

## OFFLU summary report from the WHO vaccine composition meeting, February 2024

23<sup>rd</sup> February 2024

Since 2011, the World Organisation for Animal Health (WOAH) 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 Meetings (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 WOAH-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 WOAH 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 2983 avian influenza outbreaks were reported between September 2023 and February 2024. 12 LPAI H3, 9LPAI H5 and 1 HPAI H7 and 2 LPAI H7 sequences were submitted through the OFFLU network. 485 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. 349 of which were submitted through the OFFLU network, including: 464 clade 2.3.4.4b (19 viruses antigenically characterised from Asia, Americas, Europe and Africa and the Antarctic); 2 clade 2.3.2.1a (11 antigenically characterised from Asia outside the reporting period) and 7 clade 2.3.2.1c sequences. H9 sequences were analysed including 21 G1 sequences from Africa and Asia (4 antigenically characterised from Asia) sequences were analysed from *within the reporting period*.

There were over 680 swine influenza detections within the reporting period in 24 countries in 11 regions from 39 lineages from Europe, the Americas and Asia between July 2023 and January 2024. 215 H1 sequences submitted through the OFFLU network; 100 1A lineage (1 antigenically characterised); 58 1B lineage (2 antigenically characterised); 57 1C lineage (3 antigenically characterised); 47 H3 sequences submitted through the OFFLU network (1 antigenically characterised).

During the consultation, which OFFLU Avian and Swine experts from IZSve and USDA-ARS attended, along with the OFFLU Scientist, two new A(H1) CVVs were recommended: A/Catalonia/NSAV198289092/2023-like of the 1A.3.3.2 lineage and A/England/234600203/2023-like of the 1B.1.1.1 lineage.

The OFFLU avian influenza report is available [here](#) and the swine influenza report is available [here](#). The WHO summary report on the genetic and antigenic characteristics of influenza viruses can be found [here](#).

A recording of the WHO information Meeting on the composition of influenza vaccines for use in the 2024 /2025 northern hemisphere influenza season can be found [here](#).