Meeting report
Regional avian influenza in Asia
2 - 4 November 2022
Geelong, Australia
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**Abbreviations and acronyms**

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Description</th>
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<tbody>
<tr>
<td>ACDP</td>
<td>Australian Centre for Disease Preparedness</td>
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<td>AI</td>
<td>Avian influenza</td>
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<td>AIVs</td>
<td>Avian influenza A viruses</td>
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<td>APHA</td>
<td>Animal and Plant Health Agency</td>
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<td>ASEAN</td>
<td>Association of Southeast Asian Nations</td>
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<tr>
<td>COVID-19</td>
<td>Coronavirus disease 2019</td>
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<td>CVO</td>
<td>Chief veterinary officer</td>
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<tr>
<td>DIVA</td>
<td>Differentiate infected from vaccinated animals</td>
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<td>ECTAD</td>
<td>Emergency Centre for Transboundary Animal Diseases</td>
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<tr>
<td>FAO</td>
<td>The United Nations Food and Agriculture Organization</td>
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<tr>
<td>HA</td>
<td>Hemagglutinin</td>
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<tr>
<td>HI</td>
<td>Hemagglutination inhibition</td>
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<tr>
<td>HPAI</td>
<td>Highly pathogenic avian influenza</td>
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<td>LBM</td>
<td>Live bird market</td>
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<td>LPAI</td>
<td>Low pathogenic avian influenza</td>
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<tr>
<td>NA</td>
<td>Neuraminidase</td>
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<td>NGS</td>
<td>Next generation sequencing</td>
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<td>OFFLU</td>
<td>Joint WOAH-FAO Scientific Network On Animal Influenza</td>
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<td>PPP</td>
<td>Public-private partnerships</td>
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<td>RAP</td>
<td>Region of Asia and the Pacific</td>
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<td>RT-PCR</td>
<td>Real-time polymerase chain reaction</td>
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<tr>
<td>SAARC</td>
<td>South Asian Association for Regional Cooperation</td>
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<tr>
<td>SEAOHUN</td>
<td>Southeast Asia One Health University Network</td>
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<tr>
<td>SOP</td>
<td>Standardised operating procedure</td>
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<tr>
<td>TIPRA</td>
<td>Tool for Influenza Pandemic Risk Assessment</td>
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<tr>
<td>VCM</td>
<td>Vaccine composition meeting</td>
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<td>WOAH</td>
<td>World Organisation for Animal Health</td>
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Executive summary

Background

Since the appearance of highly pathogenic avian influenza (HPAI) A/H5N1 in 2005 in Asia, avian influenza (AI) has continued to diversify over the years, leading to a multitude of both high and low pathogenic AI (LPAI) viruses threatening both human health and poultry populations. In recent years, new subclades have spread across the globe through wild bird migration, reaching areas previously unaffected by these viruses. This is the case of A/H5Nx subclade 2.3.4.4b, which originated in Asia and has contributed to major H5N1 outbreaks in both wild and domestic populations in Europe, Africa and the Americas – including zoonotic transmission to humans.

In Asia, this subclade has persisted alongside endemic AI viruses (AIVs) such as A/H5N2, A/H5N3, A/H5N4, A/H7Nx and LPAI H9N2. This diversity of circulating AIVs creates the perfect storm for the emergence of new subclades with increased ability to infect domestic birds and humans.

Despite decades of investments into AI surveillance, further work is needed to better detect these emerging subtypes, rapidly share findings with the international community and improve early response to these new AI threats.

To address this need, the Food and Agriculture Organization of the United Nations (FAO) Regional office for Asia and the Pacific (RAP) has organised regional consultations in 2021 and 2022. Due to restrictions linked to the coronavirus disease 2019 (COVID-19) pandemic, the 2021 meeting was held online, though participants actively contributed to identify gaps and needs related to global early warning mechanisms and information sharing. During that consultation, participants designed a framework for an “ideal” global early warning system, anchored in real-time data generation from the field and rapid information sharing with national and international networks. A report from the 2021 meeting is available at the following link: https://www.fao.org/3/cc0336en/cc0336en.pdf.

During 2-4 November 2022, FAO RAP organised a follow-up expert meeting in Geelong, Australia to continue addressing the ongoing challenges posed by AI in Asia, and assess progresses made since the 2021 meeting. The objectives of the 2022 meetings were to:

1. Review progress and challenges since the 2021 expert consultation, specifically towards improved global AI early warning mechanisms and poultry vaccine composition meeting
2. Identify challenges and best practice to implement novel approaches to sampling and diagnostics of AIVs at country-level
3. Discuss advancements in next generation sequencing (NGS) and bioinformatics
4. Identify ways forward to further achieve the vision of global early warning and information sharing through the use of innovative approaches

A total of 24 experts participated in the 2022 meeting, including representatives from governments, research institutions, international organisations and reference laboratories. During the five participatory sessions of the consultation, regional AI experts actively brainstormed and jointly identified remaining gaps, needs and ways forward to reach the meeting’s objectives.
Session 1 – Introduction and setting the scene (2 November 2022)

The first session of the consultation opened the meeting by revisiting outputs of the 2021 consultation and introduced the programme of the meeting. Following a brief presentation to set the scene, participants were led in a series of facilitated exercises to identify progresses and remaining gaps related to global early warning for AI.

Progresses were grouped into the six major categories below:

1. Global coordination and sharing of data related to AI
2. Global guidance, tools
3. Better surveillance methodologies, improved efficiency
4. Piloting new approaches
5. Increased outreach & interest
6. Better understanding of disease drivers and risks

Remaining gaps were grouped and listed in the form of questions to be addressed in the rest of the consultation:

1. How do we improve One Health coordination?
2. How do we address lack of timely information sharing?
3. How to prioritize government resources?
4. How do we increase public sector engagement?
5. How do we increase wild bird surveillance?
6. How do we improve access to technical skills for new thinking?

Using the results of initial discussions, participants were led into one final exercise of the day, identifying and prioritizing activities to address the remaining gaps. Activities were prioritised based on their ease of implementation and novelty – they included:

- **Priority 1 (easy and business as usual)**
  - Implementing capacity-building activities in the region
  - Ensuring continuity of training of veterinary officers

- **Priority 2 (easy and new idea)**
  - Conducting economic impact analysis of AI outbreaks
  - Engaging with private sector to test new diagnostic approaches
  - Enhancing wild bird research: sampling and knowledge sharing
  - Anthropology: identifying dis-/incentives for data sharing
  - Improving bioinformatics skills

- **Priority 3 (hard and new idea)**
  - Developing national One Health Ministries/Platforms
  - Implementing up-to-date diagnostics in testing programmes
  - Conducting structured evaluation of AI surveillance
  - Facilitating permits for wildlife surveillance
Through inter-governmental organisations, developing international memoranda of understanding (MoU) for improve data sharing and national buy-in
Engaging with government’s Ministry of Environment, especially at the subnational levels

- **Priority 4 (hard and business as usual)**
  - Securing more funds for countries to generate sequence data

### Session 2 – Novel approaches (3 November 2022)

The second day of the consultation was the opportunity to conduct deep dives into novel approaches to conducting surveillance for early warning. As an initial discussion, participants agreed on a working definition of “early warning” that was the basis of the follow-up discussions:

*Monitoring changes in trends (including virus subtypes, risks) that provide actionable information before outbreaks/spillover*

The group then discussed the use of novel sampling approaches that can contribute to reaching this early warning definition, including prior and during outbreaks. These included sampling relevant environmental areas in the domestic bird value chain (e.g. litter, water, faeces air, cages), natural areas targeting wildlife (e.g. water bodies, faeces). Diagnostic tests discussed included real-time polymerase chain reactions (RT-PCR), antigen tests and Oxford Nanopore MinION.

As the session finished, the group identified challenges that remain in order to fully implement novel approaches to the early detection of AIVs in the Asian context. These included:

1. The need to improve acceptance of new methodologies/technologies by governments and institutions
2. Developing protocols/procedures to manage positive identification of AIVs through novel approaches
3. Monitoring trends in a continuous way to ensure a good baseline for the approaches
4. The need to calibrate and validate these novel technologies
5. The need to provide decision-makers with more background

### Session 3 – Bioinformatics, data sharing (3 November 2022)

The next session focused on uses of bioinformatics, especially in the context of data analysis and sharing. The group identified some needs and barriers affecting the implementation of bioinformatics technologies in Asia. They included:

- **Needs:**
  - Infrastructure – reagents, computers, data storage, all-in-one units
  - Enabling environment – advocacy, policy
  - Standardization, consistency of analyses
  - Training
  - Global guidance/best practices that is adaptable
  - Antigenic cartography
Better pipelines for better results

**Barriers:**

- Cost – maintenance, reagents
- Data – security, privacy, sovereignty
- Inconsistent equipment
- Trust – acceptance, understanding
- Reference database
- Quality assurance
- Lack of knowledge transfer/retention
- Technology advances too fast to keep up
- Delays due to batching
- Automated pipelines to facilitate uses in the field

Further discussions on bioinformatics addressed several topics relevant to the technologies, such as: resources, data management, evolving technologies, application for early warning and collaboration needs.

Lastly, the group discussed different uses for sequencing and bioinformatics in different epidemiological contexts: 1) vaccine composition, 2) outbreaks, 3) research, 4) ongoing surveillance and 5) early warning.

**Session 4 – Linking with vaccination strategies (3 November 2022)**

The last session of the second day was devoted to discussing advances in poultry vaccine composition (VCM), an output listed in the previous 2021 consultation.

A presentation from the Joint World Organisation for Animal Health (WOAH)-FAO Scientific Network On Animal Influenza (OFFLU) Poultry vaccine matching activities have been conducted by the United Kingdom’s Animal and Plant Health Agency (APHA), in collaboration with FAO and OFFLU. APHA has selected reference antigen for their panel and is producing matching high resolution chicken antisera. The current panel is mostly representatives of 2.3.4.4.b clades circulating at the moment. Clade 2.3.2.1.c is also included, using virus from Indonesia isolated in a quarantined bird. Currently, the goal is to pilot poultry vaccine matching activities with a limited number of clades and expand to additional AIV clades in the future.

Discussions on the topic highlighted challenges related to ongoing poultry VCM and proposed solutions:

- **Challenges**
  - Virus considered are Western-centric – what are the benefits for Asia?
  - What are appropriate vaccine monitoring procedures?
  - Impacts of illegal vaccination
  - How to address the possibility of reverse genetics for vaccines and intellectual property
  - Vaccine production is time-consuming – especially the quality assurance process
• Solutions/ideas
  o Decentralising sera beyond reference laboratories can improve representativeness of AIVs mapped
  o Engaging with the private sector from the beginning can highlight needs and partnerships – e.g. H9 and H7 vaccine market
  o Including H9 viruses and utilising formal requests from international organisations can raise interest and participation from multiple countries
  o Discussions on harmonizing technologies at VCM should occur
  o Monitoring trends in vaccine technologies can offer new opportunities – e.g. recombinant AI vaccines?
  o Can there be a universal influenza vaccine?

A last brainstorming activity with the group focused on improving post-vaccination surveillance and the group discussed the following ways forward in Asia:

• Ensuring use of correct local clades/antigen for surveillance – especially for H5 AIVs
• Capturing genetic evolution through genomic surveillance (i.e. not just hemagglutination inhibition [HI])
• Using sentinel birds to monitor situation
• Ensuring robust testing sensitivity by increasing sample size, especially when conducting surveillance in vaccinated populations
• Addressing current challenges, including:
  o Increased cost from increased serological surveillance
  o Increased training needs
• Conducting continuous surveillance of vaccinated flocks using novel approaches such as air filters, water in LBMs following a “smart cities” approach – the private sector may be interested, especially regarding air sampling at their facilities
• Leveraging regional experience in Asia, where post-vaccine monitoring already is ongoing in the by governments and private sector (e.g. Malaysia, Indonesia)

**Session 5 – Where do we go next (4 November 2023)**

On the last day of the consultation, a summary of the consultation was presented to participants, who had a final opportunity to comment on any of the topics covered in the preceding days.

The final exercise of the consultation consisted of paving the way forward to address the gaps and needs identified during the entire meeting. In facilitated sessions, participant formulated an overarching goal to reach in order to achieve an “ideal” early warning system for AI.

*To reach an “ideal” early warning system by 2033, we need: open access real-time global database for: diseases, populations, risks; continuous surveillance in risk areas with quality assurance diagnostics; including wildlife and environment; and with overall accepted global governance.*
The group then conducted a back-casting exercise to identify the relevant milestones to achieve the stated goal by 2033. These included:

- **Governance and partnerships enabling data sharing**
  - Improved partnership framework with private sector
  - Reduced negative impacts of detection/reporting/vaccination
  - Global agreements for fair and equitable data sharing
  - Better use of data to inform vaccine matching activities

- **Novel approaches in sampling, diagnostics and data analysis incorporated into countries’ surveillance activities**
  - Routine use of novel approaches at country-level, incorporating:
    - Remote sampling technologies
    - Field-based assays
    - Environmental sampling
    - Bioinformatics
  - Global guidance and validation processes to facilitate use of novel approaches by governments
  - Promoting the use of NGS as the platform of choice for AIV detection supported by streamlined pipelines
  - “Smart” farms and LBMs where environmental sampling is conducted in consistent way

- **Improved risk evaluation and prediction**
  - Development of global real-time bird migration models
  - Improved traceability along the poultry value chain
  - Integration of big data and artificial intelligence into predictive and early warning systems

Before closing the meeting, participants agreed on actions to take to ensure the outputs of this consultation are used for action. Specifically these include:

1. Using the proposed timeline as guidance to plan activities around early warning for AI, including with:
   a. Potential donors (e.g. World Bank, Asian Development Bank, and other funds dedicated to emerging infectious diseases in the wake of the COVID-19 pandemic
   b. Committees and work groups that are developing similar early warning strategies
2. Further including the environmental sector into One Health activities
3. Consolidating communications between international organisations (e.g. WOAH, FAO) during the early part of the timeline
Background and objectives

Background

Since its appearance in 2008, highly pathogenic avian influenza (HPAI) H5Nx clades have steadily evolved, leading to antigenically and genetically distinct isolates. This virus variety has led to a ten-fold rise in avian influenza A viruses (AIVs) (notably H9N2 and H5Nx subclades) detections bird populations between 2020 and 2019 (FAO, EMPRESi), leading in many outbreaks in both domestic and bird population, as well as several human infections.

In early 2020, HPAI events caused by H5N8 were reported across various continents. This was followed by a global spread of A/H5Nx subclade 2.3.4.4b throughout Europe, Asia, Africa and more recently the Americas. In addition, A/H5N5 viruses were identified in Europe and Asia, while A/H5N6 and A/H5N8 continue to be present in China and Southeast Asia since early 2019, along with sporadic outbreaks of A/H5N2, A/H5N3, and A/H5N4. Lastly, A/H7Nx and endemic LPAI H9N2 viruses continue to circulate sporadically throughout the world and are a major concern for the poultry industry. The global AIV situation goes beyond outbreaks in poultry and wild bird outbreaks and numerous zoonotic infections have been reported in humans and other mammalian species in the past few years. Subtypes include A/H7N4, A/H9N2, A/H10N3, A/H3N8, and, most concerning, A/H5Nx clade 2.3.4.4b viruses.

Despite decades of investments into AIV surveillance, further work is needed to better detect emerging subtypes. Currently, numerous stakeholders and countries only perform AIV surveillance, response, and prevention on an ad-hoc basis. It is vital to move away from responding reactively and to focus on proactive prevention and control. Connecting and aligning the work done by these various stakeholders will be critical to generate a true global “early warning” system that will facilitate rapid communication and data sharing prior to outbreaks caused by emerging HPAI subtypes. In addition, global availability of genomic data and viral isolates is essential to the success of vaccination programs in both humans and animals, and to develop/revise critical diagnostic strategies. These include innovative sampling and diagnostic methodologies such as environmental sampling, which will provide countries in Asia and the Pacific with more cost-effective ways to detect AIV and other endemic and emerging pathogens of concern in areas of high risk.

In 2021, the Emergency Centre for Transboundary Animal Diseases (ECTAD) at the Food and Agriculture Organisation of the United Nations (FAO) Regional Office for Asia and the Pacific (RAP) organised an online expert consultation to discuss challenges and ways forward related to global AIV surveillance and early warning. During the meeting, several key themes were discussed, including incorporation of novel technologies and sampling strategies, improving bioinformatics technologies for faster data analysis, and better use of surveillance outputs to inform zoonotic risk mitigation and poultry vaccine strategies. To build upon the outputs of the previous meeting, FAO RAP, in collaboration with the Australian Centre for Disease Preparedness (ACDP) organised an in-person meeting to address progress and continuing challenges related to the action points from this initial consultation with the overarching goals of improving global early warning systems, as well as discuss novel sampling and diagnostic methodologies for AIV surveillance.

Objectives
Based on expert feedback, it was decided to build upon outputs of the previous avian influenza consultation and target discussion of this meeting on “Better detection and better response” to emerging AIV threats.

The specific objectives of the meeting were to:
5. Review progress and challenges since the 2021 expert consultation, specifically towards improved global avian influenza (AI) early warning mechanisms and poultry vaccine composition meeting
6. Identify challenges and best practice to implement novel approaches to sampling and diagnostics of AIVs at country-level
7. Discuss advancements in next generation sequencing (NGS) and bioinformatics
8. Identify ways forward to further achieve the vision of global early warning and information sharing through the use of innovative approaches

Date and venue
The avian influenza expert consultation was planned directly following the World Organisation for Animal Health (WOAH)’s Regional Expert Group Meeting for diseases of poultry in Asia & the Pacific, held in Geelong, Australia between 31 October and 2 November 2022. This was chosen due to the presence of the relevant avian experts from the region attending the WOAH meeting, to which FAO ECTAD RAP was also invited to present.

It was decided to organise the FAO expert consultation from 2-4 November 2022 at the Rydges hotel in Geelong (see Appendix 1 for full agenda).

Participants
An invitation to participate in the FAO expert consultation was sent to both avian disease experts invited to the preceding WOAH meeting, as well as additional experts whose expertise is essential to reach the objectives of the consultation.

In total of 24 experts (9 females, 15 males) participated in the FAO meeting, including representatives from governments, research institutions, international organisations and reference laboratories (see Appendix 2 for details of the participants).

Overview of consultation programme
The consultation was organised into five sessions addressing specific topics and building upon each other:

- **Session 1**: Introduction and setting the scene
- **Session 2**: Novel approaches
- **Session 3**: Bioinformatics, data sharing
- **Session 4**: Linking with vaccination strategies
- **Session 5**: Where do we go next
Session 1 – Introduction and setting the scene

The first session of the FAO expert consultation on avian influenza built upon the presentations provided during the WOAH Avian Disease meeting, which already highlighted the avian influenza situation in the region of Asia and the Pacific.

Progresses and remaining gaps

After a short initial presentation describing the general overview of the meeting agenda and objectives, participants were directly led into a first facilitated exercise in small groups to identify progress and remaining gaps (Fig.1) since the 2021 FAO avian influenza consultation (Fig.2). Individual feedback for progresses was then categorized and organized by themes (Tables 1). Individual gaps were also grouped together under six over-arching questions to resolve (Table 2).

Figure 1. Participants brainstorming on progresses made and remaining gaps related to early warning and information sharing for avian influenza threats (top), with progresses (bottom left) and gaps (bottom right) identified during the session.
Figure 2. The proposed “ideal early warning framework” as discussed during Session 5 of the Regional avian influenza expert meeting (30 November – 3 December 2021)
Table 1. Themes highlighted during the brainstorming of progresses related to early warning and information sharing for avian influenza threats.

<table>
<thead>
<tr>
<th>Major themes</th>
<th>Details on progresses</th>
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| **Global coordination and sharing of data related to AI** | • Better use of virtual technologies to coordinate work at a distance (E.g. Zoom platform)  
• Inclusion of environmental groups into Joint WOAH-FAO Scientific Network On Animal Influenza (OFFLU) network  
• ACDP pipeline developed to get authorization from regional submitters to upload virus data to OFFLU for vaccine matching activity  
• Being proactive – New/emergent notifications now actively chased by FAO/OFFLU to collate available data and share globally guidance summaries, leading to improved early warning  
• At a global level, sharing of information on circulating strains has improved (epidemiological information)  
• There appears to be better collaboration/partnerships for early warning and global data sharing on zoonoses between WHO/OFFLU, especially related to vaccine composition meetings (VCM), Tool for Influenza Pandemic Risk Assessment (TIPRA) |
| **Global guidance, tools** | • Published avian influenza risk-based active surveillance guidance (FAO)  
• Letter of agreement between FAO and Université Libre de Bruxelle to develop AI early warning decision support tool (FAO)  
• Development of an interface model for wild birds/poultry for Africa & Eurasia |
| **Better surveillance methodologies, improved efficiency** | • At a national level, there’s been an increase in accurate screening tests for surveillance and early warning, including education for laboratory personnel, proficiency testing at the regional level  
• New wild bird/poultry interface surveillance conducted in some countries  
• Due to silent infection in ducks, crow passive surveillance in some countries has been implemented and is now more effective  
• All regional diagnostic laboratories are capable of detecting type A influenza  
• Some countries reported surveillance activities conducted by Ministry of Environment using simpler diagnosis systems |
| **Piloting new approaches** | • Trial of novel sampling and collection methods  
• Starting to compare “Gold standard” with novel detection methods, especially using metagenomics  
• Availability of advanced sequencing methods for metagenomics and low copy numbers  
• Advances in AIV sequencing on Nanopore, including field-forward potential  
• Field-forward bioinformatics pipeline for real-time AIV on Nanopore |
Increased outreach & interest

- Australia: impact of Japanese equine encephalopathy outbreaks stimulated intersectoral data sharing between animal and human health
- Australia: improved analysis and sharing (publications) of sequences from wild birds and availability to the public
- Australia: increased awareness of susceptibility to AI of wild bird populations

Better understanding of disease drivers and risks

- More research conducted on social determinants of health (especially following COVID-19)
- Global monitoring of wild bird dynamics
- Australia: increased understanding of environmental drivers of AI dynamics in wild birds and poultry
- Traceability of movement and control for some bird species (e.g. fighting cocks)
- Better identification of hotspots for migratory birds since 2017
- Australia: comprehensive analysis of 10 years’ worth of AI surveillance data reveals host range, factors modulating host competency; also analysis of wild bird sequences in the past 15 years reveal virus movement

Table 2. Themes highlighted during the brainstorming of gaps related to early warning and information sharing for avian influenza threats.

1. How do we improve One Health coordination?

- Lack of coordination between donors – duplication of same activities
- Lack of coordination between environment and animal sector
- Lack of training of environmental authorities for passive surveillance
- Little collaboration between disciplines
- Ministries/department silos still inhibit collaboration
- Barriers in bilateral collaboration between countries (e.g. Japan & Russian Federation)
- Legal and political frameworks unclear on sample/data ownership and sharing
- Lack of genuine One Health collaboration
- Disruptions due to COVID-19 restrictions (e.g. no face to face meetings)
- Lack of funding for disease investigation
- Australia: little clarity on surveillance purpose and actions associated with results
- WOAH/FAO reference labs that characterize viruses are not notification authorities

2. How do we address lack of timely information sharing?

- Sharing of sequence data is still low (but to be improved next year)
- Lack of available information (in real time) between adjacent subnational jurisdictions in some countries
- Challenges in data sharing between jurisdictions
- Need more publically available sequence data to inform research
- Lack of timely data sharing (e.g. in Australia)
- Limited info sharing on AIVs isolates, including low pathogenic avian influenza (LPAI)
3. How to prioritize government resources?

- Limited number of few people available to conduct activities – especially at country-level
- Few succession plans for experts, leading to repeated work following experts’ leave
- Lowering interest from new veterinary graduates to work in public practice, leading to lowering of human resources
- Human resources – lack of personnel due to transfer and retirements
- Difficulty in maintaining trained staff due to funds being project-based, in addition to movement of staff
- Transfer of staff
- Gaps in maintenance of laboratory facilities, leading to limited funding for repair, services
- Obsolete equipment used for fast detection of outbreaks
- Limited computational power/infrastructure
- Lack of budget, lack of manpower, lack of experts
- Funds
- Country reliance on donor funding

4. How do we increase public sector engagement?

- Lack of public-private partnerships (PPP)
- Need more public/private partnerships
- Poultry industry deny access for surveillance – how can we respond if we don’t know what’s there?
- Less cooperation from farmers, esp. commercial producers to notify diseases
- No PPP, reduced funding

5. How do we increase wild bird surveillance?

- Lack of information on wild birds susceptible to HPAI viruses, leading to spread of silent infections
- Surveillance in wild birds is limited to specific areas – more locations needed
- Limited information on migration patterns and drivers and potential role of species other than *Anatidae*
- Wild bird surveillance regimes are largely uninformative for revealing epidemiology and for early warning
- Systems are designed to protect poultry but HPAI kills millions of wild birds and there is little interest in systems for the benefit of wild birds
- Need more involvement from wildlife experts, ecologists
- Sample bias in wild birds – samples usually taken from breeding sites (many tests lead to many positives)

6. How to we improve access to technical skills for new thinking?

- Need for more innovative research and staff
- Need to increase capacity in analysis of sequence data
- Lack of capacity/capability, sustainability in high consequence “Global South”
- Lack of capacity for data interpretation and communications
• Need increase in genotype to phenotype characterization
• Reliance on outdated diagnostics
• Need for more bioinformatics trainings
• Surveillance gaps – need for improved methodologies for early detection and identification at the subnational levels
• Lack of surveillance in wildlife populations and at interface with domestic
• Limited interest in early warning systems in wild birds leading to early warning gaps related to hotspot identification for migratory birds
• Limited active surveillance in wild birds and environmental sampling at congregation sites
• Minimal active surveillance (not reactive or syndromic) in poultry
• Ministries of Agriculture and industries are not convinced of the benefits of surveillance and data sharing
• Targeted surveillance on high-risk populations only in poultry and live bird markets (LBMs)

Addressing gaps with decision-makers
Following the initial brainstorming session, participants were invited to develop potential recommendations to address the gaps identified in Table 2. An initial discussion in plenary identified major stakeholders who play an important role in implementing potential actions to take (i.e. decision-makers).

Participants individually identified the three most important decision makers who would be consulted to address the gaps. Stakeholders listed by the group included:

• Government institutions
  o Ministry of Agriculture, Chief veterinary officers (CVO)
  o Ministry of Environment
  o Ministry of Finance
• Academia
• Industry
• Ornithologists and bird experts
• Ministry of Environment
• International organisations: FAO, WOAH, Quadripartite

Different participants assumed the role of the various stakeholders to assess whether the proposed solutions from the rest of the group were either: not feasible, maybe feasible, or fully feasible (Fig.3).

Potential solutions that were decided to be feasible where then plotted on a four by four table based on whether the solution was novel (“business as usual” vs “new idea”) and the difficulty to implement (“easy” vs “hard”) (Fig. 4).

The table allowed participants to prioritise proposed solutions based on the ease of implementation and novelty of the idea:
• **Priority 1** ("Easy and business as usual"): this category represents the "low hanging fruit", proposed ways forward that are already part of institutions’ mandates/activities and are relatively simple to implement.

• **Priority 2** ("Easy and new idea"): solutions under this category are those that are also easy to implement, and are relatively novel approaches to addressing early warning/surveillance gaps.

• **Priority 3** ("Hard and new idea"): these consists of novel approaches that may resolve some of the perceived gaps, however they may be challenging to implement due to various barriers. The cost-benefit of these ideas should be considered prior to investing in them.

• **Priority 4** ("Hard and business as usual"): these ideas rank in the lowest priority to implement, largely due to the fact they are already part of institutions’ mandates and may be quite challenging. This does not mean that these proposed solutions should be abandoned, rather than focusing on novel approaches and feasible solutions may be more cost-effective.

The exercise marked the end of the consultation’s first day and a brief presentation was given to participants on the programme for the following days prior to closing the session.

![Image of group activity to prioritise potential solutions to gaps identified. Top: role-playing with different decision-makers to identify feasibility of proposed solutions, Bottom: outputs of the brainstorming session](image-url)

**Figure 3.** Group activity to prioritise potential solutions to gaps identified. Top: role-playing with different decision-makers to identify feasibility of proposed solutions, Bottom: outputs of the brainstorming session.
Session 2 – Novel approaches to AI early warning

The second day of the consultation started with an initial discussion linking novel approaches and strategies with early warning activities. This served as an introductory component for larger discussions around bioninformatics later in the day (Session 3).

The group agreed on a definition for early warning, to ensure that novel approaches discussed are fit for purpose. The working definition for early warning for the purpose of the consultation consisted of:

*Monitoring changes in trends (including virus subtypes, risks) that provide actionable information before outbreaks/spillover*

**During outbreaks**

The group discussed a number of sampling approaches that could be used during outbreak situations, including sampling of:

- Hosts
- Environment
  - Farm - litter, water, faeces, air in farms or outside the outbreak area
  - Natural areas (targeting wildlife) – water bodies, faeces
- Animal transportation areas – e.g. cages

Assays to perform on the samples above include real-time polymerase chain reaction (RT-PCR) tests, antigen tests and in some instances Oxford Nanopore MinION.
Prior to outbreaks

Early warning activities that can be implemented prior to outbreak situation, to monitor changes in risks or detect disease incursions at the earliest time.

The group discussed opportunities to use air sampling in various strategic areas within the poultry value chain, including in live animal markets, farms, hospitals, slaughterhouses, areas where poultry workers congregate and other hotspots identified during previous risk assessments. Specifically, sampling air on vents and wastewater outside of major poultry farms or markets can be a cost-effective way to detect circulating viruses.

The group discussed the possibility of using feathers – which are vascularised – as a novel sampling tool for both domestic and wild birds.

These novel approaches could be used in a continuous manner to develop a baseline, as well as during period of high risks.

As the session finished, the group identified challenges that remain in order to fully implement novel approaches to the early detection of AIVs in the Asian context. These included:

6. The need to improve acceptance of new methodologies/technologies by governments and institutions
7. Developing protocols/procedures to manage positive identification of AIVs through novel approaches
8. Monitoring trends in a continuous way to ensure a good baseline for the approaches
9. The need to calibrate and validate these novel technologies
10. The need to provide decision-makers with more background

Session 3 – Bioinformatics, data sharing

An initial discussion of the needs and challenges related to bioinformatics started this session (Table 3).

Table 3. Bioinformatics needs and barriers – summary of initial brainstorming

<table>
<thead>
<tr>
<th>Needs</th>
<th>Barriers</th>
</tr>
</thead>
<tbody>
<tr>
<td>• Infrastructure – reagents, computers, data storage, all-in-one units</td>
<td>• Cost – maintenance, reagents</td>
</tr>
<tr>
<td>• Enabling environment – advocacy, policy</td>
<td>• Data – security, privacy, sovereignty</td>
</tr>
<tr>
<td>• Standardization, consistency of analyses</td>
<td>• Inconsistent equipment</td>
</tr>
<tr>
<td>• Training</td>
<td>• Trust – acceptance, understanding</td>
</tr>
<tr>
<td>• Global guidance/best practices that is adaptable</td>
<td>• Reference database</td>
</tr>
<tr>
<td>• Antigenic cartography</td>
<td>• Quality assurance</td>
</tr>
<tr>
<td>• Better pipelines for better results</td>
<td>• Lack of knowledge transfer/retention</td>
</tr>
<tr>
<td></td>
<td>• Technology advances to fast to keep up</td>
</tr>
<tr>
<td></td>
<td>• Delays due to batching</td>
</tr>
</tbody>
</table>
The participants then built on this initial brainstorming exercise to discuss several key considerations to promote use of bioinformatics technologies in more detail.

**Resources**

Bioinformatics technologies can be resources-intensive, both in terms of human and laboratory resources. They can be challenging to implement at the national level them without proper continuous budget and investment. In addition a regional approach to trainings may be difficult to implement due to countries’ unequal capacities and more country-specific approaches may be more useful.

**Data management**

Experts discussed the need to identify minimum data fields that would be needed for early warning, while balancing countries’ concerns over data security and sovereignty. This issue can be exacerbated by bioinformatics platforms that are cloud-based. Outputs of data analyses also represent a challenge to ensure they can be easily and rapidly used by decision-makers. Data collection/management strategies that are fit for purpose (e.g. early warning, research, etc.) must be developed.

**Evolving technologies**

Sequencing equipment is continuously updated, leading to multiple generations of systems that may have specific qualities over others, depending on the context (Table 4). Providing consistent and standardised analyses across a region is highly challenging due to the rate of change of the technology, differing computing platforms, and use of non-portable devices.

**Table 4. Differences between first-, second- and third-generation sequencing technologies**

<table>
<thead>
<tr>
<th>1st generation sequencing</th>
<th>2nd generation sequencing</th>
<th>3rd generation sequencing</th>
</tr>
</thead>
<tbody>
<tr>
<td>- E.g. Sanger</td>
<td>- E.g. Illumina</td>
<td>- E.g. Nanopore MinION</td>
</tr>
<tr>
<td>- Familiar to use</td>
<td>- Provides deep sequencing</td>
<td>- Reagent supply</td>
</tr>
<tr>
<td>- Cheap, relatively quick</td>
<td>- Costly and time</td>
<td>- Not as cost effective as</td>
</tr>
<tr>
<td>- No full genome analysis</td>
<td>- consuming</td>
<td>Sanger (though cost</td>
</tr>
<tr>
<td></td>
<td>- Useful for research</td>
<td>per genome better)</td>
</tr>
<tr>
<td></td>
<td>- Standard sequencing for</td>
<td>- Users have control</td>
</tr>
<tr>
<td></td>
<td>information</td>
<td>over genome and can</td>
</tr>
<tr>
<td></td>
<td>- Maintenance cost around</td>
<td>conduct analyses on</td>
</tr>
<tr>
<td></td>
<td>30 000 USD/year</td>
<td>their own</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Maintenance cost</td>
</tr>
<tr>
<td></td>
<td></td>
<td>around 1000 USD/year</td>
</tr>
<tr>
<td></td>
<td></td>
<td>(for MinION)</td>
</tr>
</tbody>
</table>
Applications for early warning

In order to use metagenomics effectively for early warning, bioinformatics will have to be accurate and conducted in a frequent, routine manner. In some situations, batching of samples throughout the year is done, where multiple samples may be sequenced once yearly. This strategy is useful for research purposes, however it does not fit the needs for early warning and the experts agreed that sequencing samples at minimum on a quarterly basis should be done for better information sharing and regional awareness of circulating AIVs. Table 5 provides additional details on different uses of sequencing and bioinformatics based on their purpose.

Table 5. Uses of sequencing and bioinformatics based on different objectives

<table>
<thead>
<tr>
<th>Use</th>
<th>Type of sequencing needed</th>
<th>Bioinformatics analysis method</th>
<th>Frequency of analyses</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vaccine composition</td>
<td>- Hemagglutinin (HA)</td>
<td>- Assembly</td>
<td>6-12 months</td>
</tr>
<tr>
<td></td>
<td>- Sanger</td>
<td>- Alignment</td>
<td></td>
</tr>
<tr>
<td></td>
<td>- Illumina for batched</td>
<td>- Basic data cleaning</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Neuraminidase (NA) mapping</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Antigenic cartography</td>
<td></td>
</tr>
<tr>
<td>Outbreak situation</td>
<td>- Full genome (minimum HA and NA)</td>
<td>- Assembly / Alignment</td>
<td>Ideally as soon as possible (within 3-5 days) though in reality it is often done after 1-3 months</td>
</tr>
<tr>
<td></td>
<td>- 1st, 2nd, 3rd generation sequencing</td>
<td>- Phylogenetics</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Metaphylogenetics</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Receptor</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Antigenic sites of outbreak strain</td>
<td></td>
</tr>
<tr>
<td>Research</td>
<td>- Full genome</td>
<td>- Assembly / Alignment</td>
<td>Done in batches, depending on research needs (Illumina can be quite cost effective in this situation)</td>
</tr>
<tr>
<td></td>
<td>- 2nd generation sequencing</td>
<td>- Phylogenetics</td>
<td></td>
</tr>
<tr>
<td></td>
<td>- Very deep sequencing</td>
<td>- Metaphylogenetics</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Receptor</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Antigenic sites of outbreak strain</td>
<td></td>
</tr>
<tr>
<td>Ongoing surveillance (e.g. for viral monitoring)</td>
<td>- Full genome – more focused on HA and NA</td>
<td>- Assembly / Alignment</td>
<td>Quarterly, monthly, weekly</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Phylogenetics</td>
<td>Must be done in routine way to obtain proper baseline</td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Metaphylogenetics</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Receptor</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>- Antigenic sites of outbreak strain</td>
<td></td>
</tr>
</tbody>
</table>
**Early warning**

<table>
<thead>
<tr>
<th>Early warning</th>
<th>Metagenomics</th>
<th>Automated pipelines &amp; real-time reporting</th>
<th>Quarterly, monthly, weekly</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>Must be done in routine way to obtain proper baseline</td>
</tr>
</tbody>
</table>

**Collaboration & coordination**

A participatory and collaborative process is essential to ensuring long-lasting application of bioinformatics technologies at country-level that can also inform the broader international AI community. Sensitivities around information sharing between countries continue to present barriers to efficient international early warning mechanisms. Involving stakeholders early on can provide deep understanding of their main concerns related to data sharing, and how to mitigate/address them (e.g. reluctance to share data due to impact on trade/tourism, publication in scientific journals, etc.).

The opportunity to partner with the private sector can offer cheaper alternative to conduct bioinformatics analyses, as it requires fewer costs than maintaining in-house capacities and uses existing logistics for sample transport. Challenge of governments’ reluctance to send samples to private companies will need to be addressed.

At a government-level, outreach should be conducted to CVOs to support reporting of AI directly from the field rather than the laboratory – especially when field assays are used.

In addition to CVOs, technical staff (e.g. laboratory workers, bioinformatics focal point) should receive the appropriate trainings to understand bioinformatics well enough to rectify problems that may arise. The support of international organisations and experts can be useful for that process, for example development of guidance and best practices that can be adapted to country contexts, and updated frequently to keep up with the progress in the technology.

Lastly, the group discussed the possibility to require annual reports from laboratories on bioinformatics results to be made available for early warning purposes, as well as the difficulties arising from the lack of consistency in nomenclature of circulating and emerging AI clades.

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**Session 4 – Linking with vaccination strategies**

The afternoon of the second day of the AI consultation was dedicated to discussing progresses made towards poultry VCMs, following up on the recommendations from the 2021 FAO ECTAD Regional Consultation.

**Update on vaccine matching activities (OFFLU)**

Dr. Frank Wong from ACDP started the session with a presentation updating participants on the vaccine-matching work done by the Joint WOAH-FAO Scientific Network On Animal Influenza (OFFLU).
In his presentation, Dr. Wong started by laying the grounds on what makes a good AI poultry vaccine – he proposed the following points:

1. Antigenic match of the seed strain to virus circulating in the region
2. Ability to induce immunity
3. Ease of administration
4. Ability to differentiate infected from vaccinated animals (DIVA)
5. Availability

Poultry vaccine matching activities have been conducted by the United Kingdom’s Animal and Plant Health Agency (APHA), in collaboration with FAO and OFFLU. APHA has selected reference antigen for their panel and is producing matching high resolution chicken antisera. The current panel is mostly representatives of 2.3.4.4.b clades circulating at the moment. Clade 2.3.2.1.c is also included, using virus from Indonesia isolated in a quarantined bird. Currently, the goal is to pilot poultry vaccine matching activities with a limited number of clades and expand to additional AIVs clades in the future.

Frank highlighted some challenges in conducting this work, as well as ways to move forward:

- A robust surveillance system is needed at country-level to ensure vaccination breakdowns are identified and reported.
- The end goal of the poultry vaccine matching work is to make the results available to anyone
- Movement of virus to reference laboratories should be done in a timely fashion for characterization is essential for successful vaccine matching – however reference laboratories cannot act as data sharing
- Illegal vaccinations can negatively affect the usefulness of poultry vaccine monitoring activities
- The impact on trade from reporting of circulating AIVs at country-level should be taken into consideration
- Hemagglutination inhibition (HI) under harmonized pipeline
- The benefits of virus sharing are not always clear for countries and laboratories

Dr. Wong also commented on some of the discussion points from the previous sessions. For example, one of the critical gaps when talking about standardisation and harmonisation is that governments often defer to WOAH standards; however, these may take 3-5 years before being published and can be outdated already at the time of publication – this is especially true for rapidly-evolving technologies such as bioinformatics. A better approach would be to provide a list of best practices that can be rapidly adapted by countries, rather than producing more prescriptive guidance. If more specific guidance is developed, it should be made with adaptability in mind and they can be considered as living documents to keep up with evolving technologies. Lastly, it is important to ensure that guidance is applicable at a global level and the products developed can be used by the global South.

The issue of technology was also brought up and available software or operational systems to analyse phylogenetic trees may be different between countries. If decision-makers are using different systems, they may not be able to interpret the same phylogenetic tree.
As a final point, there is the need to keep updated with new AIVs datasets, and a dedicated bioinformatician at country-level can maintain national databases up to date, with the support from global poultry vaccine monitoring meetings which can provide updated reference data sets.

Discussion on poultry vaccine composition

Following Dr. Wong’s presentation, facilitators posed the following questions to the group to guide plenary discussion:

1. Are countries interested in having this data available?
2. How else could OFFLU provide beneficial data to countries?
3. What do you want from us?
4. Are countries willing to share viruses with red labs to be used in these studies?
   a. If no, why?
   b. What would it take to prove that data is safe/won’t affect publications/won’t be misused?
   c. Is this a “political no” or a “pragmatic no”?
5. What are the other barriers towards surveillance data sharing?

Outputs of this discussion session are summarised in Table 6, and were formulated as challenges to overcome and potential solutions/ideas to move forward.

Table 6. Key summarised points from the discussion around poultry vaccine matching activities

<table>
<thead>
<tr>
<th>Challenges</th>
<th>Solutions/ideas</th>
</tr>
</thead>
<tbody>
<tr>
<td>- Virus considered are Western-centric – what are the benefits for Asia?</td>
<td>- Decentralising sera beyond reference laboratories can improve representativeness of AIVs mapped</td>
</tr>
<tr>
<td>- What are appropriate vaccine monitoring procedures?</td>
<td>- Engaging with the private sector from the beginning can highlight needs and partnerships – e.g. H9 and H7 vaccine market</td>
</tr>
<tr>
<td>- Impacts of illegal vaccination</td>
<td>- Including H9 viruses and utilising formal requests from international organisations can raise interest and participation from multiple countries</td>
</tr>
<tr>
<td>- How to address the possibility of reverse genetics for vaccines and intellectual property</td>
<td>- Discussions on harmonizing technologies at VCM should occur</td>
</tr>
<tr>
<td>- Vaccine production is time-consuming – especially the quality assurance process</td>
<td>- Monitoring trends in vaccine technologies can offer new opportunities – e.g. recombinant AI vaccines?</td>
</tr>
<tr>
<td></td>
<td>- Can there be a universal influenza vaccine?</td>
</tr>
</tbody>
</table>
Improving post-vaccination surveillance

The last discussion of the second day covered the specifics of post-vaccination surveillance and the group identified the following ways forward in the context of Asia:

• Ensuring use of correct local clades/antigen for surveillance – this is especially relevant for H5 AIVs
• Capturing genetic evolution through genomic surveillance (i.e. not HI)
• Using sentinel birds to monitor situation
• Ensuring robust testing sensitivity by increasing sample size, especially when conducting surveillance in vaccinated populations
• Addressing current challenges, including:
  o Increased cost from increased serological surveillance
  o Increased training needs
• Conducting continuous surveillance of vaccinated flocks using novel approaches such as air filters, water in LBMs following a “smart cities” approach – the private sector may be interested, especially regarding air sampling at their facilities
• Leveraging regional experience in Asia, where post-vaccine monitoring already is ongoing in the by governments and private sector (e.g. Malaysia, Indonesia)

Session 5 - Where do we go next

The last day of the consultation started with an initial summary of the outputs so far, and provided participants with the opportunity to revisit some of the discussions from previous sessions. Following the discussion, the group conducted a back casting exercise to identify the steps to reach in order to reach a defined goal.

Participants’ feedback on previous discussion sessions

Bioinformatics. The group first revisited the topic of bioinformatics and consolidated the general needs related to this topic. These included:

• Needs for:
  o Infrastructure: reagents, computers, data storage, all-in-one units
  o Enabling environment: advocacy, policy
  o Standardisation, consistency of analyses
  o Training
  o Adaptable/updatable global guidance and best practices
  o A multi-disease and systematic approach to implementation of bioinformatics capacities in the region. This can motivate national governments to invest in these technologies, as they can be applied to more than AI – especially if national laboratories’ interest are focused on foot and mouth disease and African swine fever
**Vaccine composition.** The next topic that the group chose to revisit was poultry vaccine composition. Participants reiterated the needs for the following:

- Decentralisation of testing beyond reference laboratories
- Harmonisation of technologies
- Antigenic cartography – especially with standardized operating procedures (SOPs)
- Training of national focal points

The group then discussed some challenges to overcome in both of the areas above.

Promoting harmonization of technologies has not gained traction and there are questions on how to best deliver sequencing proficiency testing. Sanger sequencing is no longer the norm and NGS uptake is not high in Southeast Asia – even considering 2nd generation technologies. Some laboratories are progressing to NGS, though not all are able to implement it yet. Questions were raised on how to best facilitate this uptake.

A proposed option would be to start with Sanger technologies and give forward and reverse sequences as a set. Training exercises could be conducted to verify and align phylogenetic trees as initial proficiency tests (e.g. using MinION and Lumina outputs for proficiency testing).

Lastly, the topic of antigenic cartography was brought up during the consultation. Participants discussed antigenic cartography activities in Indonesia and how streamlining efforts were put in place such as pre-screening using reference serum. This has allowed to identify targets for full panel and saved reagents and work.

**Looking to the future – back casting exercise**

The last activity of the consultation consisted of a back-casting exercise, where participants state a goal to reach by 2033, and then back track to identify what hypothetical milestones during 2023-2033 have led to achieving the goal.

To get started, participants were asked to brainstorm in plenary on what criteria/milestones would be needed to reach the vision of the “ideal” early warning system (Fig.2). Individual input from participants was categorized to formulate the overarching goal to reach by 2033, which was formulated in the following statement:

*To reach an “ideal” early warning system by 2033, we need:*

1. *Open access real-time global database for: diseases, populations, risks;*
2. *continuous surveillance in risk areas with quality assurance diagnostics;*
3. *include wildlife and environment; and*
4. *with overall accepted global governance.*

Some individual input from participants were left uncategorized.
Using the statement above as end-points to reach by 2033, participants then placed their individual sticky notes on a timeline spanning 2023-2033 (Fig.4) to link milestones with targeted dates of implementation (Fig.5).

Responses gathered during this exercises could be grouped into the following themes:

- **Governance and partnerships enabling data sharing**
  - Improved partnership framework with private sector
  - Reduced negative impacts of detection/reporting/vaccination
  - Global agreements for fair and equitable data sharing
  - Better use of data to inform vaccine matching activities

- **Novel approaches in sampling, diagnostics and data analysis incorporated into countries’ surveillance activities**
  - Routine use of novel approaches at country-level, incorporating:
    - Remote sampling technologies
    - Field-based assays
    - Environmental sampling
    - Bioinformatics
  - Global guidance and validation processes to facilitate use of novel approaches by governments
  - Promoting the use of NGS as the platform of choice for AIV detection supported by streamlined pipelines
  - “Smart” farms and LBM where environmental sampling is conducted in consistent way

- **Improved risk evaluation and prediction**
  - Development of global real-time bird migration models
  - Improved traceability along the poultry value chain
  - Integration of big data and artificial intelligence into predictive and early warning systems
Figure 4. Conducting the back-casting exercise
Figure 5. Major milestones to reach the objectives of an “ideal” early warning system in Asia (ASEAN = Association of Southeast Asian Nations; SAARC = South Asian Association for Regional Cooperation; SEAOHUN = Southeast Asia One Health University Network)
Conclusions and ways forward

The objectives of this expert consultation were to:

1. Review progress and challenges since the 2021 expert consultation, specifically towards improved global AI early warning mechanisms and poultry vaccine composition meeting
2. Identify challenges and best practice to implement novel approaches to sampling and diagnostics of AIVs at country-level
3. Discuss advancements in NGS and bioinformatics
4. Identify ways forward to further achieve the vision of global early warning and information sharing through the use of innovative approaches

The participatory process of the consultation was essential to obtain experts’ feedback and jointly identify progresses, gaps and ways forward.

During the 2021 AI expert consultation, participants developed a conceptual framework for the “ideal” early warning system for AI (Fig. 2). In this iteration, a roadmap and milestones was identified to reach this framework, especially focusing on the implementation of novel technologies and bioinformatics.

Participants discussed ways forward and using outputs of this consultation to keep the momentum going and continue to enhance early warning networks for AI in Asia. Specifically these include:

1. Use the proposed timeline as guidance to plan activities around early warning for AI, including with:
   a. Potential donors (e.g. World Bank, Asian Development Bank, and other funds dedicated to emerging infectious diseases in the wake of the COVID-19 pandemic
   b. Committees and work groups that are developing similar early warning strategies
2. Further include the environmental sector into One Health activities
3. Consolidate communications between international organisations (e.g. WOAH, FAO) during the early part of the timeline
### Annex 1 – Participant list

<table>
<thead>
<tr>
<th>No.</th>
<th>Name</th>
<th>Organisation</th>
<th>Country</th>
<th>Day 1</th>
<th>Day 2</th>
<th>Day 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Breed, Andrew</td>
<td>DAFF, representing CVO Dr. Schipp</td>
<td>Australia</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
</tr>
<tr>
<td>2</td>
<td>Butler, Jeff</td>
<td>ACDP</td>
<td>Australia</td>
<td>N</td>
<td>Y</td>
<td>Y</td>
</tr>
<tr>
<td>3</td>
<td>Claes, Filip</td>
<td>FAO RAP</td>
<td>Thailand</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
</tr>
<tr>
<td>4</td>
<td>Dadang Abdullah, Sarah</td>
<td>Department of Veterinary Services</td>
<td>Malaysia</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
</tr>
<tr>
<td>5</td>
<td>Gabrielson, Julia</td>
<td>DAFF</td>
<td>Australia</td>
<td>Y</td>
<td>N</td>
<td>N</td>
</tr>
<tr>
<td>6</td>
<td>Hanim Mohd Saeid, Faizah</td>
<td>Veterinary Research Institute/Department of Veterinary Services</td>
<td>Malaysia</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
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<tr>
<td>7</td>
<td>Huynh, Tiffanie</td>
<td>DAFF</td>
<td>Australia</td>
<td>N</td>
<td>Y</td>
<td>N</td>
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<tr>
<td>8</td>
<td>Karlsson, Erik</td>
<td>IPC/FAO RAP</td>
<td>Cambodia</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
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<tr>
<td>9</td>
<td>Keyburn, Anthony</td>
<td>ACDP CSIRO</td>
<td>Australia</td>
<td>Y</td>
<td>Y</td>
<td>N</td>
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<tr>
<td>10</td>
<td>Lam, Janice</td>
<td>DAFF</td>
<td>Australia</td>
<td>Y</td>
<td>Y</td>
<td>N</td>
</tr>
<tr>
<td>11</td>
<td>Lamielle, Gaël</td>
<td>FAO RAP</td>
<td>Thailand</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
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<tr>
<td>12</td>
<td>Luczo, Jasmina M.</td>
<td>ACDP</td>
<td>Australia</td>
<td>Y</td>
<td>Y</td>
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</tr>
<tr>
<td>13</td>
<td>Mire, Junki</td>
<td>NIAH</td>
<td>Japan</td>
<td>Y</td>
<td>N</td>
<td>N</td>
</tr>
<tr>
<td>14</td>
<td>Morrissy, Chris</td>
<td>FAO</td>
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Annex 2 – Meeting concept note and agenda

Better detection, better response:

A regional consultation on avian influenza surveillance in Asia

2-4 November 2022
Geelong, Australia

BACKGROUND

During the last 2 years of the COVID-19 pandemic, outbreaks and human infections with avian influenza A viruses (AIVs) (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 A/H5Nx is continuing and increasing globally. Numerous outbreaks throughout Europe, Asia and Africa appear genetically closely related. A/H5N1 (both 2.3.4.4 and 2.3.2.1 subclades) also continues to circulate globally and recently A/H5N5 viruses were identified throughout the year in Europe and Asia, while A/H5N6/8 has been detected in China and Southeast Asia since early 2019. Sporadic outbreaks of A/H5N2, A/H5N3, and A/H5N4 were also reported. In addition to HPAI H5Nx viruses, sporadic A/H7Nx and 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 and other mammalian species in the past few years. Subtypes include A/H7N4, A/H9N2, A/H10N3, A/H3N8, and, most concerning, A/H5Nx clade 2.3.4.4b viruses.

Overall, despite decades of detected AIV circulation, there is a need to maintain and improve AIV surveillance. Currently, numerous stakeholders and countries still only 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. These approaches can benefit from innovative sampling and diagnostics methodologies such as environmental sampling, which will provide countries in Asia and the Pacific with more cost-effective ways of detecting AIV (and other endemic and emerging pathogens of concern) in areas of high risk.

In 2021, the Food and Agriculture Organisation of the United Nations (FAO) Regional Office for Asia and the Pacific (RAP) organised a regional consultation of expert to discuss challenges and ways forward related to global avian influenza surveillance and early warning. During the meeting, several key themes were discussed, including incorporation of novel technologies and sampling strategies, improving bioinformatics technologies for faster data analysis, and better use of surveillance outputs to inform zoonotic risk mitigation and poultry vaccine strategies. To build on the outputs of the previous meeting, FAO RAP, in collaboration with the Australian Centre for Disease Preparedness (ACDP) will organise an in-person meeting to address progress and continuing challenges related to the action points from this
initial consultation with the overarching goals of improving global early warning systems, as well as discuss novel sampling and diagnostic methodologies for AI surveillance.

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 progress and challenges since the previous AI consultation, specifically towards improved global AI early warning mechanisms and poultry vaccine composition meeting
4. Discuss novel diagnostic technologies (i.e.: multiplex PCR, point-of-care testing)
5. Discuss advancements in next generation sequencing (NGS) and bioinformatics
6. Discuss best practices for novel sampling strategies (environmental surveillance, pooling) to enhance surveillance at country-level

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)
- Avian influenza experts, including from the following institutions: Nextstrain Initiative, Erasmus, Johns Hopkins University and others
- International and regional partners

DATES AND VENUE

The meeting will consist of a 2-3 day face-to-face consultation with experts, directly following the World Organisation for Animal Health (WOAH)’s reference laboratory meeting in Geelong, Australia due to the opportunity to have relevant experts already present during WOAH’s meeting.

Dates: 2-4 November 2022

Venue: Geelong, Australia

EXPECTED OUTPUTS

1. Meeting summary
2. Review of progress from previous consultation’s action points, especially related to:
   a. Global avian influenza early warning system
   b. Avian influenza vaccine composition meeting
3. Review of novel sampling, diagnostics, and analysis strategies for zoonotic influenzas
4. Ways forward to pilot and implement novel sampling, diagnostics and analysis strategies
ANOTATED AGENDA (TENTATIVE)

Session 1: Introduction and setting the scene

FAO will provide introductory presentation on meeting objectives, expected results, and program. Information on global overview of AI situation and key updates on relevant global initiatives will be given.

Session 2: Where are we now?

This session will consist of reviewing the progress from the previous AI regional consultation held in December 2021 which focused on early warning and surveillance for AI at a global level. This will be the opportunity to review the Early Warning Framework developed during the previous meeting, and discuss the upcoming poultry vaccine composition meeting.

Session 3: New samples, new techniques

Innovative tools for bioinformatics were introduced during the last consultation. During this session, these will be explored in more detailed, and linked with applied novel surveillance methodologies and analyses, such as best practice for environmental or air sampling for better detection of AIVs.

Session 4: Where do we go next

This last session will bring together all points raised during the previous sessions. The participants will discuss next steps to continue address challenges and opportunities for global early warning mechanisms, incorporating novel technologies and surveillance methodologies in the context of an evolving AI situation in Asia and globally.