

OFFLU summary report from the WHO vaccine composition meeting, September 2023

29th September 2023

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 over 2835 avian influenza outbreaks were reported between February 2023 and September 2023 reported in animals. 8 LPAI H3, 3 LPAI H5 and 13 LPAI H7 sequences were submitted through the OFFLU network. 1368 HPAI H5 sequences were analysed from *within the reporting period* representing the diversity of viruses circulating in Asia, Europe, Africa and the Americas. 281 of which were submitted through the OFFLU network, including: 220 clade 2.3.4.4b (22 viruses antigenically characterised from Asia, Americas, Europe and Africa); 9 clade 2.3.2.1a (9 antigenically characterised from Asia); 17 clade 2.3.2.1c and 14 clade 2.3.2.1e sequences. 117 H9 sequences were analysed which were submitted through the OFFLU network. 11 Y280 (5 antigenically characterised from Asia) and 10 G1 (11 antigenically characterised from Africa and Asia) sequences were analysed from within the reporting period.

There were 512 swine H1 and H3 influenza detections from 30 genetic clades in 12 countries from Europe, the Americas and Asia between January and July 2023. 191 unpublished H1 sequences were submitted through the OFFLU network; 104 1A lineage (1 antigenically characterised); 22 1B lineage (4 antigenically characterised); 65 1C lineage (4 antigenically characterised). 49 unpublished H3 sequences were submitted through the OFFLU network (1 antigenically characterised).

The OFFLU avian influenza report which was presented at the September 2023 VCM is available [here](#) and the swine influenza report is available [here](#).

After consultation, two new CVVs are proposed based on available data. This includes an avian A(H9N2) Y280 lineage -like virus and an Swine A(H3N2)v 1990.4a lineage -like virus. A recording of the WHO information Meeting on the composition of influenza vaccines for use in the 2023 northern hemisphere influenza season can be found [here](#)

The WHO summary report on the genetic and antigenic characteristics of influenza viruses can be found [here](#)