.3.2.1a HPAI event in Nepal.

We note 1 report of H7 LPAI in domestic birds, and 23 reports of H7 HPAI in domestic or captive birds - one of which was H7N9 in a zoo bird in China. 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. There was 1 report of the poultry-adapted H9N2 (Nepal) for this period and 1 report of an H9N2 human case in China. There was one report of H3N1 viruses in poultry in France.

Sequence data for 61 H5, 11 H7, and 11 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.

Table 1: A geographic summary of circulating subtypes and clade designations for outbreaks for which we have sequence data (Bold - sequence data available and lineage confirmed).

Pathotype and subtype	H5/H7/H9 CVV_lineage	Country	Year (unless 2019)
HPAI H5N1	2.3.2.1c	**Laos**	2018
		VietNam	
		India	
		China	
	2.3.2.1a	**Nepal**	
	2.3.2.1a	**Bhutan**	
HPAI H5N6		China	
		Cambodia	
HPAI H5N8	2.3.4.4b	**Russian Federation**	
	2.3.4.4b	**Israel**	
		Namibia	
		Iran (Islamic Republic of)	
	2.3.4.4b	**Bulgaria**	
	2.3.4.4b	**Nigeria**	
	2.3.4.4b	**Iraq**	
HPAI H5N2	2.3.4.4c	**Taiwan**	
HPAI H5	2.3.4.4e	**Philippines**	2018
LPAI H5		**United States**	
		Denmark	
HPAI H7N3		Mexico	
HPAI H7N9		China	
		Japan	
LPAI H7		**Canada and USA**	
H9N2		China	
	G1	**Nepal**	

Global swine influenza A virus events in animals

H1 and H3 events for the current reporting period. For this reporting period there are no variant strains. Variant strains were previously identified from the 1B lineage in the US, the H3 lineage in the US and with the 1C 2.1 and 2.3 lineages in Europe and China.

Swine influenza A virus vaccination

Economic losses to pork producers due to influenza A virus (IAV) infections are substantial and a global problem, ranking among the top three major health challenges in the swine industry. Swine IAV was also ranked in the top zoonotic diseases of priority by public health officials. Currently, H1 and H3 subtypes circulate in pigs globally, associated with different combinations of N1 and N2 subtypes; however, the origin, gene constellation, and antigenic makeup of IAV vary greatly on different continents. Vaccination is one means of mitigating the effects of IAV disease, and vaccines are most effective if the strains included closely match the currently circulating strains in pigs. Genetic analyses provide panoramic views of the virus landscape at the sequence level and, thus, can aid in the selection of well-matched swine IAV vaccine strains, but is not sufficient alone. Additionally, a major challenge in selecting appropriate swine IAV vaccine strains is the co-circulation of multiple lineages of viruses in the same region, requiring multivalent or broadly cross-reacting antigens. Due to this complex IAV ecology in swine, new vaccination strategies and vaccine platforms are needed. The hemagglutinin (HA) viral protein is the major target of neutralizing antibodies, which are widely considered to be correlated with protection. Virus variants that are not recognized by previously elicited antibodies can render traditional vaccines that primarily elicit humoral responses ineffective, and therefore result in the need for vaccine strain reformulation and re-vaccination. In the future, new vaccine platforms may be on the market that will provide alternative options to those currently available.

It should be recognised that along with commercially produced vaccine, multivalent autogenous vaccines are used within production systems, and these are generally not standardised for antigen, formulation or immunogenicity.

Swine influenza A viruses

Haemagglutination inhibition (HI) assays were performed with ferret anti-sera and guinea pig red blood cells. H3N2 assays were performed with oseltamivir. Antigenic data were generated by the Animal and Plant Health Agency (APHA), UK, and by the

National Animal Disease Center (NADC), USDA-ARS, US. Ferret sera was kindly provided by WHO-CC (CDC) and NIH-Centers of Excellence in Influenza Research and Surveillance (CEIRS). Phylogenetic and sequence analyses were performed at NADC and Royal Veterinary College (RVC). We acknowledge NIH-CEIRS for funding the swine pandemic risks pipeline which supported ferret sera generation and NIH-CEIRS and the USDA IAV in Swine Surveillance Program for collection and sequencing of contemporary viruses for the antigenic and genetic analyses.

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