Summary of the OFFLU Swine Influenza virus Group Meeting 2012

27 – 28 March 2012,
OIE HEADQUARTERS, PARIS, FRANCE

Day 1

Welcome – Bernard Vallat (Director General of OIE)

On behalf of OIE and FAO Dr Vallat welcomed all the participants and thanked them for their outstanding efforts. He thanked the National Institute of Health (NIH) and St Jude’s Children’s Hospital for supporting this meeting. OIE and FAO believe that influenza surveillance in swine is important for both human and animal health. Dr Vallat offered his support to this OFFLU SIV group which convenes the world’s leading experts to coordinate influenza surveillance in swine at a global level and provides a sustainable platform for sharing and analyzing influenza surveillance data. He acknowledged the challenges in implementing influenza surveillance in pigs, highlighting the problems that can be caused by naming influenza viruses inappropriately – for example pandemic H1N1 2009 virus as ‘swine flu’ – which has no benefit for public health but can damage agricultural economies and livelihoods.

OFFLU fully supports research to better understand and identify public health and animal health risks from influenza viruses, and advocates for investments in veterinary services including laboratories, surveillance, and applied research.

Introductions – Kristien Van Reeth

Professor Kristien Van Reeth introduced the 21 group members including two new members – Drs Ariel Pereda (Argentina) and Nguyen Tung (Viet Nam)
SIV surveillance in the USA is currently generating a greater number of sequence deposits to GenBank due to a federally funded US Department of Agriculture (USDA) system and NIH funded projects. SIV is endemic in the USA and it is not reportable. There are various streams of SIV surveillance in the USA including a structured national system (USDA), and state or regional surveillance where samples are sent directly by producers/veterinarians to state diagnostic or research laboratories. USDA surveillance is passive, anonymous, and voluntary; samples are only identified by state and collection date and may not provide an accurate indication of prevalence due to lack of submissions from some regions; it also does not include actively collected samples from sub-clinically infected pigs. The majority of surveillance and outbreaks are handled at the state or private level.

**Summary of surveillance data from the USA:**

In the USDA system between Oct 2009 – Jan 2012, a total of 6 855 samples were submitted (H1N1 24%, H1N2 40%, A(H1N1)pdm09 14%, H3N2 20%, and mixed 2%). Any isolates can be shared by contacting USDA NVSL. Using “A01” as a search string in the virus strain name (with search tools available in most commonly used influenza virus web-based interfaces that link to GenBank: http://www.ncbi.nlm.nih.gov/genomes/FLU/Database/nph-select.cgi?go=database or http://www.fludb.org/brc/influenza_sequence_search_segment_display.do?method=ShowCleanSearch&decorator=influenza will identify viruses from the USDA surveillance system.

At the University of Minnesota Veterinary Diagnostic Laboratory (UM-VDL, the US laboratory with highest case load of swine influenza submissions), between August 2010 – March 2012, 21 000 samples were tested for SIV and 20% were positive (H1N1 33%, H1N2 38%, H3N2 25%, and mixed 4%). H10 has also been identified once as a cause of respiratory disease in one diagnostic submission from pigs – this has been identified on serology and PCR/sequencing (HA2 portion of the gene only) but it has been difficult to grow the H10 virus. Many submitters to UM-VDL chose not to participate in the USDA surveillance system.

SIV in USA swine are diverse with complex evolutionary patterns. Phylogenetic analysis of H1 genes illustrates the evolution of multiple cluster types (alpha, beta, gamma, delta, and pandemic) from viruses in USA swine populations. Antigenic cartography of H1 viruses correlates with the phylogenetic clusters and demonstrates the antigenic diversity of these viruses. In the diagnostic serology, H1 viruses are quite variable in antigenic cross-reactivity and delta viruses are completely unpredictable. Collaborations with USDA and UM-VDL and phylogenetic analysis by NIH demonstrated at least 50 introductions of A(H1N1)pdm09 from humans into swine (e.g. reverse zoonosis, anthrozooonosis) throughout the world since 2009. The M gene from pandemic A(H1N1)pdm09 was detected in all subtypes and cluster types of SIV found in USA swine populations indicating frequent reassortment. A human lineage N2 gene was incorporated into endemic SIV in the USA around 2002-2003. Alpha H1 have not been detected in the past 2 years; Beta H1 were common in 2008 but have steadily declined and Delta-1 have dramatically increased. Gamma H1 have decreased since 2009, but appeared to increase in first quarter of 2012. Delta-2 appears to have disappeared since 2010. H3 cluster viruses have shown increased genetic variation recently, but cross-reactivity in H1 assays with standard H3N2 reference antigens have not yet been significantly affected.

Variant H3N2 (H3N2v) infection studies were conducted at USDA ARS, including a human isolate of H3N2v, a TRIG-H3N2, and an H3N2/A(H1N1)pdm09 reassortant isolate from swine. The TRIG-H3N2
replicated most efficiently in the swine host, the H3N2v and the H3N2/ A(H1N1)pdm09 reassortant also replicated and caused lesions but less efficiently. This suggests that the pandemic M gene may not confer a selective advantage in the swine host. At least 6 different 8-gene combinations have been identified in US swine H3N2 viruses since the emergence of the A(H1N1)pdm09.

In the USA pigs are vaccinated for SIV (mainly with autogenous vaccine). SIV is often isolated from vaccinated pigs because vaccines reduce viral shedding but may not prevent it. Vaccine studies at USDA-ARS have repeatedly shown vaccine-associated enhanced respiratory disease (VAERD) when there is induction of whole virus antibodies that lack cross-reactive HI or SN activity. VAERD is not seen when MLV or Adenovirus-vectored HA vaccine is used. VAERD includes a dysregulated pro-inflammatory and anti-viral response and is histologically characterized by an increase in tracheitis, necrotizing bronchiolitis and alveolitis with edema, hemorrhage, and neutrophil influx followed by lymphocytic infiltration and peribronchiolar cuffing. The role of complement activation, opsonized uptake of virus, and a low level of primed T-cells Cell Mediated Immunity are suspected to be part of the mechanism.

NIH CEIRS – Richard Webby

Swine surveillance activities are conducted in Argentina (many influenza viruses detected); Hong Kong/Southern China (many influenza viruses detected); Sri Lanka (recently started surveillance); and West Africa, Cameroon, Congo, Uganda (where very few viruses or no viruses have been detected); USA (many viruses detected with approximate detection rate of 4.5%); human-swine interface surveillance in Alberta, Canada; Colombia (positive detections for SIV on farms and in slaughterhouses). Funding for the current CEIRS programme ends in March 2014. A request for proposals to continue the CEIRS-funded projects after 2014 will likely be publicised soon, offering opportunities for OFFLU and SIV surveillance in general.

US Public Health – Ruben Donis

In June 2007 in the USA, the Council of State and Territory Epidemiologists (CSTE) voted to make novel influenza A infections in humans nationally reportable to the National Notifiable Disease Surveillance System (NNDSS). Novel influenza A viruses are those that are different from currently circulating human H1 and H3 viruses and includes those that cannot be subtyped using standard methods and reagents. Since July 2011, 12 human cases of variant H3N2 (H3N2v) have been detected in 5 states in the USA, one case of H1N1v and one case of H1N2v. The H3N2v virus has 7 gene segments from triple reassortant H3N2 North American swine viruses and the M gene from a human A(H1N1)pdm09 virus.

The H3N2v are antigenically similar to A/Minnesota/11/2010 which was selected as a vaccine candidate for pandemic preparedness. There is minimal to no protection from current seasonal influenza vaccine and children may be more immunologically susceptible. The viruses are resistant to adamantanes but sensitive to oseltamivir. The H1N2v isolated from humans were genetically close to North American swine influenza viruses of the H1N2 subtype. These H1N2v cross react with A/Brisbane/59/2007 like viruses and are sensitive to amantadine, rimantadine, oseltamivir and zanamivir.

Europe/European Surveillance Network for Influenza in Pigs (ESNIP) – Ian Brown

ESNIP is a so-called “co-ordination and support action” in the 7th Framework Programme of the European Commission (EC). Funding is from 2010 – 2013.
ESNIP 3 has 25 partners including researchers from universities and research institutes, and vaccine manufacturers actively engaged in SIV surveillance. ESNIP 3 is coordinated by the Animal Health and Veterinary Laboratories Agency (AHVLA) in the UK; ESNIP partners submit viruses to the AHVLA virus bank.

Goals are set to generate surveillance data, epidemiological data, antigenic data and maps (cartography), genetic characterization (phylogenography, genotypic data), virus database and repository and to stimulate network interaction. There is a strong focus on data generated through passive surveillance.

http://www.esnip3.com/project_summary.html

Professor Ian Brown, ESNIP3 co-ordinator presented a concise overview of the SIVs reported so far by various ESNIP3 partners:

Approximately 7000 cases of influenza A have been detected during 2010 – 2013.

**UK:** 60% of SIV are A(H1N1)pdm09, 35% European H1N2 (with human-like H1) and 5% avian-like H1N1

**Belgium:** European H3N2, avian-like H1N1, and European H1N2 have been isolated.

**France:** 2 isolations of pH1N1 and avian-like H1N1, European H1N2 and rH1N2 (avian-like H1 X H1N2 European) have been isolated

**Italy:** European H3N2, avian-like H1N1, European H1N2 and A(H1N1)pdm09 have all been isolated

**Germany:** European H3N2, avian-like H1N1, European H1N2 and a single case of A(H1N1)pdm09 have been detected. In addition there appears to have been detection of an A(H1N1)pdm09/H3N2 reassortant

**Poland, Slovakia:** Avian-like H1N1 and un-typed influenza A

**Hungary:** European H3N2, A(H1N1)pdm09, rH1N1 (avian-like H1N1 X A(H1N1)pdm09)

**Spain:** European H3N2, avian-like H1N1, European H1N2

**Denmark:** Avian-like H1N1, H1N1 ‘European variant’ (avian-human), and A(H1N1)pdm09

**Canada – John Pasick**

The commercial pig population in Canada is 12 million, with Quebec, Ontario, and Manitoba accounting for about 75% of the pig production. Overall submission for SIV testing is low because SIV in Canada is not reportable and there is no nationally coordinated SIV surveillance program. Recent CFIA initiatives have made it easier to license influenza vaccines for use in pigs and the hope is that this will stimulate surveillance activity. Swine triple reassortant H3N2 and A(H1N1)pdm09 reassortant viruses have been identified in Quebec pigs, Ontario turkey, and Nova Scotia mink.

The PROCINORTE workshop on influenza A virus molecular diagnostic techniques (Winnipeg, Canada, 6-9 December 2011) is focused on the harmonization of diagnostic methods with an emphasis on sequencing in USA, Canada, and Mexico. The molecular diagnostic techniques have been compared at the bench level. Potential areas for collaboration were identified.

**Brazil – Janice Ciacci Zanella**

SIV is not reportable in Brazil and there is no national coordinated surveillance plan. However a grant in 2009 to undertake surveillance for porcine reproductive and respiratory syndrome virus (PRRS), pseudorabies virus and SIV led to increasing levels of surveillance with sampling in 106 farms covering 7 Brazilian states (30 pigs of 60 to 85 days old per farm). Sera and nasal swabs were collected for anti-NP antibodies (IDEXX MultiScreen ELISA) and Flu A PCR, respectively.
To date, out of 646 nasal swabs or lung samples 17.18% were positive for influenza A by RT-PCR. 46 virus isolates were obtained. In 25 viral sequence analyses, 16 showed high identity with A(H1N1)pdm09, 5 were closely related to an American H3N8 equine influenza virus. Four virus isolates, based on the sequence analyses of HA, NA, M, NP, PB1, PB2 and PA genes proved to be a new H1N2 influenza A virus which had not yet been described in Brazil. In addition, the sequence analyses of the new H1N2 virus has proved to be an arrangement where the genes for glycoprotein (H1 and N2) are of human origin (delta cluster) and the internal genes (M, NP, PB1, PB2 and PA) are derivatives of the A(H1N1)pdm09 that has been circulating in pigs in Brazil over the past two years.

60% of farms tested are seropositive for influenza A (influenza vaccines are not used in Brazil). Feral swine have also been tested and some were positive for A(H1N1)pdm09. A study by Rajao et al. in 2012 showed that one state in Brazil has a high prevalence (64.7%) of influenza A and retrospective serology studies showed flu A antibodies prior to 2009 in Brazil but not for A(H1N1)pdm09.

Argentina/South America (SA) – Ariel Pereda

In South America reports about SIV are generally scarce. CEIRS funded surveillance of 14 swine farms across Argentina and found serological profiles with breeding herds serologically positive, weaned pigs possessing maternal antibodies, antibodies waning in late nursery pigs, and rising in finishing pigs. Isolates found in Argentina include a human H3N2 virus adapted to swine, A(H1N1)pdm09 in many farms, and recombination of the A(H1N1)pdm09 with the HA and NA from a Human like δ2 SIV. In Colombia there was evidence of classic H1N1 and A(H1N1)pdm09 circulating in swine populations. Peru has serological AGID positives but no PCR or virus isolation to report. Bolivia, Ecuador, Colombia and Peru have been trained on influenza diagnostic testing but no results are forthcoming yet because other swine diseases that are prevalent get more focus. Future activities include further surveillance, animal studies at University of Maryland on South Argentina influenza isolates, and vaccine development.

China – Hualan Chen

China has 1.4 billion pigs (43% of the world’s production) with many in backyard farms, and in close contact with poultry and humans. There is no systematic surveillance and SIV vaccination in pigs is not implemented.

At least 5,000 samples have been collected from pigs per annually in recent years.

Subtypes detected from 2002 to 2008 included H1N1, H3N2, H9N2, H1N2 and H5N1. H5N1 was found only in 2001 and 2003, and only on 2 occasions. Serological surveillance in 2008 showed 62% of sampled pigs seropositive to H3, 14% to H1, 0.03% to H9, and 0.02% to H5. H9N2 viruses are closely related to strains circulating in poultry. H5N1 viruses isolated from pigs are genetically similar to the viruses isolated from ducks in China, and the H5 of swine have different pathogenicity.

Recent SIV surveillance showed pandemic H1, delta H1, classical H1, and avian-like H1. The avian like H1 has caused a human infection. There are varying H3N2 genotypes in China.

Studies have been carried out to assess the protection conferred by an inactivated H1N1 vaccine against infection with A(H1N1)pdm09, endemic swine H1N1 and H1N2 in pigs, showing cross protection against homologous and heterologous challenge.

In summary, multiple subtypes of SIV have been detected in pigs in China. The co-existence of A(H1N1)pdm09 and other virus subtypes e.g. avian-like H1N1, H9N2 and H5N1 may produce new
reassortants with pandemic potential. Systematic surveillance and analysis of SIVs are now priorities for research in China.

Research has been supported by the Ministry of Agriculture and Ministry of Science and Technology (MOST). A China-EU collaboration project for swine influenza surveillance has been promoted by ESNIP3.

Hong Kong – Malik Peiris

Update on Hong Kong slaughterhouse surveillance. 4 000-5 000 pigs are slaughtered daily in Hong Kong with only 5-20% coming from Hong Kong itself. Increased diversity and co-circulation of multiple SIV lineages has been noticed since 2002. Through surveillance of swine in Hong Kong abattoirs from January 2011 to January 2012, 94 isolates were obtained from 5409 nasal swabs with an isolation rate of 1.7%. Of these, only 29 are wholly A(H1N1)pdm09, the others are all varying reassortments (Fan et al. J. Virol. 2012; 86(4):2375-2378).

A study of H3N2 human reassorted with internal A(H1N1)pdm09 genes showed that more than 40% of humans of all ages have 1:40 antibodies against the H3N2 reassortant. Humans do have cross-reactive antibodies with these swine reassortant viruses (Perera et al. EID 2011; 17:1897-9). Sero-conversion of humans to A(H1N1)pdm09 results in higher and more cross-reactive anti-flu antibodies to other swine H1N1 viruses.

Hong Kong has also evaluated cELISA assays for swine sero-epidemiology against a panel triple reassortant (TRIG), Eurasian avian-like, and classic swine influenza viruses.

Thailand – Sujira Parchariyanon

To estimate the prevalence of SIV in Thailand, a programme of serological surveillance was undertaken between 2010 and 2012. 900 sera samples were collected from pigs in 15 provinces. HI was performed using 3 antigenic types for H1 and two antigenic types for H3. Antibodies to A(H1N1)pdm09 are widely prevalent in pigs in all provinces and dominant compared to those to H3. Older pigs showed a higher rate of sero-positivity. Some farms have used vaccination. Virological analysis will be performed in collaboration with NIAH, Japan during 2011–2015. When positive the pooled nasal swabs were tested by PCR and cultured on MDCK cells. 4 provinces were tested so far and 5 isolates have been obtained in 2011, 9 isolates in 2012, and reassortant H3N2 with A(H1N1)pdm09 in 2011.

Other collaboration studies include human animal interface SIVs infection with the Armed Forces Research Institute of Medical Sciences (AFRIMS) (2012-2014), SIVs surveillance in Nan province (2010 – 2011) and FAO funded projects with one completed and one in progress.

Japan, Thailand and Viet Nam – Sujira Parchariyanon (on behalf of Dr Saito)

The following results were obtained through collaborative activities led by National Institute of Animal Health (NIAH), Japan.

In Japan in 2010-2012, H1N2 subtypes (classical H1/Human like N2) were isolated from sows and fattening diseased pigs from the municipal animal hygiene service center. In 2011 A(H1N1)pdm09 and H3N2 triple reassortant viruses were isolated from imported pigs at a quarantine station.

In Thailand, A(H1N1)pdm09 and reassortant virus H3N2/A(H1N1)pdm09 were isolated in 2011-2012.
In Viet Nam, from northern region 9 isolates of H1N1 and from southern region 15 isolates of H1N1, 16 isolates of H1N2 and 20 isolates of H3N2 were detected.

**Viet Nam – Nguyen Tung**

In cooperation with Japan, serological and virological surveillance was undertaken in Viet Nam during 2009 – 2011. Serological studies, by HI, in slaughter houses showed antibodies positive for H3 and H1, and negative for H5.

Virological surveillance of swabs taken on farm and in slaughter houses reported A(H1N1)pdm09, H3N2 and H1N2. H3N2 and H1N2 viruses were reassortants between human seasonal influenza viruses and triple reassortant virus. Earlier serological studies conducted in 2009 using IDEXX ELISA kit (Influenza A) showed seropositivity across all ages.

Upcoming studies include SIV surveillance as part of the FAO EPT+ project, which also includes full genomic characterization of viruses, linking molecular information with agro ecological information to identify hot spots of disease transmission, and better understanding of the viral evolution at the human-animal interface.

**Australia and Asia-Pacific – Frank Wong**

*Australia*: SIV is considered exotic in Australia and is reportable to the national animal health agencies. Three outbreaks of A(H1N1)pdm09 in commercial piggeries were reported in 2009 (New South Wales, Victoria, Queensland) during the peak of human infections in Australia at that time, and one confirmed case was investigated in 2011 (Western Australia) indicating more recent incidence of the virus in Australian pigs. A(H1N1)pdm09 detected in commercial pigs in 2009 represented the first ever report of influenza in Australian swine. Phylogenetic analysis showed that the A(H1N1)pdm09 viruses from the separate cases were distinguishable, with closest identity to viruses circulating in the human population in the same region. Evidence suggests these were separate human to pig spill over transmissions and no reassortment with non-pandemic influenza A viruses have been found to date. With the exception of A(H1N1)pdm09, Australia is still considered to be free from SIV and there is no support for active surveillance.

Most information from South East Asia comes from Viet Nam and Thailand with SIV surveillance and information largely non-existent from other countries in the region. Recent HI screening of more than 1000 sera samples in Indonesian commercial pigs showed highest prevalence of H3N2 (61%) followed by 15% to Thai 2000 Eurasian H1, 11% to classical H1, 0.4% to A(H1N1)pdm09, 0% to H9 and H5.

**Discussion**

Weak to strong cross-reactivity occurs in serologic analysis of SIVs and caution must be applied when interpreting SIV serological results so as to avoid making assumptions or incorrect conclusions. Pig anti-sera against influenza A viruses in general (especially pigs that are exposed naturally to several viruses) are broadly cross-reactive. Moreover, this has been further complicated following the introduction of A(H1N1)pdm09 to pig populations. A sensitive assay such as NP ELISA that will detect multiple antigenic types versus HI should be considered for serological surveillance.

In South Asia – Thailand, Viet Nam, Japan, and China – some questions were raised as to how related or different the lineages of H1 and H3 are between and among these countries. Thailand viruses may appear to be unique; however pigs are exported from Thailand to Cambodia and Viet Nam, so there
is potential for sharing of viruses. Studies on networks of pig movements in South Asia might be helpful to better understand the relationships and complicated make-up of the viruses in these regions.

**FAO contribution – Filip Claes**

FAO has Technical Cooperation Projects (TCP), field offices, active scientific networks, and partnerships with national governments (National Veterinary Services which includes national labs and epidemiological units). The Emerging Pandemic Threat Plus (EPT+) program (2012-2013), funded by USAID, focuses on understanding the role of livestock as a potential reservoir for pandemic disease threats initially focused on influenza. Within this project active swine surveillance is planned in 4 countries: Viet Nam, Bangladesh, P.R. China, and Thailand. FAO developed an EPT+ sampling protocol and circulated it for comments by the SIV group.

Through a global TCP on A(H1N1)pdm09, serological and virological surveillance was conducted in 2010-2011 with regional participation in South East Asia, Caribbean and Latin America.

Preliminary results for the South East Asia showed seroprevalence rates of 7%, 61%, and 65% in Lao PDR, the Philippines, and Viet Nam respectively. Samples sizes were 2019 for Lao, 920 for Philippines and 165 for Viet Nam. No PCR positives were found and no viruses were isolated during this TCP.

FAO tools that might be useful to the SIV group activities are:

- EMPRES-i Global animal disease information system that includes disease tracking, analysis models, surveillance models and genetics models
- GLIPHA – Global Livestock production and health atlas (agro-ecological data, population data, production data, updated maps)
- Risk Modeling and Risk Assessment

OFFLU SIV group expertise is needed to help with harmonization of approaches, addressing capacity needs, optimizing surveillance approach and contribution to risk modeling. To assist in the EPT+ project a series of questions in the areas of sample type, optimal age of pigs for sampling, virus culture, virus typing, serosurveillance and participation in risk modeling was put forward to the group members.

FAO suggested a revised SIV group model, an open network free to expand, overall management by OFFLU executive committee, split the group into several technical activities by expertise e.g. diagnosis, surveillance, risk modeling (analogous to avian Flu model). OIE added that it understood OFFLU to be one network encompassing all animal influenza expertise, including equine, swine and avian, the SIV group being one technical group with defined objectives working within this network.

**WHO global update and SIV Surveillance data contribution to VCM, specifically, “Public health risks from influenza viruses circulating in swine.” – Liz Mumford**

The global incidence of human infections and the overall threat to public health from these viruses is not clear but it is apparent that there are an increasing number of reported human cases of variant (v) influenza in humans. The WHO International Health Regulations (IHR) requires that member states report human cases of influenza with pandemic potential, that is if the virus has demonstrated the capacity to infect a human and the HA gene is not a variation of those in influenza viruses circulating widely in the human population. Human infections with influenza viruses also found in pig populations – including H1N1, H1N2, and H3N2 subtypes of several lineages – have been reported between January 2011 and March 2012 from several continents, with the USA
reporting most of the cases worldwide. Most of these cases reported contact with pigs, and most are clinically mild. No human deaths have been reported.

WHO conducts routine public health risk assessment for influenza at the human-animal interface. However, there is not a full understanding of the determinants of risk and baseline surveillance data is sparse. More epidemiological, clinical and virological information is needed from animal health, public health and at the interface.

Nominations for Sub-Committee to draft Terms of Reference

The SIV group nominated a Sub-committee comprising Drs Van Reeth, Vincent, Pasick, Brown, Webby, Peiris and Lewis to gather on the morning of the second day to draft terms of reference for the SIV group, which would then be presented to the larger group for discussion, further comments, and their endorsement.

REPORTS ON THE PROGRESS OF ACTION ITEMS FROM 2011 MEETING

As an OFFLU Technical Activity, the SIV Group brings together the world’s leading SIV experts. The group has consolidated global SIV data and shares this with the wider scientific community through the OFFLU annual meetings and the OFFLU website. A global SIV review article, which is currently in draft, will be an important deliverable for the OFFLU SIV group in providing a clear picture of global SIV situation.

The OFFLU SIV group can be rapidly mobilized in response to emerging influenza events in animals or at the human-animal interface. The group was actively engaged by WHO, FAO, and OIE following detection of the variant H3N2 in 2011 in humans, shared data and provided technical advice for public health risk assessments. In addition to this, experts have been promoting the group at international scientific conferences.

Experts have also been working on the following specific action items:

Publication of lists of viruses and diagnostic tests by region – Marie Gramer

A list of diagnostic assays and viruses by region will be made public when completed. This guidance document will provide a basis for improving SIV diagnosis and detection. The draft document was presented to the group. The whole group will comment on this. The document can serve as a virtual depository for gene sequences. Once posted online it would be useful for experts to run these tests or analyze these sequences, to decide what viruses to use or which virus genes to compare.

Harmonization of laboratory protocols for influenza in pigs – Ian Brown

Harmonization is needed for the surveillance programs and designs, sampling, pooling, test algorithms, test type (serology, virus isolation), test specification (regional relevance), and test quality assurance (ring trials, accreditation). This action item will refocus on specific testing algorithms combined with assays available. The current algorithm on the OFFLU website needs to be revised.
Publication of OFFLU SIV group statement – Ruben Donis

The OFFLU SIV group statement includes the following points and introduces OFFLU SIV group activities and goals.

- **Problem:**
  i. SIV (and cross-species viruses) circulating in swine
     1) Causing mortality/morbidity in swine and
     2) People – besides other societal and economic impacts (pandemics)
  ii. Lack of global coordination is a major problem
  iii. Goals of the group: reduce global burden of subclinical and clinical infections (morbidity and mortality) in pigs.

- **Approach:**
  i. Advocacy
  ii. Global surveillance: epidemiology, virological, collection, sharing
  iii. Provide information to support evidence-based interventions
  iv. Outcomes assessment

- **Expected results:**
  i. Reduce the impact of SIV for all species worldwide.

Preparation of SIV Surveillance Funding proposal – Kristien Van Reeth

It would be difficult for the OFFLU SIV group to apply for specific research funding. In hindsight, this action item may be premature and a bit overambitious. The OFFLU SIV Group meeting was envisioned to be something small and sustainable allowing the experts to come together, share data and make recommendations, in a somewhat similar way as the equine influenza surveillance group, which doesn’t have dedicated funding. The OFFLU SIV group should establish its credibility by achieving clearly stated and simple objectives with impact. This cannot be done individually but requires the group effort and expert time and data put together. An important deliverable has already been achieved – the sharing, presenting, and commenting on data. It is also important that funding for next years’ group meetings is available from NIH CEIRS (R. Webby).

Global SIV review paper – Amy Vincent

A draft manuscript has been circulated, many group members have provided input and the draft is coming together nicely. The content is captured in the review paper itself. The journal to which the review will be submitted needs further discussion. It was proposed that the authorship of this paper is the OFFLU SIV group and the acknowledgements or the supplementary information will list all the individual members of the group.

DAY 2

Subcommittee Report on the Terms of Reference

The OFFLU SIV group is a technical activity under the umbrella of OFFLU. The terms of reference (TOR) were drafted prior to the start of the general meeting of the 2nd day by a small group of experts. The TOR were presented, edited, and accepted by all the group members. The ToRs will be presented to the OFFLU EC and SC for approval.

**Mission statement:**

The OFFLU SIV Group objectives are to:
- Provide expert opinion and technical advice to international organisations and other relevant stakeholders
- Gather, exchange, and disseminate global knowledge of SIV and keep under continuous review
- Identify and define gaps in knowledge in surveillance and research
- Evaluate and communicate information regarding viruses posing potential risk to veterinary and public health

To achieve these objectives the OFFLU SIV Group will conduct activities at the request of the OFFLU Steering committee or on its own initiative.

The activities are to:
- Proactively gather, interpret and exchange data on SIV relevant to diagnosis, surveillance and control
- Recommend appropriate diagnostic testing algorithms and assays relevant to diagnosis and control of SIV
- Identify and share reference reagents
- Advocate approaches, and identify resources required to address the gaps in knowledge
- Foster and facilitate collaborations to address objectives and activities
- Disseminate the information generated from the activities through the Offlu website, Offlu technical meeting, publications, and other appropriate fora
- Formally meet once per year to define and review the activities
- Report meeting minutes to the Executive and Steering Committees and post a final report on the OFFLU website
- Convene ad hoc teleconferences as needed to share updates and facilitate continued progress on activities or respond to emerging needs or requests

Group Discussion on the future of the OFFLU SIV Group

Regarding Structure:

Questions were raised about the membership of the OFFLU SIV group. Members of the SIV group expressed that the OFFLU SIV group as a small group is in general more efficient at getting work done, and the funding of such is easier to achieve and the activity is therefore sustainable. Furthermore, the experts participating in the OFFLU SIV group have their own, separate funding that allows them to perform SIV activities in their home or core regions and then bring the results to the OFFLU SIV Group to share. A similar example is the OIE Equine Surveillance Panel – a small group working with limited resources (no dedicated funds) that provides recommendations for strain selection for equine influenza vaccines based on a review of existing global equine influenza surveillance data.

Involvement in temporary or short term SIV research or surveillance conducted in a region does not automatically make that expert suitable for the OFFLU SIV Group. Providing expert opinion is still the core requirement of any member of the SIV core Group. FAO reminded that some recognised SIV experts are not members of the SIV group (e.g. ANSES, FLI, IZSVe); moreover some of them are experts of FAO Reference Centres in animal
influenza. However the coordinator or leader of a regional surveillance network (such as ESNIP) would represent that network and the experts in the network.

The core SIV Group will stay small and will comprise of SIV experts with substantive surveillance data to share and a significant track records covering years of experience.

Establishment of ad hoc membership is foreseen. This membership would seek to improve SIV surveillance globally. A definition or set of criteria may be needed to define suitability of members attending on an ad hoc basis, including that they are involved in SIV activities, have expertise to contribute, and have SIV data to share.

Regarding rotation of the Chairs or Co-Chairs of the SIV Working Group

The proposed structure is that the group has a Chairperson and Deputy Chairperson and that the term of the Chairperson is one time unit and the term of the Deputy Chair is two time units with the Deputy Chairperson moving into the Chairperson position to allow for continuity.

The roles and responsibilities of the Chairperson and Deputy Chairperson are to drive activities, to work with the OFFLU Secretariat to set the agenda of any meetings or teleconferences in coordination with FAO and OIE OFFLU FPs, to be the point of contact for OFFLU SIV Group, to facilitate communication to the OFFLU Secretariat of the SIV group accomplishments.

It is to be reminded that nomination mechanisms of OFFLU Technical Activities were previously defined by the OFFLU SC. Therefore, this proposal for appointment of the SIV group chair should be reviewed and endorsed by the OFFLU SC. The OFFLU secretariat will circulate the technical activity governance document to the group, once approved by the OFFLU SC.

Funding for OFFLU SIV Group Meetings

Support from Dr Richard Webby and NIH Center for Excellence is available for the next couple of years. Participants from Thailand and Viet Nam were sponsored by FAO this year.

Define Activities and Outcomes of the 2012 Meeting

1. Define one year work plan, including working group activity leaders for action items/outcome

   1. Publication of lists of viruses and diagnostic tests, and testing algorithms by region: Marie, Malik, Sabrina, Janice, Ariel, Ian, Sabrina, Richard, Takehiko, Sujira, Frank – by June 15
   2. Write and publish SIV Group publication of network’s statement: Ruben, Ian, Liz, John - by May 15
   3. Publish a paper on SIV Review and OFFLU activities surveillance: Amy, Marie, Kristien, Filip
      a. Group feedback on current draft by April 15
      b. Recirculate an updated draft by May 15
      c. Group feedback on updated draft by June 1
      d. Submission by July 15
   4. Review technical documents on SIV Surveillance and Diagnostics (Gwen, Ruben, Ariel, Frank)
      a. FAO EPT+ Sampling Protocol, for example, comment by April 15, Finalize May 1
   5. Update group advocacy slide and make poster (Janice, Amy, Nicola, Gwen, Kristien) May 1
      a. REPORT USE OF SLIDES OR POSTER TO SECRETARIAT
Present at IPVS 2012 (Janice and Kristien), June 2012
Present at ISIRV Neglect Flu Meeting (Nicola, Marie, Ariel) March 2013
Present at Australasia Virology Meeting (Frank)

6. Write a one page concept note for funding to maintain group (Richard, Liz, Keith) May 1
7. Update research priorities for SIV (Kristien, Amy, Ruben, John, Hualan) May 15
8. Define and develop a minimum reference panel of sera for global SIV (Ian, Kristien, Sabrina, Hualan) Sept 1
9. Global antigenic cartography (Nicola) Sept 1

2. Planning of next meeting:

Venue: FAO, Rome, Italy
Year: 2013
Date: To be decided by e-mail by circulating proposed dates to the group members
Participants (L to R):

Front row: Janice Ciacci Zanella (Brazil), Sabrina Swenson (USA), Amy Vincent (USA), Nicola Lewis (UK), Sujira Parchariyanon (Thailand), Nguyen Tung (Vietnam)

Second row: Keith Hamilton (OIE), Hualan Chen (China), Gounalan Pavade (OIE), Frank Wong (Australia), Richard Webby (USA)

Third row: Filip Claes (FAO), John Pasick (Canada), Ariel Pereda (Argentina)

Fourth row: Ian Brown (UK), Gwenaelle Dauphin (FAO), Ruben Donis (USA)

Fifth row: Kristien Van Reeth (Belgium), Marie Gramer (USA)

Not in picture: Liz Mumford (WHO), Malik Peiris (Hong Kong)