



Food and Agriculture
Organization of the
United Nations

Meeting report
Regional avian influenza in Asia
30 November – 3 December 2021
Virtual meeting



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Abbreviations and acronyms

AIV	Avian influenza virus
AU-PANVAC	Pan African Veterinary Vaccine Centre
COVID-19	Coronavirus disease 2019
DIC	Disease Investigation Center (Indonesia)
ECTAD	Emergency Centres for Transboundary Animal Disease
EFSA	European Food Safety Agency
EMA	European Medicines Agency
FAO	Food and Agriculture Organisation of the United Nations
GF-TADs	Global Framework for the Progressive Control of Transboundary Animal Diseases
GISRS	Global Influenza Surveillance and Response System
HA	Hemagglutinin
HI	Hemagglutinin inhibition
HPAI	Highly pathogenic avian influenza
ILI	Influenza-like illness
IPC	Institut Pasteur du Cambodge
JHU	John Hopkins University
LBM	Live bird market
LFT	Lateral Flow Test
LISN	Longitudinal Influenza Surveillance Network
LMIC	Low and middle-income countries
LPAI	Low pathogenic avian influenza
OFFLU	OIE/FAO Network of Expertise on Animal Influenza
OIE	World Organisation for Animal Health
ONT	Oxford Nanopore Technology
PCR	Polymerase chain reaction
RAP	Regional Office for Asia and the Pacific
ROK	Republic of Korea

RT-PCR	Real time PCR
SARI	Severe acute respiratory infections
SARS-CoV-2	Severe acute respiratory syndrome coronavirus 2
SOP	Standard operating procedures
US CDC	United States Centers for Disease control and Prevention
USD	United States dollars
VAHIS	Viet Nam Animal Health Information System
VCM	Vaccine composition meeting
WHO	World Health Organisation

Executive summary

Between 2020 and 2021, detection of avian influenza viruses (AIV) has increased as they spread around the globe. During the COVID-19 pandemic, outbreaks and human infections caused by AIV (notably H9N2 and H5Nx 2.3.4.4 subclades) have increased ten-fold compared to 2019 detections. Highly pathogenic avian influenza (HPAI) H5N1 continues to circulate globally and recently H5N5 viruses were identified in Europe and Asia, while H5N6 has been found in China and Southeast Asia since early 2014. Specifically H5 subclade 2.3.4.4b is involved in numerous outbreaks throughout Europe, Asia and, more recently, Africa and North America, becoming the predominant H5 clade circulating globally.

The impact of both HPAI and low pathogenic avian influenza (LPAI) viruses on global poultry production can be devastating, especially when new AIV subtypes are introduced into naïve populations. In addition, the zoonotic potential of H5 HPAI clade 2.3.4.4b viruses has been demonstrated, as seen with influenza A(H5N8) human infections in the Russian Federation, and contributed to the rise of human cases caused by influenza A(H5N6) in China.

In light of this evolving situation, there is a need to maintain and improve AIV surveillance in Asia. It is vital to move away from responding reactively and to increase the focus on proactive prevention and control using inter-sectoral approaches. It is critical to connect and align efforts to generate an “early warning” system linking national, regional and global levels to improve communication and data sharing before the next outbreak occurs. In addition, global availability of genomic data and viral isolates is essential for vaccination programs in both humans and animals, and for development/revision of critical diagnostics

To address these challenges, the Food and Agriculture Organisation of the United Nations (FAO) Regional Office for Asia and the Pacific (RAP) conducted a virtual consultation between 30 November and 3 December 2021 to review knowledge and gaps related to AIV surveillance in Asia, and propose novel ways forward for detection, surveillance, and response.

The objectives of this regional consultation were to discuss and agree on the following:

- Update current information on prevalence, genotypic, and antigenic characteristics of AIV in Asia
- Discuss AIV surveillance activities, including lessons learned from previous surveillance and the current COVID-19 response, which can support AIV early warning
- Determine major gaps and needs of AIV surveillance, and how they can be addressed
- Discuss novel technologies and sampling strategies for improved surveillance
- Explore possible utilisation of AIV surveillance data, including the coordinated animal sector AIV Vaccine Composition discussion/forum

Due to the ongoing COVID-19 pandemic situation, it was decided to conduct this consultation through online platforms, and thus the meeting was divided into five sessions from 30 November to 3 December. A total of 61 participants attended at least one session, with an average of 44 participants per session (Annex 3). Attendees included many experts in the field of avian influenza from international organisations, research institutions, reference laboratories, country veterinary services and more.

The consultation was divided into five major sessions, addressing specific aspects of AIV surveillance and early warning.

Session 1 (“Introduction and setting the scene”) on 30 November 2021 introduced the consultation’s objectives and provided participants with a summary of the current AIV situation at a global level in both human and animal populations, with presentations from FAO and the World Health Organization (WHO).

This was directly followed by **Session 2** (“What do we need for inter-regional collaboration and early warning?”), which started with a presentation from the OIE/FAO Network of Expertise on Animal Influenza (OFFLU) about the challenges with AIV genetic diversity, evolution and their impact on vaccine composition. Representatives from Erasmus, Human Link and Harbin Veterinary Research Institute presented on the AIV situation in Europe, Middle East and Asia, respectively. The rest of the session was devoted to discussing the data needs for better inter-regional collaboration, to track emerging subclades, and assess their pandemic potential along with vaccine efficacy.

On 1 December 2021, **Session 3** (“What are we doing, and what are we missing?”) started with a presentation of regional AIV surveillance methodologies used by FAO’s Emergency Centres for Transboundary Animal Disease (ECTAD) in Asia. Experiences in AIV surveillance at the from Indonesia, Viet Nam and Cambodia, were then shared by the Indonesian Disease Investigation Center (DIC) in Wates, FAO ECTAD Viet Nam, and Institut Pasteur du Cambodge (IPC), respectively. Afterwards, a discussion with participants highlighted the important aspects of early warning at both country and global levels, as well as ways to facilitate rapid sharing of sequences between the levels.

Session 4 (“Novel ways to look for and improve understanding of AIVs”) was held on 2 December 2021 and focused on new ways to sample, diagnose and analyse test results, leading to a better understanding of AIV epidemiology. This included the use of alternative sample types for AIV surveillance conducted by IPC in Cambodia, advanced viral genome sequencing with John Hopkins University’s Applied Physics Laboratory, and sharing the example of the Nextstrain tool for tracking AIV evolution and transmission by the Nextstrain Initiative. A facilitated discussion then further identified novel surveillance methods. The group also addressed feasibility for implementing these resources in the Asian context, including sustainability, cost, training needs, and how they can support rapid data sharing for better early warning mechanisms.

Lastly, **Session 5** (“Utilisation of AIV surveillance data to improve responses”) occurred on 3 December 2021 and was the opportunity to brainstorm with participants on the “ideal early warning framework”. Based on the discussions during the previous sessions, a proposed early warning framework was presented that brings together the roles of each levels (national, regional, international), major players, available resources and gaps to address. Participants had the opportunity to reflect on this proposed framework and provide feedback. The second part of the session was dedicated to discussing the possibility of a dedicated animal influenza vaccine composition meeting (VCM) to provide global guidance on influenza vaccine utilisation. The group touched on aspects of feasibility, funding and the role of different stakeholders including the private sector.

The session ended with concluding thoughts reflecting on the entire meeting, and provided with next steps to keep the momentum going.

Specifically, the meeting noted:

- 1) Participants acknowledge surveillance efforts at country level should meet country needs and identified areas that may improve contribution of country surveillance information for regional and global public good, such as the use of novel technologies for diagnostics and bioinformatics.
- 2) Participants identify ongoing challenges related to sharing sample data and other relevant information including potential negative impacts on livelihoods following detection. As such, they recommend support for establishing enabling environments and policies for timely and open data sharing without stigmatization and ensuring equitable benefits for all parties involved.
- 3) Novel approaches and technologies can help improve timeliness, efficacy and cost-effectiveness of surveillance. Participants agree to contribute to efforts for an enhanced regional and global early warning system through:
 - a. Developing and supporting application of tools and methodologies to improve surveillance, risk assessment, genetic data analysis and interpretation for policy and decision making, and
 - b. Strengthening country capacity to utilize appropriate tools and technologies that fit for purpose.
- 4) Participants recognize the need to reinforce and operationalise international early warning networks (linking with OFFLU) for AI, aligned with the human health system (e.g. WHO's Global Influenza Surveillance and Response System [GISRS] network, and other systems in other sectors).
- 5) Participants support establishing a global platform to advise on vaccine composition for animal influenza vaccines, similar to the human influenza VCM led by WHO.

The following action items arose from the meeting:

- 1) Developing an action plan to progress early warning system framework, in consultation with member states
- 2) Developing a concept note for potential donors of a poultry AI VCM for a possible initial two-year pilot project
- 3) Gathering information about vaccines produced by the private sector to gauge their level of interest for participation in VCM
- 4) Developing costing structures to present to potential donors for the VCM

Background and objectives

Unlike the dearth of human seasonal influenza detections during the last two years, detection of AIVs is continuing as they circulate around the globe. Indeed, during the COVID-19 pandemic, outbreaks and human infections with avian-origin influenza A viruses have increased ten-fold compared to 2019, notably involving H5Nx HPAI viruses of clade 2.3.4.4b and low pathogenic AI H9N2 virus subtype.¹ H5Nx HPAI viruses have steadily diversified into multiple clades since 2008 leading to antigenically and genetically distinct virus strains. Since early 2020, outbreaks caused by H5Nx HPAI viruses were reported across various continents, and the subclade 2.3.4.4b has become the most predominant worldwide. An unprecedented H5 HPAI epizootic caused by closely-related viruses has stricken poultry and wild bird populations across Europe, Asia and, more recently, Africa and North America. In the past two years, H5Nx HPAI subclade 2.3.4.4b viruses have shown important diversification of subtypes in Eurasia with detections of H5N1, H5N2, H5N3, H5N4, and H5N5 virus subtypes. H5N1 HPAI has now become the predominant subtype circulating in Eurasia, Africa, and North America replacing H5N8. H5N5 viruses were also identified throughout the year in Europe and Asia, while H5N6 was detected in China and Southeast Asia since early 2014. In addition to HPAI H5Nx viruses, endemic LPAI H9N2 viruses continue to circulate throughout the world and are a major concern for the poultry industry. Besides poultry and wild bird outbreaks, numerous zoonotic infections have been detected in humans in the past few years, involving H7N4, H9N2, H10N3 LPAI viruses, and, most concerning, H5N8 and H5N6 HPAI viruses of subclade 2.3.4.4b.

This challenging situation showcases the need to maintain and improve AIV surveillance at all levels. Currently, numerous stakeholders and countries conduct surveillance, response, and prevention activities on an ad-hoc basis. It is vital to move away from responding reactively and to increase the focus on proactive prevention and control using inter-sectoral approaches. In the near future, aligning efforts to generate an “early warning” system will be crucial, especially around communication and data sharing prior to the next outbreak. In addition, global availability of genomic data and viral isolates is essential for vaccination programs in both humans and animals, and for development/revision of critical diagnostics. Although the COVID-19 pandemic has ravaged the public health and economic sectors, it has brought about a renaissance in laboratory capacity and highlighted the need for coordinated, connected networks that can quickly identify and respond to endemic and emerging pathogens. Following the strengthening of the human seasonal influenza programme, it is important to also bolster and refine the global avian influenza network, starting with the Asia-Pacific region, as it has traditionally been the epicentre for AIV emergence and spread.

To address these challenges, FAO RAP conducted a virtual consultation between 30 November and 3 December 2021 to review knowledge and gaps related to AIV surveillance in Asia, and propose novel ways forward for detection, surveillance, and response.

The objectives of this regional consultation were to:

1. Update current information on prevalence, genotypic, and antigenic aspects of AIV in Asia

¹ <https://empres-i.apps.fao.org/>

2. Discuss AIV surveillance activities, including lessons learned from previous surveillance and the current COVID-19 response, which can support AIV early warning
3. Determine major gaps and needs of AIV surveillance, and how they can be addressed
4. Discuss novel technologies (i.e.: multiplex polymerase chain reaction [PCR], point-of-care testing, next generation sequencing) and sampling strategies (environmental, pooling) for improved surveillance
5. Explore possible utilisation of AIV surveillance data, including the coordinated animal sector AIV Vaccine Composition discussion/forum

Session 1 – Introduction and setting the scene (30 Nov 2021)

The first session of the series consisted of a brief opening by the Regional ECTAD RAP Coordinator. This was followed by presentations from representatives FAO and WHO providing background on AIV issues related to animals and public health, respectively.

1.1. Kachen Wongsathapornchai (FAO ECTAD RAP Regional Coordinator) – Introduction

Kachen welcomed all participants, introduced the avian influenza (AI) situation and outlined the structure of the AI consultation and its objectives. The expected results of the consultation included a meeting summary, an agreed way forward on priority areas, and agreed ways forward to ensure sharing of information between animal and human sectors.

1.2. Sophie VonDobschuetz (FAO Animal Health Global Surveillance Coordinator) – Presentation: Global overview of avian influenza situation in animals

Sophie delivered a global overview of AI in animals, including the role of wild bird migratory routes in global spread of the virus, and describing avian influenza events globally since October 2020.

1.3. Katelijjn Vandemaele (WHO Global Influenza Programme) – Presentation: Global update on human infections with AIV – challenges and gaps

Katelijn provided insight on the occurrence of human cases of avian influenza globally. Influenza A(H5N6) is most on the radar at the moment, with a recent rise in human cases in China, and Lao PDR.

Session 2 – What do we need for inter-regional collaboration and early warning? (30 Nov 2021)

Session 2 immediately followed the previous session, and provided more insight on genetic diversity and evolution of AIVs, as well as the situation in specific parts of the world, including Europe, the Middle East,

and Asia. The presentations led to a facilitated discussion with participants to jointly identify needs for regional collaboration to better track and assess emerging AIV subclades and efficacy of vaccines.

2.1. Ian Brown & Nicola Lewis (OFFLU) – Presentation: Challenges with genetic diversity, evolution, vaccine composition

In a presentation prepared by Nicola, Ian described tracking of genetic diversity in influenza A viruses over many years, which are constantly evolving towards increased host fitness, and the ability to survive and multiply in poultry. He noted the limited information regarding host diversity at the wild bird-poultry interface. There is a need to assess risk more effectively, to look at what is circulating enzootically, and to conduct surveillance more intelligently for better control of AIVs.

2.2. Ron Fouchier (Erasmusus) – Presentation: Active influenza surveillance in Europe - Early warning approaches

Europe has faced several H5Nx HPAI outbreaks over the last decade. Since 2014, clade 2.3.4.4 appeared, possibly coming from Asia, and was introduced into Europe, and North America. Integrating analyses of birds' migratory routes and ecology is essential, and a project from the European Food Safety Agency (EFSA) is identifying sites across bird migratory routes of birds for risk-based early warning and surveillance. The project identified viruses isolated in the Russian Federation that spread to Europe over the last few years. While Europe invested in passive surveillance in wild bird and poultry populations, there is also the need to conduct active surveillance in wild birds to understand which species are key virus carriers and play a significant role in AIV transmission.

2.3. Ghazi Kayali (Human Link) – Presentation: Avian influenza in Eastern Mediterranean Region

Ghazi presented on the AI situation in the Middle East and North Africa regions. Some AIVs are enzootic and continue to represent a threat to both humans and animals, including G1-like H9N2 viruses. Reporting of AIV outbreaks has decreased in the past four years, however this is from areas that are often prone to armed conflicts and political unrest, so capacity for detection and sequencing is limited. This is a major challenge, as the region plays an important role in epidemiology of AI. The situation in the region is dynamic, with multiple introductions of HPAI, reassortment events, and establishment in local poultry. Some challenges noted during the presentation included: underreporting of AI in the region (especially important for LPAI), poor policies for poultry vaccination.

2.4. Hualan Chen (Harbin Veterinary Research Institute) – Presentation: H5 avian influenza situation in Asia and the control strategy in China

Hualan presented the H5 AI situation in Asia and control strategies in China. Last year the country detected H5N8 virus and the government started monitoring the situation. Clade 2.3.4.4b was not seen in China in poultry for several years, and many samples were taken from poultry as well as 300 samples from wild birds – H5N8 was found in wild birds. Control strategies in China include using compulsory vaccination against H5 and H7, where 72.5 percent of poultry farms are vaccinated, though nearly half of ducks and geese are not vaccinated. The country has successfully eliminated human infection with A(H7N9) due to

poultry vaccination. This led to reduced prevalence of the virus in poultry, with only three cases seen in the last four years. Hualan acknowledged that sharing information is important and emphasized that using vaccination to stop birds being infected is recommended, along with strong surveillance systems.

2.5. Discussion: What data are needed for inter-regional collaboration, better track emerging subclades, and assess their zoonotic potential and efficacy of vaccines?

Moderated by Erik Karlsson from IPC

The participants discussed several needs to enhance international collaboration on AIVs. Amongst them included:

- Better alignment of surveillance studies in human, poultry and wild birds;
- Rapid data sharing, especially sequence data – which is crucial to link AIV events together and identify adaptation markers. This is particularly important for countries that do not vaccinate in order to enable early depopulation in risk areas; and
- Increased data collection and sharing around human/mammalian cases to identify and address risk factors – this requires early detection and reporting.

Several comments were made regarding the impact of vaccination strategies on AIVs outbreaks. Specifically, it was noted that there are challenges similar to those of COVID-19 in terms of access to vaccines. AI vaccines are only produced in limited countries, which impacts implementation of poultry vaccination at a larger scale. Recommendations on poultry vaccination strategies² were published by OFFLU to support countries in implementing vaccine programmes. Some country experiences with vaccination were discussed:

- China produce and sells vaccines to other countries (e.g. Egypt). A key component of the country's vaccination strategy is collaboration between private manufacturers and reference centres for quality control.
- Indonesia conducts vaccine matching to ensure effectiveness against circulating AIV strains and the country does not import additional vaccines from abroad. No significant AIV outbreak are noted since 2017. H9N2 and H5N1 subtypes are commonly detected in the country.

Lastly, the topic of a global AIV surveillance system was discussed. An important aspect of this concept is rapid sharing of virus sequences between different experts at the international level. Participants highlighted some barriers to this information sharing. For example, laboratories may be less willing to share sequences prior to publication in scientific journals, which can take some time – though it was noted that this process is easier with reference laboratories. A proposed solution was to collaborations with scientific journals so that sharing pertinent virus information for early warning purposes would not affect publication. Signing an acknowledgement of data confidentiality/restriction to access GISAID database can also facilitate early sequence sharing on the platform.

² https://www.offlu.org/wp-content/uploads/2021/01/OFFLU_Recommendations_Beijing_Dec_2013_final.pdf

Session 3 – What are we doing, and what are we missing? (1 Dec 2021)

Session 3 focused on surveillance for AI and examining different methodologies, through a panel of presentation, followed by a discussion on the feasibility of multi-sectoral coordinated surveillance.

3.1 Gaël Lamielle (FAO ECTAD RAP Regional Surveillance Coordinator) – Presentation: Overview of regional AI surveillance methodologies

Gaël provided an overview of AI surveillance methodologies in Southeast Asia with a focus on FAO-supported surveillance. The goals for surveillance are to get an improved understanding of the circulating AI subtypes, and to promote capacity-building and country ownership of activities, which is important for sustainability. Gaël outlined the sampling methodologies for each of the countries where AI surveillance is supported by FAO, and described the varying levels of ownership each country takes for their surveillance, noting that COVID-19 slowed activities significantly. FAO will continue promoting country ownership to transition FAO's role from operational to technical support, update AI active surveillance guidance, and support a platform for regional early warning and rumor tracking.

3.2 Hendra Wibawa (Government of Indonesia, Disease Investigation Center Wates) – Presentation: Influenza virus monitoring (IVM) network: an integrated vet. Lab. Network for molecular surveillance on avian influenza

Hendra provided a comprehensive presentation of AI surveillance in Indonesia. Recent reports noted sporadic cases of HPAI H5N1 and LPAI H9N2 in poultry, but no human cases. The last human case reported was in Bali in 2017. Hendra outlined the Influenza Virus Monitoring (IVM) network and testing surveillance samples from the field and the benefits of IVM, including the process for updating vaccine seed strains.

3.3 Pawin Padungtod (FAO ECTAD Viet Nam Country Team Leader) – Presentation: Viet Nam avian influenza surveillance

Pawin acknowledged Viet Nam's Department of Animal Health for transparency and willingness to share information. The objectives for surveillance in the country are threefold: 1) early detection, 2) monitoring circulating viruses, and 3) vaccine matching. In Viet Nam, surveillance of influenza is primarily done at live bird markets (LBMs), and using pen-side PCR surveillance at the border. Longitudinal Influenza Surveillance Network (LISN), established in 2016, tests samples from animal, humans and wildlife collected from the same province during the same years to search for viruses that could lead to a pandemic, including influenza. Viet Nam uses the Viet Nam Animal Health Information System (VAHIS) to collect daily outbreak data for priority animal diseases (African swine fever, foot and mouth disease, lumpy skin disease, AI). The county uses both locally produced and imported AI vaccines. Lastly, Pawin noted that the government of Viet Nam, led by Ministry of Health (MOH), has taken ownership and customized the Joint Risk Assessment (JRA) tool according to Viet Nam legislations.

3.4 Erik Karlsson (IPC, Deputy Head of Virology Unit) – Avian influenza in the time of COVID-19: Stories from Cambodia

Erik described risk-based active surveillance activities that IPC conducts in collaboration with government, FAO and other partners in Cambodia. The aims for surveillance are to determine: 1) virus prevalence in poultry in LBMs, 2) virus diversity (subtypes, clades, co-infections), and 3) areas of high risk and risk of introduction of new subtypes. Erik described factors affecting AIV prevalence, especially how it appears to positively correlate with festival periods. He also noted changes from COVID-19's impact leading to increased biosafety and biosecurity. In 2021, a human case of influenza A(H9N2) was detected in Cambodia, prompting a joint One Health investigation involving the human and animal health sectors and international partners such as the World Organisation for Animal health (OIE), WHO, FAO and United States Centers for Disease control and Prevention (US CDC). Erik reiterated the need to maintain surveillance, share data, and inform widely, including for LPAI as it still poses a risk for zoonotic infections. This requires a One Health approach and novel techniques, focusing on the wild bird-poultry interface, poultry trade practices and movement for early warning.

Expanded longitudinal surveillance in high-risk human populations (e.g. LBM workers) is a critical part of early warning for spillover, influenza-like illness (ILI)/ Severe acute respiratory infections (SARI) through GISRS coupled with high-risk populations like LBM workers (ILI/seroprevalence) ideal.

3.5 Panel discussion: What are important aspects of early warning at the country level and what would be needed at the global level?

Moderated by Gaël Lamielle (FAO RAP)

Panelists: Frank Wong, Ian Brown, Hualan Chen, Yoshihiro Sakoda

The panellists took turn answering the questions posed by the facilitator. Participants were also invited to provide their perspectives. Major topics discussed included:

1) What are important aspects of early warning at the country level?

- a.* Early information sharing can provide a target to anticipate what to look for and what is coming, and inform vaccine choices. Information sharing between animal and human sectors is also important. For example, Viet Nam detects numerous types of viruses continually but there have been no human outbreaks since 2014. Year-round sample collection for monitoring and surveillance for early detection can contribute to outbreak prevention.
- b.* Early warning activities can identify other routes of introduction (e.g. wild birds rather than poultry movement/trade), which is important to predict potential outbreaks in animal and human populations. Joint Risk Assessment (JRA) in animal and human sector, and coordination between sectors are essential for early warning system to work.
- c.* Early warning would benefit from more targeted, active longitudinal surveillance. Logistics for these activities represent a challenge, FAO-supported activities must be sustainable with countries taking ownership of their surveillance system. Resources are still limited for most laboratories to do sequencing. Working with other international laboratories presents the issue of sharing live samples, which are regarded as a national biological resource.

2) *What would be needed to enhance early warning at the global level?*

- a. Coordinated longitudinal surveillance at wild bird-poultry interface, data availability, timely sharing, and use of data for vaccine efficacy monitoring.
- b. Epidemic intelligence regarding the situation in neighboring countries, in order to predict incursions and protect each other.
- c. It would be useful to understand each country's surveillance structure for context at the international scale. This allows for understanding of risk pathways for global spread in a timely manner, and helps to decide on surveillance and tools required at country-level.
- d. There is a need for a public database platform for the Asia region, countries can be encouraged to share information in parallel of publishing papers.
- e. Disease notification is important, if sequence is available. It is more helpful for countries to perform stamping out, and to develop diagnostic reagents and vaccines.

3) *How do we facilitate rapid data sharing of sequences?*

- a. Reduce perceived risk from early sharing of genomic sequences
 - i. Only publish key reference findings, sharing one genome with a certain context can be sufficient
 - ii. Implement a consortium requiring signed agreement of terms to participate
 - iii. Information-sharing systems should have mechanisms to address political or fear-based barriers, therefore avoiding 'pointing fingers' at a country or region
 - iv. Advocacy about benefits and risks is needed, messaging about negative impacts for national contributors (e.g. trade). OIE could play a role by providing clarity in OIE Terrestrial Code on disease freedom
- b. Incentives for rapid data sharing
 - i. Country governments need to get something back for sharing their data. If frequent sharing is required, frequent feedback (e.g. periodic reports) should be provided.
 - ii. There must be clarity about the purpose of data being shared. For example, this gained traction for VCM because there was a clear purpose for use of data.
 - iii. AIV genetic analysis and AI vaccine monitoring in the region is crucial, particularly for endemic diseases. Vaccinating countries must ensure vaccination effectiveness.
 - iv. For example, St. Jude CEIRR group (Universidad de Chile/Universidad Católica de Chile) in Chile shares sequences ahead of publications and publishes all sequences in GenBank but doesn't receive feedback from international agencies. South America is one of the least sampled areas of the world, so improved data sharing would be beneficial.
- c. Structure/attributes and platform for rapid data sharing
 - i. WHO's sequence database to inform vaccine composition can act as a model for a GISRS for the animal sector.

- ii. Can develop private compartment for immediate sharing of sequences, which are kept up to date, and owned by contributors. This would be better than waiting for an update every 6 months. This can possibility get things going first for early warning, then information can be pushed to open domains as soon as possible.
 - iii. Sharing needs should be streamlined, and creating a platform can enable this (e.g. the antimicrobial resistance data platform)
 - iv. OIE has a pipeline project initiated to update genetic information in timely manner, based on OIE's World Animal Information System (WAHIS). It involves reference laboratories and authorities – need to enable sharing with international scientific community.
 - v. Speed is important. Results should reach people who need them quickly enough to enable response/preventive actions. E.g. producers need to know if the vaccines are still working for recent viruses in a timely manner (days, weeks not months after the emergence and spread of a vaccine-break virus). Countries can routinely apply vaccine efficacy monitoring by simple hemagglutinin inhibition (HI) tests using vaccine anti-serum as soon as viruses are detected.
- d. Participants discussed China's vaccine monitoring and efficacy. It is believed that vaccines slow the rates of reassortment and changes in antigenic variation. Vaccine efficacy is monitored closely with active surveillance of wild birds and domestic poultry and analysis. If viruses differ to a vaccine strain, and the vaccine not completely protective, updating vaccines in use is considered.

Session 4 – Novel ways to look for and improve understanding of AIV (2 Dec 2021)

This session was focused on novel ways that can be used to more efficiently detect AIV, including new tools. An initial panel of presentation provided examples of these resources, followed by a facilitated discussion on implementation of these techniques in the Asian context.

4.1. Erik Karlsson (IPC, Deputy Head of Virology Unit) – Presentation: Getting out of the lab: Field technologies and alternative sample types for AIV surveillance

Erik provided examples using novel technologies in the field in Cambodia. Collecting environmental samples in LBMs and farms can provide insight on range of circulating virus subtypes, levels of contamination, and points of high risk for transmission. Some advantages of the methodologies discussed included: cost-effectiveness, simplicity, rapidity, flexibility, convenience, non-invasiveness. Some disadvantages and gaps included: unknown sensitivity, variable results, loss of species-specific information, inhibition of molecular detection, dependence on surveillance objectives, degradation of samples, and limited standard operating procedures (SOPs)/best practices.

For example, environmental sampling can be improved through use of air samplers, sampling at water filtration/pumps, and use of drones for hard-to-reach places. Pen-side solutions (RT-PCR, rapid diagnostic tests) and dipsticks may be used in an early warning systems to look at real time surveillance in the field.

Next steps include: conducting this work in a more collaborative manner while maintaining realistic cost and sensitivity, conducting further comparative studies, using novel technologies, bringing the laboratory to field, rapid data sharing (e.g. phone apps connecting directly to laboratories).

4.2. Peter Thielen (John Hopkins University [JHU] Applied Physics Laboratory) – Presentation: Advancing Viral Genome Sequencing to Enable Sustainable Surveillance

Peter presented his work with viral genome sequencing. With the COVID-19 response increasing capacity and use of technology, the timelines for generating sequence data have greatly reduced. The aim is shortening these timelines even further so that information is available at the point where it is generated in laboratory samples. Technology has decreased processing time from 33 hours to 7 hours. For genetically complex samples, rapid classification software for real-time influenza characterization can help by allowing classification separated by: influenza type, segment, subtype, host, hemagglutinin (HA) clade, year, and strain. This can act as a data triage step by adding influenza-specific layers of taxonomy.

The team at JHU implements sustainable genomic epidemiology research, and conducts trainings in many countries, including virtual workshops to train people to use this software and conduct sequencing. JHU established Basestack,³ an open software package for operational genomics, purpose-built to enable minimally-trained users to generate and analyse DNA sequencing data. AIV genetic characterization capabilities have quickly advanced, including through enabling and emerging technologies, consideration of sustainable implementation for laboratories (e.g. Indexed AIV RT-PCR, Nanopore sequencing, etc.) and deployable analytics (e.g. Basestack). These platforms are primed for broad deployment of standardized surveillance methods.

4.3. Louise Moncla (Nextstrain Initiative) – Recorded presentation: Nextstrain as a tool kit for tracking avian influenza virus evolution and transmission

Louise pre-recorded a presentation about open-source software Nextstrain. The software can reconstruct disease transmission through the use of phylogenetic trees. Louise demonstrated use of Nextstrain to investigate a case of influenza A(H5N8) in a human poultry farm workers from the Russian Federation. Using sequences from humans and chickens, they could determine if the event was related to wild birds, the route of transmission, and whether there were any human adaptations. Users can visualise real time tracking of influenza virus evolution, identify a cluster for the specific isolate, visualise reassortments, view evidence of zoonotic transmission, onward transmission, and human-adapted mutations, allowing a story to be reconstructed about what happened.

4.4. Discussion: How can we use these technologies to improve early warning in the region? How can we adapt these technologies to country contexts?

³ <https://github.com/jhuapl-bio/Basestack>

Moderated by Filip Claes (FAO ECTAD Regional Laboratory Coordinator)

Participants provided feedback along the following topics:

- 1) Environmental sampling:
 - a. In Chile, Cox1 gene-barcoding is used for wild host species identification using two different sets of nested primers and comparing results in both BLAST and BOLD (<https://www.boldsystems.org/>). After running over 120 barcodes in the last couple of month, BLAST seemed to be more accurate.⁴ A similar approach is also used in the Republic of Korea (ROK). This generated questions on whether there a better host identification methods for genetically close bird species.
 - b. Host ID barcoding done at the same time as sample sequencing with multiplexed amplicon-based systems for influenza can provide information on different species and viral genome at once. Questions were raised on whether same efficiency of PCR between the two and whether the process requires separation prior to combination.
 - c. Some key environmental methods used in swine field include rope sampling (pigs chewing on rope to collect saliva samples). This provides a high amount of samples, and a first step of screening is important. Experiences using environmental sampling have shown mixed results in Chile when the environment is too dirty. The approach works best under cleaner conditions (e.g. industrial farms)
- 2) Tools/technology
 - a. Basestack⁵ – Platform for rapid and real-time analysis of Oxford Nanopore Technologies (ONT) generated sequencing data. Allows for visualization to rapidly triage and identify host, presence of virus and anomalies, with rapid turnaround. Main visualization and interpretation targets can be used by the non-bioinformatician to move from data to intervention. Prioritization based on previous work with infectious disease physicians and lessons learned from 2009 H1N1 pandemic, which was complex reassortment from an animal reservoir. For more in-depths information, such HA cleavage sites, etc. a specialist would be needed.
 - b. Tools for analyzing Illumina data (in a laboratory setting rather than field setting) – incorporating StaphB toolkit and others into Basestack more recently. If there is an open-source software package available, it can be deployed with a user interface within Basestack.
- 3) Gaps and opportunities for utilization of technology
 - a. Methods are needed to concentrate samples prior to amplification and sequencing. Not so much for avian settings with higher loads, but in zoonotic or swine settings where sequencing platforms aren't sensitive enough. A number of probe pull down sets have been assessed/used with wildly varying results.
 - b. Can have a step consisting of PCR in the field looking for highest M gene value, then can optimise what goes through the system, and prioritise high viral load to get data quickly.
 - c. Broader consideration of other zoonotic or priority pathogens, e.g. multiplexing for different pathogens, bioinformatics for ONT and Illumina, might improve sustainability.

⁴ The following primers seemed to work best: : Chu DK, Leung CY, Gilbert M, Joyner PH, Ng EM, et al. (2011) Avian coronavirus in wild aquatic birds. *J Virol* 85: 12815–12820

⁵ <https://github.com/jhuapl-bio/Basestack>

- d. Challenges have been related to computational facilities available, size of data, training of personnel, wide variation in level of background knowledge, but technology (e.g. Basestack) could address this.
- e. Other challenge is resourcing/staffing in laboratories, where there may not be a specific bioinformatician. It is difficult to maintain a qualified group of people with staff turnover, affects the sustainability even with software package.

Is there a cheap way to get lots of samples, would lateral flow work? Any experience with pre-concentration method?

- 1) Metagenomics is used in wild animals, with different Illumina probe sets. The problem is that it's based on what is already available in GenBank. For influenza, multisegmented PCR works well for amplification step, and custom sets can be developed based on sequences available. Not sure if pull down plus multisegmented PCR would work.
- 2) Can use materials from lateral flow tests (LFT) to sequence coronaviruses, but it is better to run them in parallel as the same sample for LFT and sequencing can be used. It is convenient if it can be used in field, then take to lab for sequencing. This technique has not seen much success however.

Are there any ways to go outside the lab with enough quality control?

- 1) Existing data can help determine if genome is bad.
- 2) Spike collection buffers before sampling, then later check how much has degraded, also conduct internal controls for PCR. For field gel, it is possible to check bands.
- 3) Testing at reference laboratories and in the field are two different things, we need to identify priorities for each to decide when to use the technology for specific purpose. This capability might change how we interpret this information.
- 4) Can conduct quality assurance procedures by coordinating with reference laboratories and local capacity in field, we need to empower them to enrich data.
- 5) Regional collaboration on the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) showed through information sharing that technologies and methods are becoming more standardized, we can adopt standards for analyzing data regionally.

What is the feasibility for these technologies to be integrated into system to serve as early warning?

- 1) Cost-related aspects:
 - a. Set up for dipstick, portable PCR, and MinION cost around 10 000-15 000 United States dollars (USD).
 - b. The investment it would take for a laboratory to go from PCR testing to generating sequencing on their own can be based on the typical "startup" for a few hundred SARS-CoV-2 samples. This includes sequencing hardware, around 20 000 USD. Analyzing a set of samples costs about 600 USD per sequencing runs, but a lot of samples can be analysed on one sequencing run. Cost per sample ends up being in range of 10-100 USD/sample.
- 2) Training aspects:
 - a. Training programs for bioinformaticians would be well received. GISRS network now moving forward to implement sequencing so the challenge remains the bioinformatician component.

- b. For Basestack, focus on training people on how the systems work together to ingest data into a surveillance system as quickly as possible, generating data products sent to centralized location for in-depth analysis. Need to consider how to use in regional level system.
- 3) Sustainability
- a. These systems are not sustainable if experts are needed to operate them. Therefore purpose of the software is to provide a user-friendly package of tools for laboratory technicians or similar staff to use. This is not a “black box” for bioinformaticians, but it might be for wet lab technician.
 - b. New software package can be developed to do the work if new pathogens are identified
 - c. Expanding the Basestack support team. The team is able to develop and supply tools to make process easier, leading to a community of practice more skilled over time, possible to leverage international networks of laboratories.
 - d. No control over prior experience or training. We need to ensure that people using tools/software are able to interpret what information means for decision-makers or in outbreak situation.

There is the need for sharing sequences. How can technology help with this type of early warning sharing sequences and how can we make this happen to make real change in future?

- 1) Generating sequences in bulk and using online systems to enable tracking of mutations and markers.
- 2) Countries’ overall goals of surveillance network is an important consideration. We can remove technical bottlenecks, e.g. using software with GISAID format for immediate upload, and to share in limited way with regional data pool.
- 3) A fast pipeline from sampling to sequencing, to visualization clearly helps with reporting to government/decision-makers. The faster the data is generated, the sooner it can be shared/progressed through political clearance processes.
- 4) We need mechanisms to share through Nextstrain and GitHub repositories. There is also a need to manage controlled access for regional group of experts and share information for disease control purposes before being made available to everyone.
- 5) National data sharing does not fit with the global/regional emergence of pathogens. There is a reluctance to move back to small-scale regional or national data sharing, which also not in the interest of FAO or WHO.
- 6) Use network of groups to get information to where it needs to be, ensure no duplication, data sharing as quickly as possible, rather than data hoarding.
- 7) Harnessing the speed and interpretability is still contingent upon the ability to act on the signal. E.g. epidemiology and health office staff at provincial/district level must be prepared to move at the speed of these platforms.
- 8) Using these technologies as a “local” deployment rather than cloud-based analysis needs to consider sharing of sequences found at country level with international community. Integrated software system enables transfer of data in a way that is sensitive to country needs while maximizing data sharing potential.
- 9) The person running the machine does not usually have the authority to share the sequence. It is necessary to also build capacity to analyze and interpret the results so that these people

communicate the significance of findings with authorities. There have been efforts to address this with training courses on the interpretation of genetic analysis for non-technical staff.

Session 5 – Utilisation of AIV surveillance data to improve responses (3 Dec 2021)

The final session of the series gave participants the opportunity to discuss what an “ideal early warning system” could look like, integrating elements at country, regional and global levels. A final brainstorming session was also conducted to discuss feasibility of a poultry influenza vaccine composition meeting (VCM) to provide global guidance on poultry vaccination programmes based on circulating AI strains.

5.1. Discussion: the ideal global early warning system – would this work?

Moderated by Gaël Lamielle (FAO ECTAD Regional Surveillance Coordinator)

Based on the discussions during the previous sessions, Gaël introduced a framework for early warning of AI events and facilitated a discussion to receive feedback from the participants on this approach, as well as challenges, gaps and opportunities to reach this scenario.

Initial comments on the proposed early warning approach included:

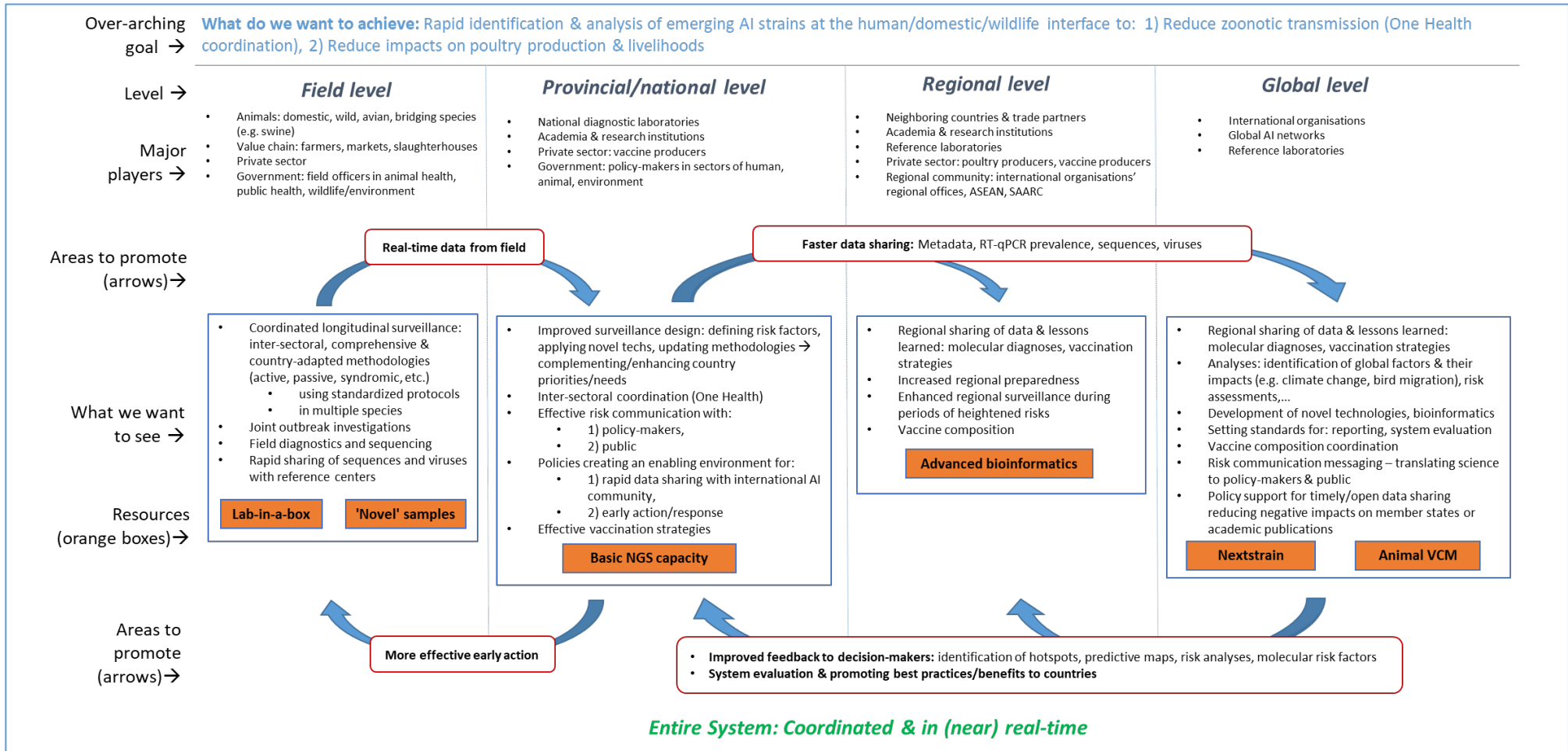
- Including pigs in field-level surveillance
- Including the role of different surveillance methodologies jointly, such as active, passive and sentinel surveillance
- Promoting the importance of a One Health approach from the top, including the importance of integration between animal and human surveillance ; the concept of One Health needs to be enforced to bring the sectors together
- Emphasizing the importance of information/data sharing as early as possible with international community
 - Timely data sharing can be achieved by using: novel technologies to sequence in the field and analysis packages that can enable immediate sharing on public database. WHO is encouraging timely sharing of data for viruses with pandemic potential
- Parameters such as climate change should be part of the early warning system. For example, the role of climate change and the impact on bird migration is most relevant but would need to be well-defined in relation to early warning.
- Incorporating early risk communication with the public (not just relevant ministries) based on virus detection in birds to reduce risk of infections in humans, therefore reducing the pandemic risk.
- Field level surveillance should include both domestic and wild birds (including wild birds in zoos/captivity), and stakeholders should include national parks/rangers (wild bird surveillance) and poultry slaughterhouses (allows traceability).

- The sections of the framework related to “How” and “why” need to be further explored at the national provincial level.

Following the discussion, meeting participants were polled on whether they agreed with the early warning framework in principle and the majority of those who voted were in favour of this draft framework (19/22 voted yes).

The “ideal early warning framework” was later updated to include the comments listed above, and sent out to participants for additional input. A final proposed version of this framework is included in this report (Fig. 1).

Figure 1. The proposed “ideal early warning framework” as discussed during Session 5 of the Regional avian influenza expert meeting (30 November – 3 December 2021)



During this session, participants also discussed some challenges and gaps that can slow the development of an efficient early warning mechanism at country, regional and global levels – including:

- Limited national investment and commitment can lead to low sustainability
- The need to validate new technologies with national and international standards, including: 1) sequencing and subtyping viruses using field PCR techniques, and 2) managing data generated from difference sources – e.g. from field and reference laboratories. Currently no reporting standards exist for these new technologies and no framework is in place to understand how to implement them.
- For strains of most concern (Gs/GD/96-lineage H5Nx viruses) information is shared reasonably quickly with sequences on GISAID within a few weeks. However, there is a need to change OIE's WAHIS reporting requirements to allow countries to share LPAI (other than H5 and H7) data in wild bird or environmental samples. Currently, it is not compulsory to report these subtypes in WAHIS and this information is therefore not readily available.
- Regional level communication is still lacking in many regions.
- Some warning messages already exist for H5Nx in wild birds, however there is often a short window of time between incursion and spillover to poultry (e.g. as seen in Japan and ROK). This means that there is little that farms can do beyond tightening biosecurity.
- If the objective is to reduce zoonotic transmission, a baseline to measure achievements should be established, which includes: standard serology studies and analyses for populations at the wildlife/domestic/human interface, in addition to counting sporadic human cases.
- There is a reluctance to share sequences early due to potential impacts on research publication. A potential suggestion to mitigate this included:
 - Requesting scientific journals to grant additional points if isolates' sequences are shared ahead of publication, with higher points for earlier sharing, and avoidance of embargos on sequences once uploaded.
- There must be better incentive to encourage countries to share sequences or viruses. Countries must see what they get in return – i.e. the reciprocal benefit for sharing data can inform their own outbreak situation. A poultry VCM could also be as such a benefit for countries.
- Current early warning surveillance may not be translating into risk reduction, e.g. improving biosecurity on poultry farms. This could be partially due to challenges in making higher risk production systems more biosecure, or when doing so changes the production system (such as the need to house free ranging chickens).
- Compared to ease of early detection of HPAI in birds, the current system is not adapted to have the same timeliness for identifying the establishment of swine H1 virus in birds. Samples picked up cannot be typed because swine influenza virus primers are not used regularly in birds, and country protocols may not include all subtypes due to budget. However, full genome sequencing could improve this, and a longitudinal system may be able to pick this up, especially if focused on high-risk interfaces.
- Integration and analysis of data at national/regional/international level in anything approaching real time is a challenge – it does not happen automatically and simply making data available is not the endpoint.

Discussions continued along the theme of existing frameworks and intersectoral coordination, including the following points:

- The current early warning system is not broken but needs tweaking. In the past two years, FAO headquarters issued warnings of wild bird cases coming to Asia; cases found quickly, and sequences were available within two weeks. There were also hints that clade 2.3.4.4b viruses were capable of infecting humans.
- Part of this framework already exists. For example, when H5N8 was detected in Russia, Viet Nam and Cambodia requested sequence data to update their surveillance. Are there novel approaches or technologies that could enhance the resolution and speed of data sharing in the system?
- Better coordination with GISRS and other existing systems, where countries conduct surveillance and reporting during “peace” and “war” times, including for LPAI, would enable us to be ahead of the curve and warn countries of potential human infections.
- Early warning could identify interspecies spillover (e.g. swine, humans) and inform spillover risk mitigation measures, with adjustments ILI and human-targeted surveillance.
- The OIE Terrestrial Code avian influenza chapter on diagnostic techniques is up for major revision by reference laboratories, including molecular aspects and different technologies. It is unclear if the differences between field and reference labs are well-defined.
- Early warning findings should be interpreted broadly and can go beyond warning for new incursions to include warning of continuous presence, new hosts affected, and human health risks.

5.2. Panel debate: What is the utility and feasibility of a poultry vaccine composition meeting (VCM)?

Moderated by Filip Claes (FAO ECTAD Regional Laboratory Coordinator)

Panelists: Sophie VonDobschuetz, Gounalan Pavade, Magdi Samaan, Frank Wong, Leslie Sims

The objective of this facilitated discussion was to assess the interest for a poultry VCM, and discuss its feasibility, and specific questions were directed to the panellists for their input.

- 1) *Do we still think that an animal health VCM is a good idea?*
 - a. The consensus from the panelists was ‘Yes’.
- 2) *How can it function and what is stopping it from happening?*
 - a. Funding and resources are needed and OFFLU can provide support. The current challenge is that there is currently no permanent OFFLU scientist focused on delivery, and other OFFLU members volunteer their own time. OFFLU/FAO are recruiting a person full-time to do this work and drive it forward.
 - b. Resources and coordination are essential. There needs to be a network of reference laboratories to pull together baseline panel to produce poultry antisera. A few laboratories are doing that for the WHO VCM. Investment is needed to add poultry VCM. COVID-19 has hindered progress for reference laboratories to collaborate. Reference laboratories in different regions must be considered because not every country is vaccinating poultry against AI.

- c. Some data is already available to use (e.g. OFFLU published a report with information on genetic strains and sites, can include cross HI testing data), even if it is not the full picture. Interest from vaccine manufacturers may increase. We can start with what is available, then coordinate with the human side.
 - d. We can start with meaningful data for countries, as they see value in it, it will gather more momentum. Globally many countries are affected by AI, which may push towards vaccination. With new countries using vaccines and others doing monitoring and matching, global guidance on manufacture would be considered of major global value for countries. Increased use of vaccination for AI prevention and control will also increase funding interest.
 - e. One benefit seen in countries using up to date vaccines is the sharp decline in human cases compared to when vaccines are mismatched.
 - f. Recommendations for use of vaccination must be clearly highlighted in OIE Code to protect member countries from losing their freedom status. We need to progress this technically. Some countries are using vaccinations without guidance on how to monitor or update vaccines.
- 3) *We need engagement from OFFLU network, countries, governments, and private sector – how can we get the private sector engaged?*
- a. We need to provide value for all stakeholders – show the private sector how they will benefit. Some vaccine producers may be happy to carry on their activities like they have done in the past, so they may feel threatened by this idea. But the objective is not to tell them which vaccine to use or not to use, but rather to make science available to all.
 - b. The private sector will be more willing to be involved once they see that vaccination will be ongoing. The private sector already involved in a few European countries to produce vaccines (H5), but are cautious as vector vaccines may give broader coverage.
 - c. The private sector will be interested in this data as they do not have access to it from countries. The Global Framework for the Progressive Control of Transboundary Animal Diseases (GF-TADs) steering committee has set HPAI as a global priority and discussed resistance to use of vaccines.
 - d. OIE already has agreement with private sector, and OFFLU private-public partnerships are part of the discussion. The equine influenza sector already meets annually, technical inputs for multiple stakeholders to update vaccines for multiple sectors.
 - e. There is mutual interest for the public health and private sector to update vaccines. Pharmaceutical companies fund activities for surveillance, including for seasonal influenza. So engagement of the private sector in the whole process would be supported, with more effective vaccines and increased profits in return.
- 4) *One Health, One Wallet – how can this be funded? Can public health support funding for a poultry VCM?*
- a. A shared One Health objective is to reduce the burden of AI, but the use of public health sector funds for veterinary side needs further discussion.
 - b. Private funding can also be used, and we must develop framework and concept to prove to donors that we can deliver this with lasting impact and sustainability. It is suggested to

pilot a project for two years to establish a VCM framework to develop poultry vaccines. This needs Tripartite endorsement, and the wider group within OFFLU can drive it forward. WHO has the experience to get donor funding.

- c. Vaccines will make money, and if a company can make good vaccine, farmers will pay for it. Unless a company is expected to distribute a vaccine for free, funding is not a concern. Countries use their own strains so it is difficult to recommend one strain – it may be beneficial for sales if vaccine companies to adhere to recommendations so their vaccine is fit for purpose.
- d. FAO, USAID are supportive to employ someone to manage OFFLU next year, who will support poultry VCM as well. It is helpful to understand costs to make packages for the right funding entity.
- e. OIE is supportive, as AI is a priority within the Tripartite. A list of vaccines produced by private sector is needed to understand their interest to engage in this, including how information utilised by private sector.

5) *Additional inputs from the panellists and participants regarding funding and support for the poultry VCM:*

- a. Low- and middle-income countries (LMIC) need to justify their contribution to the global good. Is there a mechanism for the global community to cover the cost for less resourced countries (apart from intermittent projects)?
- b. Similar to GISRS, human vaccine manufacturers pay for surveillance and benefit financially from surveillance generated by countries, justifying sharing information beyond the region along seasonal migration routes. A global system on the poultry side would be a major improvement.
- c. OFFLU is an important participant during the WHO VCM for providing a global picture.
- d. Regional vaccine quality control mechanisms like the European Medicines Agency (EMA) or the Pan African Veterinary Vaccine Centre (AU-PANVAC) are missing in Asia, but they may promote willingness to produce safe vaccines that can be used in other countries in the region.
- e. Regularly updating vaccines can reduce incidence of cases in poultry and humans.
- f. Human vaccine manufacturers are forced to use the recommended vaccine viruses by country regulations and are vested in vaccine selection. Their commercial advantage comes from the platform rather than the antigen. The WHO network provides standardised vaccine seeds so commercial sponsors get something back.
- g. OFFLU is not a legal entity, and cannot set up framework to commercially exploit vaccine sales, the challenge is that vaccines must be tailored for specific regions. Personnel costs can be modest, and could include small group of international junior scientist research fellows.

Conclusions and way forward

Dr. Kachen Wongsathapornchai (FAO ECTAD Regional Coordinator) provided the participants with a summary of the major discussion points of the consultation series, along with the way forward to continue the momentum on surveillance, early warning and poultry VCM.

The meeting noted:

- 1) Participants acknowledge surveillance efforts at country level should meet country needs and they identify areas that may improve contribution of country surveillance information for regional and global public good.
- 2) Participants identify ongoing impediments related to sharing sample data and other relevant information, and as such recommend to facilitate an enabling environment and policies for timely and open data sharing without stigmatization and ensuring equitable benefits for all parties involved.
- 3) Novel approaches and technologies can help to improve timeliness, efficacy and cost-effectiveness of surveillance. Participants agree to contribute to efforts for an enhanced regional and global early warning system through:
 - a. Developing and supporting application of tools and methodologies to improve surveillance, risk assessment, genetic data analysis and interpretation for policy and decision making, and
 - b. Strengthening country capacity to utilize appropriate tools and technologies that fit for purpose.
- 4) Participants recognize the need to establish and operationalise an international early warning networks (linking with OFFLU) for AI, aligned with the human health system (e.g. WHO GISRS network, and other systems in other sectors).
- 5) Participants support the concept of establishing a global platform to advise on vaccine composition for animal influenza vaccines, similar to the human influenza VCM led by WHO.

The following action items arose from the meeting:

- 1) Developing an action plan to progress early warning system framework, in consultation with member states
- 2) Developing a concept note for potential donors of a poultry VCM for a possible initial two-year pilot project
- 3) Gathering information about vaccines produced by the private sector to gauge their level of interest for participation in VCM
- 4) Developing costing structures to present to potential donors for VCM

Annex 1 – Meeting concept note

Toward Mitigating Pandemic Influenza Risk:

A regional consultation on avian influenza surveillance in Asia

30 November – 3 December 2021

Virtual Meeting – 18:00hrs to 20:00hrs Indochina Time (ICT)

CONCEPT NOTE

BACKGROUND

Unlike the dearth of human seasonal influenza detections during the last 2 years, avian influenza viruses (AIV) continue to be detected as they circulate around the globe. Indeed, during the COVID-19 pandemic, outbreaks and human infections with avian influenza A viruses (notably H9N2 and H5Nx subclades) have increased ten-fold over 2019 detections (FAO, EMPRESi). Highly pathogenic avian influenza (HPAI) H5Nx clades have steadily evolved since 2008 leading to antigenically and genetically distinct isolates. Since early 2020, H5N8 outbreaks were reported across various continents, and recently the detection of subclade 2.3.4.4b is increasing. Numerous outbreaks throughout Europe, Asia and, more recently, Africa appear genetically closely related. H5N1 also continues to circulate globally and recently H5N5 viruses were identified throughout the year in Europe and Asia, while H5N6 was detected in China and Southeast Asia since early 2019. Sporadic outbreaks of H5N2, H5N3, and H5N4 were also reported. In addition to HPAI H5Nx viruses, endemic LPAI H9N2 viruses continue to circulate throughout the world and are a major concern for the poultry industry. Besides poultry and wild bird outbreaks, numerous zoonotic infections have been detected in humans in the past few years. Subtypes include H7N4, H9N2, H10N3, and, most concerning, H5N8 and H5N6 clade 2.3.4.4b viruses.

Overall, there is a need to maintain and improve AIV surveillance. Currently, numerous stakeholders and countries perform AIV surveillance, response, and prevention activities on an ad-hoc basis. It is vital to move away from responding reactively and to increase the focus on proactive prevention and control. In the near future, it is critical to connect and align efforts to generate an “early warning” system, especially in regard to communication and data sharing before the next outbreak occurs. In addition, global availability of genomic data and viral isolates is essential for vaccination programs in both humans and animals, and for development/revision of critical diagnostics. Although the COVID-19 pandemic has ravaged the public health and economic sectors, it has brought about a renaissance in laboratory capacity and highlighted the need for coordinated, connected networks that can quickly identify and respond to endemic and emerging pathogens. Following the strengthening of the human seasonal influenza programme, it serves to also bolster and refine the global avian influenza network, starting with the Asia-Pacific region as it has traditionally been the epicentre for AIV emergence and spread.

Therefore, the Food and Agriculture Organisation of the United Nations (FAO) Regional Office for Asia and the Pacific (RAP) will conduct a virtual consultation between 30 November and 3 December 2021 to define the state of the field and propose novel ways forward in AIV detection, surveillance, and response.

OBJECTIVES

The meeting aims to:

1. Update current information on prevalence, genotypic, and antigenic aspects of AIV in Asia
2. Discuss risks of emerging strains for poultry production and public health in Asia
3. Review AIV surveillance activities at the country/regional levels, including lessons learned from previous surveillance and the current COVID-19 response to be used in AIV early warning,
4. Determine major gaps, needs and ways forward to enhance AIV surveillance
5. Discuss novel technologies (i.e.: multiplex PCR, point-of-care testing, next generation sequencing) and sampling strategies (environmental, pooling) for improved surveillance
6. Explore possible utilisation of AIV surveillance data, including the coordinated animal sector AIV Vaccine Composition discussion/forum

PARTICIPANTS:

- FAO/OIE Reference Laboratories for influenzas
- WHO Collaborating Centres for influenza
- ASEAN Reference Laboratories
- OIE/FAO global network of expertise on animal influenza (OFFLU)
- Invited countries representatives
- Invited influenza experts
- Invited poultry and swine industries with ongoing surveillance activities
- International and regional partners

DATES AND VENUE

30 November – 3 December 2021 at 18:00hrs to 21:00hrs Indochina Time (ICT)

The consultation will be organized virtually via Zoom. Zoom links will be provided later.

EXPECTED OUTPUTS

1. Meeting summary including
 - a. AIV situation,
 - b. Surveillance activities, gaps and needs
2. Agreed ways forward on priority areas and action points related to novel technologies, sampling strategies, research and information sharing
3. Agreed ways forward for possible establishment of animal sector AIV Vaccine Composition group

Annex 2 – Meeting agenda

Toward Mitigating Pandemic Influenza Risk:

A regional consultation on avian influenza surveillance in Asia

30 November – 3 December 2021

18.00 – 20.00 Indochina time (ICT)

Join Zoom Meeting

<https://fao.zoom.us/j/92218523799>

Meeting ID: 922 1852 3799

Passcode: 48001483

The event will consist of a series of three consultation meetings with experts in the field of avian influenza viruses (AIV) to gain a better understanding of the current situation in Asia and discuss strategies to improve surveillance and early warning. Participants will include representatives from international organisations, reference laboratories, research institutions, public health and the private sector, amongst others. The meeting will be the opportunity for these experts to share valuable information on evolution of AIVs in Asia including circulating and emerging clades in animals and humans, discuss lessons-learned from previous surveillance as well as the impact of the COVID-19 pandemic, and identify novel approaches and technologies for rapid diagnostics and data sharing. Outputs from the meeting will guide the implementation of novel surveillance strategies for AIV in Asia and identify next steps for the possible establishments of an AIV vaccine composition group.

Objectives

- Update current information on prevalence, genotypic, and antigenic aspects of AIV in Asia
- Discuss AIV surveillance activities, including lessons learned from previous surveillance and the current COVID-19 response to be used in AIV early warning,
- Determine major gaps and needs of AIV surveillance, and how they can be addressed
- Discuss novel technologies (i.e.: multiplex PCR, point-of-care testing, next generation sequencing) and sampling strategies (environmental, pooling) for improved surveillance
- Explore possible utilisation of AIV surveillance data, including the coordinated animal sector AIV Vaccine Composition discussion/forum

Sessions

1. Introduction and setting the scene

2. What do we need for inter-regional collaboration and early warning?
3. What are we doing, and what are we missing?
4. Novel ways to look for and improve understanding of AIV
5. Utilisation of AIV surveillance data to improve responses

Detailed agenda

Day 1: 30 November 2021			
18.00-20.00 Indochina Time (ICT)			
Moderator: Gaël			
Session 1: Introduction and scene setting			
Time	Duration	Topic	Who
18.00-18.10	10min	Welcome and Introduction of Consultation <ul style="list-style-type: none"> - Key issues for discussion - Meeting objectives - Expected results - Picture 	Kachen Wongsathapornchai (FAO RAP)
18.10-18.20	10min	Presentation: Overview of the current avian influenza situation in animals	Sophie von Dobschuetz (FAO HQ)
18.20-18.30	10min	Presentation: Update on human infections with AIV – challenges and gaps	Kaat Vandemaele (WHO)
Session 2: What do we need for inter-regional collaboration and early warning?			
Time	Duration	Topic	Who
18.30-18.40	10min	Presentation: Challenges with genetic diversity, evolution, vaccine composition (including mixing between regions)	Nicola Lewis (OFFLU)
18.40-18.50	10min	Presentation: Early warning approaches in Europe	Ron Fouchier (Erasmus)
18.50-19.00	10min	Presentation: What is Africa/ME doing to screen for viruses & gaps	Ghazi Kayali (Humanlink)
19.00-19.10	10min	Presentation: Focus on Asia – FAO reference centre for AI	Hualan Chen (Harbin veterinary research institute)
19.10-	45min	Discussion: <ul style="list-style-type: none"> - What data are needed for inter-regional collaboration, better track emerging subclades, and 	Facilitation:

19.55		assess their zoonotic potential and efficacy of vaccines?	Erik Karlsson (IPC)
19.55-20.00	5min	Closing of the day	FAO RAP

Day 2: 1 December 2021			
18.00-20.00 Indochina Time (ICT)			
Moderator: Filip			
Session 3: What are we doing, and what are we missing?			
Time	Duration	Topic	Who
18.00-18.05	5min	Debrief of day 1 and introduction to day 2	FAO RAP
18.05-18.15	10min	Presentation: Overview of surveillance strategies in the region and their fitness for purpose	Gaël Lamielle (FAO RAP)
18.15-18.25	10min	Presentation: Example from the field – Indonesia & IVM	Dr. Hendra Wibawa (Indonesia DIC Wates)
18.25-18.35	10min	Presentation: Example from the field – Viet Nam & LISN	Pawin Padungtod (FAO ECTAD Viet Nam)
18.35-18.45	10min	Presentation: Example from the field – Cambodia & IPC	Erik Karlsson (IPC)
18.45-19.55	70min	Discussion: Panel with expert opinions and discussion <ul style="list-style-type: none"> • Questions to countries: do country surveillance methodologies fit their objectives? What information is missing, what are remaining gaps? • Questions to panelists: Do country surveillance methodologies meet the needs of the international AIV community? What can be done to better align needs? 	Facilitation: Gaël Lamielle (FAO RAP) Panelists: - Frank Wong (ACDP) - Ian Brown (OFFLU) - Hualan Chen (HaVRI)

			- Yoshihiro Sakoda (Hokkaido University) - Nicola Lewis (OFFLU)
19.55-20.00	5min	Closing of the day	FAO RAP

Day 3: 2 December 2021			
18.00-20.00 Indochina Time (ICT)			
Moderator: Kachen			
Session 4: Novel ways to look for and improve understanding of AIV			
Time	Duration	Topic	Who
18.00-18.05	5min	Wrap up of previous days & introduction	FAO RAP
18.05-18.20	15min	Presentation: Field technologies and alternate sample types - field PCR & environmental sampling (including air)	Erik Karlsson (IPC)
18.20-18.35	15min	Presentation: Advances in AIV sequencing capacities and speed	Peter Thielen (Johns Hopkins University)
18.50	15min	Presentation: Computational and bioinformatics needs to support novel diagnostics	Louise Moncla (pre-recorded)
18.50-19.55	65min	Discussion: Panelists and open discussion <ul style="list-style-type: none"> • How can we use these technologies to improve early warning in the region? • How can we adapt these technologies to country contexts? 	Facilitation: Filip Claes (FAO RAP)
19.55-20.00	5min	Closing	FAO RAP

Day 4: 3 December 2021			
18.00-20.00 Indochina Time (ICT)			
Moderator: Erik			
Session 5: Utilisation of AIV surveillance data to improve responses			

Time	Duration	Topic	Who
18.00-18.05	5min	Present day's objective	FAO RAP
18.05-18.15	10min	Summary of what has been learned so far Day 1: What we know currently Day 2: What are we doing, and what are we missing Day 3: What tools can we improve and what can we integrate?	FAO RAP
18.15-19.00	45min	Discussion: What do YOU want to see as a coordinated AIV surveillance and response system? How can we have better information sharing? How can surveillance data be better utilized?	Facilitation: Filip Claes (FAO RAP)
19.00-19.45	45min	Panel debate: What is the utility and feasibility of a Zoonotic vaccine composition meeting (VCM)?	Panelists: - Nicola Lewis (OFFLU) - Ian Brown (OFFLU) - Gounalan Pavade (OIE) - WHO
19.45-19.55	10min	Summary Recommendations for Moving Forward Action Points Final Thoughts	FAO RAP
19.55-20.00	5min	Closing	FAO RAP

Annex 3 – Participant list

Name	Institution	Country	Day 1	Day 2	Day 3	Day 4
Akiko Kamata	<i>FAO Headquarters</i>	Italy	Yes	Yes		Yes
Ali Rizqi A	<i>FAO Indonesia</i>	Indonesia	Yes		Yes	Yes
Andrew Clements	<i>USAID</i>	USA	Yes	Yes	Yes	Yes
Angelique Angot	<i>FAO Headquarters</i>	Italy	Yes	Yes	Yes	
Aspen Hammond	<i>WHO Global Influenza Programme</i>	Switzerland	Yes			Yes
Audi Harsono	<i>FAO Indonesia</i>	Indonesia			Yes	Yes
Chakradhar Tosh	<i>Bhopal AI Reference Laboratory</i>	India	Yes	Yes	Yes	Yes
Claudia Pittiglio	<i>FAO Headquarters</i>	Italy				Yes
Dan Schar	<i>USAID</i>	Thailand	Yes	Yes	Yes	Yes
Dessie Eri	<i>Disease Investigation Centre Wates</i>	Indonesia	Yes			
Erik Karlsson	<i>Institut Pasteur du Cambodge</i>	Cambodia	Yes	Yes	Yes	Yes
Farida Zenal	<i>FAO Indonesia</i>	Indonesia	Yes	Yes	Yes	Yes
Filip Claes	<i>FAO RAP</i>	Thailand	Yes	Yes	Yes	Yes
Frank Wong	<i>Australian Animal Health Laboratory</i>	Australia	Yes	Yes	Yes	Yes
Gael Lamielle	<i>FAO RAP</i>	Thailand	Yes	Yes	Yes	Yes
Gavin Smith	<i>Singapore Duke-NUS Medical school</i>	Singapore	Yes	Yes	Yes	Yes
Ghazi Kayali	<i>Human Link</i>	Lebanon	Yes			
Giovanni Cattoli	<i>Joint FAO/IAEA Centre</i>	Austria	Yes	Yes	Yes	

Gounalan Pavade	<i>OIE</i>	France	Yes	Yes		Yes
Gyeongbeom Heo	<i>Animal and Plant Quarantine Agency</i>	Republic of Korea			Yes	
Hendra Wibawa	<i>Disease Investigation Centre Wates</i>	Indonesia		Yes		
Hualan Chen	<i>Harbin Veterinary Research Institute</i>	China	Yes	Yes	Yes	Yes
HyunKyu Cho	<i>Animal and Plant Quarantine Agency</i>	Republic of Korea				Yes
Ian Brown	<i>APHA</i>	United Kingdom	Yes	Yes	Yes	Yes
Ivancho Naletoski	<i>IAEA</i>	Austria		Yes	Yes	
Jeff Gilbert	<i>FAO Headquarters</i>	Italy	Yes	Yes		Yes
Kachen Wongsathapornchai	<i>FAO RAP</i>	Thailand	Yes	Yes	Yes	Yes
Karoon Chanachai	<i>USAID/RDMA</i>	Thailand	Yes	Yes	Yes	Yes
Katelijn Vandemaele	<i>WHO Headquarters</i>	Switzerland	Yes	Yes		
Ken Inui	<i>FAO RAP</i>	Viet Nam	Yes	Yes	Yes	Yes
Kwang Nyeong Lee	<i>Animal and Plant Quarantine Agency</i>	Republic of Korea	Yes		Yes	Yes
Leslie Sims	<i>Asia Pacific Veterinary Information Services</i>	Australia				Yes
DIC Wates	<i>Disease Investigation Centre Wates</i>	Indonesia	Yes	Yes		
Louise Moncla (via recording)	<i>Nextstrain Initiative</i>	United States of America			Yes	
Lushi Liu	<i>FAO China</i>	China	Yes			

Luuk Schoonman	<i>FAO Indonesia</i>	Indonesia	Yes	Yes	Yes	Yes
Madhur Dhingra	<i>FAO Headquarters</i>	Italy	Yes			
Magdi Samaan	<i>WHO Headquarters</i>	Switzerland	Yes	Yes	Yes	Yes
Michael O'Leary	<i>USAID</i>	USA	Yes	Yes		Yes
Mugyeom Moon	<i>FAO RAP</i>	Republic of Korea	Yes	Yes	Yes	Yes
Oanh Kim	<i>USAID</i>	Viet Nam	Yes	Yes	Yes	Yes
Paolo Roberto Motta	<i>FAO RAP</i>	Italy	Yes	Yes		Yes
Pawin Padungtod	<i>FAO Viet Nam</i>	Viet Nam	Yes	Yes	Yes	Yes
Pedro Jimenez-Bluhm	<i>Universidad de Chile</i>	Chile	Yes	Yes	Yes	Yes
Peter Black	<i>FAO RAP</i>	New Zealand	Yes	Yes	Yes	Yes
Peter Thielen	<i>John's Hopkins University</i>	United States of America	Yes	Yes	Yes	Yes
Richard Webby	<i>St. Jude Children's Research Hospital (CEIRS)</i>	United States of America	Yes	Yes	Yes	Yes
Rindu Putri	<i>FAO RAP</i>	Indonesia	Yes	Yes	Yes	Yes
Ron Fouchier	<i>Erasmus MC</i>	Netherlands	Yes	Yes	Yes	Yes
Sarah Van Dyk	<i>FAO RAP</i>	Australia	Yes	Yes	Yes	Yes
Sophie Von Dobschuetz	<i>FAO Headquarters</i>	Italy	Yes	Yes	Yes	Yes
Sri Handayani Irianingsih	<i>Disease Investigation Centre Wates</i>	Indonesia	Yes	Yes	Yes	
Todd Davis	<i>US CDC</i>	USA	Yes			
Tosapol Dejyong	<i>FAO RAP</i>	Thailand	Yes	Yes	Yes	

Tran Huynh	<i>FAO Headquarters</i>	Viet Nam		Yes		
Vijaykrishna Dhanasekaran	<i>University of Hong Kong</i>	China		Yes	Yes	Yes
VJ Singh	<i>Bhopal AI Reference Laboratory</i>	India	Yes			
William Dundon	<i>IAEA</i>	Austria			Yes	
Xavier Roche	<i>FAO Headquarters</i>	Italy	Yes		Yes	Yes
Yongmyeong Kang(/w other colleagues)	<i>Animal and Plant Quarantine Agency</i>	Republic of Korea	Yes	Yes		
Yoshi Sakoda	<i>Hokkaido University</i>	Japan		Yes		
Total per day			49	44	40	41