



Summary of the OFFLU Swine Influenza Virus (SIV) Group Meeting University of Minnesota, Minneapolis, 19 - 20 March 2014

Participants: Amy Vincent (USA), Ariel Pereda (Argentina), Ian Brown (UK), Yohannes Berhane (Canada), , Kristien Van Reeth (Belgium), Marie Culhane (USA), Nicola Lewis (UK), Richard Webby (USA), Ruben Donis (USA), Sabrina Swenson (USA), Takehiko Saito (Japan), Young Ki Choi (Republic of Korea), Blesilda C. Verin (FAO), Gounalan Pavade and Keith Hamilton (OIE)

Through teleconference - Gwenaelle Dauphin and Filip Claes (FAO), Liz Mumford (WHO) – limited number of sessions

The meeting started with a report on progress with the previous meeting's action items.

Diagnostic tests (Marie Culhane):

A list of currently available diagnostic tests for detecting swine influenza viruses (SIV) was presented. In the USA, the Flu A Matrix real time RT-PCR (Spackman) assay was reported to be working well. Routine and commercial assays are also available with 98% sensitivity and specificity. Diagnostic sample types can include respiratory tract samples (tissues/secretions), bronchial swabs, nasal swabs, oral fluids, tracheal swabs, aerosols, water and environment. Data has demonstrated that there is a negative correlation between PCR cut off (ct) value and virus recovery.

There was a discussion on the relative merits of different sampling techniques for SIV surveillance. Although environmental samples can be useful for SIV surveillance, samples taken from the respiratory tract are most sensitive, followed by nasal swab samples and then by oral fluid sampling. Ropes left in pig pens, which groups of pigs 'mouth', have also been used as a practical sampling technique for SIV surveillance. The advantage of rope/oral fluid sampling is that multiple animals can be sampled and skilled personnel are not required to restrain and sample the animals. Oral fluids are useful for detecting and subtyping influenza viruses and reveal herd status (positive or negative) relatively quickly and easily. However, for successful virus isolation and subsequent full characterization of viruses, it was suggested that the best practice is the collection and submission of respiratory tract samples or respiratory secretions from pigs showing acute clinical signs and/or from pigs in higher risk groups (nursing pigs, replacement gilts, or weaned pigs with waning maternal immunity).

There are commercially available serologic assays (ELISA) that can be used for screening pigs for antibodies to SIV. To determine the strain of flu against which the antibodies were formed it is necessary to follow-up positive screening ELISA results with strain-specific hemagglutination inhibition (HI) tests. It is too early to produce guidance on HI testing reagents until regional circulating strains are determined.

Global antigenic cartography (Nicola Lewis):

Nicola Lewis presented antigenic maps illustrating the antigenic relationships between different influenza viruses (isolated from pigs) within and between different regions of the world where SIV surveillance data were available. To get a more complete global antigenic picture attempts were being made to develop collaborations with scientists in regions where data were currently unavailable. Cross validation studies had been completed to demonstrate that swine and ferret antisera produced according to standard protocols yielded comparable results for defining antigenic distances between different SIV of subtypes H1 and H3.

The global antigenic cartography map illustrates multiple and distinct H1 and H3 clades currently circulating in pigs world-wide. At the human and swine interface, at least 35 separate introductions of human H3 into pigs have been identified by phylogenetic analysis. Fewer introductions of H1 from humans to pig populations have been identified, but the results may have been biased by the sampled populations and because A(H1N1)pdm09 was counted as a single introduction from humans to pigs. There is also evidence that some of these introductions from humans into pigs become endemic within the pig population, and evolve antigenically within the animal host. For example, H3 viruses that are circulating in pig populations in Europe are very different from their counterparts circulating in humans. Thus, it is clear that reverse zoonosis (introductions of influenza viruses to the pig population from the human population) is important for driving antigenic diversity amongst influenza viruses circulating in pig populations and assessing the relative risk of these viruses being re-introduced into the human population should be assessed.

It was demonstrated that swine influenza viruses of subtype H1 have significant clade diversity both genetically and antigenically. At the same time, there was also significant cross-reactivity between some strains of differing H1-lineage (e.g. 'classic' and 'avian'). Human seasonal H1 and delta H1 genetic lineages tend to cluster antigenically whilst the avian and classic H1 genetic lineages tend to form more of a "cloud" of overlapping non-discrete antigens.

Reference panel of sera (Ian Brown):

The purpose of this activity was to define a minimum set of sera that would enable the preliminary subtyping of the HA of all strains of SIV from different parts of the world. Multiple H1N1, H3N2, and H1N2 viruses have been identified for serum development. The sera generated from these viruses were hyper-immune and therefore highly cross reactive. Sera produced against viruses that were circulating further back in time (closer to parent) were generally better for detecting larger groups of viruses compared to more recent viruses of the same lineage. The next steps in this activity would include assembling a panel of sera to be shared with partner institutes for preliminary evaluation of the suitability of the sera. Longer term planning would need to consider how a panel would be produced and distributed to additional groups of diagnosticians and scientists.

Regional specific diagnostic assays (Ian Brown):

During the meeting a survey was conducted among meeting participants to obtain information on regional specific diagnostic protocols and assays used in their countries. Six of 10 respondents indicated that they use the OFFLU algorithm http://www.offlu.net/fileadmin/home/en/resource-centre/pdf/SIV_algorithm.pdf or a modified version of it for diagnostic testing. The majority of

respondents used a combination of diagnostic test methods, with most using a PCR targeting the M gene as the initial screening tool. Confirmatory subtyping was through mainly HI or genetic sequencing of the HA, with some laboratories using PCR, or multiple tools. The majority of laboratories were not seeking technical assistance to identify virus subtypes because they were able to do this in their own laboratories. Most of the laboratories used an ELISA test for screening for serum antibodies and then subtyped positive samples using the HI test. The majority of laboratories were using virus strains from their own country and using more recent circulating strains for the HI test.

Harmonization of laboratory protocols (Ian Brown):

During the meeting an additional survey was conducted among meeting participants to collect information on laboratory protocols for SIV diagnosis. A total of 8/12 laboratories indicated that they essentially used diagnostic protocols that were based on the OIE Manual of Diagnostic Tests and Vaccines for Terrestrial Animals. A total of 5/11 of the laboratories said that they conduct their testing under a third party quality assurance scheme. At least half of the respondents participated in some form of proficiency testing (PT)/ring trial and expressed interest in participating in a global PT if this was offered by OFFLU. Multiple sources of PT's were reported with the majority of participants utilizing PT's for PCR. Caution should be taken when recommending specific PCR assays because an assay that works well for viruses circulating in one region may not be able to detect different viruses circulating in another region.

Update on SIV Chapter in the OIE technical disease cards (Sabrina Swenson):

The SIV chapter update in the OIE technical disease cards had not yet been completed. The updated chapter would need to account for a new template required by OIE and to ensure that the information provided is accurate and up to date and reflects the information in the Terrestrial Manual chapter on swine influenza.

OFFLU STAR IDAZ meeting on influenza research agenda (Keith Hamilton):

The OFFLU and STAR IDAZ (EU-funded project concerned with improving coordination of research activities on the major infectious diseases of livestock and zoonoses) would be jointly holding a consultation to develop a global animal influenza research at OIE headquarters in April 2014. This meeting would engage technical experts from the fields of avian, swine, equine, wild birds, donors and policy makers in order to identify and align research priorities to develop a strategic agenda for global animal influenza research. The group was asked to prioritize a list of predetermined research priorities to be considered at the meeting. Several of the research-orientated SIV group experts had been invited to this consultation.

EMPRES-i genetic model (Blesilda Verin/Gwen Dauphin):

EMPRES-i is a global/regional FAO web-based animal disease information system that includes disease tracking, analysis models, surveillance models and genetics models <http://empres-i.fao.org/>. In 2013 a genetic module was released to the public that combines within EMPRES-i epidemiological information, genetic characterisation and geomapping in the analysis of influenza epidemiology and ecology including possible virus reassortments. A link was developed to act as the interface between EMPRES-i disease events and publicly available influenza virus sequences available at Open Flu

database. The link computes potential outbreak events with sequences. FAO has made this tool available for scientists and policy makers. http://www.offlu.net/fileadmin/home/en/resource-centre/pdf/EMPRESi_genetic_module.pdf Future developments planned include: continued validating of links to sequence and influenza events, cluster information, molecular markers, segment origin predictions and links with other influenza specialized databases such as IRD. It was suggested in this meeting that a possible compartment could be created within EMPRES-i to host and share swine influenza virus data.

EPT+ project (Blesilda Verin):

To improve the understanding of livestock as a reservoir for potential pandemic influenza viruses in South East, East and Southern Asia, FAO coordinated activities under the USAID funding to undertake influenza surveillance as part of the broader Emerging Pandemic Threat (EPT) Program in South and South East Asia. The aim of the EPT+ program (a subprogram of the EPT) was to increase the detection of diverse progenitor viruses with zoonotic potential within targeted agro-ecological systems in countries where the greatest genetic diversity were likely to occur. The focus of the program included: (a) surveillance for influenza viruses, (b) identification of risk factors for virus diversity, and (c) determination of the role of value chains in virus diversity. Highlights of the phase 1 activities were: China completed laboratory testing of samples, Viet Nam has developed suitable methodology for efficient detection and isolation of Swine Influenza Viruses, Bangladesh conducted surveillance in pig populations and established One Health laboratory networking, and review of influenza risk models.

Current status of SIV by region and activity updates

Canada (Yohannes Berhane):

Canada conducted SIV surveillance in 3 provinces (namely Quebec, Manitoba, and Ontario) where the highest population of swine were located. Virus had been isolated from 67 out of 93 PCR positive samples with subtypes H1 (n=31) and H3 (n=20) identified by HI testing. Full genome sequencing of the viruses of H1 subtype showed that they possessed the same gene constellation as the A(H1N1)pdm09, with the exception of 2 viruses that had both TRIG and A(H1N1)pdm09 gene segments. Viruses of the H3 subtype that had been sequenced appeared to possess a mixture of the TRIG with A(H1N1)pdm09 genes. Six swine influenza viruses were also isolated from turkeys in the year 2011 – 2013.

Work is underway to develop a Luminex based multiplexed fluorescent microsphere immunoassay (FMIA) for the detection of antibodies to SIV infection; the FMIA will be able to subtype and differentiate antibodies to H1 and H3 viruses. For this purpose codon optimized influenza A virus nucleoprotein and the HA1 subunit of the hemagglutinin protein from different clusters of H1 and H3 has been expressed. The most suitable antigen from each cluster of H1 and H3 subtypes would be selected for use in the multiplexed FMIA. The project was being conducted in collaboration with Bio-Vet Inc.

USA surveillance (Sabrina Swenson, Marie Culhane):

The USDA surveillance program monitored SIV changes nationally. In 2013 there continued to be strong participation from pig farmers and the pork industry. Influenza viruses were detected all year

round in pigs and peaked in the autumn and spring time. Surveillance was targeted to samples from sick pigs, pigs linked to public health investigations for novel flu cases in humans, and pigs exhibiting influenza like illness at exhibition events.

From October 2011 to January 2014, a total of 38,350 samples were tested in the USDA system. The predominant subtypes isolated were H1N1, H1N2 and H3N2. A(H1N1)pdm09 was rarely detected in 2011 and 2012. There was also minor but consistent detection of mixed subtypes, usually from oral fluid submissions. The majority of viruses isolated possessed the A(H1N1)pdm09 matrix gene. The National Veterinary Services Laboratories (NVSL) has a repository of around 2400 SIV. Full genome sequencing was done for representatives of each subtype and for representative viruses of each submitted state.

The University of Minnesota was a participant in USDA surveillance system and, in addition to the USDA program, the university also received samples from pig farms not participating in the voluntary USDA system. The laboratory received diagnostic samples from multiple states outside Minnesota and other countries such as Canada and Mexico. An approximately equal distribution of H1N1, H1N2, H3N2, was detected; however some viruses of subtype H3N1 and some human seasonal H3 spillover into the pigs was also detected. The laboratory routinely conducted full length sequencing of the HA, NA, and M genes and several viruses were subjected to full genome sequencing. Many viruses were referred to biological companies for further characterization.

USA research (Amy Vincent):

Globally, 3365 full length HA sequences from SIV (2000 – 2013) have been deposited into GenBank. USA accounted for 77% of the SIV HA sequences in Genbank, of these 90% of the endemic viruses possessed the A(H1N1)pdm09 matrix gene. H1N1 viruses predominately contain the gamma cluster HA and delta cluster HA predominated in H1N2 viruses. Historically, a gradual reduction in the number of A(H1N1)pdm09 had been seen but recently there had been a small but relative increase in the frequency of A(H1N1)pdm09. There appeared to be a recent increase in spillover of this virus from human to pigs, however the numbers were too low to be statistically significant. An expansion in the diversity of H3 was noticed with the predominant sub clusters being alpha/beta. The introduction of a new N2 subtype in 2002 appeared to be more successful in maintaining itself compared to the 1998-lineage N2. Antisera for cross HI and antigenic cartography have been developed. Delta 1 and delta 2 have limited cross-reactivity and further antigenic mapping of human and swine H1 is in progress. An H3N2 genetic and antigenic study was recently published. There were 6 amino acid sites in the H3 that correlated with antigenic divergence (Lewis NS, Anderson TK, Kitikoon P, Skepner E, Burke DF, Vincent AL. Substitutions near the hemagglutinin receptor-binding site determine the antigenic evolution of influenza A H3N2 viruses in U.S. swine. *J. Virol.* 2014 May; 88(9):4752-63). These were the same 6/7 amino acid sites found in humans for H3 and were located around the receptor binding site of the HA. The antigenic clusters were not predicted by the genetic cluster for H3. Next steps include point mutations and reverse engineering of H3 viruses to test impact of specific mutations.

USA NIH Centers of Excellence in Influenza Research and Surveillance (CEIRS) (Richard Webby):

In the USA field surveillance was targeted at gilts (approximately 6 months of age) and piglets (approximately 3 weeks of age). SIV was detected throughout the year with detection level of 5% in both groups, although gilt development units showed a higher (8%) level of detection.

Collection of sera, nasal swabs, and tracheal swabs from abattoir and backyard farms in Colombia was under progress. The project had been expanded to include an additional geographic area in Colombia and was focusing on collecting diagnostic samples from using swabs and rope. Approximately 15.5% of samples had tested as positive and were identified as A(H1N1)pdm09. NIH CEIRS surveillance had also been expanded into other countries including Benin, Bulgaria, Cote d'Ivoire, Ghana, Sri Lanka, and Uganda. A small number of positive samples have been identified in Sri Lanka and Uganda.

Brazil, Argentina/South America (Ariel Pereda):

In Brazil, surveillance was focused on commercial farms, captive wild pigs, feral pigs, and diagnostic laboratory submissions. Collected diagnostic specimens included nasal swabs, oral fluids, lung, and sera. A total of 68 viruses (3 from nasal swabs and 65 from lung samples) had been isolated. The viruses detected included subtypes H3N2, H1N2, H1N1, and A(H1N1)pdm09. Three partial gene (H, N, and M) sequences were completed on 37 viruses and full genome sequencing completed on 9 viruses. All of the viruses isolated from the surveillance programme had an A(H1N1)pdm09 matrix.

In Colombia surveillance was conducted using oral fluid based on real-time PCR and included testing for influenza, PRRS, and porcine circovirus 2. Oral fluid samples performed better for virus detection than swab samples. Vaccination for influenza was not practiced in Colombia and there appears to be no clear seasonality based on serosurveillance.

In Chile four viral subtypes including A(H1N1)pdm09, H1N2, H3N2, H1N1pdm09-like have been identified. Vaccination for influenza was practiced in commercial herds and began in 2011/2012. Serologic data indicated that A(H1N1)pdm09 was highly prevalent and data suggested there was potential antigenic drift occurring in pandemic H1N1 strains.

In Argentina there was continuous surveillance for influenza in pig farms. The viruses had changed over time with A(H1N1)pdm09 being the predominant virus. There was evidence to support reassortment of viruses. The main subtypes present in pig farms are delta H1N1 and H1N2, H3N2 cluster 2 and A(H1N1)pdm09. Vaccination for influenza was initiated in Argentina.

In Guatemala, due to the lack of funds in 2013, influenza surveillance was discontinued.

European swine influenza network (ESNIP) (Ian Brown):

Twenty-five partners, including vaccine manufacturers had been involved in the ESNIP project. Regional variation in the epidemiology of SIV had been observed. Although there was reluctance by some to report the presence of A(H1N1)pdm09 virus in swine, it was detected in some regions. Seventeen unique genotypes were identified, of which 3 are historic and no longer present in pigs.

Entirely avian-like H1N1 virus remained the predominant virus (32%) followed by H1N2 (21%) and H3N2 (18%). A(H1N1)pdm09 gene segments were detected in viruses in countries in which the virus had not been reported and the new introductions appeared to be primarily from humans. The ESNIP project has helped to harmonize surveillance and diagnostic procedures. Currently there is no immediate prospect for continued funding for the ESNIP network, although commercial companies have expressed interest to fund annual meetings.

Europe research (Kristien Van Reeth)

“Flupig” is a research project (July 2010 – December 2014) that is funded by the European Commission. It involves 10 international partners and is coordinated by Ghent University. It aims to better understand 1) the role of pigs in the emergence of novel pandemic influenza viruses and 2) the extent of cross-protection between different influenza virus subtypes and lineages and underlying immune mechanisms (see www.flupig.ugent.be for full information about the project). During 2013, most research groups have focused on aim 1. They have worked together to try to adapt wholly avian H1N1 and H9N2 influenza viruses to pigs by serial pig passage, and to examine their transmissibility between pigs as well as between ferrets (as a model for humans). Though the serial pig passages resulted in an enhanced replication efficiency of some avian viruses in the pig, none of the research groups could obtain fully swine-adapted avian viruses that transmit efficiently between pigs. Preliminary data suggest that parental and pig-passaged avian viruses transmit more readily between ferrets than between pigs. The results of these studies will be published in the near future.

Japan/South East Asia (Takehiko Saito):

There was no systematic surveillance system for SIV in Japan and therefore there were very few isolates for characterization. During 2013, 6 viruses were isolated and both A(H1N1)pdm09 and H1N2 were detected. The H1N2 viruses possessed classical swine HA and human-like NA genes. The internal genes were either all A(H1N1)pdm09 or a mixture of classical swine and A(H1N1)pdm09.

In Vietnam surveillance involved collection of 800 nasal swabs in July and December 2013 for virus isolation. 20 viruses were isolated representing both Northern and Southern regions. A(H1N1)pdm09, H1N2, and H3N2 were detected.

Thailand (Bandit Nuansrichy):

In Thailand 1610 samples were collected in 2013 from five provinces and 13 viruses were isolated, of which 8 belonged to A(H1N1)pdm09 and 5 belonged to H3N2. Future surveillance activities were planned through a human-animal interface project focusing on subtypes H3 and N2 in pigs, humans, ducks, chickens and bats.

South Korea (Young Ki Choi):

In South Korea, North American-like triple reassortant swine and European like SIV were detected. All diagnostic samples were sourced from slaughter facilities and therefore there was no information available on the clinical presentation. In 2011-2012, epidemiologic surveillance was conducted in the

largest swine production provinces. Multiple reassortant viruses had been identified. One of the novel reassortants was an H1N2 SIV bearing a Eurasian avian-like swine hemagglutinin and a Korean swine H1N2-like neuraminidase in the internal gene backbone of the H3N2pM-like virus. The first sero surveillance detections were reported in 2013. Research studies evaluating viral growth in multiple cell lines, virulence in mice and ferrets were undertaken. In 2012 a high prevalence of H3N2 and in 2013 H1N2 viruses were reported. The new viral types detected are thought to be associated with importation of pigs because the South Korean pig population had been decimated during the 2008 FMD outbreak.

Global SIV HA overview and framework for cluster designation (Amy Vincent/Nicola Lewis):

A global phylogenetic cluster naming system was proposed based on criteria adapted from avian influenza H5 genetic diversity to be suitable for the global influenza A virus genetic dataset from swine and humans. The naming system was proposed for several reasons: 1) To communicate the genetic relationships between influenza viruses circulating in swine among different geographic regions 2) To communicate the genetic relationships between swine and human seasonal influenza viruses. 3) To provide a benchmark to monitor and identify significant genetic evolution of the influenza virus HA gene in the future. The group has been working with the Influenza Research Database (fludb.org) to provide the HA gene cluster names based on the new system for a web-based cluster determination tool for query sequences with free public access.

The OFFLU SIV group had an ongoing collaboration among its members to characterize the antigenic relationships among swine influenza viruses and with human influenza viruses. The hemagglutinin (HA) surface protein is the primary target of the immune response and is the main antigenic component of human and swine influenza A virus vaccines and thus the focus of the OFFLU swine group activity. Assessing the antigenic relationships among the HA's of multiple subtypes circulating in pigs and people and understanding the relative HA evolution in these hosts over time was key to improve vaccines and understanding the relative risk of future interspecies transmission events as well understanding potential susceptibility of human populations to both existing and emerging subtypes. Genetic analyses of swine viruses revealed reoccurring incursions of human seasonal influenza viruses and variants of these introductions continue to circulate in different pig populations worldwide. Antigenic analyses of influenza viruses in pigs showed significant antigenic diversity among strains circulating within and between geographic areas and will have important implications for swine influenza vaccine strain selection. These independent incursion events occurred at different time points in different geographic regions and maintenance of such diverse viruses within pigs for long periods of time also pose a risk of re-introduction into the human population. This globally compiled information should be used in risk assessment for pandemic preparedness as swine are a reservoir for viruses with human potential, exemplified by the 2009 H1N1 pandemic. A publication will be prepared to share the cluster naming criteria and system publicly. The manuscript is contingent upon release of unpublished genetic data from OFFLU participants.

Demonstration of a swine HA sequence cluster typing tool by Influenza Resource Database (IRD): (Richard Scheuermann and Catherine Macken)

Information about the Influenza Research Database (IRD) system can be found at www.fludb.org. The database is a free open access web resource that has no usage restrictions. It supports a wide range of information about influenza viruses, including genome sequence, functional genomic, proteomic, and structural genomic data. IRD provides a comprehensive, integrated database supporting influenza virus research and surveillance and is based on information integrated from public venues and submitted directly to IRD. There are multiple searching and analysis tools available for use. The site also provides video tutorials, primer design tools, information on publications, and links to important sites. Users can set up personal workspaces for controlled access analysis that can be maintained for private use. (Squires RB, Noronha J, Hunt V, García-Sastre A, Macken C, Baumgarth N, Suarez D, Pickett BE, Zhang Y, Larsen CN, Ramsey A, Zhou L, Zaremba S, Kumar S, Deitrich J, Klem E, Scheuermann RH. 2012. Influenza Research Database: an integrated bioinformatics resource for influenza research and surveillance. *Influenza and Other Respiratory Viruses* 6:404-416).

IRD is currently developing and testing a suite of algorithms for a web-based tool to determine the clade of viruses based on the HA. H1 subtype genes and the U.S. cluster designations have been used to develop the prototype. Two general methods of genomic sequence classification have been evaluated by blast-based and tree-based methods. Blast-based analysis is highly accurate provided classes are well separated, simple to implement, simple to update as viruses evolve, robust to quality of sequences, and fast. Tree-based analysis is highly accurate even when classes are closely related, more complicated than blast-based methods from both conceptual and implementation standpoints, allows for detection of transitional sequences, more sensitive to bad sequences, and fast. The tree-based analysis has provided more accuracy compared to the blast based method with the data tested thus far.

One year work plan (2014-15)

- Update chapter on swine influenza in the OIE technical disease cards (Sabrina, Ian, Takehiko, Ariel, Emanuela Foni) : September 2014
- Develop set of viruses and hyperimmune sera for preliminary subtyping (Ian) : October 2014
- Serologic panel for viral antigenic cartography (Richard and Nicola) : July/August 2014 to complete discussion (testing date to be assessed later)
- Harmonization of lab protocols (Marie) : November 2014
- OFFLU press release on reverse zoonosis information with appropriate caveats (Keith, Gwen) : June 2014
- OFFLU-STAR-IDAZ meeting minutes for group (Keith) : June 2014
- Revisit SIV testing algorithm (Sabrina, Ian, Kristien) : July 2014
- Linking OIE and OFFLU web sites for swine influenza documents (Gounalan, Kristien) : September 2014
- Maintenance/expansion of antigenic cartography work (Nicola) : Initial discussions at STAR-IDAZ meeting in April 2014
- Discussion with the OFFLU steering committee for similar approach regarding avian and swine on harmonization and information distribution (Ian and Kristien) - October 2014
- Publish scientific nomenclature (Amy, Nicola) : Need to obtain more information first ; send e-mail to committee members requesting more data – June to October 2014
- Inform OFFLU steering committee of new nomenclature and provision of data to other providers (Ian) : April 2014
- Poster update and submission to IPVS (Amy, Sabrina) : June 2014

Planning for next meeting:

2015 OFFLU SIV meeting tentatively scheduled for Ghent in June.

Group photo



Front row (L to R): Gounalan Pavade (OIE), Blesilda Verin (FAO), Sabrina Swenson (USA), Nicola Lewis (UK), Kristien Van Reeth (Belgium), Ariel Pereda (Argentina), Takehiko Saito (Japan), Keith Hamilton (OIE)

Back row (L to R): Ian Brown (UK), Carlos A Diaz (USA), Young Ki Choi (Rep. of Korea), Marie Culhane (USA), Yohannes Berhane (Canada), Richard Webby (USA)

Amy Vincent (Not in picture).