Summary of the OFFLU Swine Influenza Virus (SIV) Technical Meeting
WOAH Headquarters, Paris, 3 - 4 April 2024

Participants: Amy Baker (USDA, USA), Chiara Chiapponi (IZSLER, Italy), Clement Meseko (NVRI, Nigeria), Gaëlle Simon (ANSES, France), Helen Everett (APHA, UK), Huanliang Yang (CAAS, China), Junki Mine (NIAH, Japan), Kristen Van Reeth (Ghent U, Belgium), Marie Culhane (Minnesota U, USA), Nicola Lewis (Crick Institute, UK), Tommy Lam (Hong Kong U, Hong Kong), Yohannes Berhane (NCFAD, Canada), Amelia Coggon (FAO), Lidewij Wiersma (FAO), Gounalan Pavade (WOAH), Mariana Delgado (WOAH), Yuka Moribe (WOAH)

Through Zoom – Janice Ciacci Zanella (EMBRAPA, Brazil), Mia Torchetti (NVSL, USA), Rejane Schaefer (EMBRAPA, Brazil), Todd Davis (CDC, USA).

Dr Montserrat Arroyo, WOAH's Deputy Director General for International Standards and Science, extended a cordial welcome to the OFFLU swine influenza experts, appreciating their continuing efforts in sharing global swine influenza surveillance data and understanding its epidemiological situation. Dr Arroyo, acknowledged the contribution of this expert group since 2011, underscoring its important role in assessing the impact of influenza viruses on both animal and human health, and recognised the diverse expertise encompassing animal and public health sectors, including the involvement of the 4 WOAH Reference Laboratories for swine influenza as well as the active involvement of the Tripartite (FAO, WHO and WOAH).

Dr Arroyo also thanked the group's contributions to updating the WOAH Manual's Chapter 3.9.7. Influenza A virus in swine, adopted in 2023. Dr. Arroyo recognized the valuable input of the group's SIV data to the WHO Vaccine Composition Meetings (VCM - February 2024 report), which serves as a key information for pre-pandemic candidate vaccine viruses for update of human vaccines against zoonotic viruses of concern.

To conclude, Dr. Arroyo thanked the experts for their robust support of OFFLU's initiatives and also acknowledged the CDC's financial support for this meeting.

Updated surveillance data and research activities - 2023

The OFFLU Swine Influenza technical activity experts presented the status of Swine influenza virus (SIV) by region and recent updates on the research activities (See **Annex 1** for agenda of meeting).

- **Surveillance and characterization of Eurasian Avian-like H1N1 swine influenza viruses in China (Dr Huanliang Yang)**

  The Eurasian avian-like H1N1 (EA H1N1) viruses were predominant in pigs in China between October 2013 and December 2019 and genomic analysis of 319 representative viruses revealed that these EA H1N1 viruses formed eight different genotypes through reassortment with viruses of other lineages circulating in humans and pigs, and two of these genotypes (G4 and G5) were widely distributed in pigs. Animal studies indicated that some strains have become highly pathogenic in mice and highly transmissible in ferrets via respiratory droplets. Moreover, two-thirds of the EA H1N1 viruses reacted poorly with ferret serum antibodies induced by the currently used H1N1 human influenza vaccine, suggesting that existing immunity may not prevent the transmission of the EA H1N1 viruses in humans. Further studies indicated that EA H1N1 virus could become more lethal in mice and more efficient in transmission in ferrets via respiratory droplets by accumulating mutations in its acidic polymerase (PA) gene and that the PA gene bearing these mutations was predominant in the 2009/H1N1 viruses in humans and progressively increased in the 2009/H1N1 viruses in swine.

- **Swine influenza viruses from Hong Kong and Vietnam (Dr Tommy Lam)**

Genomic sequencing and phylogenetic analysis of swine samples from Hong Kong of China between 2021 and 2023 shows that the majority of the swine influenza A viruses belong to 1.C.2.3 (H1) and 3.2000.4 (H3). The swine samples from Vietnam between 2020 and 2023 are also classified similarly by their HA genes, whereas some older Vietnam samples during 2016-2019 have found to form a new clade, 1.C.2.7 (tentative name). These emerged viruses of Eurasian and North American origins have occasionally exchanged gene segments between themselves, resulting in the reassortant genotypes. H1 swine influenza viruses appear to reassort their gene segments between geographic continents more frequently than H3 swine influenza viruses do. It is important to monitor the circulation and evolution of the Asian swine influenza viruses for better pandemic preparedness.

- **Genetic diversity in Influenza A virus of swine in Japan (Dr Junki Mine)**

From 2018 to 2023, surveillance efforts in Japan yielded the isolation of 619 influenza A viruses of swine (IAVs-S) from 7972 nasal swabs collected from 43 farms. More recently, in the 2023-2024 period, 97 IAVs-S were isolated from 965 nasal swabs across 21 farms.

Continued surveillance activities proved that there are three genotypes based on HA genes (H1 1A.5.1; H1 1A.3.3.2; H3) circulating in Japan. Out of these three genotypes, H1 1A.5.1 IAVs-S, are uniquely evolved in Japan and are most isolated in recent years. H1 1A.5.1 and H3 IAVs-S are localized, while H1 1A.3.3.2 IAVs-S are isolated throughout Japan. Additionally, the HA genes of H1 1A.5.1 and H3 IAVs-S formed one cluster respectively, while HA genes of H1 1A.3.3.2 IAVs-S in Japan derived from different origins. These results suggest that H1 1A.5.1 and H3 IAVs-S might have adapted to swine, while H1 1A.3.3.2 IAVs-S might not be enough.

- **Recent swine flu research at Ghent University, Belgium (Kristien Van Reeth)**

Dr Van Reeth presented a brief overview of recent swine influenza research at Ghent University, Belgium. She started with a summary of a paper entitled “Sequential vaccinations with divergent H1N1 influenza virus strains induce multi-H1 clade neutralizing antibodies in swine”. This was published in Nature Communications in 2023 (14(1):7745. doi: 10.1038/s41467-023-43339-3). This was followed by an introduction of two ongoing research projects. The FLUZOVA project is funded by the Belgian federal public service. It is about swine influenza surveillance with emphasis on vaccine strain selection and zoonotic risk. The EPICVIR project is funded by ICRAD (International coordination of research on infectious animal diseases). It aims to compare the transmission dynamics, pathogenesis and immune response of emerging porcine influenza and coronaviruses. It includes partners from six European research institutions or universities.

- **ESFLU (European Swine Influenza Network) COST Action (Dr Gaëlle Simon)**

In 2022, European Swine Influenza Network (ESFLU) was established to forge a multidisciplinary network across Europe focused on swine influenza A virus. This network aims to facilitate the exchange of information, increase awareness, and enhance pandemic preparedness. ESFLU gathers 159 members in an interdisciplinary One Health approach, from 30 participating countries 25 of them participating in the management committee.

The first year's activities (November 2022 – October 2023) and achievements of the ESFLU Working Groups (WGs) were introduced:

- WG1: Strengthen the capacity in Europe for the identification and characterisation of swine influenza virus.
    - Produce standardize diagnostic protocols,
    - Training school on swine IAV diagnostics,
    - Short term scientific mission on diagnostic and sequencing.
- WG2: Increase sharing and analyses of surveillance and virology data.
    - Collection of data: Sequences from 250 swine IAV strains detected in 16 countries have been collected and analysed, leading to a first common report on swIAV genetic diversity in Europe – European swine influenza network report on swine influenza A viruses evolution and diversity in Europe from October 2022 to September 2023 (zenodo.org) https://doi.org/10.5281/zenodo.10598312
    - NGS Pipelines ring trial\Phylodynamic STSM
- WG3: Foster knowledge exchange on surveillance and management measures to improve control of swine IAV in pig herds.
    - Review on current surveillance schemes and swine IAV vaccines, guidelines for control.
- WG4: Dissemination, communication, and awareness.
    - Linkages with OFFLU: Collected swIAV sequences have been shared with OFFLU after diversity reduction: first sequences sent in December 2023 for VCM February 2024 (WG2)

- **Diagnostic activity in Italy, present and future perspectives (Dr Chiara Chiapponi)**

In the absence of a current centralized national surveillance program for IAV-S in Italy, IZSLER laboratories have undertaken virological surveillance initiatives funded by National and European research program. These are executed in partnership with field veterinarians and the private sector, involving the analysis of diverse sample types such as blood, carcasses, and nasal swabs. The year 2023 witnessed a significant detection rate of IAV-S: 10% in lung samples and 30% in nasal swabs. Annually, an estimated 100 IAV-S positive samples undergo sequencing, revealing notable genetic variability, particularly from imported swine populations. This underscores the necessity for the development and deployment of refined diagnostic methods, specifically enhanced molecular and serological genotyping techniques, to effectively monitor and manage the evolving landscape of IAV-S in Italy. Sequences data are regularly shared with the OFFLU-VCM group and recently IAV-S has been included in the Italian Pandemic Plan laboratory network due to its importance at the human-animal interface. The future research development will try to follow the increasing genetic variability of IAV-S, considering new molecular techniques for rapid and full informative genotyping as well as development of recombinant antigens able to detect serological positivity against multiple genetic HA lineages.

- **A decade of swine influenza A virus surveillance and the first report of an H1N2v case in Great Britain (Dr Helen Everett)**

In the UK, where reporting swine influenza is not mandatory, the submission of samples for analysis is optional and typically guided by clinical signs. The most detected strains are from clades 1B.1.1 (H1hu) and 1A.3.3.2 (H1pdm09), while detections of clade 1C.2.2 occur infrequently. It's notable that there have been no findings of swine adapted H3N2 viruses since 1997. Recently, a human case of H1N2v with the 1B.1.1 HA segment was identified. Continuous surveillance in the UK underscores the ever-evolving nature of Swine Influenza Virus, mirroring the global imperative for vigilant monitoring to evaluate pandemic risks. Embracing a One Health approach is crucial in managing the interface between human and animal health, particularly for addressing spillover events.

- **USDA perspective on current endemic swine strains (Dr Amy Baker)**

In the USA, surveillance efforts for swine influenza have evolved to prioritize genomic sequencing, enabling the monitoring of various clades and genotype proportions. Recent data from the first quarter of 2024 revealed that clades 1A.1.1.3, 1A.3.3.3, and 1B.2.1 constituted 60.9% of all H1 detections, while clades 2010.1 and 1990.4.a accounted for 28.4% of all H3 detections. Notably, equal proportions of the N1 and N2 subtypes were observed, with the triple reassortants gene pattern being the most commonly detected. Regular reports are issued quarterly, providing insights into the prevalence of different strains, with representative HA and NA genes for each clade identified. This surveillance program has also identified multiple novel spillover events from humans to pigs, detecting viruses with completely human genome constellations. This underscores the importance of ongoing monitoring efforts to assess pandemic risks and ensure a comprehensive One Health approach to managing the interface between human and animal health and this surveillance contributes and underpins the OFFLU contribution to the WHO’s vaccine composition meeting.

- **USA surveillance update on HPAI in Dairy Cattle (Dr Mia Torchetti)**

An update was provided from the National Veterinary Services Laboratories Services on the detections of H5N1 clade 2.3.4.4b high pathogenicity avian influenza in dairy cattle. Various different testing methods are being carried out on milk, nasal swab samples and other samples and tissues. Whole genome sequencing carried out on PCR positive samples identified a previously reported minor genotype – B3.13, and representative sequences and virus have been made available to researchers. Measures have been put in place to limit spread and the USDA are working with producers and the bovine industry.

- **Experimental infection of pigs with HPAI 2.3.4.4b H5N1 from US isolates (Dr Amy Baker)**

The recent detection of Highly Pathogenic Avian Influenza (HPAI) in mammals raises concerns about the potential risk to humans, particularly if the virus adapts to mammalian hosts. Pigs are also susceptible to HPAI. Historically, Low Pathogenic Avian Influenza (LPAI) has been periodically detected in commercial swine herds in the USA. Additionally, serological evidence of swine exposure to the 2.3.4.4b clade virus has been observed on multi-species farms in Italy. While direct transmission of mammalian isolates among pigs appears limited, the potential for reassortment with endemic swine influenza strains presents a significant concern. In the United States, the likelihood of HPAI entering conventional confinement swine operations is considered low, yet maintaining heightened awareness and precautionary measures is vital. Ongoing follow-up studies are further examining various genotypes to assess this risk comprehensively.

- **Swine-to-Turkey IAV 1A, 1B & 3.1990.4.1 IAV in US Turkey Breeders Hens (Dr Marie Culhane)**

Turkey breeder hens consistently experience a reduction in egg production, known as egg drop, following each introduction of Influenza A Virus (IAV). Surveillance data from the USA indicates a regular exchange of IAV between swine and turkey populations. These four case studies provided evidence of swine-to-turkey IAV transmission.

  - In November 2015, an IAV H3 of clade 3.1990.4.a
  - In May 2016, an H1 virus from clade 1A.3.3.2.
  - In December 2020, an H1N2 virus from clade 1B.2.1
  - In December 2023, an H1N2 virus from clade 1A.1.1.3

To combat the impact of IAV on turkeys, particularly the egg drops in breeder hens, vaccination has been a key strategy. These vaccines are periodically updated to reflect the latest research and analysis of turkey IAV sequences. The application of these vaccines has been helpful in controlling IAV infections in turkey populations. Alongside vaccination, preventive measures include testing for IAV using methods like NP ELISA serology and antigen detection by PCR prior to flock movements. This helps in ensuring that infected flocks do not spread the virus, particularly as the virus can transmit within different houses of the same flock, although not typically between separate flocks. This approach underlines the importance of surveillance and proactive measures in maintaining the health and productivity of turkey populations.

- **Swine influenza virus surveillance in Canada (Dr Yohannes Berhane)**

The National Centre for Foreign Animal Disease (NCFAD) in Canada collaborates with multiple provincial and private veterinary laboratories on passive surveillance of influenza A swine (IAV-S) in Canada. The project is funded annually by the Public Health Agency of Canada (PHAC) and Canadian Food Inspection Agency (CFIA). In 2023, there was an incursion of H3 2010.1 into the province of Ontario. At the moment H3 2010.1 is the most predominantly (60 to 70% cases) circulating H3N2 virus in Ontario. The other most predominantly circulating strains of IAV-S in Canada in 2023/24 are H1.A.1.1 (alpha), H1 1A.3.3.2 and H3 – cluster IVB. Although there were no human cases, H3N2 cluster IV infections were confirmed in turkeys and farmed mink. Notably, high pathogenicity avian influenza virus (HPAIv) H5N1 infection trials in pigs showed that domestic pigs are less susceptible to direct infection or mortality, suggesting a lower risk of HPAIv H5Nx in pigs, though contact transmission is possible.

Serum samples that were collected from wild boars in Alberta in 2022 tested positive for HPAIv H5N1 antibodies, likely from eating infected birds. Moving forward, NCFAD plans to focus on HPAIv H5Nx surveillance in pig farms near affected poultry farms, continue monitoring IAV in swine and H5Nx in wild boars, conduct risk assessments with new H5Nx genotypes in pigs, and study H5N1/5 co-infections in pigs. These efforts aim to better understand and mitigate the risks of SIV and HPAI in both domestic and wild animals.

- **CDC update on zoonotic influenza infections in humans (Dr Todd Davis)**

Swine influenza viruses have been detected in humans between September 2023 and February 2024 and a dairy farm worker, exposed to presumably infected cattle tested positive for A(H5N1) of the clade 2.3.4.4b virus. H1N1v subtype of the clade 1A.3.3.2 was detected in Brazil and Spain with no reported exposure and exposure to swine, respectively. Additionally, the H1N2v subtype of the clade 1B.1.1.1, was detected in a human in the UK with no reported exposure to swine and an H1N1v of the clade 1C.2.2 was detected in a human in Switzerland with exposure to swine. This situation highlights the complex dynamics of interspecies influenza transmission. The genetic and antigenic properties of these viruses are diverse, however the WHO prepares candidate vaccine viruses for pre pandemic preparedness.

- **Influenza A virus in swine in Brazil (Dr Rejane Schaeter)**

Since 2009, EMBRAPA has implemented a passive surveillance program for IAV-S across nine states in Brazil, encompassing the majority of the country’s pork production. Genetic analysis over this period has confirmed the presence and circulation of IAVs in the Brazilian swine population, with a noted increase in genetic diversity in recent years. The cross-reactivity among circulating swine virus lineages is found to be limited, pointing to a significant antigenic variation between these lineages.

In the human population, particularly in the southern region of Brazil, nine cases of IAV infections have been identified since 2015. Given these findings, EMBRAPA plans to maintain vigilant monitoring of influenza through continued sequencing and antigenic analyses. This ongoing surveillance is crucial for tracking the evolution of the virus and its potential impact on both swine and human health.

- **Swine influenza : Africa surveillance update (Dr Clement Meseko)**

Continental Africa has a smaller number of pigs compared to Asia, Europe and the Americas, nonetheless significant number of pigs are found mostly in Nigeria, Uganda and Cameroon in order of pig population density. Pig husbandry is distributed into intensive commercial farms, backyard farms, feral and free ranging pigs and live animal markets. These diversity of pig holdings also come with diverse ecological conditions that influence transmission of swine influenza and other pathogens in the region.

Swine influenza data in Africa is also limited and there is no sustainable countrywide surveillance. The few available data are efforts of researchers in institutions and universities. A review of influenza A prevalence amongst backyard pigs globally shows that this sector is active in Africa with 6 studies. Other regions are Asia (11), North America (10), South America (6) and Europe (1) (*"A systematic review of influenza A virus prevalence and transmission dynamics in backyard swine populations globally" [Chauhan & Gordon 2022)*). In addition to swine influenza studies in backyard holdings, more recent surveillance data from various countries are described in the table below:

Country	Year	Study	Reference
Nigeria	2024	Influenza A virus antibodies in horses and pigs in Nigeria / H1N1pdm in 90 swine sera in Jan 2024- (unpublished data)	Adamu et al, 2024
Cameroon	2023	A/H1N1/pdm09 detected in Swine by RT-PCR	Tahmo et al, 2023
Zambia	2021	H3N2 and 8 H1N1 IAV strains were isolated from pigs	Harima et al., 2021
Ghana	2020	H3N2 and H1N1pdm09 were found in swine and human samples	Ayim-Akonor et al., 2020
Senegal	2019	Influenza A Virus in Pigs, Senegal…	Jallow et al., 2023
Kenya	2019	230 (11.56%) sera and 1(x%) of 2066 nasal swabs from pigs was positive for AIV	Osoro et. al.,2019
South Africa	2018	51 oral and nasal specimens from pigs, 44 (52.4%) and 6 (11.8%) had molecular evidence of influenza A virus	Zowalaty et al., 2022

Country	Year	Study	Reference
Uganda	2018	IAV specific antibodies in 26 (4.98%) out of 522 clinically healthy swine	Dione et al, 2018

Other recent IAVs event in other species with implication for swine in Africa includes; H5N1 in domestic poultry (2024 and continuing); H5N1 in wild birds (2024); H5N1 in cats by PCR and Serology (2023/2024); H9N2 in poultry — farms/local chickens /LBM (2024; H5N2 reassortant (H5N1 + H9N2) in poultry (2022); H3N8 Fc-1 in donkeys (2023); H9N2 LPAI + IBV/NDV causing high mortality (2023-2024); H9N2 in pigs (Egypt). In summary, swine influenza surveillance data from Africa are few and inconsistent compared to Asia, Europe and America. Genomic data in GenBank and other repositories from Africa is also limited. Therefore, the need for funding attention cannot be overemphasised. Swine influenza virus is circulating in limited biosecurity operations and the potential for re-assortments and recombination with other IAVs is a concern.

- **WHO Collaborating Centre: Francis Crick Institute update (Dr Nicola Lewis)**

Recent variant virus detections in UK:

The UK A(H1N2)v was caused by an influenza A H1 virus from the 1B.1.1.1 lineage. The 1B viruses were first identified in the 1980s, have diversified antigenically and genetically and circulated up to present. The A(H1N2)v internal gene segments are nearly all associated wtih instances of human-to-swine spillover of the H1 human seasonal pmd-09-like viruses, particularly with ancestors that circulated in humans around 2010/2011. The NS gene of this variant shows unclear ancestry and is not directly linked to pdm09-like human seasonal strains. From human serological analyses using the variant virus and human seasonal pre- and post- vaccination panels showed an absence of human population immunity to 1B.1.1.1. strains circulating in pigs.

The challenges at the human-animal interface are significant, especially in diagnostics and assessing fitness for purpose. This was recently highlighted when sequences were deposited onto GISAID derived from human influenza virus specimens in two member states. Further analyses suggested that the HA of these viruses were genetically similar to viruses that last circulated in humans in 2004. Other gene segments were also not closely related to current human seasonal influenza strains. Subsequent collaboration and corroboration with the submitting labs and the WHOCC identified that there remain challenges the need for capacity building, particularly in assembly pipelines and low-depth NGS assembly. Clade classification on GISAID, quality checks, running trees, and visually inspecting alignments were among the lessons learned.

Moreover, the limitations of sequence data derived from oral fluids and the complexities of pooled sampling systems were discussed, highlighting the intricate nature of influenza virus surveillance and the need for ongoing adaptation in methodologies to better understand and manage these viruses.

- **IAV-s data for WHO VCM discussion (Dr Amy Baker)**

There were over 680 swine influenza detections in 24 countries in 11 regions from 39 lineages from Europe, the Americas and Asia between July 2023 and January 2024. For the February 2024 WHO VCM, 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). 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.

- **OFFLU/WOAH update (Gounalan Pavade, Mariana Delgado)**

Participants were updated on the recently adopted version of the Chapter 3.9.7. Influenza A virus in swine in the *Manual of Diagnostic Tests and Vaccines for Terrestrial Animals* . Key updates include changing the acronym for influenza A viruses of swine to IAV-S, enriching the section on the H1 virus with detailed clade classifications, and adding a new segment focused on gene sequencing. Experts were encouraged to actively communicate any potential updates or advancements in the diagnostic techniques to maintain their relevance and accuracy in the chapter.

Participants were further updated on the current organization of OFFLU Steering and Executive Committees and activities of other OFFLU technical activities. The OFFLU Secretariat announced an upcoming update to the OFFLU website, aimed at enhancing its functionalities. The Secretariat will collaborate with all technical activity experts to explore new and useful features for the website, demonstrating a commitment to making the OFFLU website more informative and user-friendly for its global audience.

- **FAO national/regional/global projects update (Lidewij Wiersma)**

FAO is involving PhD students and postdocs in various OFFLU technical activities and for assisting the Chairs in planning and executing activities and FAO considers that setting up communities of practice is important to improve communication among experts. FAO highlighted that it is involved in many other projects involving swine, which could be leveraged on to improve geographical representation of data available, and also noted that it has a sequencing service which can be made available to countries to use for example for swine influenza virus monitoring. In July 2024, OFFLU is planning to convene a global technical meeting at FAO Headquarters, inviting experts from all technical activities.

Election of new co-chair

Dr Chiara Chiapponi (IZSLER, Italy) was elected as the new co-Chair of the Swine influenza group. Dr Amy Baker (USDA, USA) continues to be the Chair of the group.

Discussion points

- The experts discussed and suggested potential new members from different regions to strengthen the global swine influenza surveillance data such as participants from the Americas, Asia and Eastern Europe. Individuals will be approached, and the item will be actioned by the SIV group chair/co-chair and OFFLU secretariat.
- The group discussed the impacts of the Nagoya protocol and permits on viral shipment between laboratories and effects this has on activities such as the vaccine composition meeting preparations and timely reporting. The group also discussed the benefits of sharing unpublished data through the OFFLU network for such activities on improving real-time surveillance.
- Issues surrounding public vs private sequence databases were also discussed, and the effects these have on activities such as using data to update nomenclature, provide reports on genome constellations which are circulating which have implications on the fitness for purpose of detection of swine influenza variant cases in the human population. The group discussed making available one-page regional updates on swine influenza viruses and their genome constellations for public health laboratories and other tripartite colleagues to ensure that seasonal and swine influenza viruses circulating in humans can be discriminated. This item will be actioned by the OFFLU scientist and the swine influenza group leads.
- The need for networks to be mapped was discussed and it was decided that OFFLU will develop a point of contact list with visualization for WHO, FAO and WOAH Reference labs with influenza expertise for the OFFLU website which can serve as a point of reference.
- Discussion about what other information OFFLU could provide on the website, suggestions from experts included surveillance guidelines, surveillance algorithms, what commercial reagents and subtyping assays are available, any recommendations from the OFFLU swine group and webinars from OFFLU website giving information on hot topics, research updates and novel techniques.

Action items and Workplan

- Leverage other swine virus expertise (ASFV, PRRSV….) test samples collected for other disease for FLU if MTA allows; sequencing services through FAO/International Atomic Energy Agency
- Nomenclature for FHA and NA clades (contact Tavis Anderson)
- Develop one-page summaries on regional IAV-S diversity to share with public health.
    - ✓ OFFLU scientist work with quadripartite to create a template.
    - ✓ OFFLU will formalize a plan for distribution.
- Develop a point of contact list for WHO, FAO and WOAH ref labs with influenza expertise for website.
- Increase visibility of OFFLU to increase regional coverage.
    - ✓ Send to OFFLU Secretariat the meeting links and information when giving experts are giving public webinars so information can be updated onto OFFLU website.
    - ✓ Represent OFFLU at professional/society meetings.

- OFFLU experts to send any information on training opportunities to the OFFLU secretariat.

Annex 1. Agenda

OFFLU Swine Influenza Virus (SIV) Technical Meeting
3 - 4 April 2024
WOAH Headquarters, Paris, France

<table>
<tr><th colspan="2">DAY 1 - Wednesday 3 April 2024</th></tr>
<tr><td colspan="2"><u>Chair</u>: Amy Baker and Janice Zanella</td></tr>
<tr><td>9.30 – 10.00h</td><td>Welcome - Montserrat Arroyo (WOAH DDG)
Introductions and objectives for the meeting – WOAH/FAO/Chairs</td></tr>
<tr><td colspan="2">Updated surveillance data and research activities - 2023</td></tr>
<tr><td>10.00 – 10.45h
(15 min. each)</td><td>Asia
• China – <i>Huanliang Yang</i>
• Hong Kong – <i>Tommy Lam</i>
• Genetic diversity in Influenza A virus of swine in Japan – <i>Junki Mine</i></td></tr>
<tr><td colspan="2">10.45 – 11.15h Group photo and coffee break</td></tr>
<tr><td>11.15 – 12.15h
(15 min. each)</td><td>Europe
• Recent swine flu research at Ghent University, Belgium– <i>Kristien Van Reeth</i>
• ESFLU (European swine influenza network) COST Action – <i>Gaelle Simon</i>
• Diagnostic activity in Italy, present and future perspectives – <i>Chiara Chiapponi</i>
• A decade of swine influenza A virus surveillance and the first report of an H1N2v case in Great Britain – <i>Helen Everett</i></td></tr>
<tr><td>12.15 – 13.00h
(15 min. each)</td><td>America
• USDA perspective on current endemic swine strains – <i>Amy Baker</i>
• Experimental infection of pigs with HPAI 2.3.4.4b H5N1 from US isolates – <i>Amy Baker</i>
• NVSL, USA update – <i>Mia Torchetti</i></td></tr>
<tr><td colspan="2">Lunch break 13.00 – 14.00 h</td></tr>
<tr><td>14.00 – 15.00h</td><td>Americas
• St. Jude update – <i>Richard Webby</i> (virtual presentation)</td></tr>
</table>

(15 min. each)	- Update on 1A and 1B H1 flu in turkeys– ***Marie Culhane*** - Canada – ***Yohannes Berhane*** - Brazil – ***Rejane Schaefer*** (Virtual presentation)
15.00 – 15.15h	**Africa** - Nigeria – ***Clement Meseko***
15.15 – 15.45h (15 min. each)	- CDC update – ***Todd Davis*** (Virtual presentation) - Crick Institute update – ***Nicola Lewis***
Coffee Break 15.45 – 16.15h	
16.15 – 17.30h	IAV-S data for WHO VCM discussion – ***Amelia Coggon, Amy Baker***

DAY 2 - Thursday 4 April 2024	
Chair: Amy Baker and Janice Zanella	
9.00 – 9.10h	OFFLU/WOAH update – ***Gounalan Pavade***
9.10 – 9.20h	FAO national/regional/global projects update – ***Lidewij and Amelia***
9.20 – 9.30h	Election of new co-chair
9h30 – 10.00h	Review of current and future group representatives needed to fully capture global swine influenza surveillance data and research activities (**All**)
10.00 – 10.30h Coffee Break	
10.30 – 12.00h	For discussion: - Swine influenza A virus vaccines and barriers to updating vaccine antigen composition. - Surveillance algorithm - Regional Swine Influenza Meetings Workplan - Future workplan and role of the OFFLU swine influenza group and its visibility - What the group needs from OFFLU and if/how we need to improve
12.00h End of the meeting	