



## OFFLU summary report from the WHO vaccine composition meeting

27<sup>th</sup> September 2024

Since 2011 the World Organisation for Animal Health (WOAH, founded as OIE) and the Food and Agriculture Organization of the United Nations (FAO)'s Network of Expertise on Animal Influenza (OFFLU), have attended the World Health Organisation (WHO) bi-annual Vaccine Composition Meeting (VCM) organized by the Global Influenza Surveillance and Response (GISRS) team. The need to update candidate vaccine viruses which may be prepared as part of the pandemic response for zoonotic influenza is assessed during the meeting. OFFLU brings important data from the animal health community which provides the context around zoonotic avian and swine influenza cases in humans. Zoonotic diseases with pandemic potential caused by animal influenza viruses remain a threat to the international community and OFFLU works towards helping to improve pandemic preparedness by strengthening the WOAHO-FAO-WHO tripartite response.

The OFFLU VCM team gathers data through the network in the form of sequences, surveillance data and phenotypic data from avian and swine contemporary circulating influenza viruses. This collaborative effort between animal influenza laboratories strengthens the data available for analysis and contributes to evidence-based decision making. OFFLU would like to thank, and specifically acknowledges the involved WOAHO and FAO country offices, WHO CCs, OFFLU network laboratories, research programs and collaborators for the significant and kind contributions of epidemiological information, sequence data and antigenic characterisation of viruses. OFFLU acknowledges GISRS, GISAID, EMPRES-I and WAHIS. OFFLU also thanks all colleagues involved in the data analyses, information sharing and the generation of its reports.

There were 843 avian influenza outbreaks were reported between February 2024 and September 2024. 14225 HPAI H5 sequences were analysed from *within the reporting period* representing the diversity of viruses circulating in Asia, Europe, Africa the Americas and the Antarctic. 225 sequences submitted to OFFLU were analysed, of which 260 clade 2.3.4.4b (30 viruses antigenically characterised from Asia, Americas, Europe and Africa); 18 clade 2.3.2.1a (5 antigenically characterised from Asia), 79 clade 2.3.2.1c sequences, 2 clade 2.3.2.1e sequences and 6 non Gs/Gd-lineage H5 LPAI viruses. 17 H7 viruses were submitted to OFFLU, of which 3 were HPAI. 29 H9 viruses of the B4.7 lineage were submitted to OFFLU and 2 viruses of the B4.5 lineage (formally known as Y280). 5 G5.5 (3 of which antigenically characterised from Africa) and 37 G5.7 viruses were submitted to OFFLU (formally known as G1). 8 H10 viruses were submitted to OFFLU.

There were over 1009 swine influenza detections within the reporting period in 15 countries in 9 regions (3 continents) from 32 lineages. 284 H1 sequences were submitted through the OFFLU network; 115 1A lineage (2 antigenically characterised); 11 1B lineage (2 antigenically characterised); 158 1C lineage (7 antigenically characterised); 26 H3 sequences submitted through the OFFLU network (0 antigenically characterised).

**A new antigenically like A/Cambodia/SVH240441/2024 CVV was proposed for Gs/Gd lineage clade 2.3.2.1c viruses. A/Jiangsu/428/2021-like CVV was proposed for H10 viruses. A new antigenically like A/Pennsylvania/27/2024 CVV was proposed for H1 clade 1A.1.1.3 variant viruses.**

The OFFLU swine and avian reports which were presented at the September 2024 VCM are available [here](#). A recording of the WHO information Meeting on the composition of influenza vaccines for use in the 2024 southern hemisphere influenza season can be found [here](#). The WHO summary report on the genetic and antigenic characteristics of influenza viruses can be found [here](#).