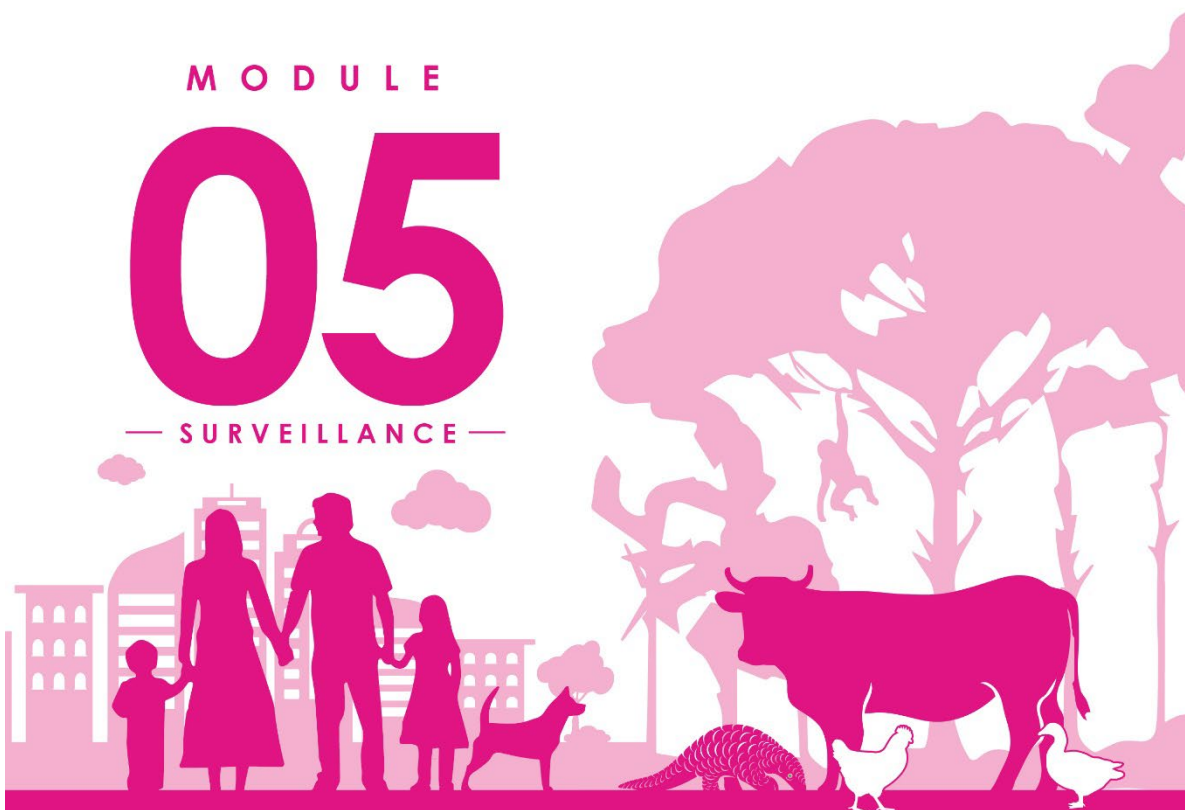


M O D U L E

05

— SURVEILLANCE —



How to Design and Conduct Risk-Based Surveillance at the Human-Animal Interface

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How to Design and Conduct Risk-Based Surveillance at the Human–Animal Interface

INTRODUCTION

In 2018, the FAO-WHO-WOAH Tripartite (the Tripartite) called for the development or improvement of coordinated One Health surveillance systems within member countries and regional networks (FAO, WOA H, and WHO, 2019). Surveillance systems, whether they are risk-based or not, are defined as ongoing efforts, whether active or passive, aiming at detecting cases of disease (Thacker and Berkelman, 1988). Risk-based surveillance takes advantage of information about known or suspected high-risk targets to narrow surveillance efforts, often as a way to optimize use of limited resources (Bordier et al., 2020). This approach naturally aligns with One Health systems that target both human and animal populations, and ideally employ environmental monitoring as well (Berezowski et al., 2023). However, sector-specific resources and authorities remain as major gaps in achieving effective coordination among human, animal, and environmental monitoring and response activities (Sharan et al., 2023). This module aims to provide guidance on the design and execution of risk-based surveillance at the interface of human–animal–environmental health, where the risk of spillover is known or suspected to be higher.

RISK-BASED ONE HEALTH SURVEILLANCE APPROACHES

To carry out risk-based One Health surveillance, One Health authorities (typically ministries of health, agriculture and animal health, natural resources, and the environment) interact with community partners, One Health researchers, their networks, and policymakers to conduct activities in an iterative way (WHO, 2017b). In the context of early detection and rapid response, regional and local surveillance programs are critical to identify initial cases of spillover, document potential human-to-human transmission, and inform efforts to intervene to avert outbreaks, emerging epidemics, and pandemics (Berthe et al., 2022; Tufts University Consortium, 2022). At national and international levels, triangulation of data from disparate sources, including human, animal, and environmental domains, and considering the potential for transboundary movement of disease, aids in understanding the scope of the event, transmission pathways, and potential intervention points (Figure 5-1). Within surveillance systems, disease reporting and laboratory networks may rely on established mandatory reporting requirements at multiple levels of governance or institutional structure (Nsubuga et al., 2006), whereas syndromic surveillance may use emerging technologies, such as text data mining and intelligence (AI) based systems (Box 5-1) (Zeng et al., 2021). Sampling programs may be part of established initiatives, such as occupational health surveillance (Lele, 2018), or may rely on clinical populations and research initiatives for some or all of the data. In this, the data integration and decision-making may be based on One Health approaches, although the individual surveillance systems may not be.

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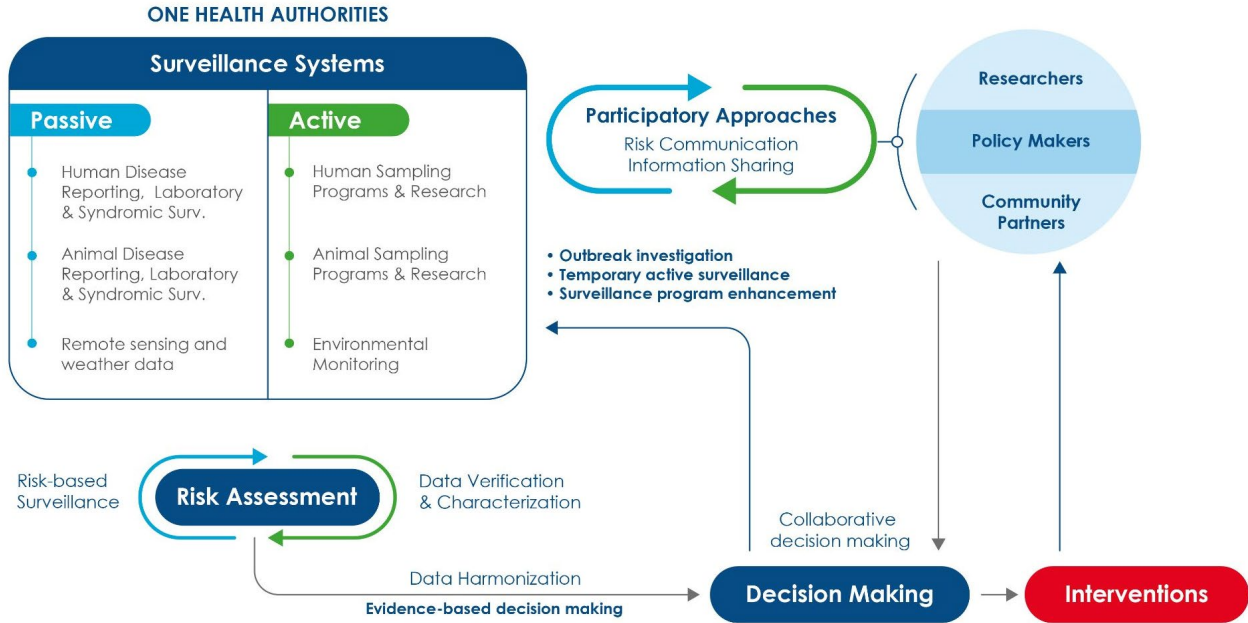


FIGURE 5-1 Interactions among partner groups and iterative activities for One Health surveillance, risk assessment, and decision-making using participatory approaches.

Risk-based approaches often aid in the prioritization of targets for surveillance or intervention and may be based on traditional risk assessment processes used widely on a global scale for public health efforts. When these are targeted to One Health approaches and context, activities typically involve identification of higher-risk human and animal populations and geographic regions or high-risk microenvironments (e.g., live animal markets). Ultimately, information from surveillance systems often guides risk assessment and decision-making, e.g., restrictions on trade or transport of animals or their products or the initiation of infection control, enhanced biosecurity or quarantine measures in response to an ongoing outbreak (Thacker and Berkelman, 1988). For example, during the 12 years of avian influenza surveillance from 1999 to 2011 in Hong Kong, the authorities implemented a series of interventions to control outbreaks of the H5N1 influenza virus in live poultry markets and poultry farms (Leung et al., 2012). These included (1) implementation of a monthly rest day, (2) a mandate that all poultry in live poultry markets be sold or slaughtered at the end of each day, (3) a requirement that poultry stalls be cleaned and disinfected and (4) that stalls must be left free of live poultry for 1 day before restocking, (5) prohibiting the sales of live quail, and (6) a complete ban on holding live poultry overnight in 2008. These have been shown effective in reducing viral amplification and persistence in live poultry markets while also mitigating the risk of avian influenza transmission to humans (Leung et al., 2012).

Known zoonotic pathogens can be regularly monitored with animal surveillance and functioning veterinary service systems. The World Organization for Animal Health (WOAH) publishes Performance of Veterinary Services (PVS) standards that are widely used to track national veterinary capacity and surveillance (WOAH, 2019; WOAH, 2023). However, the PVS primarily addresses domestic animal health standards. Notably, wildlife are most likely to harbour a new zoonotic pathogen with pandemic potential that can either directly spillover into people or pass through an intermediary domestic animal host (Module 3; Jones et al., 2008). It is likely that emerging pathogens will evade detection until they cause noticeable illness or mortality in humans

or animals identified through surveillance activities. WOAHA also has published a National Wildlife Health Surveillance framework (WOAHA, 2022), but the use of such surveillance systems remains the exception rather than the rule (Machalaba et al., 2021). For example, surveillance of Lao PDR's wildlife trade only recently detected a high prevalence of leptospirosis (20%) in all traded animals as well as rickettsial species responsible for murine typhus, revealing a 'substantial risk for exposure through handling and consumption of wild animal meat' (Nawtaisong et al., 2022; Phongmany et al., 2006).

Participatory approaches, in which community members are engaged in the design and conduct of surveillance systems, can enhance quality of reporting and accelerate detection and response efforts (Mariner et al., 2011). Ideally, community-based participatory approaches to surveillance and response efforts are built on and oriented to what communities identify as priorities, and the efforts typically are conducted by community members (Palmer and Duclos, 2023). However, specific activities may fall along a spectrum of community engagement and participation, from community-led efforts to those led by national authorities or researchers who work with communities to incorporate their needs into surveillance and mitigation efforts. Participatory and public-based surveillance of small livestock holdings can greatly expand the number of engaged observers within a national, regional, or local framework. For example, there is a mobile-phone-based Participatory One Health Digital Disease Detection (PODD) project in Thailand, and a similar project in Africa: Enhancing Community-Based Disease Outbreak Detection and Response in East and Southern Africa (DODRES). Other examples are wildlife health surveillance networks, such as the WildHealthNet initiative (Privot et al., 2023) and the Wildlife Conservation Society's SMART FOR HEALTH. When communities themselves define high-risk priority interfaces, they are more likely to engage in implementation of interventions to reduce or mitigate the risks.

DESIGNING ONE HEALTH SURVEILLANCE AT THE HUMAN-ANIMAL INTERFACE

One Health surveillance efforts that address high-risk human-animal-environmental pathogen interfaces and their potential for use in monitoring programs aid in spillover detection and response (Bordier et al., 2020). Surveillance efforts can take numerous forms and be either passive or active (Figure 5-1) (Nsubuga et al., 2006). Passive collection of human or animal health data relies on reporting disease from human and animal healthcare providers, local health departments, local animal health ministries, and similar groups (Murray and Cohen, 2017). Disease reporting therefore may be less timely or depend on the provision of a diagnosis (Jajosky and Groseclose, 2004). Other passive systems include clinical, reference and public health laboratories and networks that compile and report information about pathogen detection and other pathogen characteristics, and given sufficient resources, include pathogen genomic sequencing and analysis to identify key virulence factors (e.g., the polybasic cleavage site in the hemagglutinin of avian influenza viruses). Such efforts aid in the detection of novel variants, and guide investigation of outbreaks using genomic epidemiology supported by meta-data, ideally including host and geotemporal data (Nsubuga et al., 2006). Remote sensing and other sources of weather data also may be important to inform prediction of outbreak events based on risk factors related to temperature, rainfall, sea surface temperature and wind patterns (e.g., vector-borne diseases or cholera) (Kuhn et al., 2005). Finally, syndromic surveillance relies on reporting at the population

level (e.g., via intelligence (AI) systems) (Box 5-1) of clusters of cases based on symptoms rather than disease diagnosis (Groseclose and Buckeridge, 2017). Surveillance for influenza-like illness is an example of this, where healthcare systems may monitor the number of people with respiratory symptoms as their primary presenting complaint, where pharmacy systems track purchase of common over-the-counter medications used to alleviate respiratory symptoms, or where AI algorithms track online queries related to respiratory illness. Syndromic surveillance at the individual host level (e.g., presentations of foetal demise, encephalitis, or haemorrhagic fever) often are reportable and provide early warning of emerging infectious diseases (Henning, 2004).

In contrast, active collection of surveillance data and/or samples relies on trained personnel, often at regional or national levels in ministries of health or agriculture, who administer surveys, collect samples and aggregate data, or perform other information-seeking activities (Murray and Cohen, 2017). This may be augmented by targeted programmatic or research activities by non-profit organizations or academic partners, e.g., via the Southeast Asia One Health University Network (SEAOHUN). Active surveillance often provides more timely results better targeted to higher-risk populations but also has higher resource costs in personnel, materials, and other supplies (Nsubuga et al., 2006). These efforts also may require more substantial investments in One Health workforce expertise, although it is important to note that expertise is essential for a wide range of surveillance efforts. Further, investment in programs that use active sampling approaches, such as collection of environmental DNA (eDNA) for non-targeted sequencing, or targeted sequencing of pathogens, can inform passive approaches (Rishan et al., 2023). There are numerous approaches to surveillance (Table 5-1) which may be used alone or in combination depending on the goal of the surveillance activity.

Syndromic Surveillance

Risk-based monitoring for severe respiratory and neurologic syndromes or foetal demise in humans and animals relies on accurate and comprehensive knowledge of key risk factors, including occupational or other behavioural risk factors and pathogen epidemiology (Sosin and DeThomasis, 2004). Syndromic surveillance allows for earlier detection of clusters of similar disease in time or geographic region, and therefore can be particularly important for novel diseases because these may be threat-agnostic, i.e., the hazard does not need to be known in advance (Henning, 2004). Syndromic surveillance can be limited by lack of human health or veterinary care-seeking or access, non-specific (e.g., fever) clinical or subclinical presentations, or lack of reporting mechanisms (Elliot et al., 2020).

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TABLE 5-1. Approaches to surveillance activities

Surveillance Approach	Description	Role in Risk-Based Approaches
Syndromic surveillance	Use of symptom data to identify clusters of disease in time or space	Identify populations or areas of higher risk
Laboratory surveillance	Use of laboratory reporting data or specimens to identify clusters or diagnose outbreaks	Identify related strains across time and space to inform response and outbreak investigation
Seroepidemiological studies	Use of biospecimen repositories (serum samples) for novel targets	Inform knowledge of risk factors
Environmental surveillance	Active sampling of environmental media for pathogens	Environmental locations informed by risk analysis
Event-based surveillance	Use of information outside of normal reporting systems to identify disease clusters	Identify populations or areas of higher risk

Laboratory Surveillance

When samples from humans or animals are collected through routine health assessments, i.e., a test ordered by a physician, laboratory detection of pathogens can be used to identify unexpected clusters of pathogens ([Nsubuga et al., 2006](#)). When bacteria are cultured or viruses detected as part of these efforts, further characterization of the pathogen (antimicrobial susceptibility, genomic sequencing) can aid in identification of related strains of the pathogen, and this can help to enhance case identification for outbreak investigations that are more likely related in terms of transmission events. This approach requires laboratory standardisation in diagnostic testing, lab accreditation and quality control programs, and access to reference laboratories for confirmation. This also requires the robust maintenance of laboratory biosafety and biosecurity standards ([Taylor et al., 2017](#)).

Seroepidemiological Studies

In addition to activities that target sampling of humans or animals and use of the biospecimens for microbiological and immunological assays to detect known or emerging diseases or host responses to them ([Murphy, 2008](#)), some activities can use established repositories such as blood donation banks or military archives to identify prevalence of prior exposure ([Cariappa et al., 2004](#); [Zhang et al., 2020](#)). These benefit by being more population-based and feasible to access, assuming the repositories have been established and maintained in a way that allows such use. Access to standardised protocols and reagents is also an important enabling factor. However, biorepositories for animal specimens are limited and national laboratories may not have resources for longer-term storage of samples (Module 4), which offers an opportunity for resource investment. Another consideration is the use of salivary antibody testing in lieu of blood antibody testing for high-risk human populations (such as animal or abattoir workers) who are averse to blood draw for serological testing, if salivary antibody tests are available ([Pisanic et al., 2020](#); [Thomas et al., 2023](#)). Given that few salivary biospecimen repositories exist, this may require active surveillance and *de novo* sample collection.

Environmental Surveillance

Environmental surveillance may include wastewater (including litter, manure, and effluent from markets), bioaerosol and surface sampling, as has been done for influenza virus of swine origin in swine production facilities (Anderson et al., 2017; Prost et al., 2019) or for *Chlamydophila psitacii* (bioaerosols) in slaughterhouses (Dickx et al., 2010). Locations of high concentrations of animals in the human food chain (and thus associated with exposure) include animal production facilities, wet markets, slaughterhouses, and abattoirs (Al-Gheethi et al., 2021; Clark, 2022; Lin et al., 2021). High-throughput DNA sequencing can be used to identify animal species (Suminda et al., 2022) kept in live animal markets and whether they are illegal species, which can inform enforcement efforts. For example, one study demonstrated that airborne eDNA used to monitor and confirm animal species was sufficiently sensitive to detect dead animals fed to zoo animals as well as rodents (Lynggaard et al., 2022). Additionally, environmental surveillance should include monitoring anthropogenic changes related to land use and deforestation, as these actions may put animals under stress and impact viral ecology and spillover through altered proximity dynamics.

Event-Based Surveillance

In contrast to classic surveillance activities in which collection occurs routinely and action may be based on defined criteria, such as thresholds for number or rates for cases, event-based surveillance captures information through less formal channels and outside standard reporting systems. An early warning system can be established from event-based surveillance, identifying unusual health events or trends in human and animal health, which can serve as signs of disease emergence. For example, this could take place through media reports or community groups and may be verified through formalized processes; the World Health Organization has published guidance for establishment of these systems (WHO, 2014). For example, Lao PDR has adopted an event-based surveillance system and has a [standard operating procedure \(SOPs\)](#) with four components: community engagement, health facility-based surveillance, hotline, and media monitoring; the WHO is providing technical support. These activities (i.e., considering the network, actors within the system, their role, etc.) inform policy development. Affordable monitoring of targeted specific species, especially those identified as reservoirs and intermediate hosts, can be implemented as a crucial component of wildlife disease surveillance, especially in the context of constraints on diagnostic capacities (Kelly et al., 2021). A remaining challenge is that this requires ample time for development of government support, and there are additional challenges of sustainability.

BOX 5-1

Artificial Intelligence and One Health

Artificial intelligence (AI) plays an increasingly crucial role in One Health, which focuses on the intersection of human, animal, and environmental health (Ezanno et al., 2021). AI methods can help organize the vast amounts of data that are central to the One Health approach by detecting outbreaks, predicting disease spread patterns, contributing to drug discovery, and optimizing resource allocation for interventions across different species and ecosystems (Malik et al., 2021; Seifman, 2023; Qureshi et al., 2021). AI methods can integrate large amounts of data from different sources and synthesize information across multiple systems, helping scientists understand zoonotic diseases and identify potential interventions (Pillai et al., 2022). For example:

1. Machine Learning algorithms analyse large datasets to identify patterns and predict disease outbreaks, track environmental changes, and assess the effectiveness of interventions.
2. Deep Learning techniques assist in image and sequence data analysis for medical imaging, tracking wildlife movements, and analysing genomic sequences.
3. Natural Language Processing enables the extraction of valuable insights from textual data, such as medical records, One Health-related reports, scientific literature, and social media posts.
4. Network Analysis methods can efficiently and accurately model complex interactions among hosts, pathogens, vectors, and environmental factors to help develop disease transmission pathways, identify key nodes for targeted interventions, and predict disease spread patterns within and across populations.
5. Predictive Analytics, such as Bayesian networks and decision trees, can forecast disease outbreaks, assess the impact of climate change on disease distribution, and optimize resource allocation for disease control measures.
6. Robotics and other autonomous systems are used for surveillance, sample collection, and monitoring environmental parameters in remote or hazardous areas, facilitating data collection in challenging environments (forests, oceans, and disaster zones) to support early warning systems and ecosystem health monitoring.

One Health approaches are based on data, and AI methodologies offer efficient and creative ways to harness data for good. However, AIs are accompanied by concerns with bias, access, cost etc. The concepts of “FAIR(ER)” (Findable, Accessible, Interoperable, Reusable, Ethical and Revisable) are essential to address deep-seated inequities that characterize so many global arenas. Calvin Wai-Loon Ho published a call for a One Digital Health Framework (Ho, 2022) that argues for:

“a dedicated global ODH framework that also augments current ABS provisions in the CBD and NP as an ABS+ Framework. In essence, this ODH framework should apply to both human and non-human biological materials and related data, put into effect the FAIRER principles (more aligned with global justice under the SDGs) through arrangements like federated data systems, and shift toward multilateralism.”

RISK-BASED APPROACHES

Regardless of the approach used for surveillance, selection of surveillance targets (human populations, animal populations, environmental sites) can rely on risk assessment and target interfaces established or suspected to be of higher risk to maximize use of limited resources, i.e., identify targets for surveillance or intervention that have a higher benefit-to-cost ratio. Risk-based approaches also can inform interventions, such as restriction of the live trade of high-risk reservoir

host species in urban markets where alternative protein sources are available (Module 2). Wildlife meat products still may carry pathogens (Espinosa et al., 2020), but any unobserved processes of pathogen amplification or viral recombination and evolution are reduced. In this, there are dual needs for coordination—first to interpolate data and biosurveillance strategies, e.g., through identification of common targets (Box 5-2), and second to integrate surveillance with response and control efforts (Nsubuga et al., 2006; Zinsstag et al., 2020).

Approaches to risk-based surveillance in animal populations benefit from consideration of infection dynamics within any given host population (Stark et al., 2006). For example, reservoir animal hosts often carry infectious agents without showing many or any symptoms of disease and may not shed the infectious agent (virus, etc.) routinely, which limits the utility of methods that rely on pathogen detection or isolation (Module 4) unless sampling occurs during periods of high shedding (e.g., during stressor events). Similarly, risk-based environmental strategies need to consider the detection method (PCR, pathogen isolation, etc.) and the stability of that target over time given the organic matrix of the waste or wastewater, since agents may die, and genetic material may degrade given environmental conditions and time. On the other hand, certain host genera or species (i.e., kinds of animals), such as bats, rodents, and birds (Table 4-5; Module 4), are in a higher-risk category for potential to carry established and novel zoonotic agents, including those with pandemic potential.

Box 5-2

Avian influenza example

Although laboratory-confirmed cases of highly pathogenic avian influenza viruses have been associated with high mortality in humans (59%), true infection rates are unknown in the absence of sound seroepidemiological studies (Butler, 2012). Prior studies have identified seroprevalence ranging from 0 to 3.2% depending on exposure, HPAI viral subtype, and clade. One longitudinal study in southern China, however, revealed 54.2% live poultry market workers were seropositive with antibodies to H7N9 virus, suggesting that this workforce is at higher risk and may be a useful target for active surveillance activities (Wang et al., 2014). Incidence of infection among poultry workers varies, with incidence density higher for H5N1 clade 2.3.4 (3.8/1,000 person-months) compared to other H5N1 clades (0.3/1,000 person-months for clade 2.3.2.1 and H7N9 viruses (1.6/1,000 person-months) in one study from Beijing, China (Yang et al., 2016).

The use of new risk assessment tools to predict virus emergence or identify areas of higher risk for spillover events can guide selection of target populations (Salerno et al., 2017; Vora et al., 2023). Classic risk assessment techniques adapted from assessment of environmental toxins include problem formulation, hazard identification, exposure assessment, risk characterization, risk management, and risk communication, ideally within a participatory approach framework (NRC, 2009). These may be important to consider because of their widespread use for other public health activities at regional, national, and international levels, including decision-making that involves large industries. The International Union for Conservation of Nature (IUCN)-WOAH *Guidelines for Wildlife Disease Risk Analysis* (2014) is one more recently developed disease risk assessment tool based on classic risk assessment processes adapted for and intended to inform animal value chain decision-making around movement of wildlife and wildlife products. A tool that focuses on the pathogen rather than on the target population is the Influenza Risk Assessment Tool (IRAT) developed by the U.S. CDC (Cox et al., 2014); this is a 10-element assessment

conducted by influenza experts that helps to prioritize virus strains in terms of their pandemic potential.

The Tripartite has produced three operational tools to help support One Health risk-based surveillance activities: the Multisectoral Coordination Mechanism Operational Tool ([MCM OT](#)) the Joint Risk Assessment OT ([JRA OT](#)), and the Surveillance and Information Sharing OT ([SIS OT](#)). Specifically, the MCM OT offers a process to establish and strengthen governmental multisectoral coordination to manage zoonotic diseases and other health events at the human–animal–environmental interface; the JRA OT is an expert-based process to conduct One Health risk assessment; and the SIS OT provides a process to help support coordinated surveillance activities and information sharing, for example, the [Tripartite Zoonoses Guide](#). Other tools include the Strategic Tool for Assessing Risks ([STAR](#)).

Recommendations On how to Conduct Risk-Based Surveillance at the Human–Animal Interface

Recommendation A: Use aids developed for risk-based approaches to prioritize resources and target high-priority areas and populations

Whether risk assessment is used in the selection of target human or target animal populations (Box 5-3) or environmental sites or not, there are strengths and limitations to different approaches (Table 5-2). Common considerations include whether a population is well enumerated or otherwise defined—specifically whether there are lists of known people or identified locations with known numbers and types of animals—and whether or not a population is accessible—specifically whether employers or community leaders will allow engagement or whether animal owners will allow access for surveillance purposes (Box 5-4). Another key consideration for the animal populations is not just whether they are identified at the group level (e.g., a herd of cattle linked to the geographic location of a farm) but also whether they are identified at the individual level (e.g., animal identification tattoos, tags, or other devices for domestic animals). National or regional requirements for individual animal identification—or requirements tied to global trade or compliance with International Health Regulations—may aid in enumeration efforts and improve traceback in the event of an outbreak.

GUIDELINES FOR COUNTERING ZOO NOTIC SPILLOVER

TABLE 5-2. Strengths and limitations of different populations of humans or animals used as surveillance targets— as identified by risk-based approaches for active and passive surveillance activities

Population	Strengths	Limitations
Humans		
Occupational cohorts—animal (e.g., livestock producers, other food industry workers, wildlife traders/hunters, fisheries/forestry workers, veterinarians/allied professionals)	<ul style="list-style-type: none"> • May be enumerated/well-defined • Have known animal exposures 	<ul style="list-style-type: none"> • Accessibility may be inconsistent (e.g., supervisor permissions, risks of retribution from employers for participation)
Occupational cohorts—human (e.g., physicians/allied professionals, military)	<ul style="list-style-type: none"> • May be enumerated • May have existing occupational surveillance programs 	<ul style="list-style-type: none"> • Accessibility may be mixed (e.g., military agreement/security, opportunity costs to participate)
Age-based cohorts	<ul style="list-style-type: none"> • Birth cohorts or babies may be enumerated and tracked through other programs 	<ul style="list-style-type: none"> • Enumeration requires national census or other database
Cohorts based on comorbidities (e.g., immunosuppression)	<ul style="list-style-type: none"> • May be enumerated (via health records, if available) 	<ul style="list-style-type: none"> • Vulnerable populations (rural or lacking healthcare coverage) may not be included
Animals		
Domestic livestock/aquaculture	<ul style="list-style-type: none"> • May be enumerated 	<ul style="list-style-type: none"> • Accessibility may be mixed (e.g., owner/producer permissions)
Domestic working animals	<ul style="list-style-type: none"> • May be enumerated 	<ul style="list-style-type: none"> • Accessibility may be mixed (e.g., owner/producer permissions)
Domestic pet animals		<ul style="list-style-type: none"> • Often not enumerated
Captive wildlife	<ul style="list-style-type: none"> • May be enumerated 	<ul style="list-style-type: none"> • Accessibility may be mixed
Farmed wildlife	<ul style="list-style-type: none"> • May be enumerated 	<ul style="list-style-type: none"> • Accessibility may be mixed (e.g., owner/producer permissions)
Free-ranging wildlife	<ul style="list-style-type: none"> • Higher-risk population 	<ul style="list-style-type: none"> • Often not enumerated
Mosquito or other vector pools	<ul style="list-style-type: none"> • Target vector population • Integrates risk across human and animal host targets 	<ul style="list-style-type: none"> • Often not enumerated

Box 5-3
Rabies example

Although mammals generally are susceptible to rabies virus and able to transmit it into human populations, surveillance of human rabies cases identified that 99% of human rabies cases come from the bite of an infected dog, particularly in Asia and Africa (WHO, 2018a). This has guided the global efforts of the Tripartite and the Global Alliance for Rabies Control to reduce human cases—the ‘Zero by 30’ strategic plan—largely through dog vaccination campaigns (WHO, 2018b). This is an example of a risk-based approach used to identify a target animal population and focus resources strategically as well as to simplify approaches to improve feasibility.

Box 5-4
Indonesia Surveilans Triangulasi example

A surveillance program known as ‘Surveilans Triangulasi’ was jointly organized by Directorate General of Livestock and Animal Health, Indonesia Agriculture Ministry, in collaboration with USAID and FAO, has been operating since 2015 (FAO, 2023; Muflihanah, 2017; Muflihanah, 2021). The program was initiated in Kabupaten Maros, Sulawesi Selatan Indonesia. This archipelagic region, marked by its abundant biodiversity, wildlife, and a dense population of domestic animals such as cattle, buffaloes, goats, pigs, and horses in backyard farms, also features bats in both their natural habitats as well as within residential areas. Some local tribes consume bats as a local delicacy and believe in their medicinal value. Ponelo Island has fruit varieties that attract bats, and locals allow their livestock to graze freely in the farms, where they consume leftover fruits dropped by bats. This situation increases the risk of disease spillover (FAO, 2023; Muflihanah, 2017; Muflihanah, 2021).

The program is a collaborative effort involving various sectors, including veterinary services, agencies such as FAO and PREDICT, and local communities in Ponelo Island. During the program, passive surveillance measures were undertaken, and engagement with local communities aimed to foster an understanding of interactions between wild and domestic animals, and humans based on the One Health concept (FAO, 2023). This approach promotes a balance in the human ecosystem and safe coexistence and addresses the threat of emerging zoonotic diseases. Outputs of this program includes the establishment of disease surveillance systems and the implementation of enhanced biosecurity measures. As a result, heightened surveillance of wild birds and poultry has led to a reduction in the frequency of major outbreaks, ultimately increasing farmers’ profits from livestock sales.

Data Harmonisation and Interpolation

When surveillance efforts are not well coordinated across domains, animal disease data and meta-data for samples may not be the same (i.e., harmonized) (Kuchipudi et al., 2023; Bellet et al., 2012). Furthermore, data are collected and stored in ways that limit analysis because the data cannot be combined or compared (i.e., interpolated). Ultimately, this threatens not just the speed with which emergent outbreaks or new strains of infectious agents can be identified but challenges the ability of surveillance systems to detect smaller outbreaks or outbreaks that do not occur on a regional level. Conversely, systems that allow for comparison of data along the animal value chain and in human risk cohorts, such as animal workers or other vulnerable community populations, can allow for identification of outbreaks (Box 5-5). Ideally, these systems are built on routine

surveillance functions but are able to adapt to emerging infectious disease threats using an All Hazards Preparedness model, in which capabilities are strengthened to detect and respond to both routine threats and emerging risks. The Viral Emergence Research Initiative, founded in 2019 at George Washington University in the US ([VERENA](#)), and the associated Pathogen Harmonized Observatory ([PHAROS](#)) are developing frameworks based on molecular mechanisms to explain viral dynamics at a planetary scale.

Box 5-5
Group B Streptococcus example

In 2015, Singapore faced an unprecedented outbreak of Group B *Streptococcus* (GBS) linked to consuming raw freshwater fish ([Kalimuddin et al., 2017](#)). It has been shown that eating *yusheng*, Chinese-style raw fish dish typically made with freshwater fish like Asian bighead carp (*Hypophthalmichthys nobilis*) or snakehead fish (*Channa* spp.) are major risk factors ([Chau et al., 2017](#)). In fact, prior to the 2015 outbreak, GBS was not considered as a foodborne pathogen ([Muthanna et al., 2023](#)). Updated policies and guidelines concerning the sale of ready-to-eat raw fish dishes using raw freshwater fish, including a public advisory issued in July 2015, significantly reduced the number of cases ([Tan et al., 2016](#)). Following the outbreak, genomic evaluation of GBS isolates collected through routine clinical surveillance and various project activities found that freshwater fish in Singapore continue to carry GBS ST283, leading to a suspicion that fish in regional aquaculture operations may be colonized ([Chen, 2019](#)). It was subsequently determined that GBS ST283 is widespread in Southeast Asia and may have been responsible for human disease for over 25 years, with potential expanding intercontinental dispersal and human–fish host switching ([Schar et al., 2023](#)). This example also highlights the role of genome sequencing of pathogens and use of surveillance technologies to identify cross-species transmission and uncover novel routes of exposure, which can directly inform interventions.

Recommendation B: Ensure data collection is coordinated and interoperable across human, animal, and environmental domains

Data should be collected and managed in a way that permits analysis across domains, including consideration of coordinated targets (coordinated according to type of sample, pathogen target, and relevance for potential human–animal transmission events). Data must be standardised at a global scale, follow best practices, and be fed directly into AI-enabled databases capable of tracking the evolution of the agents of interest and flagging potential spillover events. Existing genome databases such as [GISAID](#), [NCBI](#), [Nextstrain](#) etc., can be improved and built on for this purpose. Ideally, systems should allow for the integration of metadata, including from Geographic Information System ([GIS](#)), weather, and land-use data based on spatial interpolation with case data to improve risk assessment, given the influence of spatial, temporal, and weather factors on disease emergence and transmission. An example is the [PHAROS](#) open-access wildlife disease database that requires spatiotemporal metadata for submissions.

Improved interoperability of One Health data is foundational to faster and more complete assessment of outbreaks from spillover or intentional release events. In the long term, improvements to data completeness and dataset interoperability are critical for development of automated processes for data reporting, interpolation, and assessment, with the potential for further automation of analysis through machine learning or other intelligence approaches (Box 5-1). In this, especially for some of the latter approaches, deposition of data into the public domain is

important; while funded research may have publication mandates, the same may not be true of governmental or non-governmental program activities.

SURVEILLANCE TECHNOLOGIES

Surveillance technologies include digital and laboratory resources for the detection and monitoring of pathogens and human or animal disease (Kostkova et al., 2021). With technological approaches, there often is a trade-off between more complex but more precise, accurate, sensitive, and specific assays and these performance characteristics of simpler, more accessible testing. For example, low-cost point-of-care (POC) diagnostics may be more readily available and provide faster results but have challenges with limits of detection, false positives, and/or false negatives (Wang et al., 2016). Additionally, results may not be reported in a systematic manner. In addition, POC tests are more readily available for human compared to animal populations, particularly for livestock or wild animal populations (Velayudhan and Naikare, 2022). Further, serological, or molecular assays do not yield infectious pathogens for full identification or phenotypic characterization. Depending on the context, point-of-use tests or other technologies that are user-friendly, i.e., not requiring laboratory equipment to run, may have advantages that outweigh the disadvantages, particularly in resource-limited or rural settings with limited access to regional or national laboratory networks (Heidt et al., 2020).

Where viruses from specific families are sought, molecular detection has frequently focused on well-conserved regions of the viral genome. Assays using pan-CoV primers optimized for coronavirus polymerase targets aim to detect viruses across *Alpha-*, *Beta-*, *Gamma-* and *Delta-coronaviruses*. For filoviruses, a panel of assays with both agnostic targets aimed to encompass the viral family (*L* or *NP* genes) and specific to certain genera (*NP* gene of *Ebolavirus*) and viruses (EBOV) have been developed and implemented (Koehler et al., 2014). Similarly, an *L* gene target has been used for broad detection of paramyxoviruses (Tong et al., 2008; Jin et al., 2021). Assay sensitivity is enhanced using a nested approach (Hanlon and Nadin-Davis, 2013), but may be limited for cryptic (including animal) viruses underrepresented in genomic databases, impeding optimal primer and probe design.

Next-generation sequencing has become progressively more accessible and versatile for pathogen discovery and characterization as well as for hypothesis generation around viral evolution and ecology (Gupta and Verma, 2019). There are three broad approaches that are progressively more agnostic, including amplicon-based sequencing of known targets such as SARS-CoV-2, bait-capture assays targeting broader viral families, and metagenomics, which is an unenriched and non-specific approach (Rehn et al., 2021). Critically, viral genomics and metagenomics can be leveraged to generate novel insights into viral ecology and drivers of spillover by transforming data into knowledge using key metadata and appropriate analytical approaches (Roux et al., 2021).

Recommendation C: Repurpose or maintain existing diagnostic capacity for future emerging zoonotic future threats

The COVID-19 pandemic caught many countries off guard in early 2020 (Hiscott et al., 2020; Singh et al., 2021) despite earlier reports of the discovery of SARS-CoV-2 in China in December 2019 (CDC, 2023a) and the earlier emergence of SARS-CoV in China in 2002-2003. Many countries adopted the wait-and-see strategy, expecting the epidemic to spike and wane off

(Wise, 2021). When local SARS-CoV-2 infections were reported, numerous diagnostic laboratories were unequipped and unprepared (Lippi et al., 2023; Tang et al., 2023) despite the procurement of real-time PCR equipment during the 2009 H1N1 influenza pandemic.

Since the World Health Organization (WHO) declared that COVID-19 is no longer a global health emergency (Fadel and Aizenman, 2023), diagnostic capacity has gradually declined due to fiduciary and workforce reprioritization. For example, in Malaysia, SARS-CoV-2 diagnostic laboratories are being repurposed for human papillomavirus screening program which is nested within the Action Plan Towards the Elimination of Cervical Cancer in Malaysia 2021-2030 (Malaysia Ministry of Health, 2021) and other real-time molecular assays for syndromic surveillance. Onsite health screening posts, such as airports or immigration checkpoints, along with their standardised procedures should be maintained, as an essential component of global mitigation measures (CDC, 2022b). Further, maintenance of standardised procedures and attention to quality control should be maintained between health crises. This may result in the maintenance of technological investments and the training of the future workforce as an ongoing preparation for the next pandemic.

Recommendation D: Strengthen interpandemic surveillance including broad virologic assays

Building on the existing technologies in the diagnostic laboratories, syndromic surveillance should be adopted and intensified, and advanced technologies such as next-generation sequencing (NGS) strategically applied. Many pathogens endemic to humans are zoonotic in origin (Rahman et al., 2020), and surveillance is the key to further understanding the natural and intermediate hosts (Pepin et al., 2010).

Unlike many bacteria and fungi that are more readily cultivable and/or have robust barcoding protocols (Lebonah et al., 2014; Xu, 2016), viruses lack a single consensus barcoding region. However, family-wide consensus primers are often available. Despite the availability of next-generation sequencing (NGS) technologies that boast the potential of whole genome sequencing (Qin, 2019), the majority of NGS platforms remain costly to acquire and effectively implement (Schwarze et al., 2020). While NGS capabilities are often available in-country through medical, animal health, or research institutions, the public containment strategy learned during the COVID-19 pandemic made centralized diagnostics and outsourcing a challenge, especially in countries with lands separated by sea.

The development of multiplexed virus discovery kits using family-wide consensus primers would allow rapid detection of novel and emerging viruses, enabling a preliminary warning system in anticipation of further characterization.

Compatibility of reportable data

Monitoring the trajectories of outbreaks and pandemics is important to position resources for rapid deployment and to enhance surveillance in at-risk populations (Qasmieh et al., 2023; WHO, 2022b). For novel pathogens, this may require rapid investment in new tests for pathogen detection. Other than laboratory-based diagnostic tools, rapid tests or point-of-care testing platforms must be developed such that in-country capability is available to develop and validate new tests quickly with upscaling capability for mass screening. The ideal criteria for these tests must be:

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1. Economical
2. Stable at ambient temperature
3. Have reasonably high sensitivity and specificity
4. Usable without a corresponding analyser/reader (standalone)

For example, the use of national mobile applications such as [MySejahtera](#) (Malaysia), [TraceTogether](#) (Singapore), [Mor Prom](#) (Thailand), etc. allows real-time information to be made available to the population, including vaccination status and contact tracing while allowing individuals to upload essential data about their COVID-19 status. Such applications should ideally be repurposed and maintained for future public health emergencies. Although some emerging high-tech diagnostic technologies, such as biosensors, isothermal amplification, aptamers, etc. are promising, more research should be done to allow rapid development, validation, and scalable implementation. Further, better integration of data on livestock, domesticated pets, and wildlife with development or deployment of surveillance technologies and monitoring by field workers across different animal services or governmental agencies, or by community volunteers, is needed in Southeast Asia to alert local authorities, although some examples exist, such as the Participatory Surveillance App by the [Thailand PODD](#), which is an example for event-based surveillance opportunities.

Further Recommendations for One Health Surveillance

Current surveillance systems to detect emerging pathogens and/or outbreaks among animal populations require better integration of animal and environmental surveillance data with human disease surveillance efforts.

Recommendation E: Conduct value chain analyses and exposure assessment to identify high-risk populations

Using approaches that include engagement of experienced stakeholders at the local level, conduct national and regional value chain analysis and exposure assessment in terms of occupational and consumer exposure to identify how people are in direct or indirect contact with animals and animal products, whether these are domestic or wild animal populations. This can include:

- Determining locations of farms, other production facilities, and processing facilities, identifying the species they serve, and categorizing these (qualitatively or quantitatively) in terms of likely risk.
- Identifying obvious screening points (e.g., transboundary, processing) for active surveillance activities.
- Facilitating the adoption of integrated biosecurity approaches to enhance disease detection and management within the value chain.

CONCLUSION

Regardless of the kinds of surveillance activities that are used to collect, interpolate, analyse and act on data across human, animal, and environmental health domains, these data are intended to inform decision-making and, ultimately, interventions or other programmatic activities to address the challenge of zoonotic disease spillover. In this, attention to sustainability of these

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programs, including the expertise within the One Health workforce at local, regional, and global scales, is a key consideration. This includes One Health-oriented training in laboratory and data-based approaches (qualitative and quantitative) to inform and conduct risk assessment, training in implementation of evidence-based intervention strategies, and guidance in effective communication strategies (which likely will differ according to audience and context). Further, given that surveillance inputs and intervention or other implementation outputs from these systems rely on strong community engagement, attention to local value systems, cultural norms, and unintended consequences of such outputs is essential for such activities to be successful (Module 7). Strong bidirectional communication systems (between public health authorities and communities or other partner groups) can improve situational awareness and enhance engagement around control measures. Indeed, understanding of the externalities and other consequences of changes along the animal value chain (Module 6) may help to uncover potential barriers to implementation and allow for more engaged action, with a goal of participatory approaches to community implementation. Finally, integration of surveillance and response systems, including engagement of decision-makers and coordination across human, animal, and environmental sectors, is needed for surveillance activities to inform public health measures to mitigate risks.