Understanding the dimensions and gaps in wildlife health surveillance for zoonotic risk management

Alice. C. Hughes[1*], Alexandre Caron[2,3], Nazli Demirel[4], Sharon Calvin[5], Serge Morand[6], John Weaver[7]

1. School of BioSciences, University of Melbourne. alice.c.hughes@unimelb.edu.au
2. ASTRE, University of Montpellier, CIRAD, INRAE, MUSE, Montpellier, France
3. International Livestock Research Institute, ILRI, Nairobi, Kenya
4. Institute of Marine Sciences and Management, Istanbul University, Istanbul, Turkiye
5. Public Health Agency of Canada, Ottawa, Canada
6. HealthDEEP, CNRS - Kasetsart University - Mahidol University, Bangkok, Thailand
7. Weaver Consulting International, Hong Kong

Abstract

Following the Covid 19 pandemic, One Health has been a topic of increasing global awareness, with the development of various global strategies and action plans to manage and counteract risks as well as identify potential risks. However, despite these calls for action, little work has been conducted to establish a global baseline on policies related to One Health, particularly dealing with the transmission and risks of zoonoses between non-human animals and humans. Here we explore the national and international policy linked to One Health, related to both domestic animal husbandry and international import, and spanning livestock, companion animals and wildlife, as well as comparable measures for plant health. We also assess the standards for data collation during analyses of zoonotic pathogens, particularly around the recording of key ecological and ecophysiological parameters which may be critical to modelling and managing risks of spillover into the future. We find that regulations around One Health focus primarily on livestock and common pets, whereas regulations for other animals are far more variable (or absent), and phytosanitary surveillance often focuses on a subset of pathogens. Furthermore, whilst some high income economies do have regulations for animal and plant health for import, how this is monitored and enforced varies, and it is typically limited to a subset of conditions. Yet, even for those with the strictest entry requirements, virtually no systematised monitoring of wildlife health is in place, and standards around recording of ecological parameters are entirely absent. As a consequence, despite ambitious plans around health, major gaps still exist, with little evidence of concerted efforts to reconcile these gaps.

Introduction

Recent years have seen the rising awareness of the risk of pathogen spillover from wildlife in various contexts, with the Covid-19 pandemic bringing these risks to the forefront of concerns in preventing future pandemics. Understanding these risks is crucial, as up to 75% of human pathogens have a zoonotic origin (Jones et al. 2008; Sun et al., 2024), including many pathogens with high rates of mortality such as Ebola, MERS and SARS-CoVs, as well as those which have recently spread widely within humans globally, such as Mpox. To break this down further, around 80% of viruses, 50% of bacteria, 40% of fungi, 70% of protozoa and 95% of helminths of humans have zoonotic origins (Asokan & Asokan 2016). Wildlife, hosting the known and unknown pathogen diversity, have contributed significantly to the burden of current human diseases. However, today, given the extensive wildlife/domestic animals/human interfaces (WDHI) created by anthropological drivers, the risk of spillback and transmission of pathogens and parasites from humans and domestic animals into wildlife becomes also a risk for species and biodiversity conservation. For example, feral cats and dogs are known to spread gut parasites to wild carnivores (Liu 2018) as well as various other outbreaks, such as the spread of African Swine Fever into wild pig species from domestic pigs across Asia (Luskin et al., 2023). Consequently, understanding the distribution of parasites and pathogens in wildlife and at WDHI remains a crucial topic if we are to manage risks into the future. This is especially true in the face of changing climate, and continued degradation of biodiversity and fragmentation of habitats, all of which may act to exacerbate risks (de Garine-Wichatitsky et al., 2021).

The mechanisms of spillover, whilst multifaceted, should therefore consider the diversity of WDHI, as well as the health status of wildlife (Lambin et al., 2010). These interactions provide a two-way interface for the exchange of pathogens, and thus understanding where these may occur, as well as factors which drive them or exacerbate susceptibility (i.e. factors which increase eco-physiological stress) provide a window to allow the prediction of spillover (Caron et al., 2021). Broadly, interactions which pose a risk can occur in a number of situations, but highest among them will be via the hunting and trade of wildlife (or their parts) (wildlife trade -where highly stressed animals, often from different ecosystems will come into contact with other animals and humans) and in the landscape, especially where native habitat has been lost and fragmented (Ortiz et al., 2022; Perfecto et al., 2023). This fragmentation increases movement (and stress), increases exposure to other stressors (such as agrochemicals), increases energy needs (Torquetti et al., 2021), and increases the interface between wildlife with domestic animals and humans (WDHI), providing optimal conditions for spillover to occur. For example, in southern Africa, the African buffalo (*Syncerus caffer caffer*) has coevolved with many African-origin pathogens and presents a risk of pathogen spillover into cattle (Caron et al., 2013). Understanding buffalo behavioral ecology and the dynamics and drivers of buffalo and cattle contact is necessary to manage pathogen transmission and disease spread that can impact local livelihoods (Miguel et al., 2013; Caron et al., 2016).

Understanding the roles and identities of marine hosts have become central to understanding spillover risk at ocean-coastal-human interfaces (see Text S1). Even though stressors, including fisheries effort, coastal infrastructure exposure, and effluent discharge, overlap directly with wildlife exposure interfaces in coastal and offshore waters, potential spillover risk is rarely examined (Ioannou et al., 2025). Marine disease ecology in turtles (Manes et al., 2023) and marine mammals (Uhart et al., 2024; Ioannou et al., 2025) highlight that host demography and stress-linked immune suppression are widely recognised as key components of wildlife disease risk (Manes et al., 2023), yet post-trade screening and associated host metadata are inconsistently captured in public pathogen records, often requiring the exclusion of entries missing basic fields such as host identity, collection date, or location (Chen et al., 2025). Changes in ocean connectivity as a consequence of glacial melt drove the spread of phocine distemper between the Atlantic Ocean and the Pacific Ocean through the Arctic Ocean (Barratclough et al., 2023; VanWormer et al., 2019). Yet proactive measures to detect and manage zoonotic spillover risks remain variable, with protocols and programs for biosurveillance not widely streamlined, and few mechanisms to manage risks in natural systems (Haider et al., 2020).

From a policy perspective, One Health was included in an annex of the Global Biodiversity Framework and in an agreement of the Global Action Plan on Biodiversity and Health from CBD-COP16 (IISD 2024; Hughes, 2023; Hughes 2025), the Pandemic Agreement (WHO 2025), and the IPBES NEXUS assessment (IPBES 2024). The One Health High Level Expert Panel (OHHLEP) has also outlined potential actions to reduce risks of spillover, by taking a holistic approach to spillover, and shifting from reactive to proactive approaches (OHHLEP 2023; FAO 2025a).

Yet despite increased attention throughout the pandemic, efforts to collate data to understand these risks have been fragmented. This is in part due to the exponential growth in research programs trying to understand different facets of risk, whilst one of the largest organisations examining wildlife related landscape risks (EcoHealth) was defunded in 2025 (Committee on Oversight and Government reform, 2025; Kaiser, 2024). With major alliances exploring various elements of One Health, and the Convention of Biodiversity (CBD) drafting guidelines for the standardised selection of One Health indicators, it is crucial to identify and understand the proliferation of databases collecting information relevant to spillover risk, as well as the major gaps in data collection, programs, and existing data "standards" (as well as gaps and omissions) (FAO, UNEP, WHO, and WOAH. 2022).

Virologists undertaking field-research may fail to collect (or correctly identify) the species hosting different viruses. For example, the bat initially found to host similar viruses to SARS-CoV2 (RaTG13) was initially listed as *Rhinolophus sinicus* before bat scientists called for barcoding and determined the species was in-fact *Rhinolophus affinis (Kendra Phelps/Aaron Irving pers comm)*. Likewise, locality information, such as coordinates, date of capture, or habitat conditions are rarely recorded when virologists work alone (Russo et al., 2017). These factors provide vital insights in understanding the landscape context of spillover, or how these risks change across space, time, and taxa. For example, research on *Pteropus alecto* (Eby et al., 2023; Becker et al., 2023) has shown that spillover can be predicted by understanding the ranges of bats, loss of habitat, and climate conditions. These factors determine winter-bloom patterns in their major winter food sources, and thus both the ecophysiological stress level (low food increases stress, as well as movement to access sufficient food) and the probability that these animals will forage in the shade trees in horse-paddocks, where interactions between bat faeces and horses provides the opportunity for spillover to occur. Thus, mitigating these risks would require systemwide interventions, including identifying, assessing and modelling risk across landscapes, especially given that degraded habitats host more competent zoonotic hosts (i.e Kane et al., 2024; Marcolin et al., 2024; Debnath et al., 2023; Gibb et al., 2020; Cortez et al., 2021). Furthermore, peridomestic species, and those commensal on humans may provide a particular risk for exchange, and whilst the risks from various flies may have been examined; risks more widely may have highly variable monitoring (Gamble et al., 2023). Also, in some instances species movement across landscapes, and between ecosystems may act to transfer zoonoses between natural ecosystems as well as degraded and converted landscapes (Plowright et al., 2024). Furthermore, understanding these systems may benefit from the contributions of indigenous communities, and collaborations may help characterize ecological and epidemiological processes (Caron et al., in review).

Clearly, to advance the field we need to: 1) better understand what is currently being measured, collated, and shared in terms of health requirements for organisms in trade, in the wild, and in captivity; 2) examine the standards of data collection, including the opportunities presented by local knowledge and citizen science, around different facets of One Health; and 3) determine how we can measure progress to better enable the use of such data for modelling, hazard identification and assessing health risks. This need for better surveillance is highlighted in the OHHLEP whitepaper (OHHLEP 2023) and the recent "Framework for early warning of animal health threats" (FAO 2025), yet progress towards improving monitoring and data-collation is still unclear, despite scoping of what is needed within the Quadripartite One Health Intelligence Scoping Study (OHISS - FAO et al., 2022). The need for this data and indicators has become especially apparent in recent years. Here we examine the data landscape, as well as the standardisation and implementation of monitoring in various facets of the system (livestock, wildlife, and wildlife trade). We also explore associated phytosanitary risks to provide an overview of regulations for plant health, which provides interesting parallels to the mechanisms to control and manage zoonotic pathogens, and has both economic and ecological implications when outbreaks do occur. We also explore the need for key metrics to better understand dimensions of risk, and thus enable more proactive management going forwards.

Methods

We sequentially followed the path of spillover and detection, from biosurveillance in wildlife populations (and the reference material available for analysis), to wildlife trade and collection of wildlife, surveillance in livestock and companion animals, and following this potential spillover into human populations. We then map out various elements of the Global Health Security index to assess capacity and regulations, before exploring modelling frameworks which data can feed into.

Biosurveillance of wildlife and collation of pathogen data

To understand national programs to monitor wildlife health we used the search-term "*Could you collate a list of initiatives monitoring wildlife health (plants and animals) for the UN regions of Asia in addition to Oceania and the Pacific. Please collate a table noting the country, the search term in the appropriate National language, the organisations responsible, the URL of any existing initiatives or programs, the scope of the programs, the organisms surveyed, and conditions being monitored for. For any countries with no programs just not "undetected"*". The search was repeated, and regions were sequentially replaced with each UN subregion until records were collated for all regions, and as before all URLs were then manually searched to assess their veracity. This search was then repeated with a modification to state "*monitoring health of wild animals in trade*" to explore wildlife trade pathogen monitoring, then collated and checked as before. In addition we searched for "wildlife trade pathogen", "wildlife trade disease" and "wildlife spillover" (to capture trade and biosurveillance) in OpenAlex. General summaries were created for the first two search-terms, whereas for the third we downloaded the excel of results (1,286 entries). We then extracted the country of research from any title where it was provided, or was inferable from locality data, or endemic species to explore where this type of research is being undertaken.

To collate platforms and data collating data on pathogens we included both keyword searches (host virus database) and assessed recent publications for the datasets used or where data was stored for various studies. In addition, based on these databases we explored the standards applied to data collection to identify gaps. In addition, we used Claude AI with the search "*Could you collate a list of databases hosting data on hosts and viruses, please include the responsible authority, url, scope of database, year the database started (if known, note NA if unknown), geographic scope (if specified), and taxa covered (if specified)*". All listed databases were then manually checked via either URL (when present) or searching the name provided. All outcomes were then collated into a single excel sheet, with the scope and size of the database (i.e. number of samples, species, pathogens etc) noted. Other key facets (e.g. provision on specific information on individuals sampled such as site, seasonal data, and key ecological traits) was also assessed. However, based on recent papers on spillover, many more ecologically orientated pathogen databases were not included in initial search outcomes, consequently a "snowball" approach was implemented to then search for links on various websites, for example the Chinese National Genomics Data Center (https://ngdc.cncb.ac.cn/) collated information from 224 platforms hosting molecular data on pathogens, but many of these pertained to virus structure etc and often did not provide information on hosts. Data was collated to determine the size, scope and aims of various databases and to determine their coverage in terms of the types of data being collated on animals and their pathogens.

International animal and plant trade

For National phytosanitary and biosecurity guidelines we also used Claude AI with the search-term "*Could you tabulate a list of national guidelines on biosafety and phytosanitary schemes for imports of animals and plants. Please list country, brief guidelines and standards and the URL, please do this in turn for each country in each UN region for which data is available, and note the search term in the national language for the country, could you turn this into a single table with columns for country, UN region, search-term, Phytosanitary legislation-scope, Phytosanitary legislation-regulation names, Biosecurity legislation-scope, Biosecurity legislation-regulation names, quarantine requirements, any other details, url*".

Livestock biosecurity

To examine domestic regulations we also included "*Could you create a table for all countries in the UN regions of Asia and Pacific, and Oceania for all countries where there are national regulations for biosecurity measures on keeping livestock, please tabulate the result including "country, search term in appropriate language, regulation name, scope of regulation, appropriate ministry, URL. Only include countries for which domestic regulations exist*". This was then repeated for each UN region until all were complete (as a region based approach was found to be necessary to avoid gaps in assessment).

Checking and calibration

All URLs from each set of searches were manually checked in Google, and where no url was provided the names of associated ministries were searched for and added. Where necessary the "web-archive" (https://web.archive.org/) was also examined, this was also important where there were geographic or firewall-based blocks on accessing links. For both searches for ministries and agencies responsible for animal health searches were very effective at finding responsible agencies for many countries based on our cross-validation of manual searches. To verify the accuracy of information disclosed, a selection of the directives, laws and regulations stipulated to be in place for different countries were manually searched to ensure the information provided was accurate and consistent with information made available by the appropriate agencies. For example, all the EU laws and protocols were requested, then individually checked through independent searches to ensure that the data was comparable and that the original search was accurate.

Assessing capacity and implementation

In addition we used the "*Global Health Security index*" for 2021 (https://ghsindex.org/) to map various facets of One Health related to wildlife, livestock and companion animals. Many of these indices only show “100” or “0” (and may lack data) so were not mapped, however for all facets which were relevant to biosecurity, biosurveillance, animal health, or veterinary coverage as well as preparedness for epidemics (particularly epizootics) and data-sharing were mapped. Outputs from the initial searches as well as all country ISO2 codes and country names were uploaded to notebook lm (https://notebooklm.google.com/, and the prompt “*Could you rank the strictness of international regulations for zoosanitary and phytosanitary guidelines for each country, the need for quarantine for animal imports (strict, variable, absent), record columns for zoosanitary (regulations on animals) and phytosanitary (regulations on plants) into two different columns. Include further columns on "strictness of biosecurity monitoring for domestic animals"; "biosurveillance of wildlife", "biosecurity_monitoring_wildlifetrade" as well as the country name and iso2 code (also one column for each), for any country where there is no data on regulations note "unknown"*””. All columns where the outcomes were unknown were then manually checked using previous outputs and Google, and outputs mapped; these were consistent with previous analysis and helped showcase variable patterns of One Health monitoring. Lastly we mapped the numbers of papers from the *spillover monitoring* we had from OpenAlex to assess this mode of attention.

Results

Biosurveillance of wildlife

A number of existing bodies have developed global initiatives focusing on One Health, especially since the Covid-19 pandemic. IUCN has formed a working group with the WHO (WHO-IUCN Expert Working Group on Biodiversity, Climate, One Health and Nature-based Solutions), in addition a One Health High Level Expert Panel (OHHLEP) has been developed based on a “Quadripartite collaboration on One Health” composed of the World Health Organization (WHO), Food and Agriculture Organization (FAO), World Organisation for Animal Health (WOAH) and United Nations Environment Programme (UNEP) (Geneva Environment Network 2024; Mettenleiter et al., 2023).

Based on these groups a number of new work-programs have been developed, though for these to work effectively they need national level support (which varies with capacity, i.e. the number of animal healthcare workers; Figure 1). The Quadripartite has initiated a “One Health Joint Plan of Action (OH JPA)” which aims to better manage threats to the health of humans, animals, plants, and the environment and prevent potential future pandemics (FAO, UNEP, WHO, and WOAH. 2022; WOAH 2024). This joint plan aims to include cross-sectoral measures to identify and monitor the risk of zoonotic spillover, reverse environmental degradation, and to “Mainstream the health of the environment and ecosystems into the One Health approach”. The One Health High-Level Expert Panel (OHHLEP) has also worked to develop a shared consensus on what constitutes One Health, and develop frameworks to facilitate the integration of One Health approaches throughout society (Adisasmito et al., 2022). Likewise, the One Health Commission aims to assess One Health risks from a systems perspective (NOAA 2025a; One Health Commission 2025). Initiatives to improve capacity have also been launched (i.e. WHO 2025c), and even global agencies (Global Health Security Agenda (GHSA) and WOAH Performance of Veterinary Services Pathway; Belay et al., 2017; Zoonotic Disease Integrated Action (ZODIAC); IAEA 2025) developed, yet initiatives, and data remain fragmented (OHHLEP 2022).

Some initiatives (such as Connecting Organisations for Regional Disease Surveillance-CORDS, which includes six regional member networks) have worked to collate data in a standardised way and network regions. There have also been multiple proposals for more overarching approaches to monitor wildlife populations from a health perspective (WAHIS, Ahmed Hassan et al., 2023; WHO 2024), as well as new networks to increase surveillance capacity (e.g. International Pathogen Surveillance Network (IPSN); WHO 2025a, Global Early Warning System (GLEWS+) FAO 2025); likewise WCS has launched a wildlife health intelligence network (https://wildlifehealthintelligence.net/) with the associated HAWK (Health And Wildlife Knowledge) database under development (Montecino-Latorre et al., 2025). However, it is challenging to assess the successful implementation of such initiatives at present, and efforts remain fragmented and unstandardised (Sharan et al., 2023).

Coordination of One Health monitoring in marine systems is progressing primarily through government-led alliances, proposal-driven surveillance networks, and national-level capacity expansion, with long-term operational continuity remaining constrained by limited regional workforces and dependence on external funding structures (Seth and Fralin, 2016; Tuholske et al., 2021; Carvalho et al., 2023; Ioannou et al., 2025). Pathogen detection records relevant to ocean-linked hosts are increasingly held within broad biodiversity and health databases (e.g. WAHIS), but these data sources are predominantly optimized for genetic characterization and host-range linkage, rarely structuring consistent ecological provenance or demographic metadata fields which limits cross-system interoperability and indicator evolution for marine wildlife health inference (Norman et al., 2023; Smith et al., 2022; Fountain-Jones et al., 2024). Furthermore, whilst increasing efforts to better link human health with disease outbreaks in wildlife, as well as more general traceability are improving (e.g. GOARN, 2025), the lack of biosurveillance for most wildlife species (necessary to detect when pathogens may be circulating in wildlife) (Figure 3c), and lack of core standards for data recording and deposition hamper the ability to analyse data to facilitate more proactive management strategies. Regional initiatives, such as PREACTS have also increased both biosurveillance and capacity across developing economies (https://www.preacts.org/).

Baseline environmental monitoring is crucial, both for preventing and detecting spillover from occurring (Stephens et al., 2021), and preventing the spread of panzootics (epidemics in wildlife, which can also result from, or be exacerbated by trade; for example, crayfish fever (Jussila et al., 2015; Milbank & Vira 2022)). Additionally there are increasing efforts to integrate ecology and ecological monitoring into biosurveillance efforts (e.g EarthRanger-Wall et al., 2024; Hassell et al., 2025). Previously the EcoHealth alliance conducted broad-scale assessments of pathogens in wildlife (Vanhove et al., 2020), but these efforts are now largely conducted by independent scientists, without overarching standards for key parameters, or platforms for data sharing.

Exceptions to this do exist in the form of long-recognised insect disease vectors, for example the use of drones to collect eDNA for malaria detection (Ip et al., 2025), yet these approaches focus on a subset of known pathogens (especially those with high rates of incidents and mortality such as malaria) and have not yet been applied to emerging infectious diseases, or epizootics, where more standard means of biosurveillance may be needed. Likewise, programs to monitor Antimicrobial Resistance are ongoing, yet there are not currently shared standards, but some data on antimicrobial resistance and use is now available for much of the world, though major gaps exist in the African continent (One Health Trust 2025).

At present there are few strategies and programs to monitor wildlife health, especially at a global level. The World Animal Health Information System (WAHIS: https://wahis.woah.org/#/home) does record outbreaks of diseases in animals to facilitate management, there are no standardised efforts to upload such data (whilst the overall WOAH website provides broader information on animal pathogens). At present whilst guidelines may exist for some parts of the process (i.e. data upload), they are frequently not implemented, whereas other components (such as biosurveillance) have very little standardisation. Likewise, the WHO also monitors and maps pathogens with pandemic potential (https://portal.who.int/pandemichub/newsmap/). Various agencies also monitor various pathogens of concern, for example Avian Flu (CDC 2025; WHO 2025). This includes monitoring platforms (Supplement 4). Some other pathogens also have their own tracking platforms such as influenza (GISRS) and Rift Valley Fever viruses. Some other global platforms also exist, for example PADI-web (Platform for Automated extraction of Disease Information from the web: https://padi-web.cirad.fr/en/; Valentin et al., 2020) which extracts key epidemiological data (diseases, dates, symptoms, hosts and locations) from online sources using web-scraping, and MEDISYS (European Commission 2025).

At a national level, monitoring also varies with sustained programs and entities only existing in a small number of countries (Supplement 4). This includes various national agencies (in some countries) such as Wildlife Health Australia with steering committees to monitor pathogens in wildlife, and to include sampling in wildlife (Wildlife Health Australia 2025; Department of Agriculture, Fisheries and Forestry 2025). The United States hosts the USGS National Wildlife Health Center (NWHC) as well as the USDA led National Wildlife Disease Program (NWDP), and the active WHISPers database (https://whispers.usgs.gov/home), whilst Canada has Canadian Wildlife Health Cooperative (CWHC); both of which include surveillance of various pathogens (with a special focus on Avian Influenza viruses). Some European countries (Norway, Sweden) have long-running programs, whilst France has SAGIR and the UK has a number of programs (e.g Human Animal Infections and Risk Surveillance; HAIRS), these systems also enable citizens to report wildlife death. Various European nations also have programs focused on the detection and monitoring of African Swine Fever (ASF) in wild boars (Montecino-Latorre et al., 2025). However, whilst in high income economies these are government programs, in other regions, such as across the African continent these programs are led by WOAH (i.e https://ebo-sursy.woah.org/). These programs, focus on pathogens, such as for Lassa fever and Ebola, are generally organised into specific programs (such as EBOSURSY followed by ZOOSURSY) and funded by the European Union - which leaves them susceptible to international funding cuts. Exceptions to this exist, with Kenya and South Africa both having their own national biosurveillance programs under the auspices of various ministries. Other initiatives within Africa, such as in Guinea have also shown very variable success in zoonotic monitoring (Bongono et al., 2025). Many regions, especially in the African continent are locally focused on pathogens which also have relevance (i.e. economic costs) within agricultural systems (i.e. Marcelino, et al., 2025).

Asia shows a similar pattern, with few countries having government led schemes on biosurveillance of wildlife (Japan, South Korea, Singapore), some university led programs (Thailand) whereas other regions typically fall under initiatives from WOAH, WCS and WHO, as well as initiatives such as Wildhealthnet (Pruvot et al., 2023). These efforts mean that understanding of pathogens may be limited to a very small subset of taxa and regions, with little long-term knowledge of pathogens which may be circulating in wildlife in the region. South America shows similar patterns, where outside Brazil (where the Brazilian Institute of Environment and Renewable Natural Resources leads the CETAS program for rescued wildlife), other programs are typically organised by NGOs such as WCS. Thus, the risks in, and from wildlife remain neglected in most of the world, and a lack of centralised frameworks for standard setting and data-sharing hamper efforts to better understand and manage risks. These efforts are complemented by the fragmented work of scientists (i.e. Montecino-Latorre et al., 2020, 2022; Wacharapluesadee et al., 2021; Zhou et al., 2021), and without mechanisms for the standardised sharing of such data, the value of this work remains limited.

Given the importance of forestry (which requires long-term investment, and may be harder to manage once a pathogen establishes than in cereal crops; Vettraino et al., 2025), plant pathogens are more closely monitored (Forest research 2025; Carnegie & Nahrung 2019; Carnegie et al., 2022). Many temperate regions also have various programs to limit these risks, as well as at least some degree of monitoring within National forests. In addition some countries will have citizen science programs to track the progress of various pathogens. Using indigenous knowledge systems as data-rich sources based on observation and learning over large time-scale has not yet been extensively used in wildlife health surveillance but environmental monitoring tools (e.g. EarthRanger, Wildhealthnet) could in principle tap into this knowledge.

Databases of pathogens

Data on pathogens, and more recently viromes, has been hosted by a diversity of sites, and whilst some of the elements of these databases (coverage, scope) have been previously reviewed (i.e Ritsch et al., 2023), how this relates to assessing risks, remains limited.

Repositories may host either physical samples (National Infectious Diseases Biorepository (NIDB): https://www.ncid.sg, in addition to various National Infectious Diseases Banks: https://nidb.nhri.edu.tw/) or sequence data, in some instances including millions of records. Multiple different databases exist with data on pathogens (Supplement 1), many of these are focused on a particular disease (e.g. flu, hepatitis) and most focus either solely on humans, or on a subset of animals (e.g humans, mice, rats, chickens). For example, the Chinese National Genomics data-centre database (https://ngdc.cncb.ac.cn/) lists 224 databases on pathogens, but most of these are intended for the better understanding of the genetic diversity of various pathogens, and in some cases their structure. Other repositories also showcase a diversity of pathogens, but most are general (i.e specific to a pathogen without detailed case-based information) and do not hold case/sample specific information (https://www.hsls.pitt.edu/obrc/index.php?page=viruses). These databases rarely include information which extends beyond lab contexts, i.e. they fail to provide data for wild individuals, the origins or conditions, and have rather been developed to enable study of the pathogen. Few platforms host more dynamic information, such as changes in the virome in natural settings, but some databases do contain this information (e.g https://nextstrain.org/). Some databases include data on pathogens and hosts (e.g https://www.mgc.ac.cn/cgi-bin/ZOVER/main.cgi, ViralZone; ViralHost; NCBI Virus; VirHostNet; European Nucleotide Archive, Host-Pathogen Interaction database; BioGRID5.0; String), which exist to understand host range, but rarely go past cataloguing targeted known hosts (i.e Lamy-Besnier et al., 2021). Some host specific databases also exist including fish (http://bioinfo.ihb.ac.cn/fvd/html/homepage.html), rodents (https://www.mgc.ac.cn/cgi-bin/DRodVir/), bats (https://www.mgc.ac.cn/DBatVir/) and plants (https://www.dpvweb.net/; Plant Virus Database), but even these focus on the association of species and what pathogens they have been found to carry, rather than the conditions where these animals or plants have been sampled from. Only GLOBII enables tracking of the individual studies between hosts and their pathogens at an individual level. These datasets (Supplement 1) provide an overview of what some taxa can carry, but do not allow for any mapping of risk in most instances. Furthermore, the lack of individual data generally precludes analysis of risk across time, or demographic states.

New databases with a focus on One Health have developed (Verena 2025) with the aim to better cross-reference species distributions and ecology with other environmental factors. Other programs such as "SpillOver" collates data and facilitate decisions at all levels to identify potential spillover and direct management responses (i.e. see SpillOver 2025). In contrast to most of the above platforms, which were developed principally for virologists and in some instances to develop vaccines etc, newer platforms have been developed to better reflect species ecology, spillover risks and other ecological variables, such as the Global Virome in One Network (VERENA; https://www.viralemergence.org/virion; currently hosts 3767 vertebrate hosts and over 9000 viruses). Building on this, the Pathogen Harmonized Observatory (PHAROS; https://pharos.viralemergence.org/) allows tracking of current zoonotic outbreaks though like many population monitoring databases, spatial and taxonomic coverage is a product of individual research programs rather than any standardised overarching strategy. Likewise Pathoplexus includes zoonoses with known spillover risks, including the spatial and temporal elements needed for modelling and tracking (https://pathoplexus.org/) and some platforms monitor pathogens of known risk to wildlife (Zooanthroponosis, i.e. https://euring.org/migration-mapping/bird-flu-radar), but these are platform, taxa and pathogen specific. Similar initiatives also exist for various human pathogens (https://www.healthmap.org/en/ ; https://www.who.int/initiatives/eios ; https://www.promedmail.org/).

Programs and initiatives examining risks associated with wildlife trade

Much of the focus on pathogen spillover has centred on the wildlife trade. However, wildlife trade is complex, with the risks varying with the species, scale, uses and drivers of trade, as well as the forms of the animals (alive, dead), sources (wild, captive, ranched) and origin (country/region). Domestic subsistence trade has very different risks (including likely local acquired immunity in human populations), from international trade, and even meat vs fur vs pet trade includes different species and practices, which all impact on the potential risk.

Initiatives have included global programs, such as expanded work within CITES on species monitored under the convention (i.e. CITES et al., 2025; Borsky et al., 2020; Can et al., 2019), to more regionalised and national initiatives. New regulations (i.e. China's wildlife protection laws) have focused on the risks associated with the procurement, and farming of wildlife (Zhao et al., 2024). However, wildlife trade whilst drawing an increased focus, still lacks the comprehensive measures needed for monitoring (Figure 3b). Furthermore, industries such as fur-farming can include both captive bred and wild-caught animals, and unlike most commercial livestock systems, lack a means of tracking individuals, or assessing pedigree, making preventing laundering of wildlife into these systems challenging, even when animals are presumed captive bred. Thus, these systems provide the ideal conditions for spillover, with fur-farms in particular often hosting high numbers of competent hosts, including individuals from diverse origins, combined with overcrowding and poor hygiene standards (Zhao et al., 2024). Likewise risks associated with the release of gamebirds, despite the risk of avian influenza (H5N1) has continued with little oversight (Wille & Barr 2022; Stokstad 2022; Rueness et al., 2022; Horton 2024; Carrell 2022). These gaps in monitoring, combined with a lack of standard biosafety regulations, highlight that when pathogen risks have not been associated with economic risk, little standardised and stratified monitoring may have been developed.

Conversely, given the high value of illegal wildlife trade and associated pathogen risks, UNODC has launched various regional projects such as the SAFE project, which focuses on pandemic risk from the Southeast Asian wildlife trade. Other dedicated organisations and programs have also been launched, such as the International Alliance of Health Risks in Wildlife Trade: https://alliance-health-wildlife.org/; and Health in Harmony: https://www.healthinharmony.org/). Yet despite this, very few national level programs focus on pathogens associated with the wildlife trade (Supplement 5), with most programs led by organisations such as WCS (as in the case of Vietnam). However, both Kenya and Tanzania do have systems and mobile units (the FAO supports these programs). This highlights that whilst the international dialogue has centred on pathogens associated with wildlife trade, this is not reflected in programs at the national level.

Interestingly, if we look at research on this topic (i.e. “pathogens wildlife trade” in Open Alex) we see that whilst this was clearly a topic of interest during the pandemic (going from only 15 to around 50 articles annually between 2019 and 2020) high rates of publishing only lasted from 2020-2023, before returning to around 20 articles annually (Figure 3d). Notably, the USA led in this research, with 148 of the 427 papers (35%) on the topic coming from institutions in the USA. The term “wildlife trade disease” gives the same pattern but yields 1177 results, with 25% coming from the USA, and the drop is around 120 to 60 from 2023 onwards. When we use the term “wildlife spillover” (to capture both of these trends) we find 1286 papers (of which 40% are authored in the US). This does not show the same decline as the studies focused on trade and continues to show the publication of around 130 articles annually from the pandemic on. In terms of where the research is being conducted (1152 papers were present once duplicates were removed, of which 496 could be resolved to country, with 122 different geographic countries/regions noted). In terms of geographic coverage, Europe had the most countries at 24 countries, whereas Africa had the second highest number of countries (23) and the highest proportion of papers (28%). This was followed by North America, which whilst only having two countries had 20% of all studies, this was followed by Asia (21 countries, 17% of studies), whilst Europe only had 15% of studies. In terms of countries, the US was unsurprisingly the best studied at 68 studies, followed by Australia at 25 studies, and India with 18. Various African countries, as well as China and Canada all had more than 10 studies within the search (Figure 3d).

International animal and plant trade

Livestock and plants are the major focus of international biosecurity regulation (Figure 1). These regulations include several different components, firstly the health requirements of any animals or plants for them to enter a country (which may require certification) and secondly, potential quarantine regulations following import. Many countries require some degree of phytosanitary and biosafety certification as a condition of import, in addition to quarantine programs for various nations, with Australia, New Zealand, Japan and Singapore having the most stringent regulations (Figure 1). For certification, many countries have now transitioned "ePhyto" and "eCert" systems to facilitate trade whilst outlining standards. However, whilst electronic certification should make monitoring easy, the collation and publication of collected information is highly variable (see Supplement 2). In addition the process necessary for procuring the necessary certification to satisfy import regulation, such as veterinary clinics, and if external checks are required, varies; as does the level of health checks at ports of entry.

Regulations have been developed to reduce the risk of importing pathogens which could be economically costly, or pose a risk to humans, whereas broader risks (i.e. threats to wildlife) may not be as systemically monitored. Animal regulations are often taxa specific, frequently limited to livestock for food, and various pets (typically dogs and cats), whereas other taxa may be less regulated (many species imported as "exotic pets"). However, some countries have a total ban on the import of certain taxa such as Singapore and Australia (Figure 1). Some countries also standardise their animal health regulations to provide continuity and comparability between domestic and international regulations, such as for Canadian animal health (Government of Canada 2025).

Conditions typically covered by animal import regulations in countries with "strict" regulations still often focus on a subset of "notifiable diseases" (Figure 1), for example, within the EU Regulation 2016/429 on transmissible animal diseases ("Animal Health Law") and the Delegated Regulation (EU) 2020/687 outline the framework which includes control of certain diseases, and the methods for reporting and control (e.g. rabies, brucellosis, which animals must be free from to satisfy import conditions). This framework currently includes 63 animal diseases and five categories of control which set out the level of monitoring, and implications when identified, of which categories A-D require control of the movement of any animal noted to have the condition (DG-SANTE 2021). These regulations, whilst some of the most stringent globally, generally only monitor for a limited subset of conditions, with various levels of reporting demanded for export/import, and do not focus on pathogens of particular risk to wildlife. Furthermore, though the TRACES NT system was developed to facilitate monitoring of trade from a biosafety perspective, the limitations of conditions covered means emerging or wildlife pathogens may go undetected (https://webgate.ec.europa.eu/tracesnt/login).

Animal quarantine regulations, when present range from comprehensive, to selective (i.e. all live animals entering Australia are subject to quarantine, though length, and ability to import varies depending on origin (Biosecurity Act 2015), whereas in a region like Hong Kong quarantine regulations largely apply to certain animals coming from countries where rabies has not been eradicated; (Public Health (Animals and Birds) Ordinance Cap. 139 and the Rabies Ordinance Cap. 421) (Supplement 2). For certification of being rabies free some countries (i.e. New Zealand) may require both rabies titre tests and extended (180 days) quarantine for import of mammals from certain non-approved countries.

For plants, some countries put most effort into a subset of particularly high-risk pathogens even within declarations of "pest/disease free" certifications (e.g the UK; Summers 2022). Regulations on plant imports may be more universal in terms of taxonomic coverage, for example under EU Plant Health Law 2016/2031 almost all live plants require phytosanitary certificates. Regulatory structures are improving, and making greater use of "*e*" (electronic) certification in many regions, however how this interacts with how any form of condition is assessed, or how information is stored and shared may continue to vary. Phytosanitary standards are showing increasing "regional harmonisation" efforts, with the EU showing some of the best examples of regionally harmonised standards to enable trade (i.e. see Petrovan et al., 2025). However, dedicated repositories for pathogens in imports have not been developed. Furthermore, whilst databases may note the number of exports rejected for failing to satisfy these biosecurity related conditions, further details are unlikely to be collated or shared in a standard form.

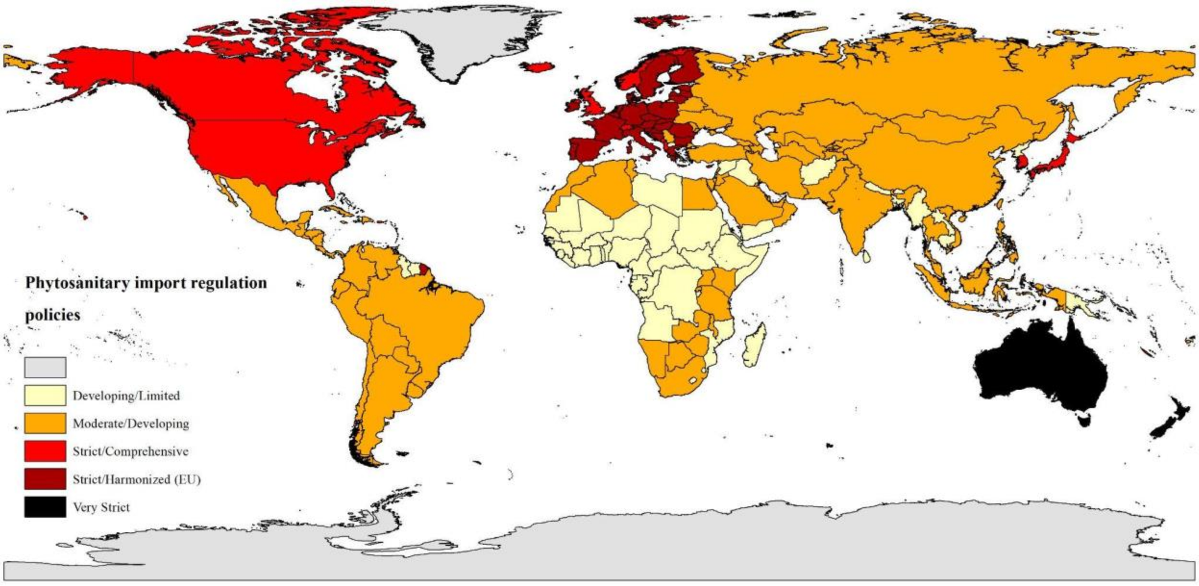
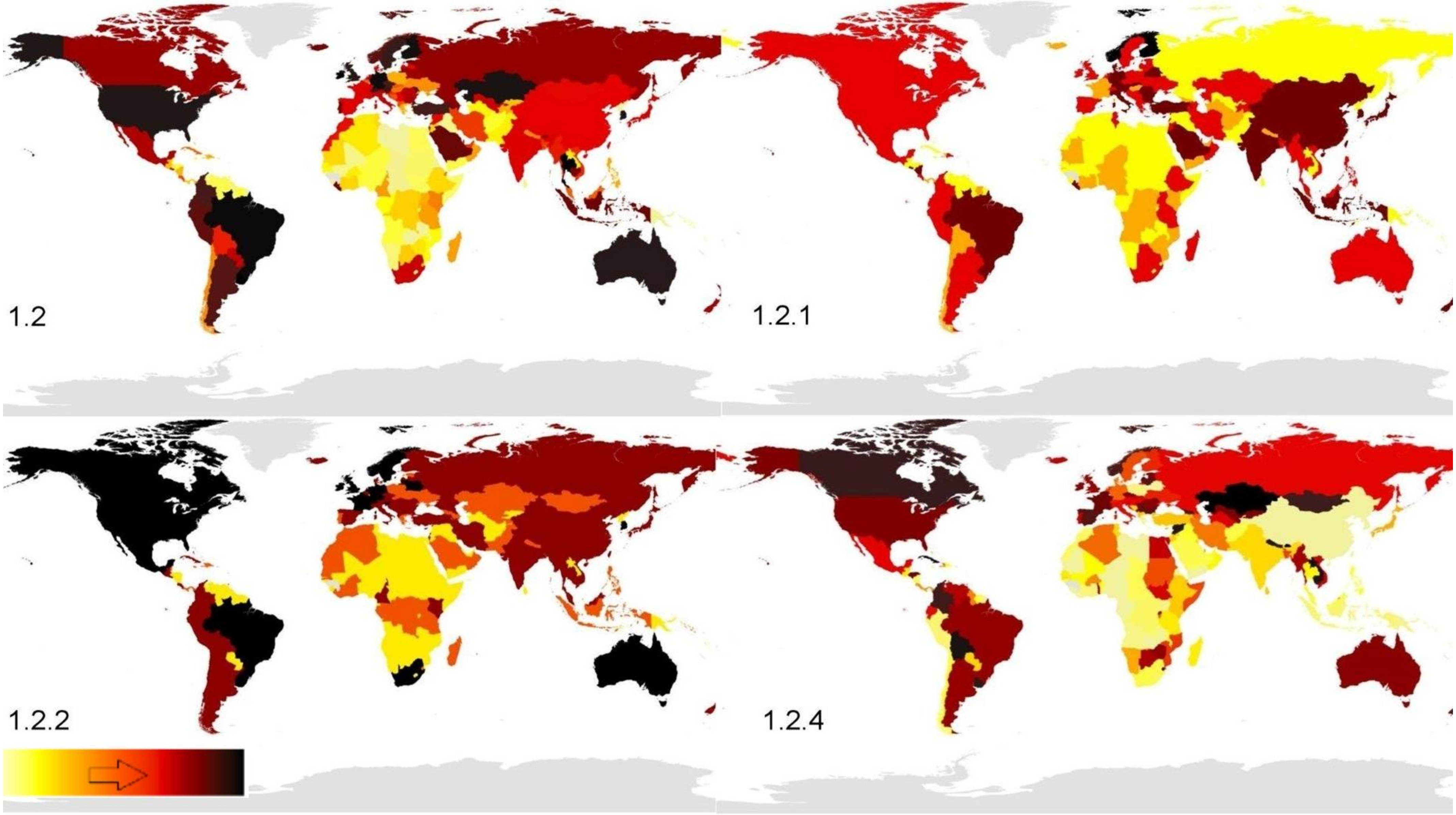


Figure 1. Strictness of phytosanitary (and zoosanitary) regulations for imports based on searches. The regulations for the imports of plants and animals are generally interrelated so the strictness of both is comparable in most countries. Harmonised refers to regionally standardised regulations, between countries. Developing/Limited- Some regulations may exist but they are very limited or may not be effectively implemented. Moderate/Developing - regulations do exist and are normally implemented, but may not be totally comprehensive, or have consistent frameworks to ensure implementation, Strict/comprehensive- strict regulations for a single country, Strict/harmonised- regulations are strict and applied across a number of countries within a union (such as the EU), Very strict- the import of animals and plants is very limited and has very strong regulations.

Generally at least some regulations fall within the remits of National Plant Protection Organisations (currently including 185 parties), which may also host the list of reports of national plant pathogen outbreaks, at least for notifiable conditions (IPPC 2025). Plant import regulations can be very strict (particularly for island nations such as the UK). Within the UK DEFRA has a plant health portal (https://planthealthportal.defra.gov.uk/) complete with plant passports and strict regulations as a condition for import (DEFRA 2025; Gov.UK 2025). Guidance on what can be imported is based on a "Pest Risk Analysis" (Gov.UK 2017). Whilst in the EU the European Food Safety Authority assesses and manages risks of plant pathogens (ESFA 2025), whilst EPPO helps develop the standards (EPPO 2025). As plant trade is a major global commodity it is closely regulated (Petrovan et al., 2025), but often impacts on the environment are largely focused on forestry areas.

Beyond the major focus on livestock and common pets (cats, dogs etc), specific measures exist to restrict the import of classes of animal known to pose a particular risk of bringing in pathogens. For example, some regions (Europe, the United States) heavily restrict the import of wild birds to counter the risk of associated pathogen spread; US Wild Bird Conservation Act, EU bird directive. The United States also lists various taxa, including most caudates (salamanders) as "high risk" (injurious species) within the Lacey Act (FWS 2025), restricting the import of animals to reduce the spread of fungal pathogens, especially *Batrachochytrium salamandrivorans,* as well as various fish pathogens (though certification with live fish, or dead fish of listed species can still be imported). Notably, whilst recent analysis has highlighted the zoonotic risks within CITES listed species (i.e. at least 25% of reported trades included animal families with known associations with zoonotic diseases, though data does not exist for all species; UNEP-WCMC & JNCC 2021; CITES 2023), there is a lack of systematic data collection in addition to even larger gaps for wild species traded outside CITES.

Thus, whilst various "health" requirements for imported livestock are common, the focus may be on a subset of pathogens with varying measures used for their detection. Likewise regulations may exist for common pets (cats, dogs) but often focus on a limited number of pathogens, and species. This means that animals may carry pathogens without being detected, particularly if not a "standardised" or common species in trade, or if the pathogens are not listed as under surveillance or if a pathogen is not looked for in a given species. Many of these tests have been instituted from an economic standpoint, hence a focus on pathogens which are either known to be transmissible to humans (such as rabies and other priority Transboundary Animal Diseases) or present economic risks and may be hard to control. Increases in the transmission of such pathogens (i.e African Swine Fever, Lumpy skin disease) can also lead to temporary restrictions, or even bans on certain species being internationally traded between various countries being enacted. Regulations generally fall under departments of agriculture, and, or customs authorities, and in some cases different roles and responsibilities will fall across different agencies within a country. Thus, whilst regulations, though not universally present (some developing economies are still developing approaches) are generally in place, normally certification for trade does not require screening of exported or imported animal individuals, and is unlikely to include pathogens outside a very limited list. Exceptions are limited, though countries such as Australia have much more stringent regulations, even banning until recently the import of unpasteurised cheeses (Van Caenegem et al., 2017).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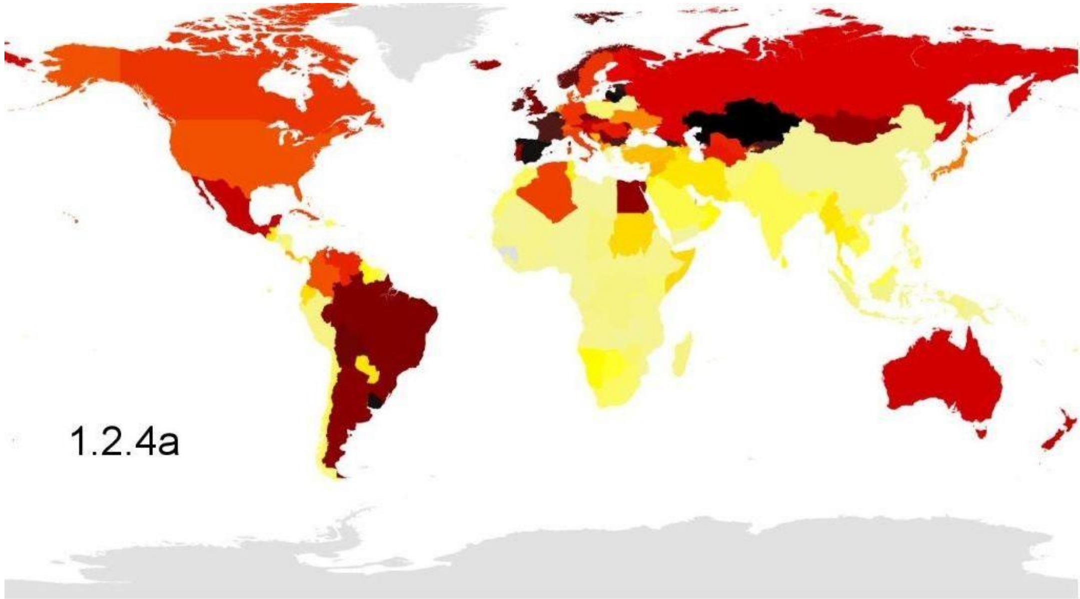
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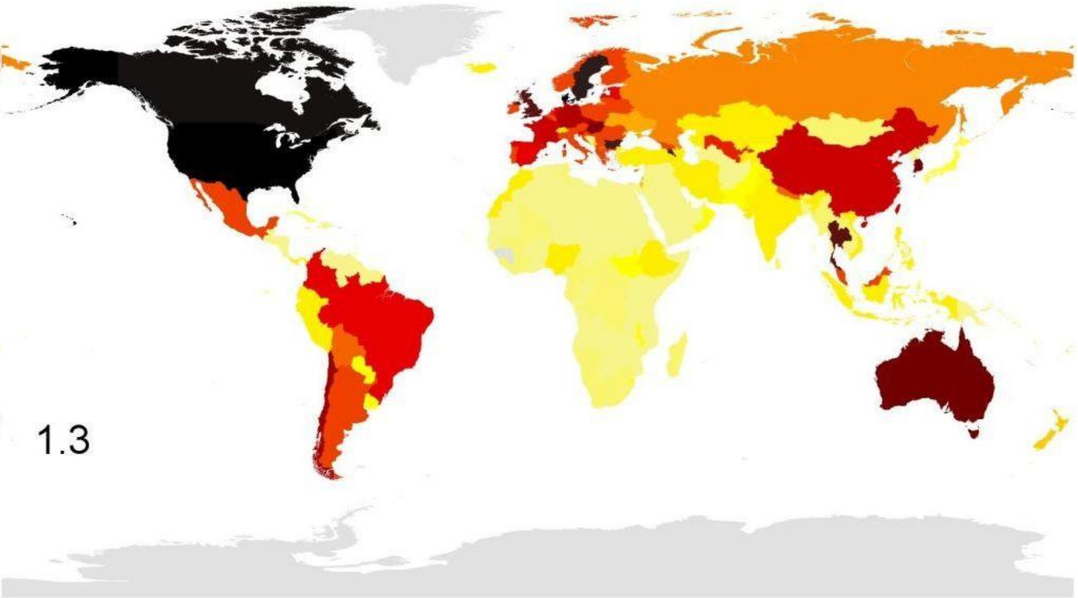
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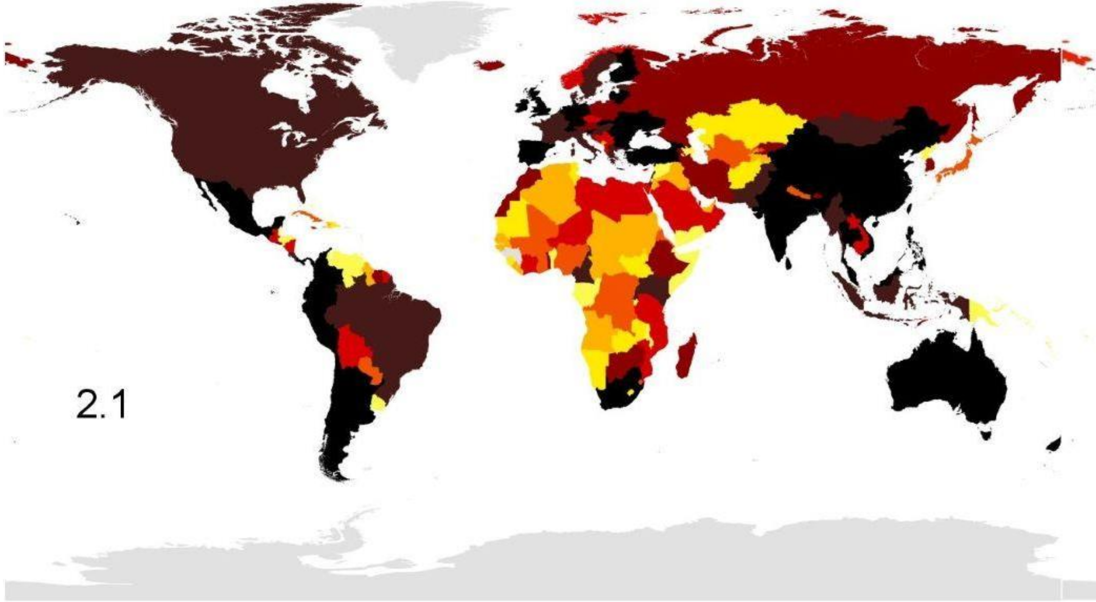
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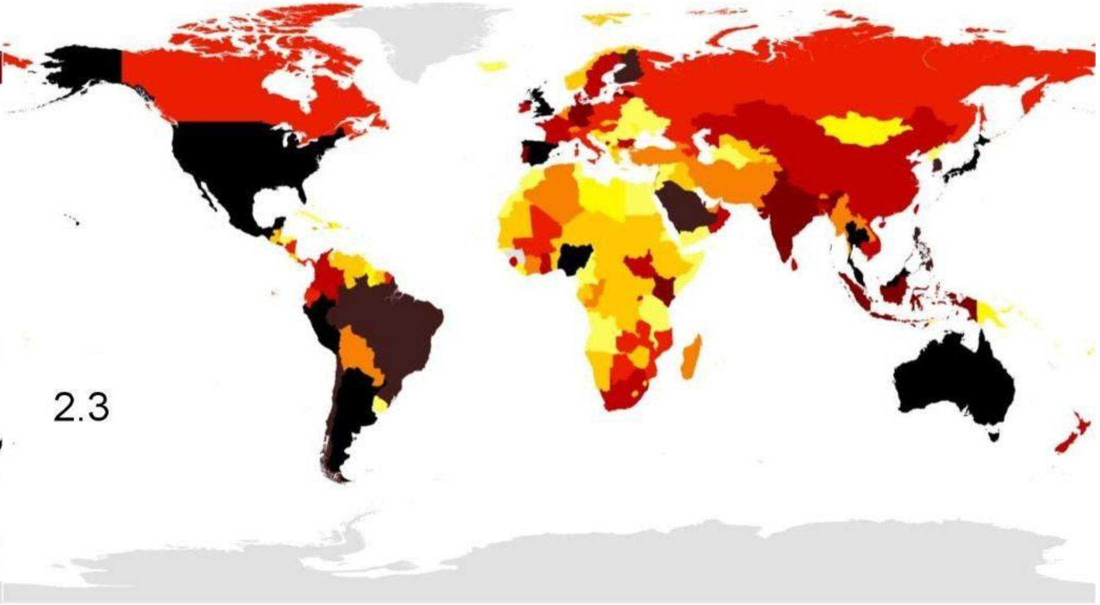
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Figure 2. Global Health Security Index (2021) analysis for various parameters with a maximum score of 100. Index 1.2: Zoonotic disease; an aggregate indicator which examines preparedness for diseases that originate in animals which may spread to humans (maximum 77). 1.2.1: National planning for zoonotic diseases/pathogens (maximum 100), 1.2.2: Surveillance systems for zoonotic diseases/pathogens (maximum 100). 1.2.4: Animal health workforce (maximum 93). 1.2.4a: Number of veterinarians per 100,000 people (maximum 100). 1.3: Biosecurity (maximum 89), 2.1: Laboratory systems strength and quality (maximum 88), this provides a measure of capacity for analysis and surveillance. 2.3: Real-time surveillance and reporting (maximum 100), this provides a measure of monitoring and reporting capacity. Methods are provided in GHS 2021. Further maps are provided in Supplemental Figures. All figures show a scale from low/limited to high/developed in coloured progressively from Yellow-Red-Black.

In addition, regulations around the trade of soil (generally prohibited due to soil pathogens and pests) and plants (see Petrovan et al., 2025) are common. Again, these focus primarily on preventing the import of pathogens and pests which may be economically burdensome, and the detail required as well as the level of monitoring within ports can vary considerably. Soil biodiversity, including potentially unknown pathogens, composes close to 60% of the global biodiversity and is still largely unknown (Anthony et al., 2023). Island nations, due to high invasion risk often have more stringent regulations around imports and health, but the collation of this data more broadly is limited.

Livestock biosecurity

Livestock and poultry represent a common intermediate host in the case of many zoonoses (i.e Hendra: Becker et al., 2023; Bird flu: Klaassen et al., 2023; Tuberculosis: Byrne et al., 2024). Thus detecting pathogens in livestock may represent the first sign of zoonoses already in wildlife (as well as a pathogen which could spill back into wildlife), and a key point of intervention to prevent further spread (Figure 5). Welfare and biosecurity standards vary significantly by country and region (Figure 2), significant efforts have been made in high income economies to enable the tracking of individual animals to allow tracing and control of any outbreak event as well as regulations for the standards under which livestock are kept (Supplement 3). Animals in agricultural settings are often subject to various welfare and biosecurity regulations (Figure 3a). Within the EU a harmonized framework (Animal Health Law) stipulates biosecurity requirements for livestock production. Likewise, Japan, South Korea and Australia stipulate mandatory biosecurity requirements, whereas many countries only have recommended standards and may have inspections to ensure animals are kept in alignment with various stipulations. Many high-income economies have mechanisms for the registration of livestock, for example NLIS (Australia), NAIT (New Zealand), EUCAS (the EU), CLTS (Canada) and a recent (and ongoing) transition to digital registration and tracking in the UK, as well as comparable regulations in common European trading partners. South American Nations have also developed increasingly rigorous systems for tracking, in part driven by EU import requirements. Many of these systems register and track individual animals, generally from birth, and include millions of animals (for example the UK alone is estimated to have 32 million sheep, and all sheep and cattle are registered), highlighting the massive effort made to ensure facilitate the ability to trace outbreak origins, and thus manage any related outbreak events. The US has a more basic system of tracking under USDA, which does not provide the same level of detail for tracking as is present in other high-income economies.

These systems (e.g registration etc) are generally complemented by systematic frameworks for welfare, including both generalised (i.e. the Five Freedoms approach within Europe) and taxa specific approaches to enhance animal welfare (which are occasionally driven by import regulations, such as in the case of Chile, which has higher regulations due to the requirements of trade partners). These regulations can include housing, transport and even slaughter restrictions. Vaccinations are also frequently mandated, for Category B diseases within Europe, and a suite of other livestock pathogens in other regions; this is particularly important to satisfy any export requirements which may be present. However, whilst high-income economies generally have high levels of domestic regulation, inspection and enforcement varies in developing economies. In higher income economies national competent authorities have mechanisms to ensure compliance (in some instances to meet export requirements), whereas in lower income countries, regulations and their enforcement are considerably more variable. Eradication of pests and pathogens within countries also shows heterogeneous monitoring, with for example programs catalogued in some instances in GERDA (https://b3.net.nz/gerda/), which whilst it includes 108 countries to date, is much more comprehensive in higher income economies (i.e. 317 programs in the US, 200 in Australia, but at maximum two (and in many instances zero) for most African and Asian Nations). Furthermore the assessments may be complemented by global initiatives such as the Global Burden of Animal Disease, though implementation may be limited (https://gbads.woah.org/). Reporting and monitoring systems such as EMPRES+I- provide an almost real-time assessment of pathogen outbreaks, largely in livestock, though the standardisation of mechanisms to ensure these systems are up to date and representative may be limited.

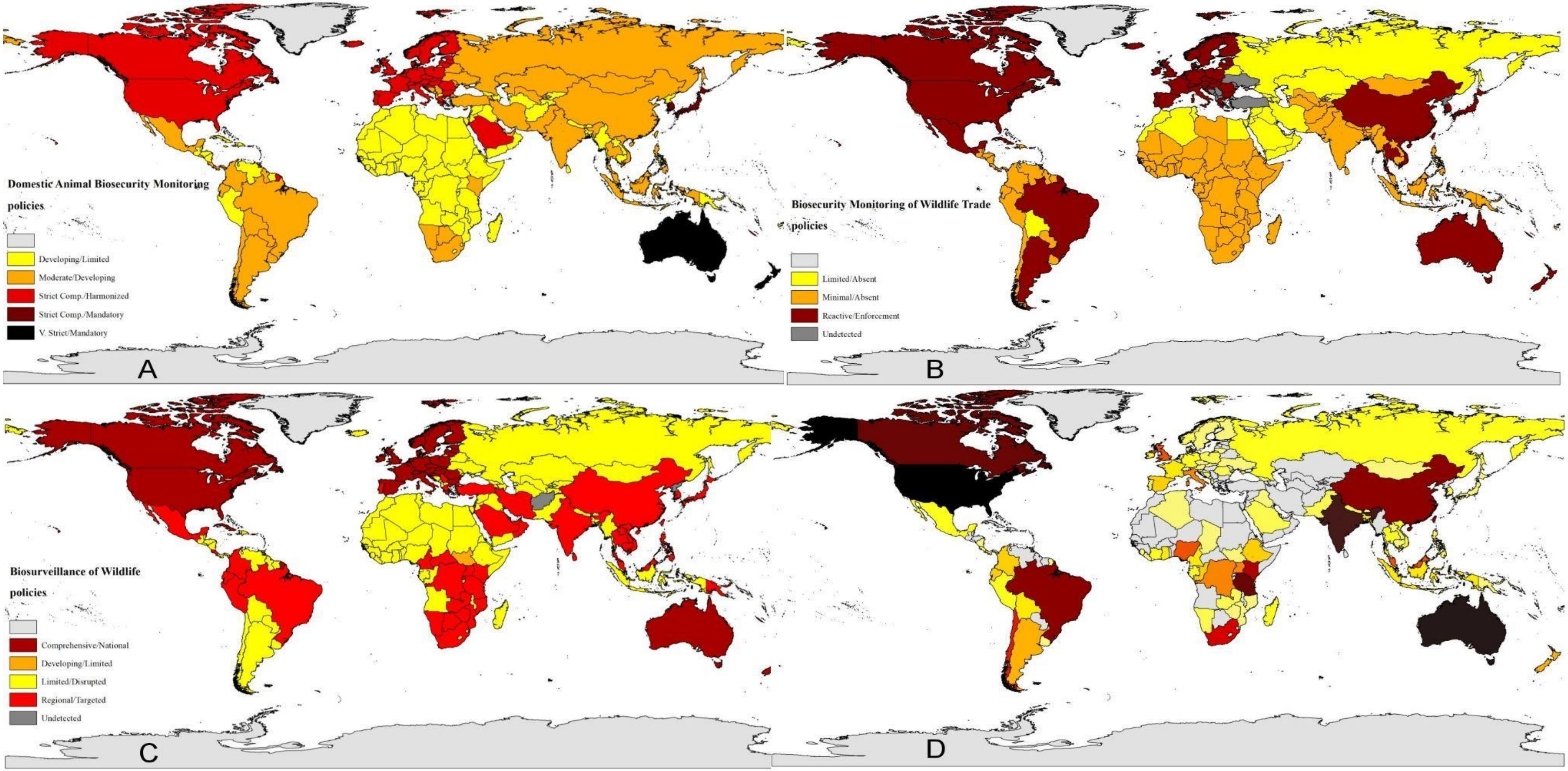


Figure 3. A. Domestic regulations for livestock based on search analysis. B. Regulations for monitoring the health status of wild animals during trade, C. Surveillance of the health status of wildlife and D. "Wildlife spillover" publications from OpenAlex, with a maximum of 68 (in the United States) shown in black, scale of number of publications goes from Yellow-red-black, with grey areas showing no publications. Limited/disruptive indicates that very few and very limited regulations exist, and

may rarely if ever be applied or have no mechanisms for implementation, Developing/Limited- Some regulations may exist but they are very limited in scope or may have limited implementation. Moderate/Developing - regulations do exist and are normally implemented, but may not be totally comprehensive, or have consistent frameworks to ensure implementation, Strict/comprehensive- strict regulations for a single country, Strict/harmonised- regulations are strict and applied across a number of countries within a union (such as the EU), Very strict- the import of animals and plants is very limited and has very strong regulations.

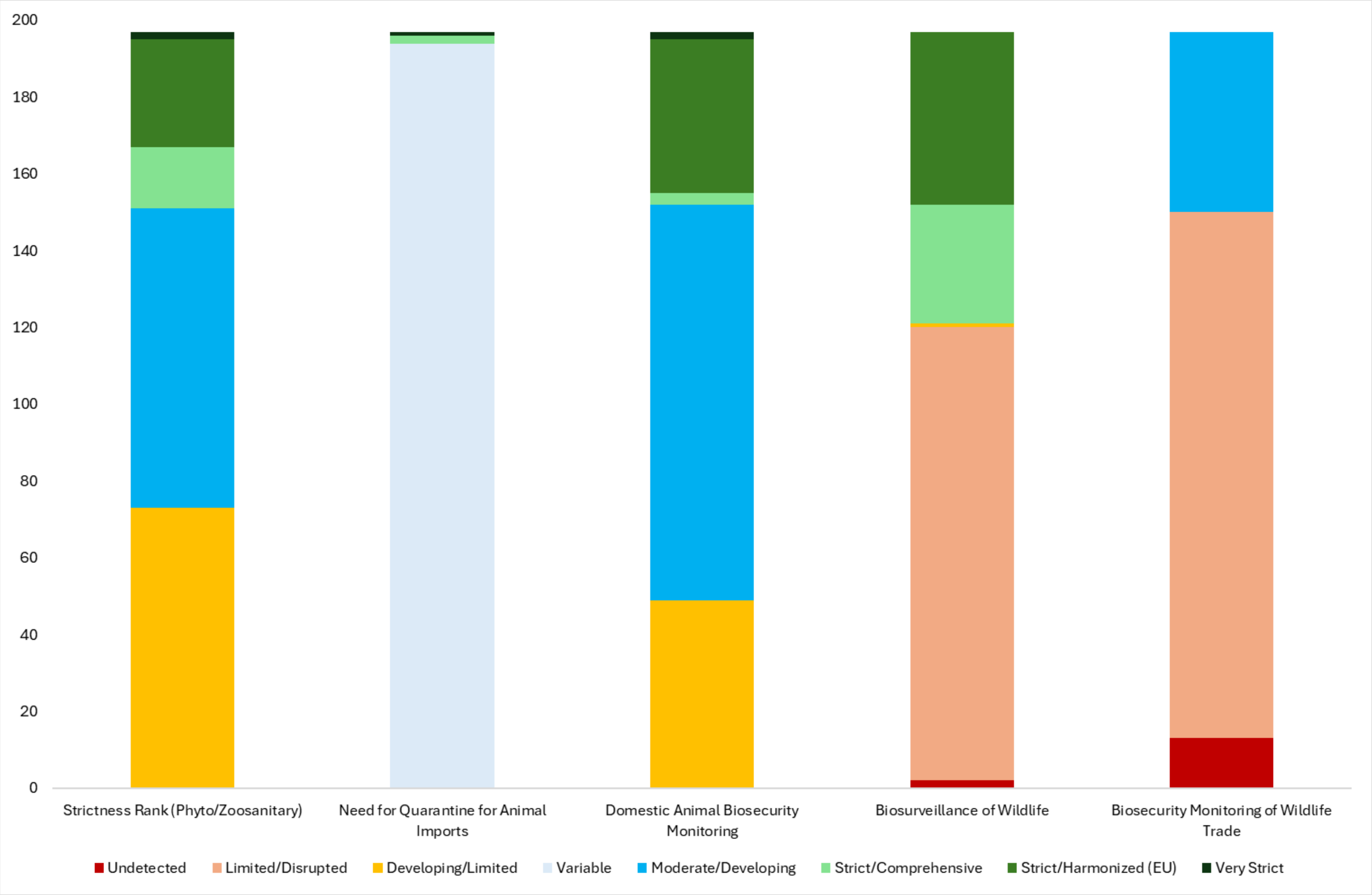


Figure 4. Ranking of status of systems for monitoring of key elements of One Health monitoring showing the number of countries with different levels of regulatory coverage for key elements of One Health. Undetected indicates that no relevant regulations or standards were detected. Limited/disruptive indicates that very few and

very limited regulations exist, and may rarely if ever be applied or have no mechanisms for implementation, Developing/Limited- Some regulations may exist but they are very limited in scope or may have limited implementation. Moderate/Developing - regulations do exist and are normally implemented, but may not be totally comprehensive, or have consistent frameworks to ensure implementation, Strict/comprehensive- strict regulations for a single country, Strict/harmonised- regulations are strict and applied across a number of countries within a union (such as the EU), Very strict- the import of animals and plants is very limited and has very strong regulations. “Variable” indicates that standards vary between taxa, and various other conditions, or may in some cases show sub-national differences.

Gaps in standards

Many previous studies which aimed at collating data on little known and emerging pathogens, including epizootics, lack ecological measures. Without such data any inference of patterns of risk is limited or completely impossible. Guidance and standards, not only for the protection of personnel, but for ecological elements are clearly needed (Goulet et al., 2024).

Wild species are in progressively greater direct, or indirect contact with humans, and domestic animals through various pathways, including hunting and trade, and the progressive fragmentation of natural habitats, increasing exposure between wildlife and domesticated animals (e.g. peri-domestic wildlife and zoos) (Goulet et al., 2024). These multiple interaction types should be the focus and the opportunity to collect relevant data and metadata concerning ecological and epidemiological aspects of these populations relevant to zoonotic risks. Whilst there are routine requirements for biosecurity and phytosanitary data for species in trade, many of these efforts are focused on livestock and common pets (cats and dogs), and data on pathogens as well as standardisation of field limited to a subset of pathogens (particularly in animals). In research more broadly, collection of pathogens from wild species often lacks provenance or ecological data, this means that any further analysis remains challenging. Organisations such as GBIF (the global biodiversity information facility) are developing taskforces to standardise and mobilise data and to create research frameworks to host such data; yet given that data collection is dominated by virologists, standards for data collection from wildlife more widely requires more attention if we are to use the data effectively and efficiently. These taskforces also consider the collection and access to such data based on FAIR (Findable, Accessible, Interoperable, Reusable) and CARE principles (i.e. see Jennings et al., 2019), as well as ethical dimensions (Moyano-Fernández 2025). Work is also being done to develop FAIR standards for data collected on human and animal pathogens, to enable the more efficient, effective and accurate use of such data (Nasr et al., 2025, 2025A; Neves et al., 2023; Infectious diseases toolkit 2025). The application of these principals is crucial to ensuring data can be used efficiently, yet the application of these frameworks is still limited. Given the lack of efforts to systematically collect data on pathogens in wildlife, understanding risks remains challenging (Figure 4).

For wildlife trade, standardising parameters to collect including basic health metrics, demographic parameters, and a more comprehensive screening of pathogens rather than a more reactive approach, with a narrower definition of pathogens of particular interest. It is also important to note, that whilst the scale at which trade is occurring (see Marshall et al., 2025), the same basic measurements likely need to be recorded to assess animals state and origins, as well as the conditions during any form of transport or housing. Furthermore, consumption of wildlife can occur, even when this was not the main driver for its collection, thus screening of animal health remains important during all forms of trade. Likewise, for data collected from ecological systems, information on the individuals that samples were collected from, the locality, date, and basic information on the actual individuals (e.g. species, sex, reproductive status, weight, and if possible linked health data on injuries, parasitism). These factors have known links to spillover risk (i.e. Eby et al., 2023), yet a failure to collect such data more widely precludes further analysis, and the generation of insights into different species and systems.

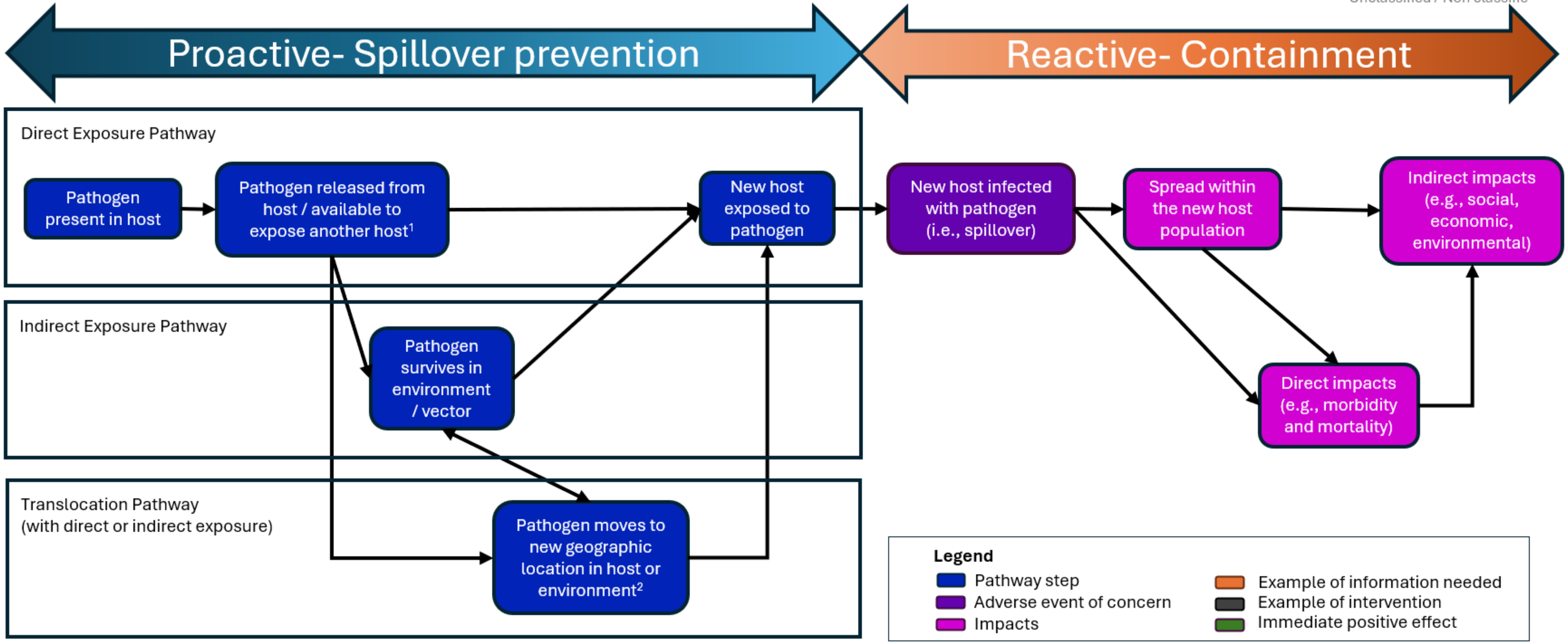
Standards gaps described for terrestrial wildlife surveillance also apply to the aquatic systems, where persistent connectivity and mobile marine hosts operate without standards for monitoring design or reporting completeness (McCallum, et al., 2003). For example, mandatory depth-provenance standards for wildlife pathogen records are largely absent, despite vertical habitat structure determining exposure timing and detection probability for many marine taxa (Carvalho et al., 2023; Clessin et al., 2023; Cohen et al., 2018). Surveillance frameworks also lack criteria recognizing over-filtration pathogen sink dynamics in filter-feeding communities (Bidegain et al., 2016; Glidden et al., 2021). In addition, effluent discharge is a recognized pathogen source, but there are no standardized fields linking wastewater outflows, coastal fronts, and wildlife exposure interfaces in One Health reporting schemas, limiting the ability to attribute pathogen fronts to ecological exposure rather than detection effort alone (Knap et al., 2002; Seth and Fralin, 2016; Tuholske et al., 2021; Ioannou et al., 2025). Microbial recovery signals such as shifts in co-occurrence connectivity and network structure are described across coral, fish, and marine mammal outbreak studies, yet no standards require their inclusion as formal surveillance indicators, leaving recovery comparisons dependent on analytical preference rather than codified monitoring obligations (Rosales et al., 2025; Glidden et al., 2021; Cantrell et al., 2020; Cohen et al., 2018).

Frameworks for modelling

When sufficient data is available, modelling can provide a useful approach for assessing probable risk, but requires an underpinning of reliable and representative data to ensure models are useful and informative, especially under changing conditions (Figure 5). Many models to assess probable spread have been developed in recent years, all reflecting different elements of One Health and associated risks, (Coronaviruses: Lapuz et al., 2025; Ebola: Lee-Cruz et al. 2021; West Nile virus: Tran et al. 2014; Durand et al. 2017; African Swine fever: Faustini, 2025; Various pathogens; McNeill et al., 2023). Additionally, event-based surveillance systems are being developed to strengthen and better integrate environmental risk factors (Boudoua et al. 2025), with various platforms providing reporting of outbreaks online (i.e. WHO and WAHIS), whilst new efforts to develop regional models are underway (WWF efforts for Southeast Asia; Martin et al., in prep). Modelling risks generally requires integrating data on landscape structure and fragmentation, and data on human populations, and livestock populations and production systems (as well as companion animals), climate, and species ecology and ecophysiology. Modelling can also enable interventions to either modelling of potential spread within a species (i.e. between populations) where containment may be most appropriate, or may map potential for spillover (i.e. see Lapuz et al., 2025); both of which require targeted actions to proactively reduce transmission or propagation of pathogens (i.e see Figure 5).

Risks may be highest during times of physical stress, thus events such as hibernation, migration and reproduction all carry with them increased risk. Notably, migration is important from two perspectives; firstly as a major driver of stress (often posing extreme ecophysiological demands on individuals) and secondly potentially transferring pathogens over extended distances (i.e. Avian Flu; Lycett et al., 2019; Stokstad 2022). Recent analysis synthesising 1834 studies highlighted 760 pathogens associated with 1438 bird species, with migratory birds hosting the highest pathogen richness (found in 593 species) (Qiu et al., 2025). The importance of better understanding pathogen prevalence in migratory species has also been highlighted as an area in need of further research by the Convention of Migratory species, including understanding the interface between migratory species and livestock; which provides a particularly high risk of spillover (WCMC 2024; Kipperman et al., 2024). Thus understanding migration routes and potential pathways could allow actions to either reduce contact with potential intermediate hosts (i.e. see Plantneeds 2024; https://waterfowlalertnetwork.com/), or to vaccinate them to reduce risk of infection (Capua & Marangon 2006, AU Gov 2026).

Example Risk Pathway



Biosurveillance + Habitat data	Monitoring of Infection dynamics	Pathogen survival	Trade data	Host interface and behaviour	Host immune status	Potential spread dynamics	Treatment options	Vulnerabilities
Habitat management, creation of barriers	Vaccination of reservoir [3], improve host immunity	Environmental clean up	Trade restrictions, Veterinary checks, Quarantine	PPE, create barriers- fencing, disrupt interactions [4]	Vaccination of new host	Biosecurity for new hosts	Treatment	Address inequalities
Reduced spread in/between reservoir/intermediate hosts	Reduced shedding	Reduced pathogen accumulation	Reduced geographical spread	Reduced exposure of new hosts	Lack of susceptible hosts	Containment of cases	Reduced severity	More robust populations

Figure 5. Example risk pathway for spillover of a pathogen to a new host, including direct and indirect exposure and translocation to a new geographic area. Below the pathway, examples are provided of the information needed to assess the different steps, potential interventions, and the immediate positive effects of those interventions. Notably, "spill-back" can occur from intermediate hosts back to reservoir (initial) hosts, or from humans to either stage. Reactive strategies also include building capacity and preparedness for limiting potential spreads. All steps have multiple options, and in many cases options are highly dependent on the host type (i.e vaccinating bats or rodents is impractical - 3). 1-Details depend on transmission routes of pathogen (e.g., pathogen shed in feces, viremia for blood-borne infections). 2-This includes all ways that the pathogen could move, such as legal and illegal trade (of domestic animals or wildlife), wind-blown arboviral vectors, or ballast water of container ships, etc. 4-Disrupting interactions may involve physical barriers or removing resources that attract reservoir hosts. Some elements, such as trade also need to consider welfare (stress, risk of injury) as well as biosafety during housing and transport. Processes for monitoring of plant health may be similar, though often receive less attention than animal pathogens.

Furthermore, these temporal events interact with changes in climate, and shorter-term extreme climate events may impose additional stressors, or change behaviour and movement as well as causing both direct increases in stress, and altering access to food. At a landscape scale, loss and degradation in the landscape, or factors which force animals outside core habitat (such as climate induced reductions in food supply) increase the energy expenditure required to forage sufficiently, forcing animals into stressful conditions, increasing the interface with domestic animals which wildlife may either receive pathogens from or pass them onto, as well as potentially exposing animals to other stressors such as agrochemicals. All these factors should be considerations in model development, and yet all of these require higher resolution data from animals (or plants) collected from the wild; thus at present our best insights into how these systems function come from a handful of well-studied species (such as *Pteropus alecto*- Eby et al., 2023), and through theoretical modelling based on a subset of these parameters. In terms of managing these issues (i.e. see Figure 5), different modes of intervention will be needed, especially once a pathogen is detected. In the case of *P. alecto* for example, the loss of foraging trees is a major component of creating the interface over which spillover occurs, thus if mango trees in horses paddocks were felled (to remove the probability of flying foxes foraging adjacent to horses) and fruiting trees planted within forested areas to provide an alternate food supply both less energy would need to be expended for them to forage (less stress, lower shedding and less exposure to contact pathogens) as well as less interface to spill pathogens into horses.

Synthesis and directions moving forwards

Globally a heterogeneous picture of biosurveillance for One Health emerges from our study, and despite regulations focused on the international trade of taxa in some jurisdictions (particularly higher income economies) most of these are focused on livestock and pets, whilst wildlife biosurveillance, even during import is frequently neglected (Figure 4). Despite a global pandemic, and the development of robust reports aiming to monitor, identify and mitigate risks, we still do not collect basic information on the health of most wildlife. Focus centres on animals and plants exported commercially (largely for food) or for companion animals, with notable gaps for taxa where trade is less well monitored (i.e. see Hughes et al., 2026). Thus monitoring of international trade biosecurity is often mismatched with major elements of global trade (see Hughes et al., 2026), where the growing volume of exotic and ornamental pet trade is poorly accounted for in biosecurity monitoring and requirements. Quarantine protocols often follow the same patterns. Health data for routine screening of animal facilities and the international trade of species tends to focus on a subset of pathogens for animals, with a broader range generally considered for plants. For both welfare and biosecurity structures and standards, often involving standardised routine inspections, responsible bodies have been developed in higher income economies, but are often lacking or have weak enforcement in developing economies.

Within wildlife trade, there is a lack of monitoring of what species are in trade (Hughes et al., 2026), before even considering the associated pathogen risks. Programs tend to be focused by region or taxa, and whilst initiatives such as that of CITES have focused on a more diverse selection of taxa, it is still often limited to a subset of species, and biosafety concerns likely remain a low priority. Furthermore, some national trade inventory systems, such as LEMIS have identified injurious species which pose a major risk of bringing with them various pathogens (FWS 2025). Circumventing these risks also requires care, for example to manage the risks associated with the aquaria trade in the Caribbean. The One Health zoonotic disease prioritization (OHZDP) tool can be adapted to identify and manage risks (Douglas et al., 2024). Other tools have been developed to identify potential risks as a means of early surveillance (e.g ESSENCE; Burkom et al., 2021); yet such tools are often industry and regionally specific, with relatively few shared between regions. Frameworks like these can be optimised to reflect risks and use this as a basis for either restricting imports, or for targeting biosurveillance efforts to prioritise where risks are highest.

Whilst approaches have been implemented to use data from domestic animals for early warning (Lin et al., 2023), clear guidelines are needed for the collation of data from wildlife, including ecologically relevant measures on the condition of the animal, as well as ecosystem metrics. Likewise, measures to enhance the ability to track wildlife, and their pathogens are likely needed to reduce the risks of spillover, and identify when trafficking or laundering may have taken place. Given that at present we lack basic data of even what is in trade (Hughes et al., 2026), effective monitoring of associated risks represents a further frontier which has not been well examined aside from basic regulations (zoosanitary regulations and certification), and efforts to catalogue and database risk remain conceptual.

General biosurveillance and baseline ecological monitoring remains an area in urgent need of research, and the development of funding and standards to generate the data needed to monitor and manage potential risks. Very few countries have nationally-funded programs which adequately address wildlife related risks, with many existing programs (largely in high income economies) focused only on avian flu, whilst for plant pathogens the focus is often dominated by pathogens likely to impact on forestry. Other lower and middle income countries often rely on externally funded projects or programmes, which rarely provide enough capacity building and sustainability to deliver solid monitoring processes. Recent years have seen a proliferation of databases to monitor pathogens, however, most of these have been developed to collate pathogen data, but not species ecology data, leaving major gaps in our ability to monitor and manage risks. In ocean and coastal systems, advancing monitoring standards also depend on embedding marine ecological context, depth-resolved sampling, pathogen persistence envelopes, and host-condition fields into existing surveillance systems. These systems also need to be supported by evidence of marine pathogen spread, stressor co-occurrence, and aquatic trade networks. Such measures also require tailored indicator qualification and cross-interface data schemas to avoid under-estimating introduction likelihood and to strengthen multi-taxa ocean reporting frameworks (Glidden et al., 2021; O'Hara et al., 2021; Demirel et al., in prep). There is currently a major disconnect between many of the major agreements, and the means to assess and manage risks. Given the crucial relevance of species ecology in our ability to monitor, manage, model or mitigate risk, ensuring we have clear data on the individuals sampled will be crucial moving forwards.

Reporting platforms, especially from WHO and WAHIS have been developed in recent years to enhance communication and reporting, but the actual collection and collation of data is still generally lacking, especially for risks related to wildlife. Major priorities include not only synergising information within these major domains (international wildlife and plant trade, domestic regulations, and biosurveillance of wildlife), but determining the standards for data collation within each. Despite the multiple high-level entities and panels which have come into existence in recent years, how we operationalise monitoring at scale, or develop standards, remains an area where further work is urgently needed. This operational gap echoes operationalization issues common across One Health initiatives globally. Standards and tools need to be developed, tested and refined in order to better monitor wildlife health and its consequences in terms of zoonotic risks.

Following the development of standards, national OH platforms should have the capacity to adapt and adopt these standards and tools for their local contexts. Once such standards have been agreed, then more field-based One Health task forces can explore routes to implementation. Thankfully in most cases, authorities already exist to do some of the work, and by standardisation, the generation of interoperable data will enable development of, and access to tools to process this data effectively. However, the responsibilities over wildlife and livestock health and the management of zoonotic risks is often spread over multiple ministries (e.g., ministry of health, agriculture and environment). The development of processes and tools for effective wildlife-origin zoonotic risk therefore requires a level of coordination and collaboration that only a OH approach can provide. Furthermore, given the superficial and fragmented data that exists at present, it may seem daunting to begin a process to standardise and collate such data, yet, given the economic incentives for biosecurity, once such standards have been developed, it could actively reduce challenges for existing authorities in this space. These mid- to long-term objectives represent the type of complex task that One Health initiatives can implement incrementally over an extended period. Lastly, whilst we know the multifaceted-costs of these pathogens on societies and nature, understanding their impacts on wildlife, domestic animals, and humans, especially in a changing world is crucial; yet to do this will require data which currently either does not exist, or is too fragmented and unstandardised to feed into the frameworks needed to enable management, or even provide warnings of potential issues until they may already be challenging to control.

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Supplements

Supplement 1. Online databases and compilations of pathogens and the parameters within each database

Supplement 2. National regulations for zoosanitary and phytosanitary conditions for the import of animals and plants.

Supplement 3. Regulations for biosafety and monitoring for livestock at a National level.

Supplement 4. Programs and initiatives for monitoring wildlife health and pathogens.

Supplement 5. Regulations and initiatives for monitoring the health status of wildlife in trade.

Supplemental Figures

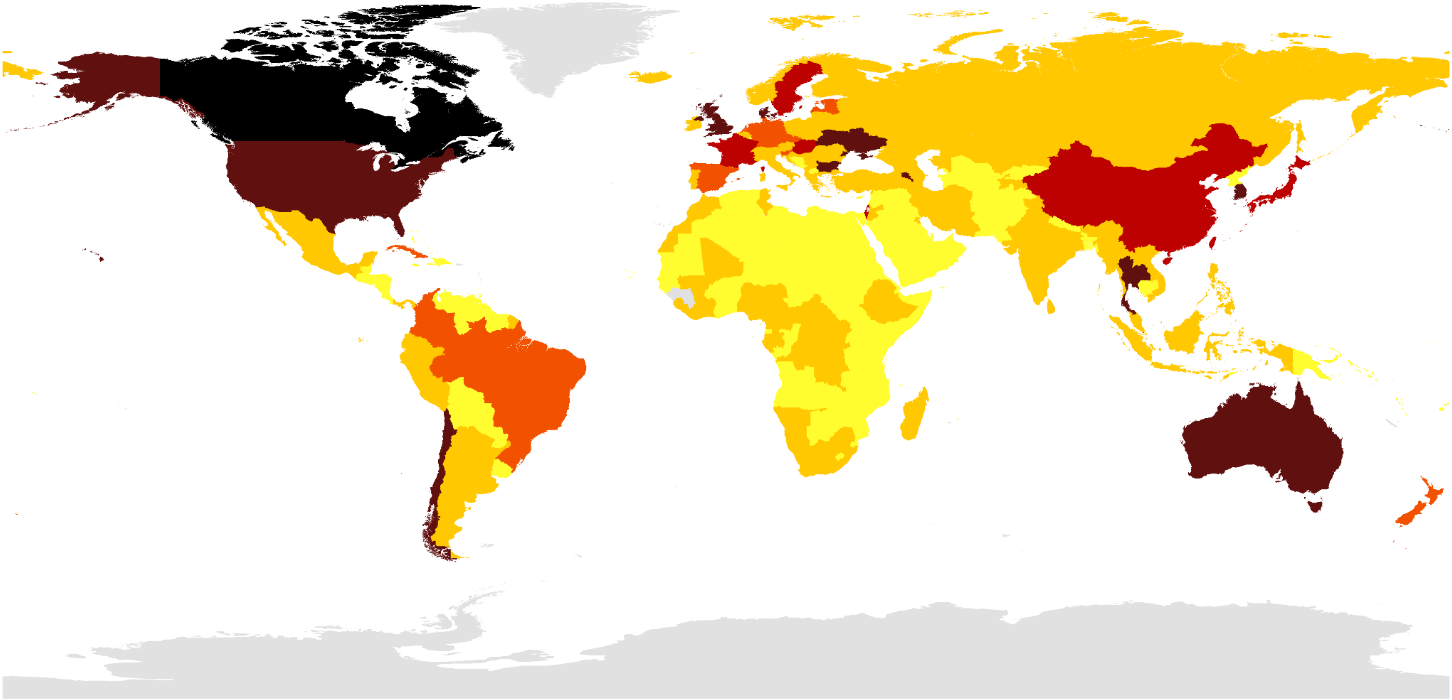

Figure S1. Global Health Security Index (GHS). Indicator 1.3.1) Whole-of-government biosecurity systems (maximum 100)

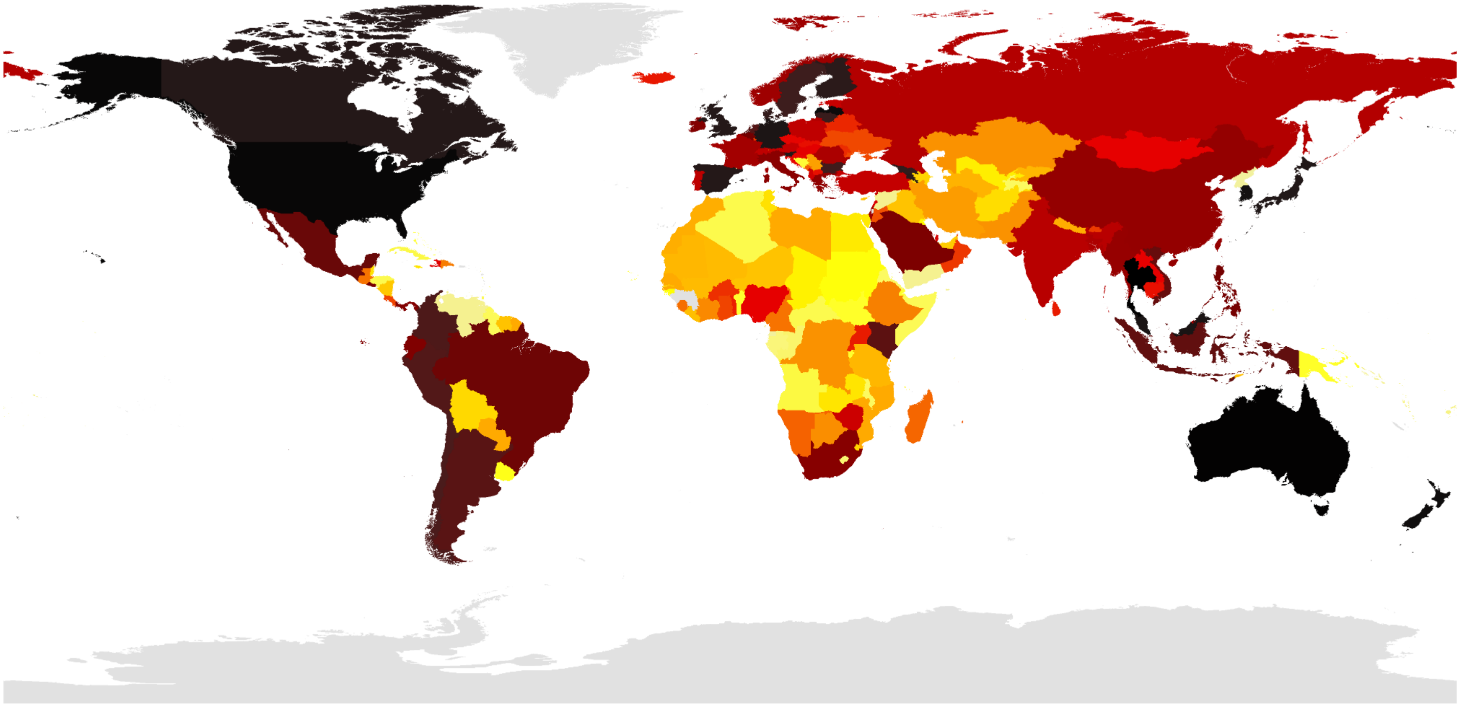

Figure S2. GHS Indicator 2. Early detection & reporting for epidemics of potential international concern (maximum 92).

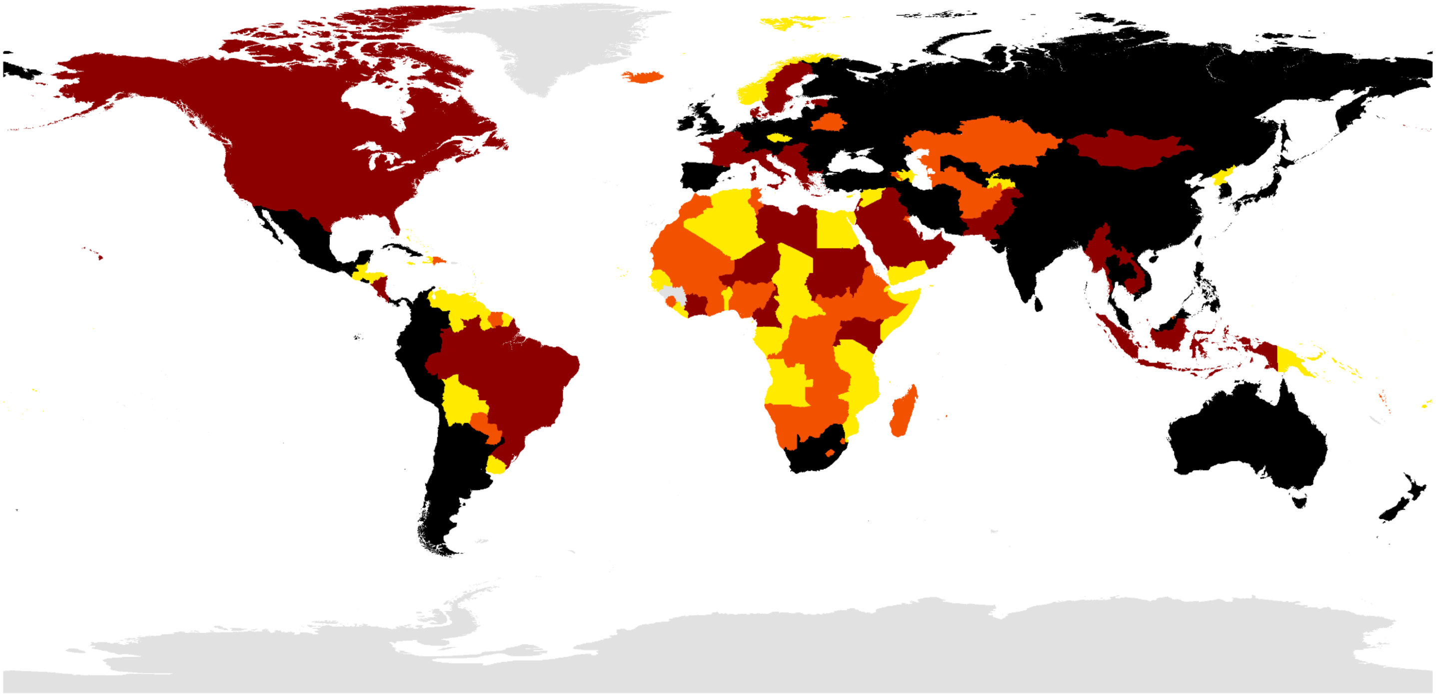

Figure S3. GHS Indicator 2.1.1. Lab capacity for detecting priority diseases (maximum 75).

Supplemental Text

Text S1: Risk patterns in Marine systems

However, marine pathogen spread shows patterns that differ markedly from terrestrial pathogens in pace and transmission context, and ocean connectivity enables host contact and environmental pathogen persistence over exceptionally large spatial scales (McCallum, et al., 2003). The absence of long-term physical barriers in many marine regions supports pathogen survival outside hosts and allows currents to act as persistent dispersal highways rather than short-lived disturbance vectors (Golan and Pringle, 2017; Smith et al., 2022). Semi-enclosed seas and coastal fronts concentrate population contact (Cantrell et al., 2020), while circumpolar seaways open seasonally and increase multi-regional host mixing (Rosales et al., 2025). Vertical stratification of salinity and temperature influences pathogen persistence and exposure timing for marine organisms (Clessin et al., 2023; Bidegain et al., 2016; Vezzuli et al., 2013). Outbreak reconstructions in belugas (Stone et al., 2023), pelagic fish (Rosales et al., 2025), stony corals (Cohen et al., 2018), and filter-feeding bivalves (Carvalho et al., 2023) show that marine disease spread is mediated by currents and prolonged seawater survival phases, producing dispersal velocities that challenge surveillance boundaries and risk attribution. However, monitoring and surveillance in marine system remains limited and variable (Chen et al., 2025).