

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) organised by the Global Influenza Surveillance and Response (GISRS) team. During the meeting, the need to update candidate vaccine viruses for potential pandemic response to zoonotic influenza is assessed. 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 has been a recent update to this nomenclature to reflect the genetic diversification of the A(H5) viruses, particularly clade 2.3.2.1c, to add 2.3.2.1d, e, f, and g^[1]. Where relevant, updated clade nomenclatures have been adopted in this report.

There were 3040 avian influenza outbreaks reported between September 2024 and February 2025. 1640 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. 409 sequences submitted to OFFLU were analysed, of which 218 clade 2.3.4.4b (38 viruses antigenically characterised from Asia, Americas, the Antarctic, Europe and Africa); two clade 2.3.2.1a, 79 clade 2.3.2.1e sequences (previously known as clade 2.3.2.1c), 8 clade 2.3.2.1g sequences (previously known as clade 2.3.2.1c), and 102 non Gs/Gd-lineage H5 LPAI viruses. Seven H7 viruses were submitted to OFFLU. Four H9 viruses of the B4.5 lineage and 11 H9 viruses of the B4.7 lineage were submitted to OFFLU (previously known as Y280 ^[2]). Five G5.6 viruses and 1 G5.7 viruses were submitted to OFFLU (formally known as G1 ^[2]). Three H10 viruses were submitted to OFFLU.

There were over 829 swine influenza detections within the reporting period in 16 countries in 9 regions (3 continents) from 33 genetic clades. 194 H1 sequences were submitted through the OFFLU network; 129 1A lineage (9 antigenically characterised); three 1B lineage (8 antigenically characterised); 62 1C lineage (6 antigenically characterised); 62 H3 sequences submitted through the OFFLU network (9 antigenically characterised).

A new antigenically like A/Victoria/149/2024 CVV was proposed for Gs/Gd lineage H5 clade 2.3.2.1a viruses. A new antigenically like A/Fujian/2/2024 CVV was proposed for Gs/Gd lineage H5 clade 2.3.4.4h viruses.

The OFFLU avian report which was presented at the February 2025 VCM is available [here](#). The OFFLU swine report which was presented at the February 2025 VCM is available [here](#). A recording of the WHO information Meeting on the composition of influenza vaccines for use in the 2024 northern hemisphere influenza season can be found [here](#).

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

[1] Ort JT, Zolnoski SA, Lam TT-Y, Neher R, Moncla LH. Development of avian influenza A(H5) virus datasets for Nextclade enables rapid and accurate clade assignment. *BioRxiv* 2025:2025.01.07.631789. <https://doi.org/10.1101/2025.01.07.631789>.

[2] Fusaro A, Pu J, Zhou Y, Lu L, Tassoni L, Lan Y, et al. Proposal for a Global Classification and Nomenclature System for A/H9 Influenza Viruses. *Emerging Infectious Disease Journal* 2024;30:1. <https://doi.org/10.3201/eid3008.231176>.