Summary of the OFFLU Swine Influenza Virus (SIV) group technical meeting
Zoom videoconference, 9 December 2020 (13h-14.30h Paris time)

Participants: Amy Vincent (USDA, USA), Ariel Pereda (INTA, Argentina), Frank Wong (AAHL, Australia), Gaelle Simon (ANSES, France), Janice Ciacci Zanella (EMPRAPA, Brazil), Kristien Van Reeth (Ghent University, Belgium), Marie Culhane (U Minnesota, USA), Nicola Lewis (APHA/RVC, UK), Todd Charles Davis (CDC, USA), Rachell Tell (NVSL, USA), Yohannes Berhane (NCFAD, Canada), Young Ki Choi (CBNU, Rep. Korea), Huanliang Yang (HVRI, China), Richard Webby (St. Jude, USA), Gounalan Pavade and Patricia Pozzetti (OIE).

Apologies –Taiko Saito (NIAH, Japan) and Clement Meseko (NVRI, Nigeria).

Dr Gounalan Pavade, OFFLU Secretariat welcomed the experts. Due to the Covid-19 pandemic situation, the technical meeting was organised by zoom video conference.

The experts presented the status of Swine influenza virus (SIV) by region and recent updates on the research activities of SIV.

Ongoing SIV surveillance in Europe and creation of a regional sub-group (Gaëlle Simon):

In 2019-2020, SIV passive surveillance conducted in France revealed novel incursions and diffusion of HA-1C viruses belonging to 1C.2 genogroup. This led to a strong modification in the proportions of most frequently detected genotypes as compared to previous years (NB: a detailed description of HA-1C and HA-1B viruses identified in France from 2000 to 2018 has been published recently: https://www.mdpi.com/1999-4915/12/11/1304). Thus, $H1_{av}N2$ viruses belonging to a lineage of Danish origin were responsible of many respiratory outbreaks in the North-Western part of France. Surveillance in 2021 will say if these viruses are evolving toward an enzootic circulation, potentially replacing previous enzootic viruses, i.e. $H1_{av}N1$ with a HA-1C.2.1 and/or $H1_{hu}N2$ with a HA-1B.1.2.3. Several virus strains containing one or more genes from H1N1pdm were also identified sporadically, whereas H3N2 viruses were no more detected since 2016. Altogether, 18 different genotypes were identified in France since 2009.

In Spain, the numbers of HA and NA lineages, and their combinations, are increasing. $H1_{av}N2$ viruses, that were undetected until 2017, now count for the most prevalent lineage. Seven new genotypes, undetected during ESNIP3 (Watson et al., 2015), are now present in Spain. Whereas H1N1pdm virus represents only 6% of the isolates, there were up to 30% of strains with one or more H1N1pdm internal genes. Viruses with H3-Gent/1984 have been replaced by viruses with H3-Malaysia/2004, however in a different combination of internal genes as compared to the H3N2 SIV bearing H3-Malaysia/2004 that was first described in Denmark in 2017.

In Italy, there is also an increasing number of genotypes. The highest diversity is observed among H1N2 subtype. HA genes belong to clades A, B, C, and the highest diversity is reported among HA-1C. Novel reassortants derived from A/sw/Italy/4675/2003-like $H1_{hu}N2$ with a N2 deriving from the human H3N2 strain A/HK/208-/1997. H3N2 viruses, all belonging to H3-Gent/1984 lineage, are circulating but are detected less frequently than H1N1 and H1N2.

In Hungary, among 457 submissions, there were 18.6% positive farms, from 13/19 counties. 58 strains were submitted to HA/NA subtyping. H1 genes belonged to HA-1A, -1B and -1C clades. There were no H3 strains. Four isolates were submitted to WGS, identifying a $rH1_{av}N1$ with pdm09 internal genes, a $rH1_{av}N2$ (with N2 from the Gent84 lineage), a $rH1_{av}N2_{hu}$ (seasonal H3N2 mid 90') and a $H1_{av}N1$.

Ceva Santé Animale also contributes to SIV surveillance in several European countries. From January to September 2020, 579 farms have been detected SIV positive in 12 countries. H3N2 viruses were detected in Germany and Spain only. The panoplies of the different virus subtypes (and H1 clades) identified vary enormously from one country to another.

On the initiative of Ceva, a "SIV European network" is in the process of consolidation, grouping nine public institutes from eight EU countries (to date). The main objectives are to increase sharing of surveillance data, improve diagnostic tools and flows, and built scientific forum for discussions about SIVs and swine influenza (incl. vaccination). Besides its own ambitions, another objective could be to engage with OFFLU for established linkages. Thus, this "SIV European network" could become a regional sub-group of OFFLU SIV group, in order to help participating countries in sharing information at the international level, promote EU contributions to the WHO Vaccine Composition Meetings, and potentially take part to some OFFLU discussions. This proposal has been submitted to the OFFLU SIV Group and was well received by most members. Next reflections should focus on the formalization of the creation of such a regional sub-group, especially since the same issues arise in other parts of the world.

SIV in Belgium and Netherlands (Kristien Van Reeth):

The lab is testing samples from pigs with respiratory disease in Belgium and the Netherlands for influenza A viruses. During 2020, 59 samples were submitted to the lab and 32 of these were influenza positive. Subtyping of the HA by HI showed the following distribution: 16 isolates H1av, 7 H1pdm, 8 H1hu, one H3. Characterization of the NA and internal gene segments is pending. A manuscript describing the results of surveillance from 2014 – 2019 has been submitted for publication. This 5-year surveillance also showed a predominance of H1 influenza A viruses, and of the avian-like H1 subtype in particular. Nineteen of the 2014 – 2019 H1 isolates were characterized by whole genome sequencing: 18 had an M gene segment from the 2009 pandemic H1N1 virus and 3 had a "novel" genetic constellation that had not been described before. In September 2019, a Eurasian avian-like swine influenza A virus was isolated from a farmer and his pigs in the Netherlands. A short communication ("dispatch") about this isolate will soon be published in Emerging Infectious Diseases (A. Parys et al., EID Volume 27, Number 3—March 2021).

Japan (Taki Saito):

Around 1,900 nasal swab specimens were collected from domestic pigs through active surveillance project in 2019 – 2020. Isolated 144 SIV consisting of 118 H1N2 and 12 H1N1 strains (14 strains not characterized yet).

Suspension of active surveillance in Thailand and Vietnam as the project expired in 2019 and there is no more budget for the surveillance abroad.

South Korea (Young Ki Choi):

South Korea still follows the FMD vaccine strategy and recently African swine fever viruses were also reported in wild bores. Therefore, a strict control policy for swine farms is followed. Thus, only the registered persons can access the swine farms under strict control and this caused some limitation to access the large numbers of clinical specimens. With these circumstances, some H1N2 and H3N2 subtypes were isolated from nasal swabs specimens, but none of the swine H1N1 subtype. Genetic characterization revealed that the H1N2 viruses have the HA genes of European avian-like H1 lineage which was reported in China recently. However, the NA gene was originated from 2005 Ontario-like lineage (the same lineage of recent Korean H3N2) while the 2019 isolates clustered with old North American triple assortment lineage suggesting at least two different NA gene lineages. The H3N2 viruses shared all gene segments with recent North American swine viruses. To evaluate their pathogenic potential, animal experiments are ongoing.

China (Huanliang Yang):

Recently in China's pig production, the number of small and medium sized pig farms decreased gradually. Quarantine certificate is required for pigs transported across provinces. Pigs are not routinely vaccinated against swine influenza. Sporadic human infections with SIVs have been occasionally reported. The objectives of the surveillance program are to gain a better understanding of epidemiology, genetic and antigenic diversity of SIV in China, update diagnostic assays and vaccine seed stock products. This is supported by the national surveillance plan for SIV in pigs.

In January 2020, sample collection and testing were carried out in the first stage over 1800 nasal swabs from Guangxi province. In November – December 2020, sample collection and testing were carried out in the second stage over 13,600 nasal and tracheal swabs from 17 provinces. All samples were collected through abattoir-based surveillance. Also 1600 serum samples collected and tested.

282 strains of SIVs were isolated from samples collected in 2019, while 23 strains of SIVs were isolated in 2020 samples so far and work is still in progress. Viruses isolated from 2016 – 2020 include Eurasian avian like H1N1, H1N1/09, H1N2 and H3N2. Based on the lineage classification, three genotypes of H1N1/09 were found in 2019 – 2020 surveillance namely Genotype 1, Genotype 2 which is called 'G5' and Genotype 3 which is called 'G4'. The previous surveillance results from 2011 to 2018, identified a recently emerged genotype 4 (G4) reassortant Eurasian avian-like (EA) H1N1 virus, which bears 2009 pandemic (pdm/09) and triple-reassortant (TR)-derived internal genes and has been predominant in swine populations since 2016. Results of HI test showed that the positive rates of Eurasian avian like H1N1, pH1N1/2009 and H3N2 were 52%, 7.6% and 50% respectively.

To conclude, SIVs are widely found in pig populations. Multiple subtypes and genotypes of influenza viruses co-circulated in pigs in China during 2019 – 2020. Triple reassortant Eurasian avian like H1N1 SIVs containing the four RNP genes (encoding PB1, PB2, PA and NP) from 2009/H1N1 became predominant among pigs in China.

Australia (Frank Wong):

Australia conducts only syndromic surveillance for influenza in domestic swine and the samples go to Australian Centre for Disease Preparedness (ACDP). Novel reassorted H1N2 and H3N2 influenza viruses were detected in Australia swine populations since 2012 to present, containing old human IAV genes. In 2018, a 15-year-old female adolescent in South Australia was infected with swine influenza A(H3N2) variant virus. The virus contained HA and NA genes derived from 1990s-like human seasonal viruses and internal protein genes from influenza A(H1N1)pdm09 virus, highlighting the potential zoonotic risk that swine influenza A virus poses in Australia. [Update since meeting: In January 2021, a second isolated human case with a nearly identical A(H3N2)v was detected in the same state (reported to the WHO in March 2021)].

H1N1pdm like viruses have been detected from samples collected each year and was in continuous circulation in Australian swine populations since 2009, contributing to the apparent SIV reassortment diversity in Australia and also involved in ongoing human-swine interface interactions. Phylogenetic analysis showed independent evolutionary drift of this diversity over the past ten years in humans and pigs. Most of the genetic analysis have been published and ongoing research planned for improving HI assessments of H1 and H3 antigenic relationships and diversity.

USA (USDA-NADC) update (Rachell Tell/Amy Vincent/Tavis Anderson):

The USDA surveillance system for swine influenza continued through fiscal year 2020 (FY20) with similar levels of submission as FY19. There were over 8,000 isolates with HA and NA sequences contributed to the repository at the National Veterinary Services Laboratories (NVSL) since the program inception. Over 1,700 underwent whole genome sequencing (WGS). The number of isolates selected for WGS was recently increased from approximately 20 to 30 per month. Many phylogenetic clades of H1, H3, N1, and N2 co-circulated in US swine populations. H1N1 and H2N2 represented approximately 35% each of overall detections, with 1A.3.3.3 (gamma) paired with classical N1, 1B.2.1 (delta-2) with N2-98, 1A.3.3.2 (H1N1pdm09) paired with pdm-N1 were most frequently detected H1s, although 1A.1.1 (alpha) and 1B.2.2 (delta-1) were consistently detected at lower levels. H3N2 represented approximately 30% of detections, with 1990.4.a (IV-A) paired with N2-02 and 2010.1 paired with N2-02 most frequent of the H3 detections. Reassortment between the North American TRIG lineage (T) and human H1N1pdm09 (P) was apparent in the WGS analyses, with the internal gene constellations of TTTTPT, TTTPPT, and TTPPPT (in the order of PB2, PB1, PA, NP, M, and NS) most frequently detected.

A rigorous phylogenetic system was developed to provide a globally consistent nomenclature of swine H3 virus hemagglutinin (HA) evolution. This system established 13 co-circulating lineages and grouped them based on the decade in which the lineage was first detected following human-to-swine transmission. A web-accessible annotation tool was developed that can assign these biologically informative categories to new sequence data. The annotation tool assigned the combined data set of 4276 H3 sequences to the correct clade more than 99% of the time, and provided generic classifications for avian, equine, canine, and human H3 HA data. A pair of IAV analytical software tools were in development, octoFLUdb and flutile. Both tools were made available on github (flu-crew/octoFLU). octoFLUdb is a general-purpose graph database that links public genetic data to lab data and metadata parsed from public sequence records. The flutile tool manipulates and analyzes IAV data, including the translation of nucleotide to amino acid sequence, the generation of annotated amino acid comparison tables, and the selection of representative sequences from defined genetic clades. Future work includes the development of an interactive graphical summary tool that synthesizes swine influenza strains and displays genetic diversity across time and location, with hosting on a public facing website.

USA research updates:

University of Minnesota College of Veterinary Medicine (Marie Culhane):

A research study was conducted at the University of Minnesota College of Veterinary Medicine (Laboratory of Montserrat Torremorell and Marie Culhane), to understand how population dynamics, immunity and farm managements factors affect influenza transmission in order to develop protocols to control and eliminate the disease.

The summary statements of research findings - Sows are not a significant source of influenza at farrowing. Sows become infected during lactation (i.e., piglets are the source of infection). Influenza infections can start very soon after piglets are born. Limiting pig contact and changing farm protocols (e.g., no cross-fostering after processing, handling of the pigs with new/clean gloves, plastic boot covers if entering crates, no nurse sows) can help decrease transmission but prevalence at weaning was not altered. Fomites and hands of personnel may be a main driver of influenza spread. Interventions should be implemented at the farm level since interventions at the room level are not enough to fully stop transmission between rooms. Vaccination is critical to help decrease infection levels.

What noise does flu make? (Richard Webby):

Two groups of 60 pigs (0-7 days post wean) known to be infected with IAV. Recording devices were used to capture pig cough sound signatures. Twelve samplings, conducted on Monday, Wednesday and Friday each week over 4 weeks were performed. Nasal wipes, nasal swabs, one oral fluid sample per group, air sample collected. Nasal wipes appear to be the preferred sample type (need up to 42 samples to have 95% confidence). Increased cough is associated with a higher likelihood of detecting IAV with nasal swabs. Pen or group-based sampling resulted in poor detection of infection under these conditions.

Brazil update (Janice Zanella):

Respiratory infections caused by influenza A virus (IAV) became frequent in Brazilian swine herds following the introduction of H1N1pdm in 2009. IAV is commonly detected in swine showing mild to severe acute respiratory disease, as the only pathogen, or in association with other viral or bacterial agents. Previous investigation revealed substantial genetic diversity of IAVs detected in pigs. H3N2 and H1N2 swine IAV from Brazil were characterized to be most closely related to human seasonal influenza viruses that circulated during the late 1990s and early 2000s. Viral diversity increased after reassortment with co-circulating H1N1pdm09 virus internal genes. There is no official monitoring of influenza virus in pigs in Brazil. Embrapa Swine and Poultry research team studies and characterize contemporary genetic and antigenic evolution of this important respiratory pathogen since 2010.

Nasal swabs and lung samples were collected from commercial swine in herds located in seven Brazilian states and sent to a veterinary diagnostic laboratory for screening of respiratory agents involved in the porcine respiratory disease complex. IAV positive samples by RT-PCR were submitted for virus isolation in SPF chicken eggs and/or MDCK cells, and genetic sequencing. RNA was extracted from pig samples and RT-PCR using PathAmp FluA reagents amplified the eight gene segments. DNA libraries were prepared and submitted for sequencing using Ion Torrent system. Influenza genomes were assembled using Newbler v.2.9. H1 and H3 hemagglutinin (HA) gene alignments were generated for these sequences alongside a random sample of global human and swine IAVs downloaded from the Influenza Research Database. For each alignment, a maximum likelihood phylogeny was inferred, and statistically supported clades of viruses that demonstrated onward transmission in Brazil are identified. An HA1 amino acid consensus was determined for each clade, and representative strains are identified for antigenic characterization. The representative H1 and H3 IAV were tested by hemagglutination inhibition (HI) using a panel of swine sera against global swine and human seasonal IAV, with newly generated monovalent swine anti-sera against Brazilian swine IAV.

From 2019-20, partial and complete gene sequences were generated for 48 SIVs isolated from 2016 to 2018 in Brazilian swine farms. Sequence of gene segments H1s, H1pdm, H3, N1 and N2 were analyzed. All H1N2 and H3N2 viruses sequenced so far have the internal gene segments derived from H1N1pdm. Results indicated five co-circulating clades of viruses were identified within three subtypes. These particular H3N2 and H1N2 SIV clades appear to be specific to Brazil.

Antigenic maps were generated from the HI data. Antigenic distances (1 AU equals a 2-fold loss in HI titer) demonstrated significant variability among IAV within each clade, and at least 4 AU distance from putative human-seasonal precursor viruses to representative circulating swine strains.

These data demonstrated the role and importance of human-to-swine transmission in the evolution and diversity of swine IAV in Brazil. Five co-circulating clades of viruses were identified within three subtypes. Antigenic characterization of representative isolates suggested that Brazilian swine IAV are regionally unique and swine vaccines may have limited efficacy. The swine IAV also demonstrated antigenic divergence from human seasonal strains and therefore may also pose a zoonotic risk.

Latin America (Ariel Pereda):

In Argentina research in influenza on INTA includes wild birds, equines and pigs. The swine production in Argentina, as in all Latin America differs per region of the country. Argentina has approximately 1.3 million sows, 40% of the farms are commercial and 60% are in Buenos Aires, Cordoba and Santa Fé Provinces. Little research or investigation is done on wild boars.

Swine influenza surveillance is voluntary including 300 samples processed per year and the detection of 40-50 positive cases. INTA has characterized 59 viruses identified, and the pandemic H1N1 influenza virus (H1N1pdm2009) was the first that caused influenza endemic in Argentina. Today, most of the identified influenza viruses in swine have the H1N1pdm2009 internal genes.

In 2020 we received samples from 27 different farms al around Argentina, but mostly form the central region (Córdoba, Buenos Aires, Santa Fe and San Luis) with only 7 being positive to Influenza A. Those positive samples (29) were nasal swabs (6) and lung tissues (23).

The subtypes characterized in Argentina since 2008 from 59 isolates are: 39 H1N1pdm09, 13 H1N2 human like, 5 H3N2 Human like, 2 H1N1 human like. On top of this, 130 RNA´s form these samples were sent to UGA for full length sequencing.

Until now, introductions of human viruses are not related to Brazilians or Chileans, however, Argentina imported 1,500 breeding stock of Brazil (single source). There are 2 commercial vaccines licensed in Argentina, both contain non-circulating antigens in Argentina. No information about the use of these vaccine is available. In the 90's there was the reassortment. Today there are 4 subtypes, mainly after the introduction of the H1N1pdm2009.

In Guatemala, all the results come from the research group at Universidad del Valle de Guatemala – Centro de Estudios en Salud, leaded by Dra. Celia Cordón Rosales. Guatemala started the first study in influenza in wild birds in 2005. In 2010 started to do serology and then virology analysis to detect influenza in pigs. From 2010 – 2011, a total of 3 H1N1pdm2009 and human viruses distinct from the vaccine virus were founded.

A study performed in departments with high prevalence in previous surveys (Chimaltenango, Escuintla, Guatemala, Sacatepéquez and Santa Rosa) was started in 2018. Nasal swabs were taken from animals with clinical like-flu signs (nasal secretion, ocular secretion, cough and / or sneezing). Also, antibodies were tested in samples from Classical Swine Fever survey across the country. The results were: 6.8% (36/524) swabs tested IAV-positive by RRT-PCR; 15.8% (83/523) serums tested Antibodies-positive by ELISA; and 2.7% (16/523) individual positive for AIV in PCR and ELISA .

From the National surveillance of Classical Swine Fever Serum Survey a total of 1,024 sera received, the 10% were positive by ELISA. Swine IAV infection rate in Guatemalan swine populations has ranged from 6-12% during the last 10 years. Guatemalan viruses represent a unique group of sequences, suggesting independent evolution from other A(H1N1)pdm09 viruses circulating in Central America and whose zoonotic risk remains to be determined.

Canada (Yohannes Berhane):

Surveillance of influenza A viruses in Canadian pigs is continuing. Got funding from Public Health Agency of Canada (PHAC) to continue the surveillance work. Due to COVID-19, there is a delay in isolation and sequencing the influenza A swine positive samples on time. A case of variant Influenza A (H1N2)v was detected in central Alberta in October 2020. Received the full genome sequencing information from the Canadian public health agency. The hemagglutinin gene of the H1N2v virus belongs to clade 1A.1 (Alpha) H1 subtype influenza A viruses. In contrast to other 1A.1 clade viruses, this virus does not contain the 2 amino-acid deletion in the HA gene. More surveillance study to be done if there exist other 1A.1 clade viruses without the 2 AA deletions in pigs from the same area.

Nigeria and other African countries update (Clement Meseko):

Though Africa has a smaller number of pigs compared to America, Europe and Asia, nevertheless sizeable stocks are raised in countries like Nigeria, Ghana, Uganda and Kenya. It is also important to note that less than optimal biosecurity and weaker veterinary infrastructure in Africa make many cohorts of piggery in these countries and more likely source of pathogen emergence and circulation. Swine influenza surveillance is yet to receive deserved attention, therefore surveillance efforts by few scientists with little or no funding is limited but risk based.

Swine influenza surveillance in Nigeria for instance is focussed on slaughter slabs, live pig markets, high density pig farms and mixed farms. Yearly but seasonal surveillance in slaughter slabs revealed high prevalence of H1N1pdm 09 in pigs since it was first introduced from human during the 2009 pandemic. Both genetic materials and antibody are regularly detected. There is also evidence of interspecies transmission of avian influenza H5N1 from poultry to pigs (Nigeria and Egypt) and observation of influenza virus transmission from pigs to poultry in mixed species farms. For further information refer to https://www.nature.com/articles/s41598-018-24371-6.

It is important to note that Ghana reported fatal H1N1pdm09 among boarding school students (4 deaths and 44 hospitalised in December 2017), evidence of H1N1pdm09 has also been reported in pigs in that country and hence the risk of future human infection from swine should be critically evaluated in Africa.

The potential for interspecies transmission and genetic reassortment of influenza in pigs (the traditional mixing vessel) require continuous surveillance and monitoring especially in Africa where co-mingling occurs.

Public health updates:

Swine influenza A virus infections in 2020 (Todd Davis):

Human infections with A(H1)v:

Country	Subtype	Age (yrs)	Sex	Onset date	Outcome	Exposure
Netherlands	H1N1v (1C.2.2)			Sept 2019	Recovered	Exposure to swine
Germany	H1N1v (1C.2.2)	2	M	06/15/2020	Recovered	Exposure to swine
Brazil	H1N2v (1B.2)	22	F	04/13/2020	Recovered	Possible exposure to swine
Canada	H1N2v (1A.1.1)			October 2020	Recovered	Exposure to swine

Status of influenza A(H1)v candidate vaccine virus development:

Candidate vaccine viruses in preparation	Clade	Type	Institution	Availability
A/Iowa/32/2016-like (H1N2)	1B.2.2.1	Reverse Genetics	CDC	Pending
A/Netherlands/3315/2016-like (H1N1)	1C.2.1	Conventional	NIBSC	Pending
A/Ohio/35/2017-like (H1N2)	1B.2.1	Conventional	NIBSC	Pending
A/Hessen/47/2020-like (H1N1)	1C.2.2	Conventional	NIBSC	Pending

Human infections with A(H3N2)v:

Country	Subtype	Age	Sex	Onset Date	Exposure
USA	H3N2v	18	M	6/30/20	unknown

Status of influenza A(H3N2)v candidate vaccine virus development:

Candidate vaccine viruses in preparation	Type	Institution	Availability
A/Ohio/13/2017-like	Reverse Genetics	CDC	Pending
A/Ohio/28/2016-like	Conventional	NIBSC	Pending

OFFLU swine group updates for WHO VCM technical activity (Nicola Lewis):

OFFLU swine influenza experts contribute data to WHO VCM in the last couple of years to provide global diversity of IAV in pigs. For the next VCM in February 2021, the timelines were presented. A data request letter will be sent for data submission and sharing before 18th December 2020. HA and NA genetic sequences are preferred for submission or only the HA sequences if available. If viruses can also be shared, antigenic characterisation can be done by APHA (UK) and USDA (USA) with harmonised reagent panels with CDC. A preliminary report will be submitted to WHO by end of January 2021 before the zoonotic teleconference. The seasonal and zoonotic meetings of WHO VCM will be held in February - March 2021 and followed by report release.

Basically, the epidemiological data is presented by micro react map by clades and geographical locations circulating in the last six months. Sequences are collated and harmonised. Phylogenetic analysis trees are done for H1 and H3 viruses. The highlight of contributions includes, OFFLU data identified 6 1B genetic clades not captured otherwise, HI assay data generation is harmonised and amino acid comparison to current vaccines.

Follow up from action points of previous technical meeting (February 2019, Paris, France)

1. The OFFLU swine influenza group activities poster will be updated by Janice

- The poster was not updated since IPVS 2020 was cancelled and postponed to 2022.

2. South America regional meetings will continue to be led by Ariel and Janice.

- No progress regarding this meeting since there are no funds for surveillance in swine influenza nor face-to-face meetings in 2020 due to the Covid-19 pandemic.

3. The potential for African regional meetings will be explored by Clement and Yohannes to include surveillance information from Uganda, Ghana, and perhaps South Africa.

- The potential for African countries involvement to gather swine influenza surveillance data is underway. Dr Yohannes Berhane (Canada) in parallel to an OIE twinning project is working to collect samples in live animal markets and farms in Ghana for surveillance. Contacts were also made with investigators in Nigeria, Kenya, Uganda and Cameroon. Further networking is planned during the meeting of African Network for Influenza Surveillance and Epidemiology (ANISE) later in 2020 which was postponed due to COVID-19 situation.

4. Regularity of OFFLU swine influenza group meetings will be approximately every 18 months. The next meeting can be tried around September 2020 subject to funding availabilities. There will be an International Pig Veterinary Society (IPVS) meeting in 2020 at Brazil. It may be a place to have an OFFLU Swine meeting and possibly an exhibitor table. Janice will follow up.

- The 2020 IPVS meeting in Brazil in June has been rescheduled due to the Covid-19 pandemic. Plans to have an OFFLU swine influenza side meeting during the rescheduled meeting in Brazil later in 2020 was on table, but this meeting was cancelled finally. Due to the current global health situation, the next face-to-face meeting cannot yet be envisaged, hence this videoconference.

5. Possible manuscripts to be written by the group

a. SIV surveillance summaries by region: South America, Asia, Africa, Europe.

- South America and Asia: Pending

- Europe: a group of several public institutes is meeting on a regularly basis at the instigation of Ceva Santé Animale. A common paper, aiming to summarize the viruses currently circulating in the different countries and trying to explain virus strain propagation and evolution in Europe is in the process of reflection and organization.

b. Swine-people interface with CDC – important to synthesize all information in a review: before and after, as the last review was published in 2011 (March 2020).

- Related to this topic, articles on swine-human interface have been published by members of the group since the last technical meeting

Anderson TK, Chang J, Arendsee ZW, Venkatesh D, Souza CK, Kimble JB, Lewis NS, Davis CT, Vincent AL. 2020. Swine Influenza A Viruses and the Tangled Relationship with Humans. Cold Spring Harb Perspect Med. 2020 Jan 27:a038737. doi:10.1101/cshperspect.a038737. Epub ahead of print. PMID: 31988203.

Rambo-Martin BL, Keller MW, Wilson MM, Nolting JM, Anderson TK, Vincent AL, Bagal UR, Jang Y, Neuhaus EB, Davis CT, Bowman AS, Wentworth DE, Barnes JR. 2020. Influenza A virus field surveillance at a swine human interface. mSphere 5:e00822-19. https://doi.org/10.1128/mSphere.00822-19.

Activity plan for 2021

1. Year 2019 – 2020 report from the SIV group to be prepared and posted on the website.

2. Send SIV data before 18 December for the February 2021 VCM meeting.

3. Update the H1 – 1C.2 clade nomenclature

4. To explore how regional subgroups can assist in feeding data to the main SIV group

Election of new co-chair to replace Dr Taki Saito:

Dr Janice Ciacci Zanella (EMPRAPA, Brazil) was elected as the new co-chair of the Swine influenza group. Dr Gaelle Simon (Anses, France) continues to be the Co-Chair of the group.

Next meeting:

Next virtual meeting to be considered in June 2021 for 1.5 to two hours duration without any country presentations and with a focus on specific topics like VCM, follow up on action plans.