



AUSVET

Avian disease surveillance in the Asia and the Pacific region

Prepared for The World Organization for
Animal Health (WOAH)

December 2022

Disclaimer

This report is for the use of the client only and is confidential information. If you have received a copy of this report in error, please delete it and notify the sender. Ausvet gives no warranty that the information contained in this report is correct or complete and shall not be liable for any loss howsoever caused, whether due to negligence or other circumstances, arising from use of or reliance on this information.

© 2022 Ausvet

This work is copyright and, apart from any fair use as permitted under the *Copyright Act 1968*, no part may be reproduced without written permission from the publishers, Ausvet. Requests and inquiries concerning reproduction and rights should be addressed to Ausvet at the address below.

Ausvet

Level 1, 34 Thynne St, Bruce, ACT 2617 Australia

www.ausvet.com.au

ABN: 64 613 142 9

Contact: alison.hillman@ausvet.com.au

Contents

Abbreviations and acronyms.....	vi
Summary	7
1 Introduction	9
2 Review of avian disease surveillance in the Asia and the Pacific region	11
2.1 Summary findings	11
2.2 Summaries of avian influenza surveillance programs in five Members.....	15
2.2.1 Japan.....	15
2.2.2 Republic of Korea.....	15
2.2.3 Australia	16
2.2.4 India.....	17
2.2.5 FAO contributions to avian influenza surveillance activities in the Asia and the Pacific region.....	19
2.2.6 Institut Pasteur du Cambodge in Cambodia	19
2.2.7 Siberian Wild Birds Surveillance Program.....	20
2.3 Commentary from consulted sources regarding surveillance in the region in relation to avian influenza data sharing.....	21
2.3.1 Practicalities of consent to sharing of data.....	21
2.3.2 Minimum data set.....	22
2.3.3 Desirable additional data.....	22
2.3.4 Difficulties in categorisation of host species between countries	23
2.3.5 Timeliness of reporting.....	23
2.3.6 Desirable database outputs	24
3 Proposed approach for harmonised and cost-effective surveillance programs for avian diseases in the Asia and the Pacific region	25
3.1 Approach to surveillance for early detection of infection.....	25
3.1.1 Domestic gallinaceous poultry production and pet birds	26
3.1.2 Domestic waterfowl production	27
3.1.3 Live bird markets.....	27
3.1.4 Wild birds.....	27
3.2 Surveillance for vaccine matching	28
3.3 Use of surveillance data to improve the understanding of AI epidemiology in poultry, live bird markets and wild birds.....	28
3.4 Surveillance for identification and estimation of the value of intervention points to reduce the risk of zoonotic AI in humans.....	28



3.5	Harmonisation of capture of data, and harmonisation of data after upload into a database.....	29
3.5.1	Harmonisation of data upon integration into a database.....	29
3.5.1	Harmonisation of capture of data.....	30
4	Review of avian disease occurrence and surveillance data in the Asia and the Pacific region.....	31
4.1	World Animal Health Information System	31
4.1.1	WAHIS public interface.....	31
4.1.2	WAHIS data available through SharePoint.....	41
4.1.3	The Handistatus database.....	44
4.2	The Hokkaido University Influenza Virus database	45
4.3	Other systems collating avian influenza sequence and surveillance data	47
4.3.1	GenBank and the Influenza Virus Resource.....	47
4.3.1	The GISAID Initiative.....	47
4.3.2	EMPRES-i+.....	47
4.3.3	Nextstrain.....	48
4.3.4	Influenza Research Database	48
4.3.1	OFFLU.....	48
5	Surveillance information system design for avian influenza in the Asia and the Pacific region.....	49
5.1	General comments on the approach to sharing data.....	49
5.2	Proposed aims of an information system to collate avian influenza data in the Asia and the Pacific region.....	51
5.3	Consultation and recruitment of participating Members and laboratories	51
5.4	System ownership, governance and management.....	52
5.4.1	Technical management of the database system	52
5.4.2	Database users and permissions.....	52
5.5	Summary of proposed technical aspects of an information system	55
5.5.1	System architecture and hosting.....	55
5.5.2	Type of data captured	56
5.5.3	Transfer of data into the database.....	57
5.6	Reporting from the database.....	62
5.6.1	Dashboard reporting.....	62
5.6.2	Automated generation of reports.....	63
5.6.3	Scalability of reporting	63
5.7	Sharing or reporting of data to third parties, and its use in research and publications.....	63



5.8 How a new information system for the Asia and the Pacific region may be different from existing systems.....	64
6 Proposal of a template for avian influenza surveillance data collection	65
7 References	66

Tables

Table 1	WOAH Asia and the Pacific Region Members.....	9
Table 2	WOAH Asia and the Pacific Region Reference Laboratories for Avian Influenza.....	9
Table 3	Summary of approaches to avian influenza surveillance	13
Table 4	Example ‘Quantitative data’ from WAHIS database.....	32
Table 5	Data available in the WAHIS system (‘Quantitative data’) from 2018 – 2021.....	33
Table 6	Example ‘Disease situation’ data from WAHIS database	36
Table 7	Example of the ‘List of control measures’ data from the ‘Surveillance and control measures’ section of the WAHIS database	38
Table 8	Example of the ‘Official vaccination data’ from the ‘Surveillance and control measures’ section of the WAHIS database.....	38
Table 9	Example of the ‘List of control measures’ data from the ‘Surveillance and control measures’ section of the WAHIS database	38
Table 10	WAHIS data available through SharePoint (WOAH, 2022a).....	41
Table 11	Exported data from the Hokkaido University Influenza Virus Database	46
Table 12	User group types, suggested bodies for user groups, and suggested default access levels for various database user groups	54
Table 13	Example of a database table containing data from samples from individual birds	59
Table 14	Example of a database table containing data from pooled samples.....	60
Table 15	Example of a database table containing serological surveillance data.....	61

Figures

Figure 1	Approach to data sharing related to regulation.....	49
Figure 2	Recommended approach to successfully engage data providers to voluntarily share data.....	50



Abbreviations and acronyms

Abbreviation	Definition
AI	Avian influenza
API	Application Programming Interface, a form of machine to machine data communication
CSV	Comma-separated values file
CT	Cycle threshold
ELISA	Enzyme-linked immunosorbent assay
FAO	Food and Agriculture Organization of the United Nations
GF-TADs	Global Framework for the Progressive Control of Transboundary Animal Diseases
HA	Haemagglutinin gene
HPAI	High pathogenicity avian influenza
LPAI	Low pathogenicity avian influenza
NA	Neuraminidase gene
NGO	Non-governmental organization
PCR	Polymerase chain reaction
SSe	Surveillance system sensitivity
WAHIS	World Animal Health Information System
WHO	World Health Organization
WOAH	World Organization for Animal Health



Summary

Avian influenza (AI) is a transboundary threat in the Asia and the Pacific region. It can have marked economic and welfare implications through its effects on poultry production and health, and may entail considerable public health risk.

This project reviewed existing avian influenza reporting systems and the types of surveillance currently being undertaken in the Asia and the Pacific Region, and proposed approaches to harmonised and cost-effective surveillance across the region, alongside an information system design to meet the requirements of WOAHA Members for avian disease surveillance in the region. Avian influenza is specifically considered in this report as an exemplar avian infectious disease for which timely sharing of data could be valuable for regional WOAHA Members. However, the described information system design is relevant to sharing data on a wide range of avian diseases.

Surveillance activities and reporting of data

Of the reviewed national avian influenza surveillance activities, early detection of disease incursions, particularly of subtypes and strains that are novel or of particular importance, is a common goal. In Members where vaccines are used, surveillance is an important part of vaccine matching strategy. A non-governmental organisation consulted worked in avian influenza surveillance to identify areas for disease interventions to reduce zoonotic risk to humans. The approach to surveillance varies substantially between programmes, including the use of active surveillance, target populations, and the approach to sampling and testing of domestic poultry and wild birds.

For the surveillance goal of early detection of disease, it is recommended that the most effective and cost-effective approach in gallinaceous poultry production and pet birds is passive surveillance—and so surveillance resources in these sectors should focus on enhancing passive surveillance. For domestic waterfowl and other species where subclinical infection can be relatively common, and in live bird markets and wild bird populations, active surveillance may be a valuable additional tool, and most efficient if risk-based. For vaccine matching, data arising from both passive and active surveillance can be of value.

A range of data sources and information sharing for avian influenza data in the region exist, including the World Animal Health Information System, the Hokkaido University Influenza Virus database, GenBank and the Influenza Virus Resource, the GISAID Initiative, EMPRES-i+, Nextstrain and the Influenza Research Database. They encompass a range of outputs, including outbreak reporting, sharing of genetic sequences, and analyses including disease mapping and phylogenetic trees. Data contributions vary between mandated reporting, ad hoc voluntary reporting and data scraping. Capture of surveillance efforts in detail was lacking, and there was limited or no capacity for linking test results for multiple infections to the same sample. Timeliness of reporting and a lack of coverage of a range of avian diseases/ disease subtypes were raised by stakeholders as other key limitations of current data sharing arrangements.



Proposed additional data sharing activities

It is proposed that any additional information sharing platform for avian diseases in the Asia and the Pacific region should be developed with Members retaining authority over the data through a clearly defined governance structure. This would help to ensure the system is of value to Members (filling in gaps of information that are important to them and not currently available by other means) and responsive to their evolving needs; and in doing so, encourage trust and thus participation in the data sharing process. It is essential that consideration is given to the security, flexibility and scalability of the system in system architecture and hosting.

It is recommended that the system captures disaggregated data—individual test results—rather than summary reports. Disaggregated data can be used more flexibly and with greater precision in analyses and output options than summary data, and allows for linking of the results of multiple tests performed on a single sample. A minimum set of covariate data were considered to be host, species and location. Additional data of value relate to the reasons for sampling, sampling and testing methodology, management factors and co-infections. Machine-to-machine transfer of data with API authorisations is recommended, from the laboratories to the information system directly (on the approval of the data owners—the Members), for optimal security and minimisation of labour, error and reporting delays. Alternative options of data transfer include emailing of spreadsheets to a database, or upload through a web interface.

Reporting is suggested to include a dashboard display, email notifications, frequent automated reports (e.g. monthly) and intermittent ‘informed reports’ (e.g. quarterly; drafted automatically and then completed with interpretation and other commentary from experts). The nature of dashboard displays and reports are expected to be specifically guided by Member needs, and automatically updated with new submissions of data.

It is recommended that sharing of data and reports from the system is controlled by the information system Management Committee, which would be centred around the authority of contributing Members. If data are to be shared with third parties, including researchers, other collaborators and regulators, it is expected that the sharing would require specific Management Committee approval and occur in accordance with clearly defined and delimited data requests with conditions around data security and publishing of the data or resultant analyses.

In contrast to existing data sources, a new information system for the purposes of reporting on avian disease surveillance in the Asia and the Pacific region would

- aim to capture disaggregated negative test data (as well as positive test data) for multiple avian diseases, for reporting purposes that include detailed mapping of surveillance efforts. This also allows for linkage of multiple test results undertaken on a single sample.
- aim to capture data on the surveillance type, approach to sampling, and testing methods, to allow for epidemiological inferences of improved validity.
- combine data that are not available collectively in existing databases, to enable rapid and inexpensive analyses that can incorporate more detail
- operate under the authority of contributing WOAHA Members, with output that is tailored specifically to the needs and mutually agreed terms of the Members.
- have the capacity to be rapidly responsive to evolving requirements of regional Members, such as expanding the range of data capture, reporting on additional diseases, and adjusting or adding to the information system outputs.
- have the capacity to be considerably more timely with reporting and analyses involving a broad range of avian diseases compared to existing systems.



1 Introduction

Avian influenza (AI) is a viral infection that can have marked economic and welfare implications in poultry production and health, and may entail considerable public health risk. Reflecting this, cases of highly pathogenic avian influenza (HPAI) are reportable to the World Organization for Animal Health (WOAH), and many countries have surveillance programs for early detection of AI in poultry (including, but not limited to, HPAI).

In the Asia and the Pacific region (Table 1), avian influenza is a regional transboundary threat. Many national surveillance programs targeting AI exist in the region, with five WOAH reference laboratories at a regional level (Table 2) in addition to many national laboratories involved in surveillance diagnostics.

Table 1 WOAH Asia and the Pacific Region Members

WOAH Members for the Asia and the Pacific region				
Australia	Fiji	Laos	New Caledonia	Thailand
Bangladesh	India	Malaysia	New Zealand	Timor-Leste
Bhutan	Indonesia	Maldives	Pakistan	Vanuatu
Brunei	Iran	Micronesia (Federated States of)	Papua New Guinea	Vietnam
Cambodia	Japan	Mongolia	Philippines	
China (People's Republic of)	Korea (Democratic People's Republic of)	Myanmar	Singapore	
Chinese Taipei	Korea (Republic of)	Nepal	Sri Lanka	

Table 2 WOAH Asia and the Pacific Region Reference Laboratories for Avian Influenza

Location	Laboratory
Australia	Australian Centre for Disease Preparedness, Commonwealth Scientific and Industrial Research Organisation
China (People's Republic of)	National Avian Influenza Reference Laboratory Animal Influenza Laboratory of the Ministry of Agriculture Harbin Veterinary Research Institute, CAAS
India	Indian Council of Agricultural Research (ICAR) National Institute of High Security Animal Diseases (NIHSAD)
Japan	Hokkaido University Research Center for Zoonosis Control
Korea	Animal and Plant Quarantine Agency Ministry of Agriculture, Forest and Rural Affairs

Sharing of surveillance data between Members can be of value to surveillance strategy within Members, and in management of avian influenza risk. In line with the GF-TADs objectives, and the recommendations from the WOAH Regional Expert Group Meeting for diseases of poultry in the Asia and the Pacific region, the objectives of data sharing between Members may span

1. Diagnostic capacity development (particularly, to allow laboratories to refine RT-PCR probes in line with circulating strains of avian influenza and other diseases).



2. Timely and cohesive region-wide sharing of avian disease detections in domestic poultry and wild birds, to inform preparedness and response activities in the region, and sharing of data relating to detection of novel infections or strains of infections in the region.
3. Sharing information on poultry and wild bird surveillance activities undertaken in the region.
4. Increasing the understanding of the epidemiology of avian diseases in the Asia and the Pacific region.

This project

- reviewed the types of surveillance currently being undertaken in the Asia and the Pacific Region,
- proposed approaches to harmonised and cost-effective surveillance across the region,
- reviewed existing avian influenza data reporting systems, and
- proposed an information system design to meet the requirements of Members for avian disease surveillance in the Asia and the Pacific Region.

Avian influenza is specifically considered in this report as an exemplar avian infectious disease for which timely sharing of data could be valuable for regional WOAHA Members. However, the described information system design is relevant to sharing data on a wide range of avian diseases.



2 Review of avian disease surveillance in the Asia and the Pacific region

2.1 Summary findings

Surveillance in the Asia and the Pacific region is undertaken by national and/or jurisdictional governmental agencies, and by local and international non-governmental agencies, research institutes and universities (often in collaboration).

Various surveillance goals for avian influenza were identified across the Members in discussion with stakeholders.

- Early detection of disease incursions, particularly of subtypes and strains that are novel or of particular importance, was a common goal across surveillance programmes in the region).
- In Members where vaccines are used, surveillance is an important part of vaccine matching strategy.
- An non-governmental organisation consulted worked in avian influenza surveillance to identify areas for disease interventions to reduce zoonotic risk to humans.

Some surveillance programs include active surveillance as well as passive (general) surveillance. For active surveillance, populations targeted include domestic poultry and wild bird species. In many cases, domestic poultry surveillance is limited to passive surveillance, with active surveillance primarily occurring in wild bird populations. In some areas of the region where transmission of avian influenza from wild birds is known to be particularly important to public health and domestic poultry production, there can be substantial surveillance efforts targeting wild birds (for example, in Japan, Korea and Australia). Meanwhile, there are areas of the region where very limited wild bird surveillance activities are occurring (for example, areas of southeast Asia).

Specifics of the approaches to sampling and testing can vary substantially between Members, in consideration of the surveillance goals of that Member and the resources available for avian influenza surveillance. For example, variations were considerable in

- the target populations for surveillance,
- the number of samples collected and sampling frequency,
- the approach to pooling of samples (whether samples are pooled at the time of collection, or pooled in the lab, and whether oropharyngeal and cloacal samples are pooled), and
- testing procedures—whole genome sequencing is common, but not uniform across the region.

Contributors highlighted the variations between sampling and testing guidelines used for poultry disease surveillance. For example, in regards to collecting and pooling cloacal and oropharyngeal samples from birds, the WOAAH guidelines (WOAH, 2022b) and FAO guidelines (Rose et al., 2006; Whitworth et al., 2007) differ from those previously provided by WHO. These variations are likely to relate to differences in priorities in sampling avian populations between programmes.



Approaches of four Members and three NGOs are summarised below, based on consultation where possible, and otherwise through published information (Table 3).



Table 3 Summary of approaches to avian influenza surveillance

Member/ Organisation	Surveillance objectives	Target population(s)	Surveillance type	Sample type; frequency of testing
Japan	Detection of HPAI and LPAI in poultry	Poultry (sampling dead poultry)	Passive	Dead poultry; as indicated
	Detection of HPAI in wild birds	Wild birds	Passive	Dead and rescued birds; As indicated
		Wild populations of water birds	Active	Faecal samples collected from the environment; up to three times in migratory and winter periods (occasionally more ¹)
Republic of Korea	Early detection of HPAI and LPAI viruses in poultry and wild birds	Poultry	Passive	As indicated
		Poultry, particularly targeting chickens, ducks, Korean native chickens and quail ²	Risked-based active	Quarterly testing, and testing prior to slaughter. During winter and HPAI outbreaks, sampling at least once a month ³
		Wild birds	Passive	As indicated
		Wild birds	Risked-based active	Live capture and testing, and faecal sampling; primarily during winter
Australia	Early detection of AI infection	Domestic poultry (dead birds)	Passive	As indicated
	Detect AI viruses in wild bird populations	Wild birds	Enhanced passive	As indicated
India⁴	Early detection of clinical disease and infection, inform control strategies, demonstration of freedom from disease	Commercial poultry kept at high population densities, domestic ducks, backyard poultry, and live bird markets, especially those at border areas.	Passive Risk-based Active (targeting chickens and ducks)	As indicated Specific plan determined at State level
		Wild/migratory birds	Passive	As indicated
			Active	Specific plan determined at State level
FAO	Activities vary according to the Member's needs. Active surveillance in live bird markets is a shared feature across Members.			
Institut Pasteur du Cambodge	Early detection of novel strains of AI, to identify areas for interventions to reduce disease risk to humans	Live bird markets (ducks and chickens)	Active	20 ducks and 20 chickens randomly sampled at 16 time points per year



Member/ Organisation	Surveillance objectives	Target population(s)	Surveillance type	Sample type; frequency of testing
Siberian Wild Birds Surveillance Program		Wild birds	Active	Spring and Autumn

¹ E.g. during an outbreak

² For surveillance purposes, each shed of birds on a farm is considered a separate flock

³ Up to every week in duck flocks

⁴ Recommended approach from India's Action Plan for Prevention, Control and Containment of Avian Influenza; state governments have discretion in undertaking surveillance in view of local conditions (Government of India, 2021)



2.2 Summaries of avian influenza surveillance programs in five Members

2.2.1 Japan

Japan has a surveillance program for avian influenza in wild birds and captive birds (run by the Ministry of Environment) and a surveillance program for AI in poultry (run by the Ministry of Agriculture, Forestry and Fisheries). The primary aims are detection of HPAI in wild birds, and detection of HPAI and LPAI in poultry. The program involves passive surveillance through sampling of dead or rescued birds, active monitoring, and environmental testing (water bird faeces) (Moriguchi et al., 2021). Active monitoring is informed by a prioritised list of target species, and involves collection of waterbird faecal samples up to three times in the migratory and wintering periods (occasionally more, for example if there is a known outbreak of HPAI in Japan).

From dead or rescued birds, tracheal or oropharyngeal swabs and cloacal swabs are tested using rapid test kits. Samples that test positive are then sent to one of four national reference laboratories for confirmatory testing. Samples that test negative using rapid test kits are then tested with reverse transcription-loop-mediated isothermal amplification (RT-LAMP) method. Samples that are positive by this test are also subject to confirmatory testing. Confirmatory testing involves virus isolation, then haemagglutination inhibition and neuraminidase inhibition and/or rt-PCR. H5 and H7 subtypes are sequenced at the hemagglutination cleavage site region, and/or chickens are inoculated with the virus to confirm pathogenicity. Virus isolation and testing is undertaken in accordance with WOA standards (WOAH, 2022b).

Waterbird faeces are tested using molecular tests at the Animal Quarantine Service or the National Institute for Environmental Studies. Positive samples are subject to confirmatory testing procedures at national reference laboratories, which are undertaken as per protocols for dead or rescued birds.

2.2.2 Republic of Korea

The Republic of Korea's surveillance program aims for early detection of HPAI viruses and LPAI viruses in poultry and wild birds.

Since 2008, surveillance activities have occurred year-round. Poultry farms are targeted for periodic and occasional viral detection tests—periodic tests are usually performed quarterly, and occasional testing occurs just prior to slaughter. However, during winter (October to February) and during HPAI outbreaks, the active surveillance scheme sampling increases in frequency, e.g. from quarterly to monthly, or up to every 1 – 2 weeks in duck flocks. Within the protected zone of an HPAI outbreak, all poultry flocks are tested more frequently—up to once a week for duck flocks—until movement controls are lifted. For testing purposes, each shed of birds on a farm is considered a separate flock. The major target species of surveillance include chickens, ducks, Korean native chickens and quail.

Passive surveillance is also an important part of the poultry surveillance activities, and in the case of chicken farms, this is the primary mode of detection of the virus (through reporting farmers).

There is year-round active surveillance in wild bird species, including faecal sampling and sampling of captured live birds. Most of the samples are collected and tested during winter, with target locations for sampling and the number of samples to be taken pre-defined considering the



pattern of visits and stay of migratory birds. For live bird capture and testing, major target species include mallards, spot billed ducks, mandarin ducks, common teals, pintails, Baikal teals and widgeons. In terms of passive surveillance, dead wild birds may also be reported, transported to and tested at an Institute under the Ministry of Environment.

Given the extensive surveillance, field sampling strategy is devised in line with the primary aim of the active surveillance, which is early detection of virus incursions. Cost effectiveness is important, particularly given that they are working within the constraints of laboratory capacity against the large number of birds to be sampled. In testing on farm, 20 oropharyngeal samples are collected as two pools of 10 samples, and 20 cloacal samples (or faecal samples) are collected as two pools of 10 samples. Pooling occurs in the field.

Most isolated viruses are sequenced using next generation sequencing. In 2021, over 500,000 samples (mostly pooled) were tested. Samples are not routinely or commonly tested for Newcastle disease or infectious bursal disease.

Surveillance data are collated at the national level, by the Animal and Plant Quarantine Agency. The raw data are not shared with other countries, though summarised results or key information from the surveillance may be—for example, processed data or statistics are shared with other WOAAH Members during international meetings, and with OFFLU for WHO vaccination composition meetings.

2.2.3 Australia

In domestic poultry, surveillance is based around passive or syndromic surveillance activities, particularly

- clinical surveillance (daily monitoring of flocks, with post mortem examinations and monitoring of production parameters),
- investigation of clinical disease for which avian influenza may be a differential diagnosis, and
- flock testing for export consignments (Commonwealth of Australia, 2010).

There is also some opportunistic testing—for example, where there is an infectious bursal disease outbreak or toxicity outbreak, samples from those birds will be routinely tested for AI. Tests include competitive ELISA, haemagglutination inhibition, agar gel immunodiffusion, reverse-transcriptase PCR and virus isolation (NAHIS, 2022). There are also intermittent active surveillance activities in the poultry industry, which can be associated with outbreak response, research, or industry / jurisdictional initiatives (Commonwealth of Australia, 2010).

The passive surveillance activities are run at the jurisdictional level, with jurisdictional Chief Veterinary Officers working closely with industry. Infections are confirmed through testing of samples at the Australian Centre for Disease Preparedness laboratory; the laboratory reports back to the jurisdiction. The jurisdiction is responsible for notifying the country's Chief Veterinary Officer for reporting to the WOAAH. Summary data are collated in the National Animal Health Information System, a national database that is broadly accessible (NAHIS, 2022). Jurisdictions hold their own detailed data; depending on the jurisdiction, they may allow aspects of it to be published (for example, in GenBank).

In wild bird populations, there are risk-based active surveillance activities and enhanced passive surveillance activities in wild birds undertaken as part of the National Avian Influenza Wild Bird Surveillance Program, coordinated through Wildlife Health Australia (Wildlife Health Australia, 2022a). The program is funded at the federal level, for implementation at the jurisdictional level.



As for poultry, jurisdictions control the accessibility of the data and report to the national chief veterinary officer.

Objectives of this program are

1. to regularly detect avian influenza viruses by sampling wild birds, in order to:
 - contribute to a better understanding of avian influenza virus genetic variation and gene flow of subtypes, ecology and epidemiology to support industry and human and wildlife health strategic risk assessment and management;
 - generate avian influenza virus sequence data required to monitor genetic diversity and variation of avian influenza viruses circulating in Australia and maintain a contemporary Australian avian influenza virus sequence ‘library’; and
 - maintain fit-for-purpose diagnostic tests and national laboratory diagnostic capacity and capability.
2. to share and communicate data nationally, and internationally.
3. to contribute to One Health through regular communication of avian influenza virus data to the Department of Health with specific analysis of wild bird avian influenza viruses for likelihood of infection and transmission in humans.
4. to exclude AI viruses, specifically H5 and H7, through investigation of significant, unexplained or mass mortality events in wild birds (Wildlife Health Australia, 2022a).

Their activities target waterfowl in locations where there is known mixing between the waterfowl and birds of the shorebirds order, and where the waterfowl are in close proximity to poultry and humans. The enhanced passive surveillance activities seek to detect or exclude AI viruses as the cause of mass mortality and morbidity events in wild birds (Wildlife Health Australia, 2022a).

A subset of samples from the wild bird surveillance are also tested for Newcastle disease (Animal Health Australia, 2021).

Generally, faecal and environmental samples are tested as part of the wild birds program—it is relatively rare to get direct bird sampling. If samples are pooled, it is 3–5 swabs per pool, from the same sample source. In practice, costs involved means that samples are usually pooled in the field, rather than in the lab; this is done in consideration of the primary focus of the surveillance program, which is early detection of new strains via metagenomics: the implications of pooling are less important for this goal. Whole genome sequencing is done at the Australian Centre for Disease Preparedness laboratory. Data from this surveillance are reported to the eWHIS system, which is not an open database, though requests for data can be made (Wildlife Health Australia, 2022b). Data displayed includes maps and phylogenetic trees.

2.2.4 India

India’s Action Plan for Prevention, Control and Containment of Avian Influenza lists surveillance objectives of

- early detection of clinical disease and infection,
- assessment of the temporal and spatial patterns of the disease to improve effectiveness of control efforts, and
- demonstration of country freedom from disease (Government of India, 2021).



Surveillance activities are undertaken by Indian state departments of Agriculture and Forestry in line with the plan, though with room for discretion regarding local conditions (Government of India, 2021).

The Action Plan encourages risk-based approaches to surveillance, in terms of target population and other risk factors for infection. Recommended risk considerations in terms of target population included

- commercial poultry kept at high population densities,
- domestic ducks,
- backyard poultry,
- wild/migratory birds, and
- live bird markets, especially those at border areas.

Other risk considerations are considered in terms of geography

- the number and activity of live bird markets in the area,
- the disease situation in neighbouring areas,
- locations historically affected by AI or in the vicinity of such locations,
- areas bordering other countries, and
- national sanctuaries, wetlands and lakes used by migratory and wild birds, in consideration of their proximity to domestic poultry, and captive birds.

In domestic poultry, passive surveillance is based on observation of unusual mortality, and is the primary source of samples tested from populations of geese, turkeys, guinea fowl, quail and ‘other’ domestic species. Active surveillance is also employed in domestic poultry, particularly targeting chickens and ducks. Surveillance strategy is based multistage or cluster random sampling.

In wild bird populations, both active and passive surveillance for AI are used. As for domestic poultry, passive surveillance is based on observations of unusual mortality. For active surveillance, faeces of wild birds are tested; active surveillance does not target any particular wild bird species.

Samples collected in passive surveillance may include whole dead birds, tissues, cloacal and oropharyngeal swabs, and serum. Samples collected in active surveillance include swabs (cloacal and oropharyngeal) and serum. Environmental samples are also tested as part of both active and passive surveillance, especially from live bird markets.

Samples are tested at India’s WOAHA Reference Laboratory for Avian Influenza in Bhopal, the Indian Council of Agricultural Research’s National Institute of High Security Animal Diseases. In the laboratory, samples are pooled for testing. Complete genome sequencing is carried out using Sanger’s method. Newcastle disease is routinely tested for alongside AI.

Approximately 100,000 birds are sampled per year. The Government of India (i.e. national level) owns the data collected through surveillance, through the Department of Animal Husbandry and Dairying.



2.2.5 FAO contributions to avian influenza surveillance activities in the Asia and the Pacific region

FAO work in partnership with a number of Members in the Asia and the Pacific region. Surveillance activities vary between these Members to suit that Member's needs, but active surveillance in live bird markets is a shared feature. In some Members, active surveillance is undertaken on farm and/or in slaughterhouses; pooled environmental samples are also sourced in some cases (e.g. bird faeces or environmental water). Serosurveillance and egg testing are not common, though serosurveillance is considered potentially useful for early detection in waterfowl.

The protocols for avian influenza surveillance vary between Members that FAO work with. Samples are often pooled for H & N testing, depending on resources. FAO guidelines (Rose et al., 2006; Whitworth et al., 2007) include

- pooling samples in the lab, rather than in the field,
- restricting pooling to 5 samples or fewer,
- pooling only the same location and species, and pooling the oropharyngeal and cloacal swabs separate, and
- ideally, testing the M-gene on pools, then revisiting individual samples separately if positive.

However, in practice sampling may not always reflect these standards.

The administration structure of surveillance in some Members is complex, with provinces or states leading their own surveillance, with varying priorities and capacities. For example, classifications of birds (into species or other taxonomic groups) is tailored to each Member's circumstances and priorities in undertaking surveillance.

The surveillance results belong to the respective Member's government, with no obligation to share the data with the FAO. Members may delay reporting of data to WOAHP for administrative reasons and are generally considered unlikely to want to share additional data to those currently reported.

Blocks to sharing of sequences in these Members include that researchers won't share sequences whilst drafting a publication, and publication turnaround time can be considerable. Currently, considerations are being made as to whether this situation can be improved upon through agreements with journals.

2.2.6 Institut Pasteur du Cambodge in Cambodia

The Institut Pasteur du Cambodge undertakes avian influenza surveillance in Cambodia. Aims of program include early detection of novel strains of the virus, particularly in consideration of zoonotic risk—i.e. preventing disease in humans. Through this work, areas for interventions to reduce disease risk to humans are identified; this can include interventions to reduce risk in birds to then reduce risk to humans.

The Institut was monitoring human cases of AI and surrounding birds from 2004 to 2013, commencing around the time where HPAI became endemic in Cambodia. From 2011, the Institut has undertaken active surveillance at live bird markets in conjunction with animal health authorities.



Currently, the active surveillance involves sampling approximately 7,000 – 8,000 chickens and ducks per year (20 ducks and 20 chickens randomly sampled at 16 time points a year at live bird markets). This level of surveillance has been occurring consistently since 2015. The major Cambodian live bird markets, and bird markets in major centres, are well covered by the surveillance; coverage is more limited in remote areas. Cloacal swabs and oropharyngeal swabs are taken and tested separately by swab type: samples are tested in pools of 5, and then swabs from M gene positive pools are tested individually. Where the RT-PCR CT score is <25, the samples are put in the sequencing pipeline; where the CT score is ≥ 25 , the virus is isolated in eggs first.

The Institut is also doing some wild bird and poultry interface studies, involving sampling of wild bird faeces from the environment in conjunction with sampling nearby poultry.

The Institut's work does not undertake routine surveillance on farms. However they have some targeted activities—for example, the Institut has started value chain tracking to try to identify points where virus is amplified in the population

The Institut has in house sequencing. They report cases of HPAI to local authorities very quickly, and in addition report routinely to the WOAHA every 6 months. Reporting is often facilitated by OFFLU.

In animal outbreak investigations, the Institut will sometimes be involved in testing samples, if requested (for example, if the animal lab is overwhelmed). The Institut also assists sequencing and virus isolation if needed.

The Institut is mainly funded through USAID and FAO, and collaborates with FAO, the WOAHA and others in some programs. Regarding data ownership, the Institut has an agreement with the Cambodian government that it doesn't need sign off for uploading sequences to GenBank. However, reporting and publications will always go through a government approval process.

There is good coverage of veterinary epidemiologists across the provinces, through the Cambodian Applied Veterinary Epidemiology Training (CAVET) program. Usually they are in charge of response activities, and educate community leaders and producers, who often have good knowledge of avian influenza. However those new to farming can have poor knowledge. Barriers to reporting include concern about farms being shut down and a lack of compensation. Additionally, the farmers can be somewhat acquiescent to die offs of birds at certain times of the year and accept them, which can also influence reporting.

The Institut has a good relationship with related institutions in Laos and Thailand, but are not undertaking surveillance there at this time.

2.2.7 Siberian Wild Birds Surveillance Program

The Siberian Wild Birds Surveillance Program undertakes active surveillance of wild birds in south Western Siberia, a location crossed by several significant flyways. During spring and autumn migration, hunt-harvested or net-captured wild birds (most commonly of the order Anseriformes) are routinely sampled by cloacal samples; oropharyngeal swabs are not routinely undertaken. Samples are individually tested, after virus isolation in embryonated chicken eggs according to the WHO procedure (World Health Organization, 2011). Whole genome sequencing is undertaken where possible (Sharshov et al., 2017).



The Siberian Wild Birds Surveillance Program laboratory owns the data that are collected. They collaborate with organizations in Japan, China and Korea, with some sharing of data within the framework of the collaborations.

2.3 Commentary from consulted sources regarding surveillance in the region in relation to avian influenza data sharing

All participants in the consultation process identified the high value of sharing of avian influenza data between Members in the region. Information priorities included

- regional early warning,
- collation of genetic data, particularly regarding subtypes and strains that can affect both animals and humans, and with capture of sequences of the full genome wherever possible,
- linkage of genetic data to data regarding host species, Member and time of sampling,
- collation of data on surveillance activities in the region, and
- up-to-date information on vaccine efficacy in the region.

2.3.1 Practicalities of consent to sharing of data

Consultation indicated a good relationship between WOAHA Reference Laboratories for Avian Influenza, and national laboratories more generally, in the Asian and the Pacific region. This includes regular sharing of summary data at meetings such as WOAHA Regional Representation for Asia and the Pacific's Regional Expert Group Meetings for Diseases of Poultry in Asia and the Pacific. Such data sharing has the permission of the respective governments, but these data are not captured in any databases. Further to this broader sharing of data, in some cases there are close working relationships between certain Members where additional data are shared.

Unsurprisingly, the main obstacles to regional data sharing were unanimously nominated as political and legal blocks. The data involved are sensitive to the data owners (the Members), so concerns about third parties having access to them are predictable; and in the case of notifiable infections and genetic data, there can be legal barriers to sharing of information with other countries. In almost all cases of consultation, the data involved in the respective surveillance program were owned by governmental authorities. Surmounting these challenges would require

- demonstration of the value of the system to Members submitting data,
- instilling confidence in the security of contributing data in the system, and
- meeting all legal requirements in data sharing agreements.

Considering these obstacles, there were suggestions of piloting a database between a few select Members (with access to the shared information restricted to those Members). The database could then be readily expanded to include further Members as the benefits of the system were demonstrated and confidence grew in participation. Suggestions of Members within which to pilot the database included Members of ASEAN, or niches of Members that already have a close working relationship regarding sharing of avian influenza surveillance data. Alternatively, a suggestion was for piloting a database through the WOAHA Reference Laboratories for Avian Influenza. In all cases, the approval of the respective Member would remain a requirement for sharing of that Member's data; and only contributing Members (or Reference Laboratories) would have access to the shared data.



2.3.2 Minimum data set

The key information to be captured in a shared database (minimum data set) was identified as

- the subtype or strain of AI identified, including sequences (whole genome sequencing where ever possible; at a minimum, HA and NA gene sequences).
- the host species from which the positive sample came.
- the time the sample was collected (ideally dd/mm/yy, or mm/yy).
- the geographical location at which the sample was collected, at a suitable level of granularity.

These data include comprehensive reporting of negative test results as well as positive.

This type of data is equivalent to those captured by WAHIS for H5 and H7 AI prior to 2022 (i.e. including LPAI as well as HPAI), but also includes capture of data on other subtypes of AI and sequence information (these data are not available in WAHIS). It was commonly suggested that such linking of virological and basic epidemiological data may be the most useful outcome of a shared database system.

Minimum data set information was considered to be of value in diagnostics, preparedness activities through timely sharing of data on the detection of novel and/or zoonotic subtypes and strains, and as an early warning system for neighbouring areas. It may also enable an improved understanding of influenza A epidemiology in the region, regarding infections found in various host species and locations, and variations in detection across time and space within the region. This would be particularly pertinent to distribution of subtypes or strains of concern, such as zoonotic subtypes and the 2.3.4.4b H5Nx clade.

In collecting data on the host species, the formatting and level of detail in species descriptions was highlighted as a challenge in data sharing (Section 2.3.4).

2.3.3 Desirable additional data

The following data would be valuable to improve understanding of epidemiology in the region, where capture is possible:

- the reason for testing (for example, disease investigation/passive surveillance, active surveillance, opportunistic testing);
- the location use-type category of the sample (for example, farm, live bird market, wild bird, zoo, pet, other);
- the type of sample tested (e.g. oropharyngeal swab, cloacal swab, mixed swab, tissue sample, faeces, environmental sample);
- the type of test undertaken on the sample;
- all test results associated with a particular sample (e.g. M-gene testing results and serology);
- for pooled samples, the number of birds in the pool;
- where relevant, a unique identifier to link results from different tests undertaken on samples from the same bird or same pool of birds (e.g. oropharyngeal swab and cloacal swab);
- where relevant, a unique identifier to link any individual bird samples to the pool from which it came (i.e. for samples which were tested individually after a pooled sample was positive);



- coinfection data;
- for domestic poultry, whether the bird(s) were managed free-range or not;
- for domestic poultry, whether the bird(s) were managed in a premises rearing multiple bird species; and
- the size of the at-risk population.

Coinfection data were identified as a gap in surveillance, most particularly regarding Newcastle disease and infectious bursal disease. The availability of coinfection data was expected to vary across Members, given variation in the approaches to coinfection screening between laboratories. For example, some routinely screen for Newcastle disease alongside AI, whilst others rarely concurrently test for Newcastle disease. As yet, coinfection data have not been available through the regional network of laboratories alongside the avian influenza data reporting, but there have been discussions and presentations related to this topic at regional meetings.

2.3.4 Difficulties in categorisation of host species between countries

Host species has an important role in the epidemiology of AI spread. However, the categorisation of host species from which surveillance samples came was nominated as a particularly problematic aspect in interpretation of results across shared regional data. It was thus highlighted as an important consideration in harmonisation of surveillance systems across the region. Examples of issues given were

- Domestic birds tend to be categorised or reported to a level which suits the circumstances of the respective Member, and so can be quite different between Members.
- Individual wild birds may be described to species level, or more broadly up to simply being reported as a ‘wild bird’. This may be attributable to difficulties in identification (for example, due to degradation or damage to wild bird carcasses), inadequate record keeping or reporting, a lack of knowledge in wild bird identification by people involved in sampling, or ambiguities in sample origin (e.g. environmental sampling).
- Samples taken from the environment (including faecal samples and other environmental samples) may be labelled as ‘wild bird’, or labelled to a broader taxonomic level such as ‘Anseriformes’, or may be labelled by the dominant or likely only species in the region of sampling.

2.3.5 Timeliness of reporting

Real-time sharing of surveillance data was considered the ideal, as it would be particularly valuable in early detection. However, the ability to share results as soon as test results are available at the laboratory is not considered a realistic prospect, particularly regarding notifiable avian diseases (e.g. subtypes of avian influenza notifiable to the WOAAH). For example, legal barriers may be in place to reporting of notifiable infection data to a source other than the WOAAH. Further, Members may require a detailed investigation before confirming and then reporting the presence of infection to the WOAAH, and only at this point would there be any possibility of sharing data in a different context.

Of note regarding timeliness, in terms of delays between observation of clinical symptoms/ sampling to analysis of the sample at a laboratory, it was commented that national laboratories that do not have the resources or capacity for whole genome sequencing may send samples to WOAAH reference laboratories in certain circumstances, and it is rare that these samples are received by the reference lab in a timely manner. Further, where national laboratory capacity is



exceeded, samples may be sent to other Members for testing, potentially with a considerable delay.

2.3.6 Desirable database outputs

Desired output displays nominated were:

- a dashboard with autogenerated and interactive phylogenetic trees similar to those available in Nextstrain (Hadfield et al., 2018; Nextstrain, 2022a);
- interactive maps and summary data with filtering options, similar to those available through a number of existing platforms;
- accessible code to approved and registered users; and
- email notifications of upload of data, particularly regarding subtypes and strains of particular concern.
 - For example, alerting Members to new records of subtypes/ strains of virus detected at a given time and location, with genomic sequence data, as soon as it is uploaded.
 - Notifying members of changes to sequence data over time if required.

Particularly important aspects of these outputs are agreed to be presentation of surveillance efforts over time and space, presentation of LPAI data, and presentation of surveillance data of other AI subtypes that are not well covered in other AI data information systems.



3 Proposed approach for harmonised and cost-effective surveillance programs for avian diseases in the Asia and the Pacific region

The appropriate approach to surveillance depends on the specific aims of surveillance. For avian diseases in the Asia and the Pacific Region, existing surveillance programs have goals that include early detection of AI incursions and novel subtypes and strains in poultry and wild birds, vaccine matching, improving the understanding of avian influenza epidemiology in poultry, and identification of intervention points where the risk of zoonotic avian influenza infections in humans can be reduced.

Approaches to harmonised and cost-effective surveillance programs will thus be considered in view of such goals and the need to balance the approach to surveillance across them.

3.1 Approach to surveillance for early detection of infection

The performance of an early detection surveillance system is influenced by the Surveillance system sensitivity (SSe) (Cameron et al., 2020). This is a function of

- Target population surveillance coverage.
 - For optimal early detection surveillance system sensitivity, the entire target population needs to be under surveillance; with incomplete coverage the ability of the surveillance system to detect the infection early is compromised, as the early infections may occur outside of the population under surveillance.
 - Whilst there may be well-established population risk factors for disease incursions, incursions themselves are single events and can occur randomly and unpredictably in population strata that are not considered high risk (e.g. geographic areas or species that are generally considered at low risk). Therefore, if the surveillance aim is early detection of all incursions, exclusion or under-representation of lower-risk strata from surveillance activities means that an incursion in these strata may not be detected within the time frame nominated in surveillance goals.
- The temporal coverage of surveillance of the target population.
 - For optimal early detection surveillance system sensitivity, the target population needs to be under continuous surveillance to ensure that early infections can be detected promptly. Early infections may occur in between surveillance efforts in discontinuous surveillance approaches, with corresponding delays in the time-to-detection.
- The sensitivity of detection of the infection.
 - If the infection in the population under surveillance is relatively easy to detect, it is more likely that early cases of infection incursion will be detected in a timely manner.
 - Tools in detection of infection in the population under surveillance may start with detection of clinical symptoms or changes in production indices, or may rely more heavily on the use of diagnostic tests (Cameron et al., 2020).



Passive surveillance approaches are therefore cornerstone of early detection of disease incursions, in consideration of avian influenza in poultry and many other important avian diseases. Passive surveillance systems can achieve a relatively high surveillance system sensitivity in a cost-effective manner, given a large proportion of the target population (domestic poultry) are being observed frequently by producers for clinical symptoms that can be marked in certain host species.

In contrast, active surveillance strategies tend to be substantially less sensitive in the early detection of disease incursions, as target population coverage and temporal coverage are relatively limited in the absence of exceptionally large—and likely unfeasible—resource commitments (Cameron et al., 2020). Nevertheless, in some circumstances passive surveillance may be inadequate as a stand-alone tool for early detection. In these cases, supplementation with active surveillance approaches may be necessary to raise sensitivity in early detection of infection (Cameron et al., 2020)—for example, in wild birds where clinical signs or mortality may be minimal and/or difficult to observe. Targeting such active surveillance strategies based on risk, to augment passive surveillance for early detection of infection, is most efficient and effective when based on detailed and objective risk data.

3.1.1 Domestic gallinaceous poultry production and pet birds

In domestic gallinaceous poultry production, typically all poultry are observed frequently by the farmers/ producers, and clinical symptoms of disease and/ or changes in production metrics are sensitive indicators of the presence of avian influenza. Similarly, pet and zoo birds tend to be observed frequently over time. In these cases, passive surveillance and syndromic surveillance can be highly sensitive tools for early detection of AI incursions in these groups—particularly if farmers/producers, local communities and authorities are knowledgeable about AI, farmers and pet/zoo owners are willing and able to report their suspicions to animal health authorities, and animal health authorities are adequately resourced to investigate these observations. The sensitivity of a passive surveillance system can be aided by direction of resources to enhancing passive surveillance as a priority, including maintenance/expansion of animal health worker resources across Members and communities, and community education across the population involved in bird husbandry regarding avian diseases and disease notification. Reducing disincentives to reporting is also a critical component of maximising passive surveillance system sensitivity (for example, ensuring compensation of any hardships that reporting disease has on the farmer).

In consultations, a heterogenous distribution of knowledge and resources in the region was reported. In some Members, governments and/or NGOs have invested heavily in veterinary epidemiology/ animal health worker training and employment, and in community education programmes, resulting in excellent community knowledge and resourcing to investigate potential AI outbreaks. However, other Members are relatively poorly resourced, and so less able to undertake activities to enhance passive surveillance, compromising surveillance system sensitivity. New farmers were highlighted as an area of potentially weakness in passive surveillance system sensitivity, due to inadequate knowledge of AI. Consideration of how to encompass or specifically target this group of the population in passive surveillance enhancement activities is therefore an important part of maximising system sensitivity.

It is noted however, that certain subtypes or strains of avian influenza may not result in a readily discernible clinical expression of infection. If early detection of these strains was considered to be of value, an active surveillance strategy may be required (as per domestic waterfowl production (Section 3.1.2)).



3.1.2 Domestic waterfowl production

In domestic waterfowl (and possibly some other domestic avian species), population coverage and temporal coverage of passive surveillance may be very good. However, subclinical infection across an infected flock is more likely than in gallinaceous poultry, meaning that observation for clinical symptoms and/or monitoring production metrics may be relatively insensitive in detecting AI infection. In this circumstance, supplementation of passive surveillance with active surveillance approaches may be appropriate to increase surveillance system sensitivity in early detection of infection.

For avian influenza, a risk-based or sentinel approach may be taken in domestic waterfowl populations, to maximise the cost-effectiveness in using active surveillance to increase surveillance system sensitivity for early detection of infection (as compared to using representative-sampling survey approaches). For example, if a certain novel AI strain of concern is known to be relatively common in domestic poultry in a contiguous Member, an active surveillance effort may target waterfowl production in the vicinity of the border with that Member, or a sentinel surveillance program may particularly focus on production sites closer to the border. Similarly, if certain subtype(s) occur in another Member with whom a large number of poultry are traded, subsets of producers heavily involved in trade across that border may be targeted in an active surveillance program for early detection of infection incursions. Production systems with relatively poor biosecurity practices, or on high-risk wild bird migratory pathways, are also options for risk targeting.

3.1.3 Live bird markets

In live bird markets, passive surveillance should be encouraged, but in practice the likelihood of reporting may be limited by particularly acute disincentives to reporting suspected infection to authorities, and in species where subclinical infection may be relatively common. Improving passive surveillance sensitivity in early detection of infection could be approached by working to reduce disincentives to reporting.

As for domestic waterfowl production (Section 3.1.2), risk-based active surveillance can be used to improve the sensitivity of surveillance for early detection of infection in live bird markets. The risk basis for sampling would be targeting birds with clinical symptoms consistent with AI infection, and species where subclinical infection is relatively likely to occur.

3.1.4 Wild birds

In wild birds, population coverage is inherently poor, and so passive surveillance is a relatively insensitive tool for early detection surveillance. Active surveillance strategies are similarly limited in early detection surveillance sensitivity, given limited population coverage and limited temporal surveillance coverage. In these cases, a targeted combination of approaches to surveillance is most likely to maximise sensitivity of detection of AI incursions in these populations.

Passive surveillance can be enhanced by educating communities and groups with an interest in wildlife on reporting of wild bird mortalities (particularly mass die-offs) or wild birds with clinical symptoms consistent with AI presented to wildlife carers or animal clinics for care. This also requires resourcing of the relevant authorities to enable investigation of suspected AI cases in wild birds. Improving ease of reporting (for example, through provision of apps or advertising phone numbers for reporting to appropriate audiences) may improve the sensitivity of this pathway.



Risk-based active surveillance strategies can target species of birds and migratory pathways considered high risk for spread of avian influenza, and particularly in regions in close contact with poultry production (especially where production is free-range) for the benefit of early warning to poultry production. Areas of congregation of wild birds considered a substantial risk for AI could also be targeted (e.g. wetlands associated with migratory bird populations). The Siberian Wild Birds Surveillance Program (Section 2.2.7) and the Wildlife Health Australia National Avian Influenza Wild Bird Surveillance Program (Section 2.2.3) provide examples of approaches to risk-based active surveillance relevant to risk in the respective regions.

3.2 Surveillance for vaccine matching

Information from both passive and active surveillance is of value to vaccine matching strategies. Passive surveillance provides information on the types of strains circulating, whilst active can provide information on their relative frequency. It is thus expected that sufficient surveillance information for vaccine matching could be made available through a surveillance system designed primarily in consideration of other surveillance goals.

3.3 Use of surveillance data to improve the understanding of AI epidemiology in poultry, live bird markets and wild birds

Passive surveillance can provide information of descriptive epidemiological value, such as where subtypes and strains of infections have occurred in time and space, and species demonstrated to host the infection.

For robust analytical inferences about the epidemiology of avian influenza, such as estimating the prevalence of or risk factors for infection of various AI subtypes, a representative approach to sampling is required. In Members where AI infection is relatively common (or in studying species in the region where AI is relatively common, or studying subtypes of AI in the region that are common, for example), this could occur through utilisation of active surveillance data where available, or appropriately designed periodic sampling surveys. However, there are some important considerations of the validity in doing so at a regional level.

- Variations in the methods of active surveillance between Members may influence the validity of using these data analytically at a regional level.
- In Members or species where AI infection is rare, or in studying AI subtypes and strains that are relatively rare, the sample sizes required for statistically robust analytical inferences from surveillance or survey data may be unfeasibly large.
- The non-uniform approach to pooling samples for testing may compromise the ability to use even the active surveillance data to make analytical inferences (Section 2.3.4).

3.4 Surveillance for identification and estimation of the value of intervention points to reduce the risk of zoonotic AI in humans

This and related objectives require representative data obtained as part of a designed-for-purpose analytical observational and interventional studies. Such data are of value in contributing to surveillance, but are beyond the scope of design of surveillance systems.



3.5 Harmonisation of capture of data, and harmonisation of data after upload into a database

Jurisdictions capture and categorise data in a way that is locally meaningful, and so jurisdictional data may not integrate seamlessly at a regional level for drawing region-wide inferences.

In the short term, harmonisation of data after upload to the information system database is an imperfect but practical solution. It also allows for an exercise in highlighting inconsistencies in data submissions, to consider how these may be able to be rectified in the longer term.

In the longer term, Members may pragmatically continue to support such *post hoc* harmonisation, or may agree to standardise the capture of certain data for shared benefit in interpretation. Standardisation of data capture can require a long process of consultation and implementation within Members.

3.5.1 Harmonisation of data upon integration into a database

In the short term, the goals of a shared data system should be capture of all relevant data, and utilisation of that data to the best ability at a regional level.

Sequence data may be relatively easy to harmonise from across the region in the database. If sequences have been uploaded to Genbank, and irregularities are detected in data submission for a record with a linked Genbank code, the irregularities can be automatically cross-checked or overwritten by scraping of Genbank data.

Particular concerns were raised about categorisation of bird species in a shared information system (Section 2.3.4). Achieving a broad-level nested categorisation may be the most realistic short-term goal. For example, sufficient data may be submitted to achieve sampled bird categorisations at one or more of these levels:

- ‘wild bird’ vs ‘domestic’,
- taxonomic order, and
- an open-field species label.

It may also be possible to use available data to achieve categorisations of

- ‘free range’ vs ‘non free range’ (including caged pet or zoo birds),
- for domestic poultry, the type of production (e.g. laying hens, breeder ducks).

At relatively high levels of taxonomic classification, useful inferences may still be able to be drawn at a regional level, and there may be a relatively large proportion of records successfully classified to these higher levels, either directly or through mining an open-field species description. However, if using the species descriptions available through WAHIS submissions as a precedent, there may be considerable amounts of missing data.

For further precision in harmonising species data after submission, as an example from an existing animal health information system, there is the use of a national zoo species list to automate categorisation of species by a hierarchy of taxonomic levels. An international system is likely to require creation of synonyms for each species (e.g. taxonomic name (or names, if superseded taxonomic names are still in use) and common name(s)), with a common code assigned to the synonyms. This approach can require a considerable amount of manual intervention in data management in the early stages of setting up an animal health information system.



In cleaning data during submission to the database, with a view to harmonisation across the region, it is essential that all steps taken in harmonisation are clearly recorded, and then considered in interpretation of surveillance data at a regional level.

3.5.1 Harmonisation of capture of data

Harmonisation of capture of data represents surveillance methodology: sampling and testing methods, and the way data are categorised and recorded before data are shared. Across a region with many Members, and in some cases many jurisdictions that run their own surveillance programs within Members, harmonisation of capture of data can be an extremely challenging undertaking. There are potential legislative or policy barriers, a very large number of departments and staff to be engaged in harmonisation endeavours, resourcing limitations and a dependence on the skill and motivation of those reporting the data on the success of harmonisation of methodology.

For example, in the capture of genomic data for AI in surveillance testing, Members will not necessarily sequence all AI genes, and there can be variations in methodology for those that do. This can be related to the resources available to the Member (or jurisdiction of the Member), and the Member's (or Member jurisdiction's) priorities in resource allocation for surveillance. Considering this, it is extremely difficult to achieve harmonisation of capture of genomic data at a regional level in the absence of allocation of considerable amounts of external funding where resources are limited.

Motivation and skill are particularly relevant to the capture and reporting of wild bird data. To achieve harmonisation in the capture and categorisation of nominated wild bird species in submitted data, relatively high taxonomic level capture may be relatively achievable and yield relatively high accuracy and readily utilisable data. In line with categorisations after submission to the database mentioned above (Section 3.5.1), Members' processes could be harmonised to record the nested levels of 'wild bird' vs. 'domestic', taxonomic order of the bird, and an open-field species label (where known), particularly through laboratory information management system categories. The creation of an ID tool for reporting countries to use in their data systems may also be of value.

The harmonisation, or lack thereof, of the capture of surveillance data also requires consideration in interpretation of surveillance data at a regional level. This can in many cases be improved by the provision of search interfaces that allow easy categorisation of the data, often from within existing systems.



4 Review of avian disease occurrence and surveillance data in the Asia and the Pacific region

There are a range of sources of data regarding avian influenza already in existence. These include data collated in the World Animal Health Information System (WAHIS), the Hokkaido University Influenza Virus database, Genbank and the Influenza virus resource, the GISAID Initiative, EMPRES-i+, Nextstrain and the Influenza Research Database.

4.1 World Animal Health Information System

The World Animal Health Information System (WAHIS) collates and displays summary notification data on high pathogenicity avian influenza (HPAI) H5 and H7 subtypes; and prior to July 2021, low pathogenicity avian influenza (LPAI) H5 and H7 subtypes (WOAH, 2019). Data are sourced from notifications from Member countries (Table 1). Notification of cases to WAHIS occurs immediately upon the Member authorities confirming the occurrence; routine reporting of disease investigation and surveillance efforts occurs every six months.

Data from WOAHA notifications since 2005 can be viewed and downloaded from the WAHIS public interface (Section 4.1.1), and through SharePoint (Section 4.1.2). Historical data (1996 – 2004) are also available through the separate Handistatus database (Section 4.1.3).

For avian influenza, there are multiple disease reporting categories. Across 2018 – 2021, which was used for data description, categories were

- ‘High pathogenicity avian influenza viruses (poultry) (inf. with)’;
- ‘Low pathogenic avian influenza (poultry) (2006-2021)’; and
- ‘Influenza A viruses of high pathogenicity (Inf. with)(non-poultry including wild birds)(2017-)’.

4.1.1 WAHIS public interface

There are two sections of data displayed on WAHIS- the ‘analytics’ dashboard and the ‘reports’ dashboard.

4.1.1.1 ‘Analytics’ section

The WAHIS ‘analytics’ dashboard displays involves sections: ‘Quantitative data’, ‘Disease situation’, ‘Animal Health capacity’, and ‘Surveillance and control measures’.

4.1.1.1.1 ‘Quantitative data’

For each avian influenza category, data are downloadable by CSV. Data for CSV download are described in Table 4 and Table 5, with description based on review of the 2018 – 2021 data for the three relevant influenza categories in the Asia and Oceania regions. Data represent a mix of data from Six-monthly reports and from Immediate notifications and follow up reports.



Table 4 Example 'Quantitative data' from WAHIS database

Year	Semester	World region	Country	Administrative Division	Disease	Serotype/ subtype/ genotype
2021	Jul-Dec 2021	Asia	Country X	Admin. Division Y	Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-)	H5N2
2021	Jul-Dec 2021	Asia	Country X	Admin. Division Y	High pathogenicity avian influenza viruses (poultry) (Inf. with)	H5N1
2021	Jul-Dec 2021	Asia	Country X	Admin. Division Y	High pathogenicity avian influenza viruses (poultry) (Inf. with)	H5N1
2021	Jul-Dec 2021	Asia	Country X	Admin. Division Y	Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-)	H5N1
2021	Jul-Dec 2021	Asia	Country X	Admin. Division Y	Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-)	H5N1

Animal category	Species	Outbreak_id	New outbreaks	Susceptible	Cases	Killed and disposed of	Slaughtered	Deaths	Vaccinated
Domestic	Birds	-	-	-	600	0	0	600	-
Both animal categories	-	-	1	-	-	-	-	-	-
Domestic	Birds	-	-	1 823	-	1 823	0	0	-
Both animal categories	-	-	1	-	-	-	-	-	-
Wild	House Crow	-	-	-	173	0	0	173	-



Table 5 Data available in the WAHIS system ('Quantitative data') from 2018 – 2021.

These data have been filtered to only include those from the 'World regions' of 'Asia' and 'Oceania'

Data field	Values	Comment
Year	2018, 2019, 2020, 2021	
Semester	'Jan-Jun YYYY' and 'Jul-Dec YYYY (YYYY = for the respective 'Year')	
World region	[Restricted to Asia, Oceania]	
Country	[many; countries in the Asia and Oceania regions]	
Administrative Division	[many; administrative subdivision of the respective country]	
Disease	'High pathogenicity avian influenza viruses (poultry) (Inf. with) 'Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-) 'Low pathogenic avian influenza (poultry) (2006 – 2021)'	
Serotype/ Subtype/ Genotype	'-', 'not typed', 'other', 'H5', 'H5;H5N2', 'H5;H5N2;H5N5', 'H5N2;H5N5', 'H5N1', 'H5N2', 'H5N5', 'H5N6', 'H5N8', 'H7N4', 'H7N6', 'H7N7', 'H7N9'	Multiple serotypes reported concurrently
Animal category	'Domestic', 'Wild', 'Both animal categories'	'Both animal categories' is only associated with Six-monthly report figures
Species	Many avian species listed by common name, 'Anatidae', 'Corvidae (unidentified)', 'Birds', 'Cattle', 'Equidae', 'Sheep/goats (mixed herd)', 'Swine', '-'	Many categories, from 'birds' and 'wildlife (species unspecified)' to species-level common names (not taxonomic); other mammalian taxa included in 'poultry' categories (e.g. 'cattle'). For the 'Animal category' variable value 'Wild', the 'Species' description was often at a high resolution of taxonomy, using common names; the broadest 'Species' label was Wildlife (species unspecified). For the 'Animal category' variable value 'domestic', the 'Species' value was typically 'Birds'. Where a '-' value exists in 'Species' and also in the 'Outbreak_id' column, the row of data represents a 'total species' row, indicating the total number of new outbreaks in the 6-month reporting time period.
Outbreak_id	'-' or 5 digit numeric identifier	Rows with a '-' value come from a six-monthly report; rows with other values come from immediate notifications or follow-up reports.



Data field	Values	Comment
		Where a '-' value exists in 'Outbreak_id' and also in the 'Species' column, the row of data represents a 'total species' row, indicating the total number of new outbreaks in the 6-month reporting time period.
New outbreaks	'-' or numeric (between 0 and 50)	Number of new outbreaks at the epidemiological unit level (a group of animals with the same likelihood of exposure to a pathogenic agent). Where multiple species are involved in an outbreak, only one species is assigned the new outbreak count (i.e. a value >'0'). So in this situation, for the same 'Outbreak_id', there will be one 'Species' specific row containing the number of new outbreaks across all involved species for that reporting period; the other 'Species' rows will be assigned '0'. '-' values for 'New outbreaks' that are associated with '-' values for 'Outbreak_id' and a species grouping value for 'Species' represent rows to delimit the number of 'Susceptible' epidemiological units, and the number of 'Cases', 'Killed and disposed of', 'Slaughtered', 'Deaths' and 'Vaccinated' for a given 6-month reporting period.
Susceptible	'-' or numeric (between 1 and 6,632,634)	No. individuals susceptible; no information at holding or flock level. '-' values are usually associated with 'total species' rows for calculating the number of new outbreaks.
Cases	'-' or numeric (between 0 and 6,632,634)	No. individual cases; no information at holding or flock level. '-' values are usually associated with 'total species' rows for calculating the number of new outbreaks.
Killed and disposed of	'-' or numeric (between 0 and 4,052,045)	'-' values are usually associated with 'total species' rows for calculating the number of new outbreaks.
Slaughtered	'-' or numeric (between 0 and 2,755)	'-' values are usually associated with 'total species' rows for calculating the number of new outbreaks.
Deaths	'-' or numeric (between 0 and 1,853,744)	'-' values are usually associated with 'total species' rows for calculating the number of new outbreaks.
Vaccinated	'-' or numeric (between 0 and 625,025)	'-' values associated with 'total species' rows for calculating the number of new outbreaks.



The dashboard display comprises

- a histogram of the number of new outbreaks of the category (in bins of 6 months), and
- a line graph of the number of deaths, number of cases, number killed and disposed of and number of susceptible [hosts] for that infection, in bins of 6 months.

These data are filterable by World region, country, animal type, disease, serotype/ subtype/ genotype, animal category, species and year.

4.1.1.1.2 'Disease situation' section

For each avian influenza category, data are downloadable by CSV. Data for CSV download are described in Table 6.

The dashboard display comprises a table and three maps, which are filterable by disease, country and animal category.

- A table and a map of country status for that infection in six-month intervals, in the categories of:
 - '1 Present',
 - '2 Present limited zones',
 - '3 Inf./Infest.',
 - '4 Inf./Infest. limited zones',
 - '5 Suspected',
 - '6 Suspected limited zones',
 - '7 Absent', '8 Never reported',
 - '9 No information', and
 - '- No data available'.
- A 'disease status' map, with a raster display categorised as 'present', 'suspected', 'absent in the country', 'no information provide in report for selected disease(s)' and 'no report available or no outbreaks were reported in the area for a disease present in the country'. The map provides a temporal animation which allows visualisation of the change in disease status of geographical units over time.
- An 'outbreak presence' map with icons for 'Domestic', 'Wild', 'Mixed', 'Resolved', 'Continuing' and 'Cluster'. This map also has an animator for visualising outbreaks over time.
- An 'outbreak presence grouped by event' map with icons for 'Domestic', 'Wild', 'Mixed' and 'Cluster'.



Table 6 Example 'Disease situation' data from WAHIS database

Year	Semester	Region	Country	Disease	Animal category	Occurrence code	Disease status
2022	Jan–Jun–2022	Asia	Country X	High pathogenicity avian influenza viruses (poultry) (Inf. with)	Domestic	Disease limited to one or more zones	Present
2022	Jan-Jun-2022	Asia	Country X	Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-)	Wild	Disease limited to one or more zones	Present



4.1.1.1.3 'Surveillance and control measures' section

For each avian influenza category, data are downloadable by CSV. Data for CSV download are described in Table 7.

The dashboard display comprises one map and three tables. For each avian influenza category, this section contains:

- A 'Presence of control measures' map, shaded by 'Control Measure' (presumed integer scale, though the legend displays a graduated scale)
- A 'List of control measures' filterable table, with each entry indicating a control measure used by a given country for a given 6-month binned time period for the given categorisation of animal category/ species.
- An 'Official vaccination data' filterable table of the type of vaccination used and the number vaccinated in vaccinating countries for the respective country and year/semester. The 'number of vaccinated' variable represents the number of birds vaccinated; there is no reference to the number of holdings/ flocks (though the number of holdings/flocks is reported through the annual reports, Section 4.1.1.2.3).
- A 'targeted surveillance data' filterable table was created in 2021 (thus data are currently sparse). It will indicate the number of samples collected by targeted surveillance in a certain country, for specified semester and type of bird.



Table 7 Example of the 'List of control measures' data from the 'Surveillance and control measures' section of the WAHIS database

Year	Semester	Region	Country	Disease	Animal category	Species	Control measure
2020	Jul-Dec 2020	Asia	Country X	High pathogenicity avian influenza viruses (poultry) (Inf. with)	Domestic	Birds	Ante and post-mortem inspections
2020	Jul-Dec 2020	Asia	Country X	High pathogenicity avian influenza viruses (poultry) (Inf. with)	Domestic	Birds	Control of wildlife reservoirs

Table 8 Example of the 'Official vaccination data' from the 'Surveillance and control measures' section of the WAHIS database

Year	Semester	Region	Country	Disease	Animal category	Species	Vaccine type	Number of vaccinated
2018	Jan-Jun 2018	Asia	Country X	High pathogenicity avian influenza viruses (poultry) (Inf. with)	Domestic	Birds	-	-
2018	Jan-Jun 2018	Asia	Country X	High pathogenicity avian influenza viruses (poultry) (Inf. with)	Domestic	Birds	-	2229343

Table 9 Example of the 'List of control measures' data from the 'Surveillance and control measures' section of the WAHIS database

Year	Semester	Region	Country	Disease	Animal category	Species	Number of samples collected
2018	Jan-Jun 2018	Asia	Country X	High pathogenicity avian influenza viruses (poultry) (Inf. with)	Domestic	Birds	-
2018	Jan-Jun 2018	Asia	Country X	High pathogenicity avian influenza viruses (poultry) (Inf. with)	Domestic	Birds	-



4.1.1.1.4 'Animal Health Capacity' section

This section is under development, and so was not available at the time of review. However, 2005 to present data can be accessed on demand. Some data from 1996 to 2004 is available through the Handistatus historical WOAAH records (Section 4.1.3).

4.1.1.2 'By reports' section

The WAHIS 'By reports' dashboard displays involves the sections 'Animal disease event', 'Six-monthly report' and 'Annual report'.

4.1.1.2.1 'Animal disease event' section

The 'Animal disease event' reports notifications that the WOAAH has received from reporting countries for a given disease event, including immediate notifications and follow up reports. The event data are downloadable in XLXS and PDF format, with a map in PNG also downloadable. XLXS files of the reports include a row per species affected for data relating to an event, and a summary row for all species.

4.1.1.2.2 'Six-monthly report' section

The 'Six-monthly report' summarises notifications that the WOAAH has received from reporting countries. A report is available for a given country, in a given 6-monthly period, with separate reports for aquatic and terrestrial species. Six-monthly reports are exportable as PDFs.

4.1.1.2.3 'Annual report' section

At the time of reviewing the report, the 'Annual report' reports link was not functioning.



4.1.1.3 Data available for coinfections of relevance to avian influenza detection

In the WAHIS system, data are available for Newcastle disease and infectious bursal disease, two important coinfections for consideration in avian influenza data. However, there is no ability to link data on these infections to avian influenza surveillance data, if any were concurrently identified in a disease outbreak investigation or in surveillance activities.

4.1.1.4 Public interface data expansion

There are plans to expand the amount of data available on the WAHIS public interface, including more sophisticated mapping. Currently, all these data are available through the WAHIS SharePoint system, though in the absence of dashboard display (Section 4.1.2).



4.1.2 WAHIS data available through SharePoint

The full set of WAHIS reporting data from 2005 are available through a SharePoint system (WOAH, 2022a). This system is designed to grant access to all data from the notifications, and application for access is unrestricted. WAHIS are extracted weekly to an XLSX file, with the date of extraction in the title of the file, and uploaded to SharePoint. All data are displayed in each file, up to the date of extraction (i.e. 2005 – present). The first section of columns of the file is related to an outbreak event; the second section of columns provides location data; and the final section of columns reports details of the event (Table 10). A data description file is available alongside the data files in SharePoint.

Table 10 WAHIS data available through SharePoint (WOAH, 2022a)

Data field	Field description	Values / comments relating to AI data
epi_event_id	ID of the event	
disease_id	ID of the disease	
reporting_level	Indicates if the outbreak is reported at the level of disease, serotype/subtype/genotype, or strain.	'Disease'; 'serotype/subtype/genotype'; 'strain'
strain_eng	Name of the detailed strain in English	
strain_fr	Name of the detailed strain in French	
strain_esp	Name of the detailed strain in Spanish	
sero_sub_genotype_eng	Name of the serotype/subtype/ genotype in English	
sero_sub_genotype_fr	Name of the serotype/subtype/ genotype in French	
sero_sub_genotype_esp	Name of the serotype/subtype/ genotype in Spanish	
disease_eng	Name of the disease in English	
disease_fr	Name of the disease in French	
disease_esp	Name of the disease in Spanish	
iso_code	ISO Code of the reporting country/territory	
country	Name of the country/territory	
region	Geographical Region	Asia, Africa, Oceania, Americas, Europe
reason of notification	Reason for notification to OIE	'Change in epidemiology'; 'Emerging disease'; 'First occ in country'; 'First occ in zone'; 'New host'; 'New pathogen'; 'New strain in country'; 'New strain in zone'; 'recurrence disease'; 'recurrence strain'; 'unusual/new host'.
event_start date	Start date of the event	
event_confirmation_date	Confirmation date of the event	
event_closing_date	Closing date of the event	
date_last_occurrence	Date of last occurrence	Only relevant for recurrences
Terra_Aqua	Disease of terrestrial or aquatic animals	'Aquatic'; 'Terrestrial'
Report_id	ID of the report	



Data field	Field description	Values / comments relating to AI data
IN_FUR	Immediate notification or follow-up report	'TN' = immediate notification; 'FUR' = follow-up report
Report_number	Rank of the report in the event	
Report_Nat_Ref	National reference of the report	Optional value
Reporting_date	Date of the report	
Outbreak_id	ID of the outbreak/cluster	
Outbreak_Nat_Ref	National reference of the outbreak/cluster	Optional value
Outbreak_start_date	Date of start of the outbreak/cluster	
Outbreak_end_date	Date of end of the outbreak/cluster	
Is_cluster	Single outbreak or cluster of several outbreaks	'FALSE' for single outbreak; 'TRUE' for cluster
N_outbreaks_cluster	Number of outbreaks (if 'Is_cluster' variable = FALSE); or number of outbreaks within a cluster (if 'Is_cluster' variable = TRUE)	'1' for single outbreak; '[>1]' for number of outbreaks in the cluster.
Epi_unit	Epidemiological unit of the outbreak/cluster	Backyard, farm, forest, livestock market, natural park, not applicable, other, slaughterhouse, village, zoo.
Longitude	Longitude of the outbreak/cluster	
Latitude	Latitude of the outbreak/cluster	
Location_aprox	Exact location or approximate	'False' = exact; 'true' = approximate
Location_name	Location of the outbreak/cluster	
Ob_area_id	ID of the area of the outbreak/cluster	
level3_area_id	ID of the level 3 area of the outbreak/cluster	Lowest level areal unit
level3_unique_code	ID of the level 3 area of the outbreak/cluster	Lowest level areal unit
level3_name	Name of the level 3 area of the outbreak/cluster	Lowest level areal unit
level2_area_id	ID of the level 2 area of the outbreak/cluster	Medium level areal unit
level2_unique_code	ID of the level 2 area of the outbreak/cluster	Medium level areal unit
level2_name	Name of the level 2 area of the outbreak/cluster	Medium level areal unit
level1_area_id	ID of the level 1 area of the outbreak/cluster	Largest level areal unit
level1_unique_code	ID of the level 1 area of the outbreak/cluster	Largest level areal unit
level1_name	Name of the level 1 area of the outbreak/cluster	Largest level areal unit
country_area_id	ID of the area of the country/territory	
country_unique_code	ID of the area of the country/territory	
country_name	Name of the area of the country/territory	
is_wild	Outbreaks/clusters in wild or domestic species	'true' = wild species; 'false' = domestic species
wild_type	Type of wildlife (if 'is_wild' = TRUE)	'captive'; 'feral'; 'wild'
water_type	Type of water	Relevant for diseases of aquatic animals
Species	Name of species	Species level or broader
quantitative_unit	Unit of counting cases	Animal



Data field	Field description	Values / comments relating to AI data
susceptible	Number of units of susceptible animals in the outbreak/cluster	
cases	Number of units of affected animals in the outbreak/cluster	
dead	Number of units of dead animals in the outbreak/cluster	
killed_disposed	Number of units of animals killed and disposed of in the outbreak/cluster	
slaughtered	Number of units of animals slaughtered/killed for commercial use in the outbreak/cluster	
vaccinated	Number of units of animals vaccinated in response to the outbreak/cluster	
morbidity	% morbidity, by species by outbreak/cluster	Only available for recent outbreaks/clusters
mortality	% mortality, by species by outbreak/cluster	Only available for recent outbreaks/clusters



4.1.3 The Handistatus database

Data of HPAI notifications to the WOAAH from 1996 – 2004 are available through the Handistatus database, searchable by disease or by country (WOAH, 2016).

- The ‘multiannual animal disease status’ for a nominated region and disease.
 - HPAI disease status in a table across 1996 – 2004 for each country.

- The ‘multiannual animal disease status’ for a nominated country and disease.
 - A table containing information on the occurrence of reported HPAI outbreaks across 1996 – 2004. This includes species group affected; the number of outbreaks, cases and deaths; control measures; the number of animals destroyed, slaughtered and vaccinated; and notes (for example, on fulfilling requirements for proof of freedom of disease in the aftermath of an outbreak).

- The ‘annual animal disease status’ for a nominated country.
 - A table containing information on the occurrence of reported HPAI outbreaks, by listed disease and filterable by year. This includes species group affected; the number of outbreaks, cases and deaths; control measures; the number of animals destroyed, slaughtered and vaccinated; and notes (for example, on fulfilling requirements for proof of freedom of disease in the aftermath of an outbreak).

- The ‘annual animal disease status’ for a nominated disease and region.
 - A table containing information on the occurrence of reported outbreaks of HPAI, by country of that region and filterable by year. This includes species group affected; the number of outbreaks, cases and deaths; control measures; the number of animals destroyed, slaughtered and vaccinated; and notes (for example, on fulfilling requirements for proof of freedom of disease in the aftermath of an outbreak).

- The ‘monthly animal disease status (List A)’ for a nominated region and disease.
 - HPAI disease status in a table across each month of the year, filterable by year.

- The ‘monthly animal disease status (List A)’ for a nominated country and disease.
 - A table with the number of new outbreaks of HPAI reported to the WOAAH for each month.
 - A separate table for each month, with detailed of outbreaks in that month (number of new outbreaks in that month; the total number of outbreaks in the month; Locations of outbreaks; species group(s) affected; and numbers of susceptible, cases, deaths, destroyed, slaughtered animals).

- ‘Zoonoses (human cases)’ by country.
 - A table of listed zoonotic diseases and the number of human cases in that country, filterable by year.



- ‘Zoonoses (human cases)’ by disease.
 - For a given listed zoonotic disease and region, a table of countries with the number of reported human cases per country, filterable by year.
- ‘Veterinary personnel’ by region.
 - For a given region, a table of countries with the number of veterinarians and technical personnel per country.
- ‘Veterinary personnel’ by country.
 - For a given country, a table of the numbers of veterinarians broken down by activity (government officials (central and local); in laboratories, universities and training institutions; private practitioners; and other); and of the number of technical personnel broken down by activity (animal health assistants (with formal training); Animal health auxiliaries; involved in food hygiene, including meat inspectors). The table is filterable by year.

4.2 The Hokkaido University Influenza Virus database

The Hokkaido University Influenza Virus Database contains information on Influenza A viruses in a range of host species, including humans. It has a ‘Virus Stock Search’ category and a ‘Related Papers Search’ category.

The ‘Virus Stock Search’ allows the user to search for virus records of interest by a range of categories, including

- AI strain name (e.g. A/duck/Vietnam/D533/2011),
- HA subtype,
- NA subtype,
- Sampling year,
- Country/Region of sampling,
- Host (this may have been recorded at species level or at a higher taxonomic grouping, per Section 2.3.4),
- Wild/domestic,
- Sampling source (e.g. swab or tissue type),
- Plasmid clone,
- Sequence,
- Pathogenicity, and
- Regulation.

The search results can be exported as a CSV (e.g. Table 11). Sequences meeting the nominated criteria can then be downloaded as a text file.



Table 11 Exported data from the Hokkaido University Influenza Virus Database

Name	HA	NA	Pathogenicity	Regulation	Year	Country/ Region1	Country/ Region2	Country/ Region3	Host	Host/Wild	Sampling source
A/chicken/Ismailia/144CA/2014	5	1	HPAIV	1	2014	Ismailia	Egypt		Chicken	0	Oropharyngeal and cloacal swabs
A/chicken/Ibaraki/1/2005	5	2	LPAIV	0	-	Laboratory					-

Plasmid	Sequence	Pub. num	Coordinates_ Latitude	Coordinates_ Longitude	Contact	Sequence_ PB2_id	Sequence_ PB2_size	Sequence_ PB2_sequence	Sequence_ PB1_id	...
	PB2, PB1, PA, HA, NP, NA, M, NS	1				LC106039	0		LC106048	
PB2, PB1, PA, HA, NP, NA, M, NS	PB2, PB1, PA, HA, NP, NA, M, NS	1					2280	ATGGAGA...	PB2, PB1, PA, HA, NP, NA, M, NS	



The ‘related papers’ section allows for a search of citations for papers related to the sequencing data presented in the cite. The user can search by

- Name (of AI strain),
- Author,
- Title,
- Journal,
- Issue,
- Year, and/or
- pubmed_id

Academics associated with the development and maintenance of this database expressed a reluctance to focus any further collation of surveillance data in the Asian and the Pacific region on this database (with modifications or additions to the database where deemed to be of value). A preference was expressed for development of a new system.

4.3 Other systems collating avian influenza sequence and surveillance data

4.3.1 GenBank and the Influenza Virus Resource

GenBank is the USA National Institute of Health’s open access genomic sequence database, and collates sequence data, including AI sequences (Schoch et al., 2020). The Influenza Virus Resource is an extension that can be used to search for and compare avian influenza virus genomes from Genbank (National Centre for Biotechnology Information, n.d.)

4.3.1 The GISAID Initiative

The GISAID initiative is an open access repository for genomic data of influenza viruses (GISAID, 2022a). Genomic sequences with associated epidemiological data are stored in a sequence repository that is linked to Nextstrain (see below, Section 4.3.3). Users can access data for free, but must identify themselves and agree to the Database Access Agreement (GISAID, 2022b); one of the requirements of that agreement is for the data user to acknowledge the source of sequences used in their work. The Agreement aims to reduce the hesitancy amongst researchers to rapidly share sequence data, by increasing confidence in the researchers’ retention of intellectual property (compared to open access repositories where use of the data are anonymous, such as Genbank (see above, Section 4.3.1)). It was reported from people consulted for this project that there are cases of exclusive submission of avian influenza sequences to GISAID for this reason.

4.3.2 EMPRES-i+

EMPRES-i+ Global Animal Disease Information System is administered by the FAO. It sources data from FAO country or regional project reports, FAO field mission reports, partner Non-Governmental Organizations (NGOs) and Cooperating institutions, government ministries of agriculture and health, FAO in-country representations or other United Nations parties, public domains, the media and web-based health surveillance systems (FAO, 2022a). Sourced data includes avian influenza (FAO, 2022b).

The system displays maps and temporal charts of avian influenza cases, as well as other descriptive charts (such as cases by host species and region, and frequency histograms of different serotypes). Maps and temporal charts can be filtered by animal type (captive, domestic,



wild, environmental sample), diagnosis status (confirmed, denied, suspected) and time frames. Displays are variable by host species, diagnosis source (for example, WOAHA, FAO officer, media, national authorities), humans affected/deaths, and diagnosis status. Data points are presented with GPS locations. Data can be downloaded as raw data (CSV), or as maps and charts, or as a report. The website also provides information on laboratories by region and by regional network.

4.3.3 Nextstrain

Nextstrain is a project that aims to aid epidemiological understanding of pathogen spread and evolution and improve outbreak response (Nextstrain, 2022a). It collates information on AI strains of zoonotic significance—H5N1, H5Nx, H7N9 and H9N2—from human and animal hosts (Hadfield et al., 2018). The output displays are phylogenetic trees (with five options for presentation), filterable by time, host species, region and country. Helpfully, it can be installed on individual computers and run locally, allowing rapid development of new analyses. The code for Nextstrain is open-source, available through github (Nextstrain, 2022b) and via the website (Nextstrain, 2022a).

4.3.4 Influenza Research Database

The Influenza Research Database is a collaboration of the University of Chicago and J. Craig Venter Institute, funded by the U.S. National Institute of Allergy and Infectious Diseases. It imports and integrates publicly available genomic, proteomic, annotation surveillance and experimental influenza data (Influenza Research Database, 2022a). The dashboard outputs include an extensive variety of descriptive and analytical tools, including phylogenetic trees, sequence alignment and PCR primer design (Influenza Research Database, 2022b).

4.3.1 OFFLU

OFFLU is a joint WOAHA-FAO scientific network on animal influenza (OFFLU, 2020). It works with WOAHA/ FAO Reference Centres and National Laboratories for Avian Influenza to collate outbreak and sequence data. Information on zoonotic subtypes (H5, H7 and H9, and other subtypes shown to spillover into humans) is then shared with World Health Organization systems, for use in pandemic preparedness and risk analysis.

OFFLU produces six-monthly reports summarising the epidemiological data of past six months, with information on subtypes and clades, phylogenetic analyses and antigenic data for recently circulating strains. OFFLU also has links on their webpage to WAHIS (Section 4.1) and EMPRES-i+ (Section 4.3.2) web pages. OFFLU does not present disaggregated data to other parties in other formats (e.g. through a dashboard).



5 Surveillance information system design for avian influenza in the Asia and the Pacific region

5.1 General comments on the approach to sharing data

Data sharing can occur within and outside of regulation. The report authors observe that the approaches to successfully capturing data differ between these circumstances.

In regulation, parties are compelled to provide data which they may not otherwise choose to share. In these cases, data are used by the regulatory authority (-ies) for regulatory purposes. The authority(-ies) may provide feedback to those contributing data, but the value and timeliness of this feedback is not a priority and so may be of limited benefit to the data provider—for example, if the feedback doesn't meet their needs, or is not delivered in a timely fashion (Figure 1).

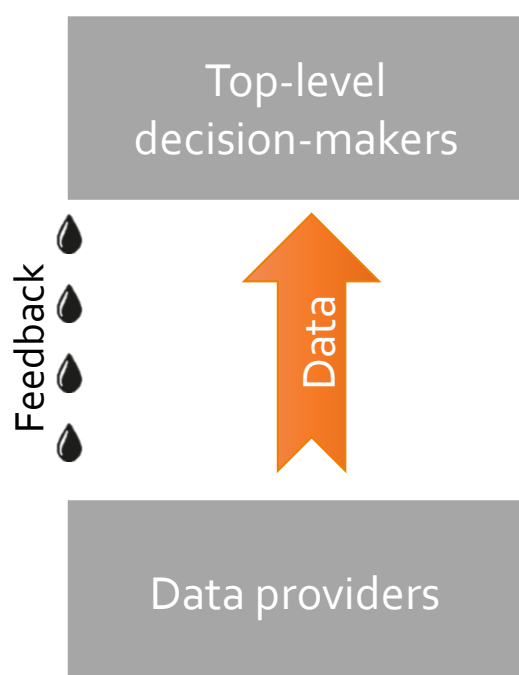


Figure 1 Approach to data sharing related to regulation

Data providers are compelled to report data. Priorities of top-level decision makers or regulators centre on regulatory purposes or high-level decision making, and so while results may be made available to the data providers, they are not necessarily of high value to them.

Outside of a regulatory framework, where there are no obligations to share data, data cannot be expected to be readily shared in the absence of clear and substantial benefit that incentivises the participation of those sharing the data. This is particularly the case for data that are considered sensitive by the data holders. Simply requesting access to the data is unlikely to yield broad participation or temporally consistent data sharing, given the real and/or perceived risks and potential increases in workload to be taken on by data providers. In the report authors' opinion, the most successful and sustainable incentive for participation in data sharing is centring the



needs of the data providers (in this case, WOAAH Members) in providing immediate and substantial benefit upon their sharing of data to the information system (Figure 2). This may involve immediate analyses and production of reports that specifically meet their needs, for example.

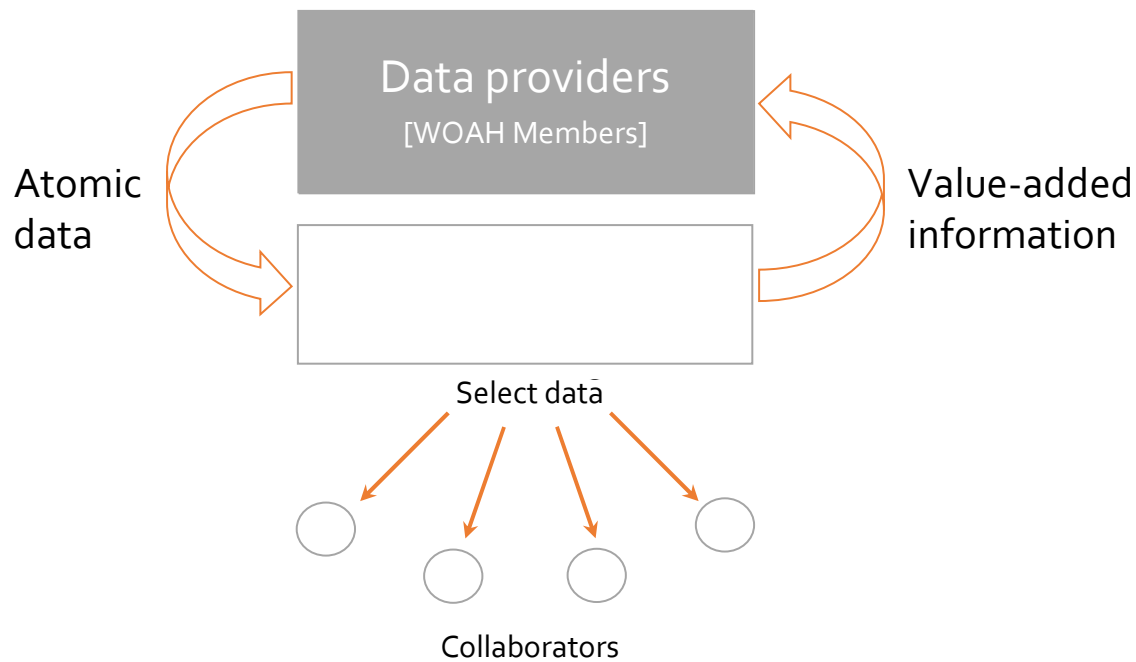


Figure 2 Recommended approach to successfully engage data providers to voluntarily share data

Data providers submit data into the information system, and get immediate value-added information relating to the submission of data that is valuable for them and thus motivates participation. As a by-product of this situation, data are available that may also be useful to other parties, such as collaborators. Where data providers consent, data may be shared from the information system directly to them.

Alongside inherent incentives to participate, cost and risk to the data providers need to be minimised in information system design.

In the context of an information system for avian disease occurrence in Asia and the Pacific, the foundation of meeting all of these criteria is establishing a governance structure based around the authority of contributing Members. By Members retaining authority around the use and sharing of data, there may be an improved willingness to contribute as perceived risk of sharing may be lower, compared to systems based on mandated sharing of data to third parties.

Further to Members retaining authority over the data, having the database hosted by an independent party can also encourage trust that data will not be used surreptitiously by authorities. It is expected that an information system will start small, either in data contributors or scope of data submission (or both); but with the opportunity to build trust, it is expected that the system will be able to scale up in size.

5.2 Proposed aims of an information system to collate avian influenza data in the Asia and the Pacific region

As avian influenza surveillance in the Asia and the Pacific region is very complex, involving many players and considerable sensitivities to data sharing, and in view of feedback from consultations (Section 2.3), it is proposed that in the first instance the information system should be pragmatically limited in scope to

1. Diagnostic capacity development (particularly, to allow laboratories to refine RT-PCR probes in line with circulating strains of avian influenza and other diseases).
2. Timely and cohesive region-wide sharing of avian disease detections in domestic poultry and wild birds, to inform preparedness and response activities in the region, and sharing of data relating to detection of novel infections or strains of infections in the region.
3. Sharing information on poultry and wild bird surveillance activities undertaken in the region.
4. Increasing the understanding of the epidemiology of avian diseases in the Asia and the Pacific region.

This equates to summary information that is shared quite freely already during regional meetings. In both the consultations for this project (Section 2.3) and in discussions at the WOAHA Regional Avian Disease Expert Group Network Meeting for Asia and the Pacific (held in Geelong, Australia, 31st October to 2nd November 2022) there was expression of a willingness to share these data in a new system of data capture. The system could mirror this intermittent reporting at meetings, but yield faster communication and constant access to relatively up-to-date summaries from across the region for all Members.

The scope of the information can be expanded as the information system evolves, in accordance with directions from the Management Committee (Section 5.4).

5.3 Consultation and recruitment of participating Members and laboratories

Extensive consultation and agreement on Terms of Reference and security are required to enable confidence in data contributors (Members) that

- their data will be secure and used only in accordance with pre-agreed terms, and
- the information system offers value to them that justifies their efforts in contributing (for example, through demonstration of examples of the output that they could expect to have access to in the first iteration of such an information system).

Managed information sharing between a few agreeing Members may be appropriate initially—creating a functional system with limited partners, but with a capacity to expand over time as confidence builds in the system's value and security (Section 2.3.1). Processes and specifics of consultation and recruitment, and legal considerations (particularly regarding sharing of notifiable disease data, and meeting the obligations of the Nagoya protocol), are important but beyond the scope of this project.



5.4 System ownership, governance and management

Key roles in the operation of an animal health information system include the system owner, management committee, secretariat and manager.

The system owner provides governance, adopts the appropriate internal policies for management of the system, allocates funding, manages contracting and authorises access of external parties to the data in line with established policies. It has been suggested that the WOAHA Asia and the Pacific Expert Reference Group, or the WOAHA Asia and the Pacific Reference Laboratories for Avian Influenza, could fulfil this role.

A good governance structure is vital to successful implementation and ongoing support of an information system, and ensuring the system is of value. Developing the governance structure is thus an essential first step in developing the information system; and for an information system that spans multiple independent parties, the governance structure must be clear and widely accepted.

In the governance structure, the Management Committee develops policies that control data access and usage, defines data standards, regulates the use of the database, and manages priorities in the future growth of the information system, with assistance of technical expertise. It is suggested that all participating Members and WOAHA Reference Laboratories for Avian Influenza would be represented in the Management Committee. As an example from a current animal health information system, iSIKHNAS (an integrated real-time information system for collecting, managing, reporting and using data to support animal health and production in Indonesia) is managed by a committee of senior staff from a number of related directorates general and organizational sub-units (previously subdirectorates) (iSIKHNAS, 2015).

Within the governance, the Secretariat provides administrative leadership, to facilitate the flow of governance to management. The secretariat is an independent party that is not aligned to any particular Member; this role may be best fulfilled by WOAHA or another non-partisan organization.

5.4.1 Technical management of the database system

Technical management of the system requires designated management staff to have full access to the data and data system, under appropriate security agreements. Technical management could be administered internally where adequate skills and resources are available (for example, within WOAHA). Alternatively, a private company involved in information system management could be contracted to manage and administer the system. The advantages of this approach are that it ensures independence and helps to alleviate concerns data contributors may have about the data being accessed by authorities in a non-transparent way.

5.4.2 Database users and permissions

The types of database users will fall broadly under the categories:

- System owner,
- Management Committee,
- Secretariat,
- System manager and administrators (administrators being the staff of the system manager involved in the IT side of the database management),



- Members,
- WOAHP Reference Laboratories for AI,
- Regional national laboratories,
- Collaborators such as FAO, OFFLU and the World Health Organization,
- Non-participating Members and future collaborators, and
- Public.

Users and permissions can be accommodated flexibly within a database structure, and access levels can be altered depending on governance agreements. A suggestion of default access levels, in accordance with industry requirements communicated through consultation for this project, is provided (Table 12).



Table 12 User group types, suggested bodies for user groups, and suggested default access levels for various database user groups

User groups (suggested bodies for user group):	Access level:					
	Login?	Submit detailed data?	View / download detailed data ^{1?}	View / download summary data ^{1?}	Edit categories?	Receive periodic reports ^{1?}
System owner and Management Committee (e.g. governance group comprised of participating Members)	✓	✗	✗	✓	✗	✓
Secretariat (e.g. WOAHA)	✓	✗	✗	✓	✗	✓
System manager (e.g. WOAHA internal staff, or an external information systems management company)	✓	✓	✓	✓	✓	✓
Members ²	✓	✓ ²	✓ ³	✓	✗	✓
WOAHA Reference Laboratories for AI	✓	✓ ^{3,4}	✓ ³	✓	✗	✓
Regional national laboratories	✓	✓ ^{3,4}	✓ ³	✓	✗	✓
Collaborators (e.g. FAO, OFFLU, WHO)	✓	✗ ⁵	✗	✓	✗	✓
Non-participating Members ⁶ / future collaborators ⁵	✓	✗	✗	✓	✗	✗ ⁷
Public	✗	✗	✗	✗	✗	✗ ⁷

¹ Data displays and reports can be tailored to a specific user group.

² If data transfer is not automated, there could be one person submitting data per Member, or one person submitting per surveillance program for the Member (e.g. domestic poultry program vs. wild bird program).

³ Detailed data access and displays would be for their Member; the Members cannot submit or view other Members' detailed data.

⁴ Data could be submitted directly from laboratory databases, where permission is obtained by data owner (usually the Member's government) (Section 5.5.3.1).

⁵ The Management Committee may agree to collaborations in which collaborators contribute data to the information system (Section 5.5.3.3).

⁶ Non-participating Members or future collaborators may be granted restricted and temporary access, to demonstrate the value of the system to encourage future participation.

⁷ This is flexible, in line with the directives of System Owner based on Management Committee policy. As for all other categories and aspects of access, the system will allow for it. For example, there may be an agreed need to make certain summary data available to non-participating Members or to the public.



5.5 Summary of proposed technical aspects of an information system

5.5.1 System architecture and hosting

It is recommended that a spatially-enabled relational database (for example PostgreSQL) is used, hosted by a cloud service provider.

5.5.1.1 Database security

International best practice security standards should apply to any database that is implemented; and it must be ensured that security features meet all local data privacy and security laws.

Cloud-based hosting of the information system is recommended to ensure integrity of the hardware, as leading cloud service providers provide physical security that is expensive to match with on-premises solutions.

Security is also an important consideration in the upload of data into the database (Section 5.5.3). Machine-to-machine connections for automated or manually-timed transfer of laboratory data with API authorisations entail optimal security in data transfers, and ensure data transfer occurs strictly according to data sharing agreements. If Members prefer submissions to be undertaken manually by email of excel spreadsheets to the system, or uploading of data using a web-based interface, the use of secure browsers and email providers to do so is required.

As well as the authorisation discussed under users and groups (Section 5.4.2), the information system is recommended to have restricted access using contemporary cybersecurity risk mitigation approaches. Access and authentication management, such as multi-factor authentication (a combination of username, password and a token or message-based confirmation to an external device) and full encryption of access is to be expected, as well as regular secure backup of data.

In developing an information system, it needs to be recognised that there will be ongoing costs regarding security updates and system maintenance, in addition to the hosting and general management costs. Most security breaches are resolved by changes to system security processes, which invariably require changes to the way the application behaves.

5.5.1.1 Database flexibility and scalability

Cloud-based hosting of the information system is also recommended so that it can be readily scaled (presuming all the correct agreements are in place) to match current needs. For example, the information system is expected to start small, likely increasing in the number of data contributors over time, and perhaps increasing in the range of data captured where the Management Committee agrees to do so. It may also make sense to scale the database based on seasons, as surveillance efforts (and thus data input into the system) are expected to vary substantially between seasons. Systems built on local solutions often cannot scale well due to security or application constraints.



5.5.2 Type of data captured

It is recommended that the system captures disaggregated data—individual test results, both positive and negative—rather than summary reports. Disaggregated data can be used more flexibly in analyses and output options. In line with consultation findings (Section 2.3.2), the minimum data required per test result are

- the test result, and if positive the subtype or strain of AI identified, including sequences.
- the host species from which the sample came.
 - An information system would be able to use the submitted species data from different Members to create new categories of species that are cohesive across the data set. This is expected to be hierarchical in nature and require the regional species categorisations to be very broad (for example, categorising host species first into wild bird and domestic birds, and then into broad taxonomic categories, such as at Order level for wild birds, where possible (Section 2.3.4).
 - The use of database synonyms facilitates the process. There would be a process in the first period of running the information system (particularly through the busy times of year for surveillance activities) where manual intervention/ updating of synonyms would be required to develop completeness in the cohesive species categories.
- the date the sample was collected.
- the geographical location at which the sample was collected.
 - A level of granularity for geographical location data expected to be acceptable is Member level, or first administrative division level (state, province, district or equivalent; a first administrative division level would be particularly valuable for interpretation of data from geographically large Members in the region, such as China, Australia, India and Indonesia).
 - Further increases in the granularity of the geographical location data would be of value, but may be difficult to reach agreement on.

As per consultations (Section 2.3.3), additional data of interest may span:

- the reason for testing (for example, disease investigation/passive surveillance, active surveillance, opportunistic testing);
- the location use-type category of the sample (for example, farm, live bird market, wild bird, zoo, pet, other);
- the type of sample tested (e.g. oropharyngeal swab, cloacal swab, mixed swab, tissue sample, faeces, environmental sample);
- the type of test undertaken on the sample;
- all test results associated with a particular sample (e.g. M-gene testing results and serology);
- for pooled samples, the number of birds in the pool;
- where relevant, a unique identifier to link results from different tests undertaken on samples from the same bird or same pool of birds (e.g. oropharyngeal swab and cloacal swab);
- where relevant, a unique identifier to link any individual bird samples to the pool from which it came (i.e. for samples which were tested individually after a pooled sample was positive);



- coinfection data;
- for domestic poultry, whether the bird(s) were managed free-range or not;
- for domestic poultry, whether the bird(s) were managed in a premises rearing multiple bird species; and
- the size of the at-risk population.

5.5.3 Transfer of data into the database

5.5.3.1 Laboratory data

Automated transfer of laboratory data from laboratory management systems to a database is recommended where possible, particularly for non-notifiable infections. Machine-to-machine connections with API authorisations occur strictly according to data sharing agreements. By avoiding manual transfer of data, the automated approach avoids placing time burdens on staff to arrange submissions, avoids the risk of transcription error (depending on the methods of data extraction for submission, and whether manual cleaning of data is undertaken before transfer), and ensures the frequency of submission of data is in line with agreed policies. Laboratory information management systems usually have a series of inbuilt ‘check points’ (for example, a pathologist may be required to sign-off test results, the implications of the test results, and funding source). These can be used to regulate transfer of data, to ensure that it does not occur before the Member who owns the data is ready to share it. Additionally and importantly, the API approach typically overcomes issues with data inconsistency as the information systems require data to meet validation standards before they are accepted into the database.

Alternatively, data can be transferred from laboratory management systems to a database with the timings of data transfer managed manually. In these cases, automated reminders would be sent to delegated staff within Member(s) in the absence of expected submission. This may be a preferred approach, particularly for notifiable infections, in consideration of the high level of sensitivity of such data, the reporting obligations and potential legal impediments to sharing such information.

Data submissions can also occur external to a LIMS system. For example, a Member could periodically email data to the information system’s database using a uniform template (for example, excel spreadsheets), or could upload such data into a system by a web interface. There could be one person responsible for submitting data per Member, or one person submitting per surveillance program for the Member (e.g. domestic poultry program vs. wild bird program). A suggested approach to database structure is outlined in Table 13, Table 14 and Table 15; this also reflects excel template structure for emailing to the database (Section 6).

Automation of data validation is important in allowing for rapid and inexpensive integration and analysis of uploaded data, and incorporation of it into reporting outputs—this should represent no manual intervention between data capture, management, generation of reports and reporting to Members. In both automated and manual processes of data transfer, there is expected to be automated error checking in place providing immediate feedback to those submitting data. If an upload is unsuccessful, this entails provision of precise information as to why an upload was unsuccessful for the data provider to rectify. If an upload is successful, a summary of the uploaded data is provided to the data provider for review, so they can check for obvious errors in the transferred data.



5.5.3.2 Other data

Data from external, open access data sources can be scraped and incorporated into the information system for reporting of AI data. For example, data could be matched from Genbank for generation of phylogenetic trees; national and NGO data sources containing information on poultry demographics could be incorporated for descriptive reporting and analytics; and meteorological and agricultural data sources for environmental data relevant to descriptive reporting and analytics.

Integration of all useful data, either in one system or available in one system through interoperability, is important to allow immediate (automated) analysis at low cost.

5.5.3.3 Collaborators' data

The Management Committee may reach agreements with collaborators for additional data sharing (e.g. non-governmental organisations or research organisations heavily involved in avian disease testing the region). In these cases, data could be submitted by collaborators through any of the mechanisms outlined in Section 5.5.3.1, where permitted to do so by data owners.

5.5.3.4 Timeliness of data transfer

The frequency of data sharing is expected to be agreed on and put into policy by the Management Committee.

5.5.3.5 Maintenance of data dictionaries

The methods by which samples were obtained, and the definitions by which data were categorised before submission to the information system, require clear description and updating by involved Members. This ensures that merging and reporting of data across the region is done accurately and in consideration of data limitations. For example, detail of the sample collection and testing methods, methods for categorising bird species, and methods for categorising sample types are required. The use of shared resources (often in the form of an API provided by regional organizations or experts) can be built into an information system, helping to reduce the burden of this maintenance.



Table 13 Example of a database table containing data from samples from individual birds

Database table would include variables for all genetic sequences; abbreviated here for simplicity of presentation

<i>Minimum data (excluding genomic data)</i>										<i>Further information of value</i>							
Bird ID	Holding ID	Wild_bird	Taxonomic order	Species-free text	Date	Location	Test type	Result	Subtype	Surveillance	Sample type	Test type	Pool ID ¹	Newcastle Disease	Infectious bursal disease	Free-range	Multispecies premises
1	102	No	Galliformes	broilers	DD-MM-YY	Member 1	RT-PCR	0		Passive	Cloacal swab	RT-PCR	766	NT	NT ²	0	0
1	102	No	Galliformes	broilers	DD-MM-YY	Member 1	RT-PCR	1	H5N8	Passive	Oropharyngeal swab	RT-PCR	767	NT	NT	0	0
2	NA	Yes	Anseriformes	Tufted duck	DD-MM-YY	Member 2	RT-PCR	1	H5N6	Active	faeces	RT-PCR	NA	No	NT	NA	NA

¹ To link results where a pool tested positive, and then individuals from that pool were tested

² NT = not tested

		<i>Genomic data</i>									
[Bird ID]	[Holding ID]	Subtype	Clade	Strain	HA_ct	Genbank	HA	HA_complete	HA_codon_start	
[1]	[102]	H5N8	2.3.4.4b	A/Chicken/...	20	MZ701931	atggagaaca..	no	1		
[2]	NA	H5N6	2.3.4.4	A/Wild_duck/..	17	-	atggaagtaa...	yes			



Table 14 Example of a database table containing data from pooled samples

Database table would include variables for all genetic sequences; abbreviated here for simplicity of presentation

<i>Minimum data (excluding genomic data)</i>								<i>Further information of value</i>							
Pool ID	Holding ID	Wild bird	Taxonomic order	Species-free text	Date	Location	Result	Surveillance	Sample type	Test type	Pool Size	Newcastle Disease	Infectious bursal disease	Free-range	Multispecies premises
766	102	No	—*	broilers	DD-MM-YY	Member 1	1	Passive	Cloacal swab	Rt-PCR	5	NT	NT	0	0
767	102	No	—*	broilers	DD-MM-YY	Member 1	1	Passive	Oropharyngeal swab	Rt-PCR	5	NT	NT	0	0

* Example missing data

		<i>Genomic data</i>													
[Pool ID]	[Holding ID]	Subtype	Clade	Strain	HA_ct	Genbank	HA	HA_comple	HA_codon_	te	start			
[1]	[102]	H5N8	2.3.4.4b	A/Chicken/...	20	MZ701931	atggagaaca..	no	1						



Table 15 Example of a database table containing serological surveillance data

<i>Minimum data</i>									<i>Further information of value</i>					
Wild bird	Taxonomic order	Species—free text	Date	Location	Test	Number tested	No. positive	Serovar	Surveillance	Test type	Newcastle disease	Infectious bursal disease	Free-range	Multispecies premises
No	—*	broilers	DD-MM-YY	Member 1	Serology	120	0	H7N9	Passive	HIT	NT	NT	0	1
No	—*	ducks	DD-MM-YY	Member 2	Serology	20	0	H7N9	Passive	HIT	NT	NT	1	0

* Example missing data



5.6 Reporting from the database

Reporting from an appropriately structured database can be set up automatically. In this case, reporting can be as frequent or intermittent as decided by the Management Committee, with Members and collaborators able to access reports on demand through web access. Frequent autogenerated reporting can be important to maintain engagement of contributors of data, and it is recommended that they are produced and distributed on emailing lists at least one a month, with additional reports available on demand. More detailed reports that are drafted automatically but then incorporate expert interpretation and discussion of results are also recommended, with regular production and distribution (e.g. every three months).

Dashboards are a more advanced option than automated reporting, allowing users to interact with the data for specific purposes, rather than only having access to pre-structured and automated reports. Theoretically, if data are uploaded automatically from laboratories (with Member permission) then dashboard reporting can be in real time; but as discussed, in this case real-time reporting is unlikely to be feasible (Section 2.3.5). Nonetheless, elements such as mapping interfaces showing the distribution of surveillance efforts and infections do provide opportunity for members to understand better the implications of new reports of disease presence in the region on their own national flocks.

5.6.1 Dashboard reporting

For approved and registered users, a dashboard system could autogenerate all outputs identified as being of value to the region in AI surveillance (Section 2.3.6). These include interactive phylogenetic trees, maps, tables and charts, as well as accessible code, and with download of summary data from across the contributing Members.

There are excellent examples of valuable information displays across existing systems, including WAHIS, the Hokkaido University database, Empres-i+, Nextstrain and the Influenza Research Database (Section 4). Outputs can be modelled on the outputs considered of value in the context of this information system's goals, and expanded on with additional and novel outputs where needed, as guided by the Management Committee. As the usefulness and accuracy of any analyses is heavily dependent on quality and quantity of data available, it will be essential to have sufficient information on the data origins with expert guidance to inform the feasibility and value of potential data outputs (Section 5.5.3.5).

For example, maps and figures of a similar concept to WAHIS and Empres-i+ could be replicated, with expansions such as

- density mapping for exploring spatial clustering of infection with access to negative data and/or by drawing in poultry demographic data from open data sources, where available)
- basic trend analyses (e.g. on environmental variables incorporated into the database from external open access sources)
- using the right data, prevalence estimates of endemic subtypes and strains (though these figures are likely to only be made available to the Member to which the estimates relate.

There are well established approaches to estimating prevalence using pooled samples.

For example, in Nexstrain there are a variety of 2D dendrograms that are filterable by features such as time and space. A similar approach could be taken, and/or a 3D approach may be considered of value to improve the display of complex phylogenetic trees, as well as being able to display additional information (for example, on the relative frequency of sequences).



Additionally, there are a swathe of advanced tools available for dashboard reporting—for example, PCR primer design tools, and tools for sequence alignment, as per the Influenza Research Database (Influenza Research Database, 2022b).

5.6.2 Automated generation of reports

Email alerts could be set up by users, to enable them to receive email notification of new data uploads, or upload of data on specific subtypes or strain of interest, or based on proximity. Monthly automated reports could be devised, as a summary of AI information nominated as of value to contributing Members for frequent reporting. For example, it could include highlight data relating to particular subtypes/strains of interest or novel sequences, alongside summary data such as the numbers of positive tests of each subtype and strain, with description of infected host species, geographical locations (at an agree level of granularity), the timing of sampling and the origin of the sample (e.g. passive vs active surveillance).

Quarterly ‘informed’ summary reports could be set up to automate a draft summary of the quarterly data, for manual addition of commentary/ interpretation of findings by an expert group, alongside social aspects of the system (for example, Members or laboratories joining the information sharing, or personnel changes).

5.6.3 Scalability of reporting

Reporting from the information would be readily scalable. If the Management Committee agrees on new reporting outputs, or expansion of existing outputs, the information system can readily accommodate this in the short term (days or weeks), presuming all the correct agreements are in place.

5.7 Sharing or reporting of data to third parties, and its use in research and publications

It is expected that sharing or reporting of data to third parties would only occur if mutually agreed to do so by the Management Committee (representing the Members), in accordance with clearly defined and delimited data requests.

Early in the process of developing a system, it is recommended that the Management Committee establish policies and guidelines around sharing of data to outside parties (including researchers, collaborators and regulators). If data sharing is agreed to in principle in certain circumstances, it is expected that any data requests will be subject to the approval of the Management Committee in a formal application process. This would include consideration of the aims of the research, the data required and the security standards under which the data will be held and used. It would also include conditions around the publication of shared data or resultant analysis.



5.8 How a new information system for the Asia and the Pacific region may be different from existing systems

In contrast to existing data sources, a new information system for the purposes of reporting on avian disease surveillance in the Asia and the Pacific region would

- aim to capture disaggregated negative test data (as well as positive test data) for multiple avian diseases, for reporting purposes that include detailed mapping of surveillance efforts. This also allows for linkage of multiple test results undertaken on a single sample.
- aim to capture more data on reasons for sampling, approach to sampling and testing methods, to allow for epidemiological inferences of improved validity.
- combine data that are not available collectively in existing databases, to enable rapid and inexpensive analyses that can incorporate more detail
- operate under the authority of contributing WOAHP Members, with output that is tailored specifically to the needs and mutually agreed terms of the Members.
- have the capacity to be rapidly responsive to evolving requirements of regional Members, such as expanding the range of data capture, reporting on additional diseases, and adjusting or adding to the information system outputs.
- have the capacity to be considerably more timely with reporting and analyses involving a broad range of avian diseases compared to existing systems.

Additionally, by retaining control of data and contributing to decision making on how the system operates, including data inputs and outputs, Members may have increased confidence in sharing an expanded range of data, compared to that currently captured in other databases.



6 Proposal of a template for avian influenza surveillance data collection

As discussed above, automated transfer of laboratory data from laboratory management systems to a database is a secure and recommended approach to sharing of data from the region (Section 5.5.3). The advantages of this approach include

- minimising labour requirements from participating Members, and thus avoiding disincentives to participation,
- ensuring data is available to the database in the most timely manner possible, and
- avoiding potential transcription error.

Nonetheless, submission by emailing of data to the database is another option, where that is the preference of participating Member (Section 5.5.3). It would be the responsibility of the Member to work with their existing systems to produce the suitable data (e.g. an excel spreadsheet).

Suggested templates for excel spreadsheet submissions correspond exactly to the suggested structure of the database (Section 5.5). This involves separate spreadsheet reporting for individual sample results (Table 13), pooled sample results (Table 14) and serological surveillance results (Table 15).

For baseline data collection, data for the HA sequence are shown (Table 14 and Table 15); the HA variables would be repeated for all sequences in the data, for completion wherever the sequence was undertaken. If the lab has submitted sequences to Genbank or GISAID, the accession number could be provided in the absence of the other information: using the code, the relevant information to be scraped off the relevant site and thus minimise manual labour in collating the data.

Of desirable additional data, results of M-gene testing could be reported; and the presence of Newcastle disease and infectious bursal disease are considered as binary variables (presence: yes or no) at a basic level, but data collection could be expanded to include submission of information on testing methodology and sequencing data for these infections as well. As previously discussed, it should be relatively easy to scale the database to accommodate further information (Section 5.5.1.1). However, compliance in obtaining that information, particularly if submission is occurring manually, is best achieved with relatively focussed and concise information requests.



7 References

- Animal Health Australia, 2021. Animal Health in Australia System Report. Canberra.
- Cameron, A.R., Meyer, A., Faverjon, C., Mackenzie, C., 2020. Quantification of the sensitivity of early detection surveillance. *Transbound Emerg Dis* 10.1111/tbed.13598. <https://doi.org/10.1111/tbed.13598>
- Commonwealth of Australia, 2010. National Avian Influenza Surveillance Dossier 173.
- FAO, 2022a. EMPRES : Global Animal Disease Information System AIMS [WWW Document]. URL <http://aims.fao.org/news/empres-global-animal-disease-information-system> (accessed 4.8.22).
- FAO, 2022b. Empres-i+ Global Animal Disease Information System [WWW Document]. URL <https://empres-i.apps.fao.org/> (accessed 4.8.22).
- GISAID, 2022a. GISAID - Initiative [WWW Document]. URL <https://www.gisaid.org/> (accessed 5.27.22).
- GISAID, 2022b. GISAID EpiFlu Database Access Agreement [WWW Document]. URL <https://www.gisaid.org/registration/terms-of-use/> (accessed 5.27.22).
- Government of India, 2021. Action Plan for Prevention, Control and Containment of Avian Influenza (Revised – 2021).
- Hadfield, J., Megill, C., Bell, S.M., Huddleston, J., Potter, B., Callender, C., Sagulenko, P., Bedford, T., Neher, R.A., 2018. Nextstrain: real-time tracking of pathogen evolution. *Bioinformatics* 34, 4121–4123. <https://doi.org/10.1093/bioinformatics/bty407>
- Influenza Research Database, 2022a. Data Sources [WWW Document]. Influenza Research Database. URL <https://www.fludb.org/brc/dataSources.spg?decorator=influenza> (accessed 4.26.22).
- Influenza Research Database, 2022b. Analysis Tools [WWW Document]. Influenza Research Database. URL https://www.fludb.org/brc/analysis_landing.spg?decorator=influenza (accessed 4.26.22).
- iSIKHNAS, 2015. How is it managed? - Wiki Sumber Informasi iSIKHNAS [WWW Document]. iSIKHNAS. URL http://wiki.isikhnas.com/w/How_is_it_managed%3F (accessed 4.11.22).
- Moriguchi, S., Hosoda, R., Ushine, N., Kato, T., Hayama, S.-I., 2021. Surveillance system for avian influenza in wild birds and implications of its improvement with insights into the highly pathogenic avian influenza outbreaks in Japan. *Prev Vet Med* 187, 105234. <https://doi.org/10.1016/j.prevetmed.2020.105234>
- NAHIS, 2022. Avian influenza summary results.
- National Centre for Biotechnology Information, n.d. Influenza Virus Resource [WWW Document]. URL <https://www.ncbi.nlm.nih.gov/genomes/FLU/Database/nph-select.cgi?go=database> (accessed 5.27.22).



- Nextstrain, 2022a. Nextstrain CLI [WWW Document]. Nextstrain. URL <https://docs.nextstrain.org/projects/cli/en/stable/> (accessed 4.26.22).
- Nextstrain, 2022b. Nextstrain [WWW Document]. GitHub. URL <https://github.com/nextstrain> (accessed 4.26.22).
- OFFLU, 2020. Joint OIE-FAO Scientific Network on Animal Influenza [WWW Document]. URL <https://www.offlu.org/> (accessed 5.27.22).
- OIE, 2019. World Animal Health Information Database (WAHIS). World Animal Health Organization, Paris, France.
- Rose, K., Newman, S., Uhart, M., Lubroth, J., 2006. Wild bird highly pathogenic avian influenza surveillance: sample collection from healthy, sick and dead birds, FAO animal production and health manual. Food and Agriculture Organization of the United Nations, Rome.
- Schoch, C.L., Ciuffo, S., Domrachev, M., Hotton, C.L., Kannan, S., Khovanskaya, R., Leipe, D., Mcveigh, R., O'Neill, K., Robbertse, B., 2020. NCBI Taxonomy: a comprehensive update on curation, resources and tools. Database 2020.
- Sharshov, K.A., Yurlov, A.K., Li, X., Wang, W., Li, L., Bi, Y., Liu, W., Saito, T., Ogawa, H., Shestopalov, A.M., 2017. Avian influenza virus ecology in wild birds of Western Siberia. *Avian Res* 8, 12. <https://doi.org/10.1186/s40657-017-0070-9>
- Whitworth, D., Newman, S., Mundkur, T., Harris, P., 2007. Disease sampling procedures, in: *Wild Birds and Avian Influenza: An Introduction to Applied Field Research and Disease Sampling Techniques*. FAO.
- Wildlife Health Australia, 2022a. National Avian Influenza Wild Bird Surveillance [WWW Document]. Wildlife Health Australia. URL <https://wildlifehealthaustralia.com.au/ProgramsProjects/WildBirdSurveillance.aspx> (accessed 2.24.22).
- Wildlife Health Australia, 2022b. eWHIS- Wildlife Health Information System [WWW Document]. URL <https://wildlifehealthaustralia.com.au/ProgramsProjects/eWHIS-WildlifeHealthInformationSystem.aspx>
- WOAH, 2022a. Periodical data extractions OIE-WAHIS [WWW Document]. URL <https://oieoffice365.sharepoint.com/sites/PeriodicaldataextractionsOIE-WAHIS> (accessed 6.30.22).
- WOAH, 2022b. Chapter 3.3.4. Avian influenza (including infection with high pathogenicity avian influenza viruses), in: *Terrestrial Manual*. World Organisation for Animal Health.
- WOAH, 2016. HANDISTATUS II [WWW Document]. URL <https://web.oie.int/hs2/report.asp> (accessed 6.30.22).
- World Health Organization, 2011. Manual for the laboratory diagnosis and virological surveillance of influenza. World Health Organisation.

