



OFFLU Swine Influenza Experts Technical Meeting
28-29 April 2026
WOAH Headquarters, Paris France

The WOAHA Deputy Director General for Global Frameworks and Capacity Building, Dr Baba Soumare and FAO Senior Animal Health Officer, Dr Madhur Dhingra, welcomed the participating experts and acknowledged their valuable contribution in sharing global swine influenza surveillance data and updates on the scientific advancements on the disease. Although swine influenza is not a WOAHA-listed disease, its monitoring remains essential due to its implications for both animal and public health. In this context, FAO and WOAHA highlighted the importance of sustained, coordinated surveillance efforts led by experienced experts and supported by strong veterinary services as the most effective approach to achieving long-term, sustainable outcomes.

WOAHA and FAO expressed the parent organisations strong commitment to the OFFLU swine influenza expert activities which comprises specialists from both animal and public health sectors worldwide. The expert group has played a key role in generating and sharing surveillance data, fostering collaboration, and contributing to global scientific knowledge since its creation from 2011. The opening remarks concluded by expressing appreciation for the experts' continued support and to have a productive discussions during the meeting.

Update surveillance data and research activities since April 2024:

Australia

Detection of influenza A in pigs is reportable in some Australian states, however swine influenza surveillance in commercial/production pigs in Australia remains passive with positive laboratory detections often opportunistic. The first confirmed IAV detection in Australian pigs occurred in 2009, following the introduction of H1N1pdm09 virus from humans to pigs. In July-August 2012 (and separately in 2016) unique H1N2 and H3N2 IAV reassortants were also detected in commercial pigs in Western Australia and Queensland consisting of genes derived from past human pandemic and seasonal IAV lineages. These showed that some IAV gene lineages have likely been maintained in Australian pig populations for at least 50 years. H1 clade 1A.3.3.2, 'other-human' H1 clades 1B.2 and 1B.3, and old-human origin H3 IAVs continue to evolve in isolation in Australia separate from other global swine IAV populations, with H1 clade 1A.3.3.2 viruses present in all sampled swine-producing state jurisdictions. Most Australian swine IAV gene clusters form long branches that could be directly traced back to their seed human IAV, indicating the absence of direct relatedness to swine viruses elsewhere in the world. Therefore, swine IAVs in Australia are left to independent

evolution. Australia has reported two laboratory-confirmed human cases of variant H3N2 cases, in 2018 and 2021, from the same state of South Australia. These H3N2v viruses are genomically similar, with their virus gene segments most closely related to those in H3N2 and H1N1 IAVs maintained in Australian swine. Pilot serology screening of healthy market progeny and sows in at least two eastern Australian states in 2025 indicate moderate to high influenza seroprevalence. Ongoing efforts are being made to reduce the genetic surveillance knowledge gap on swine influenza viruses circulating in Australian swine production systems. Some focused antigenic surveillance analysis is also being planned together with the OFFLU swine influenza and VCM technical activity groups.

China

For the period November 2024 – April 2026, 28800 nasal and tracheal swab samples from 18 provinces were collected and analysed. All samples were collected through abattoir based surveillance. 160 strains of swine influenza virus (SIV) were isolated from samples collected in 2024 and more than 100 strains of SIVs were isolated from samples collected in 2025. Surveillance results suggested that the majority of the influenza viruses circulating in pigs were H1N1 subtype. Influenza viruses of H1N2, H3N2 and H9N2 subtypes were also isolated from the samples. The lab constructed phylogenetic trees for the HA and NA genes of 126 viral strains isolated in 2023 and 2024. Evolutionary analysis showed that both the HA and NA genes of H1N1 subtype swine influenza viruses belonged to the EA H1N1 Group 1 branch. Also the lab completed whole-genome sequencing of 319 representative virus strains (2013-2019). Based on genomic characteristics, these viruses were classified into 8 distinct genotypes (G1–G8). Whole-genome sequencing revealed that all EA H1N1 viruses isolated in 2023 and 2024 belonged to genotype G5. Whole-genome sequencing revealed that all H3N2 viruses isolated in 2023 and 2024 belonged to genotype G1.

Results of HI test showed that the positive rates of EA H1N1, 2009/H1N1, and H3N2 were 40.1%, 22.5%, and 20.4%, respectively. Results of HI test showed that the positive rates of EA H1N1, 2009/H1N1, and H3N2 were 33.9%, 14.7%, and 19.4%, respectively.

Hong Kong and Vietnam

Longitudinal surveillance at the Van Phuc slaughterhouse in Hanoi, which sources pigs from 23 provinces across the country were tested. Monthly visits to slaughter houses and collected swabs and sera from 300 animals as they enter the supply chain in Hong Kong and Vietnam. The viruses were isolated and characterized. The results indicate subtypes H1 - 1C.2.3 and H3 - 3.2000.4 subtypes were circulating in Hong Kong during period 2021 – 2026 and subtypes H1 – 1A.3.3.2, 1B.2, 1B.2.2.1, 1C.2.3, 1C.2.4 and H3 – 3.1990.3, 3.2000.4 were circulating in Vietnam during period 2013 – 2026.

The current swine influenza genotyping tools available are flu-crew.org/octoFLU (USDA maintained platform for automated clade classification) and Flu genome influenza virus genotype tool – [flugenome.org / FluGenome](https://flugenome.org/) (web tool for comprehensive genotype analysis).

Japan

From April 2024 to December 2025, 3,900 nasal swab samples were collected from 28 pig farms in 11 prefectures in Japan. Out of them, 340 strains were isolated (detection rate of 8.7%) and possessed HAs classified as 96 1A3.3.2 and 244 1A.5.1. Some reassortment events between those IAVs-S were found. Two genotypes (H1 1A.5.1; H1 1A.3.3.2) are circulating throughout Japan. While almost H1 1A.3.3.2 IAVs-S are sporadically isolated throughout Japan, In one case, apparent adaptation to pigs are found.

Belgium

During the 2024–2025 surveillance period, 308 diagnostic samples were collected from 3 different sources, of which 55 swine influenza A viruses (swIAV) were successfully isolated. The predominant subtype was European avian-like H1N1 (56%), followed by European human-like H1N2 (25%) and H1pdm09N2 (12%), while H3N2 was not detected. Analyses of the origin of all 8 gene segments revealed 11 genotypes, including 5 novel ones in Belgium, reflecting ongoing reassortment and viral evolution. Phylogenetic analysis confirmed the co-circulation of three major H1 clades: 1A.3.3.2, 1B.1.2.1, and 1C.2.2.

Isolates were antigenically characterized using cross-HI and HI assays. The cross-HI assays revealed strong cross-reactivity between recent Belgian isolates and European strains from the same clade, but no cross-reactivity with North American swine strains or the 2022 human vaccine strain. All tested swIAV strains showed cross-reactivity with swine influenza vaccine strains; however, post-vaccination swine sera reacted to higher titers with the older vaccine strains than with the 2024–2025 Belgian isolates. This effect was most pronounced for clade 1A.3.3.2 viruses and highlights the need to update swine influenza vaccine strains to better match currently circulating Belgian swIAV.

Italy

Swine Influenza A viruses (IAV-S) continue to exhibit high genetic and antigenic diversity, driven by frequent reassortment events and sustained viral evolution. Italy plays a central role in the European swine influenza landscape due to intensive pig production systems and active live swine trade with several European countries. This presentation provides an updated overview of the circulation, genetic composition and diagnostic implications of IAV-S detected in Italy, with a focus on recent trends observed through national diagnostic activities.

Since 2012, multiple IAV-S subtypes have co-circulated in Italy, including H1N1, H1N2, H3N2 and H3N1, with marked temporal shifts in subtype prevalence. Detailed genotype analyses conducted from January 2025 onwards highlight extensive reassortment among H1 and H3 lineages, involving avian-like, pandemic-derived and human-like gene segments. In particular, H1N1 and H1N2 viruses exhibit a wide range of genotypes, dominated by H1av-1C and H1pdm-1A lineages combined with diverse NA and internal gene constellations. Antigenic analyses further confirm substantial

variability within H1C lineages and the emergence of new human-derived H3N2 genotypes, with evidence of reduced cross-reactivity in hemagglutination inhibition assays using sera from vaccinated animals.

Surveillance data from wild boar populations in Emilia-Romagna indicate low but detectable IAV-S positivity, supporting the role of wildlife monitoring within an integrated surveillance framework. In parallel, advances in diagnostic approaches, including the evaluation of COBRA-based antigens in indirect ELISA assays, demonstrate potential improvements in the serological detection.

United Kingdom

An update of IAV-S genetic diversity in Great Britain and detailed analysis of trends observed during the period 2014-2022 as recently published (Mollet BC et al, 2026 <https://doi.org/10.1099/mgen.0.001668>) was presented. Recent results from the Defra-funded Great Britain swine influenza surveillance programme was also discussed. A finding of note was the detection of an H3N2 influenza A virus in a pig herd in England (detected by another laboratory in Dec 2025, confirmed by an APHA detailed investigation in Jan 2026). The strain isolated had envelope glycoproteins with genetic similarity to viruses from the 2022 human seasonal clade 2b (subclade G.2) corresponding to clade 2020.1 (swine) and N2 human seasonal clade A.2.2.2. The remaining genes were derived from A/H1N1 pdm09 viruses. This gene constellation suggests that a reassortment event occurred within pigs, most likely within the wider pig population in Great Britain.

A report is published:

<https://assets.publishing.service.gov.uk/media/69a6aecf3b5b78231d1a9ad7/Quarterly-GB-pig-disease-surveillance-emerging-threats-report-Oct-Dec-2025.pdf>

An isolate has been shared with the WIC (Crick Institute) and antigenic analysis is ongoing at APHA and the WIC.

SwIAV diversity in Europe: outcomes from the ESFLU Network

IAV-S diversity at the scale of Europe based on data collected within the European Swine Influenza Network, with a focus on the 10-2024/09-2025 period compared to the 10-2023/09-2024 period was presented by Gautier Richard, Anses, France. Full-genome genotyping (via a modified OctoFlu database) and maximum-likelihood phylogenies (via Nextstrain) approaches were used to map the spatiotemporal distribution of IAV-S on 717 strain sequences for the 10-2024/09-2025 period.

20 distinct lineages made up of 17 HA clades and 8 NA clades were identified. The H1A/N1P (H1pdmN1pdm) lineage was the most geographically widespread across Europe, though it was not necessarily the most frequent in every individual country. The H1C/N1EA (H1avN1av) lineage was the second most widespread overall, but it was usually the most frequently detected lineage within

the individual countries surveyed. The H1C/N2G (H1avN2) lineage was the third most widespread in Europe. Conversely, H3 lineages remained rare in Europe.

Analyses at the HA/NA clades level revealed contrasting diversity between each country as well as major differences in the IAV-S sampling. Some countries however displayed similar HA/NA clades distribution, like Belgium and The Netherlands, or Denmark and Italy. Within each country, the proportion of HA/NA clades combination remained stable between the two analysed periods.

At the full genome level, thanks to the use of a new international nomenclature to annotate IAV-S genotypes, 75 different genotypes were identified in the 2024–2025 period from 523 strains, an increase from 53 in the previous period. The most widespread genotypes remained similar between both studied periods, i.e. H1C.2.2/N1EA/EEEEEE, H1A.3.3.2/N1P/PPPPPP, H1C.2.2/N1EA/EEEEPE and H1C.2.4.1/N2G.2/PPPPPP. While most genotypes were specific to individual countries, several were repeatedly found shared between two countries (e.g., Belgium and the Netherlands; Italy and Denmark), suggesting either co-evolution or cross-border transmission spillovers, with the example of the H1C.2.4.3/N2G.2/PPPPPE genotype between Denmark and Italy.

France

A focus on France was also presented by Gautier Richard based on the French national IAV-S surveillance program. Following a sharp modification of the IAV-S diversity in 2020 after the introduction of the H1C.2.4.2/N2G.2/EEEEEE genotype from Denmark (Richard et al. 2025, Virus Evolution), the IAV-S genotypes distributions remained stable up to the considered period (March 2026). However, an increase in H1A.3.3.2/N1P detection was identified in 2025, as well as an increase in cases involving H1C.2.1/N1EA reassortants with the M segment from the H1C.2.4.2/N2G.2/EEEEEE genotype. Several reverse-zoonotic events were documented (human seasonal H1N1 and H3N2 viruses). From the sequences shared with OFFLU, an isolate was shared with the WIC and APHA for antigenic characterization, which is ongoing.

Brazil

Swine influenza surveillance in commercial pigs in Brazil is conducted through a passive, laboratory-based network, in which swine samples that test positive for influenza by RT-PCR are submitted for viral isolation and sequencing. The network currently covers nine states (SC, RS, PR, SP, MG, MS, MT, GO, and DF) across three Brazilian regions, which together account for 99.8% of pork production in Brazil. Approximately 130 IAV-S isolates collected in 2023–2025 were sequenced, predominantly H1N1pdm, H1N2, and H3N2. Phylogenetic analyses revealed four established swine clades of H1N1pdm (1A.3.3.2) in Brazil, alongside frequent human-to-swine spillover events, many of which appear to be dead-end infections. Continued surveillance has demonstrated clade expansion (clades 2 and 4) and the emergence of four new clades. Distinct geographic patterns of clade circulation were observed, and new sampling supports links between swine clades and variant viruses (new clade 2 and the human variant ID10835 detected in Paraná State in 2021). For H1 1B

clade, substantial genetic diversity was documented. In addition to the previously characterized genetic clades 1B2.3, 1B2.4, and 1B2.6, a newly identified clade emerged and was designated 1B2.8. Three H3 clades were detected in swine, representing distinct human-to-swine transmission events: the previously characterized 1990.5 clade and two novel clades, Other-Human-2020 and 2010.4. Most of the analyzed sequences clustered within the 1990.5 clade. The Other-Human-2020 clade contains sequences from viruses isolated in 2023 in southeastern Brazil and resulted from a human-to-swine transmission event estimated to have occurred between February and October 2022. The 2010.4 clade contains sequences from viruses isolated in 2023 and 2024 in southern Brazil, with the human-to-swine transmission estimated to have occurred between December 2011 and November 2013. The human variant virus (H3N2v) detected in a child from a rural school in Campo Grande, Mato Grosso do Sul State, in September 2025 clustered within the 2010.4 lineage. Together, these findings emphasize the dynamic evolution of IAV-S in Brazil and highlight the importance of sustained genomic surveillance at the swine–human interface for pandemic preparedness.

Canada

Genomic surveillance of swine influenza viruses (SIV) in Canada for the current reporting period reveals circulation both H1 and H3 virus subtypes. H1 viruses remain genetically diverse but are overwhelmingly dominated by the 1A.1.1.3 (alpha-del) lineage, which persists as the primary circulating genotype across provinces and throughout the surveillance period. While pdm lineage viruses continue to circulate at lower but stable levels, beta appear only sporadically, indicating limited but ongoing diversity within the H1 viral population. Instances of spill over infections of pdm and alpha-del to domestic poultry were also reported. In contrast, H3 SIV circulation is characterized by strong dominance of the 2010.1 human-like lineage, which accounts for more than 80% of sequenced genomes and has expanded geographically since its first detection in Ontario in April 2023 and subsequent emergence in Québec in November 2024. Minority H3 lineages (C IV, C IVA, C IVB2, C IVI) persist at low frequencies and vary by region, reflecting localized diversity. There was a spill over infection in domestic poultry associated with C IV.

Studies, on the analysis of sialic acid (SA) receptor distribution across porcine mammary gland and respiratory tissues were conducted at Vaccine and Infection Disease Organisation (VIDO) and NCFAD. Porcine mammary gland and respiratory tissues display both avian-type (SA α 2,3) and mammalian-type (SA α 2,6) sialic acid receptors, with tissue-specific expression patterns that influence influenza A virus (IAV) attachment and replication. Mammary gland tissue shows strong SA α 2,6 expression, while nasal turbinate, bronchioles, and alveoli exhibit balanced or elevated levels of both receptor types. Correspondingly, bovine and avian H5N1 viruses bind robustly to mammary and lower-airway tissues, whereas swine H1N2 shows stronger binding in bronchioles and alveoli. Primary epithelial cell cultures from these tissues support replication of diverse IAV strains, with bovine H5N1 replicating rapidly across all cell types, avian H5N1 showing slower but steady replication, and swine H1N2 and human H1N1 demonstrating tissue-specific replication

advantages. Collectively, these findings indicate that porcine mammary and respiratory tissues provide a permissive receptor and cellular environment for multiple IAV lineages, underscoring their potential role in cross-species transmission and viral adaptation.

USA

USDA Animal and Plant Health Inspection Service (APHIS), in cooperation with federal, state and industry stakeholders, continue the [National Surveillance Plan for Influenza A Virus in Swine](#) to monitor circulating viruses, identify interspecies transmission events in swine populations, and better understand endemic and emerging influenza A virus ecology. USDA APHIS recently updated the IAV in swine surveillance plan algorithm to expand eligible sample types and remove the requirement for clinical signs, while increasing the PCR cycle cut off and adding reimbursement option for whole genome sequencing. The changes increase inclusion of diagnostic samples and the focus on whole genome sequencing. In partnership with the Agricultural Research Service National Animal Disease Center, sequence data from surveillance are summarized in an online resource called octoFLUshow (<https://www.flu-crew.org>), and APHIS publishes [quarterly reports on this program](#) on the IAV in swine website. Endemic swine H1 from 10 clades of 1A and 1B lineages, along with H3 from 7 clades of 1990.4, 2010.1, 2010.2, and 2020.2 lineages continue to be detected in the US. The 2020.2 clade emerged from recent human seasonal H3N2 incursion from 2023-24, followed by reassortment and sustained transmission in swine. Research highlights from published papers include patterns of genomic diversity and movement of viruses in pigs in the US; development and deployment of new sequence analysis tools; impact of weaning and maternal antibodies on human seasonal H3 infection in pigs; continued impact of H1N1 human seasonal spillover into swine; and detection of endemic H1 and H3 in feral swine indicated interface with commercial swine in Texas.

University of Minnesota

Pigs are key amplifying hosts for reassortant influenza A virus (IAV). Understanding reassortment at the individual pig level and its impact on viral diversity and fitness is critical to mitigating risks to animal and human health. We characterized the genetic diversity and replicative fitness of reassortant IAV recovered from individual pigs under field conditions, demonstrating high genotypic diversity, frequent multi-genotype infections within single animals, and rapid viral turnover. All identified genotypes were capable of replicating in both swine and human respiratory epithelial cells, although with varying fitness. These findings provide insight into the extent of reassortment in naturally infected pigs and highlight the potential for under-detection of circulating variants, with implications for surveillance and vaccine strain selection.

In the U.S., research on swine influenza has largely focused on breeding herds and early production stages of the growing phase, leaving a critical gap in our understanding of growing pigs, which represent ~90% of the national herd. We conducted a longitudinal study of 63 wean-to-finish herds in the U.S. Midwest, showing that IAV is nearly ubiquitous at the herd level, with early infection after placement and prolonged, heterogeneous detection throughout the production cycle. Multiple lineages (H1N1, H3N2, and H1N2) co-circulate within and across sites, with evidence of mixed

infections, lineage turnover, and re-emergence of closely related strains. Phylogenetic analyses also identified occasional human-to-swine spillover events, underscoring the importance of the human–swine interface. Overall, these findings highlight the highly dynamic nature of IAV in growing pigs and the need for improved surveillance strategies to inform control and vaccine design.

Africa:

Nigeria, Malawi, Angola, Uganda, Mozambique, Cameroon, Burkina Faso, Madagascar, South Africa, and Zambia rank among the top 10 African countries by pig population, with populations ranging from approximately 12 million in Nigeria to 1 million in Zambia. Pig production systems across these countries are diverse and include large-scale industrial operations, commercial pig estates, backyard farming, and rural free-range husbandry systems.

Despite the substantial pig population across the continent, only a limited number of countries have reported swine influenza virus (SIV) infections, with occasional detections documented in Cameroon, Nigeria, Ghana, Togo, Benin, Uganda, and Kenya. The predominant strain reported has been Influenza A(H1N1)pdm09. Most surveillance data are based on serological evidence (antibody detection), while direct virus detection remains limited, with relatively few genomic sequences from the region available in international databases.

Swine influenza is likely underreported in Africa due to weak and poorly structured surveillance systems, greater prioritization of other swine diseases such as African Swine Fever (ASF), and limited laboratory diagnostic capacity for SIV, especially when compared to avian influenza virus (AIV) surveillance. Consequently, swine influenza is often identified through sporadic research activities rather than routine outbreak investigations. It is likely that SIV circulates in more African countries than currently documented, but remains undetected or unpublished.

Africa has also contributed evidence of avian influenza virus infections in pigs, including the detection of avian-origin H5N1, H5N8, and H9N2 viruses, highlighting the importance of avian–swine interactions and interspecies transmission. Poultry-to-swine transmission of AIV has been reported in Nigeria (H5 subtype) and Egypt (H5 and H9 subtypes), while evidence from Ghana remains under investigation.

In a recent study conducted between November and December 2025 within a pig farm complex in Lagos, Nigeria, 125 pooled swine nasal swab samples were screened for the Influenza A matrix gene using RT-PCR. Of these, 19 samples (15%) tested positive, with cycle threshold (Ct) values ranging from 26 to 33. Further analysis is ongoing to determine whether these detections are associated with avian-origin influenza viruses in swine.

In conclusion, data on swine influenza in Africa remain limited, fragmented, and inconsistent compared to regions such as Asia, Europe, and the Americas. However, the potential for influenza transmission in African pig populations is considerable. The risk of interspecies transmission is likely

among the highest globally, creating opportunities for viral reassortment and recombination among circulating influenza A viruses. This underscores the need for strengthened surveillance, improved diagnostic capacity, and enhanced genomic monitoring across the continent.

DAY 2

Election of new chair

Dr Tommy Lam (Associate Professor, School of Public Health, The University of Hong Kong) was elected as the new co-Chair of the swine influenza technical expert group. Dr Chiara Chiapponi (IZSLER, Italy) will continue to be the Chair of the group.

Review of current and future group representatives needed to fully capture global swine influenza surveillance data and research activities

The meeting focused on discussing the future of the swine influenza surveillance network and funding opportunities. Participants discussed expanding global representation in the group, with particular emphasis on including more experts from South Asia, Central and South America, and other underrepresented regions. The group explored options for securing funding to continue surveillance activities, including approaching public health organizations for pre-pandemic preparedness initiatives and potentially collaborating with vaccine producers for sample access. They also discussed the need for enhanced virus characterization, including antigenic cartography and ferret antiserum production, as well as the development of MTAs for sharing samples between laboratories. The conversation ended with agreement to draft a context letter proposal for funding and to identify key contacts for submission to various funding bodies.

Brainstorming on OFFLU swine influenza work plan 2026 and beyond

Strengthen global swine influenza virus surveillance and genetic characterisation by addressing gaps in standardisation of methods and data interpretation, enhancing the role of WOA Reference Laboratories in supporting virus characterisation across regions, and defining strategic approaches for sample selection and processing; this includes updating legal frameworks ([MTAs](#)) for sample sharing, developing guidance (should be guidelines about period, areas, samples, to increase the diversity of the samples and enrich the viral database instead) to optimise sample diversity and avoid duplication, securing funding for sample shipment, and fostering trust and collaboration across animal and public health sectors, with regional engagement and upcoming opportunities such as the Barcelona meeting to further advance partnerships, including with the pharmaceutical sector.

Explore the feasibility of establishing a **twining project** on swine influenza, including the identification of potential candidate laboratories. Clement will share a preliminary list of laboratories, and the Secretariat will coordinate with Regional Offices to assess suitability and

interest. In parallel, opportunities to adopt a One Health approach will be considered, including the potential involvement of the Crick Institute and the exploration of a tripartite twinning programme.

Under the OFFLU umbrella, maintain and strengthen collaboration through the genomic working group following the conclusion of the ESFLU programme/network, and develop a concept note/letter to support funding requests for its continuation; Dr Helen Everett will prepare a draft for circulation within the group, after which potential stakeholders and funding opportunities will be explored including the budget required.

Explore funding opportunities to support the **generation of ferret antisera** (Todd Davis – CDC + Crick Institute, maybe Richard Paley)

High Pathogenicity Avian Influenza (HPAI) surveillance in pigs Discussion

The group discussed HPAI surveillance and research in pigs. Amy shared that while there is no targeted surveillance for HPAI H5 in commercial swine, diagnostic samples from commercial farms would be tested, and research with feral pigs showed some H5 serologic positives but high rates of endemic H1 and H3 seropositivity. The discussion covered response plans, with Mia Torchetti noting that USDA Veterinary Services is developing plans with options including depopulation, though industry prefers to limit movement restrictions. The group also discussed experimental infection studies, with Amy reporting variable results across different H5 strains in pigs, including neurologic disease in some cases and limited transmission between pigs.

Phylogenetic Classification Tools for Influenza

The meeting focused on discussions about phylogenetic classification tools and methods for influenza virus analysis. Gautier presented a new tool based on phylogenetic classification that will be published as a paper and made available online for public use. Tavis demonstrated several algorithms his team has developed, including one for phylogenetic scaffold construction, a maximum likelihood placement tool, and a reassortment inference method. The group discussed the challenges of balancing detailed classification with practical utility, particularly in regions with sparse surveillance data. They also explored the potential for harmonizing classification approaches across different influenza virus types while acknowledging the need for different levels of granularity depending on the context, whether studying swine, avian, or human influenza.

Influenza Surveillance data sharing tools

The group discussed data sharing and genotyping tools for influenza surveillance. Tavis demonstrated a new USDA web server that visualizes wildlife and agricultural animal surveillance data for avian influenza, showing how it can display genotypes by location and time. The team discussed challenges with private sequence data and potential solutions, including using reference data sets hosted by GISAID. They also addressed the need for better regional representation in surveillance and discussed the importance of human seasonal vaccine strain inclusion in antigenic

characterization. The group reviewed upcoming deadlines for sequence data submission and VCM-related meetings scheduled for September.

Swine Influenza surveillance collaboration

The meeting focused on swine influenza surveillance and research collaboration. Todd Davis explained the requirements for TIPRA and IRAT assessments, highlighting the need for genetic data, geographic distribution information, and phenotypic characterization of viruses. The group discussed challenges in obtaining swine influenza data due to it not being a notifiable disease and the importance of sharing specimens through networks. They addressed the process for designating viruses as PIP biological material and the role of collaborating centers in vaccine development. The meeting also covered logistics for importing viruses into the US and UK, with discussions about material transfer agreements and permits. Participants explored opportunities for continued funding of swine influenza surveillance activities, particularly expanding beyond Europe to other regions. The group considered creating a bioinformatics subgroup and organizing webinars to disseminate information and attract new members to the network.

Summary of new tasks set and action points for the group to work on:

1. Explore establishing a sub-group or a specific technical activity to discuss bioinformatics coordination among various OFFLU technical activities
2. Promote flexible data-sharing agreements allowing different levels of access and reinforce the message that partial sequencing data is preferable to no submission
3. Develop guidance on minimum characterization requirements (genetic and antigenic)
4. Use WOAHA reference laboratories to support and strengthen national laboratory capacity through laboratory twinning projects; utilize FAO support to connect laboratories for technical collaboration
5. Explore sustainable funding options for ferret antisera production
6. Coordinate with CDC and reference centers to optimize existing antisera capacity. Follow up with national laboratories on serum production capabilities
7. Communicate clearly with stakeholders about the relevance of vaccine strains and updates
8. Maintain links with relevant regional scientific platforms (e.g. ESPHM, IPVS) to support global objectives
9. Draft and circulate a proposal letter outlining priorities, timelines, and funding needs.
10. Organize an OFFLU swine influenza webinar to inform on its activities and deliverables.

Annex 1: Agenda

OFFLU Swine Influenza Experts Technical Meeting
28 - 29 April 2026
WOAH Headquarters, Paris, France

DAY 1 - Tuesday 28 April 2026	
Chair: Amy Baker and Chiara Chiapponi	
9.30 – 9.45h	Welcome – Baba Soumare (WOAH DDG) Introductions and objectives for the meeting – Amy/Chiara
Updated surveillance data and research activities since April 2024 meeting	
9.45 – 11.05h (20 min each)	Asia • Australia – Frank Wong (virtual) • China – Professor Yang Huanliang (virtual) • Hong Kong – Tommy Lam • Japan – Junki Mine
11.05 – 11.30h Group photo and coffee break	
11.30 – 13.00h (20 min each)	Europe • Ghent University, Belgium– Maha Masoudi • SwIAV diversity in Europe: outcomes from the ESFLU Network - Gautier Richard • Italy – Chiara Chiapponi • UK – Helen Everett
Lunch break 13.00 – 14.00 h	
14.00 – 15.40h (20 min each)	America • USDA surveillance – Amy Baker (virtual) • NVSL, USA update – Mia Torchetti (virtual) • University of Minnesota - Juan Mena Vasquez • Canada – Yohannes Berhane • Brazil – Rejane Schaefer
Coffee break 15.40 – 16.10 h	
16.10 – 16.30h (20 min)	Africa • Nigeria – Clement Meseko
16.30 – 17.30	Public health update • CDC update – Todd Davis (virtual) • Crick Institute update – Nicola Lewis

DAY 2 - Wednesday 29 April 2026	
Chair: Amy Baker and Chiara Chiapponi	
9.30 – 10.00h	Election of new co-chair
10.00 – 10.30h	Review of current and future group representatives needed to fully capture global swine influenza surveillance data and research activities (All)
10.30 – 11.00h Coffee Break	
11.00 – 12.30h	Brain storming on OFFLU swine influenza work plan 2026 and beyond - Action items stemming from research and surveillance updates from first day - Setting new tasks and action points for the group to work on
12.30 – 13.30h Lunch break	
13.30 – 14.30h	- HPAI infections in swine (Round table discussion)
14.30 – 15.30h	- New upcoming international swIAV segments classification tool based on Nextclade (Gautier Richard) - Questions and discussion on OFFLU contribution to this tool
15.30 – 16.30h	Coordination and improvement of IAV-S data for biannual WHO VCM - VCM Lead, participation in VCM - Data collation and analysis discussion
16.30 – 16.40h	Closing remarks (Gregorio Torres, WOA)

Annex 2: List of Participants

OFFLU Swine Influenza Members

Chiara Chiapponi
IZSLER,
Italy

Amy Baker
USDA
United States of America
Virtual attendance

Frank Wong
ACDC
Australia
Virtual attendance

Rejane Schaefer
EMBRAPA,
Brazil

Maha Masoudi
Ghent University
Belgium

Yohannes Berhane
CFIA
Canada

Yang Huanliang
HVRI
China (People Rep. of)
Virtual attendance

Gaelle SIMON
Anses
France

Gautier Richard
Anses
France

Tommy Lam
HKU
Hong Kong

Junki Mine
NIAH
Japan

Clement Meseko
NVRI
Nigeria
Virtual attendance

Helen Everett
APHA,
United Kingdom

Nicola Lewis
Crick institute
United Kingdom

Juan Mena Vasquez
University of Minnesota,
United States of America

Mia Kim Torchetti
USDA
United States of America
Virtual attendance

Todd Davis
CDC/Influenza Division
United States of America
Virtual attendance

FAO

Lidewij Wiersma
Virtual attendance

Lorcan Carnegie

Madhur Dhingra
Virtual attendance

WOAH Headquarters

Gregorio Torres

Gounalan Pavade

Mariana Delgado

Annex 3: Group picture

