Summary of the OFFLU Swine Influenza Virus Group Meeting 2017

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Surveillance in pigs by continent-updated surveillance data and research activities:

Australia (Frank Wong):

It remains challenging to get surveillance information on circulation of swine influenza virus (SIV) in Australian swine populations. In year 2012, novel genotypes H1N2 and H3N2 SIV were detected. Again in December 2016, the H1N2 and H3N2 genotypes were re-isolated from same piggery in Western Australia, with 98-99% sequence similarities between 2012 and 2016 isolates.

The current studies include, characterization of these viruses in terms of pathogenesis and zoonotic potential of novel Australian influenza A viruses using the ferret models of disease, determining the extent of disease caused these influenza viruses in pigs the origin host species, and determining the infectivity and growth characteristics of the novel Australian SIV isolates by *in vitro* assays. The antigenic relationships, and molecular determinants of infectivity and pathogenicity of the novel Australian influenza A viruses are also being investigated.

Japan (Takehiko Saito):

Active and passive surveillance for SIV was done in Japan in 2016-2017. By active surveillance 189 viruses were isolated from 3217 nasal swabs belonging to 33 farms and by passive surveillance 5 viruses were isolated. The subtypes detected include predominately A(H1N1)pdm09, H1N1-swine HA and NP, H1N2-swine HA and human NA and H3N2-human HA, human NA. SIV possessing either Classical H1 HA or human-like H3 HA with most of the human A(H1N1)pdm09 virus derived internal genes have co-circulated in Japanese pig populations. H1 genes of swine A(H1N1)pdm09 viruses isolated from 2015 to 2017 in Japan were derived from 5 distinct human isolates. H3 genes of H3N2 SIV in Japan were derived from a human ancestral virus circulating around 2000.

Thailand (Takehiko Saito):

In Thailand, 35 SIV were detected from 808 nasal samples from two provinces belonging to four farms. The subtypes detected include predominantly A(H1N1)pdm09 and seasonal H3N2 human lineage. At least 3 introductions of human A(H1N1)pdm09 viruses had established swine A(H1N1)pdm09 lineages in Thai pig population. Thai H3N2 lineage possessing seasonal human-like surface antigens has been circulating in Thai pig population since 2005. H3 genes of Thai H3N2 SIV are derived from a human ancestral virus circulating in the late 1990. Genotypes of H3N2 SIV in Thailand and Japan are same but all of the origins of each segment are different.

Vietnam (Takehiko Saito):

In Vietnam, 83 SIV were isolated in 2016 from 1680 nasal swabs from 5 provinces belonging to 28 farms. The subtypes detected include predominantly A(H1N1)pdm09 in north and south, H1N2 (two versions) and H3N2 (two versions). There is continuing genetic reassortments which generate the novel combination of gene segments. Unlike human population, pre-2009 human-like H1 viruses still have circulated in Vietnamese pig population. Antigenic drifts of Vietnamese classical and pre-2009 human-like H1 and human-like H3 SIV are evident.

Vietnam (Nguyen Tung):

In Vietnam, the coordinated surveillance for influenza and potential pandemic pathogens is through longitudinal influenza surveillance network (LISN). The main objective of this network is to monitor and characterize influenza viruses and other potential pandemic pathogens and risk assessment using the aligned surveillance results. The surveillance covers human, poultry, swine and wildlife at provincial, regional, and national levels. The goal is to do more virus characterization, strengthen analysis and strengthen capacity.

Surveillance for SIV was initiated in 2013 in order to understand better on gene pool of influenza A virus in pig population, risk factors for virus transmission, circulation, and evolution across sectors based on production systems and value chains. Risk-based surveillance was done targeted at high risk populations involving large commercial breeding/fattening farms with low farm biosecurity. Sampling design involve collection of 30 nasal swabs from 5-8 week old and 9-12 week old pigs with max of 30 nasal swabs/farm and sera from 10 piglets/farm. H1 and H3 SIV were isolated in pigs in Vietnam.

Wildlife Surveillance in Viet Nam involve surveillance targeting high-risk interfaces for disease transmission between wildlife and humans by screening for viral pathogens of pandemic potential and building local capacity for surveillance and laboratory diagnostics.

South Korea (Young Ki Choi):

Nasal swabs (farms) and lung tissues (slaughter house) were screened for SIV surveillance. It remains challenging to obtain materials for analysis. The subtypes detected were 4 isolates of H1N1 (2016), one isolate of H1N2 (2015) and 4 isolates of H3N2 (1 in 2015 and 3 in 2016). Genetic analysis showed that 3 different subtypes of SIVs are co- circuiting in South Korea (H1N1 pdm09 –like virus, avian like H1N2, and TRIG H3N2 along with H3N2pM). Overall sero positive rate was about 32% during the 2016-2017 swine sera. Comparison of sero prevalence of antibodies against different swine influenza virus lineages showed high positivity for A(H1N1)pdm09 (39.5%) and followed by EA avian-like H1N2 (20.3%) andH3N2pm/H3N2 (19.9), respectively.

Europe and other region not covered (Nicola Lewis):

SIV cases from Europe and non-USA not covered elsewhere from other experts was shared. A swine influenza A(H1N1) variant virus related to the Eurasian avian lineage was dctected in the Netherlands in 2016 which is genetically similar to some strains from ESNIP3 project. The virus has been shared by our colleagues in the Netherlands and full antigenic characterization is planned at Animal and Plant Health Agency (APHA) in upcoming weeks. It is published in Eurosurveillance (vol 21, issue 48, Dec 01, 2016) http://eurosurveillance.org/ViewArticle.aspx?ArticleId=22660.

A swine influenza A(H1N1) variant virus case also occurred in Italy in October 2016. Eurosurveillance, Vol 22, Issue 5, 02 February 2017. (http://eurosurveillance.org/ViewArticle.aspx?ArticleId=22707).
The H1avN1 infections that occurred in the Netherlands and Italy were both human cases.

In Colombia, Chile, Spain and Italy, H1 and H3 viruses detected. Sharing of isolates and data, and additional characterization including sequencing ongoing and will be antigenically characterized against HI panels using both ferret antisera and swine antisera.

France (Gaelle Simon):

Passive surveillance information on SIV is obtained through RESAVIP (French national network for SIV surveillance), ANSES investigations in farms, local studies with regional investigators and surveillance programs conducted by medical companies. Around 10 strains selected every 3 months for sequencing and antigenic subtyping done and propagated in eggs and antisera generated in pigs. More than 50% of swine respiratory cases are matrix gene positive with 75-80% of positive subtyped.

From 2010-2016 multiple H1 and H3 viruses identified with H1N1 most prevalent (H1avN1 68.3%, H1huN2 24% make up the most of the H1). Pandemic virus is primarily detected in low swine density areas in central France. H1huN2 variant first detected in 2012 and 2 H1huN2 sub-populations in co-circulation during 5 years at least. Converting to new H1 nomenclature, the H1 viruses identified in France are H1pdm, European H1hu, H1hu, H1av (Anderson et. al 2016). In summary, 3 subtypes (H1N1, H1N2, H3N2), 8 lineages, 14 genotypes were seen in France from 2010 – 2016. In 2016-2017 first detections of reassortants with internal genes from H1N1pdm were noticed.

SIV new research update (Kristien Van Reeth):

The European Surveillance Network for Influenza in Pigs (ESNIP) is no longer funded by the European commission and there is currently less coordination in Europe for SIV surveillance. Kristien Van Reeth presented an overview of the most important research papers on swine influenza that were published in 2016 and 2017. The new publications related to SIV surveillance, diagnostics, transmission and epidemiology, pathogenesis, immune response, vaccination, interspecies transmission and public health aspects.

USA surveillance (Sabrina Swenson):

USDA surveillance program for influenza A virus in swine was presented. It includes three data streams: case-compatible swine accessions submitted to the NAHLN system, swine populations epidemiologically linked to a human case of influenza A virus and swine exhibiting influenza-like illness (ILI) at commingling event such as auctions, markets, fairs, or other swine exhibition events. The surveillance plan was drafted in 2008 and later modified in 2009 to be specific for pdm H1N1 and then broadened in 2010 to account for more subtypes. From 2012 the lab improvised the laboratory algorithm testing methods and in 2014 the Ct cut off values for virus isolation was implemented. In 2015 external review of the surveillance program was conducted and in 2016 a stakeholder meeting was held and the algorithm changed for efficiency. The changes include matrix PCR cost no longer borne by the program, lower CT cutoff values for further covered testing and selecting only one sample per herd for subtyping.

The NVSL holds a repository of around 6100 viruses representing around 37 states. Full genome sequencing is done on select isolates of interest at NVSL. The lab provides confirmative testing and public health investigations. In fiscal year 2016, a total of 22771 samples were tested in the USDA system. The predominant subtypes isolated were H1N1, H1N2, and H3N2 with a minor detection of H3N1. 26/33 (79%) of the H3’s in fiscal year 2017-Quarter 1 were the newly emerged Human-like H3s. Human-like H3 has now been identified in 11 states.

In July-August 2016, country fair associated zoonotic transmissions were detected in seven country fairs of Ohio and Michigan. 18 human infections were reported with detection of H3N2v and all linked to swine exposure at these fairs. Swine sampled at each of the fairs were positive for H3N2 virus. Human viruses were genetically related to the swine viruses detected from the same fairs.

USA herd-based research (Marie Culhane):

Montse Torremorell leads a team of researchers at the University of Minnesota Swine Disease Eradication Center dedicated to understanding transmission of and developing control measures for SIV in breeding herds. The objectives of their research are to 1) assess herd-level prevalence and seasonality of influenza in a pig production system; 2) associate influenza prevalence with meteorological conditions; and 3) characterize influenza genetic diversity at the system level. The active surveillance program for 2011 – 2016 tested nasal swabs and oral fluids from 60 swine farms over 58 months. The results indicated that influenza is widespread in pig farms, influenza prevalence was seasonal across the years evaluated, influenza prevalence increased during fall, peaked in winter and spring, and decreased in summer month and influenza detection dynamics may be partially associated with air absolute humidity. During infections of influenza in swine, the air and surfaces in swine housing facilities contain detectable levels of viable influenza virus representing an exposure hazard to swine and people. Potential routes for influenza indirect transmission include air/droplets inside animal holding areas and contaminated surfaces.

USA research (Amy Vincent):

In Quarter 1 fiscal year 2017, H1 delta-1 and gamma viruses predominated with continued low frequency detection of alpha with a 2 amino acid deletion. In H3, human like H3 was predominant. In NA, classical N1 represented 91% of N1 detections and the 2002 lineage N2 represented 86% of N2 detections. The 1998 lineage N2 was most frequently paired with delta-2 H1. H3 SIV continues to evolve antigenically. Human-like H3 SIV is emerging as the most frequently detected H3. There were over 100 detections of the 3rd genotype of human-like H3N2 in the USDA swine surveillance system since 2014. This genotype also infected 16 humans in close contact with swine at fair exhibits in the summer of 2016.

The Swine H1 clade classification was published (Anderson et al. MSphere, 2016; Zhang et al 2016) and the H1 Clade tool was integrated into the IRD (fludb.org) search interfaces. Strain information annotated with both US and Global H1 designation for all H1 are available. The tool can be used to search for viruses in certain clades and can be used to annotate your own unknown sequence.

ISU FLU*ture* is an interactive web-based tool developed to provide diagnostic information from an Influenza A Virus database of test results, metadata, and sequences collected at the Iowa State University Veterinary Diagnostic Laboratory. The goal of ISU FLU*ture* is to allow veterinarians, swine producers, and researchers to seek out and find trends in the data that will allow them to make informed decisions regarding influenza and swine health. ISU FLU*ture* data is derived from diagnostic samples submitted from a diverse array of swine farms and production systems around the United States and North America (http://influenza.cvm.iastate.edu/).

Vaccine platform study results with antigenically mismatched H3 viruses comparing the efficacy of HA RNA vaccine (alphavirus vectored), whole inactivated virus (adjuvanted) and live attenuated influenza virus were presented (Eugenio Abente *et al*).

Canada (John Pasick):

In 2016 the Canadian pig inventory totaled 13.7 million. The major pig producing provinces were Quebec (31.6% of national production) and Ontario (24.6%) in the east and Manitoba (22.8%), Saskatchewan (8.7%) and Alberta (11.1%) in the west. In 2016 fifty-four veterinarians participated in the Canadian Swine Intelligence Network; 20 from Quebec, 10 from Ontario and 24 from Western Canada. The swine influenza viruses described in this report are the result of ongoing passive surveillance and cooperation between provincial and federal veterinary diagnostic laboratories. H1N1pdm2009 continues to be isolated from pigs but its prevalence appears to be on the decline, although this virus was isolated from farmed mink in Atlantic Canada and breeder turkeys in Ontario and Manitoba in 2016. A clear divide appears to exist between Eastern and Western Canada with regards to the circulation of other H1 viruses with classical swine lineage clade 1A.2 (β cluster) H1N1 predominating in the east and clade 1A.1 (α cluster) H1N2 predominating in the west. Clade 1A.3 (γ cluster) and 1B.2 (δ cluster) viruses were not detected. Differences between Eastern and Western Canada were also observed with respect to H3N2 viruses. Cluster IV-B viruses were circulating in Ontario in 2015 and 2016 and in Manitoba from 2012 to 2016. Cluster IV-C viruses circulated in Quebec and Ontario between 2012 and 2014. Cluster IV-D viruses were circulating in Quebec, Ontario and Manitoba between 2012 and 2016. Cluster IV-F viruses were found in Quebec and Ontario in 2012 and 2014. A fifth uncharacterized cluster was isolated from pigs from Manitoba and Saskatchewan in 2013 and 2014. A case of H3N2v was reported in November 2016 that involved a 19 month from rural Ontario. The HA gene of this virus belonged to cluster IV-B in contrast to USA H3N2v viruses which are cluster IV-A. The remaining gene segments of this H3N2v showed >99% identity with H3N2 swine viruses isolated from Ontario pigs in 2016.

Brazil (Janice Ciacci Zanella):

Since 2009, frequent outbreaks of H1N1pdm in pigs associated with respiratory illness and since 2011, human-like H1N2 and H3N2 detected in swine in seven Brazilian states and had internal gene segments of H1N1pdm09 origin. From 2009 – 2016, 1952 nasal swabs and 165 lung tissue samples were screened by RT-qPCR, virus isolation by MDCK cells or egg inoculation, subtyping by RT-PCR and sequencing methods. 14.45% of samples tested positive by RT-qPCR, 54.91% by virus isolation and 85 samples were subtyped. The subtypes detected include H1N1, H1N2 and H3N2. Partial and complete gene sequences generated for 58 SIV. Sequenced FLUAV genome also included lung samples tested positive at surveillance at Embrapa's diagnostic laboratory (CEDISA).There were 13 introductions of human pandemic H1N1 viruses into swine in Brazil since 2009. There was one introduction of human H3N2 viruses in 1996 (H3 segment) and two introductions of human H3N2 viruses (N2 segment) into Brazil swine in 1998. There was also novel introduction of human N1 into swine in Brazil in 2006.

H1N1pdm and human-origin H1N2 and H3N2 influenza viruses are widespread in pig herds in Brazil, where they continue to evolve. Influenza A viruses of human seasonal virus origin have been circulating in swine for more than a decade. These particular H3N2 and H1N2 swIAV clades appear to be specific to Brazil. A novel introduction of a human N1 in swine was detected; the most closely related human influenza virus circulated in humans between 1977 and 2009. The human-to-swine transmission probably has occurred in 2006. These findings show the very dynamic epidemiology of influenza virus in pigs and highlight the importance of human-to-swine transmission in the generation of influenza virus diversity in swine in Brazil.

South and Central America (Ariel Pereda):

In Chile, multiple introductions of human seasonal influenza A virus resulted in high diversity and reassortment of SIV. The H3 viruses were closely related to 2 human-like H3 influenza A viruses that are different from the North American clusters. The time to most recent common ancestor (TMRCA) was estimated as early as 1987 and 2006, respectively. Phylogenetic analyses of H1 viruses revealed 3 clusters of SIV, an H1pdm cluster and two unique Chilean clusters. TMRCA of cluster A estimated to be 1994 and of cluster B was estimated to as early as 1986. Human seasonal H1N1 and H3N2 viruses were likely introduced into the swine population in Chile sometime during the late 1980s to mid-1990s, generating increased reassortment and diversity since the 1990s.

In Guatemala, active surveillance in commercial farm was done. A pilot surveillance of swine influenza is being conducted in Escuintla, southern region of Guatemala. To date, a total of 997 nasal swabs were collected from May 2016 to February 2017. Preliminary results showed 19% (186/997) of influenza A detected by RRT-PCR and 33% (62/186) for pN1 in influenza A-positive samples.

In Colombia, 790 samples were screened with 5 isolations, of which 4 were pandemic H1.

In Argentina, passive surveillance in 2015 and 2016 on 979 samples yielded 126 RRT-PCR positive with 11 isolates so far. Also active surveillance from longitudinal studies on 3 farms consisting of 1200 samples yielded 284 RRT-PCR positive.

SIV´s are endemic with multiple strains co-circulating in Central and South America. Pandemic viruses seem to be predominant in the region. There are some examples of reassortment in the region. In some cases there is a potential evidence of antigenic drift. Additional phylogenetic analyses are ongoing to further characterize these isolates, study the reassortment events and, in some cases, could be further characterized by antigenic cartography.

Nigeria (Clement Meseko):

Approximately 10 million pigs and more than 140 million poultry in intensive, semi intensive and free range husbandry systems in Nigeria. In 2015-2017, H5N1 HPAI clade 2.3.2.1c cases were reported in poultry throughout the country, specifically more outbreaks in high poultry density states of Kano, Plateau, Kaduna, Bauchi (North), Rivers (South), Anambra (South East), Lagos, Ogun and Oyo (South

West) as noticed in prior outbreaks in 2006-2007. Avian influenza outbreaks noticed higher during dry/cold November – March months.

Nigeria has the highest pig population in Africa with about 30% of all pigs in the continent. High density/confined pig farms in the south, live pig markets in the north, backyard and free roaming domestic pigs across the country. Major overlap between poultry and pigs in Nigeria is a concern on potential interspecies mixing of viruses between poultry, pigs, and people. Previously, H1N1pdm09 detected in Nigeria, Cameroon, Kenya and Togo. Recently, published studies showed pigs have antibody to H1N1pdm09 in West and Central Africa and to H1N1pdm09, H1, and H3 in Nigeria. Swine H5 sequences from Egypt were submitted in the GenBank. Genomic and serologic investigations on swine samples from Nigeria are ongoing at FLI, Germany.

CDC update (Todd Davis):

In 2016, 18 cases of A(H3N2) were identified in the USA and all cases reported exposure to swine at agricultural fairs in Michigan and Ohio. There was no human-to-human transmission. 16 viruses had a seasonal human-like H3 gene likely introduced from humans into swine in 2010 or 2011. Swine specimens from seven fairs with human infections tested positive for swine influenza A(H3N2) virus, and genetic sequencing showed the viruses were very closely related to the human viruses.

In 2016, one case of A(H3N2)v was identified in Canada. The case developed respiratory infection symptoms in Oct 2016, was hospitalized with the diagnosis of pneumonia, and recovered. The case had confirmed exposure to swine on a farm.

In 2016/2017, influenza A(H1N1)v and A(H1N2)v was reported in humans in the USA, Netherlands, Switzerland and Italy. All cases reported exposure to swine prior to onset of illness.

Candidate vaccine viruses have been developed by WHO Collaborating Centers for the following: A/Ohio/9/2015 (gamma lineage A(H1N1)v); A/Hunan/42443/2015 (Eurasian avian-like A(H1N1)v). Candidate vaccine viruses currently under development by WHO Collaborating Centers include A/Iowa/32/2016 (delta lineage A(H1N2)v) and A/Netherlands/3315/2016 (Eurasian avian-like A(H1N1)v).

SIV data for WHO Vaccine Composition Meetings (VCM) (Richard Webby):

The primary function of the WHO Consultation on the Composition of Influenza Virus Vaccines (VCM) is to select the viral components of the seasonal, human influenza vaccine for the Northern and Southern Hemispheres. The meeting is organized in February and September every year. Since early 2000, the meeting also reviews zoonotic influenza virus activity and recommends development of pre-pandemic candidate vaccine viruses as a preparedness countermeasure to cover those viruses of highest public health concern. OFFLU sends two participants to this meeting twice annual meeting. The first day of the meeting is typically dedicated to review of surveillance, genetic and antigenic data on viruses with zoonotic potential and/or viruses that have caused human infection. Data analysis has recently focused on H5/H7/H9 subtypes that circulate in birds and H1/H3 subtypes that circulate in swine populations.

The future role for the OFFLU SIV group to play in the WHO VCM was presented. The SIV group could contribute a single report with contemporary data that focuses on influenza viruses in swine that have previously been associated with human infections. The primary use of the data would be to put zoonotic infections into epidemiologic/virologic perspective. Data of most interest would include unique detection events in swine, prevalence (even relative), sequence analysis (anything relevant not in public databases), antigenic information relative to contemporary human viruses, and human serology to understand population immunity to influenza viruses in swine. In order to provide periodic updates to the WHO VCM, there might be an opportunity to produce a report once a year.

Swine risk assessment pipeline (Amy Vincent, Nicola Lewis):

An update on the swine risk assessment pipeline was provided. It involves assessing antigenic relationships between swine and human seasonal viruses to predict potential for human risk. A side-by-side comparison of swine sera and ferret sera will also be conducted. Swine and ferret sera were generated against human and swine strains. Preliminary cross-HI for the H3 viruses was done and work on cross-HI for the H1 viruses in progress. Following the swine and ferret sera comparisons, the next step will be to assess population immunity by HI with human population sera panels.

H3 clade classification discussion (Tavis Anderson):

Following on the global nomenclature system and automated annotation tool for H1 hemagglutinin genes of influenza A viruses integrated into the IRD database, now a similar nomenclature system for H3 SIV is in development. The H3 clade classification will designate existing established clades with common phylogenetic nodes, >70 bootstrap value, >93% within clade nucleotide identity, >7% between clade divergence, and evidence of detection for at least a minimum time period (>1 year). The H3 data may require modification from the H1 criteria, including altering the threshold to 5 minimum numbers of sequences per clade, and utilizing contemporary data from 2006 to present. These changes resulted in the recognition and naming of an additional five swine H3 clades.

Discussion about STAR IDAZ and DISCONTOOLS:

The group discussed about STAR IDAZ and DISCONTOOLS request for involvement of the SIV experts in their activities for contribution.

STAR IDAZ is European Commission's International research consortium on animal health. Public and private groups contribute with aim of improving research collaboration and working towards common research agenda and coordinating research funding on major animal diseases, including zoonosis. There were expectations for the SIV group members to contribute to this initiative. However there was lack of clarity on what is expected and what inputs needed for the gap analysis, as OFFLU and STAR IDAZ has already worked together to develop a research agenda document in 2014.

DISCONTOOLS is a database to identify research gaps on vaccines, pharmaceuticals and diagnostics for the control of infectious diseases of animals.

It was suggested that STAR IDAZ and DISCONTOOLS be contacted again on this issue for clarification on kind of support expected from the SIV experts and involvement primarily through the OFFLU network.

OFFLU update (Peter Daniels):

OFFLU is a global, open network of expertise on animal influenza, established jointly in 2005 by the OIE and FAO to support and coordinate global efforts to prevent, detect, and control important influenzas in animals. The network encompasses the OIE and FAO Reference Centres, other diagnostic and research facilities, and world leading experts from a range of disciplines including diagnostics, classic, and molecular epidemiology, virology, animal production, and vaccinology. The vision of OFFLU is animal health community to provide early recognition and characterization of emerging influenza viral strains in animal populations and effective management. The objectives of OFFLU include: to share technical advice, training and expertise; exchange scientific data and biological materials; collaborate with the WHO related to human-animal interface; highlight influenza surveillance and research needs, promote their development and coordination. The network primarily works through special technical activities of primary interest. The newly established groups are the influenza in wildlife and the epidemiology. The outputs of the OFFLU network are listed on the website www.offlu.net. OFFLU also interacts with WHO on regular basis at the human-animal interface to provide zoonotic influenza data for pandemic preparedness, risk assessment and update on research agendas.

WHO public health research agenda for influenza (Peter Daniels and Todd Davis):

The WHO public health research agenda for influenza was in a period of review for public comment. OFFLU experts provided recommendations and commented on Stream 1 of the research agenda titled ‘Reducing the risk of emergence of pandemic influenza’. The document was shared with the SIV group members and reviewed in the meeting. The group provided additional research objectives to strengthen/expand on the current and future goals of SIV research/surveillance since the 2009 Public Health Research Agenda.
http://www.who.int/influenza/resources/research/en/

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

The group discussed about the missing SIV information from China, Hong Kong and other countries and ways to obtain it. It was suggested that the main expert should propose alternate expert if not attending to contribute to the face to face meeting. Dr Yi Guan could be contacted to include in the SIV group for Hong Kong. For missing information from Central America/Mexico, Marie could approach Montse Torremorell on how to get information from Mexico and potentially Chile. The group discussed about holding SIV regional sub-meetings to encourage other experts involvement in the region and to discuss regional vaccine recommendations. Also the possibility of member rotation from the region to the OFFLU SIV meeting was discussed but concern was raised on the continuity of information and proper scientific background in flu of the expert.

Election of new co-chair:

- Takehiko Saito (Japan) elected as the new co-chair of the group replacing Nicola Lewis. Marie Culhane will continue as the other co-chair.

Next SIV group meeting:

- The group discussed about the potential to hold meeting in Japan in 2018 and also at the ISIRV neglected flu meeting in UK in April 2018. Nicola Lewis will look at the possibilities of holding OFFLU SIV group meeting back to back with ISIRV.

New tasks and action points for the group to work on:

1. Updating and simplification of the algorithm for posting on the OFFLU website (Sabrina, Gaelle)
2. Labs share list of sera, list of viruses and diagnostic reagents available and post it on the website
3. Linking to regional laboratories: The expert from the SIV group will link to national and regional laboratories to obtain data for contribution. South America to try regional meeting based on already planned meeting (Janice to lead the pilot project), Europe to try regional pilot meeting (Gaelle to lead) and Mexico and Chile (Marie to contact Montse), contact China for commitment to attend the meetings, Dr Yi Guan to be contacted for Hong Kong.
4. Updates to documents on website
    - Update surveillance algorithm (Sabrina, Gaelle)
    - Technical disease card (Kristien and Choi)
    - SIV Poster (Amy)
    - Sampling of pigs (Marie, Gaelle, Clement)
    - 2 FAO documents on SIV - recommendation to FAO to review and update (Lidewij)
    - Vaccine summary documents on website (USA-Marie; EU/Asia-Kristien)
    - Advertise virus repository on website (USA-Sabrina; APHA-Nicola)
5. Determined that a small summary power point slide would be developed for WHO VCM (Lidewij)
6. H3 sequence to Tavis by June 1 for analysis (2 months) and paper development (end of August) –sequences must be for viruses from the last 5 years (all experts)
7. Ariel will liaise with STAR IDAZ and provide feedback to OFFLU SIV group; recommendation that STAR IDAZ and Discontools to come to consensus on who is doing gap analysis