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Situation analysis on the roles and risks of wildlife in the emergence of human infectious diseases

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Foreword

Science does not seek definitive, inflexible, unquestionable truths – which is certainly the greatest strength of scientific inquiry. Rather, scientists gather all the available evidence and draw conclusions based on existing data, which means that policy advice informed by science will necessarily evolve as knowledge improves. A primary role of the network of >10,500 experts of the IUCN Species Survival Commission, which spans 174 countries, is to understand and inform the world about the status and trends of biodiversity and develop collaborative and inclusive conservation strategies and policies. That is the purpose of this document: to guide public opinion on the roles and risks of wildlife in the emergence of human infectious diseases and inspire world leaders and governments to pursue evidence-based actions.

Although initially motivated by the COVID-19 pandemic and its alleged link to wildlife trade, as the research for this situation analysis progressed, it became evident that there was a need for deeper scientific examination. This was necessary given the strong, mostly unsubstantiated narratives around wild animals and disease risks, whether in nature or under human management, subsistence use or exploitation. This was partly a concern because current evidence for COVID-19 as a zoonotic disease (i.e. any disease or infection that is naturally transmissible from vertebrate animals – animal reservoir – to humans) was primarily circumstantial, and while epidemiologists broadly agree on what constitutes a zoonosis, direct evidence is not always available to confirm its emergence pathway when suspected, as in this case. Although increased monitoring of human-mediated movement of wildlife around the world remains an important goal for conservation and public health, a better understanding of the role of domesticated animals and wildlife under direct domestic management as a reservoir and source of zoonosis and novel pathogens is possibly a higher priority. For example, the extensive (human) Global Burden of Disease[1], work done collaboratively by the Harvard School of Public Health, the World Health Organization (WHO) and the World Bank do not always differentiate zoonoses from other sources of infection, making any analysis of the role of zoonotic modes of transmission in human infection risk and the impact of zoonotic disease on human health almost impossible. The initial reaction of many actors in the global conservation community to COVID-19 to call for a ban on all wildlife trade was understandable, as it was perhaps successful to some extent in limiting the sale of certain wildlife for food in markets (the ban excluded livestock, marine products, wild plants, amphibian, reptiles, and other animals and products for non-consumptive use), whilst including provisions on wildlife ownership, protection and management mechanisms, and penalties for law violations. However, examination of the scientific evidence does not support the assertion that this measure would have a substantial impact on preventing future epidemics or that it has averted any of the current risks. This does not mean improved sanitary measures applied to wildlife trade are not important, quite the reverse, it is a serious gap in veterinary regulation that it is not done in many instances or is not effective. Perhaps the most important lesson of this situation analysis is that nature continues to be a critical ally to our well-being. Wild species are not enemies and we need not fear them nor try to control them in nature. Rather, the challenge rests in better understanding how our domesticated animals and human-dominated landscapes create opportunities for the establishment of an interface for, and emergence of, infectious diseases.

Jon Paul Rodríguez
Chair, IUCN Species Survival Commission

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1 Global Burden of Disease (GBD) (http://www.healthdata.org/gbd/2019).

Executive summary

This situation analysis presents a thorough, evidence-based examination of the relationship between wildlife and zoonosis, wildlife and emerging human pathogens and associated diseases, their origins, drivers, and risk factors. There is considerable divergence of opinion around the subject both within and outside the biodiversity conservation community and given the ontological challenges and highly different perspectives, contradictory narrative is unsurprising. The IUCN Species Survival Commission (SSC) focuses on biodiversity as a vital element to Earth's systems, including humanity, and therefore this work questions much of the negative narrative surrounding wildlife in the disease debates. Context is all-important and to clarify this in the analysis, the evidence of human diseases coming from wildlife is compared to diseases emerging from domestic animals and humans themselves, to provide context and proportions of the relative risk.

Emerging infectious disease (of humans) is a primary and current societal concern given the COVID-19 pandemic and, by generally accepted definitions, spans a very wide spectrum of diseases with diverse emergence pathways and underlying processes, so generalisation is uninformative. To illustrate this point, it is commonly depicted that ~70% of emerging infectious diseases of humans originate from wildlife, which is inaccurate. This figure is relevant only to human pathogens originating from animals (zoonotic), while a more accurate figure is that 43% of human emerging infectious diseases over six decades, from all sources, have wildlife origins. Further to this clarification, the diseases of pandemic concern or high risk and impact on humans, with known or probable wildlife origins are fortunately of rare occurrence, even if seemingly on the increase. This handful of novel human pathogens and diseases, nevertheless, are extremely important, as COVID-19 has shown. More relevant is the context for emergence. The increase in events is more likely due to exponential growth of human activities (domestic/farmed animal population, environmental perturbation, and globalisation), rather than any increase in the underlying rates of evolution of new pathogens from nature.

We also conclude that the vast majority of recurring zoonoses come from domesticated animals and anthropogenically disrupted habitats, directly or through food systems and other vectors, accounting for an estimated 99% of the human incidence. Direct zoonoses of significance from wildlife, directly, are rare, mostly indirect and/or vector-borne. A good example is rabies where in the United States, on average only 2-3 cases occur annually from direct exposure to wildlife.

Embedded in this complexity, the report focuses on wildlife trade, and has mined available data to try to elucidate the claims that the trade is a significant source of zoonosis and/or emerging infectious diseases. In this regard, we hope that there is more clarity of what we can and cannot assert, based on evidence and with a major outcome being evidence of the absence of evidence, which is a major gap for future generations to address and research.

The report highlights key knowledge, and provides perspective on where research, policy, interventions, and capacity building are needed to reduce risks of zoonoses and emergent animal-origin human diseases globally.

Knowledge, quantity
and quality of information

● Not all emerging infectious disease (EID) are new diseases. The overall estimated figure (from one study) is that 43% of emerging infectious diseases have ultimate origins in nature and many emerging infectious diseases are no longer acquired from wildlife. Under emerging infectious diseases, however, are included geographical, temporal, and novelty aspects that can mask relevant epidemiological context about a disease. An infectious disease may emerge due to a change in geography, a re-emergence, an increase in baseline prevalence, or a variant, so truly novel new pathogens are in the minority of emerging infectious diseases. We recommend the subcategory "Novel Emerging Infectious Diseases" (nEID), for truly novel pathogens which are the greatest threat. Novel Emerging Infectious Diseases are those that we have no prior knowledge of, do not know how to control them, and often their novelty renders immune responses inadequate, allowing for a high pandemic potential, high mortality rates and sickness, such as with COVID-19.

● The terms "zoonosis" and "zoonotic disease" are often confused and thus misapplied. According to the World Health Organisation, a "zoonosis" is any disease or infection that is naturally transmissible from vertebrate animals or an animal reservoir to humans, either directly (e.g. rabies and dog bites), or indirectly through a vector- or food-borne, such as Lyme disease (tick borne) or salmonellosis (eggs or uncooked meats). The descriptive term "zoonotic disease" (or "zoonotic origin") is often used for a disease that first originated in non-human animals, even when the disease is no longer transmitted from animals. The disease may continue to circulate within human populations and be maintained in the absence of animals or an animal reservoir. Good examples are when a causative organism has genetic origins amongst microbial communities of animals but adapts to humans becoming an "emerging infectious disease of humans," for example HIV/AIDS, COVID-19.

● Where countries record zoonosis (notifiable or reportable) or just attempt to record cases, the results show most animal-origin infections affecting humans come from interactions with domestic animals and species that thrive in human-dominated environments (regardless of the origin of the infectious pathogen).

● Knowledge of the incidence of zoonosis from any source, in particular from wildlife or wildlife trade, is often weak on specifics and is highly data deficient globally, with a few important exceptions. The global burden of (human) disease database does not account separately for zoonosis, for example tuberculosis is recorded as a single disease, whether human or animal origin, whilst estimates of zoonotic tuberculosis are around 1% of global cases. Without human case data and confirmatory diagnostics on zoonotic and emerging infectious disease pathogens transmitted or derived from wildlife species, it is not possible to determine with certainty the importance or risk of these hosts, reservoirs, or genetic origins. Furthermore, there is no consistent surveillance

of the disease and public health aspects of the wildlife trade, internationally or in many cases at national level.

● The inclusion in these terms and lists of a wide variety of pathogen-types and diseases with very different origins or epidemiology is arguably too broad to help in developing appropriate targeted, disease-specific interventions, control policies, and to improve preparedness and response, beyond general capacity building and preparedness.

● A further confusion is in the use of the term "wildlife" in situations that cover diverse animal populations and animal use systems, some of which are not part of natural ecosystems, such as wildlife farming. This lack of specificity can lead to inappropriate focus on natural populations which, based on available evidence, we understand to have a negligible role in the general context of human disease, and which can result in inappropriate policies and interventions with potential negative effects to millions of people.

● Coronavirus disease 2019 (COVID-19) is a novel human disease caused by a new betacoronavirus strain named Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2), a human adapted coronavirus with as yet no evidence of zoonosis or animal reservoir. Although an animal reservoir or the immediate ancestor has not been found yet, there is an increasing body of evidence that report findings of related alpha- and betacoronavirus in *Rhinolophus* bats, demonstrating natural circulation of related betacoronavirus in Southeast Asia, highlighting the importance of cross-border surveillance. The human transmission may have been a single or repeated spillover events from wild, farmed, or domesticated animal(s) that could be both impossible to detect or to confirm at this stage, whilst also a laboratory origin of the virus cannot as yet be discounted.

Recommendations

1. Seek cross-sectoral and interdisciplinary consensus on definitions related to zoonotic diseases and achieve common understanding.

2. Confirm and record zoonoses (in each case due to direct infection from an animal) in an open global human disease database to enable impact and risk factor analysis to prioritise research and mitigation measures.

3. Differentiate untested hypotheses from evidence-based conclusions in reporting and recommend evidence-based policy interventions for zoonosis and emerging pathogens.

4. Analyse diseases, disease processes, and risk contextually and specifically.

Emergence of human pathogens and their risk

- The role of nature in disease transmission – the structure of ecosystems and biodiversity in general – play important roles in host-pathogen dynamics. Most microorganisms are beneficial, ecosystems would likely collapse without them. Novel human pathogens and diseases have been acquired from various pathways. Of the estimated total number of microbial species on Earth (i.e. viruses, bacteria, fungi, protozoa, and helminths), human pathogens are approximately 1,400 or 0.000014% of the total estimated number of species of microorganisms (estimated between 120,000 to tens of millions); with many disappearing as well as becoming non-pathogenic throughout human history.

- Direct naturally acquired human zoonosis from a wildlife reservoir is extremely rare, except in a few diseases, such as plague and Lassa fever from synanthropic rodents (i.e. rodents that benefit from living in proximity to humans but remain undomesticated). More commonly, wildlife species may be a source, indirectly, via vectors such as ticks or mosquitos, such as Lyme disease and West Nile Virus, or maintain and shed sufficient levels of pathogens in the environment that create the conditions for human infections, for example rodents and water-borne leptospirosis.

Recommendations

1. There is no evidence-based justification for interventions such as culling free ranging wildlife to prevent wildlife zoonoses or reduce the potential for emerging infectious diseases. An unintended consequence of culling "host populations" in a cordon sanitaire can be, perversely, more rapid spread through the perturbation caused and rapid reintroduction of cleared zones. However, culling of, for instance infected mink in farms or synanthropic wildlife such as rodents around human habitation might be an appropriate measure, where risk of a zoonosis is high, and control of vectors is commonly practised.

2. Biodiversity has a central role in disease regulation and must be conserved. Increased biodiversity can reduce the prevalence of infectious diseases (dilution effect) or increase it (amplification effect), depending on landscape features, community characteristics, and type of pathogen transmission.

3. Prevention and control of zoonoses and emerging infectious diseases are best achieved through infrastructural and health systems pathways. Rethinking the current production systems, exploitation practices of natural resources and animals (domestic, farmed, and wild), and systemic inequities in the access to healthcare will be fundamental to decrease the risk of future pandemics. New spillover events and outbreaks are inevitable but preventing increasing rates of these events and the rapid global spread are feasible goals, especially if they address primordial prevention issues (drivers) rather than just preparedness and rapid response.

Wildlife trade

The overall risks of zoonosis are greater from those species traded in large volumes. The highest risk is most likely from unregulated trade where little knowledge exists of host-pathogen-environment dynamics, inter-species interactions, collection and transport practices, and exposure rates (whether domesticated, or wild animals of farmed or wild-caught origin). The degree of regulation and application of safe practices tends to be higher in sophisticated high-volume legal trade than illegal low volume trade for obvious reasons, but risk remains in both sectors. The risk is largely dependent on the specific system and conditions employed rather than a particular species. The likelihood of contracting a zoonosis from a domestic animal is 3000 times greater compared to a wild animal in trade, based on trade volumes. Evidence is lacking and it is difficult to calculate specific risk probabilities due to the lack of consistent reporting and surveillance in this system. The evidence to support the perceived risks of zoonosis or emerging pathogens from wild-sourced animal trade is particularly weak and restricted to a few events, so different trade systems have not been analysed separately in this report. Risk of novel pathogen spillover from wildlife trade is not zero, and even single events can have major consequences. Recent trends in international trade show a shift from wild- to captive-sourced species and products, though large volumes involve species that are not overseen by CITES (e.g. mink for the fur trade) and while proportionally the wild-sourced trade goes down, the total number of interactions with wild-sourced specimens is still increasing in number. Identifying high-risk practices and improving sanitary and animal welfare conditions along supply chains, whether trade is legal or illegal, are fundamental to reducing the likelihood of spillover events. However, wildlife trade must be considered with all the other potential pathways and drivers of disease emergence proportionally, in a balanced intersectoral and transdisciplinary manner, informed by evidence-based disease risk analysis.

Recommendations

1. Preventive measures must be directed at specific practices and contexts. As with livestock (and other human-animal interactions like keeping companion animals), there is an intrinsic risk associated with wildlife trade whether legal or illegal (illegal trade likely has a higher risk than legal regulated trade). In the case of livestock trade, indiscriminate bans are not imposed unless there is a tangible health risk beyond pathogen detection. Rather institutions, such as European Food Safety Authority or the US Food and Drug Administration set up to regulate and control disease risk and exposure, and formulate appropriate regulations . Current best-practice guidelines for global livestock trade provide a framework to apply to wildlife trade.

2. Lack of data warrants improved surveillance of zoonosis cases attributed to wildlife and the wildlife trade, both legal and illegal, to at least the same standards applied to the domesticated animal trade.

3. Wildlife use and trade is often linked to the livelihoods of indigenous peoples and local communities, as well as local (and national) economies in developed and developing countries; the provision of alternative livelihood activities to replace wildlife trade needs to be carefully considered and evaluated to avoid perverse negative impacts on wildlife, natural resources, and local values.

4. Top-down regulations should account for multiple jurisdictions under unified policy instruments and in consultation with a broader range of regulatory instruments and local stakeholders. Participatory approaches and behavioural science could incentivise compliance with new measures by including relevant stakeholders along supply chains, generate understanding of what drives the use and consumption of wildlife, and develop inclusive measures, thereby increasing the likelihood of the long-term survival of wildlife populations, associated ecosystem services, and reducing risks to human health.

Deforestation and landscape/ land use change

There are many uncertainties around the mechanisms and pathways by which deforestation, agriculture, infrastructure, and other land use changes affect zoonosis and pathogen emergence and prevalence (positively or negatively). Nevertheless, there are some clear relationships described for specific known and emergent diseases (mostly vector-borne), including the role of edge effects, ecotones, artificial water sources, intensified agriculture, and the range of domesticated and peridomestic animal hosts.

Recommendations

1. Human transformation of natural habitats facilitates pathogen transmission between domesticated animals, wildlife, and humans.

2. Deforestation is one of the main drivers of biodiversity loss and it can negatively affect human health. Deforestation has been linked to an increase in zoonotic disease outbreaks and vector-borne disease affecting humans, but evidence to support a universal effect of deforestation is still missing.

3. Conservation and restoration of biodiversity is central to recovery of the planet and for a sustainable human future. This will reduce existential risk from diseases and other health threats such as climate change, pollution, and collapse of biological and environmental resources vital for life, such as soil organisms, water, and oxygen.

4. Further research and clearer understanding of the mechanisms for disease emergence driven by landscape change may allow for some mitigation and identify where trade-offs are possible in the short term.

Intensified animal-based agriculture

- Animal-based food and animal product systems increase zoonosis and emerging infectious diseases risk. The role of wildlife species in intensively reared food or fur farms represents a poorly understood disease risk to humans and their domesticated animals. Globally, large-scale animal-based agriculture systems for food and other products are rapidly expanding. The biggest impacts are expected in Africa (sub-Saharan Africa, the Great Rift Valley, and equatorial West Africa), eastern areas South America (the Atlantic Rainforest in Brazil and eastern Argentina), and some areas in South and Southeast Asia. This global trend in large scale industrial production of pigs, poultry and farmed-wildlife species is coincident with pandemic emergence of highly pathogenic human or zoonotic influenzas, and coronaviruses (e.g. MERS, SARS), which constitute the main and most important emergent pathogens of international concern over the last twenty years.

- Whilst free-living wildlife are often blamed for virus origin, wild animal populations fundamentally have not changed in behaviour, ecology, or community other than in abundance (i.e. most species declining in natural areas). Some species, introduced, and/or invasive are occupying human engineered domains through habitat loss, agriculture, and food storage, leading to some species of public-health concern thriving close to humans. Therefore, the drivers facilitating the emergence of these pathogens are deeply rooted in anthropogenic impacts to the environment.

Recommendations

1. A certain way to reduce risk of zoonosis and emerging infectious diseases globally, without affecting human nutrition, health, and well-being, is to reduce dependence on intensive animal-based food production systems. Human omnivory is well suited to a mostly plant-based diet and this would have added benefits of the potential release of land currently used for livestock food crops for reforestation, biodiversity, and ecosystems recovery.

2. Research on zoonotic disease risk especially from large-scale intensive wildlife and domesticated animal farming is urgently needed.

Transport networks

In terms of directly transmitted and food-borne infections from humans and animals, and associated epidemics and pandemics, there is no doubt that the growth in transport infrastructure, and scale and rate of human, animal, and animal product movements globally, has transformed the disease landscape and increased the risk of emerging infectious diseases. The role of international people and animal movement, as seen by the rapid global spread of COVID-19 and African Swine Fever are clear examples of how global transport networks increase the risk of pandemics.

Recommendations

1. Nations should implement health certifications, quarantine, and where feasible a reduction in human and animal movements as a component of disease regulation.

2. Societies and relevant authorities must improve current monitoring schemes of diseases along the animal trade supply chain, enhancing current human and animal health organisations' (World Health Organisation [WHO] and World Organisation for Animal Health [OIE]) practices for disease control in general.

Translocation of animals for conservation and non-trade purposes

Interventions such as translocation, reintroduction, rehabilitation, and confiscation led to numerous guidelines to prevent health hazards, such as: OIE and IUCN's Guidelines for Wildlife Disease Risk Analysis (2014), IUCN's Guidelines for the management of confiscated, live organisms (2019), and IUCN's Guidelines for reintroductions and other conservation translocations (2013). When appropriately implemented, the risks posed by these activities are minimal, but never zero.

Recommendations

1. Wildlife disease risk analysis needs to be widely applied especially in rehabilitation and seizures. Actions should be regulated by the World Organisation for Animal Health (OIE) to reduce risk of zoonosis and zoonotically acquired emerging infectious diseases and this may require expansion of their mandate and capacities to address this.

Climate change

There is limited but clear and unambiguous evidence to show climate change has direct impact on the emergence of novel pathogens (nEID) with known pathogens and diseases, especially vector borne, showing both negative and positive associations in specific locations. Hypothetically, the effects of changing climate and weather on mammals and birds and their microbiomes could create stresses and modify natural immune-incompetence, in addition to changing their geographic distribution, and communities, with potential for increased disease and pathogen evolution and spillover.

Recommendations

1. Mitigation of climate change effects might be possible in some disease scenarios and these diseases should be identified and targeted.

2. It is unlikely mitigation will be possible in most vector-borne diseases as climate effects will disrupt the Earth's normal ecological cycles.

3. Climate change will create novel human-animal interfaces, modify current ecological communities, and landscapes. Nations must take a proactive stance and focus on preventive measures to reduce future emergence and re-emergence of diseases.

4. Governments need to proactively prepare for epidemics, reflect on current surveillance and rapid response practices, and adapt to new endemic infection.

5. Ignoring the climate crisis will negatively impact the health of people, animals, and the environment. Tackling climate change ought to be a priority.

Antimicrobial resistance (AMR)

AMR is both a natural process and a significant part (25%) of the so-called emerging infectious disease complex generated by human actions. AMR is accelerated by the inappropriate or excessive use of natural and synthesised antimicrobial agents. Emerging infectious diseases derived from an antimicrobial resistance organism with a wildlife origin are extremely rare, but as the genes determining resistance emerge from human, domesticated animal sources under antimicrobial use, or naturally; they inevitably find their way into the environment and can be tracked to wildlife species and ecosystems. There is potential for spillback (i.e. backward transmission from a new host back to the original host) but as yet very little evidence of this being an issue. However, wildlife species are not treated with antimicrobials (unless under human care or unintentionally through indirect pathways) so there is no likely immediate feedback or consequence to humans or domesticated animal industry. Antimicrobial resistance is a primary concern for human and animal health throughout the world. Impacts of antimicrobial resistance in free ranging wildlife appear minimal, but exists as recent MRSA evidence in European hedgehogs as a source of MRSA in dairy cattle shows. More research and ongoing surveillance aimed at the wildlife-farming interface (e.g. water run-off) and urban waste management and disposal of waste into the environment from animal farms of all types and impacts on free-ranging species is needed.

Recommendations

1. Further research is required to investigate the use and disposal of antibiotics, how it contaminates the environment, and the role of naturally occurring antibiotic resistance cycles in wildlife.

One Health approach

There is a growing recognition in society that sectoral approaches to human, animal, plant, and fungi health are not appropriate in today's globalised world, where the interface between (changing) environment, economy, human and animal populations, and multiple-host pathogen dynamics is rapidly intensifying, with uncertain outcomes and potentially unmanageable economic and existential risks. Capacity building to improve the current understanding of the environment, ecosystems, and wildlife dynamics as a third pillar to human and domestic animals in the context of One Health and diseases is globally deficient, with narratives that are poorly evidenced. Nevertheless, there are promising initiatives and contributions that recognise the importance of adopting a One Health approach, such as the Declaration and the launch of the One Health High-Level Expert Panel (OHHLEP); the adoption of WCC Motion 135 – now WCC Resolution – by IUCN *(135 - Promoting human, animal and environmental health, and preventing pandemics through the One health approach and by addressing the drivers of biodiversity loss, https://portals.iucn.org/library/ node/49807)*; the PREZODE international initiative (PREventing ZOonotic Disease Emergence), the International Alliance against Health Risks in Wildlife Trade, ZODIAC-IAEA Initiative, the Joint FAO/IAEA Division of Atomic Energy in Agriculture, the G20 Declaration (September 2021), the G7 Carbis Bay Health Declaration (November 2021), and The Rome Declaration (May 2021).

Recommendations

1. Move from reactive approaches to novel disease emergence to preventive approaches (e.g. act against the major environmental processes driving disease emergence, fund research, mitigate).

2. Prioritise the integration of international agencies addressing human, animal (domesticated and wildlife), and ecosystems health with broader sustainability agendas.

3. New agencies or agreements in global wildlife health may be needed if current animal health organisations such as OIE and UN's Food and Agriculture Organization (FAO) are not able to expand their mandates to evolving requirements.

4. Boost multidisciplinary collaboration to tackle zoonosis and emerging human and animal diseases, with a particular focus on improving knowledge of zoonosis burden, transmission risk, and its source.

5. Current bias in investment towards human and domesticated animal health should be addressed with a greater preventive focus on environmental and wildlife species health.

6. Institutional developments of ecosystems and wildlife health management systems are required. This will need intersectoral actions, capacity development, and systematic insertion of these systems into human development practices, global economies, health systems, and research agendas.

7. Global health (human) largely depends on the access to primary care and health systems. Global health initiatives ought to strive for equitable access to non-pharmaceutical interventions and pharmaceutical resources, such as vaccines, in a unified manner.

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List of acronyms

AMR	Antimicrobial resistance
CITES	Convention on International Trade in Endangered Species of Wild Fauna and Flora
CDC	Centers for Disease Control and Prevention
ECDC	European Centre for Disease Prevention and Control
EID	Emerging infectious disease
EHP	Emerging human pathogen
EVD	Ebola virus disease
FAO	Food and Agriculture Organization of the United Nations
GHSA	Global Health Security Agenda
HACCP	Hazard Analysis and Critical Control Point
HIV/AIDs	Human immunodeficiency virus infection and acquired immunodeficiency syndrome
IPLCs	Indigenous peoples and local communities
IUCN	International Union for Conservation of Nature
NGO	Non-governmental organisation
OIE	World Organisation for Animal Health, Organisation mondiale de la santé animale, Organización Mundial de Sanidad Animal.
UNDP	United Nations Development Programme
UNEP	United Nations Environment Programme
WHI	The North American Wild Harvest Initiative
WHO	World Health Organization

Structure
of the report

Key research questions

To frame an evidence-based approach to the subject of zoonoses and emerging pathogens, the study was structured around specific, relevant questions, which guided the literature review and other methods of inquiry. The questions were:

What is the significance of wildlife in Emerging Human Pathogens (EHP), Emerging Infectious Diseases (EID), and zoonoses?

Section 2 and 3 focus on disease context, natural and wildlife resources use, and includes a description of what is known more generally as the "wildlife trade" and how this compares in terms of risk to domesticated animal trade in all its forms. Key examples highlight similarities and differences between regions in terms of species, industries, and trades, and in the potential roles of traded animals in zoonosis or emerging infectious diseases.

What are the conditions and drivers for EHP, EID, and zoonoses?

Section 4 and 5 focus on the evidence for zoonoses from animals more generally (i.e. wild animals, wildlife, captive wildlife, peridomestic wildlife and domesticated animals) and possible mechanisms for or drivers of the risk of emerging human pathogens, including through the process of animal industry and companion animals as well as domestication of vectors, peridomestic wildlife or through manipulation of wildlife such as farming and their sustainable use.

What are possible solutions or mitigation measures and policies to reduce risk of EHP, EID, and zoonosis from animal use?

This is discussed in Section 6 and 7, as are the institutions and governance systems necessary to implement the actions highlighted. In the debate as to how to reduce risk of emerging diseases, the unintended consequences of measures, such as wildlife trade bans, on socioeconomic activities and the environmental benefits and costs of natural resource use are also considered.

Review methodology

This situation analysis is based on a non-systematic extensive literature review of both scientific and grey literature, guided by expert opinion, and critically assessed by members of the IUCN SSC Steering Committee, the Situation Analysis Advisory Committee, and global experts in the field of wildlife conservation, sustainable use, wildlife trade, wildlife disease, zoonosis, and emerging infectious diseases of humans.

To ensure that the process was driven by scientific evidence, credible scientific literature and analyses were consulted and re-examined (*Supplementary Information SI-1*) to locate primary data that addressed major themes in the context of zoonosis or emerging infectious disease of humans from natural resource use and wildlife trade (e.g. the number of, and which, emerging pathogens or zoonoses have been recorded from wildlife and wildlife trade and their significance). To capture relevant scientific and grey literature, we implemented a combination of forward and backward literature searches and performed a systematic search to assess the role of wildlife trade on disease emergence and zoonoses. Further to this, knowledge of the factors leading to known EIDs and zoonoses were applied in a risk framework, in the context of animal use, wildlife trade, environmental land use change (particularly via agricultural expansion and urbanisation), climate change, transportation, translocation, antimicrobial resistance, with reference to socioecology, economics and development. This was necessary given the paucity of evidence for a simple explanation of the origin of diseases like COVID-19, especially where knowledge on specific pathways and risk factors is difficult to obtain or prove. This allowed for informed discussion on the use of the precautionary principle, in any measures recommended to reduce risks that might have a significant cost to society or the environment.

The data available were re-analysed and interpreted, communicated through proposed solutions, conclusions, and recommendations, providing the key narrative for the situation analysis given in the executive summary.

This situation analysis was written by the lead authors with feedback from IUCN Species Survival Commission members and the Advisory Committee, and was reviewed extensively both internally and externally ∎

1 **||** Introduction

This report constitutes a thorough examination of the published scientific evidence around wildlife and zoonosis, emerging human pathogens and associated diseases and their origins, drivers, and risk factors, in the context of wildlife and compared to domesticated animals. All so-called wildlife/wild animals, free-living or wildlife in captivity, as well as feral domesticated species are considered in the realm of non-domesticated animals. What constitutes natural resource use, sustainable or unsustainable, is described in this context and there is a particular focus on wildlife trade. The initial focus of this situation analysis was wildlife trade but as it became clear that there is an absence of evidence on the role of wildlife trade in zoonosis or emerging disease, including COVID-19 caused by the SARS-CoV-2 virus, this scope was broadened to capture a wider perspective on wildlife-related issues pertaining to human disease. The broader proposed causes, risk factors or drivers of emerging infectious diseases (Lederberg, Shope & Oaks, 1992; Woolhouse & Gowtage-Sequeria, 2005; Woolhouse et al., 2012; Longdon et al., 2014; Johnson et al., 2020) are presented with a focus on relatively recently described human pathogens (e.g. HIV AIDs, Nipah virus, coronaviruses) rather than variants of existing pathogens, re-emerging infections or changing geographies of outbreaks and infections (e.g. antimicrobial resistant organisms, novel influenza viruses, Zika virus). The analysis provides illustrative knowledge of their epidemiology, and provides perspective on where research, policy, intervention effort and capacity building are needed to reduce risks of zoonoses and emergent animal-origin human diseases globally.

Definitions of the key terms really matter, and this analysis gives particular attention to the terms describing disease, pathogens, and their hosts *(see section 2.1. Key definitions, below)*.

In order to assess risk, identify sources or pathways of disease or disease emergence and evaluate disease burden from non-domesticated animals, a precise understanding of the wildlife population and context being considered is vital. The term wildlife as used in common parlance is far too general and non-specific and covers both free-living and captive populations, natural populations and domestically bred wildlife and feral animals. These distinct animal communities and populations are epidemiologically separate (in what is known as compartments in epidemiology) and need to be examined as such and not generically. With respect to pathogenesis of emerging pathogens there has never been any formal consideration by human and animal health authorities, through consensus, of the ontology of critical terms around animal source infections; specifically, what constitutes emergence as both a popular narrative and how medical specialists interpret and use the term. There is an urgent need for this clarity. Some terms such as zoonosis were adequately defined nearly a century ago but are now used indiscriminately and thus need to be revisited. This problem is encouraging dogma around animal sources of human pathogens, which is often unsubstantiated and if not corrected will bias policy and action. At worst this leads to misunderstanding and ill-informed popular opinions and to actions which may include persecution of wildlife. This will cause adverse impacts on society and livelihoods and will fail to result in the prevention or control of diseases.

1.1. Key definition

1.1.1. Disease terms

Disease: a disorder of structure or function in a human, other animal, fungus or plant, especially one that produces specific symptoms or pathology that affects a specific location and is not simply a direct result of physical injury. To cause a disease, a pathogen must successfully go through multiple barriers (or pathogenesis stages): host exposure (contact), adhesion (colonization), invasion, and infection.

Emerging Human Pathogen (EHP): a novel organism rather than just a variant (such as from acquired resistance in a known pathogen to antimicrobials or a re-emerging pathogen sometimes classified as EID) that is increasing in incidence and has been first reported in human disease records within the last 20 years.

Host (Figure 1): is a living organism which is capable of supporting a microorganism in its body or cells and can be further defined as: (i) dead-end host; where limited replication may occur but without excretion after infection (e.g. cattle and peste-de-petits ruminants virus); (ii) spillover host, acquires infection from a reservoir; or (iii) temporary (maintenance) host or secondary host, that results in a number of possible scenarios from dead-end infection with no onward transmission, or a stuttering chain of limited transmission under natural conditions in the new host, or secondary epidemiological cycles that usually burn out, failing to persist (e.g. humans and pigs with Nipah virus and Hendra virus and horses with spillover from bats) (Plowright et al., 2017); *(iv) vector (host)*, an animal (vertebrate or invertebrate) which is essential to the life cycle of the organism, carrying and transmitting it to other species over space and time (e.g. anopheles mosquito and plasmodium falciparum malaria agent), *(v) maintenance host*; which will support a population of the organism, indefinitely, in the host population for example cattle and bovine tuberculosis; *(vi) intermediary or bridge **host:*** provides a link through which pathogens can be transmitted from maintenance host populations or communities, and: *(1)* is competent for the pathogen or able to mechanically transmit it; and *(2)* comes into direct contact or share habitat with both maintenance and another host populations (e.g. passerine birds and highly pathogenic avian influenza) (Caron et al., 2015) and, *(vii) reservoir host*; a host which if primary (co-evolved), maintains the organism independently of other hosts, does not suffer significant disease from the organism but potentially can transmit the organism to another susceptible host, such as bats and lyssaviruses whilst; *(viii)* secondary reservoirs can establish (e.g. dogs and rabies [Lyssa] virus).

Infection: describes the invasion and multiplication of microorganisms such as bacteria, viruses, and parasites that are not normally present within the body of an animal or plant.

Pathogen: an organism causing pathological dysfunction (disease) to its host.

Pathogenesis: the processes and factors that prompt a disease or disorder, its progression and maintenance.

Pathogen jump: describes how an organism which is exposed to a new host, adapts over a relatively short time to establishing in the new host, by chance adaptation or genetic modification as a result of mutation or recombination. It then establishes in that host with disease consequences. This is sometimes described as *host switching.* The pathogen, may or may not have ongoing zoonotic or zooanthroponotic potential (Woolhouse & Gowtage-Sequeria, 2005; Longdon et al., 2014; Johnson, Roode & Fenton, 2015; Balloux & van Dorp, 2017).

Sylvatic cycle: is a natural disease maintenance or transmission cycle that involves non-human wild animals and insects.
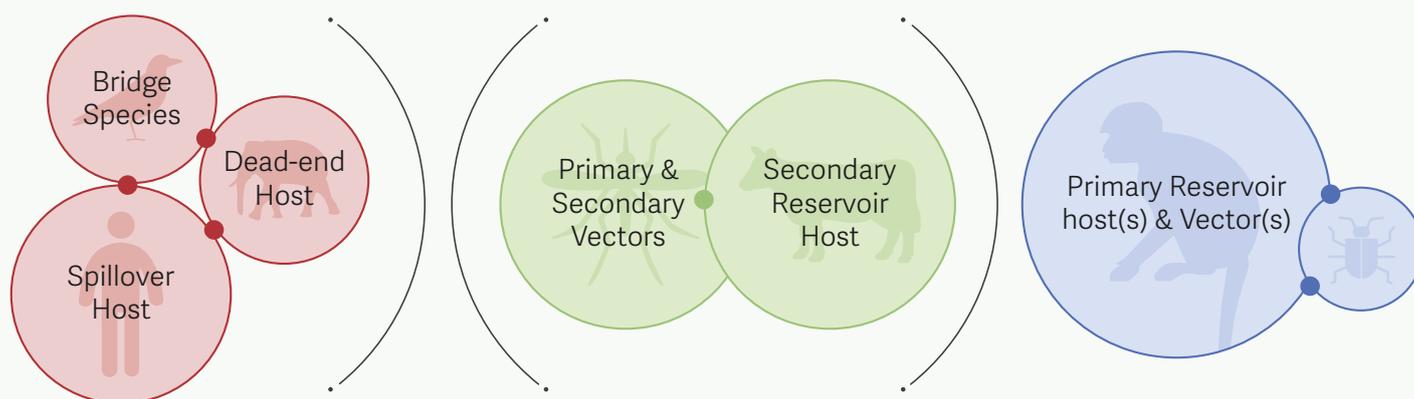
Figure 1. Hosts and boundaries

Illustration of key epidemiological infectious disease cycles showing ecological boundaries, represented by brackets, which under certain conditions are breached. This describes different types of hosts and the ecology of infection with both directly and vector borne diseases arising. *Source: Adapted by the report authors from Kock, 2015.*

1.1.2. Host terms used frequently in disease description

Emerging infectious disease (EID): it should be noted that the ontology of this term remains quite confused. Emerging infectious diseases (EIDs) are commonly defined as infectious agents that are newly identified in a population or newly evolved, or a known infectious agent that is rapidly increasing in incidence (i.e. re-ree-merging infectious agents) or expanding geographical range, host (i.e. host-switch) or vector range (WHO, 2014; Petersen et al., 2018; CDC, 2018). Some authors also use an arbitrary 20-year timeframe since its first record (CDC, 2018), but many analyses do not adhere to this which makes any statistical interpretation complicated and frequently misleading. EID is used to describe many and varied diseases even in scientific publications without using any consensus definition (Jones et al., 2008; Rosenthal et al., 2015). This further complicates interpretation and renders statements such as "70% of EID are from wildlife" in many citations quite difficult to put in context given the lack of a unified and comparable methodology (this is discussed in more detail in the introduction of Section 2).

Host shift or switch: parasite/microorganism/pathogen shifting to infect a new species of host (species jump) (Longdon et al., 2014) – equivalent to pathogen jump.

Host plasticity: characteristic usually of a virus, which enables it to infect hosts of a taxonomically and ecologically diverse range. (Johnson et al., 2015)

Infectious disease of public health significance: an infectious disease is defined by infection with a transmissible organism (i.e. pathogen) that causes pathology and dysfunction (i.e. disease) in a host, and disrupts public health systems. It can either appear and affect a human population for the first time, or has existed previously but is rapidly spreading, either in terms of the number of people getting infected, or to new geographical areas (WHO, 2014).

Species barrier: a characteristic of host(s) in which phylogeny influences the ability of a particular pathogen to adapt from one host type to another. This means that it is not able to fully cause an infection in the new host species. This is well described for viruses, where host restriction factors, determined by specific genes acting at the level of cell entry, resist infection by a particular micro-organism.

To assist in understanding particularly important novel infections like SARS-CoV-2 we suggest a narrower definition of terms in this text, to enable more precise attention to drivers and risk factors. This will facilitate better analysis and policy development for a few serious, previously unknown, and potentially pandemic infections.

Meat market in Ethiopia (2006)
Photo © Michael D. Kock

Parrot trade.
Photo © Gabriela Lichtenstein

The terms are defined as follows:

Anthropozoonosis: infection or disease that primarily affects other animals but can be naturally transmitted to humans (with the reservoir host being the other animal, e.g. human rabies from domestic dogs).

Emerging infectious diseases (EID): are clinically distinct conditions whose incidence in humans has increased (Lederberg, Shope & Oaks, 1992) and typically given temporal boundaries of the past two decades (CDC, 2018), see Box 1.

Novel emerging infectious diseases (nEID): diseases caused by truly new pathogens that have newly evolved to infect humans or have adapted to humans through host switching. In this definition we exclude re-emerging pathogens, changing pathogen geographies or old pathogen variants which have emerged because of strains with different virulence or levels of antimicrobial resistance.

Re-emerging diseases: diseases that used to be major health problems globally, regionally, or nationally, and then declined dramatically, to become again health problems for a significant proportion of the population (e.g. malaria and tuberculosis) (National Institutes of Health (US) & Biological Sciences Curriculum Study, 2007).

Spillover infection: infection from a reservoir host, that results in another species, a dead-end infection with no onward transmission or a stuttering chain of limited transmission in the new host or secondary epidemiological cycles that can be quite extensive but usually burn out, and inclusive of single events which lead to pathogen spread and independent circulation in another species (Plowright et al., 2017).

Zoonosis: any disease or infection that is naturally transmissible from vertebrate animals (animal reservoir) to humans (WHO, 2020b); either directly – via contact or aerosol, or indirectly – via food, fomite or vector (usually arthropod).

Zooanthroponosis: infection or disease that primarily affects humans but is naturally transmissible to animals (with the reservoir or maintenance host being the human, e.g. SARS coronavirus 1 and 2 – causing SARS and COVID-19).

Box 1. The Emerging Infectious Disease (EID) complex

(Novel) Emerging infectuous diseases (nEID)

Newly identified (Emerging) pathogen and diseases that were previously unknown until the first detection.

Ex: SARS, MERS, SARS-CoV2, Klebsiella hauxiensis

(Re) Emerging disease-Geographical range

Pathogens and diseases that already exist but are rapidly expanding their geographical range

Ex: Zika virus, chikungunya, dengue, West Nile fever, avian influenza A(H7N7), Oropouche virus.

Emerging diseases-newly envolved

Evolution (new variant) of previous known microorganism.

Ex: Methicilline-resistant Staphylococcus aureus (MRSA), penicillin-resistant Enterococcus, and multidrugs-resistant Mycobacterium tuberculosis (MDR-TB), and drugs -resistant Plasmodium, Leishmania and Schistosoma.

(Re) Emerging diseases-Host or Vector

Pathogens and deseases that already exist and have been recently found in a new host (i.e. host-jump, cross species jump or host-shift)

Ex: Turnip mosaic virus (TuMV), Borna disease virus, Distemper virus, avianinfluenza A(H5N5), Influenza H10N3.

Re-emerging disease-incidence

Pathogen and diseases that exist but are rapidly increasing in incidence.

Ex: MRSA, Scarlet fever, cholera, Ebola, Influenza A.

Emerging infectuous diseases

Source: Prepared by the report authors.

1.1.3. Ecological terms

Domestic or domesticated animals: those animals that have been selectively bred and genetically adapted over generations to live alongside humans; genetically distinct from wild ancestors.

Feral animals: animals of a domesticated species that now live in the wild without direct human supervision or control (e.g. *Felis domesticus*, *Canis familiaris*, and almost any other domestic species).

Peridomestic animals (synanthropic animals): animals living in and around human habitations. We extend the term for epidemiological considerations to include animal species that are free living, but that have adapted behaviourally and/or genetically over generations to living primarily alongside humans and in human landscapes (i.e. synanthropic), such as agriculture, infrastructure, housing, etc. For example, the house mouse (*Mus musculus*), common rat (*Rattus norvegicus*), many bats and some birds, such as house sparrow (*Passer domesticus*).

Semi-domestic or semi-domesticated animals: animals that appear more similar to their wild counterparts than domesticated animals and have not undergone genetic adaptations to humans and human-made environments. Commonly, humans have partial control over their food supply, breeding, mortality, and space use.

Wildlife: is, defined by IUCN as "living things that are neither human nor domesticated" and therefore inclusive of animals, fungi, and plants. For the purposes of considering human-animal disease risk, this report defines "wildlife" as vertebrate animals including all feral animals, captive wild animals, and wild animals, as proposed by the OIE (World Animal Health Organisation).

Wild animals: have a phenotype and genetic make-up unaffected by intentional (or unintentional) human selection and live independent of direct human supervision or control.

1.1.4. Wildlife trade

Animal welfare: is a complex and multi-dimensional subject with scientific, ethical, economic, cultural, social, religious, and political components. The OIE Terrestrial Code defines Animal welfare as: "the physical and mental state of an animal in relation to the conditions in which it lives and dies." (OIE, 2019a). For terrestrial animals, it includes the "Five Freedoms" described in 1965 for the conditions non-human animals should be under human care, and it is a human responsibility to provide the conditions that ensure animal welfare. The five conditions are: freedom from hunger, malnutrition, and thirst; freedom from fear and distress; freedom from heat stress or physical discomfort; freedom from pain, injury and disease; and freedom to express normal patterns of behaviour. For aquatic animals, OIE developed standards for farm fish with the exception of ornamental species, this can be found in the *Aquatic Code* (OIE, 2019b).

Domestic wildlife trade: commercial wildlife trade for which both source and end markets are in the same country.

Medicinal species: plants, animals, and derived products use in traditional and modern health practices. WHO estimates that around 80% of the global population depends directly or indirectly on the use of medicinal species.

Farmed, captive bred: in the context of wild animal, plant and fungi trade, such terms designate management and production modes that are distinct from "wild-sourcing" or "ranching", with breeding, propagation and raising taking place in controlled conditions.

Illegal wildlife trade (IWT): trade in wildlife whereby collection, production, possession, transport, processing, and wholesale or retail commerce is (or was at some point in the trade chain) in contravention of one or more applicable international, national or subnational laws or associated regulations.

Legal wildlife trade: wildlife trade that is not in contravention of applicable laws and and/or regulations at any point in the trade chain.

Ranched wildlife: rearing in a controlled (e.g. fenced, restricted) environment of animals taken as eggs or juveniles from the wild, sometimes sourced from a wild population that is long-term managed *(modified from CITES, 2020a).*

Sustainable production: legal creation of goods and services using systems and processes that limit environmental impacts; strive to preserve energy and natural resources; are economically viable and equitable; and guarantee social responsibility, by guaranteeing animal welfare and the livelihood, culture, working conditions, and health of communities.

Sustainable use of wildlife: legal and equitable use and commerce of wildlife and wildlife products that ensures long-term species survival, ecosystem functions, and protects the livelihoods of the people who depend on them.

Trade: all activities related to harvesting, processing, transportation, commercial exchange (involving money or barter), and end use of wildlife and harvested wildlife products, both at local levels and across legal jurisdictions. Wildlife trade more generally means taking and selling dead or living plants and animals and the products derived from them. Although difficult to monitor we do not exclude barter and exchange from this definition.

Wet market: Retail location where vendors offer multiple agricultural and other biological products, which may include live animals intended for human consumption or meat. In these markets, live animals may be sold, killed, and butchered on the premises.

Wild meat, bushmeat or game meat: meat from wildlife species.

Wild-sourced (or wild-caught): wild animals, fungi, plants, or their products collected or harvested from free-living (non-captive unrestricted) populations which may or may not be managed for sustainably.

Wildlife trade: refers to the commerce in wildlife (animals, fungi, and plants), inclusive of parts and products derived from them (Oldfield, 2003) ■

Meat trade (Maputo, Mozambique).
Photo © Michael D. Kock

1.2. List of relevant institutions and their mandates

Acronym	Name	Mission/Mandate
CDC *https://www.cdc.gov/*	**Centers for Disease Control and Prevention**	CDC works 24/7 to protect America from health, safety and security threats, both foreign and in the U.S. Whether diseases start at home or abroad, are chronic or acute, curable or preventable, human error or deliberate attack, CDC fights disease and supports communities and citizens to do the same. CDC increases the health security of our nation. As the nation's health protection agency, CDC saves lives and protects people from health threats. To accomplish our mission, CDC conducts critical science and provides health information that protects our nation against expensive and dangerous health threats, and responds when these arise.
CITES *https://cites.org/*	**Convention on International Trade in Endangered Species of Wild Fauna and Flora**	Aims to ensure that international trade in specimens of wild animals and plants does not threaten their survival
ECDC *https://www.ecdc.europa.eu/*	**The European Centre for Disease Prevention and Control**	ECDC's mission is to identify, assess and communicate current and emerging threats to human health posed by infectious diseases.
FAO *http://www.fao.org/*	**Food and Agriculture Organization of the United Nations**	The Food and Agriculture Organization (FAO) is a specialized agency of the United Nations that leads international efforts to defeat hunger. Our goal is to achieve food security for all and make sure that people have regular access to enough high-quality food to lead active, healthy lives. With over 194 member states, FAO works in over 130 countries worldwide. We believe that everyone can play a part in ending hunger.
IUCN *https://www.iucn.org/*	**International Union for Conservation of Nature**	Influence, encourage and assist societies to conserve the integrity and diversity of nature and ensure that any use of natural resources is equitable and ecologically sustainable.
IUCN SSC WHSG (also WHSG) *http://www.iucn-whsg.org/*	**IUCN Species Survival Commission Wildlife Health Specialist Group**	The group is commissioned to serve as a first response for wildlife health concerns relevant to conservation around the world. The focus of the group is on health impacts that relate to the conservation of species, some of which are negative to wildlife population persistence and a threat to endangered species

Acronym	Name	Mission/Mandate
IPBES *https://ipbes.net/*	**Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services**	"The Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES) is an independent intergovernmental body established by States to strengthen the science-policy interface for biodiversity and ecosystem services for the conservation and sustainable use of biodiversity, long-term human well-being and sustainable development."
OIE *https://www.oie.int/*	**World Organisation for Animal Health, Organisation mondiale de la santé animale, Organización Mundial de Sanidad Animal.**	The OIE is the inter-governmental organisation responsible for improving animal health worldwide. The mandate the OIE is to ensure transparency in the global animal disease situation; collect, analyse and disseminate veterinary scientific information; encourage international solidarity in the control of animal diseases; safeguard world trade by publishing health standards for international trade in animals and animal products; improve the legal framework and resources of national veterinary services; provide a better guarantee of food of animal origin and to promote animal welfare through a science-based approach. The adopted standards are recognised under the SPS agreement of the WTO/OMC.
UNDP *https://www.undp.org/*	**United Nations Development Programme**	To supporting countries in their development path, and coordinating the UN System at the country level
UNEP *https://www.unep.org/*	**United Nations Environment Programme**	"Our mission is to provide leadership and encourage partnership in caring for the environment by inspiring, informing, and enabling nations and peoples to improve their quality of life without compromising that of future generations"
WHO *https://www.who.int/*	**World Health Organization**	"WHO works worldwide to promote health, keep the world safe, and serve the vulnerable. Our goal is to ensure that a billion more people have universal health coverage, to protect a billion more people from health emergencies, and provide a further billion people with better health and well-being."
WTO *https://www.wto.org/*	**World Trade Organization**	"To ensure that trade flows as smoothly, predictably and freely as possible, thereby contributing toeconomic growth and development"

2 ‖ The disease context

The literature is highly variable on the definition of the terms "emerging" and "zoonosis" which makes the task and comparative analysis of events and explanation of risk challenging (see Key Definitions) (Haider et al., 2020a). It leads to a great deal of confusion and when discussing disease at the human-animal interface, there is confusion in terminology, which can negatively affect perceptions and encourage incorrect decision-making or attribution of responsibility (Rocha et al., 2020). Generally, more precision is needed as the causes for different types of emergence of human diseases can be and are often inappropriately attributed to pathogens acquired directly from animals (zoonosis) when they may, for example, have historic or evolutionary origins in other animals but are now wholly human diseases (e.g. HIV).

Human pathogens with an animal host (i.e. reservoir), which directly transmit to humans (i.e. zoonosis), are relatively unusual in human health and most often an occupational risk, with the majority of more generalised zoonosis indirect via food (accounting for a third of the zoonosis burden) and vector borne (VBD accounting for another third) (Grace et al., 2012a; Li et al., 2019; Murray et al., 2020; Vos et al., 2020). The majority of zoonoses are derived from domesticated animals and peridomestic wildlife. Direct wildlife to human zoonoses are extremely rare events (Kock, 2014). Nevertheless, broad reviews on zoonosis and its ecology (Karesh et al., 2012) show more attention should be given to understanding pathogenesis (i.e. processes and factors that prompt a disease or disorder, progression and maintenance) and host-pathogen dynamics. To cause a disease, a pathogen must successfully go through multiple barriers (or pathogenesis stages): host exposure (contact), adhesion (colonization), invasion, and infection.

Human emerging pathogens can be broadly classified as:

a) Emerging zoonosis with ongoing infection of humans by animals, requiring an animal reservoir, and a new interface providing the opportunity for infection.

b) Animal (zoonotic) or other, non-animal origin emerging pathogen, adapting to the human host and establishing a human-to-human infection (with or without a vector), with sometimes rare zoonotic transmission from sylvatic (wild animal) or domesticated animal hosts or, no further zoonotic transmission. This occurring from a chance contact or event or change in interface, new introduction into a community and other causes.

c) Human EID can also be a zooanthroponosis (i.e. humans infecting animals with the human being the reservoir host).

A good example currently of a category b) and c) pathogen is SARS-CoV-2 (causing agent of COVID-19). COVID-19 is a human disease, it is acquired by infection from humans (and not animals) and spilling into animals (zooanthroponosis). The original pathway for this emerging pathogen is not confirmed yet and until an animal reservoir is found it is not classifiable as a true zoonosis (Haider et al., 2020a). It has been demonstrated that SARS-CoV-2 can transmit

Wildlife pathology lessons.
Photo © Michael D. Kock

zooanthroponotically from humans to mink kept in artificial conditions such as fur farms (and on a couple of occasions from mink to humans) (Munnink et al., 2020b), and transmission to pet animals (i.e. cats and dogs) appears to be a regular event (Patterson et al., 2020; AVMA, 2021; Grimm, 2021), occasionally to some free-ranging wildlife such as white-tailed deer in North America where it appears circulation independent of human infection might have occurred in deer population; and wildlife in zoos (Hale et al. 2021) (see Table 4).

In our descriptors and definitions, novel EIDs (nEIDs) are caused by newly identified emerging human pathogens (EHPs). We do not focus on re-emerging infections, changing infection geographies or variants on old pathogens (especially those related to antimicrobial resistance traits), which currently are included in the generally used definition of EIDs in the literature (Lederberg, Shope & Oaks, 1992). Most emerging human pathogens (by definition) survive in humans independent of animal hosts (endemic or epidemic), whilst emerging zoonosis is rare, they are important having pandemic potential, in contrast to most zoonoses which are sporadic events and rarely epidemic.

To explain the dynamic of zoonosis and evolving infectious diseases from and to animals, a graphical representation is helpful (Figure 2) to illustrate the distinctions in disease typology as well as quantitative and proportionate aspects of the source of zoonosis and EID.

EIDs

Legend
- ● *Zoonotic EID*
- ● *Non- Zoonotic EID*
- ● *Domestic Animals*
- ● *Wildlife ***

**(i.e. peri-domestic, captive-managed/
farmed and free-ranging wildlife)*

EIDs of zoonotic origin   Ongoing zoonosis

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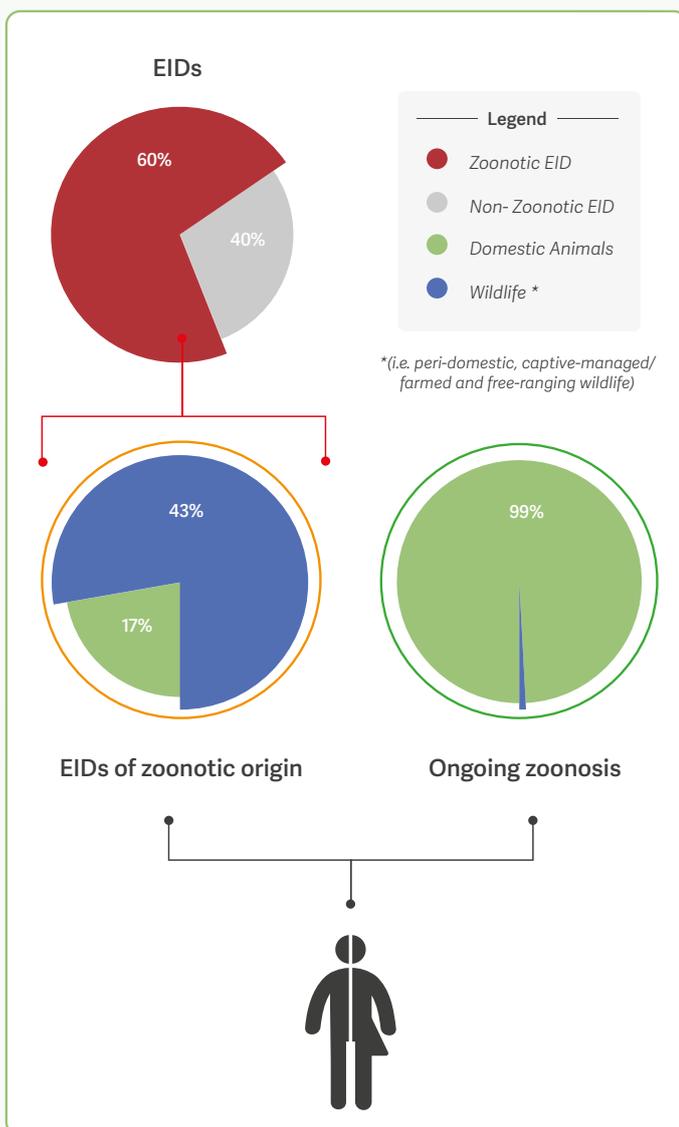
**Figure 2. Spillover sources -
from non-human animals to humans**

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Pathogen spillover from non-human animals to humans can occur through two main processes: (1) Emerging infectious diseases (EIDs, orange circle) and (2) Zoonoses (green circle). Jones et al. (2008) reported 60.3% of EIDs originated in animals (red circles) and 39.7% do not have a zoonotic origin (humans are the only known host, grey circles). Of the 60.3% of EIDs with a zoonotic origin, it is estimated that 71.8% have a wildlife origin (blue circle) while 28.2% jumped to humans from domesticated animals (green circles). Therefore, 43.3% of EIDs have a wildlife origin, with many no longer acquired from wildlife but through direct human-to-human transmission. Ongoing zoonoses (green circle) originate predominantly from domesticated animals (99%, green circles), with only 1% from wildlife (blue circle) as
 reported in Haider et al. (2020).
Source: Prepared by the report authors.

Figure 2 shows that emergence is complex and cannot easily be described in simple pathways or sometimes single hosts. Each event is probably different to some extent in terms of the risk factors and critical events leading to the outcome, but in general can be human-related, pathogen-related, and climate/environment-related (Cascio et al., 2011). New sciences have emerged to try to explain stabilities and instabilities observed in pathogen host dynamics (Hawley & Altizer, 2011) and complexities of community ecology and disease (Keesing et al., 2010; Randolph & Dobson, 2012; Levi et al., 2016) which are clearly important to understanding functional ecology when looking for explanations for these events or a lack of them.

A great deal of emphasis has been given over the last two decades on the emergence of human pathogens, by organisms and origin. Several early publications have become the dogma of emerging infectious disease (EID) communication and unfortunately have created misunderstandings. It is helpful to examine a few of these:

Taylor et al. (2001) provided a valuable contribution to the subject with clear definitions on zoonosis, excluding diseases which are not dependent on animals (e.g. zooanthroponosis) and for EID they did not include diseases as zoonotic when the circulation was primarily human to human, regardless of the origin. The data showed 1,415 known human pathogens at the time of which 61% were considered zoonotic in origin and 12% were considered emergent (175). Of the 175 EIDs, 61% were considered zoonotic, amounting to about 132 diseases. The breakdown of all human pathogens was 15% viruses, 5% protozoa, 38% bacteria/rickettsia, 22% fungi, and 20% helminth. In general, viruses and protozoa are the most emergent in behaviour whilst helminths the least.

Another analysis often quoted is (Jones et al., 2008) which looked at EID with a different methodological approach. All cases were grouped under a broad definition of zoonosis (including zooanthroponoses and where no animal reservoir was known), showing 60.3% EID as zoonotic, 71.4% of these of wildlife origin, and that bacteria were more likely to be emergent (54.3%), followed by viruses (+prions) (25.4%), protozoa (10.7%), fungi (6.3%) and helminths (3.3%). This analysis suggests that only 23 truly novel wildlife related zoonotic origin diseases are in existence, of which many are no longer acquired zoonotically as the organism has evolved and adapted to human population and most of the others are rarely acquired. The majority of diseases in this database (described as EID even if not consistent with the definition of emergent in the last 20 years at the time of reporting and they were new at least to science over the period 1940–2013) are variants, changing pathogen distributions or incidence, evolution of known organisms and of virulence or antimicrobial resistance patterns, with a few shifting host ranges (see Figure 3). Further databases have been developed and collation is ongoing in an attempt to predict likely zoonosis in the future and from which species they might originate (Wardeh et al., 2015; Wardeh, Sharkey & Baylis, 2020) but these are largely based on presence/absence of shared microorganisms and not on real disease events so uncertainty remains the dominant theme.

Emerging infectious diseases in humans: 1940–2013
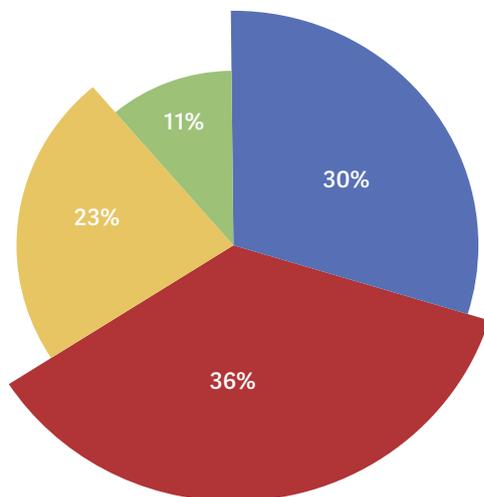
- ● New region, increase incidence, expanding, reappearence.
- ● Evolution existing organism.
- ● Drug Resistant/Increased virulence.
- ● New host range.

Figure 3. Reanalysis of emerging infectious diseases from Jones et al. (2008) and Allen et al. (2017)

Figure 3 shows the analysis of Allen et al. (2017) and Jones et al. (2008). Only 36% of these described EID fit the common narrative of truly novel emergent pathogens of humans which are so concerning, such as emergent coronaviruses. Most nEID fit the "new host range" type of EID which accounts for only 11% of the total (dataset in *SI-2*).
Source: Prepared by the report authors.

Woolhouse and Gowtage-Sequeria (2005) observed that despite the unpredictability of emergence, the organisms that jump between species have some traits in common, and many are directly trans-mitted RNA viruses (e.g. Orthomyxoviruses [Influenza], Coronavirus [SARS, MERS, COVID-19], Ebola virus, Hepatitis C virus, West Nile virus [West Nile Fever], Lyssavirus [Rabies]). Three important points arise of these analyses: 1) There are very few pathogens of humans relative to the millions or billions of potential organisms in nature that could be pathogens. 2) The majority are benign or beneficial through the microbiome to humans. 3) The abundant host popu-lations (e.g. 36% mammal biomass is human, 58% is domesticated animals (Bar-On, Phillips & Milo, 2018; Mittermeier, 2020) and inten-sifying interfaces between species will favour directly transmitted pathogens. As genetic diversity declines, invading organisms will

expand into and create pandemics in the surviving hosts. As an important component of biodiversity, wildlife is less of a threat, and more a buffer, to this process (Maillard & Gonzalez, 2006; Suzán et al., 2009; Keesing et al., 2010). Biodiversity may well be a major reason that the numbers of human pathogens relative to microbial species in nature is so low, in effect buffering this process, diluting the opportunity.

What these and other articles do not make clear is that direct wildli-fe to human zoonosis in nature is extremely rare. Most zoonosis are from domesticated animals and wildlife zoonosis involves predo-minately peridomestic or managed wildlife close to humans (Kock, 2014; Johnson et al., 2020). The analysis included in the Supplemen-tary Information (*SI-3*) on African wild meat is very informative. There was only one confirmed case of zoonotic disease (Ebola – from contact with a chimpanzee during a necropsy) from the entire con-tinental wild meat trade, whilst the zoonotic reservoir for this virus remains elusive (Leendertz, 2016). No natural reservoir has been unequivocally confirmed for Ebola (as well as for SARS-CoV-1 and SARS-CoV-2) but it is likely to be in bats, with various spillover animal (and human) hosts, with some evidence of direct (i.e. wild meat hun-ting and fruit harvesting) and indirect vectoring to humans through processed, hunted or butchered animals (Shi & Hu, 2008; Marí Saéz et al., 2015; Whitmee et al., 2015; Fairhead, Leach & Millimouno, 2021).

For the human immunodeficiency virus (HIV/AIDS) no animal re-servoir has been found, but it is widely accepted that SIV (originally from African primates) was the likely zoonotic origin of the human viruses through evolution (i.e. serial passage). There are two known variants of HIV, suggesting two separate adaptations to humans (Sharp & Hahn, 2011), resulting in the now widely known human epidemic (without any ongoing zoonosis) which likely begun many decades before it was originally thought (Korber et al., 2000; Williams & Burdo, 2009). Yellow Fever has sylvatic cycles which rarely spillover to humans, with subsequent human to human infection cycles, but these do not usually persist. Under certain conditions such as domestication of the animal vector in urban landscapes, cycles can develop with viruses migrating into urban areas and circulation is entirely between humans via anthropophilic (prefer human blood meal) vectors. To explain the recent upsurge in Yellow Fever cases in Brazil, *Possas et al. (2018)* concluded that the rapid emergence was from a combination of human behaviour and ecological changes resulting in increase in mosquito and NHP densities and their con-tacts with humans.

In many cases of EID, without evidence of zoonotic infections from reservoirs and resulting disease, we are faced with only speculation. Although a lot of attention has focused on viruses emerging in Africa due to HIV and EVD, recent events are putting the spotlight on Asia due to the coronavirus emergence as a pandemic threat. In Asia, the situation differs from Africa with a much smaller and res-tricted wildlife population and a large farmed wildlife industry invol-ving more high-risk species of human zoonosis. Attempts at viewing the landscape of emergence, include the following schematic for Europe (Figure 4), where the main conclusion is that emergence is a highly complex process and often cannot be described in isolation of environmental, social, and other epidemiological elements.

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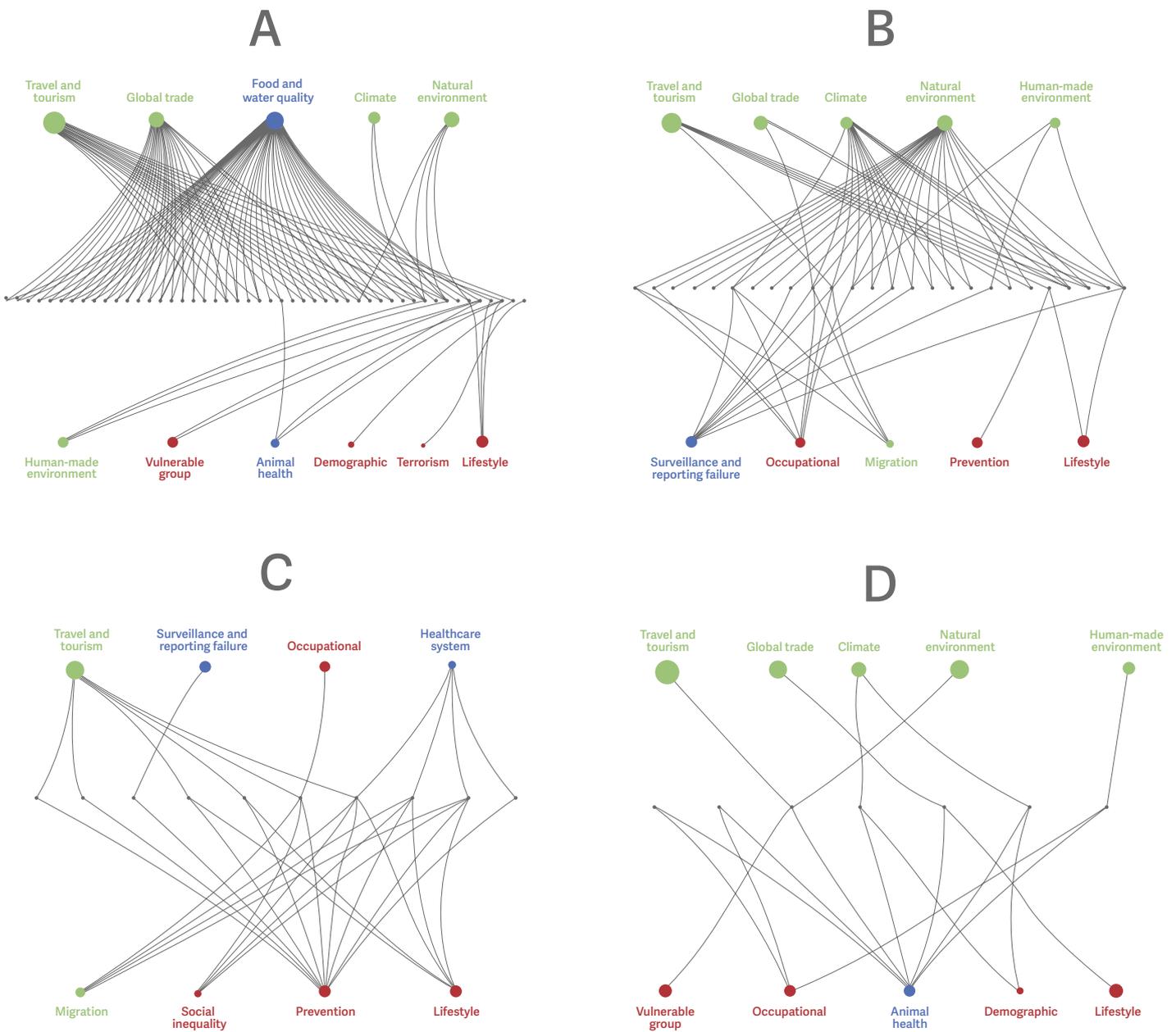
Figure 4. Infectious disease threat events (IDTEs), by contributing drivers, observed in Europe, 2008–2013

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Each black node (circle) represents and infectious disease threat event (IDTE) connected with black lines to contributed drivers. The 3 IDTE general categories are represented by green (globalization and environment), red (sociodemographic), and blue (public health systems) symbols, the sizes of which are proportional to the overall frequency of the driver. A) Foodborne and waterborne IDTEs. B) Vector-borne and rodent-borne IDTEs. C) Other zoonoses IDTEs. D) Vaccine preventable IDTEs.
Source: Semenza et al., 2016.

2.1. What are some of the drivers of disease emergence?

For zoonosis in general, a few domesticated animals are nearly 100 times more likely a source (Johnson et al., 2020) than all non-domesticated animals put together and most zoonosis is indirect through the food systems (Foodborne diseases) or VBDs. *Johnson et al. (2015)* in a further analysis showed zoonotic virus transmission risk relates mostly to increasingly abundant animal species with expanding ranges, through adapting to human-dominated landscapes, i.e. domesticated animals and peridomestic wildlife. They described a high proportion (91%) of these emergent viruses with wildlife associations but the majority of these were non-significant rare viruses or mostly transmitted by livestock. About 7% of these infections were from wildlife and of any importance to the burden of human disease, and only tens to hundreds of cases annually included wildlife reservoirs. For direct infection of humans from wildlife in nature, the conditions to bring these humans and animals and pathogens together are extraordinary and are therefore extremely rare.

The impact of humanity on nature is often proposed as an overarching cause for emerging pandemics and currently popular narrative to explain COVID-19. There is evidence for this association in some few diseases, but it is by no means relevant in every EID. The role of biodiversity (nature) in ecosystem stability and buffering of pathogen risk is best described by the *dilution effect* (Civitello et al., 2015). The *dilution effect* is related to *Zooprophylaxis*, proposed by *Macdonald (1957)* as a control method for malaria by increasing the availability of alternative hosts so that mosquito vectors prefer them over humans. The premise of the *dilution effect* is that higher community diversity can reduce infection levels and disease (Johnson & Thieltges, 2010). However, empirical data shows that the *dilution effect* is not generalisable and depends on landscapes, pathogen transmission mode, and community composition (Macdonald, 1957; McCallum, 2015; Faust et al., 2017). The process of pathogen dynamics is complex and, in some circumstances, at least theoretically, biodiversity and certain host community conditions might paradoxically create an *amplification effect* on pathogens and parasites (Randolph & Dobson, 2012). What is important in this debate is that these dynamics are sensitive to changes in community composition, environmental factors, pathogen characteristics, and during a historic period of massive perturbation in our landscapes and biodiversity loss, some consequence to disease incidence is inevitable. This has been illustrated with the Nipah virus emergence described below (Section 3.2).

Direct infection and indirect infection through cross contamination of people, animals, or surfaces with pathogens in wildlife trade are special cases, now popularly associated with emerging disease and pandemics like COVID-19. Causal factors which determine the contamination of the source(s) and contact needed for human infection from trade can relate to the original population of wildlife in nature (and associated perturbation of ecosystems), contamination of wildlife in trade, and increased susceptibility due to stress through aggregations of animals during capture or hunting, in transport and storage, in breeding farms and markets where they

are sold (Pruvot et al., 2019; Huong et al., 2020). As the focus of this situation analysis is the role of wildlife trade in disease emergence, only zoonoses with non-domesticated animal species reservoirs are considered in any depth. We consider directly transmitted infections and those indirectly through wild animal products or food. Vector-borne disease, although accounting for about 40% of EIDs, is mostly excluded as there is little evidence to suggest wildlife trade influences VBD emergence in any substantive way (Karesh et al., 2005) and analyses of any risk is limited by the lack of data on the subject of wild meat (or wildlife trade) in VBD emergence (Loh et al., 2015), making conclusions speculative. Other wildlife zoonoses, which occur outside the wildlife trade (direct natural infection) and where there is no evidence for its occurrence in trade, will be only considered only lightly as a potential risk
or to illustrate other key points around emergence of diseases.

2.2. Novel zoonotically acquired human infections

To encompass diseases such as SARS, COVID-19, and other important emergent diseases of modern times, such as HIV/AIDs, loosely described as zoonoses, we propose an additional separate heading and terminology "emerging pathogens" and/or nEIDs of humans. Where the disease is primarily a human challenge, but where humans can also infect animals with the pathogen, they are described as zooanthroponoses. Pathogen emergence is relatively rare but apparently increasing in frequency and this may be the result of an intensifying interface, or other host, pathogen, or environmental factors. Interventions to reduce spillover risk are possible at the interface if the epidemiology is well understood, but other risk factors (e.g. intra-host pathogen changes) may be impossible to predict and there is little that can be done beyond general prevention strategies.

Weiss et al. (2022) showed high impact human infections in 2020 including; zoonotic origin, zoonosis or non-zoonosis infections causing mortality. These include important endemic infectious diseases of humans like tuberculosis, contemporary emergent infections (HIV/AIDs) and recent pandemics (COVID-19 and *Candida auris*) which have caused millions and hundreds of thousands of deaths. There are two important observations relevant to this analysis, few of these highlighted diseases are acquired from wild animals and where associated, they are peridomestic or virtually domesticated species and relatively low case numbers and certainly not pandemics. It would be true to say that none of the major infectious diseases that have had significant impact on human health in 2020 have confirmed roots in wildlife trade and only four zoonoses (as opposed to zoonotic origin) are in the list—rabies from domestic dogs and Lassa fever, hanta, and plague from peridomestic or domesticated rodents (Lassa fever and Natal multimammate mouse [*Mastomys natalensis*]; Hantavirus and deer mouse [*Peromyscus maniculatus*]; and plague and fancy rat [*Rattus norvegicus domestica*]). COVID-19 links to wildlife trade remains speculative but as a

novel emerging infectious disease (nEID) it is important. Therefore, further research to establishing an epidemiologically significant link to wildlife is equally important.

nEIDs are a much more worrying contemporary issue than most described EIDs or endemic zoonosis, but fortunately these nEIDs are relatively few (estimated around 35 over the last half century or more), whilst there are about 900 different pathogens present in animal populations, around 200 cause zoonoses (WHO, 2021a). Examples of nEIDs are Ebola disease, AIDS caused by human Immunodeficiency virus, SARS, and COVID-19 coronaviruses and novel influenza viruses. nEIDs which are also emerging zoonoses, with a known animal reservoir have occurred rarely and numbers of cases are low (e.g. zoonotic avian influenza from poultry). MERS coronavirus is a good example of where we are progressing our understanding of its zoonotic origins. MERS-CoV emerged in Saudi Arabia in 2012 and continues to cause human infections, mostly acquired nosocomially, with 35% case fatality rates. For MERS-CoV there is convincing phylogenetic and epidemiological evidence that it can be acquired from Dromedary camels (probable natural reservoir) with 70 to nearly 100% seroprevalence rate (Zumla et al., 2016; Banerjee et al., 2019) and between 0–19.8% infection rates reported (Eckstein et al., 2021; Holloway et al., 2021).

Marburg virus disease (MVD) is a filovirus, an RNA virus of the same family than Ebola virus (Filoviridae) (WHO, 2021f). It affects primates, causing sporadic outbreaks of severe haemorrhagic fever in Africa. *Rousettus aegyptiacus*, an African fruit bat of the *Pteropodidae* family, are considered the natural hosts of Marburg virus and do not show signs of disease (CDC, 2021b). The Marburg virus was

first discovered in 1967 after outbreaks in laboratories located in Marburg and Frankfurt in Germany, and Belgrade (Serbia) (Siegert et al., 1967a; CDC, 2021b). The first people exposed to the virus were laboratory workers in contact with African green monkeys (*Cercopithecus aethiops*), or tissues, imported from Uganda; followed by family members and medical personnel. 31 people fell ill during the 1967 outbreak and seven died during this event. The precise initial zoonotic pathway for Marburg is unknown (CDC, 2021b), but unprotected exposure to African fruit bats excretions or aerosols (e.g. mines and caves) or infected non-human primates (e.g. occupational risk), are the most likely exposure routes. Following the initial spillover from the animal host to humans, Marburg virus spreads among people through direct human-to-human contact and indirectly through contaminated objects (i.e. fomites) (WHO, 2021f; CDC, 2021b). The risk of exposure is higher among those in contact with African fruit bats and infected primates (including people) (CDC, 2021b).

Another disease with epidemiological clarity is Nipah virus from fruit bats (reservoir) which was first reported in Malaysia in 1998 and subsequently in South Asia in humans. The route of infection involved bats contaminating fruit handled by people and/or infecting pigs as an intermediate host, to then infect people in contact with the pigs (Field, 2009). Other example is monkeypox virus, endemic to regions in Africa. Monkeypox virus was first recognised in 1958 in captive primates (Reed et al., 2004) and the first reported human cases were in 1970 in Democratic Republic of the Congo (Breman, 2000; Hutson et al., 2007). The main Monkeypox animal reservoir is unknown (Reynolds et al., 2007) but several species are susceptible to Monkeypox infection (CDC, NCEZID & DHCPP, 2015). It can be

Box 2. Directionally of pathogen transmission
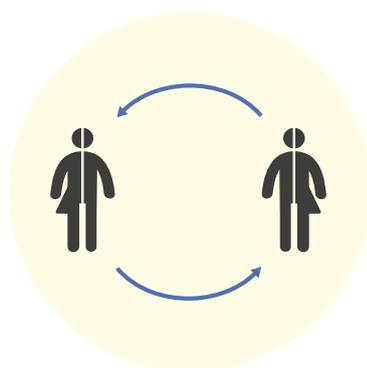
Zoonosis (or Anthropozoonosis)

Any disease or infection that is naturally transmissible from vertebrate animals (animal reservoir) to humans (WHO 2020a); either directly – via contact or aerosol, or indirectly – via food, fomite or vector (usually arthropods).

Examples: Rabies, Hendra, BSE, Echinococcosis, West Nile virus, Lyme disease, Zika, Malaria, Chagas disease, Cysticercosis, Salmonellosis, MERS, SARS, among others.
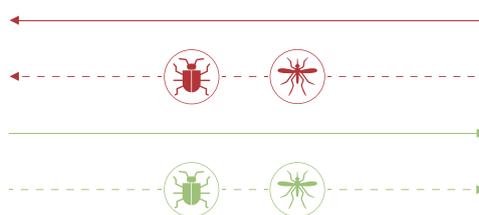
Zooanthroponosis (or Reverse Zoonosis)

Infection or disease that primarily affects humans but is naturally transmissible to animals (with the reservoir or maintenance host being humans)

Examples: *Mycobacterium tuberculosis*, SARS-CoV-2, *Giardia intestinalis*, Influenza A, Campylobacter, Cryptosporidium, *Mycobacterium tuberculosis*, Zika virus, yellow fever, and others.
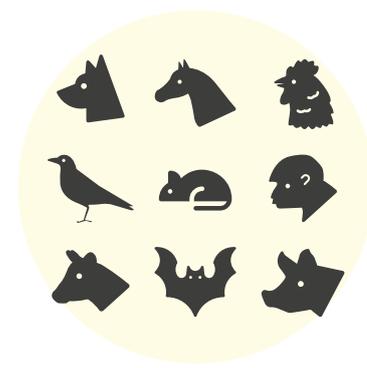
Anthroponosis

Infection or disease that is naturally maintained and transmitted from human-to-humans, with or without vectors.

Examples: Malaria, SARS, MERS, SARS-CoV-2, Norovirus, Mycobacterium tuberculosis, Measles, Mumps, Varicella Zoster virus, Variola virus, and others.

Source: Prepared by the report authors.

Malaria antigen testing.
Photo © Michael D. Kock

Ornithological studies in Lake Chuali, Mozambique.
Photo © Michael D. Kock

acquired from handling infected wild animals (i.e. primates and rodents) suffering sylvatic cycles, but human-to-human transmission is the most common route of infection (WHO, 2021b). Neither of these diseases would be described as an emerging disease by the Lederberg criteria as they are established more than 20 years and more or less static now in incidence, although MERS has clear pandemic risk.

These are also indirect zoonoses requiring the anthropogenic bridge of farming, as is the case of Nipah (i.e. pigs), and hunting/contact/trade for Monkey pox to establish infection. When an important element in the chain of transmission is broken, these zoonoses disappear so they are relatively easily managed. Cessation of pig farming adjacent to fruit farms (and bats) controlled Nipah and it is likely that if large scale camel farming were reduced or stopped in the Middle East the risk of MERS would dissipate. There is evidence of higher infection prevalence with larger herd sizes (Holloway et al., 2021). Completely stopping camel herding in the Middle East and Africa is very unlikely, but reversion to more traditional herds might well be the only way to put the disease back in the box. Current human infection prevention and control interventions are aimed at personal hygiene and the use of protective gear while handling dromedaries, regular testing of camels, strict animal movement regulations, and prevention of individuals who are at high-risk of developing a severe infection from being in contact with camels, including bodily fluids and camel products (WHO, 2019; BMJ Best Practice, 2021), but without a system change these measures may not be adequate to prevent spillover and a future pandemic.

In many other so-called zoonoses, such as COVID-19 and SARS, we do not understand the epidemiology and evidence for zoonotic reservoirs is absent. We therefore need to be much more cautious in how we describe the disease, to avoid apportioning risk or blame on wildlife, and in particular taking actions that are not likely beneficial. There might be reservoirs, but alternate evolutionary pathways also are likely, including single event spillover of organisms by chance, followed by rapid adaptation and change in the virus genome in the human population, or via serial passage in intermediate abundant animal hosts such as farmed animals. MERS-CoV may well have evolved originally from bats, but bats are now irrelevant, with a sound domesticated animal host in the camel, where the real risk remains for humans (Zumla et al., 2016).

For EID, the role of wildlife species is a chance factor in emergence requiring contact, and wildlife trade may generate regular passive spillover of a novel organism, at an intensifying interface that would not otherwise naturally occur, contributing to evolution of a pathogen and its emergence. Therefore, it is necessary to understand the disease risk in the specific context of wildlife trade, the supply chain, and current practices. This general pathway to EID was simplified in a diagram by Wolfe et al. (2007) (reproduced in Figure 5) which shows the five stages of zoonotic origin diseases; from ongoing zoonosis to subsequent adaptation and human disease without ongoing zoonotic transmission (i.e. human-to-human transmission).

STAGE   **to humans**

5 Exclusive human agent	Only from humans
4 Long outbreak	From animals or (many cycles) humans
3 Limited Outbreak	From animals or (few cycles) humans
2 Primary infection	Only from animals
1 Agent only in animals	None

Rabies   Ebola   Dengue   HIV-1 M

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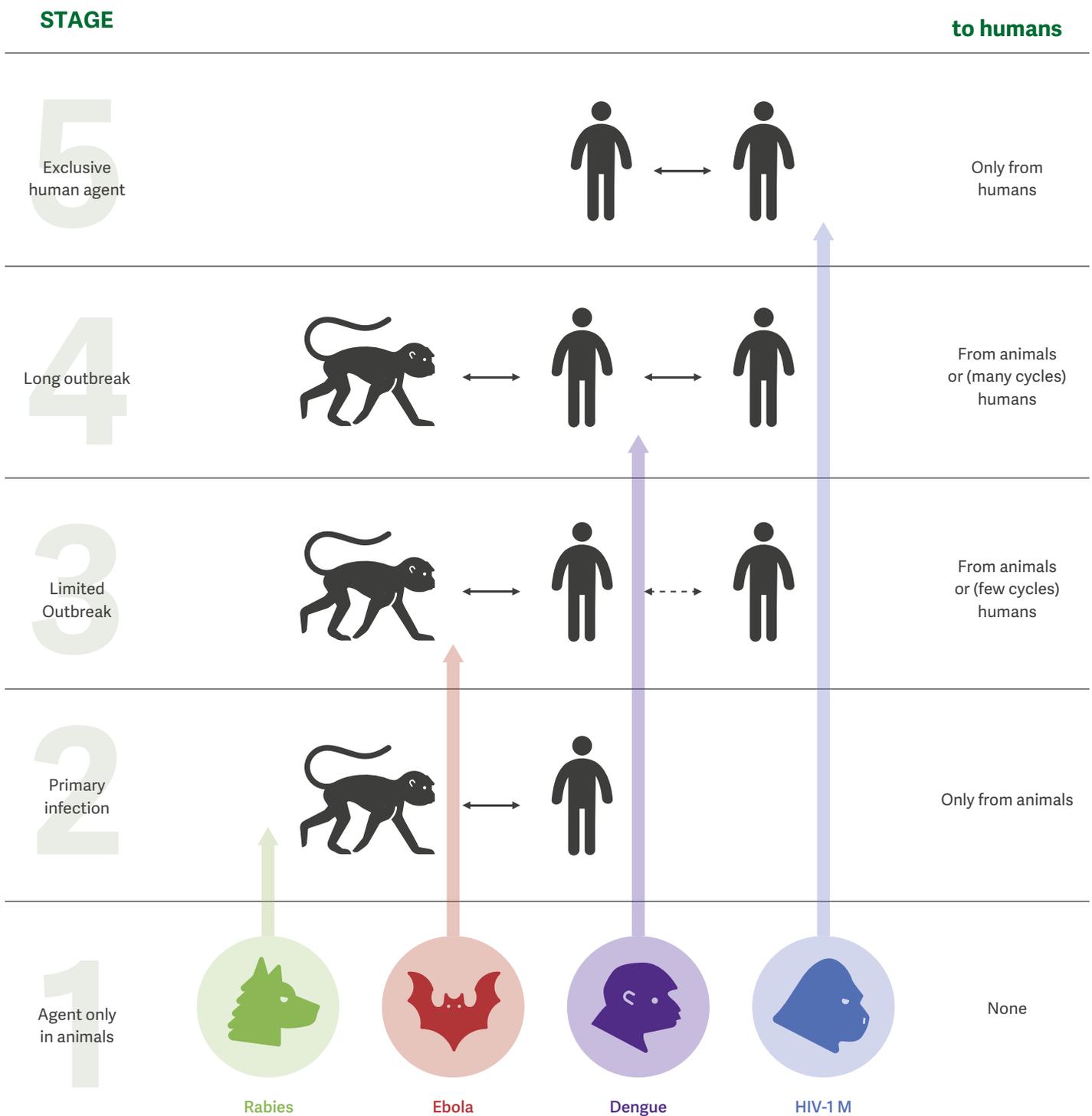
Figure 5. Illustration of the five stages through pathogens adapt to cause diseases confined to humans

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The four diseases show different stages reached in an emerging
diseases process, ranging from rabies (still acquired only from animals) to HIV-1 (now acquired
only from humans).
Source: Adapted from Wolfe et al., 2007.

2.3. One Health

The One Health integrative approach acknowledges the closed interconnections and interdependency at the interface between humans, animals, and the environment (see Figure 5) (Parkes et al., 2005; Rock et al., 2009; Coker et al., 2011; Zinsstag et al., 2011). It is interdisciplinary in principle and requires transdisciplinarity – seeking common understanding – to pursue a sustainable balance between the health of people, animals, and ecosystems alike (WHO & TDR, 2012; Queenan, 2017; FAO, OIE, WHO, and UNEP, 2021). This approach has been partly borne of the perceived crises in emerging disease over recent decades (Karesh et al., 2012; Wallace et al., 2015; Lainé & Morand, 2020), encouraging a better understanding of risk and a whole of society view to reduce the risks of disease occurrence in different ecologies associated with anthropogenic global change. A number of institutions and agencies have taken on the mandate for zoonosis and emerging infectious disease which have been identified as key One Health challenges.

The overall goal of One Health is to promote healthy humans, animals, plants, and ecosystems. In alignment with SDG 2, 3 and the GHSA, organisations such WHO, FAO, OIE have formed a tripartite One Health policy to tackle the risks to public health, animal health and global health security coming from the human-animal-ecosystem interface (FAO, OIE & WHO, 2010). However, and much against the original concepts of One Health, these agencies have narrowed the field down in accordance with their mandates. As a consequence, One Health approach has been followed through to some extent in regional and national human and animal (domesticated) health authorities but also with deficiencies. They are adopting, at least initially, a focus on AMR, zoonosis and food borne diseases. However, they are not competent, mandated, or instructed to handle the intersections between these issues and environment, ecosystems, or wildlife health; a major gap in operationalising the paradigm. Recently, to address this gap, a One Health Council was formed with the tripartite and UNEP which is a start towards addressing this major gap (Waage & Yap, 2015).

Local and international interdisciplinary networks will play a major role in identifying, preventing and adapting to strategically respond to current and future health challenges resulting from climate change (Di Marco et al., 2020; Phillips et al., 2020). A one health approach – that accounts for the links between the environment, human, animal, fungi and plant health – has shown social and economic benefits (Schelling et al., 2005; Paternoster et al., 2017) and substantial positive impacts on public health (Watts et al., 2015). Getting a clear epidemiological picture of the evolution of multi-species infections and communicating this to the public and decision-making is essential to promote common understanding, amongst not only scientists and academics but ordinary people who are at the human-animal-ecosystem interface. For example, evolution of new microorganisms or infections of new species involves complex pathways, multiple sources, and novel interactions and rarely simple solutions. This includes for the microorganisms themselves, which undergo genetic recombination, reassortment

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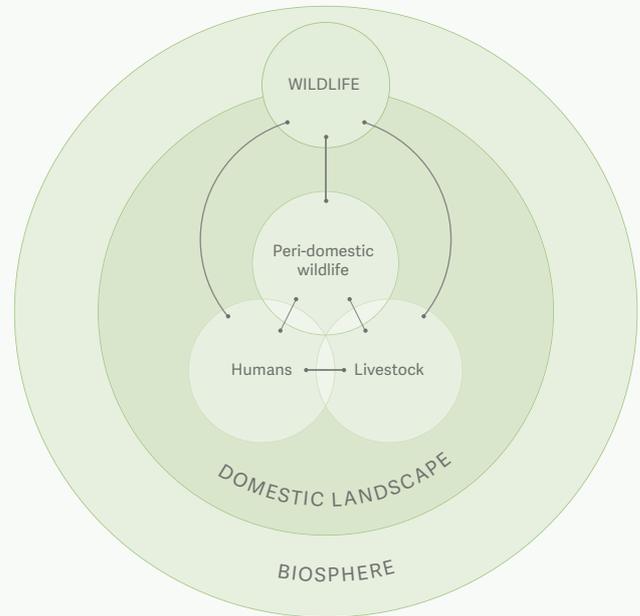
Figure 6. One Health context-interface between humans, animals, and the environment

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Pathogen flow at the wildlife–livestock–human interface. Arrows indicate direct, indirect, or vector-borne candidate pathogen flow. In each host species there is a vast array of constantly evolving microorganisms, some of which are pathogenic in the host. These are a source of new organisms for other host species, some of which may be pathogenic in the new host or may evolve in the new host to become pathogenic. If the pathogen is also transmissible in the new host species, then a new transmission cycle may be established. The rate and direction of candidate pathogen flow will depend on the nature and intensity of interaction between wildlife, livestock, and human compartments and the characteristics of the compartments
Source: Adapted by the report authors from Jones et al., 2013.

or mutation over varying timescales. Novel strains and host-pathogen interactions will arise generically and are mediated, facilitated, or eliminated through interactions between species, microbial to mega-vertebrates. However, for the outcome of these chance or circumstantially directed events to result in a novel pathogen or a zoonosis is, in truth, extremely rare, and with most pathogens unable to pass what is known as the species barrier (Sansonetti, 2006). There are estimated to be billions of types of microorganisms (including viruses, bacteria, fungi, protozoa, and helminths) and only about 1400 of these are human pathogens arisen over human history; with many disappearing as well or becoming non-pathogenic ("Microbiology by numbers," 2011) ∎

3 ‖ Wildlife trade

Having clarity on which aspects of wildlife trade are of potential concern for disease transmission, whether zoonosis or EID, is important, as is understanding the associated risks and potential impacts (Karesh et al., 2005). Across virtually all continents, natural biological resources – wild plants, animals, fungi, their parts and derivatives – sustain the livelihoods of hundreds of millions of people in developed and developing countries, especially IPLCs (Roe et al., 2020). The international commercial trade (legal or illegal) is one of the main threats to biodiversity (Butchart et al., 2010; Fukushima, Mammola & Cardoso, 2020) and a polarising topic within the conservation community (Bennett, Underwood & Milner-Gulland, 2021).

We focus on wildlife trade associated with terrestrial vertebrates, especially mammals and birds, because of the potential role of these groups in spillover and zoonotic incidents (Grace et al., 2012a; Li et al., 2019). Here, we do not consider natural resource use in indigenous settings for local consumption other than in the context of a general consideration of wild meat (non-commercial subsistence use) and hunting or butchering of wildlife. This is because local subsistence (whether truly local or part of regional or international commercial activities) wildlife consumption appears to have low zoonosis incidence even if some is undocumented or unreported (Kurpiers et al., 2016; Vliet et al., 2017). Possible reasons for this could be simply that majority of hunted-meat comes from healthy populations, whilst sick wildlife is cryptic and because local use of species for subsistence purposes leading into commercial supply chains is relatively small in volume in comparison to commercial harvesting and farming (Charity & Ferreira, 2020). In some circumstances, like hunting of primates and great apes in particular, it has been argued there is significant risk of contributing to EID or zoonoses internationally (Karesh et al., 2005; Karesh & Noble, 2009; Bezerra-Santos et al., 2021). Actual evidence of zoonosis from this source is slim but viral host switching remains a serious concern at this interface.

Major harvesting systems and extractive industries, such as mining, logging, fishing, and aquaculture, have been associated with disease emergence (e.g. Ebola virus disease, Marburg's virus; Crimean-Congo Haemorrhagic Fever Virus; (Chai, Darwin Murrell & Lymbery, 2005; Towner et al., 2006; Swanepoel et al., 2007; Olivero et al., 2017; Evans et al., 2021). We do not discuss these in detail under wildlife trade because of their mostly indirect associations with such drivers as landscape change and human intrusion rather than trade itself. Food borne bacterial diseases from fish is also a significant problem but beyond the scope of this analysis (Chai, Darwin Murrell & Lymbery, 2005).

Globally, the consumption of wild meat is extensive and a widely accepted practice in many of the countries where it occurs, despite the associated risk of zoonosis and even some discrimination when given different terms (i.e., bushmeat / game meat) according the cultural context it happens. For example, in Europe there has been an increase in the acceptance, demand, and production of wild meat (or "game") due to positive perspectives as a "healthy and environmentally friendly" alternative to meat from domesticated animals (Chakanya et al., 2020). Many virus, bacteria, and parasites are detected in wild rabbits (*Oryctolagus cuniculus*), European brown hares (*Lepus europaeus*), roe deer (*Capreolus capreolus*), and wild boars (*Sus scrofa*) (e.g. Hepatitis E virus [HEV], Toxoplasma gondii, Swine Brucellosis, Trichinella spiralis, among others) but national food security institutions have developed regulatory frameworks to oversee the consumption of wild species, from local household consumption to international trade of meat and products (Hammerschmidt et al., 2017; Meier & Ryser-Degiorgis, 2018; Diaz, Warren & Oster, 2020; Chakanya et al., 2020).

The value chain for wildlife trade (i.e. the process or activities by which "traders" add value to a wildlife product) starts from locally sourced and used (e.g. barter and exchange between local harvesters, suppliers and regional markets) to locally sourced and traded to international markets (e.g. fur trade, primates in medical research and some pet trades) (Figure 6). Traded animals from a range of species are harvested from the wild, whereas other animals are captive-bred or farm-raised (farmed); many markets are also supplied by a combination of both wild-capture and captive-bred specimens (wild, domesticated, or semi-domesticated animals) (Lyons, Natusch & Jenkins, 2017). Commercial wildlife trade in which both source and end markets are in the same country, referred to here as domestic trade, is sometimes more significant than cross-border, international, trade in terms of volumes and impacts; examples include the wild meat trade in Central Africa and the commercialisation of game species in Europe such as wild boar, pheasants, deer, among others. Various attempts have been made to get to grips with the wild meat trade and they show a complex, culturally diverse and significant commercial activity contributing to food security of people in certain regions of the world such as the Congo Basin in Africa (Chardonnet et al., 1995; van Velden, Wilson & Biggs, 2018). This domestic and international trade can involve intricate networks of harvesters, suppliers, transport routes (e.g. to urban centres or across borders), processors, distribution hubs, and markets, where many species can be kept together under sanitary conditions which vary according to national regulations and the extent of monitoring (Roe, 2008; Smith et al., 2009). Domestic wildlife trade can be as complex as international trade in terms of number of actors, transport networks, species, and products, making it challenging to describe these markets and associated dynamics (Fa et al., 2006; Coad et al., 2019).
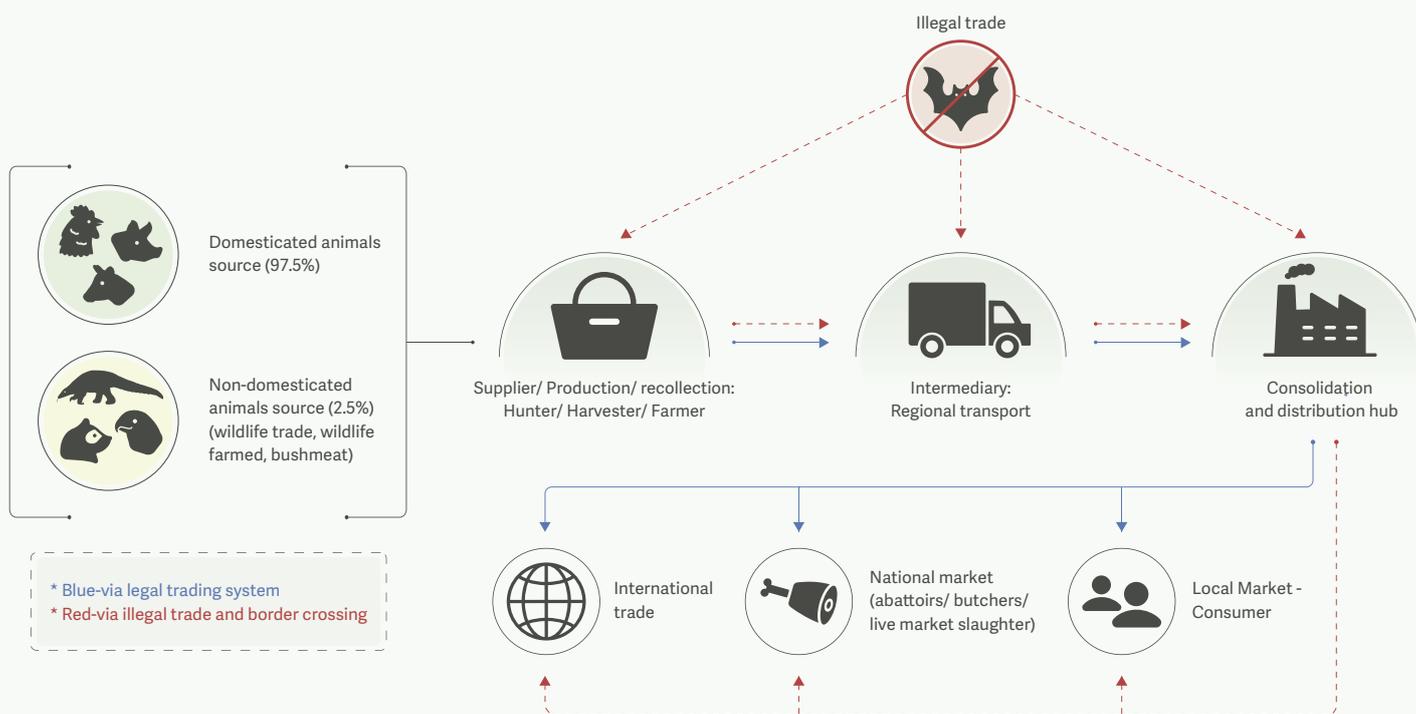
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Figure 7. Simplified meat trade chain of domesticated and non-domesticated animals.
....
Of all animal trade, 97.5% corresponds to domesticated animals whereas only 2.5% is represented by non-domesticated animals.
Source: Prepared by the report authors (created with BioRender.com).

We mainly focus on commercial openly-traded wildlife (captive or wild animals genetically distinct from non-domesticated animals animals), inclusive of parts and products derived from them; and although difficult to monitor comprehensively, there is partial and sectoral data that allows reasonable conclusions (Oldfield, 2003). We aim to demonstrate how careful use of meanings and clear focus is needed to understand and address specific problems and challenges relating to wildlife, wild animals, and emerging diseases and zoonosis. As wildlife trade has been implicated in the emergence of COVID-19, and more generally in EIDs, we explore and discuss the evidence in support of and against this supposition, expanding on the multiple social, ecological, and economic factors at play regarding the wildlife trade.

3.1. Wildlife trade in the context of sustainable/unsustainable use

The total number of people provisioned by wildlife trade for food or income on a daily basis are imprecise, but best estimates put it in the hundreds of millions (Wang et al., 2020; Roe et al., 2020), including millions of IPLC (Coad et al., 2019). The use of wild species is widespread, involving markets and actors in developed and developing countries. Whether live or dead whole organisms or their derivatives, the demand for these products spans a wide range of industries, such as food, healthcare, construction, pets; and for cultural purposes such as ornaments and luxury goods (Oldfield, 2003).

3.1.1. Positive aspects of wildlife trade

The trade in animal, fungi, and plant species, their products and derivatives has been a common practice globally since ancient civilizations ('t Sas-Rolfes et al., 2019). Wildlife trade is a common part of life today around the world and links indigenous peoples, poor, and rural communities with end consumers (Oldfield, 2003; Hutton & Leader-Williams, 2003). The use of natural resources can be consumptive (e.g. harvesting, hunting, or fishing) or non-consumptive (e.g. tourism or release fishing), for diverse purposes (i.e. primary food source, medicinal, religious, clothing and shelter, cultural, recreational or commercial). It can be legal and/or illegal, sustainable or unsustainable in terms of its impacts on species and livelihoods ('t Sas-Rolfes et al., 2019; McRae et al., 2020; Marsh et al., 2020) and often these can all be intertwined along complex supply chains.

Sustainable use is defined by the Convention on Biological Diversity as: "the use of components of biological diversity in a way and at a rate that does not lead to the long-term decline of biological diversity" (CBD, 1993). For many people, wildlife and wildlife products provide an alternative source of income in times of need, helping to maintain traditional knowledge and culture, improving the livelihoods and resilience capacity among poor, rural and remote communities, enabling millions of people to meet their physiological needs and support cultural, religious and recreational values (Oldfield, 2003; Hughes, 2003; Nasi, Taber & Van Vliet, 2011; Robinson et al., 2018; Roe et al., 2020; Lichtenstein & Cowan Ros, 2021). This deep connection can encourage community-led conservation initiatives, discouraging converting local landscapes and over-exploitation

of species just for "economically productive" uses (Oldfield, 2003; Cooney et al., 2015). Moreover, appropriate regulatory systems and effective governance can create incentives for community investment in nature, encouraging sustainable practices, which can result in positive conservation outcomes (e.g. stewardship of wildlife) and social-economic benefits for local communities, alleviating poverty, and contributing to food security (Lichtenstein, 2010; Austin & Corey, 2012; IUCN, 2016; van Velden, Wilson & Biggs, 2018). The use and trade of wildlife is driven by a number of factors – from absolute and relative poverty (e.g. protein source, income source) to for-profit commercial harvest – and when sustainable, legal and equitable, can be a valuable nature-based solution to improve rural livelihoods and support positive conservation outcomes (Challender & MacMillan, 2014; Cooney et al., 2015; IUCN, 2016; McRae et al., 2020). Demand for wildlife products internationally and related activities along supply chains has created opportunities for income generation for poor communities, especially in developing countries (Lichtenstein, 2010), therefore creating the necessary social

conditions and incentives for the implementation of sustainable use and management practices. Wildlife trade, when well-managed and accompanied by effective and equitable governance systems as well as community engagement can drive nature conservation and stewardship of biodiversity, exhibiting the value of nature to people from both utilitarian and broader cultural perspectives (Cooney et al., 2015; IUCN, 2016). A significant aspect of the wildlife trade, especially when it comes to regulation of trade, is the strong social and cultural dimension of species use and trade, and the fact that animals and plants and their derivative products can bring positive benefits to rural communities, playing an important role in their nutrition, health, livelihoods, and economy. Indigenous people own, occupy or manage land that holds 80% of the planet's biodiversity and are associated with about 40% of all terrestrial protected areas and ecologically intact landscapes (Garnier et al., 2020; Rights and Resources Initiative, 2020). This relationship varies geographically and in some continents like Asia is no longer so prevalent.

Box 3. The impact of wildlife trade bans on local livelihoods and conservation: the case of the turquoise-fronted amazon (*Amazona aestiva*) in the Gran Chaco region, Argentina

The impact of wildlife trade bans on local livelihoods and conservation projects can be illustrated by the emblematic Elé Project (1993-2006) and the sustainable use of turquoise-fronted amazon parrot (*Amazona aestiva*) in the Gran Chaco region in Argentina. The main objective of the Elé Project was habitat conservation and the sustainable management of the turquoise-fronted amazon for commercial use as a pet bird.

Historically, local people collected turquoise-fronted amazon chicks by cutting down selected trees with nests. Chicks were sold to middlemen and they reached the final markets through a long commodity chain of collectors, middlemen, stockpilers, and exporters. The unregulated high-volume trade resulted in high levels of mortality during stockpiling and transport and local collectors received an insignificant fraction of the value of the parrots in trade. The Elé project trained local harvesters to collect chicks by setting scientifically-based harvest quotas based upon a 'fixed escapement' rule of management and improved the collection method by digging a hole in the trunk instead of cutting down the trees. The collected chicks were identified with numbered rings, and trees with metal plates. The Project Elé was able to regulate trade and deliver significant livelihood benefits to the local and indigenous people countering pressures for agriculture intensification and land conversion to soybean. The surplus generated by the project enabled the creation of three protected areas and the implementation of their management plan as well as an anti-poaching activities.

Imports of wild birds to the EU were banned in 2005, following the avian flu H5N1 pandemic, as a result of the lobby from conservation organizations and European bird traders. Although avian flu originated in poultry and migrating bird populations in Asia, the ban was never revoked. The closing of this important market dismantled a well-managed programme which generated revenue to local indigenous people and protected land, resulting in increased deforestation and habitat loss. Paradoxically, while the project was closed in pursuit of the conservation of the species and following the ban, the semi-arid Chaco forests were replaced by soybean threatening not only the biodiversity of the area but also local livelihoods. The ban on chick exports to the EU illustrates how indiscriminate bans and restrictions risk being inequitable and ineffective and may inadvertently increase poverty and vulnerability. Patterns of consumption and production as well as land conversion and industrial agriculture should be revised instead.

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Source: (Rabinovich 2005; Bolkovic & Ramadori 2006; Moschione & Banchs 2006; Coconier & Lichtenstein 2014).

Management of traded species can also support habitat protection, population growth for species (McRae et al., 2020) as well as community benefits. Examples of this with little risk of introducing serious human pathogens into communities through trade are pythons in Southeast Asia and West Africa, some reptiles from Madagascar, some of the global trade in orchids, trade in southern white rhinos in South Africa (*Ceratotherium Simum*) (Knight et al., 2015) camelids in South America with vicuña fibre harvesting and trade in Andean countries (Lichtenstein, 2010), legal and sustainable trade in crocodile skins for the fashion industry, harvest and trade of hatchling Yellow-spotted River Turtles in Peru (Hutton & Leader-Williams, 2003; Bottrill et al., 2014; Knight et al., 2015; Natusch & Lyons, 2016; IUCN, 2016; Robinson et al., 2018; Hinsley et al., 2018; D'Cruze et al., 2020; Harrington et al., 2020; Hierink et al., 2020; Marsh et al., 2020). Sustainable use is particularly effective when the species are appropriately managed under community-based approaches to pursue actions consistent with conservation goals and the needs and rights of communities (Cooney et al., 2015, 2018; IUCN, 2016; Biggs et al., 2017a; McRae et al., 2020). Hence, wildlife trade, when the source populations are managed for long-term sustainability, can be a positive element to deliver the SDGs (Roe, 2008; Cooney et al., 2015). Nevertheless, there are instances where despite well-controlled settings and sustainability and sanitary practices in place, the conservation impacts could be as important as in systems with lesser control (e.g. unpredicted negative back loops). The context in which wildlife trade operates is important and should be considered in the debate considering this dichotomic perception is what leads to much of the polarisation in attitudes on the issue of use of wildlife (Bennett, Underwood & Milner-Gulland, 2021).

3.1.2. Threats from the wildlife trade

Considering the high variability of markets, actors, and drivers, one must understand the threats and risks associated with specific species and practices posed by elements throughout the wildlife trade value chain (Cooney et al., 2015; Maxwell et al., 2016; McRae et al., 2020). Drivers of trade are numerous and can include harvest incentives in source populations, incentives for processors and transporters, and heterogeneous consumers in end-markets (Hinsley et al., 2018; Sutherland, 2001; 't Sas-Rolfes et al., 2019). By appropriately targeting negative practices it is possible to maintain and maximise the positive contributions of sustainable wildlife trade to conservation and local livelihoods (CITES, 2018).

Despite efforts to achieve sustainability in terms of harvest and trade in many species in recent decades, high harvest incentives linked to high or increasing prices for some wildlife species and their products, driven in large part by international demand, has resulted in illegal harvesting and trafficking of species, undermining species conservation efforts. A good example is the international trafficking of pangolins (Challender et al., 2020a), among myriad other species (Rosen & Smith, 2010; Challender, Harrop & MacMillan, 2015a; UNODC, 2020). It can also result in detrimental effects on local ecosystems and people's livelihoods, particularly affecting incomes, assets and the well-being of indigenous people and poor communities in rural areas (UNODC, 2020). Overexploitation, in conjunction with habitat loss (mainly for agricultural purposes) and invasive species,

have been identified as the most significant threats to ecosystems and species, ecosystems and species, with intentional use recognized as a key threat for over a quarter of all threatened or Near Threatened (NT) species on the IUCN Red List (Marsh et al., 2020). While few extinctions have been documented because of international trade (e.g. Steller's Sea Cow, extirpated by whalers for their oil for lamps in Europe through intercontinental commercial exploitation (Turvey & Risley, 2006)), the overexploitation and trade (legal or illegal) in biological diversity is one of the main drivers of species decline, potentially affecting important ecological processes such as pollination and seed dispersal, and therefore forest composition, nutrient flows, and disease dynamics (Karesh et al., 2012; Harrison et al., 2013; Effiom et al., 2013; Cooney et al., 2015; IPBES, 2019). The use of vertebrate animals and wildlife products has taken place for millennia but the scale of exploitation, enhanced by globalization, now threatens many species and is a major driver of biodiversity loss (Maxwell et al., 2016). Overexploitation also poses negative impacts for many people that depend on it (Maxwell et al., 2016; Symes et al., 2018).

3.1.3. Illegal and legal international trade in wildlife species and regulation

Given the multiple social, ecological, and economic aspects of wildlife trade and its highly polarised positions taken by various communities, the need to monitor and regulate international wildlife trade and manage species populations for sustainability and ecosystem function (Duckworth et al., 2012) is obvious but inadequately addressed.

A key factor driving the international demand for wildlife species commodities is wealth (TRAFFIC, 2008; Cheng, Gao & Seale, 2015; Schwarz, Newton & Ratzimbazafy, 2017; IPBES, 2019; Stanford et al., 2020). The drivers of wildlife demand have been exacerbated by global connectivity, where consumer wealth in one community or country drives exploitation pressures in other, less wealthy communities (Marsh et al., 2020). Scarcity and high-demand of wildlife species and their products in international markets can result in a vicious cycle that intensifies illicit harvesting and uncontrolled trafficking, directly affecting animal, fungi, and plant populations in the wild resulting in socio-ecological impacts deteriorating ecosystems and people's livelihoods (IUCN, 2017a). This becomes especially severe when the management or protective measures in place in the supply areas strain local socioeconomic standards and tempt illegal actions, whilst ignoring local communities' preferences and needs (Biggs et al., 2017b; Cooney et al., 2017; van Velden et al., 2020).

The unsustainable exploitation of wildlife for international trade in mid-late 20th century, especially involving threatened and charismatic species (e.g. spotted cats, primates, crocodiles), invigorated the international community to act. This resulted in the entering into force of CITES in 1975, and during the last nearly 50 years, many civil society organizations, NGOs, and scientists have advocated governments to strengthen international and national regulations around trade and improve support for other measures such as community based natural resource management (Robinson & Bennett, 2002; Biggs et al., 2017b; Cooney et al., 2017, 2018).

Interventions to ensure trade is legal and sustainable need to be multifaceted in accordance with the intrinsic complexities of both legal and illegal wildlife trade drivers, actors, markets, and governance systems (Challender, Harrop & MacMillan, 2015a; Natusch & Lyons, 2016; Hinsley & Sas–Rolfes, 2020). Where wildlife trade is illegal and/or there is overexploitation, interventions must address the different incentives and motivations for actors along supply chains (Challender, Harrop & MacMillan, 2015a). The legal and illegal trade can have direct impacts through overexploitation of species, or indirectly such as by-catch of non-target species and introduction for commercial purposes of allochthonous species (DAISIE, 2009). As traders, both legal and illegal, adapt to different ecological circumstances, markets, and regulations, the interactions among these threats cannot be ignored, as strategies to expand and intensify production can contribute to the movement of species, increase land use change, habitat loss, and habitat degradation. This may include legislation which afford protection to species (e.g. limits or prohibits exploitation), international trade measures (e.g. CITES trade measures), seasonal, localized or size-related restrictions on offtake, devolution of access and property rights to local communities to sustainably manage harvest and trade in species, demand reduction initiatives in local or international end-markets or other context-specific measures (Challender, Harrop & MacMillan, 2015a; Biggs et al., 2017a; van Velden et al., 2020).

In response to the negative effects of wildlife trade, tougher control measures have been implemented nationally and internationally by governments, influenced to some extent by a range of actors ('t Sas-Rolfes et al., 2019). However, inadequate interventions risk the trade shifting to different yet equally unsustainable practices and may ultimately perversely increase demand for species and products and negatively impact the livelihood of millions of people (Coconier & Lichtenstein, 2014). The international legal wildlife trade and its products is a multibillion-dollar industry and has significantly increased over the past 4-5 decades in both volume and value (Harfoot et al., 2018; World Bank, 2019; UNODC, 2020).

We can broadly separate the trade into three sections:

a) The wildlife species farming (e.g. legal fur trade) is now valued at about US$ 45 billion annually globally (Fur Commission USA, 2020). A high proportion of this trade is in East Asia and supplied through legal captive breeding of foxes, raccoons, mink and other fur species. In 2013–2014, 87.2 million mink pelts were produced around the world, worth a total of £ 2.2 billion (US$3.11 billion), with 35 million produced by China alone. China also remains one of the biggest producers of fox pelts, and together with Finland was responsible for 91% of the 7.8 million fox furs produced globally in 2013–2014 (Ellis-Petersen, 2015). It should be emphasised that much wildlife trade (including for example mink, a species highly susceptible to human SARS-CoV-2 transmission, zooanthroponosis) is not CITES-regulated and these industries, including other products than fur for pharmacopeia and wildlife-food culture. Unregulated and poorly regulated wildlife farming carry a significant risk of being a pathway or reservoir for emergent diseases caused by these organisms. In addition to unrecorded legal trade in a number of wild or semi-domesticated wildlife, the illegal trade volumes suggested could be as large again as legal trade but as with much of the evidence in this area, is based on relatively little data and poorly documented ('t Sas-Rolfes et al., 2019; UNODC, 2020).
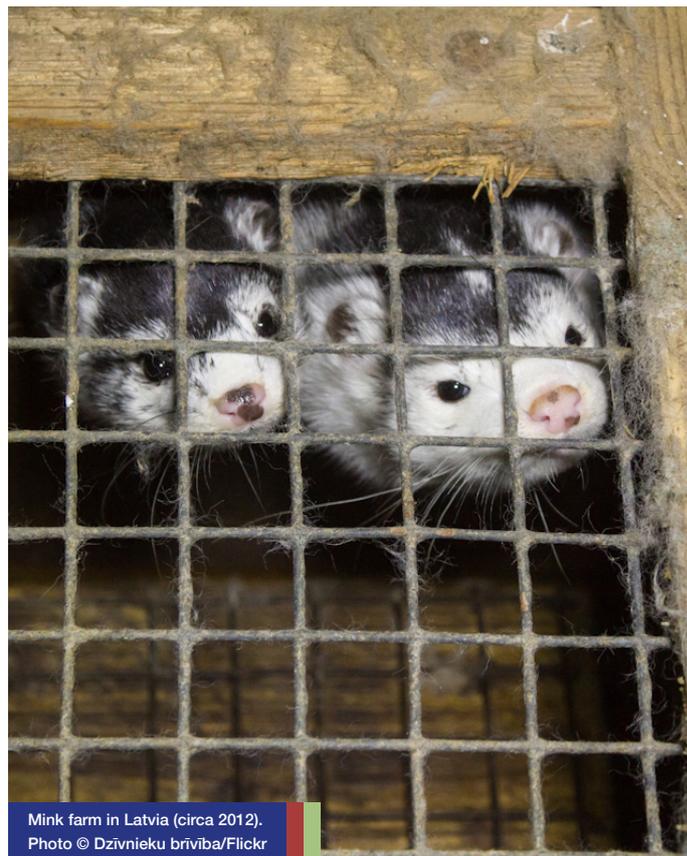
Mink farm in Latvia (circa 2012).
Photo © Dzīvnieku brīvība/Flickr

Forest rats for sale in Tomohon Traditional Market, North Sulawesi, Indonesia.
Photo © Margaret F. Kinnaird

b) An unknown percentage of the overall trade is illegal and unregulated, and this is a key threat to the long-term survival of many populations and species. For example, the Radiated Tortoise will likely not go extinct in the foreseeable future, as there are thousands in captivity and they breed effortlessly; but the hyper-exploitation of the wild populations, going from several million adults in the 1980s to under a million (and likely much less – surveys are not frequent enough to keep up) now means both disrupted ecological webs and a lost opportunity for sustainable livelihoods. Therefore, there is a need to tackle the unsustainable exploitation and illegal international wildlife trade where there is a strong biodiversity conservation component (Cooney et al., 2015; 't Sas-Rolfes et al., 2019; McRae et al., 2020).

Wild meat hanging outside a butcher (Covered Market, Oxford, UK).
Photo © allispossible.org.uk/Flickr

c) Legally traded wildlife under CITES regulation. CITES regulates the legal international trade in the species listed in its three Appendices and aims to ensure that this trade – in close to 38,000 species of animals and plants – is not detrimental to their survival in the wild (CITES, 2020b). Entering into force in 1975, CITES is the primary multilateral environmental agreement regulating international wildlife trade. It is a treaty implemented by its 183 member countries (Parties) through national legislation. It aims to ensure i) sustainability, i.e. the trade does not risk the survival of the species in the wild, ii) legality, that specimens have been obtained in accordance with national laws and regulations; and iii) traceability, meaning a product can be tracked to its origins, even after processing. The CITES Trade Database (https://trade.cites.org/) is the primary data source for legal, international wildlife trade in CITES-listed species, containing data from annual reports compiled by CITES Parties. Harfoot et al. (2018) found that the average exported yearly volume of legal wildlife increased from 9 million whole organism equivalents (WOEs) between 1975–1985 to 10 million WOEs between 2005–2014; with plants being the primary export in terms of volume (1.80 billion reported by exporters), followed by reptiles (152 million), invertebrates (79.8 million), birds (24.1 million), mammals (13 million), fish (12.8 million) and amphibians (1.07 million). A large proportion of this increase is accounted for by production systems shifting towards captive-sourced instead of wild-sourced products and live mammals, birds, reptiles, invertebrates, and artificially propagated plants. Despite criticism (Challender, Harrop & MacMillan, 2015b), the convention has proven its relevance by advancing sustainable practices of using species and harvesting products, minimizing unsustainable exploitation of some species, and promoting alternatives to the capture of wild animals, such as ranching, farming and captive breeding (Hutton & Webb, 2003; Barrios & Cremieux, 2018; CONABIO, 2018).

Understanding the distinct compartments, value chain, and volume of trade is important epidemiologically and in the determination of risk. The observation of an increasing trend in live animals originating from captive facilities in international CITES-regulated trade (versus trade in products or derivatives) is very important epidemiologically, especially when considering risk of unknown pathogens and their amplification (discussed in section 2).

3.2. Volumes, trends, and characteristics of wildlife trade in the context of disease risk

Wildlife trade data are incomplete but can provide knowledge on the extent of wildlife trade for some species, trade routes, source, and destination markets (Coconier & Lichtenstein, 2014; Natusch & Lyons, 2016; Kasterine & Lichtenstein, 2018; Harfoot et al., 2018; UNODC, 2020). Wildlife trade is dynamic, with the uses, products, species, trade routes, and markets varying across scales, time, and locations. The many dimensions of wildlife trade hamper efforts to advance our knowledge of wildlife trade practices, volumes, and use of many species, even within the legal trade of wildlife (Challender, Harrop & MacMillan, 2015a). Considering the intrinsic heterogeneous nature of legal wildlife trade, attempting to define and measure Illegal Wildlife Trade has proven to be extremely challenging, if not impossible, due to its clandestine nature ('t Sas-Rolfes et al., 2019). Currently, there are no accurate global estimates of the species involved or volumes; various estimates suggest this trade to be worth billions of dollars ('t Sas-Rolfes et al., 2019; TRAFFIC, 2020; UNODC, 2020).

A key result from this situation analysis is the finding that there is no consistent surveillance of the disease and public health aspects of the wildlife trade, internationally or in many cases at national level. Some countries include zoonosis on notifiable disease lists, for example Lyme's disease in the US, whilst in others, like in the United Kingdom, it is not notifiable. The notifiable status leads to more active surveillance and reporting, but this particular zoonosis has little or nothing to do with trade. In China, they have zoonotic disease lists, as do most countries, that they prioritise and designate for monitoring and control according to OIE and WHO guidance, but few are notifiable. For zoonosis the vast majority of the work is on detection and control of zoonosis in the domesticated and companion animal industry and not for wildlife. For example, in China wildlife disease is a split responsibility between veterinary departments and forest departments, and surveillance for wildlife disease does not work effectively and is only dealt with, sporadically, where it is considered a potential threat to domesticated animal industry or a zoonotic outbreak. It is mostly a paper exercise, multisectoral, poorly integrated and with some research from a few institutions and collaborating groups (Li In Review, 2021). Wildlife is a relatively unregulated area in terms of captivity, harvesting, production and trade in China and in many other countries, with the veterinary departments without capacity or knowledge to effectively intervene. In sub-Saharan Africa, only where there is entry of wildlife products into the formal animal-based food system (e.g. southern Africa) is there conventional sanitary management through abattoirs and application of veterinary regulation. This only captures a few species in wildlife trade for surveillance and some of these examples are referenced in this analysis (Karesh, Kock & Machalaba, 2020). This global lack of capacity or Institutions equipped to specifically deal with wildlife, and associated health risks, has been brought to the attention of the global health community recently (IUCN, 2020).

This contrasts with the transparent and recorded domesticated animal production and trade and associated notifiable diseases (OIE, 2013) (see Box 1). The human-livestock interface and associated animal trade is thousands of years old and dwarfs the wildlife trade in size. It involves local and international movements of animals and animal products. Diseases associated with trade movements and risks associated with source populations involved in trade and susceptibilities of recipient country animal industries led to development in 1963 of specific regulations and standards on trade and disease managed through the OIE and CODEX Alimentarius (FAO & WHO, 2021) with national veterinary services representation and implementation. It involves trade agreements based on sanitary conditions and disease control which facilitates trade between nations. It sets conditions on knowledge of infection risk, survey date updating and reporting of disease as it happens to enable closure of borders, trade, quarantine, and other mitigation measures. It has helped to reduce infection risk but cannot prevent infection completely as many gaps remain in pathogen movement through non-live-animal pathways which are also not captured by food trade controls, such as recycling food internationally in the animal feed production system which are known routes of transmission for porcine epidemic diarrhoea virus and African swine fever virus over recent decades (Dee et al., 2020; OIE, 2021a; Niederwerder, 2021).

Box 4. Domesticatedanimal trade, how does it work?

Early detection and quarantine measures are at the heart of the portfolio of preventive measures currently in use to stop the transboundary movement of pathogens of economic or public health importance. Since 1995, the World Trade Organisation (WTO) provides the regulatory framework of sanitary and phytosanitary measures (SPS) for international animal trade, which includes live animal trade and products and the FAO *Codex Alimentarius* provides international standards for food systems. The objective of the international agreements is to protect human, animal, and plant life from pathogens and other threats through these sources. The role of the World Organisation for Animal Health (OIE) is to guide and provide countries with the necessary epidemiological information and standards (e.g., diagnosis and test protocols) so each nation can devise their own strategies. While countries can impose restrictions to the importation of animals based on disease risk, many nations do not enact this type of measures as they could be challenged based on international trade agreements that prohibit the implementation of barriers to international animal movement based on disease risk.

Source: Prepared by the report authors.

The basis for current international disease prevention systems is monitoring and reporting of OIE-listed animal diseases at the national level in traded domesticated species. A database is set up for animal diseases of economic importance (OIE-listed diseases) and is publicly available (OIE, 2021b). This database includes the species considered as hosts (officially which sometimes excludes wildlife hosts, e.g. PPR virus) for the disease. Veterinary services provide regular reporting on OIE-listed diseases and disease outbreaks in domesticated and wild animals to OIE (but in the case of diseases where the wildlife hosts are not listed wildlife events need not be reported). Despite this anomaly, this process to facilitate trade and disease control during animal movements and transboundary commerce. However, wildlife disease reporting of non-OIE Listed diseases of wildlife to OIE through a designated focal point in each country, is voluntary, non-systematic, not capturing many events (OIE, 2020a), remaining a big gap in implementation of global reduction in disease risk. There is an increasing need to unravel the multiple factors that create high disease-risk conditions in the wildlife trade. Even in the case of regulated trade, data is lacking on the threat it poses for pandemic risks. Despite this, opinions are strong (Kolby, 2020). In order to broaden current wildlife trade management strategies – which are aimed at species conservation and livelihood protection – to include disease risk mitigation, the multiple aspects of trade need to be addressed. For some areas, such as Southeast Asia, there have been significant advances with detailed studies on the dynamics of trade (i.e. supply-chain structure its characteristics and actors, and the end-market features), the socio-ecological impacts, and the legislation and governance overseeing the national wildlife trade (Krishnasamy & Zavagli, 2020). For other regions, such as South America, important advances have been made (Rushton et al., 2005; Regueira & Bernard, 2012; Chaves, Monroe & Sieving, 2019; Charity & Ferreira, 2020; Morcatty et al., 2020) but there are still significant gaps on supply-chain structure, governance and legislation, volumes, and other relevant data ∎

4 || Threat of zoonosis and/or emerging pathogens from animal trade – the evidence

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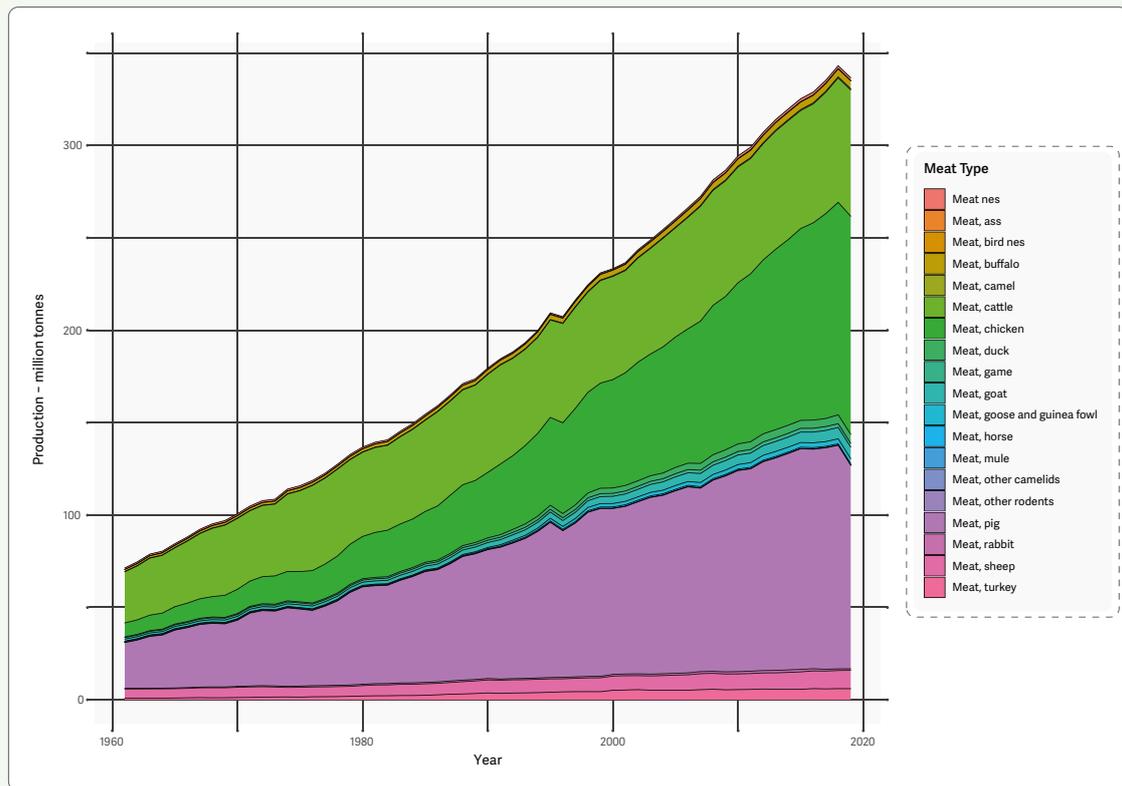
Figure 8. Global livestock meat production by animal source (1961–2019)

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Figure 8 shows the total global livestock meat production by animal source (1961–2019).
Source: Prepared by the report authors using FAO, 2021.

4.1. Volumes

Appropriately managing zoonosis and EID requires a holistic approach to address the role of animal populations (domesticated and wild). For wildlife in particular, the true role that wild species play in zoonoses and EID should not be taken out of context and should be considered proportionately to its size. Domesticated animal biomass now represents 96% of non-human mammal biomass on Earth while terrestrial wild mammals only 2% (Bar-On, Phillips & Milo, 2018). Domesticated animals are primarily food animals, providing a significant proportion of protein nutrition for humans (~25%), with a considerable companion animal population, contributing to human well-being. A smaller number are still used for transport and other activities such as ploughing in agriculture and for livestock and human security as well as horn, hair and wool products. Domesticated animal industry includes breeding and management extensively and intensively, by individuals to corporations and a complex value chain from the local to the global. The trend has been consolidation and increasing sizes of enterprises in animal production along with the rapid growth in demand globally for animal-based products. Extensive trade and regulatory systems have evolved for domesticated species partly as a direct result of animal diseases and associated risks of epidemics from moving animals around the world.

The disease aspects are largely managed by OIE, but FAO also plays a significant role. For zoonosis, WHO acts in their control and management but for a relatively small set of priority diseases (WHO & TDR, 2012). Over the last decade, FAO, OIE, and WHO created joint information systems, such as GLEW and GLEWS+ (FAO, OIE & WHO, 2006, 2021).

It is important to highlight the volume differences in, for example, the meat trade which is probably the highest risk trade for food borne zoonosis and these are shown in Figure 7. Therefore, in relation to disease risk most important distinction between the domesticated animal and wildlife trade is in relation to volumes.

4.1.1. Domesticated animal meat

In tonnage of meat (and dairy) production, domesticated animals provide the vast majority (99%) of the global source of meat (320 million tonnes a year) (Ritchie, 2017), the rest coming from non-domesticated farming or wild meat sources. A high proportion of domesticated animal meat comes from Asia and most wild sourced meat from South America and Africa (see Figure 8)
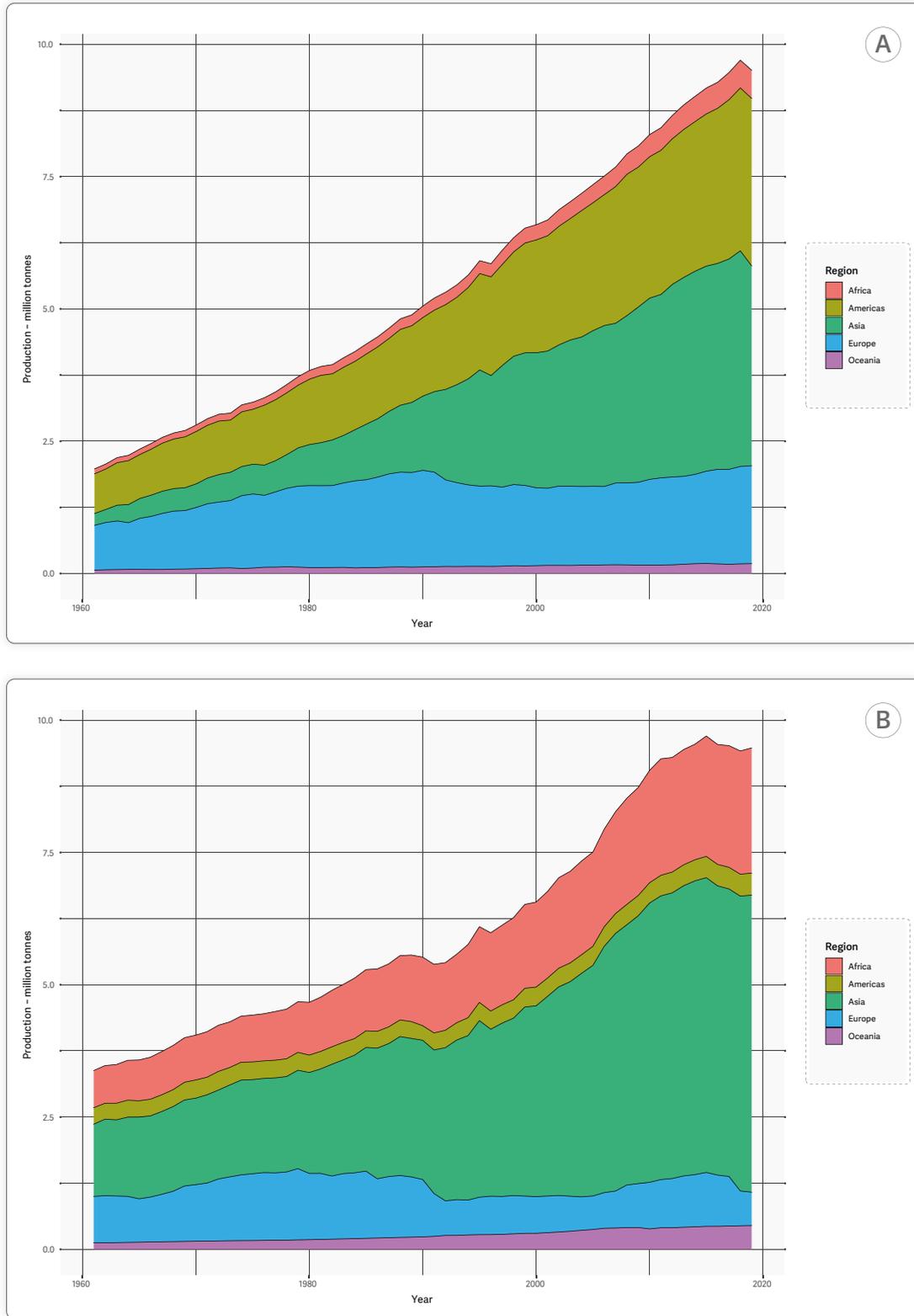
....
Figure 9. Regional proportion and changes in global livestock meat production overtime (1961-2019) globally (inclusive of all animal meat products)
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Panel (a) shows the total global regional production of conventional meat in comparison to the total global production of unconventional meat sources in panel (b).
Source: Prepared by the report authors using FAO, 2021.

4.1.2. Wildlife meat

It must be recognised though that much wild meat production is informal and at a local level and so it is not captured in formal meat production statistics. A lot of meat is consumed directly and not traded so is again not captured in datasets, for instance in North America it is estimated that 16 million people hunt for food even if primarily for recreation (see The North American Wild Harvest Initiative (WHI), (IUCN, 2017b). The State of Europe's Forests report puts the value of wild meat produced in Europe at € 0.3 billion (US$ 0.37 billion) in 2015 (Forest Europe, 2015). In South Africa it is valued at R 9.1 billion (US$ 0.56 billion/year) (Department of Environmental Affairs, Republic of south Africa, 2019). Wild meat from the Congo and Amazon basins is estimated at ~6 million tonnes a year, the areas of highest production of wild-sourced meat globally (Nasi, Taber & Van Vliet, 2011). A global estimate of "wild meat" taking these sources into consideration of ~8 million tonnes is probably reasonable, resulting in ~2.5% of meat consumed being of non-domesticated-animal origin. In Australia kangaroo harvesting is significant estimated around 3 million animals harvested annually and probably is additional to the "Wild Meat" statistic above, some of these commercial harvests seem to be considered separately only confusing these overall datasets. Australian kangaroo meat exports totalled 137,649 tonnes in 2020 (Department of Agriculture, Water and the Environment, Australian Government, 2020) up from 10,010 tons in 2008 when it was worth AU$ 34.3 million (US$ 26.54 million).

Russia accounted for at least 58 percent of the kangaroo meat market until an *E. coli* outbreak linked to the meat in August 2009 led Moscow to ban the imports. Australian kangaroo exports plummeted to 2,920 tons in 2010 as a result of this food borne zoonosis. Meat for human consumption makes up about 80 percent of total kangaroo exports, which also include meat for pet food and skins for clothing. Australia in 2011 looked toward China and East Asia with about half of exports now destined for that region (~300 tonnes annually reaching China through Hong Kong) (Animals Australia, 2011).

4.1.3. Proportional risk of wildlife trade

The theoretical threats of zoonoses emerging from the wildlife trade are similar per stock item to the domesticated animal trade, especially when we consider the stochasticity of evolutionary processes (Dobzhansky, 1982; Zhao, Abbasi & Illingworth, 2019; Fabreti et al., 2019). When the total number of traded wildlife animals is considered and within the overall provision of animal-based food, the risk is low, but never zero unless we cease the activity completely. From a food-borne disease perspective, it is roughly 3000 times more likely that humans will get a zoonosis from domesticated animal meat trade, compared to wildlife trade (based on traded volumes) (FAO, 2020a). Between 2009–2018, only 16% of the reported transactions in CITES-listed animal taxa involved species associated with one or more zoonotic diseases (UNEP-WCMC & JNCC, 2021). Different meats carry different food-borne zoonosis risks, with *Campylobacter, Salmonella, Yersinia, E. coli and Listeria spp.* being the most common and with poultry a major source. Whilst wildlife meats may carry these organisms there are only few examples of published data

from this source. In Europe alone >350,000 food borne zoonoses are recorded annually, but these are of domesticated animal origin (EFSA and ECDC, 2019), and the source of food borne zoonosis globally is shown in Table 1. A few historical examples of zoonosis from other animal products such as hair and wool are notable such as wool sorters disease due to anthrax (Bell, 2002). *Morand (2020)* explored using general additive modelling and structural equation modelling, the relationships of emerging diseases, livestock expansion and biodiversity loss. The results (2000–2019 dataset) showed a positive correlation between the increasing number of cattle and the number of threatened species, a positive correlation between the increasing number of cattle and the number of outbreaks of human diseases, and a lack of correlation between the number of outbreaks and the number of threatened animal species. While correlation does not equal causation, these data suggest the growing importance of livestock on the planet, while threatening biodiversity, increasingly puts human and animal health at risk.

Table 1. Global pathogens found in animal source foods

Animal Source Foods

Hazards	Beef	Pork	Poultry	Small ruminant meat*	Dairy	Eggs	Finfish	Shellfish [1]
Campylobacter spp.	●	●	●	●	●			
Shiga-toxin producing *Escherichia coli*	●	●		●	●			
Non-typhoidal *Salmonella enterica*	●	●		●	●	●	●	●
Cryptosporidium spp.					●			
Brucella spp.	●	●		●	●			
Mycobacterium bovis					●			
Toxoplasma gondii	●	●	●	●	●	●		
Taenia solium		●						
Trichinella spp.		● [2]						
Clonorchis sinensis							●	
Intestinal flukes							● [3]	
Opisthorchis spp.							●	
Paragonimus spp.								●

● Hazard transmitted by this and other food group (animal source or not), included in expert elicitation.

● Hazard transmitted only by one group.

[1] Including crustaceans

[2] including wild boar meat. We neglect the smallproportion of cases associated with meat from horses, bears and other animals.

[3] Included selected species of the families *Echinostomatidae, Gymnophallidae, Nanophyetidae, Neodiplostomidae* and *Plagiorchiidae*.
We neglect transmission by other foods, such as shellfish, frogs, snails and snakes.

* Small ruminant meat primarily includes goat, sheep and lamb meat.

Source: Li et al., 2019.

While the domesticated animal trade is primarily for food and pets, wildlife trade includes a wider variety of uses, from food, traditional medicines, ornaments, to the pet industry (including domesticated and captive wildlife, so-called exotic pets) and fur, hides and bones (see section 4.1.2. on Wildlife meat). Whilst the wildlife pet trade includes thousands of vertebrate species, many are not recorded in CITES, like hamsters and gerbils (examples of wild species kept as pets). This gap in pet trade data and from the informal sector including farmed wildlife species, hinders detailed disease risk assessment of these less regulated parts of animal trade, and should be included into conventional disease surveillance systems. The informal sector in China for example has its own internal dynamics with government and regulatory authorities (Gu & Li, 2020) and its scale is massive accounting for approximately 57% of the urban workers in 2013 and showing a rising trend (Liang, Appleton & Song, 2016). Individual risks of exposure to novel pathogens are also influenced by whether the animal traded is wild-sourced or captive-bred. Captivity, if for extended periods or breeding, usually leads to a filtering out of many original pathogenic organisms carried by wild-caught individuals. This is due to a variety of reasons, including loss of life cycle components or co-evolutionary drivers, to preventive treatments, with adoption of locally prevalent parasites and microorganisms adapted to the captive environment (Schulte-Hostedde & Mastromonaco, 2015), thereby reducing risk of these animals carrying novel pathogens or nEID causing organisms in trade.

These increasing figures in meat consumption (see Table 2) are accounted for mostly in terms of changes in demand in East and Southeast Asia, and whilst there is rapid growth in the domesticated and non-domesticated livestock industry in the region itself, importations continue (Zhou, Zhang & Xu, 2012; Cheng, Gao & Seale, 2015).

Table 2. Per capita meat consumption share in China (kg) in selected years

Year	Per capita meat consumption	Pork		Beef and Mutton		Poultry	
		Quantity	%	Quantity	%	Quantity	%
1995	16.18	12.51	77.3	1.21	7.5	2.45	15.2
2000	20.22	14.53	71.9	1.93	9.5	3.76	18.6
2005	25.95	17.57	67.7	2.43	9.4	5.95	22.9
2006	25.67	17.47	68.1	2.55	9.9	9.65	22.0
2007	24.73	15.59	63.0	2.62	10.6	6.52	26.4
2008	24.13	15.76	65.3	2.30	9.5	6.07	25.2
2009	26.87	17.12	63.7	2.50	9.3	7.26	27.0
2010	27.35	17.56	64.2	2.60	9.5	7.19	26.3

Source: China Statistical Yearbook (NBSC 1996–2011), in Cheng, Gao & Seale, 2015.

Another way to explore the development of zoonosis risk and prominent EID events from food-based systems in China is to look at the use of different animal meats over the period 1960 to 2019 (which includes imported products) and which encompasses the period of avian influenza and SARS virus emergence in the region (Figure 9). These data showing a slight shift from pork to beef, mutton, and poultry consumption and a large increase (7-fold) in meat consumption and importation (comparing to local production and consumption alone Table 2), thereby increasing the potential risk of zoonosis (Vijaykrishna et al., 2008). For human influenzas, derived genetically from pigs and poultry both from local and foreign sources a good example is H1N1. Influenza A H1N1 strains were circulating in pig farms in China and amongst farmers, confirming the importance of these farming systems in the pathways for the pandemic influenza which started in Mexico, transcontinental links were identified through molecular epidemiology (Garten et al., 2009a). The analysis was indicative of virus origins of the H1N1 pandemic with genes from different populations of domesticated pigs across several continents (Garten et al., 2009b). The pace of intensification in China is challenging biosecurity, evidenced in the pork industry which grew by more than 50 million tonnes since 2010 (Berthe, 2020), reaching 440 million pigs in 2018 (around 50% of the World's population of pigs that year). Between the onset of African Swine Fever (ASF) in 2018 (Wang, Sun & Qiu, 2018) and late 2019, at

least half the Chinese pig herd died or was euthanised because of ASF, with an estimated direct losses of US$141 billion (Reuters Staff, 2019; You et al., 2021). A coronavirus disease of pigs (Swine Acute Diarrhoea Syndrome or SADS-CoV) has killed millions more and has zoonotic potential (Gong et al., 2017; Edwards et al., 2020).

Although speculative, this massive loss of pork in 2019 in China might have influenced the risk of the disease emergence – such as SARS-CoV-2 – potentially in the absence of pork there may have been an increase in demand for wildlife and other meats from farms and other sources assuming that these species are a likely origin, this possibility needs to be reviewed from trade data. The suggestion by the Chinese authorities that frozen pig heads may have provided a source of SARS-CoV-2 has further muddied the waters (Xia et al., 2021; WHO, 2021e).

In addition, it is worth noting that for SARS-CoV-2, the original transmission pathway and location of the original spillover event are still unknown, 55.4% (93/168) of the reported early cases were linked to a wildlife markets in Wuhan (WHO, 2021e), either with the Huanan market (28%), other wildlife markets (22%), or the Huanan market and other markets (4.7%). This pathway is also supported with two SARS-CoV-2 early lineages (A and B), which later spread to other countries (Rambaut et al., 2020). The limited genetic diversity
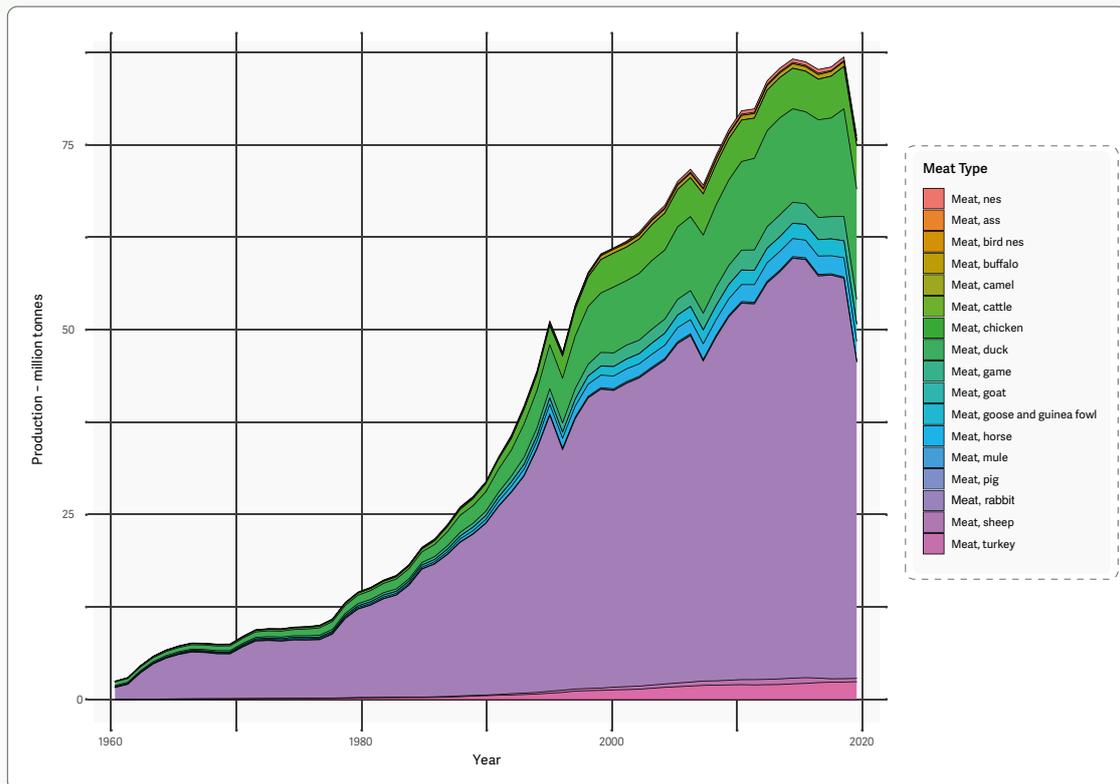
Figure 10. Change in share (%) of the different fresh meat

Change in consumption preference of multiple fresh meat sources.
Source: Prepared by the report authors using FAO, 2021.

from the Huanan market (lineage B), are consistent with the role of this market as a super-spreader (Garry, 2021), but not necessarily as point of origin or index for the epidemic and animals present may be incidental. Nevertheless, this type of research is vital to elucidate the spread pathways during the early stages of an outbreak.

In 2007 (Haberl et al., 2007) estimated the human appropriation of the potential planetary primary productivity was already 23.8%; since then, increasing global population and its demand for resources, particularly food, have led to increasing conversion of land for agricultural purposes including animal production (Leibler et al., 2009; IPBES, 2018). Today, malnutrition and food security are still a major challenge (Roser & Ritchie, 2013; United Nations, 2019) and with the human population expected to grow by 2 billion people by 2050 (United Nations, 2019), these are only expected to increase unless swift and sustainable measures are put in place by governments, businesses and the civil society. There is some positive news that

the human population is likely to peak around this point, so some space can be gained subsequently for ecological recovery (Vollset et al., 2020). Also that this current level of food demand need not increase or rely on animals at the current or projected levels (see Figure 10), with considerable potential benefits with reduction in proportion of animal-based foods in human nutrition (Berners-Lee et al., 2018). This creates a significant opportunity for removal of land from agriculture, and ecological recovery if there were science based and popularly accepted food policies, even before human population numbers begin to fall. Nevertheless, the current growing human population coupled with its needs for agricultural products and its fashion for animal resources create unique environmental pressures, and among them diverse and complex interactions among agricultural systems, natural habitats and human-dominated environments that can lead to the emergence of infectious diseases (Rohr et al., 2019).
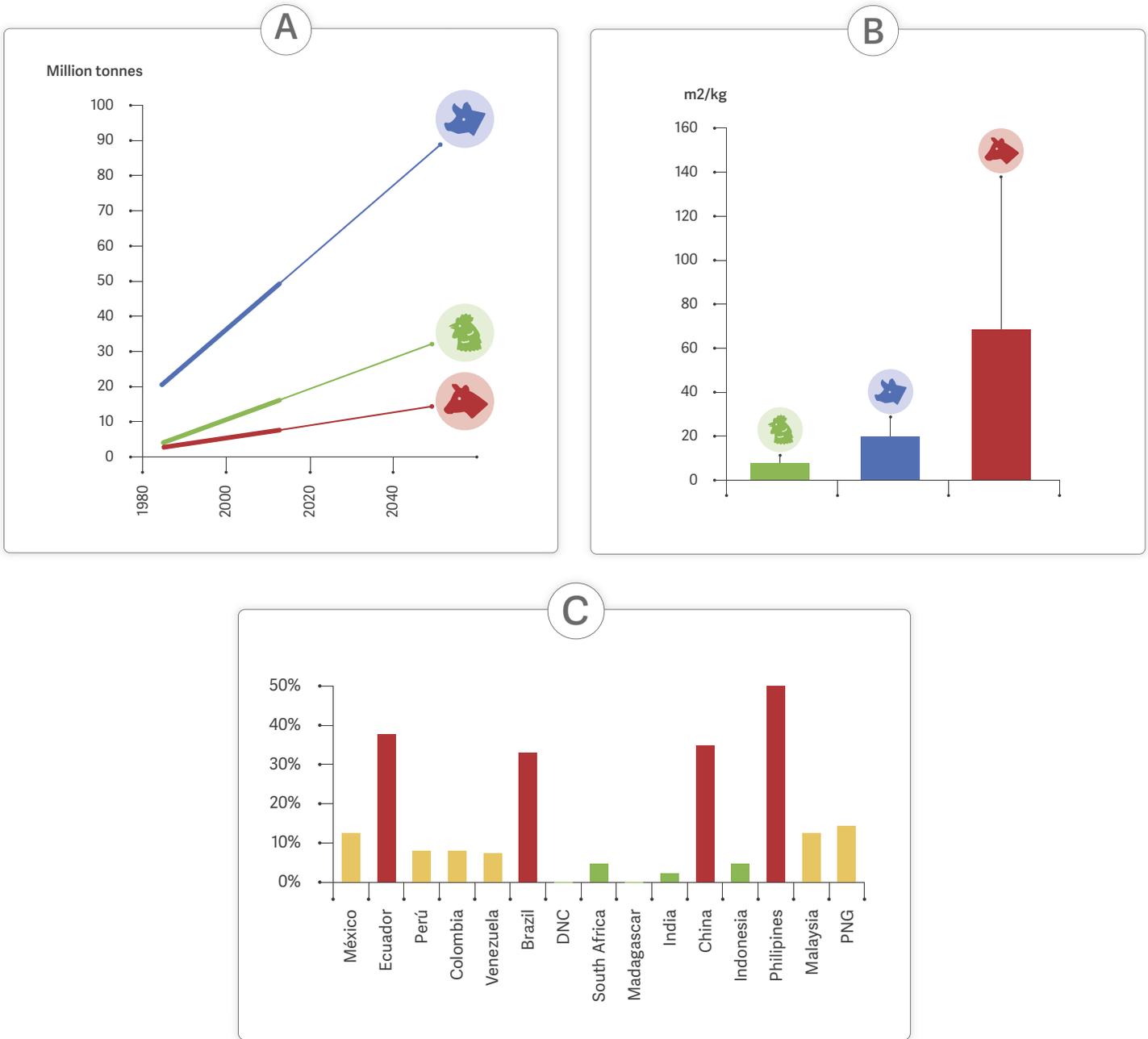
Figure 11. Projected increases in area required to produce meat in developing megadiverse countries by 2050.

(a) Extrapolating recent (1985 – 2012) production data for beef, chicken, and pork (FAO, 2014) in each megadiverse country to 2050 (data for China shown) multiplied by (b) mean area required to produce livestock biomass (Röös et al., 2013) provides (c) an estimate of area in each country required to produce livestock by 2050 as a percentage increase beyond total current agricultural area (2012) (FAO, 2014). Agricultural area expansion needs can be met by internal expansion or by agricultural expansion in other countries and importation of feedcrops and/or meat products. This analysis addresses only beef, chicken, and pork. It does not include eggs, other meat sources, or dairy, which would increase area projections.
Source: Machovina, Feeley & Ripple, 2015.
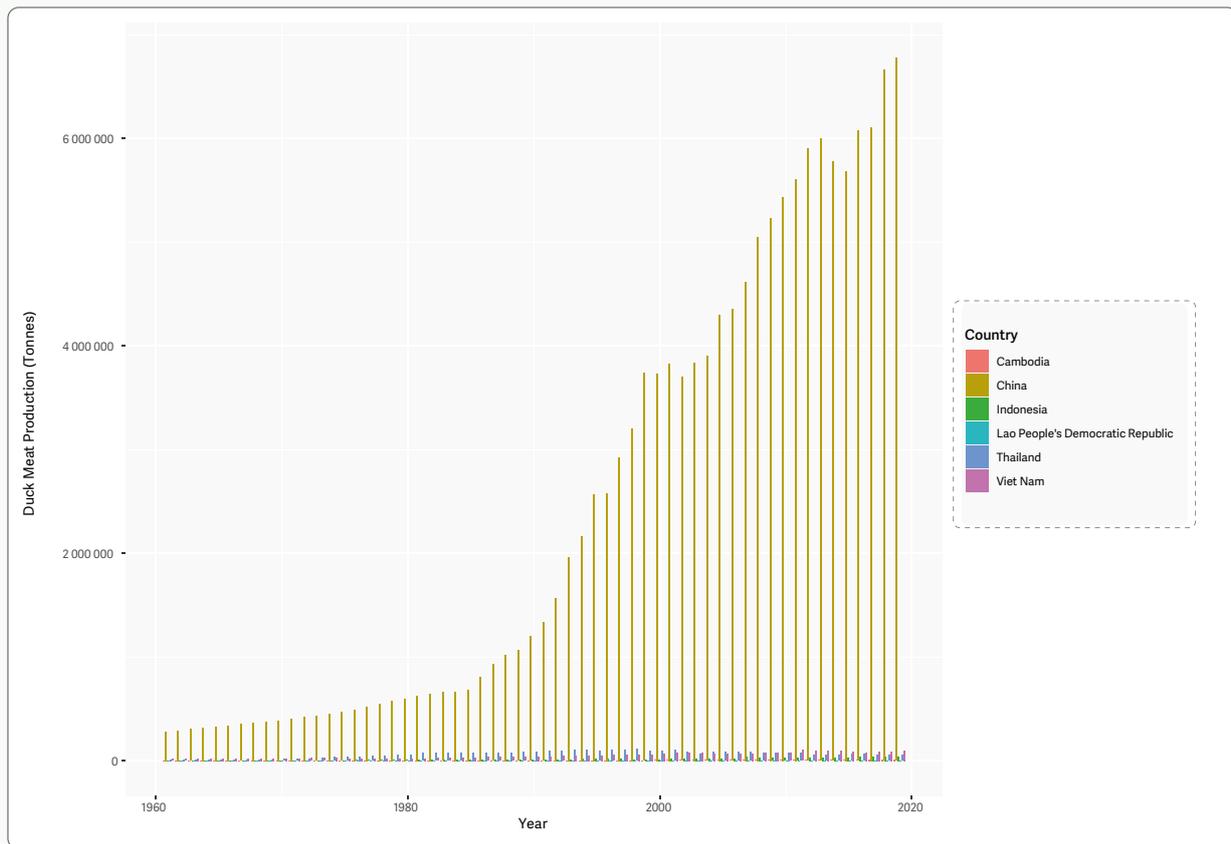
....
Figure 12. Growth in the duck industry in East Asia
....

The growth in the duck industry in East Asia and how this coincides with the emergence of highly pathogenic influenza viruses which continue to plague the world.
Source: Prepared by the report authors using FAO, 2021.

A particular risk for pandemic disease is human influenza derived genetically from recombination of the human viruses with various animal viruses. When this occurs, there is almost inevitably a pandemic. The last to be recorded was H1N1 or swine flu with genetic elements from human virus, 4 continents of pig and poultry genes showing how the globalisation and connectivity has opened up limitless evolutionary potentials for such viruses (Wallace et al., 2007). Zoonotic influenza is concerning but less significant as it tends to be localised from poultry human contact. The increase in poultry was coincident in Asia with the emergence of the highly pathogenic avian influenzas since Hong Kong flu towards the end of the 20th Century followed by Bird Flu (H5N1) in 2006 (Figure 11) and many new strains since. The role of wild birds has been widely stated and speculated upon given their potential as vectors spreading continentally virus along migration routes. Given the large air traffic in live poultry it seems unlikely the only pathway to global spread is a red flag for these pathogens, yet little attention is directed at the growth of these industries.

In 2013 a systematic review (Jones et al., 2013) was conducted by a multidisciplinary team to:

"... analyze qualitatively best available scientific evidence on the effect of agricultural intensification and environmental changes on the risk of zoonoses for which there are epidemiological interactions between wildlife and livestock. The study found several examples in which agricultural intensification and/or environmental change were associated with an increased risk of zoonotic disease emergence, driven by the impact of an expanding human population and changing human behavior on the environment."

They concluded *"... that the rate of future zoonotic disease emergence or reemergence will be closely linked to the evolution of the agriculture–environment nexus."*

This interface between humans and animals and biodiversity (wild and domesticated) is shown descriptively (*Table 3*) with diversity of context and examples of diseases to show the variable emergence patterns.

The review raised an important issue which more or less remains the same in 2021 that *"... available research inadequately addresses the complexity and interrelatedness of environmental, biological, economic, and social dimensions of zoonotic pathogen emergence, which significantly limits our ability to predict, prevent, and respond to zoonotic disease emergence".*

Table 3. Types of wildlife-livestock interface and their characteristics

Type of wildlife–livestock–human interface	Level of biodiversity	Characteristics of livestock population	Connectedness between populations	Examples of zoonotic disease with altered dynamics
"Pristine" ecosystem with human incursion to harvest wildlife and other resources	High	No livestock	Very low, small populations and limited contact	Ebola, HIV, SARS, Nipah virus in Bangladesh and India
Ecotones and fragmentation of natural ecosystems: farming edges, human incursion to harvest natural resources	High but decreasing	Few livestock, multiple species, mostly extensive systems	Increasing contact between people, livestock, and wild animals	Kyasanur Forest disease, Bat rabies, E. coli interspecies transmission in Uganda, Nipah virus in Malaysia
Evolving landscape: rapid intensification of agriculture and livestock, alongside extensive and backyard farming	Low, but increasing peridomestic wildlife	Many livestock, both intensive and genetically homogenous, as well as extensive and genetically diverse	High contacts between intensive and extensive livestock, people, and peridomestic wildlife. Less with endangered wildlife.	Avian influenza, Japanese encephalitis virus in Asia
Managed landscape: islands of intensive farming, highly regulated. Farm land converted to recreational and conservancy	Low, but increased number of certain peridomestic wildlife species	Many livestock, mainly intensive, genetically homogeneous, biosecure	Fewer contacts between livestock, and people; increasing contacts with wildlife.	Bat-associated viruses in Australia, West Nile virus in the United States, Lyme disease in the United States

Source: Jones et al., 2013.

EcoHealth Alliance (2019) estimated that 15% of the past outbreaks of EIDs were linked to agricultural activities although there is lack of specificity to what activity and apparently derived from Loh et al. (2015, UNEP (2016), and EcoHealth Alliance (2019). It is estimated that about a third of zoonosis are derived from the food system (Grace et al., 2012a) but the figures vary from region to region with higher burdens in low income and livestock dependent economics (WHO, 2015). Many of these agriculture activity-related-EIDs simply reflect growing numbers of livestock in contact with humans, as a growing food source, as well increasing proportion of homogenised landscapes attracting peridomestic wildlife species, such as rodents to concentrated food storage, crop systems and housing, raising zoonosis risk. Poultry and pigs have been identified as the priority species for risk and this is increasing as populations of these animals grow exponentially (Grace et al., 2012a). Domesticated mammals and birds in this context provide massive amplification opportunities with current relative abundance (Bar-On, Phillips & Milo, 2018). The introduction of wildlife species into intensive agricultural systems (for meat, fur, and other products) is probably the most threatening development and this is notable in landscapes such as South East Asia and China in particular.

Policies for poverty alleviation in rural agricultural landscapes over the last decades have driven an increase in wildlife species farming as product and food potential from biodiversity has been realised and exploited. Current poverty programmes need to be revisited and if the risk is confirmed, measures taken to address associated risks. Modern food production systems have reduced world hunger, and through the adoption of new technologies and better practices theoretically should have decelerated conversion of natural habitats to production systems (Rohr et al., 2019). But the paradox is that over the same time we have seen an overall massive reduction in natural land (e.g. destruction of forest in South America for soya crops expansion). In fact, these increasing efficiencies have led to perverse subsidies and investments, high demand, overproduction, forest loss, increasing land conversion rates, rural and indigenous livelihood loss, and overconsumption of food, with a dramatic rise in clinical obesity across all age groups in most industrially developed nations and beyond. Arguably the recent emerging diseases such as Ebola, Zika, Avian Influenzas H5N1/6/7/8, and COVID-19 have emerged out of global circuits of capital applied in the animal and agricultural sector and enabling exploitation of natural resources (Wallace et al., 2018; Wallace, 2020; Chaves et al., 2021). It is argued that the

current political economy, advanced technology and agriculture, far from saving species and land, has been the primary factor in biodiversity loss (Wallace, 2016; FAO, 2019). Despite the bizarre situation of excess food (and waste in production and storage) and billions overfed on unbalanced diets, and increased production efficiencies (with unaccounted externalities), the current global food system is unable to fulfill billions of people's dietary requirements, and it is expected that this will only worsen with the disruptive effects of climate change in the near future (IPCC, 2018; von Grebmer et al., 2020).

Landscape change, such as agriculture, increases the potential viral transmission risk between humans, domesticated species and peridomestic wild animals. These peridomestic species that benefit from human environments (e.g. increased in abundance) expanded their home range in response to the new habitat or due to habitat loss or are introduced into previously natural habitats, inadvertently as alien invasive species or as livestock (Everard et al., 2020). Domesticated species, primates, rodents and bats have been identified as high-risk species for zoonotic virus transmission (Johnson et al., 2015). The links between agriculture and EIDs are not only direct, but also indirect, mainly because of related impacts rising from agricultural methods and its effects (i.e. irrigation and water availability) that often increase the risk of vector-borne diseases (e.g. malaria) (Patz et al., 2004). It has been argued that the most vulnerable human populations to infectious diseases are rural populations (Rohr et al., 2019) and there is evidence for associations between agricultural landscapes and infectious diseases in South East Asia (Shah et al 2019) whilst in South Asia both urban and rural communities carry the highest global burden of zoonosis (Grace et al., 2012b; Laxminarayan et al., 2017; Shah et al., 2019). The association of rural populations with zoonotic disease is challenged by pandemics such as COVID-19 where the virus apparently emerged in urban populations. Here the principle of epidemiologically connected populations being essential for maintenance and spread of infectious disease is the key point. In isolated populations the spillover if it occurs will burn out unless connected in a network. This has been the historic experience with HIV/AIDs, EVD and now most recently the contemporary coronaviruses, they are a by-product of development.

4.1.4. Relative risk of wildlife trade

The data presented to this point show the relative risk between domesticated animal source zoonosis and wildlife source in the animal-based food systems, but to quantify the actual risks for wildlife species compared to domesticated animals in relation to zoonosis and EID is extremely difficult. The relative risk may not relate to consumption of wild animals at all but rather presence or use of domesticated and wildlife species often in artificial numbers and densities, in human domesticated environments and a range of other hypothetical mechanisms around human wildlife contact directly or through vectors. Morand (2020) showed: *"a positive association between the number of infectious and parasitic diseases recorded in humans and the total number of animal species between nations was observed. A similar positive association between the number of outbreaks of human infectious diseases, corrected for the number of surveys, and the number of threatened animal species, corrected for the number of animal species, suggests that outbreaks of human infectious diseases are linked with threatened species, a positive correlation between the increasing number of cattle and the number of outbreaks of human diseases, and a lack of correlation between the number of outbreaks and the number of threatened animal species"*. Morand & Lajaunie (2020) expanded on this examining the impact of a single crop – palm oil – pointing clearly at the trend in demographic increase in domesticated animals as the probable underlying risk factor (primary cause) for disease emergence with the likely link to wildlife and pathogen spillover from associated disturbance to natural ecosystems.

A good example is Avian Influenza, where wildlife is often linked to its emergence. Many avian influenza viruses of low pathogenicity evolve and circulate in wild birds but pathogens are diluted and frequently burn out, whilst the generation of highly pathogenic and zoonotic strains is associated with the agricultural landscape, e.g. intensive chicken production or free-ranging ducks in agricultural settings where massive epidemics arise with spill back to wild bird populations and associated vectoring (Gilbert et al., 2007, 2010; Takekawa et al., 2010; Cappelle et al., 2014).

FAO carried out a qualitative rapid risk assessment with respect to COVID-19 emergence (El Masry et al., 2020), and evaluated the likelihood of animal infection and zoonosis in this context:

"In the assessment, the uncertainty of the different levels of likelihood generally remains medium (small sample data set(s), fair correlation/good fit; reliable method) to high (lack of data, limited data, or lack of conclusive data; weak correlation or crude speculation) due to the information gaps outlined." and,

"Any measures implemented or strengthened at country level to mitigate the risk of exposure of humans and animals to SARS-CoV-2 from susceptible wild, livestock, companion and aquatic animals, should be based on the results of country-specific risk assessment and critical review of local animal husbandry and marketing practices, using the current knowledge outlined in this document.

Risk assessments should be performed according to international guidance (e.g. OIE, 2019; FAO, 2011; FAO and WHO, 2007)."

Our results coincide with these findings, and highlight that FAO includes all species, domestic and wild, and that for wildlife, the uncertainties of the likelihood of exposure are all in the high uncertainty category. The assessment goes further to caution against a blanket global approach to the wildlife trade and suggests that contextual analysis is carried out before making any decisions on banning or restricting all or any aspect of the trade.

Wildlife trade poses a risk of zoonotic disease transmission and EIDs in the same way that the domestic animal trade creates risk but for most zoonosis the wildlife contribution is negligible whilst there might be a relatively higher per capita risk of spillover of novel pathogens from wild sourced animals as has been explained. If a significant amount of legal wildlife trade is from managed environments, i.e. captive and captive-bred or farmed wildlife species, for example, the majority of wildlife mammal species traded recorded by CITES from captive bred primates for medical research (Siegert et al., 1967b; Morton, 2011) and Figure 12 , then it is these environments and populations that need to be examined first for pathogens and not free-ranging wild animals. There is a much smaller trade, under CITES regulations, in wild (once free-ranging) animals whilst the majority of wild trade in most continents constitutes wildlife products mostly, often (but not always) meat which is smoked or pelts, bones and horns and not live animals other than a few taxa such as reptiles and birds. In East (e.g. China) (Zhang, Hua & Sun, 2008; Wong, 2019) and Southeast Asia (e.g. Vietnam and Cambodia), live trade in wild mammals is relatively common, including for meat (Nijman, 2010; Cantlay, Ingram & Meredith, 2017; Alves & van Vliet, 2018; McEvoy et al., 2019; Ibbett et al., 2020).

A relatively higher risk of zoonosis from harvested or traded wildlife from natural systems is often assumed but there are no data to support this and given the increasing volumes in farmed and captive traded wildlife, this needs to be more closely examined. Total numbers of any given wildlife species traded, in most cases other than amphibians and fish, are relatively low (see section on trade volumes) and the pathways are highly diverse with tens of thousands of species involved, i.e. many species are traded in small volumes. A few species are collected and traded in large volumes and these have specific risks. For example, ~1 million farmed deer in New Zealand produce about 15,000 tons of meat exported annually (Statistics New Zealand, 2020) and harvested kangaroo in Australia produced meat exports totalling 10,010 tons in 2008 - worth US$ 38.4 million. Russia accounted for at least 58 percent of that market, until an E. coli outbreak linked to the meat in August 2009 led Moscow to ban imports (Animals Australia, 2011). Some African game species (Magwedere et al., 2012) are traded all around the world, without much data on the volumes or routes. Rodents (e.g. hamsters, squirrels, gerbils) are extensively traded but there are few statistics on domestic pet production versus wild-sourced international trade). Trade in sugar gliders is big in Asia, presumed to be mostly wild-sourced from West Papua (Lyons & Natusch, 2012). Through this wild animal trade, there is a likely heightened risk of unknown microorganisms, circulating naturally, being brought into the human domain for the first time, but quantifying these unknown risks is extremely challenging.

Imported quantity (live)

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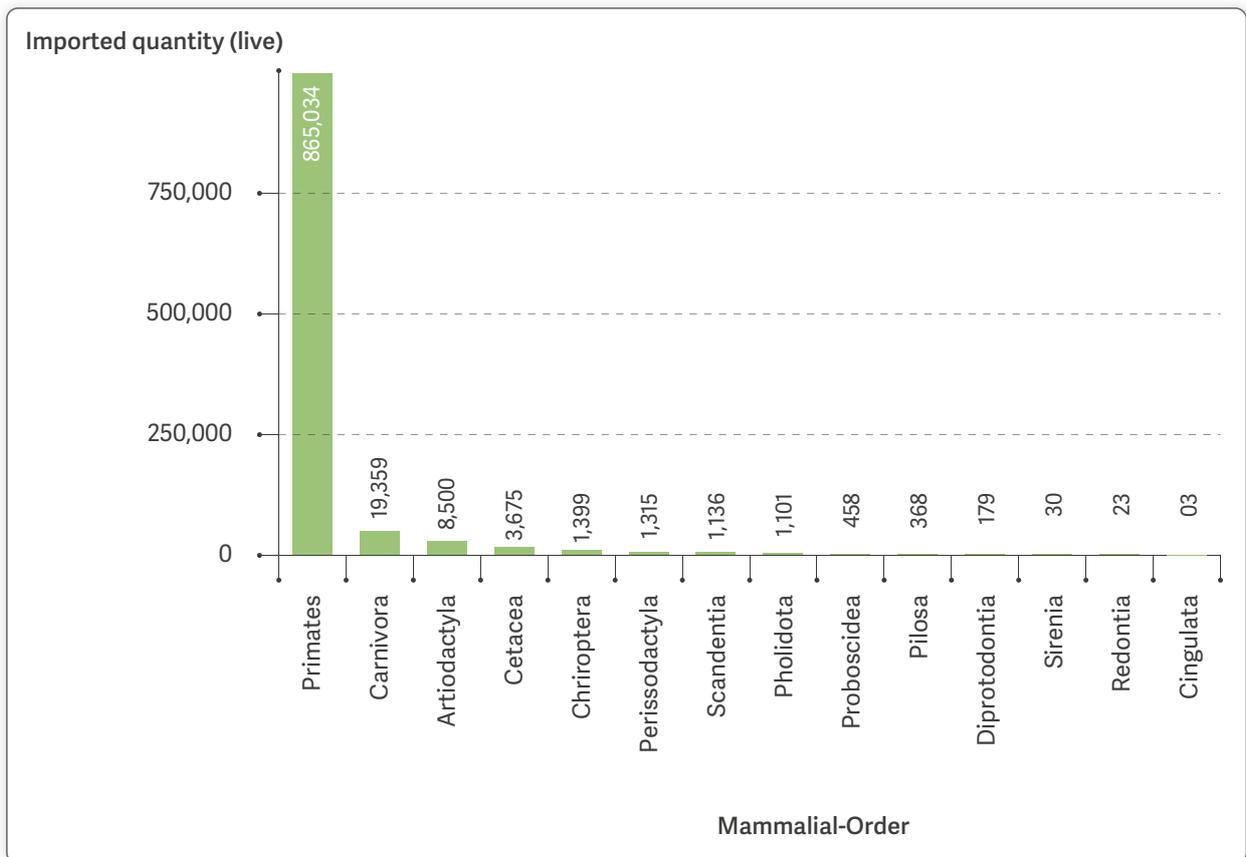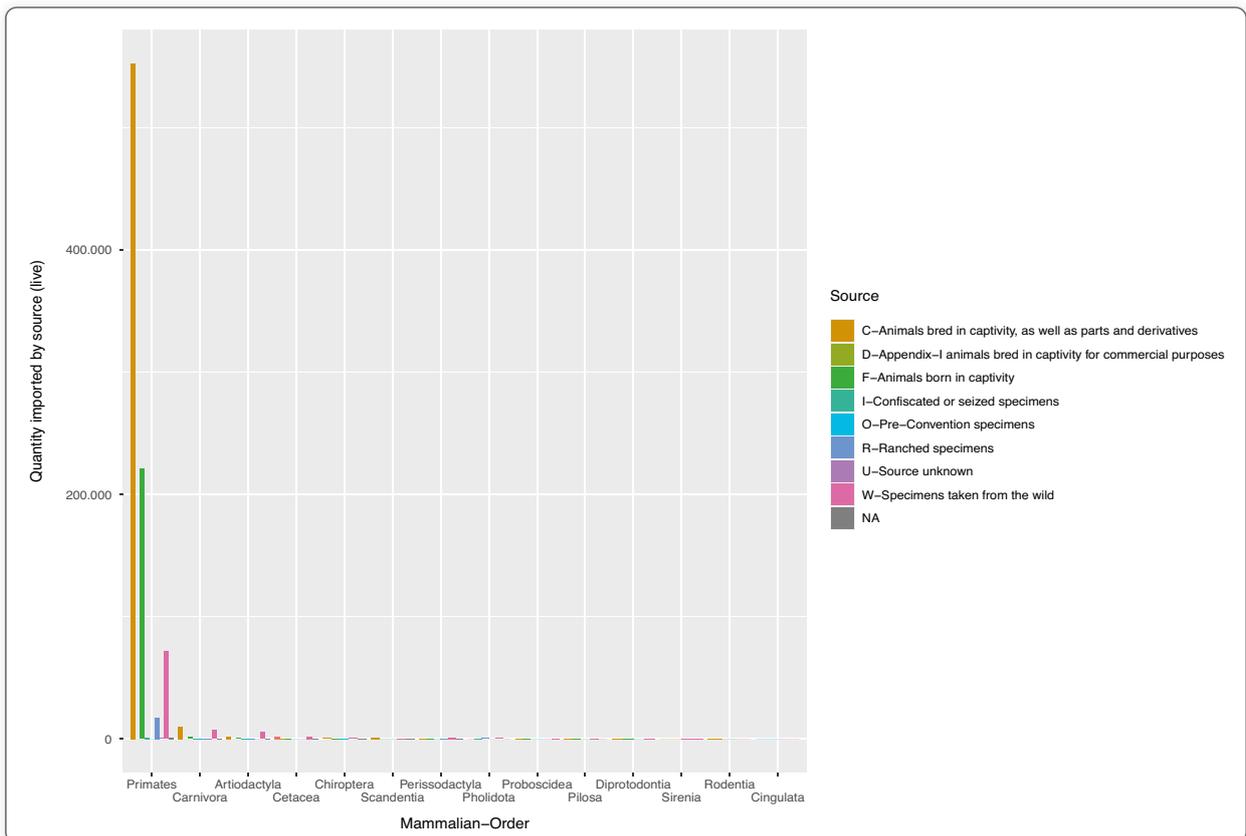
Figure 13. Quantity of imported live CITES-reported species globally

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Most mammals are primates (95.84%) followed by carnivores (2.14%).
Source: Prepared by the report authors using CITES, 2021.

4.2. Intensified and industrialised agriculture: consumer demand, food cultures, fur markets, and exotic pet trade

Less reported risk of zoonosis is related to wildlife fur and meat farming industries. There is increasing evidence and likelihood that wildlife farmed animals, such as racoon dogs (*Nyctereutes procyonoides*), masked palm civets (*Paguma larvata*) and semi-domesticated species, such as mink, are viable host species for SARS-CoV-2 virus and able to circulate the virus in their population, while there is evidence for spillover into wild or feral species associated with farms (El Masry et al., 2020; Shriner et al., 2021). The role of mink in COVID-19 zooanthroponosis and possible zoonotic events in the Netherland's and other mink farms emphasised that this is not an isolated regional issue or negligible risk (Munnink et al., 2020b). It may be that under farming conditions some of these species can act as a reservoir, if only temporarily, for human infection amongst those working in the farms but whether the virus can establish in wild populations is unknown. Whether these species may have acted as an intermediary or proximate source, host species and possible modifier/amplifier in the evolution of this pathogen and its introduction into humans remains speculative, but more plausible than it is coming from remote wildlife.

The concern around agricultural practices can extend beyond production to breeding for pet trade and exotic pets in particular. Monkeypox translocation remains one of the few and well documented examples of what is possible through trade. History shows that it can be managed through effective regulation and in this case banning of importation. Bird pet zoonosis is another well recognised issue for a few zoonosis including psittacosis (Chlamydophilosis) and salmonellosis, whilst the presence of H5N1 avian influenza virus was reported in imported birds to the EU. This was rare and no zoonosis occurred during the 2006 H5N1 epidemic across Eurasia from pet birds, all reported cases were from poultry (ECDC, 2021). It did however lead to a ban in importation – EU decision 2005/760/EC – of avian wildlife through trade at the time (EU, 2007). This ban negatively affected community conservation programmes, and resulted in an expansion of agriculture (Box 3, Coconier & Lichtenstein, 2014).

Box 5. The 1929–1930 Great Parrot Fever Pandemic

In 1929, an outbreak of Psittacosis (caused by the *Chlamydia psittaci* bacteria) was first reported in Argentina (also known as the 1929–1930 Great Parrot Fever Pandemic) when 100 cases of an unusual pneumonia were reported (**Ramsay 2003**). The patients were exposed to a large shipment of birds from Brazil which showed clinical signs of illness. Following the outbreak, Argentinian authorities outlawed the parrot trade. However, the bird trade continued, and during the following year cases were reported in more than 20 countries across Europe, North America, Africa, and Oceania (**Ramsay 2003; Honigsbaum 2019**). The 1929 event was linked to the global pet trade, then became endemic in several countries by the increasing number of local pet trade and breeders. In 2018, Virginia and Georgia authorities (United States) reported an outbreak among workers from two poultry slaughter plants (**CDC 2019**). Since 2010, there are fewer than ten cases reported annually In the US (**CDC 2019**), making psittacosis a disease of occupational concern associated with veterinarians, pet trade, and poultry production systems (**CDC 2019**).

Source: Prepared by the report authors using

The scale of the wildlife trade is significant and involves many of the high-income nations who drive demand. The proportion of CITES listed species in pet trade that derive from the wild has declined over the years as captive breeding has increased (Tensen 2016; Harfoot et al. 2018), but this may not always result in a reduction in zoonosis risk as numbers grow and many wild origin species of aquarium fish, reptiles, birds, and small mammals still remain in trade (Hutson et al., 2007; Boseret et al., 2013; CDC, NCEZID & DHCPP, 2015; Green et al., 2020) .

Since most zoonosis are derived from domesticated animals, if a significant decline in consumption of animal-based foods and product use were feasible, this would substantially reduce human disease risk. Reducing animal-based food systems may well prove to be the most important intervention in reducing the risk of further EID and in particular coronavirus emergence. There are strong arguments that humanity should shift to approximately 20% animal-based food human diet (meat, milk, eggs) (IPBES 2019)., which would substantially reduce the need for livestock and the land to support them at a time when reforestation and biodiversity recovery is essential and requires freeing up of land from agriculture and other human uses. This would not affect food security and have many other benefits such as health security (Peters et al., 2016). It would require a strong international policy on animal agriculture, rather like climate change, with collective agreement (such as the Climate Change Convention) given the compound risk and driving factors (Phillips et al., 2020). Little progress will be made otherwise and steps towards this goal would include first stopping the growth in animal production, then gradual reductions, replacing animal protein sources with improved and more diverse crop agricultural sources. Land freed up could then be recovered for natural systems of forest and other biomes..

4.3. Focus on emergence

Despite all the knowledge on zoonosis in the context of the agricultural and food sector, attention to emerging infectious diseases is recently focused on wildlife (Leibler et al. 2009) whilst the actual evidence is conflicting see Figure 2. In the context of EIDs it is important to provide accurate ecological, social and environmental context on the EIDs' emergence, transmission pathways and risks to human and animal populations (Rohr et al. 2019). This requires that we clearly differentiate diseases between (1) those organisms that arise and infect humans from a wild animal (in the wild, events which are in fact extremely rare) and (2) emerging pathogens of humans which originate from animals (domesticated and wildlife species) through spillover (as defined) in peridomestic, captive (including trade or farming operations) conditions. Given high human population, a landscape with massive growth in domesticated and wild animal exploitation and captive wildlife industries, emerging pathogens in the second category above are more likely. The repeated cycles and passage of organisms at the human-animal interface allow for the organisms to adapt over time to humans (Beare & Webster 1991; Woo & Reifman 2014). Crucially, this can occur where no wild animal reservoir exists or is significant in the epidemiology of the epidemic. Introduction of agricultural landscapes with particular emerging pathogens may go back generations and these risks establishing in the domestic environment. These novel agents (nEIDs) have high impact and require intense focus.

4.4. Coronaviruses: The SARS case

Time will tell, but it is plausible that the SARS coronavirus emergence in 2002-03 and SARS-CoV-2 (COVID-19) emerged through the farming/peridomestic/captive wildlife population (Cyranoski & Abbott, 2003; Wang & Eaton, 2007). For these viruses, likely genetic links to horseshoe bat viruses are established for SARS-CoV-1 and SARS-CoV-2 but these specific viruses have not been identified in nature amongst the 500 or so beta-coronaviruses so far detected (Latinne et al., 2020). There is some speculation on possible direct transmission of SARS like viruses from bats to humans (Wang et al., 2018; Rahalkar & Bahulikar, 2020) but these data are not conclusive. *Fischhoff et al. (2021)* combined protein structure modelling with machine learning of species traits to predict zoonotic capacity of SARS-CoV-2 across 5,400 mammals. This is suggestive of a vast range of animals that are potential hosts making the search for a source or reservoir increasingly complicated. They showed very high potential for 35 bat species, 76 rodents, 20 primates, 2 pangolin, 10+ carnivores, 5 or more herbivores and many domesticated species with many more with moderate potential . There has also been intense speculation about specific bats and pangolin (Chan & Zhan, 2020) but as with much of the data, analyses and claims are premature, and several studies raised questions about the role of pangolins (Choo et al., 2020; Frutos et al., 2020; Lee et al., 2020b). There is fairly strong evidence that the virus is not of laboratory origin (Relman, 2020; Sallard et al., 2021), although the WHO recent mission report to Wuhan did not rule it out (Sirotkin & Sirotkin, 2020), with several scientists calling for a new and more transparent investigation of the origins of SARS-CoV-2 (Bloom et al., 2021).

The high plasticity of SARS-CoV-2 (McCormick, Jacobs & Mellors, 2021) (see Table 4) – and coronavirus in general – can seed the virus into almost any animal susceptible, and in contact with infected humans further preventing a clear picture of the source. Other studies suggest the virus may have never emerged from an animal source with a low rate of evolution in the early phase of transmission; the lack of evidence of recombination events; a high pre-existing binding to human ACE2; a novel furin cleavage site insert; a flat glycan binding domain of the spike protein which conflicts with host evasion survival patterns exhibited by other coronaviruses, and high human and mouse peptide mimicry suggest human or even a laboratory source (Segreto et al., 2021; Sallard et al., 2021). The WHO mission to Wuhan (WHO, 2021e) identified that the most likely route of emergence was through an unknown intermediary species, rather than direct zoonotic spillover from horseshoe bats (Moran, 2021). Identifying the source is important to prevent further reinfections but while the search for the source continues with *in vivo* and *in silico* studies, it is important to acknowledge we may never know the exact origin of SARS-CoV-2 (Mallapaty, 2020).

Table 4. Table summarising the species that until the date of this submission have been reported to be infected by SARS-COV-2

Species	Type of infection	Suspectibility	Clinical Signs	Transmission
Farmed animals				
Ferrets (*Mustela putorius furo*)	Experimental	High	Yes (only in few cases)	Yes, between ferrets
American mink (*Neovision vision*)	Natural	High	Yes (in some cases)	Yes, between minks and from mink to humans
European rabbit (*Oryctolagus cuniculus*)	Experimental	High	No	No
Racoon dogs (*Nyctere-utes procyonoides*)	Experimental	High	No	Yes, between racoon dogs
Cattle (Bos taurus)	Experimental	Extremely low	No	No
Pigs (American Yorkshire crossbred pigs, *Sus scrofa*)	Experimental	Extremely low	No	No
Poultry (chicken, ducks, and turkeys)	Experimental	None	No	No
Companion Animals				
Dogs (*Canis lupus familiaris*)	Natural and Experimental	Low	Yes (but not observed in all cases)	No
Cats (*Felis catus*)	Natural and Experimental	High	Yes (but not observed in all cases)	Yes, between cats
Captive and Free-ranging wildlife				
Large cats - Tigers (Panthera tigris) - Lions (Panthera leo) - Puma/cougar (Puma concolor)	Natural	Medium to high	Yes, in most cases	Yes, between animals
Egyptian fruit bats (*Rousettus aegyptiacus*)	Experimental	High	No	Yes, between fruit bats
Snow Leopard	Natural	Data not available	Yes	Yes, between animals
Non-human primates	Experimental	Data unavailable	Yes (but not observed in all cases)	Yes, between non-human primates
Others				
Golden Syrian hamsters (*Mesocricetus auratus*)	Experimental	High	Yes (none to very mild in some cases depending on age)	Yes, between hamsters
Marmosets (*Callithrix jacchus*)	Experimental	High	No	No
Macaques (Macaca *fascicularis* and Macaca mulatta)	Experimental	High	Yes (none to severe in some cases)	Yes
Tree shrews (*Tupaia belangeri chinensis*)	Experimental	Data unavailable	No	Data unavailable
White-tailed deer (*Odocoileus virginianus*)	Natural and experimental	High	Subclinical	Yes, between animals

Source: Prepared by the report authors.

4.5. Special case novel emerging pathogens: coronaviruses and speculative links to wildlife

In early 2020, the emergence of SARS-CoV-2 was perceived and widely reported to be associated with wildlife trade in China, which became a predominant narrative on the emergence of the virus without any confirmatory evidence (Andersen et al., 2020; Zhang, Wu & Zhang, 2020; Xiao et al., 2020). This is the third novel coronavirus with pandemic potential to emerge in the last 20 years putting this group of viruses at the top of global health pandemic concern along with influenza viruses. The first to emerge was Severe Acute Respiratory Syndrome (SARS) caused by SARS-CoV-1, arising in China and now apparently no longer circulating and with no known animal reservoir identified. SARS was also associated with infections in markets and restaurants, where masked palm civets and raccoon dogs (meat and fur trade species, respectively) were detected carrying the virus (Cheng et al., 2007). However, these may have been reverse zoonosis and no reservoir was confirmed or endemic zoonosis cycle demonstrated for SARS to this day (Cheng et al., 2007).

The second emergence – which has proven far simpler to explain epidemiologically – was Middle East Respiratory Syndrome (MERS). MERS is mostly transmitted amongst humans and in hospital settings, and was associated to an initial spillover from its reservoir (dromedary camels). Dromedary camels are a domesticated species that is growing in number in a growing milk and meat industry in the Middle East (Zumla et al., 2016; Farag et al., 2019; Alzahrani et al., 2020). The potential spillover of MERS-CoV does not seem to result in disease in East Africa, where the camel husbandry is extensive, but the virus is also present. This regional difference shows how dynamic the epidemiology of these viruses can be and where external drivers and risk factors can be determinants in emergence of disease.

Thirdly, in COVID-19 the initial reports connected the causal virus, SARS-CoV-2, to a wildlife market in Wuhan (Haider et al., 2020a; Sheath et al., 2020). This led to some wildlife species – such as snakes, pangolins, and bats – being singled out as possible source or intermediate hosts of the virus. Xiao et al., (2021) documented the species being sold in the market between May 2017 and November 2019. There were more than 47,000 individuals from 38 species (including 31 protected species) in the market, but there were no pangolins or bats being sold at the time. Environmental samples taken in in the market in December 2019 tested positive, suggesting a role of the market in either the amplification or as the source of the outbreak (WHO, 2021). Since then, these initial claims for possible source species have been given attention and widely reported to be highly unlikely based on genetic evidence (Li et al., 2020; Andersen et al., 2020; Lee et al., 2020a), but wildlife trade remains at the centre of international discussions (Turcios-Casco & Cazzolla Gatti, 2020; MacLean et al., 2021). As a result, authorities in China rapidly enacted regulations that extensively curtailed wildlife farming for food

but with 16 species subsequently transferred to a permissible list of species that may be farmed (for fur production, medicine, research and other purposes) (Li, 2020; The National People's Congress of The People's Republic of China, 2020; Xinhua, 2020; Forgey, 2020; Koh, Li & Lee, 2021). Some conservation and animal welfare organisations issued calls for global bans on trade and consumption of wildlife; some have called for the cessation of use of wildlife (Coalition to End the Trade, 2020; Singh Khadka, 2020; Lion Coalition, 2020), others have been more specific and called for these measures in relation to wild mammals and birds (WCS, 2020). Other commentators are urging caution and recommend an evidence-based approach to risk reduction (Booth et al., 2020b; Roe et al., 2020), which also considers the potentially negative impacts of banning certain wildlife trades on biodiversity (Challender et al., 2020b). However, we are not further forward in understanding the emergence of this virus beyond the linkage with other SARS-like viruses reported in bats and pangolins (Malaiyan et al., 2021; Zhang et al., 2021), but not proven to be similar enough to be considered progenitors of SARS-CoV-2 (Moran, 2021). This is further supported by recent reports (WHO, 2021d):

"Dr Liang Wannian at WHO mission briefing in Wuhan on Feb 9: First and foremost, we have conducted testing of the samples numbering 11,000 from different kinds of animals like pig, cow, goat, chicken, duck, and goose in terms of the serum sample testing as a kind of testing sampling from the livestock and poultry from 31 provinces in China from 2019 to 2020. The testing results of those 11,000 samples of SARS-CoV-2 were all negative. We have also done the testing related to the 12,000 swab samples from different kinds of animals in terms of PCR testing. The testing results were all negative as well and also from 2019 to 2020, we have conducted PCR testing for 26,800 samples generated from different kinds of animals that are distributed in 24 provinces in China. Again, the PCR testing results were all negative. Meanwhile, as regards for the testing of the samples from the wide animal, during the sample that were collected in the period of November 2019 to Match 2020, we have conducted testing of 1,914 serum samples from 35 different species of wild animals. The testing results of this antibody testing from the serological study were all negative. Also before and after the COVID-19 outbreak, we have increased our sampling sizes from Huanan Seafood Market and also we think Wuhan Municipality and other cities in Hubei Province and also the neighbouring provinces of Hubei. We have collected 50,000 samples of the wild animals covering 300 different species. With the PCR testing of those more than 50,000 samples, the testing results were again negative."

Chinese authorities tested tens of thousands of samples in many Provinces in China, both looking for antibody and or genetic antigen footprints, including hundreds of domesticated and wildlife species in trade, farming, and markets (WHO, 2021). More than two years after the initial cases in late 2019, and despite comprehensive searches, no animal has been identified as a reservoir of SARS-CoV-2.

4.6. Examining the data on the role of wildlife in endemic (epidemic) zoonosis

We examined the literature on endemic (and rare epidemic) zoonosis in wildlife and the wildlife trade with a particular focus on the main producer-consumer continents for wild meat (Africa and South America) and wildlife species traded for food (Asia). These are the continents where the majority of known emerging human pathogens (EHP and nEID) with a zoonotic origin occurred in recent decades. Potential sources of zoonosis are alleged to be more associated with tropical and subtropical countries (Jones et al., 2008; Allen et al., 2017), where diversity and prevalence of infections is higher (GBD, 2012) and in low income countries with animal-dependent economies (Molyneux et al., 2011). How relevant these analyses are to wildlife coming from controlled environments and human management systems is questionable, and these non-specific findings and generalisations are potentially misleading especially when considering trade risks. It should be noted that the commonly cited publications referred to EID hotspots (e.g. (Morens, Folkers & Fauci, 2004; Jones et al., 2008; Dunn et al., 2010; Morse et al., 2012; Hay et al., 2013; Peterson, 2014; Allen et al., 2017; Olival et al., 2017) use a broad definition of EIDs (which includes truly novel human diseases as well as those re-emerging or subtly changing through variants, AMR, changing geographies, and increasing incidence) and analyse the same or adapted lists of pathogens based on quite limited datasets that do not differentiate wildlife source (captive or wild), and which are mostly based on literature reviews rather than primary research.

The statistics about EIDs of zoonotic origin vary, with the most commonly cited reference being that 60.3% of human EIDs originate in animals (Jones et al., 2008). This analysis is not true to common definitions of EIDs and is a flawed capture-all attempt (Morand et al., 2018). It includes a high proportion of variants on known pathogens, emerging antimicrobial resistant organisms, re-emergence and/or, first time emergence of well-known zoonosis in new geographies. Further analyses effectively confound these results entirely whilst other descriptions use different definitions and lists often in analysis, but results are directly aggregated or compared directly or erroneously (Morand et al., 2018). As a result, percentages are often misquoted and misunderstood and standardised interpretation is extremely difficult. Without proportionality or significance indicators, they are likely to misinform about real-world risk. The often misquoted 71.8% of EIDs of zoonotic origin coming from wildlife from *Jones et al., (2008)* is based on the same broad definition of EIDs and zoonosis (Morand & Lajaunie, 2020), chosen for specific academic purposes, inclusive of all known or speculative associations and evolution of pathogens with wildlife, and not endemic zoonosis with a known reservoir as defined by WHO. This makes its use as a general principle on infections acquired directly or indirectly or through evolutionary processes, fundamentally misleading as it is often used to describe all EID of humans when it only refers to those arising from animals generally. A fairer description from these data

would be that wildlife are purported to, in some way, to be the origin of 43.3% of human EID pathogens but are rarely associated with endemic (or epidemic) zoonoses. This is particularly important to understand when these figures are used in the context of CO-VID-19 and similar diseases, which are truly novel infections in new hosts for which we do not have a proven source. In order to explain proportionate risk with respect to phenomena such as COVID-19, current models need to be much more specific about the EIDs they have evaluated and what the source populations were i.e. were they truly wild animals, captive-bred wildlife, domesticated or peridomestic species, or domestic variants of species and define the associated risk factors driving spillover or emergence if known.

Most global concern is raised about zoonosis of clinical significance and epidemic or pandemic risk. This amounts to relatively few diseases that, in this analysis, are defined as nEID or EHP. This focussed approach has been suggested in order to avoid confusion and enable better targeted policy in this area of disease control (Haider et al., 2020a). The sorts of risk that truly have societal and high economic impact are more closely related to the WHO emerging diseases of concern list (WHO, 2021c). These include, for immediate attention, Crimean Congo haemorrhagic fever, Ebola virus disease, Marburg, Lassa fever, MERS, SARS, Nipah and Henipavirus, Rift Valley fever, Zika, and Coronavirus diseases. Table 5 provides the current confirmed or unconfirmed status on species as originators, maintenance hosts or reservoirs of important emerging pathogens. Based on available data, only 5 of these diseases were listed as linked to the wildlife trade (IPBES, 2020) Ebola, HIV/AIDs, monkeypox, SARS, COVID-19. But other than monkeypox, wildlife trade is not a proven source, even if infection has been shown in some species that are traded. These are Zaire ebolavirus (commonly known as Ebola virus), SARS and COVID-19. From this evidence the only justified intervention (a ban on imports) in the wildlife trade was for rodents, which were the confirmed source of a monkeypox outbreak in the USA (Reed et al., 2004; Reynolds et al., 2007; CDC, NCEZID & DHCPP, 2018).

Table 5. Table of some of high concern recently emerged/emerging pathogens of humans and the current knowledge of species role as originators or reservoir/maintenance hosts

Disease name	Origin (unconfirmed - ?)	Reservoir or maintenance hosts (RH), intermediate host (IH)	Endemic/epidemic zoonosis	Risk factors
Ebola	Bats (?)	(?) - RH Forest mammals - IH	Rare event – spillover (?)	Bush meat, West and Central African forest ecosystems fragementation
HIV-AIDs	Chimpanzee (?)	Humans - RH	None	Lentivirus spillover leading to pathogen jump – two probable spillover emergence events historically
SARS	Bats (?)	None confirmed – RH Carnivores - IH	None – single spillover event 2002	Wet markets (?), human infection
MERS	Bats (?)	Domesticated camel (C.dromedarius) – RH	Rare zoonosis – most infection human to human	Occupational risk for spillover and risk in hospital settings for human infection
COVID-19	Bats (?)	None confirmed; humans likely - RH	Human disease with confirmed zooanthroponosis and rare (2 published) zoonosis events from mink in farms.	Wet markets (?), meat processing plants but this may simply related to concentration of human hosts and ideal environment for virus to spread and persist on surfaces, moist animal products.
Nipah virus infection	Bats	Fruit bats -RH	Rare indirect zoonosis – contaminated fruit and through pig intermediate hosts (historic)	Occupational with fruit picking, pig farm workers (historic)
Hendra virus	Bats	Bats– RH Horse - IH	Rare indirect through domestic horse host	Bat food trees and horse stables.
Lassa Fever	Rodent	Rodent - RH	Endemic zoonosis West Africa	Fragmenting forest crop agriculture settlement
Kyanasur Forest Disease	Primate (?)	(?) – RH Tick - RH Cattle, monkey, small mammals - IH	South Asia	Fragmenting forest domestic animals in proximity tick vector

Source: Prepared by the report authors.

Nguni cattle in Mozambique
Photo © Michael D. Kock

The biggest problem for analysis and generating scientific eviden-ce about wildlife zoonosis is that clinical and diagnostic data are globally absent or deficient, either due to real absence of a problem or poor recognition and inadequate monitoring of zoonosis from wildlife (whether in trade, captivity or in the wild). Recent publica-tions on zoonosis provide more balanced, evidence-based views on zoonotic risk from wildlife compared to earlier texts with inherent biases. These show how important domesticated animals and peri-domestic wildlife (i.e. species that are adapted to human landscape and resources) are to zoonosis (Johnson et al., 2015, 2020; Gibb et al., 2020). Certain RNA viruses can cause nEID and EHP due to their plasticity, human-human transmissibility, and distribution, undersco-ring that we do not need to be concerned with all EIDs as currently listed in various publications:

"… the number of zoonotic viruses detected in mammalian species scales positively with global species abundance, suggesting that virus transmission risk has been highest from animal species that have increased in abundance and even expanded their range by adapting to human-dominated landscapes. Domesticated species, primates and bats were identified as having more zoonotic viruses than other species." (Johnson et al., 2020)

In contrast, Mollentze & Streicker (2020) conclude that per-species risk is homogenous; just that species-rich groups (i.e. bats, rodents) collectively carry a richer accumulation of viruses. Gibb et al. (2020) supports this shift in thinking as to the likely sources for pathogens, showing analysis of:

"… 6,801 ecological assemblages and 376 host species worldwide, controlling for research effort, show that land use has global and systematic effects on local zoonotic host communities. Known wild-life hosts of human-shared pathogens and parasites overall compri-se a greater proportion of local species richness (18–72% higher) and total abundance (21–144% higher) in sites under substantial human use (secondary, agricultural and urban ecosystems) compared with nearby undisturbed habitats."

Further Johnson et al. (2015) report,

"In general, wild animals were suggested as a source of transmission for 91% (86/95) of zoonotic viruses compared to 34% (32/95) of viru-ses sourced from domestic animals, and 25% (24/95) with transmis-sion described from both wild and domestic animals ."

We undertook further analysis (*see SI-3*) of these 86/95 reported wild animal source viruses to attempt to obtain proportionate risk compared to domesticated animals. Only 7 of the 95 described were in any way significant in terms of frequency, risk, or impact on public health, (e.g. incidence and case fatality rates [CFR] in humans) (Table 6).

Table 6. Incidence and case fatality rates of 7 viral zoonoses from 86/95 reported from wildlife (Johnson et al., 2015) including source – selected with >10 cases annually (remainder considered insignificant burden)

Viral agent	Human Cases	Case Fatality Rate	Data origin	Source
Hanta	728	36%	Average annual USA	Rodent
Lassa Fever	~300,000	2%	Modelled annual West Africa 1980s -	Rodent (Mastomys natalensis) Agri-settlement forest domain Human to human (rare)
Marburg	12 (average annual but mostly 2 major epidemics)	88%	Total reported since 1967	Bat (Rousettus aegyptiacus) Primates Human – human Mining community
Monkeypox	294	11%	Africa annual since 2016	Human-human majority, primates, rodents spillover (including one wildlife trade related)
Yellow Fever	84-170,000 annual (modelled) 7,344 (962 lab positive) ~ 500	3% 14.2% 12-33%	Africa Angola 2015-16 South America Brazil 2016-17 epidemic	Sylvatic forest and Human – human urban cycles –various mosquitos + domesticated Aedes
Nipah	~10-50	40-70%	South Asia periodic outbreaks	Bat/fruit farms
Tick Borne Encephalitis	1774	~1%	Europe	Rodent
Zika	High incidence foetal death		Global (87 countries)	Human – human majority, spillover from primates

Source: Prepared by the report authors.

Many of the 24/95 viruses coming generally from animals were more often transmitted from domesticated animals than wildlife and this is supported by data that show domesticated animals have a clear, distinct, disproportionate role in the spread of DNA and RNA viruses amongst mammals (Wells et al., 2020). Table 4 is further evidence of the relatively insignificant global burden of wild animal zoonosis, also reported elsewhere (Kock, 2014). nEID quite often have high CFR initially, given naivety in the new host, but it may decline over time as the population adapts (Lavine, Bjornstad & Antia, 2021). This is a natural evolutionary pathway as microbes are better at persisting with lower CFR (Anderson & May, 1982). High CFR pathogens, although concerning to the individual, generally do not spread rapidly so it is the lower CFR viruses which often cause the greatest overall burden. This has been well illustrated by COVID-19, where the global CFR was 2.67, with a significant variation across regions (i.e. 2.49 in Asia to 3.40 in North America) (Ahammed et al., 2021). COVID-19 CFR will probably continue dropping with vaccines, shielding of vulnerable groups, and improved treatments over time rather than any material change in virulence.

Despite earlier suggestions that wild meat poses increased opportunities for zoonotic diseases (Karesh et al., 2005; Wolfe, Dunavan & Diamond, 2007; Karesh & Noble, 2009; Smith et al., 2012) our literature and expert review (see supplementary analysis), shows little evidence for substantive ongoing zoonosis from wild animals or wildlife trade, with a few historic examples of events that are often repeated in reports and literature. One of the only concrete examples relevant to trade is the monkeypox introduction into the USA and associated zoonosis across several states. This event affected relatively few people with no deaths, after infected rodents imported from Africa transmitted monkeypox virus to humans via pet shops (Hutson et al., 2007). This led to a general ban on rodent imports from Africa directly or indirectly to the USA (CDC, 2020a).

Countries with high levels of sanitary control on export/imports of animals or animal products run a lower risk from zoonosis from wildlife in legal trade. This is further likely to be true given the high proportion of the CITES-reported trade coming from a formal wildlife use sector (farmed, captive-sourced wildlife) rather than from the wild (Harfoot et al., 2018). However, in trade more generally, there remain illegal routes, laundering through farms, and unrecorded volumes, such as personal luggage where sometimes large amounts of wildlife product, such as meat is smuggled (Temmam et al., 2017). Legal non-domesticated animal imports – the so-called exotic pet trade – also suffer a similar problem of insufficient knowledge on risk in the traded species and limited documentation of this trade, with nearly 6,000 animal species under CITES alone. For example, CITES data are not representative of overall wild animal/tetrapod trade. African rodents are not CITES-listed and there is no information available to determine (reliably) whether they were wild-sourced or captive-produced.

In an attempt to estimate the quantity of wildlife origin zoonosis irrespective of the source population (trade or otherwise), *Kock (2014)* undertook a general illustrative review of recorded zoonosis of wildlife origin from the Global Burden of Disease database (IHME, 2021) and related publications. This relatively simple analysis showed very low annual case numbers for a range of prominent

diseases. For example, rabies is acquired in 99.9% of human cases directly from domestic dogs. European Union, inclusive of 27 countries where rabies is rare or absent, reports about 1 human case every 5 years usually from bats, and 2-3 cases of wildlife source rabies are reported in the USA annually (CDC 2021). Global incidences of wildlife acquired human rabies is on the order of 10-100 annually (CDC, 2020b). Very few of these diseases illustrated exceed a figure of tens or hundreds of cases globally annually. Some notable exceptions include some rodent diseases such as plague, Lassa fever virus, hantavirus, and leptospirosis where thousands of cases occur annually (see Figure 13).
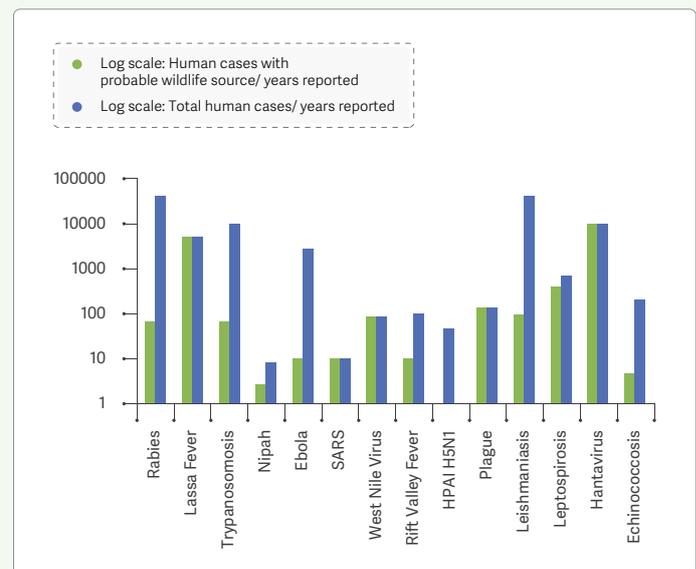
Figure 14. Estimated global mortality burden for selected wildlife zoonoses

Chart summarising key zoonosis where cases occur from wildlife source infection (light gray) compared to total human cases (dark gray). The difference is accounted for by transmission from human to human or domesticated animal to human showing the proportions (using a logarithmic scale due to the low contribution of wildlife zoonoses). *Source: Modified from Kock, 2014*

One way this potential problem of wildlife zoonosis has been examined empirically is via biological sampling for pathogens in individual traded animals as a measure of risk where data on zoonosis is absent. A US study at the John F. Kennedy airport between 2008 and 2010 showed potentially zoonotic Simian Foamy Virus (SFV) and herpesviruses detected in nonhuman primate wild meat (NHP) samples (Smith et al., 2012). All NHP samples were negative for Simian Immunodeficiency Virus (SIV) and Simian T-lymphotropic virus (STLV) sequences. All rodent samples were negative for Leptospira, anthrax, herpesviruses, filoviruses, paramyxoviruses, coronaviruses, flaviviruses, and orthopoxviruses. From this study, considering significance in humans, SFV infection (but no disease) has been reported in one study of 187 people occupationally at risk (exposed to nonhuman primates in zoos, primate centres, and laboratories): 5.3% of persons were seropositive, antibodies were detected by Western blot (WB)

Deer hunting in British Columbia, Canada (circa 2008).
Photo © Travis Nep Smith/Flickr

Bush meat market located in the village of Mbomo, on the periphery of Odzala-Kokoua National Park, Congo (Brazzaville). Meat available includes several species of duiker and monkey. Mbomo was the site of an Ebola outbreak between 2002-2003 with 128 deaths, within the local forested region large numbers of chimpanzee and lowland gorilla also died.
Photo © Michael D. Kock

analysis mainly in North America but also in Europe. However, they were not detected in traded animals. In theory, some occupational risk might be associated with the primates in the trade chain, but this remains undocumented. More recently, naturally acquired SFV infections were described in a few hunters living in Cameroon and in one person who had had contact with *Macaca fascicularis* in Indonesia, but cases are clearly rare or rarely reported and are not associated with disease.

4.6.1. Special case – African wild meat trade

We analysed a recent review by Kurpiers et al. (2016) on evidence of zoonotic diseases from African wild meat and trade and show that there is a paucity of evidence on zoonosis or zoonotic risks from wildlife and African wild meat (see Table 7).

Some of the discussion around zoonosis, and in Kurpiers et al. (2016), wildlife is centred around lists of pathogens identified in surveys and described as potential risks for zoonosis (i.e. hazards for human health). For example, studies were undertaken in the game industry in Namibia, but no evidence was found, just speculation about potential zoonosis and most of the references related to the domestic livestock industry. Much of wildlife (game) farming in southern Africa is not free ranging wildlife and part of wildlife trade, not wild meat by definition, but is likely a source of general zoonotic pathogens seen in livestock because they share the same husbandry and management risks of intensification and are often mixed together with domestic livestock. Wildlife is certainly a much lower risk than the conventional livestock industry simply based on the numbers traded in these formal wildlife ranching sectors, which require the same sanitary abattoir and processing standards as conventional livestock. These industries do not add any significant risk of emerging infectious diseases given the majority are herbivores. In conclusion, for the whole continent of Africa based on this critical analysis, there is not wide evidence for zoonosis from wildlife species in wildlife trade.

Table 7. Analysis of Kurpiers et al. (2016) contemporary review of zoonotic diseases from wildlife in Africa – highlighted events which confirm a zoonosis or suggest it

Disease	Event	Basis of Confirmation	Location	Associated species	Date source
Ebola virus	Single non-fatal case	Necropsy acquired infection	Cote d'Ivoire	Chimpanzee	(Le Guenno et al. 1995)
Ebola virus	260 human cases 71% CFR 9 other epidemics	Survey information only – hunted fruit bats eaten in one case Survey information only	Democratic Republic of Congo Luebo 2007 Various locations Africa	Fruit bat Great apes, primates, other bush meat	(Leroy et al. 2009)
Simian Immuno-deficiency Virus	Research studies, naturally acquired infection only in hunters. Zoonotic disease cases unproven.	Serology, PCR and sequence analysis	Cameroon	chimpanzee, gorilla, and monkey	(Apetrei & Marx 2004)
Nipah	497 people exposed	3-4 seropositive (associated with butchering bats) no disease	Cameroon	Bats	(Pernet et al. 2014).
Lyssa (rabies - Duvenhage)	2 cases only reported globally – 1. bat scratch whilst handling, 2. bat flew into face tourist in wildlife park camp.	Isolation from clinical cases	South Africa Kenya	Bats	(Paweska et al. 2006; Thiel et al. 2009)
Monkeypox	Circulating monkeypox	Serology positive 53/172 human samples no disease	Ghana	Bushmeat	(Reynolds & Damon 2012)
Lassa Fever	Hunted rodents bushmeat consumption	Slightly significantly higher risk of positive serology in hunters and consumers (not disease) compared to random contact.	West Africa	Rodent	Kenmoe et al., 2020; Lecompte et al., 2006; Ter Meulen et al., 1996); (Bonwitt et al. 2016)
Strongyloides fulleborni, Entamoeba histolytica and Balantidium coli Giardia intestinalis	13 faecals showed cross infection between people and primates in forested ecosystem no disease 2.1% of 48 no disease	Faecal examination	Africa		(Lilly et al. 2002) Magwedere et al., 2012

Source: Prepared by the report authors.

4.6.2. Special case – Asian wildlife trade

As mentioned in Section 4, wildlife trade is context dependant, and cannot be generalised under one umbrella. Asian wildlife trade has unique characteristics in comparison to other trade practices and markets. To some extent, with a higher adherence to farming of wildlife intensively at one end and retailing through wet markets at the other end, with a consumptive use of wildlife rooted in traditional beliefs and tradition (Thomas-Walters et al., 2020). This creates unique risks in terms of viral infection which thrives and persists under these new environmental conditions. In the case of Asia, there are few reported zoonosis directly associated with the wildlife trade, this should not be confused with potential zoonotic risk from wildlife trade (i.e. qualitative risk assessments where species are crossed with a datasets of pathogens found in that species) (Greatorex et al., 2016; Cantlay, Ingram & Meredith, 2017; Pruvot et al., 2019; Huong et al., 2020). It is assumed that the main risks of zoonosis from wildlife trade are in the live animal trade, some of which is from free-ranging wild animals, whilst the majority is farmed non-domesticated species (for meat and medicinal products from various parts of the bodies of animals, fur, and miscellaneous excretions such as civet faeces or for entertainment or as pets). The wildlife pet market was at one time driven by Europe and North America but now Asia is an emerging market (Roe, 2008; Smith et al., 2009). The scale of farmed wildlife meat and the fur trade in Southeast Asia and China puts these two industries as likely the most important traded wildlife commodity in relation to risk of zoonosis, given the large numbers and high densities of individual species kept in relatively poor sanitary conditions that are being moved alive to markets or for internal trading, usually without the strict regulations and controls applied to domesticated animal farming (Wong, 2019). The susceptibility of these species to SARS viruses adds support to these hypotheses but, whether these animal populations hold the secrets to origins of diseases such as COVID-19 is still speculation and it may well be that they simply function as amplifiers and proximate source for zoonosis. There are longer evolutionary histories of microorganisms exploiting opportunities for emergence in new hosts, which are complex and challenging to track. It will be easier to explore these complexities if we identify intermediate hosts and bridging species as this is where the real risk to human infection will lie. Scale in this context is all important. More than 14 million Chinese workers are reported to be employed in this industry (see Table 8), which shows the scale, but data on the numbers of animals and production per year are not readily available.

Table 8. Employment and direct output value of wild animal industry in China, 2016 (in a 2017 report by the Chinese Academy of Engineering on the development of the wildlife farming industry)

Industry	No. of Employment	Direct Output Value (Million CNY)
Fur Animal	7,600,000	398,483
Medicinal animal	210,800	5,027
Food animals	6,263,400	125,054
Exhibiting animals & pets	13,700	625
Experimental Animals	2,000	400
Total	14,089,900	520,616

Source: Prepared by the report authors.

This industry has been promoted in China for poverty alleviation on a regional basis to enhance rural and farming communities, and its growth is coincident with the period of the SARS-type virus emergence, suggesting this as a possible driver given the clear host adaptation to these viruses through frequent zooanthropy. Species in trade originating in fur farms which are known to have infection with SARS include mink, foxes, and raccoon dogs. These species have also recently shown to be highly susceptible to the SARS-CoV-2 virus and able to secrete or excrete it readily (Freuling et al., 2020). Masked palm civets were implicated in the SARS epidemic in 2003 (Cheng et al., 2007; Cyranoski, 2017). *Kan et al. (2005)* reported SARS investigations amongst market animals prior to a major culling exercise in China:

"The virus was identified in all 91 palm civets and 15 raccoon dogs of animal market origin sampled prior to culling, but not in 1,107 palm civets later sampled at 25 farms, spread over 12 provinces, which were claimed to be the source of traded animals."

In conclusion, it was never certain if the virus in the animals was acquired zooanthropically (from humans) or through some other pathway and no reservoir of SARS-CoV-1 or SARS- CoV-2 has yet been found.

4.6.3. Special case – Europe and North America wildlife trade

In the case of Europe and North America, the main concern is exotic pet trading, fur farming, and sport hunting (e.g. wild boar); which is significant in volume, with some importation of non-domesticated wildlife products for various food cultures (e.g. biltong – South African trade estimated at R 13,6 billion (US$ 900 million) in 2016–17) as well as illegal meat imports in luggage, particularly from West Africa (Chaber et al., 2010; Ecojust, 2020). The recent findings of SARS-CoV-2 virus infection of mink in Netherlands, Denmark, France, Spain, Sweden, Poland, Lithuania, and the United States (Cahan & 2020, 2020; Bekiempis, 2020; Koopmans, 2020; Reuters, 2020; Munnink et al., 2020b; ECDC, 2020; RFI, 2020a,b; Euronews & AFP, 2020)are of enormous concern. These are zooanthroponoses, i.e. infection or disease that primarily affects humans but is naturally transmissible to animals (with the reservoir or maintenance host being the human), with evidence of strain shifts and reinfection of humans, raising the possibility of a zoonotic reservoir and future zoonosis with this virus (Munnink et al., 2020a; Koopmans, 2020; ECDC, 2020).

Some studies have looked at the zoonotic disease risk from the trade in farmed wildlife and shown it not to be negligible, but cases of zoonosis in this trade are not apparently common or commonly reported, investigated, or documented. For example, in 2000–2005 a total of 246,772 mammals in 190 genera (68 families) were imported to the USA (Pavlin, Schloegel & Daszak, 2009) but the origins wild or captive bred could not be ascertained in the dataset. The most widespread agents of risk for zoonoses that have been reported in the species traded were rabies virus (in 78 genera of mammals), *Bacillus anthracis* (57), *Mycobacterium tuberculosis complex* (48), *Echinococcus spp.* (41), and *Leptospira spp.* (35). Genera capable of harbouring the greatest number of high-risk zoonoses were *Canis and Felis* (14 each), *Rattus* (13), *Equus* (11), and *Macaca and Lepus* (10 each). No actual zoonosis cases were documented in the study, and this scale of importation of <50,000 individuals per year is very small compared to the live domesticated animal trade, which is around 7 million individuals per year for the USA.

4.6.4. Special case – South America wild meat trade

In South America there are some estimates of the amount of wild meat traded annually (Rushton et al., 2005; Reuter, A., Kunen, J. & Roberton, S., 2018; Chaves, Monroe & Sieving, 2019), but little verifiable quantitative data, with most wild meat data skewed to primates and other mammals (Bueno et al., 2016; Reuter, A., Kunen, J. & Roberton, S., 2018). The Amazon is cited as a major contributor to the removed wildlife from forest ecosystems on earth (Charity & Ferreira, 2020). A recent report on wild meat consumption in Brazil stated that while subsistence hunting is legal in Brazil, the wild meat trade is prohibited by law. Across Amazonian states, illegal wild meat is common within regional markets and it is sold both nationally and across local borders, especially on the triple border of Brazil, Peru, and Colombia, where species such as capybara, paca, tapirs, deer, peccaries, and others are widely poached and sold (Charity & Ferreira, 2020). In Amazonas state, Brazil wild meat is a vital resource for rural communities with a mean per-capita meat consumption of 54.75 kg / person*1 year (Nunes et al., 2019) whilst over 44% of urban households consumed wild meat monthly (Parry, Barlow & Pereira, 2014) and patterns of consumption have been reviewed (Chaves et al., 2017). This practice also extends to other forested ecosystems in Brazil such as the Bahian Atlantic Forest (Castilho et al., 2019). In Colombian Amazon, the trend is down with domesticated animal origin meat increasing in volumes with wild meat becoming a luxury item (Van Vliet et al., 2015).

Beyond overviews of magnitude and species involved in Latin American wild meat consumption (Ojasti, 1993) there is little information on zoonosis relating to this wild meat trade in Brazil or any other South American countries, most of them related to vector-, food-, and water-borne diseases and landscape transformations (i.e. road network and deforestation). Vliet et al., (2017) provided a brief review of 13 studies describing parasites and bacteria in 18 wild meat species in Latin America and Caribbean which is summarised in Table 9.

Van Vliet et al. (2017) Table 9 also included data from *Kurpiers et al. (2016)* review of African wild meat (further analysed in our report see supplementary appendix *(SI-3)* and also included data from South East Asia. Here they reported a few papers identifying salmonella in axis farmed deer in Hawaii and presence of four viruses in "bushmeat" species from Asia (Nipah virus, SARS coronavirus, Ebola, A/H5N1) along with tables in annex of possible theoretical zoonosis based on pathogens reported in wild meat species. The only zoonosis cases confirmed from these viruses reported as potential zoonoses were Nipah virus via pigs in Malaysia (Mohd Nor, Gan & Ong, 2000) and suspected cases of SARS acquired from palm civets in restaurants in China (Li et al., 2005) ■

Table 9. Reported detection of zoonotic pathogens and zoonosis from wildlife in South America (Vliet et al., 2017)		
Animal Species	**Pathogen detected**	**Reported Zoonosis**
Lowland paca (*Cuniculus paca*)	*Toxoplasma gondii* *Echinococcus vogeli*	
Peccary (*Tayassu peccary*)	*Capallaria hepatica* *Brucella suis*	
Capybara	*Brucella suis*	
Ateles paniscus	*Capallaria hepatica*	
Porcupine (*Coendou spp.*) Opossum (*Philander opossum*)	*Trypanosome cruzi* (Chagas disease agent)	
Nine Banded (Dasypus novemcinctus) and Six Banded Armadillo (Euphractus sexcinctus)	Capallaria hepatica *Mycobacterium leprae* Trichinella spp. spp. *Coccidioides spp* *T.cruzi* Rickettsia typhi Pulmonary mycosis causing organisms	Leprosy

Source: Prepared by the report authors.

5 | Other elements of importance in the debate on wildlife, zoonosis, and disease emergence

The sections above provide the core situation analysis on the wildlife trade, but it is of value to describe some of the common narrative and evidence around non-trade aspects of this subject. Although not comprehensive they provide some extra background.

Considering heightened anthropogenic pressures on the environment and biodiversity there is a common narrative on these being drivers of infectious disease outbreaks, both emerging and re-emerging. This conclusion has been mostly based on modelling exercises which associate first confirmed presence of an emerging disease with various factors influencing broadly defined EID (Patz et al., 2004; Jones et al., 2008; Allen et al., 2017). Ecosystem degradation and modification are hypothesized to reduce the normal ecosystem's disease regulating capabilities (Millennium Ecosystem Assessment, 2005; Everard et al., 2020), which provide a natural barrier for the transmission of diseases from animals to humans. Socio-ecological changes at the interface also inevitably modify normal transmission dynamics and can increase human and animal exposure to potential pathogens and novel microorganisms. To better understand, and possibly predict, the role of anthropogenic impacts on the natural environment it is imperative to undertake more empirical and evidence synthesis studies linking environmental changes, pathogen epidemiology, and host ecology (White & Razgour, 2020).

5.1. Deforestation and other land use changes as an influence on emergence

Anthropogenic land use change refers to the change from one land use to another by humans for residential, agriculture, industrial, urban development, or other purposes (Lambin et al., 2001; Lambin, Geist & Lepers, 2003; Findell et al., 2017). Landscape modification is a common trait since humans moved from beginnings as small groups of hunter-gatherers to large settled agricultural communities millennia ago (Ellis et al., 2013; Steffen et al., 2015) and this change even then was associated with a shift in disease and health dynamics supported by paleopathology (Kock, Alders & Wallace, 2012). This change has accelerated in the last three centuries and it is estimated 75% of the Earth's landscapes have been significantly modified by humans (IPBES, 2019) and anthropogenic changes became planetary-altering processes (Steffen et al., 2015). Over the past century, anthropogenic impacts on natural ecosystems – such as agriculture intensification, urbanisation, and use of natural resources – reached unprecedented magnitudes, given way to a new geological epoch: The Anthropocene (Crutzen, 2002; Ellis et al., 2013; Hassell et al., 2017). Land use change occurs on a local scale, yet its additive impacts are undoubtedly now the main threat to biodiversity and a key driver of global environmental change, altering entire landscapes, significantly affecting climatic and hydrological cycles, biodiversity, and reshaping infectious disease patterns, with an emphasis on livestock, domesticated and peridomestic animals (Gottdenker et al., 2014; Newbold et al., 2015; Allen et al., 2017; McMahon, Morand & Gray, 2018; Bloomfield, McIntosh & Lambin, 2020).

The extensive network of anthropogenic modifications to the environment creates a complex array of landscape configurations, fragmenting habitats and reshaping species distributions (Mendoza et al., 2020; Bloomfield, McIntosh & Lambin, 2020). Rapid human expansion threatens the Earth's biodiversity, leading to extensive losses of wilderness areas (Watson et al., 2016) and, so far, efforts to protect them have had limited success with some exceptions such as Antarctica protected by treaty (Antarctic Treaty, 1959). Since 1990, an estimated 420 million ha of forest has been lost, and although the overall rate of decline has decreased, the rate of deforestation is still substantial at a rate of 10 million ha per year (FAO, 2020b). The loss of forest is not equivalent across the different regions nor types of forest, with most of the forest converted to other land uses (mainly agricultural and grazing lands) affecting the tropical domain (FAO, 2020b).

The loss, in particular of forested tropical regions with high wildlife biodiversity levels, has been postulated to come with important EIDs risk (Allen et al., 2017). Deforestation, fragmentation, and land cover change have been identified as main drivers of infectious disease emergence by facilitating the contact and transmission of infectious diseases, in particular vector-borne diseases (Jones et al., 2008; Gottdenker et al., 2014; Bloomfield, McIntosh & Lambin, 2020). By decreasing the total available area and fragmenting the available habitat for biodiversity, deforestation increases the edge effect in the landscape, facilitating the interactions between pathogens, vectors, and hosts (Patz et al., 2004). Landscape modifications transform biotic and abiotic factors at the local and regional scales that increase the risk of spillover events however, the mechanism of disease emergence are complex and the novel interlinks difficult to identify, which makes predicting the emergence of new zoonoses an extremely difficult (Wolfe et al., 2005).

There remain many uncertainties around precise mechanisms by which deforestation and other land use changes affect the pathogen emergence landscape (Plowright et al., 2020), but there is evidence of the positive benefits to public health of forest conservation (Pienkowski et al., 2017). There are some clear associations and a few convincing arguments and pathways described for particular diseases, with most zoonotic outbreaks not being an EID (Morand & Lajaunie, 2020). Gottdenker et al. (2014)'s extensive review of 30 years of literature on anthropogenic land use change and infectious disease showed *"Most papers (66.9%) were observational, 30.8% were review or concept papers, and few studies (2.3%) were experimental in nature, with most studies focusing on vector-borne and/or multi-host pathogens".*

This review well summarised the knowledge on this subject:

"In response to anthropogenic change, more than half of the studies (56.9%) documented increased pathogen transmission, 10.4% of studies observed decreased pathogen transmission, 30.4% had variable and complex pathogen responses, and 2.4% showed no detectable changes."

Another paper in preparation (Reaser et al., 2020) provides an excellent perspective on the subject of land use induced spillover of microorganisms. They use a broad evolutionary perspective on zoonosis but focus mostly on spillover of pathogens and provide examples, mainly from vector-borne diseases which provide the best evidence for impact on disease emergence.

Two important statements from this paper (highlighted) support our own analysis and conclusions:

"Despite the severity of the implications for human health and well-being, land use-induced spillover is not a well-studied phenomenon across ecological systems."

And further:

"However, research findings reveal that the relationships between land use change and wildlife disease are not easily generalised; different scenarios arise depending on the geographic location, ecosystem type, current and historical land uses, species of pathogens and animal hosts involved, the way the pathogens are transmitted, and animal-human dynamics of proximity."

Which emphasises why our analysis urges caution when coming to conclusions on pathways to emerging infectious diseases and simplistic solutions too commonly advocated, also supported by other authors (Pienkowski, Bickersteth & Milner-Gulland, 2019). There are a number of examples of sylvatic (wild animal) diseases which spillover after increased contact at the forest edge, directly like Ebola (assumed from multiple species association with infection of humans) or through mosquito vectors, like yellow fever (Kock, 2015). Recently this effect has been elegantly shown for Monkey Fever in India, where forest fragmentation and edge effects are critical to its emergence and where cattle are co-risk factors as tick vector abundance is promoted by the cattle (Walsh et al., 2019). The majority of zoonoses are more usually in peridomestic environments (Albery et al., 2021), where certain wildlife, especially rodents, have adapted to human landscapes and become abundant, examples are plague (*Yersinia pestis*) 1-2,000 cases per year and Lassa fever (*Lassa mammarenavirus*) <500,000 cases per year (Asogun et al., 2019). Quite fundamental to the epidemiology of new pathogens, wherever they arise, is that human populations are on the increase along with their domesticated animals, which is why the forest is fragmented and the landscape changes. Domesticated animals and synanthropic wildlife can then act as an amplifier or an evolutionary step in bringing potential pathogens to humans from nature.

5.2. Agriculture and disease emergence

The effects of deforestation and land use change are undoubtedly important for human health, domesticated animals, and wildlife populations (Patz et al., 2004; White & Razgour, 2020; Reaser et al., 2020) but in the context of disease emergence they relate not only to deforestation but also a range of other anthropic changes, most important being replacement agriculture (Shah et al., 2019), which accounts for 61% of landscape change (McFarlane, Sleigh & McMichael, 2013). A good example is agroforestry with palm oil plantations and fruiting trees which increase synanthropy with species like bats and rodents and are associated with increased disease emergence and zoonosis (Pulliam et al., 2012; Wallace et al., 2014; Morand & Lajaunie, 2020).

In more specific terms, for EIDs, science would need to prove causality from these processes, which is a much more challenging objective. With only 40% of the world's remaining forests conserving high integrity (Grantham et al., 2020), a key question is whether society

and political power will respond to calls for restoration of ecosystems in order to restore stability in pathogen dynamics? Is the threat so great that people will accept foregoing exploitation of these resources, and can they achieve their socioeconomic objectives by other means leaving nature undisturbed? If history is a teacher this is unlikely at least for the present, especially in countries which have recently emerged from relative poverty.

On the other hand if these disease phenomena are added to the other concerns for human health from climate change, pollution, etc, then a general change in development policy and economy might emerge, but its scope needs to be much more extensive than currently perceived. Saving a few protected areas or even small ecosystems will not go far enough to restore ecosystemic stability. The current 12% of terrestrial land for protection of biodiversity is totally inadequate but hard fought for and in many cases worse, it is ineffective as a protective measure. As the departing chief scientist of the Department for the Environment and Rural Affairs in the UK put it:

"to restore ecological systems that will prevent UK contributions to climate change and other negative effects of land exploitation, will require restoring 40% of the UK land to nature, basically forest".

This is the same figure given in (Leclère et al., 2020) of the land requirement for global terrestrial biodiversity recovery that will be needed from land currently transformed for human purposes. At this scale such conversion is currently socially and politically untenable so alternative solutions such as removal of perverse incentives will be important in the short term, although not guaranteed to work either.

Since most of the emergence and zoonotic opportunities occur in the domesticated or peridomestic landscape and at boundaries of human environment with natural areas, this should be a focal area for research and action (Gibb et al., 2020). If mitigation is possible through, for example, reduction in forest or habitat fragmentation this would reduce the opportunity for emergence Morand & Lajaunie (2020) reinforce the uncertainties around the narrative on EID and forest degradation and fragmentation showing in their global study that the great majority of the zoonotic outbreaks are not emerging infectious diseases, but a mixture of known vector-borne diseases and other zoonoses. They state:

"We find that the increases in outbreaks of zoonotic and vector-borne diseases from 1990 to 2016 are linked with deforestation, mostly in tropical countries, and with reforestation, mostly in temperate countries. We also find that outbreaks are associated with the increase in areas of palm oil plantations."

The criteria used for defining anthropogenic impacts and EID are very broad and mostly do not specifically relate to the rapidly evolving novel pathogens that have become of increasing concern and are of pandemic risk such as influenzas and coronaviruses (WHO, 2020a,b). It would be wrong therefore to take crude associations and justify an argument that it is generalised environment change or bio-

diversity loss that is the proximate risk factor for these EID. A main argument given for this effect is that there are new pathways for emergence caused by greater contact rates between humans and a wider landscape and biodiversity, but this is contradicted for most species by the massive decline in wildlife populations, and the chance of human-wild animal contact may well have reduced over recent centuries except for the much fewer peridomestic/synanthropic wildlife species which are now abundant (e.g. bats and rodents).

There are a few examples where environmental change has been justifiably associated with significant emergence events, such as the recent Ebola outbreak in West Africa in 2013, which was a very different case to the earlier sporadic village level rural outbreaks affecting only a few people, whereas here the disease was urbanised leading to thousands of deaths. A hypothesis was promulgated for the emergence driven by environmental change linked to global economic effects, changing agricultural practices and investment, settlement and transport networks in West African forest (Wallace et al., 2014, 2016). In other words, there may be many zoonotic events that occur without consequence, when the human host community infected cannot support sustained circulation but when certain epidemiological conditions are satisfied, such as numbers of susceptible humans and connectivity to larger populations, then the "adaptation" to the new host is "completed" through an epidemic or pandemic. The pattern for emergence of HIV/AIDs pandemic and EVD seem to have follow this pathway. The different epidemiologically important conditions may be just as critical to emergence, such as simply human and domesticated animal abundance, the suitability of human landscapes for some species, intensifying agriculture and food systems, extensive transport networks and other infrastructural changes and shifts in biophysical processes. Again, as with many analyses on EID the baselines used vary and land use change has been ascribed to underpin disease in as much as 50% of EID, 31% in analysis of more recent datasets (1944-2008) (Keesing et al., 2010) or more specifically to 22% of more strictly defined EID (1788 – 2010) (McFarlane, Sleigh & McMichael, 2013).

Further investigations are needed to better define the mechanisms by which human activities and the resulting habitat modifications have created and transformed beneficial ecosystem services such as disease buffering into *disservices*. One likely new channel is intensification of the interface between humans and other species through settlement, in complex biodiverse habitats and connectivity to large host populations through transport systems, increasing the overall risk of explosive disease transmission (Everard et al. 2020). HIV/AIDS emergence around the mid-20th Century is most likely explained by this phenomenon in Central Africa. Modified ecosystems bring wild species into closer contact with humans and their livestock, people, and domesticated animals invade wild spaces, and settlement increasing the risk of peridomestic wildlife species establishing. Thus, infectious disease transfer is theoretically likely by these processes increasing contact rates, reshaping transmission patterns and thereby, increasing the frequency of emergence and re-emergence of infectious diseases (Allen et al. 2017; Bloomfield et al. 2020). However much of this evidence base is hypothetical and based on models; true spillover risk from wild animals is far from conclusive for any disease in any context (Wilkinson et al 2018).

5.3. Animal industry and emerging pathogens

This aspect has been covered quite extensively in section 4 but it is worth reiterating here that In order to understand the landscape for emerging pathogens of humans from exploitation of animals for food and other production systems, a nuanced view is needed. Firstly, attention to emerging infectious diseases is more often focused on wildlife species, despite the fact the vast majority of different zoonosis is from domesticated species (Leibler et al., 2009) Figure 2. Post second world war, agricultural intensification and industrialization including infrastructure – hydrological engineering and factory farms – have been associated with more than 25% of all – and more than 50% of zoonotic – infectious diseases that have emerged in humans (Rohr et al., 2019).

Industrial livestock production in Brazil.
Photo © Daniel Beltra/Greenpeace
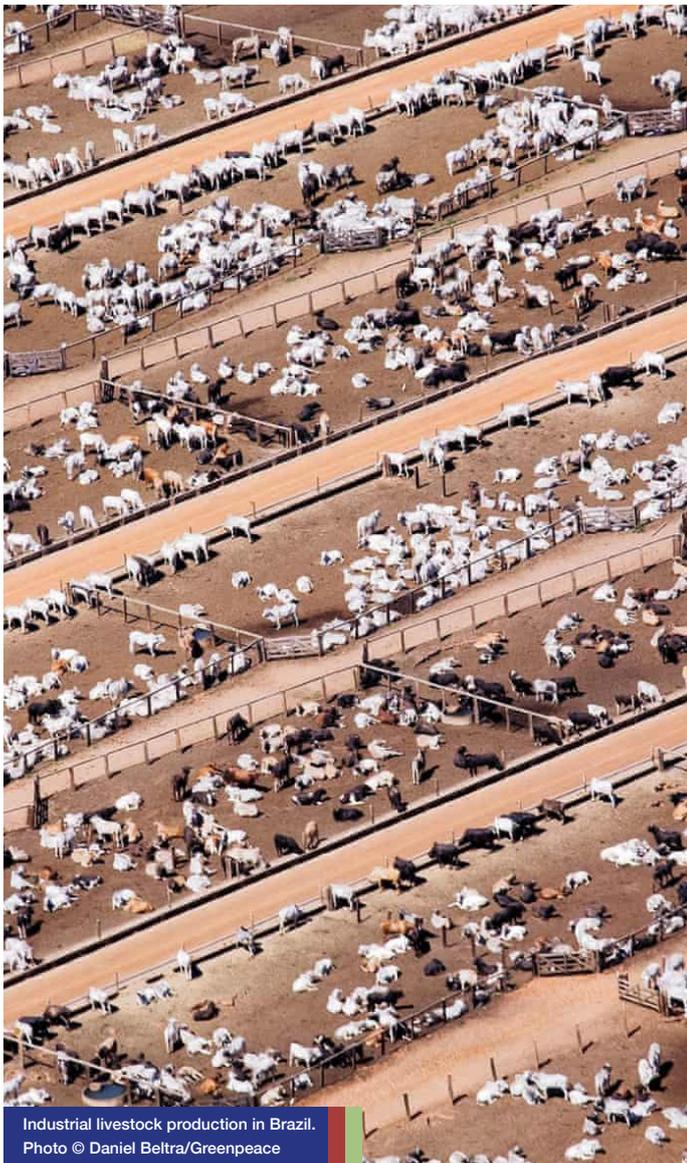
5.4. Growth and globalisation of transport networks

In terms of direct and food borne transmitted infections from animals, and associated epidemics and pandemics, there is no doubt that the growth in transport infrastructure, animals, and animal product movements globally, has transformed the disease landscape (Fèvre et al., 2006; Findlater & Bogoch, 2018; CDC, NCEZID & DHCPP, 2018; Du et al., 2020; FAO et al., 2020; Haider et al., 2020c; UNEP & ILRI, 2020; Hautefeuille, Dauphin & Peyre, 2020; IPBES, 2020; Khanh et al., 2020). This change is important for infectious disease, especially those pathogens which are transmitted directly between humans/animals, but it is also relevant for vector borne disease where movements of vectors provide opportunity for new cycles of infection. Isolated ecosystems result in slow or limited spread of diseases outside of the ecological boundaries and often there is insufficient population to sustain certain pathogens. This was likely the case early on in many diseases e.g. HIV/AIDs and EVD (Rugarabamu et al., 2020). Recent emergence of serious pathogens has been directly associated with human movements regionally and globally such as the coronaviruses. This is not a novel process and involves not only human and animal movements but also animal products, and first started thousands of years ago as people and animals (products) moved around on foot and eventually transcontinentally on sailing ships, taking months to years in past centuries. The situation today is a globalised world with almost complete interconnectedness of populations across landscapes and continents, via fast moving ships, motor vehicles or trains and leading to rapid spread of pathogens globally through air travel over a matter of hours, days, or weeks (see Figure 14). The growth in air travel has been exponential and probably the single most important factor in the COVID-19 pandemic (Haider et al., 2020c).
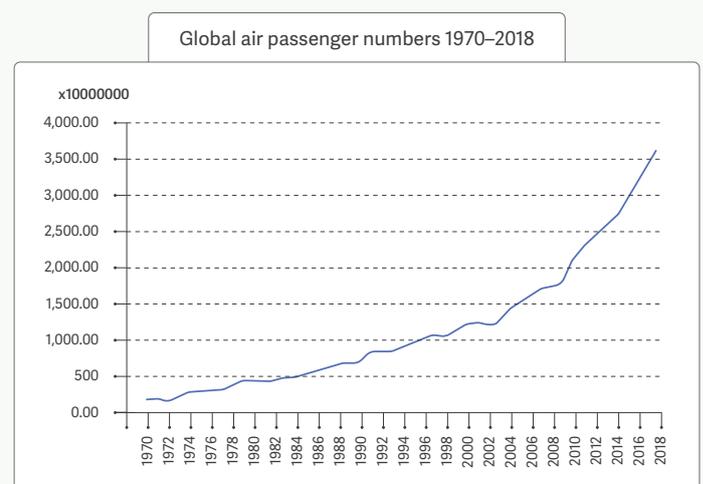

Figure 15. Graph of exponential increase in air travel passenger numbers over recent decades (thousands of millions)

Source: The World Bank, 2020.

The risk of disease from the growing international animal trade has been long recognised (Fèvre et al., 2006) and World Animal Health (OIE) was set up primarily to establish standards and guidelines for each country to develop a framework to regulate livestock trade and reduce infection risks. Every port of entry to countries has an animal and plant inspection service focused mainly on disease, collecting data, and interrogating where any anomalies in permitting exist. Despite this, capacity to detect potential zoonotic pathogens in large shipments is limited. The detection of ill and/or infected animals is largely dependent of the countries' investment on biosecurity practices and would only be likely to occur when an animal shows signs of sickness, was dead on arrival, or required quarantine; unless there are active surveillance measures in place (e.g. in accordance to the vaccination status and/or country of origin). Nevertheless, formal domesticated animal trade usually requires rigorous risk assessment and surveillance of diseases in each country. There is a major gap in this sanitary approach by OIE and governments and this relates to wildlife where trade in reality this is not effectively done. From a biosecurity angle, even if there is a requirement to monitor diseases of livestock which are reportable, very often this does not include livestock disease that occurs in wildlife nor zoonosis, and illegal trade has no control on it at all. The need for improvements generally in monitoring zoonosis has been expressed by some authors and application of Hazard Analysis and Critical Control Point (HACCP) processes which are vital to food safety should be more generalised (FAO & WHO, 2001; FDA, 2018). Despite this, the evidence remains scarce that there is risk of EID from this route as few examples of zoonosis arising or animal disease emergence through the trade are being reported.

Figure 15 shows that Africa is the only continent largely without this intense connectedness to and from populations (i.e. through movements of live animals and or their products) globally. There are some local movements that are highly significant out of Africa to Middle East for the Hajj which are not highlighted in this map (Mali, Sudan and Somalia FAO STAT on live animal trade). It does not take many animals imported into a continent, with susceptible animals infected by novel pathogens, for the recipient region to be largely impacted. The Great Rinderpest Pandemic in the 1890s started from imported cattle from India had a profound influence on the continent. Since colonial times trade in live animals into Africa (Littlewood, 1905, pp. 1903-04–05), other than some AID financed so-called improved breeds for dairy, pig, and poultry industry, trade has been minimal with the most significant being poultry into Egypt, Libya, and Uganda (Levitt, 2020; FAO, 2021) (FAO STAT on live animal trade). Many imports of animal products to Africa stopped in 1997, with the advent of bovine spongiform encephalopathy in Europe (also a zoonosis) but trade has reopened since (e.g. Ireland to Egypt in 2016). This does not mean pathogens unique to Africa do not travel and are not emerging in other continents. As rinderpest demonstrated it does not take many animals to start a pandemic. Recent examples include the emergence of African Swine Fever (ASF) in Eurasia. The transfer of ASF to Portugal from Africa in the 1950s is thought to have taken place via contaminated food waste coming from African airline flights and/or ships docking at seaports, then fed as swill to pigs (Van Schepen & Kunesh, 1981; Costard et al., 2009; Cwynar, Stojkov & Wlazlak, 2019). This first wave was eradica-

ted but followed in 2007 with a second, with the vehicle of transmission thought to be the use of contaminated meat products again fed to pigs from international ships arriving at the Black Sea Port of Poti (Terpstra & Wensvoort, 1986; Gogin et al., 2013; Lange et al., 2014). More recently Lumpy Skin Disease was introduced through the live animal trade into the Middle East and on to Turkey and Eurasia. Concerns over African-origin disease has also influenced trade in wildlife species such as tortoises, which can carry the vector for heartwater a serious disease of livestock with the tick transmitted parasite carried in many wildlife species, where they cause no harm (Burridge, Simmons & Allan, 2000). So, it does not necessarily take live animals to create disease emergence, animal products can also create hazardous conditions, and probably to a much greater degree.
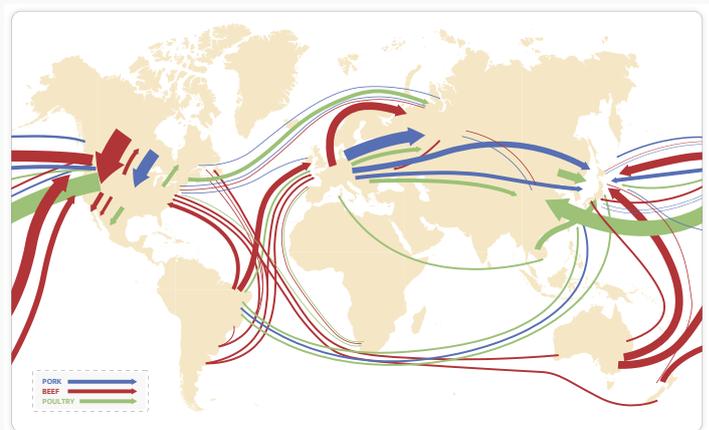
....
Figure 16. Map of the livestock trade globally showing majortrade routes in commonly traded domesticated animal-based food
....
Source: Karesh et al., 2017.

The challenge that globalisation has presented to humanity at its current population level is profound in the context of pandemics. Although the spread of disease through transportation has been known for centuries, in the modern age, COVID-19 has demonstrated the speed and extent of pathogen spread once established in a city that is interconnected nationally, regionally and internationally through air travel. Risks to different regions vary but the inability of global health security systems to prevent pandemics in this instance and with previous examples of influenza through conventional disease control measures such as quarantine. Public health messaging and monitoring is sobering (Haider et al., 2020b), without radical changes in the political economy, which is currently reliant on globalisation for growth, or through greater restrictions on air travel, the risk of repeat human and animal pandemic events remains high. Prediction, awareness, and response to nEID is clearly inadequate with current public health systems and levels of international collaboration and the feasibility of predictive systems are questionable. Sufficiently sensitive detection systems to identify the sudden emergence of a novel pathogen in an unknown species that is able to transmit to humans and also to detect the index case and

its location, globally, in real time is not likely to be practical or economically viable despite optimistic views (IPBES, 2020). The most likely effective and feasible policy to prevent pandemics is action to isolate the disease once the organism is detectable, with conventional disease control systems such as quarantine or lockdown early enough to prevent spread, and subsequently through achievement of population adherence to public health advice and regulation. *Crosier et al. (2015)* propose that in prevention of public health emergencies such as pandemics:

"Policy makers should prioritize investment in the skills and expertise required to achieve desired behaviour changes. Audience research should be conducted throughout the planning cycle to inform national communications strategies. This should include insights to inform the segmentation of public audiences, targeting of messages and consideration of content and emotional tone most likely to achieve desired behavioural outcomes".

In this context, the importance of different political systems and societal responses to public health regulations in COVID-19 outcomes has been significant. Initially, there was an unexpected and paradoxical effect in developed countries. Countries with the highest Global

Health Security Indices – a suggested measure of preparedness for pandemics and highly rated in the Joint External Evaluations by WHO (WHO, 2018) – suffering far more impact from COVID-19 (Haider et al., 2020b); this will reverberate around policy and development discussions on health systems for some decades to come. The current evidence of return on global investment in pandemic preparedness to date is weak, so improvements are justified but these are likely to be most effective through actions in the political sphere (e.g. international cooperation), behavioural health sciences, investment in public health systems, well-targeted surveillance systems and rapid response, rather than through predictive systems. Current passive surveillance systems are unlikely to detect nEID because it takes time for the health systems to detect emergence, spillover, and early circulation on the ground (i.e. abnormal incidence, atypical symptoms, etc.) whatever pathogens exist in theory (see Box 2 for examples). However, it would be sensible to at least enable more rapid control over air travel (including air cargo) in the face of epidemics of nEID (Haider et al., 2020c), improve monitoring of known zoonosis in animal-human interfaces, whatever the species, that are transported globally, through conventional animal health tracking.

Box 6. Examples of where health systems have failed to detect infectious disease emergence

HIV/AIDS is likely to have first emerged more than 50 years before being first confirmed as a disease entity (Giles-Vernick et al., 2013)

PREDICT - despite the largest focused investment in emergent pathogen detection (USAID PREDICT project) for over a decade in Africa the following has been observed:

"Although PREDICT almost certainly discovered hundreds of potential zoonoses, their true zoonotic potential is almost impossible to assess, leading to the surprising statistic that the programme only led to one conclusive discovery of a zoonosis, the Bas-Congo virus.7" **(Carlson, 2020)**

... and notably despite a focus by PREDICT on Ebola viruses, the first major EVD epidemic in West Africa was not predicted (Oliribe et al 2015 Clinical Medicine 2015 Vol 15, No 1: 54–7).

Evidence continues to emerge that SARS-CoV-2 may well have been circulating much earlier than first reported in the Hubei Provence (China) (Pekar et al., 2021) and possibly in Europe (Carrat et al., 2021).

Source: Prepared by the report authors.

5.5. Wildlife translocation

Conservation organisations and wildlife managers have been sensitised to the need for consideration of wildlife diseases and disease threats from and to wildlife in their work especially where there are interventions such as translocation, reintroduction, rehabilitation, confiscations. IUCN has catalysed a number of documents to assist in the processes, such as OIE and IUCN's *Guidelines for Wildlife Disease Risk Analysis* (OIE & IUCN, 2014), IUCN's *Guidelines for the management of confiscated, live organisms* (IUCN, 2019), and *Guidelines for Reintroductions and Other Conservation Translocations* (IUCN/SSC, 2013), while rehabilitation and training tools have also been developed through various SSC Specialist Groups (Jakob-Hoff et al., 2014; Moehrenschlager, 2017) . Disease risks associated with rehabilitation and confiscations of wildlife often involving translocations and introductions pose potential risks, but zoonosis frequency is poorly understood rather like wildlife trade risks in general.

In the formal wildlife conservation and management sectors disease issues arising during activities are relatively low risk due to the awareness and concern on this topic (Sainsbury et al., 2020). In the more informal sector of rehabilitation and confiscation which are on the increase as wildlife populations collapse and rescue of wildlife becomes a perceived benefit to conservation, the issue of disease is not so well understood and presents a more significant risk. Literature on this aspect is very limited (Kock, Woodford & Rossiter, 2010; Moehrenschlager, 2017; IUCN, 2019; Soorae, 2021) and largely overlooked in many situations (Stitt, Mountifield & Stephen, 2007).

5.6. Climate change

The human-driven increase in the concentration of greenhouse gases has caused an increase in the Earth's temperature since the 1950s. Climate change will likely have impacts on future disease emergence (Curseu et al., 2009; IPCC, 2014) as wildlife and people move due to adapt to their new environment, having very much direct impact on the emergence and rate of emergence of novel pathogens but a lot is uncertain in this respect (Hess et al., 2020). For example, the effect on mammals and birds and their microbiomes as temperatures exceed their adaptive capacity, could stress populations, create novel species assemblages, disrupt natural disease dynamics creating unusual wildlife disease emergence and potential risk for spillover events (Carlson et al., 2020). Theoretical studies on SARS-like virus emergence have postulated how shift in species diversity (e.g. bats) possibly due to climate change could have been a factor in the human emergence (Beyer, Manica & Mora, 2021). Certainly, climate change has a considerable influence on the spread of pathogens and vectors (e.g. by changing the habitat of natural hosts or expanding/reducing species' habitat) into earlier unaffected landscapes, as temperature and humidity effects change the ecologies of whole geographies, enabling establishment of vectors and changes in seasonal cyclicity of parasites.

For almost three decades, there has been scientific consensus that the Earth's climate has significantly warmed over the past 200 years and human activities are the primary source of greenhouse emissions gases and its global climatic effects (Oreskes, 2004; Cook et al., 2013, 2016). There is a growing body of evidence and interest on the links between environmental conditions and human health (WHO, 2017; Watts et al., 2018), whereas little attention has been paid to the links between emerging infectious diseases (EIDs) and environmental change (Jones et al., 2008; Di Marco et al., 2020). Climate change potentially will worsen future health risks but not everywhere or for everyone, and it will add uncertainty and complexity to our understanding of potential emerging infectious diseases by modifying the temperature, humidity and seasonality (Patz & Hahn, 2012; IPCC, 2014; Cohen et al., 2020). The climate change effects on human, animal and overall environmental health will be particularly important in climate vulnerable regions, such as the arctic, island nations, and developing and low-income nations (Blaha, 2012; IPCC, 2014; Zinsstag et al., 2018). A number of examples of animal disease emergence and mass mortality have been documented, related to weather and climate effects (Kock et al., 2018; Stephens et al., 2018).

Today, the climatic-driven diseases may seem marginal in comparison with other, more pressing, stressors. But they are already impacting the health of climatic vulnerable human populations and indigenous communities (IPCC, 2014; Dudley et al., 2015) and there is evidence that increasing temperatures and or severe weather fluctuations will likely lead to an increased transmission of diseases. Climate change disrupts the social, environmental, and economic conditions of the world (IPCC, 2014), these conditions often blur among each other and are hard to delimit. The effects on health and well-being make it increasingly important to understand the links, quantify the possible effects, and characterise the intricate connections with other phenomena (Stone, 2008; Charron, 2012;

Coal-fired power station located in the highveld province of Mpumalanga in South Africa. As emphasised at COP26 in 2021, over-reliance on coal is a significant constraint if nations are to address climate change and reduce its contribution to global emissions. Photo © Michael D. Kock

IPCC, 2014; Zinsstag et al., 2018). Hence the need to adopt a unified ecosystem approach to health, or Eco-Health (Rapport et al., 1999; Zinsstag et al., 2011) (Rapport et al. 1999), and this is further developed in the concept of One Health that accounts for humans, wildlife, pet animals, livestock, socioeconomics and the environment and social settings (Zinsstag et al., 2011; Charron, 2012; Wallace et al., 2015; Roger et al., 2016; Aguirre, 2017).

Climate change-driven health risks will impact human and animal populations in four main ways: (i) potential changes in the geographic distribution of infectious diseases; (ii) expansion of vector borne diseases some of which are zoonotic (e.g. West Nile Virus, Crimean Congo Hemorrhagic Fever); (iii) changing migratory patterns of animals (including humans); (iv) impacts to food and water security, availability and quality; among others (Patz & Hahn, 2012; IPCC, 2014). Climate change will have intricate and challenging effects on disease risk that will be difficult to predict, especially because of the intrinsic difficulty to predict the emergence of infectious diseases (Stone, 2008). It is likely that these disruption mechanisms will interact with each other and other disturbances, resulting in varying pathogen-host-environment interactions (Roger et al., 2016; Carlson et al., 2020; IPBES, 2020; Cohen et al., 2020).

The scientific consensus on climate change attributes a few major factors to this problem, fossil fuel use and other industrial processes producing CO2 and Green House Gases (GHG) and including food production, most notably animal-based food systems, whilst deforestation and ocean acidification is increasing the mitigation

challenge as it removes the main natural process for removal of excess CO2 from the atmosphere through these biomes sequestering carbon. Considerable progress is being made through the Paris Agreement but although rights to health are implicit overall public health mitigation aspects lag behind most IPCC activities (IPCC, 2018; Ripple et al., 2019).

The implementation of integrated surveillance, climate change mitigation and adaptation responses under a One Health framework can significantly benefit public health and provide a framework to mitigate the health effects of climate change (Semenza & Zeller, 2014; Dudley et al., 2015). In alignment with SDGs 2, 3 and GHSA, organisations such as WHO, FAO, and OIE have converged on a One Health policy which has recently been expanded under the One Health Council to include UNEP, bringing the environment (potentially including wildlife trade) strongly into the debate (UNEP, 2020). Local and international interdisciplinary networks will play a major role in identifying, preventing and adapting to strategically respond to current and future health challenges resulting from climate change (Di Marco et al., 2020; Phillips et al., 2020). A One Health approach – that accounts for the links between the environment, human, animal, and plant health – has shown social and economic benefits (Schelling et al., 2005; Paternoster et al., 2017) and substantial positive impacts on public health (Watts et al., 2015).

5.7. Antimicrobial resistance

AMR is considered a part of the EID complex, according to widely used definitions but its relevance to wildlife trade and free ranging wildlife is minimal and for the purposes of this situation analysis will not be covered in depth. AMR constitutes a high proportion of EID in many assessments, and this can distort the picture when considering wildlife sources, which might be able to be hosts of AMR organisms. Wildlife is not likely to feature much in the epidemiology of AMR which is much more closely associated with the human health environment and food borne transmission of resistomes from domesticated animal farming, where antibiotics are widely used (Holmes et al., 2016; Jee et al., 2018).

Nevertheless, AMR is a serious public health issue worldwide and it is mostly associated with environments with high use of antibiotics such as hospital and clinic settings and livestock systems with high use patterns. The emergence of the plasmid mrc1 in China with the use of colistin in pig farms, followed by the global dispersion of the plasmid, is a good example to highlight the importance of livestock and feed additives (and the lack of involvement of the wildlife) in the context of AMR (Liu et al., 2016; Olaitan et al., 2016, 2021). There is a spillover of resistomes into the environment through sewage and runoff etc and some absorption of these into animals including in terrestrial and marine environments. The importance of the environmental aspect of AMR is poorly understood but clearly an indicator of the source and need to control this in the human and livestock health domain. The misuse of antimicrobials in both animal and human populations has directly influenced the proportion of pathogens capable of developing antimicrobial resistance (Ayukekbong, Ntemgwa & Atabe, 2017). Exposure to antimicrobials allows bacteria, fungi, viruses, and parasites to evolve in response.
A direct consequence of this change is the ineffectiveness of common medications against these microorganisms, and an increase in the probability that these microorganisms can survive in patients (WHO, 2020c). Patients that are carrying resistant microorganisms are at an increased risk of developing poorer prognoses and death (WHO, 2020c).

In human healthcare, Methicillin-resistant Staphylococcus aureus (MRSA) is a direct consequence of antimicrobial resistance that has had significant impacts on human health. The (over)use of antibiotics over several years has led to the emergence of MRSA. The microbe is a direct result of mutation through accumulation of antibiotic resistance-conferring genes (Stapleton & Taylor, 2002). MRSA can cause a wide array of infections: skin, soft tissue, bone and joint, pneumonia, bacteraemia, and endocarditis (Siddiqui & Koirala, 2020). The responsible use of antimicrobials is necessary to prevent the development of microbial resistance and large-scale impacts on human health as a result.

One of the primary ways that antimicrobial resistance occurs is through over-prescription by both veterinary and human health-care professionals (Ayukekbong, Ntemgwa & Atabe, 2017). In food animal production, antimicrobials are used for therapeutic treatment, for parasite prevention, and to promote growth and efficiency (McEwen & Fedorka-Cray, 2002). Regardless of the reason for use in these settings, there are withdrawal times set in order to prevent drug residues in milk, meat, and egg products. Failure to adhere to withdrawal times between treatment and slaughter can result in the consumption of drug resistant pathogens by humans (Ayukekbong, Ntemgwa & Atabe, 2017). Waste that accumulates from livestock has been one of the major sources of AMR in wildlife species (Arnold, Williams & Bennett, 2016). Certain wildlife species are in close proximity to human populations. If these wildlife species are a food source in these human populations, we might see the transference of AMR into local human populations but again evidence of this actually occurring and of any significance is limited, but exists as recent MRSA evidence in European hedgehogs as a source of MRSA in dairy cattle shows (Arnold, Williams & Bennett, 2016; Larsen et al., 2022) ▪

6 || Globally acceptable pre-emptive actions and responses to human pathogen emergence from animal origins

One of the first and important actions is to obtain consensus on the international stage for policy in this arena. We review the current context for this as follows. The current COVID-19 crisis is energising old and new authors alike and a synthesis of opinion has been published to coincide with 2020 Zoonoses Day (Petrovan et al., 2020) with more than 87,000 publications on COVID-19 by October 2020 (Cai, Fry & Wagner, 2021). This section will review the major recent reports from expert groupings or commissioned, such as UNEP (UNEP & ILRI, 2020) and IPBES (IPBES, 2020); to show consistency and where appropriate, critically comment on their statements, in order to work towards a consensus to help refine practical responses and policy for prevention of emerging human pathogens.

All authors agree that the human pathogen emergence pathway arises from a complex interaction between humanity, animals, nature and the environment and that historically rare occurrence (depending on how you define EID) of new human pathogens is speeding up in recent decades. It is variously argued that it is the result of a number of factors including: human and domestic animal relative abundance and anthropogenic impacts; from climate change to deforestation, agriculture and animal-based food systems, from biodiversity loss to increased/intensified wildlife exploitation. However, as mentioned before, there is a big difference between suggesting a pathway and providing proof. At the moment hard data is lacking.

6.1. Prominent reports

In this context and in the face of COVID-19 there has been a rush to try to explain away this pandemic and its relationship with nature (Everard et al., 2020). The following section summarises the key findings from the reports that are most relevant to the situation analysis in "quotes" with our comments following in *italics*

6.1.1. UNEP Report on Pandemic Disease Emergence

- "The 7 anthropogenic drivers of disease emergence described in the UNEP report (UNEP & ILRI, 2020) are: (1) Increasing demand for animal protein; (2) Unsustainable agricultural intensification; (3) Increased use and exploitation of wildlife; (4) Unsustainable utilization of natural resources accelerated by urbanization, land use change and extractive industries; (5) Travel and transportation; (6) Changes in food supply chains; and (7) Climate change."

Drivers 1, 2, 5, 6 are indeed significant in the emergence and persistence of zoonosis, whilst for drivers 3 and 4 there is indirect evidence to suggest their role in this process (facilitating drivers). Driver 7, climate change, has a general impact on distribution of hosts, vectors, and pathogens, with associated new emergences and spreading of diseases across geographies. These are often not novel pathogens themselves (yet still described as EIDs), for which there is little direct evidence for a climate effect on their evolution, so far.

6.1.2. IPBES Workshop Report on Biodiversity and Pandemics

- "The trade and consumption of wildlife is a globally important risk for future pandemics."

Now, there is still no certainty as to wildlife consumption being a primary process for pandemic emergence. This is based on our findings that there is very limited data on zoonosis in general arising from the trade and few efforts to monitor this.

- "Wildlife trade has occurred throughout human history and provides nutrition and welfare for peoples, especially the Indigenous Peoples and Local Communities in many countries."

This corresponds to this study's findings, which is why careful assessment and evidence-based modifications to wildlife trade are important.

- "About 24% of all wild terrestrial vertebrate species are traded globally. International, legal wildlife trade has increased more than five-fold in value in the last 14 years and was estimated to be worth US$107 billion in 2019. The illegal wildlife trade is estimated to be worth $7-23 billion annually."

This has been disputed as not all CITES-listed species are in trade, and not all species in trade are CITES-listed (Challender, 2019). Non-CITES species include many species traded for their fur, this is particularly relevant given the cross-transmission of SARS-CoV-2 variants in mink farming.

- "The USA is one of the largest legal importers of wildlife with 10-20 million individual wild animals (terrestrial and marine) imported each year, largely for the pet trade. The number of shipments rose from around 7,000 to 13,000 per month from 2000 to 2015. This trade has led to the introduction of novel zoonoses (e.g. monkeypox) and disease vectors or hosts (e.g. tick reservoirs of the cattle disease heartwater) into the USA."

This corresponds to this study's findings that this is a significant concern and not widely appreciated and the monkey pox example is one of the very few examples of confirmed threats from wildlife trade for some zoonoses.

- "Wildlife farming has expanded substantially, particularly in China prior to COVID-19, where 'non-traditional animal' farming generated US$77 billion dollars and employed 14 million people in 2016."

This corresponds to this study's findings. The expansion of wildlife farming is a key issue that has not been discussed or considered in the initial emergence hypothesis for SARS and COVID-19. Reliable data on profits and employment is hard to come by to assess in detail the economic and social role of wildlife trade and confirm current estimates.

- "The farming, trade and consumption of wildlife and wildlife-derived products (for food, medicine, fur, and other products) have led to biodiversity loss, and emerging diseases, including SARS and COVID-19."

This does not correspond to this study's findings. Proof of direct causality between emerging diseases and this trade is still inconclusive beyond the identification of specific hazards and high-risk practices. No evidence is provided in the report, it is a hypothesis and it should not be treated as certainty. There is no confirmatory evidence presented as yet by the Government of the People's Republic of China, relevant international organisations, or researchers to support this statement for SARS or COVID-19 and this remains the same for many other EIDs. Much more research and monitoring are needed before we can or should ascertain direct causation.

- "Illegal and unregulated trade and unsustainable consumption of wildlife as well as the legal, regulated trade in wildlife, have been linked to disease emergence."

Unfortunately, the statement is misleading as there is very little evidence to support it as our report shows. Yes, in a few isolated examples and this corresponds to this study's findings that a risk exists but considering the volume, diversity, and multiple actors of trade it is amazing there are no more than a few reports.

- "The trade in mammals and birds is likely a higher risk for disease emergence than other taxa because they are important reservoirs of zoonotic pathogens."

This is still unclear; the evidence is still insufficient to generalise the associated risk to the trade of mammals and birds. Risk assessment is complex, hazard identification is a necessary step, but it is insufficient to understand the "risk" associated with a group of species. There are few known established reservoirs of wildlife zoonoses, such as Nipah virus and Lassa fever; and even though wild birds can act as a reservoir and vector of pathogens like H5N1 there is almost no zoonosis on record. Risk analysis requires information on intrinsic pathogen characteristics, pathogen-host interaction, system assessment, among other details that are still not fully understood. If this statement referred to domesticated and synanthropic species of mammals and birds it would capture more of the complexity of these systems, as it stands it is misleading as current evidence does not support this, perhaps because there are still many gaps to fully comprehend the hosts, pathogen, and environmental mechanisms driving these processes. Until we do, a risk-based precautionary principle should be implemented, as it can provide direction and foster effort in particular directions.

- "Regulations that mandate disease surveillance in the wildlife trade are limited in scope, disaggregated among numerous authorities, and inconsistently enforced or applied."

This corresponds to this study's findings; it is a major problem.

6.1.3. WHO-convened Global Study of Origins of SARS-CoV-2: China Part Joint WHO-China Study 14 January-10 February 2021

● "In May 2020, the World Health Assembly in resolution WHA73.1 requested the Director-General of the World Health Organization (WHO) to continue to work closely with the World Organisation for Animal Health (OIE), the Food and Agriculture Organization of the United Nations (FAO) and countries, as part of the One Health approach, to identify the zoonotic source of the virus and the route of introduction to the human population, including the possible role of intermediate hosts."

"The TORs envisaged initially short-term studies to better understand how the virus might have been introduced and started to circulate in Wuhan, China. WHO selected an international multidisciplinary team of experts to work closely with a multidisciplinary team of Chinese experts in the design, support and conduct of these studies and to conduct a follow-up visit to review progress and agree upon a series of further studies. The joint international team comprised 17 Chinese and 17 international experts from other countries, the World Health Organization (WHO), the Global Outbreak Alert and Response Network (GOARN), and the World Organisation for Animal Health (OIE) (Annex B). The Food and Agriculture Organization of the United Nations (FAO) participated as an observer."

The approach to the science and selection of some participants raised legitimate international concern and highlighted conflicts of interest. This is pertinent to the general concern over this area of scientific enquiry and our conjecture that much of the narrative around this subject is poorly evidenced and agenda driven and requiring a more independent scientific analysis of the subject matter than hitherto. This is highlighted by a call by 14 countries expressing concern that the WHO team did not have timely access to original data and samples (U.S. Department of State, 2021). Most of the currently utilised narrative is derived from a very few publications and models on human emerging infectious diseases that are believed to have been sourced from animals.

● "Following initial online meetings, a joint study was conducted over a 28-day period from 14 January to 10 February 2021 in the city of Wuhan, People's Republic of China."

"The NNDRS was notified of 174 COVID-19 cases with onset of symptoms in December 2019. Based on the analysis of surveillance data, it is considered unlikely that any substantial transmission of SARS-CoV-2 infection was occurring in Wuhan during those two months (October November 2019)."

"Many of the early cases were associated with the Huanan market, but a similar number of cases were associated with other markets and some were not associated with any markets. Transmission within the wider community in December could account for cases not associated with the Huanan market which, together with the presence of early cases not associated with that market, could suggest that the Huanan market was not the original source of the outbreak. Other milder cases that were not identified, however, could provide the link between the Huanan market and early cases without an apparent link to the market. No firm conclusion therefore about the role of the Huanan market in the origin of the outbreak, or how the infection was introduced into the market, can currently be drawn."

A central theme to the original TOR for the IUCN situation analysis was on the Wuhan Market and Wildlife Trade as a "given" for the origin of SARS-CoV-2. Our decision early on, based on the lack of concrete evidence from available data on this subject area (wildlife trade risks), was to broaden the analysis beyond this narrow perspective and this approach is supported by the WHO report which is clear from the following statements from the mission.

● "However, neither of the SARS viruses identified so far from these {bat and pangolin} mammalian species is sufficiently similar to SARS-CoV-2 to serve as its direct progenitor. "

With reference to other species.

● "In addition to these findings, the high susceptibility of mink and cats to SARS-CoV-2 suggests that additional species of animals may act as a potential reservoir."

With reference to analysis of the viral genomes and epidemiological data from the early phase of the outbreak.

● "... the sequence data also showed ... diversity of viruses already existed in the early phase of the outbreak in Wuhan, suggesting unsampled chains of transmission beyond the Huanan market cluster. There was no obvious clustering by the epidemiological parameters of exposure to raw meat or furry animals."

"The findings suggest that circulation of SARS-CoV-2 preceded the initial detection of cases by several weeks."

"Some of the suspected positive samples were detected even earlier than the first case in Wuhan, suggesting the possibility of missed circulation in other countries. "

"... the presence of SARS-CoV-2 has not been detected through sampling and testing of bats or of wildlife across China. More than 80 000 wildlife, livestock and poultry samples were collected from 31 provinces in China and no positive result was identified for SARS-CoV-2 antibody or nucleic acid before and after the SARS-CoV-2 outbreak in China. Through extensive testing of animal products in the Huanan market, no evidence of animal infections was found. "

"The supply chains to Huanan market included cold-chain products and animal products from 20 countries, including those where samples have been reported as   positive for SARS-CoV-2 before the end of 2019..."

This casts further doubt on previous dogma on this process of emergence, confirming our conclusion that Wuhan Market was probably not the originator of the epidemic even if it contributed to spread of infection. The possibility of cold chain products harbouring the virus opens up possibilities of origin extremely widely and globally. This supports our position that the assumptions made on wildlife trade as the originator were premature and remain unsubstantiated. Our decision to explore trade volumes more generally and trends in animal-based food is also supported as logical by this evidence.

"The joint international team examined four scenarios
- for introduction:

  Direct zoonotic transmission to humans (spillover);
- Introduction through an intermediate host followed by spillover;
- Introduction through the (cold) food chain;
- Introduction through a laboratory incident."

This is consistent with our conclusion and recommendations and does not specify whether domesticated or wildlife species are prioritised.

"The joint team's assessment of likelihood of each possible
- pathway was as follows:

  Direct zoonotic spillover is considered to be
- a possible-to-likely pathway;
  Introduction through an intermediate host is considered to be
- a likely to very likely pathway; Introduction through the (cold) food chain;
  Introduction through cold/ food chain products is considered
- a possible pathway;
  Introduction through a laboratory incident was considered
- to be an extremely unlikely pathway."

This is consistent with our findings, nevertheless this is mostly based on previous experience with coronavirus rather than evidence-based analysis.

6.1.4. Policies to reduce pandemic emergence related to the wildlife trade

- Building a new intergovernmental health and trade partnership to reduce zoonotic disease risks in the international wildlife trade, building on collaborations among OIE, CITES, CBD, WHO, FAO, UNDP, IUCN, and others.

Until there is sufficient evidence of zoonosis from wildlife trade to justify this expenditure it would be unjustified. Before this, monitoring activities need to be brought up at least to the same standards as currently applied for domesticated animal trade movements. Data from this monitoring should be collated and a One Health database inclusive of animal-related pathogens, infections and zoonoses should be developed for future consideration of policies and intergovernmental partnerships.

- Educating communities from all sectors in emerging infectious diseases hotspots regarding the health risks associated with wildlife use and trade that are known to pose a pandemic risk.

This seems unjustified and neo-colonial in attitude. Until data on potential EIDs is available from the trade in wildlife in a given alleged hotspot, this seems inappropriate. Nevertheless, advancing education on potential health risks from unsanitary practices, animal welfare, and biodiversity conservation has undeniable value globally whenever animal trade is concerned.

- Reducing or removing species in wildlife trade that are identified by expert review as high-risk of disease emergence, testing the efficacy of establishing market clean-out days, increased cold chain capacity, biosafety, biosecurity and sanitation in markets. Conducting disease surveillance of wildlife in the trade, and of wildlife hunters, farmers, and traders.

Expert-based processes and informed opinions, while valuable, will get us no further until further research and related data on pathways, pathogens, and zoonosis arising from wild animals in the trade are lacking. We cannot make any valid evidence-based conclusions, beyond informed recommendations. The precautionary principle should apply until there is better knowledge of specific practices, hazards, and associated risk. Future policy and management actions should be balanced against possible livelihood impacts and evaluate the probability of unexpected negative results, especially from of a ban on any species in trade. Improving supply chain surveillance systems, safeguards, and sanitary practices in markets (e.g. sanitation of markets, transport regulation, live animal containment, occupational risk assessment, animal welfare conditions, among others) are without doubt necessary. Existing protocols and best practices standards provide a route to avoid unnecessary bans that may result in undesired impacts on biodiversity and millions of people.

- Enhancing law enforcement collaboration on all aspects of the illegal wildlife trade.

This is without doubt important.

Box 7. Possible consensus statement from the analysis and other reviews on the issue of trade and wild animals in the context of zoonosis and emerging infections

In conclusion, including as to the causes for the highly varied, as currently defined, EIDs and in particular truly novel pathogens like COVID-19, we can make the following statements:

Zoonosis (under our definition) from wild animals appears to be very rare.

EID and emerging pathogens with a clear wildlife (as defined) link, even if just genetically, are concerning, but they are relatively few in number and rarely associated with wild animals (as defined) directly infecting people or present in wildlife trade.
The farming of non- domesticated species is a worrying trend, especially of carnivores for fur and meat, and is coincident with the emergence of coronaviruses in China and needs critical disease risk analysis.

However, it is probably no longer possible to prevent emerging infectious diseases of humans by interventions in a narrow frame and with response alone, or by targeting wildlife trade or specific species.

Rather like climate change, fundamental processes are now at work at a global landscape level and there will have to be fundamental changes in the human political economy and domestic animal and human populations to restore ecosystem stability and reduce emergence of diseases to preindustrial levels, thereby avoiding catastrophic individual, societal and economic impact

Source: Prepared by the report authors.

6.2. Wildlife trade

Following reports of the emergence of COVID-19, links were made between its emergence and the wildlife trade (link to evidence in above sections), principally that the disease may have emerged from the Huanan seafood wholesale market in Wuhan, Hubei Province, P.R. China. However, the source of SARS-CoV-2 remains cryptic (WHO, 2021e) but the overall risk is a concern even if poorly evidenced. There were subsequent calls after the first reports of the epidemic coming from the market from a number of organisations, including NGOs, academics and practitioners, for complete bans on wildlife trade. Some focused on banning commercial trade of particular groups, such as mammals or birds, for human consumption (WCS, 2020; Walzer, 2020) or #endthetrade and its 377 supporting organizations; (WCS, 2020; Walzer, 2020). Some called for the cessation of use of wildlife, including the breeding, domestication and trade of wildlife products (Singh Khadka, 2020). Others sought to highlight the potentially negative impacts for biodiversity and livelihoods of rapidly implementing these measures without considering the complexity of wildlife trade (Challender et al., 2020b; Roe et al., 2020; Roe & Lee, 2021). Theoretically, a range of policy options for wildlife trade could be implemented following the COVID-19 pandemic from 'do nothing' approaches to 'ban all wildlife exploitation

and trade". However, any future strategies, policies and regulations focused on wildlife trade should be informed by the best available evidence and based on risk assessments of the different options, trade-offs and synergies (Booth et al., 2020; Di Marco et al., 2020; Eskew & Carlson, 2020; Roe et al., 2020). Booth et al. (2020) provided a framework for considering this post-COVID-19, encompassing public health, wildlife and ecosystem costs and benefits of use and trade, socio-economic costs and benefits of use and trade, and potential policy options and implementation challenges.

Our analysis looked for evidence to support different options. It shows only very limited and little conclusive evidence of the wildlife trade, or wild animals more generally, being a significant source of daily zoonosis, globally. This can be easily explained when it is clear what the difference is between endemic zoonosis when compared to the emergence of novel pathogens, new variants, changing geographies, new hosts or vectors, which happen periodically but rarely is associated with new established zoonosis. However, rare emergence events, which can lead to pandemics, cannot be ignored wherever they come from but suggesting that wildlife is a source of these events, almost exclusively, is misleading.

Box 8. Identify key diseases and target for epidemiological/ ecological research

We propose more specificity with respect to a range of concerning emerging human pathogens where there is some evidence for a proximate source in wildlife or wild animals, to enable more precise examination of risk factors, derived from a clearly defined and current epidemiology - susceptibility of hosts, exposure amongst hosts, proof of infection and disease outcome. Whether emerging novel pathogens are in fact incresing in rate from wildlife sources is not easily discernible from current evidence and analyses, but the trend suggests this to be the case.

Source: Prepared by the lead authors.

When coming to a central concern in the debate around the wildlife trade and zoonosis risk a number of conclusions have been possible. Only a few examples exist of disease related long term bans on wildlife trade (see Box 4).

Box 9. Examples of bans on wildlife trade related to disease events and/or confirmed risks

Rodent imports into the USA; after the introduction of monkeypox (CDC et al., 2018; Centers for Disease Control and Prevention et al., 2015)

Following a Salmonella Typhimurium outbreak that affected 35 people across nine states the FDA banned the sale and distribution of turtles with shells smaller than 4 inches long (10.2 cm) as pets. Although animals can still be purchased or exchanged online or in small markets (e.g. at flea markets and swap meets).

Exotic birds into Europe after the Bird Flu pandemic in 2006.

The recurring ban made on kangaroo meat trade from Australia to Russia due to *E. coli* contamination (Holds et al., 2008).

Source: Prepared by the lead authors.

These examples confirm potential for wildlife trade to cause zoonotic events of significance, but these are sporadic and the overall risk of zoonosis from the generic wildlife trade appears to be low to negligible at a global scale. However, the risk that an individual species hosts a zoonotic pathogen is highly variable and some generalisations on risk are reasonable based on taxon and could be acted upon in preventive programmes or surveillance (Smith et al., 2012).

Box 10. To ban or not to ban a trade in animals

Based on evidence, it would be unjustified to implement indiscriminate measures, such as broad-ranging bans, on wildlife trade (or use and trade), or on domesticated animals or specific groups of species in trade (e.g. mammals and birds) for reasons of disease risk. However, there are specific cases of known domesticated animal and wildlife zoonosis, related to proven events and with risk of transmission from a known host reservoir, that warrant specific action, but this is best done on a case-by-case basis.

Source: Prepared by the report authors.

Any conclusion on risk is set against the absence of any kind of systematic surveillance of wildlife or wildlife trade and public health consequences for zoonotic pathogens, and the absence of surveillance of human case histories of zoonosis routinely traced to wildlife sources.

Box 11. Surveillance for infection in wildlife species in trade and public health consequences

Some effort is needed to improve the situation of a lack of surveillance of wildlife trade and disease and build up a database of risk, however challenging and unfeasible this may be, and examples are reported-on in this analysis. It is likely without any specific evidence of risk (see rodent and turtles) that individual wildlife (live or derived products) in trade carry an equal risk of carrying zoonotic pathogens, as do individual domesticated animals in trade. Therefore, at the very least, levels of surveillance currently applied to domesticated animal trade should be applied to all species in wildlife trade, with similar regulations and actions and these can be based on tried and tested HACCP processes used in livestock trade and food systems.

Source: Prepared by the report authors.

Some will argue that certain taxa are particularly risky (Johnson et al., 2020) (i.e. in orders Rodentia, Chiroptera, Primates, Artiodactyla, and Carnivora), while others will argue that the number of human-infecting viruses increases proportionately to species-rich reservoir groups, which host more virus species and therefore a larger number of zoonotic species, supporting a host-neutral model (Mollentze & Streicker, 2020). When investing in new surveillance, it need only be proportionate given that, in terms of risk, wild animals constitute a very small proportion of animals traded and an even lower proportion of reported zoonosis, nevertheless we need better data to definitely assess the overall risk associated with specific species and practices. Even if a single event can lead to catastrophic consequences, it is generally not economically feasible to invest in surveillance for such rare events, as the system is usually insensitive at this level and the only solution for *zero-risk* is a total ban on the trade of wildlife, livestock, pets, and other zoonotic sources. Investment need not be excessive and can be targeted. In the wildlife context, the most likely source of zoonosis are animals in captivity and especially where breeding is undertaken in intensive food, medicine, pet, and fur farming enterprises, so difficulties of monitoring wild animals *in situ* need not be that concerning.

Box 12. SMART regulations

Where new or revised regulations are to be implemented, they would ideally be guided by an evidence-based theory of change detailing how and why the desired changes will be expected in terms of outcomes (Biggs et al., 2017b). Approaches such as SMART regulation could also be used (Gunningham & Sinclair, 2017) . SMART regulation utilise multiple rather than single policy instruments and a broader range of regulatory actors and could be used to incentivise best practices by different actors along supply chains.

Source: Prepared by the report authors.

This advice to policymakers reviewing wildlife trade regulations in light of COVID-19 does not take into account other reasons why further regulation, or banning, of wildlife trade might be justified based on biodiversity conservation needs, animal welfare, natural resource management considerations, invasive species considerations, or otherwise. Determining which, if any, further policies or regulations on wildlife trade (including collection, production, possession, use, and consumption) to implement following COVID-19 requires an evaluation of different policy options considering the actors involved along supply chains and the benefits they derive from trade, potential impacts on biodiversity from unintended consequences from resulting illegal trade (Roe & Lee, 2021) and public health considerations. Policy evaluation should consider these factors (discussed in more detail below), and consider the possible effects, impacts and risks of different options, including the risks and benefits inherent in not imposing (further) regulations (e.g. tighter trade measures).

The nature-human nexus is a complex one and we are in a current phase of human development, where our impacts as a by-product of our population, economy, consumption patterns, transformation of landscape, and manipulation of animal biomass through domestication, have taken the planet to a critical point (IPBES, 2020). Many wild animal populations are suffering massive declines, yet humanity continues to benefit from them. Banning our interactions with wildlife is perhaps not the solution, it is human development and domesticated elements including our relationships with synanthropic species of animals which need to be rationalised. Reducing domesticated animal numbers will do a lot more towards preventing pandemics, climate change and biodiversity loss than banning wildlife trade.

The impact of regulations on biodiversity should also be considered because in some situations new measures could result in adverse impacts on species and ecosystems, for short periods or long term. Where new or revised regulations are not socially legitimate, or well-designed, and/or well enforced, they could do more harm than good. Prohibitionist approaches, for example, may not deter all actors within marketplaces, which would mean that existing legal trade in species and products may continue or expand illegally, especially where consumers in end markets consider species and products to be socially desirable. Prohibitionist approaches could also reinforce perceptions of scarcity and thus drive up prices for species and their products in illegal marketplaces, potentially increasing incentives for poaching. While in other circumstances, bans may have contributed to positive conservation outcomes, particularly when implemented in conjunction with other interventions (Conrad, 2012), but predicting their impact is challenging. The capacity – both in human and technical resource terms – of law enforcement agents and agencies is critical to the effectiveness of any new or revised wildlife trade regulations. Where new measures are being considered the capacity of agents and agencies to enforce these such measures should be

explicitly considered. For instance, major revisions to legislation and practice (e.g. increased monitoring of trade and captive facilities) may mean that additional law enforcement resources need to be committed commensurate with such changes, without which the new or revised regulations may simply be undermined by ongoing, but now, illegal activity. This is especially the case where actors perceive such regulations to be socially illegitimate and/or in countries and areas where enforcement of existing wildlife laws is currently weak (Challender & Waterman, 2017). Examples of the effectiveness of wildlife exploitation bans vary with geography, time, and governance system. When egret and alligator hunting were outlawed in the USA in the early 20th century, no compensation was provided, and hunters switched to other, more resilient species or occupations; the ban was effective because the retail market for products was easily controlled and thus collapsed (Thorbjarnarson, 1999). When Dutch and Danish mink farmers were ordered out of business, governments compensated their losses (Reuters Staff, 2021).

An important aspect of policy is to be fair and effective. In the context of disease risk, we know that animals in general pose risk and albeit rarely a high impact on public health but the greatest risk is from humans themselves and their population. If we are to recognise and mitigate zoonosis risk, it needs a cost benefit for all animal use. The first step may simply be to address subsidies. Many countries keep subsidizing harmful and inefficient agricultural practices and practitioners especially in animal-based food industries which ensures expansion, and resulting disease risk, environmental and biodiversity decline. A similar argument is clearly strong that commercial wildlife trade is of a similar impact but on a smaller scale, although less subsidised except through inflated prices in illegal highly valued commodities. This issue is far bigger than having policy of simple alternative livelihoods for wildlife collectors as this will not resolve the bigger issues of the impact of animal industry generally and may even exacerbate land use changes through agriculturalisation as an alternate. Implementing new measures without considering these factors, could be inviting policy failure and further pressure on biodiversity.

Enforcement capacity is a function of an authority's determination to address an issue; this is a governance matter of varying geographic weight, and beyond the scope of this report. It should also be noted that broad bans may be easier to enforce than current biodiversity conservation-inspired restricted bans: a blanket ban on turtle trade, for example, would replace a situation where an inspector spends time identifying a redfooted tortoise (versus a yellowfoot) in a shipment and determining its regulatory status with a shorter time identifying an animal as 'any tortoise' and determining the group's blanket regulatory status. Where it is impossible to differentiate risk at species level, higher taxon might be chosen to determine regulation, as indeed it was for rodents in the decision to ban imports and reduce the risk of monkeypox importation to the USA ■

Box 13. Strategic control of wildlife trade

Where a zoonotic risk is confirmed and cannot be mitigated through easily applied and low-cost control measures, or through targeted action, blanket bans on that trade could and perhaps should be implemented.

Source: Prepared by the report authors.

*Source: Prepared by the report authors.

7 ‖ Conclusions

7.1. Knowledge and methods

7.1.1. Quantity and quality of information

Knowledge on the incidence of zoonosis from any source, wildlife trade or any other animal system, is limited. A specific database on the global burden for zoonosis and global animal disease burden does not exist, with most reports incorporated in a variety of International and National databases and few analysed. There is a discussion on preparing a Global Animal Disease database, but this is only focused on domesticated animals and wildlife disease remains unaddressed. There is some progress on improving the Global Burden of Disease database to include zoonosis but there is no published material to the author's knowledge as yet. By the end of this report. OIE's WAHIS dataset is one of the main disease reporting tools. Other databases (e.g. EID2 and VIRION) focus on collecting and standardising novel host-pathogen association. The quality of information on zoonoses and EID of humans is reduced with lack of clarity on or appreciation of what constitutes a zoonosis and EID. This can lead to spurious associations and misidentification of drivers and risk factors in remote analysis and modelling. The use of the terms across such a wide variation of pathogen-type and diseases with very different epidemiology is arguably too non-specific to help in developing appropriate disease-specific interventions, control policies, and to improve preparedness and response plans at the speed and scale required by these events.

A challenge also exists in clearly defining wildlife, wild animals, wildlife trade and similar terms and the terms which are now widely used in situations that cover diverse animal populations and animal use systems, which are not part of natural ecosystems or ecologies. The lack of specificity in these definitions can lead to inappropriate focus on wild animal populations that are not epidemiologically important, potentially resulting in incorrect and damaging policies and interventions.

The tens of thousands of species that constitute the wildlife trade create unique challenges to addressing monitoring of the trade for infectious diseases. It is challenging enough to cover about 14 domesticated species traded globally. The only probable option in this situation is a risk-based approach to obtain the necessary knowledge through monitoring along the lines of existing protocols, such as the HACCP model for food safety, in countries where it is applied. For informal sectors, monitoring remains an acute challenge but may not be so necessary for small and local supply chains, for example locally harvest and consumed wild meat (deemed as "safe" following risk analysis).

7.1.2. Differentiate hypothesis from evidence-based conclusions

Without case data and confirmatory diagnostics on zoonosis and emerging infectious disease pathogens from wildlife species, it is not possible to determine the importance or risk of these hosts, reservoirs, or genetic origins. Some wildlife zoonosis or pathways to emerging infectious disease of humans are well understood and these are really not a great concern, but this knowledge is not available for most EIDs. The precautionary principle can be used but intervention against EIDs cannot be justified based on hypotheses alone and disease risk analysis which addresses this problem broadly is urgently needed.

7.1.3. One Health approach

This situation analysis recommends implementing a One Health approach to mitigation of wildlife disease risks, but this approach must incorporate a stronger environmental component through appropriate partnerships, as noted in IUCN WCC Resolution 135 (IUCN, Members' Assembly, 2021) and in the Addendum to the IUCN Programme 2021-2024 (IUCN, World Conservation Congress, 2021). Irrespective of our limited knowledge of the risk of zoonosis in wildlife trade and other forms of wildlife human-managed-movements we should apply, at the very least, the same standards of veterinary surveillance and biosecurity as we apply for domesticated animal trade. Monitoring should include known animal pathogens for both captive wildlife species, domesticated animals, and zoonoses from traded or translocated individuals; and more generally for novel organisms that might present risks. Case records of zoonotic infections should be tracked back to origins from all medical and public health settings, to establish possible sources and reservoirs of human pathogens that can be transmitted directly or indirectly. Advancing towards a complete implementation of the One Health will require an expansion of existing cross-disciplinary collaborations, especially expanding existing collaborations with human health professionals.

OIE seems the obvious organisation to adopt issues arising out of the wild animal sector and wildlife trade and disease but we have to be careful when assuming this. OIE has had a peripheral interest in wildlife through its "wildlife working group" for many years. The OIE mandate is for disease control in the domesticated animal industry, focused on those diseases of importance to the animal-based food economy and setting standards in diagnostics, treatments, and control measures; essentially OIE is driven by trade issues and works through the veterinary services in each country. There are even conflicts arising between these issues and wildlife conservation and health. OIE has historically been concerned about wildlife reservoirs

of domestic animal pathogens rather than wildlife health issues and this has brought at times, unwanted attention to wildlife sectors, causing considerable disturbance to natural ecologies when draconian measures for disease control are applied, such as through extensive fencing systems or reservoir reduction strategies (wildlife culling) and other interventions. In the face of the current interest in wildlife around emerging pathogens OIE has developed a new framework *OIE Wildlife Health Framework 'Protecting Wildlife Health to Achieve One Health* (OIE, 2020b) which is very welcome but the challenge is that there will be conflicts between goals for wildlife health and domesticated animal health. However, until an alternative global institution or agency more oriented to wildlife health for wildlife's sake (Karesh, Kock & Machalaba, 2020), OIE should provide standards for monitoring infectious disease in the wildlife trade, undomesticated-domestic animal interface, and for actions taken in prevention of disease transmission through trade. The same might be said for the FAO Animal Production and Health Division (NSA). FAO has provided valuable insight into the future of animal agriculture some of which is not comfortable reading (Steinfeld et al., 2006). They have considerable capacity in analysis of the interface between agricultural and natural systems and extend into the marine environment which few do in the health sphere. There have been more attempts recently to integrate wildlife and domesticated animal disease concerns with promising models for future cooperation emerging (Fine et al., 2020).

Zinsstag et al. (2018) on integrated surveillance brought out some pertinent economic arguments for improving global disease surveillance:

"The World Bank makes a compelling case for integrated human and animal surveillance (...), emphasizing that if emerging diseases can already be detected in vectors, livestock or wildlife, prior to detection in humans, very large costs could be averted (World-Bank 2012; Heymann and Dixon 2013). Savings of 344 to 360 billion USD over the next 100 years are expected from use of integrated surveillance of zoonoses with a pandemic potential (Pike et al. 2014). Savings from early detection of pathogens in vectors would not only apply to vector-borne zoonoses but also for vector-transmitted diseases like dengue fever (Li and Wu 2015)."

Policy is usually driven by economically justified arguments but in this case the predictions on savings is optimistic and the unspoken caveat is that it depends on being able to detect emerging pathogens in a timely manner and recent history is not kind to this argument as our analysis, and others, have shown in recent decades. The cost of doing this effectively may well outweigh any benefit but some degree of monitoring and strategic integrated surveillance seem entirely logical. However, we recommend that this is focused on animal trade and amongst exploited animals in farms and captivity (wildlife and domesticated) rather than in wild animals in nature, which is unrealistic. Whether organisations such as CITES can expand their mandates to do this is a point of discussion currently, but some caution is necessary. CITES in its present form has inadvertently led to constraints on wildlife disease monitoring and prevented acquisition of knowledge on this poorly understood area of health. Efforts to change this through resolutions in CITES over

recent years has been challenging and slow (CITES, 2019, 2020c), with complex proposals still under discussion and lacking simplicity, despite the names given to the resolutions such as "simplified procedures." Whether these measures will lead to improved diagnostics and research applied to disease and health in the natural world remains to be seen.

Nevertheless, general improvements in capacity to investigate and research wild animal diseases, human and animal interfaces of risk, and disease processes in the environment are also entirely sensible and highly recommended (Machalaba et al., 2020). This sort of science will go beyond species specific issues, identify risky practices and interfaces, and provide indicators of the healthiness of our environment as much as CO_2 levels and temperature does for our climate. Current health agencies are not equipped for monitoring, surveillance or investigation or research in wildlife disease and health across all necessary systems and interfaces. It is likely new institutions will be needed. To fully examine emergence of pathogens at the human-animal-environment interface, a transectoral and multidisciplinary approach is needed to create common understanding and ontology, clear definitions, identify relevant indicators, and bring together disciplines to better understand the biodiversity of microbes, prevalence and emergence of pathogens and related diseases (Wolfe et al., 2005). A One Health approach is warranted using socioecological and economic frameworks and improving capacities especially in the wildlife and environment sectors (Karesh, Kock & Machalaba, 2020).

Health governance into the future needs to take the One Health approach seriously and the gap in knowledge, capacity and focus on environmental change and wildlife in the context of health and disease requires urgent action. Therefore, we fully endorse the proposed integration of UNEP into the Tripartite FAO-OIE-WHO One Health collaboration and the need to address environment, biodiversity conservation and ecosystem services alongside public health and economic development; and also recommends widening engagement to other actors with relevant on-ground capabilities such as UNDP. We advise more generally, the adoption of transdisciplinary, intersectoral, and integrative *bottom-up* approaches across local, national, and international governance levels to integrate local communities and share relevant knowledge to develop global policy. An international agreement for tackling emerging diseases is urgently needed followed by actions necessary to identify and mitigate infectious disease threats arising in the 21st Century.

7.2. Risk factors for emergence of human pathogens

7.2.1. Wildlife trade and other forms of animal translocation and release risk to health

There is only very limited evidence presented in peer reviewed or grey literature to confirm risks of zoonosis in wildlife trade and therefore little evidence to confirm risk of EIDs arising from this pathway. However, one or two examples are pertinent and prove the possibility, such as monkeypox outbreaks in the USA, where infection was imported through the rodent pet trade, as well as food borne zoonosis from, such as *E. coli* bacteria imported with kangaroo meat (wild harvested) into Russia in 2008. It is unlikely a significant incidence of zoonosis is being missed in wildlife trade given the large numbers of people along the value chain and therefore incidence of zoonosis risk from wildlife trade is likely low to very low. However, risk of nEID from pathogen spillover from wildlife trade needs to be minimal to prevent an epidemic event in the long term via this route and this cannot be guaranteed, whatever the monitoring or control measures taken. Often the evolution of a nEID is complex and the wildlife trade element may just be one link in the chain towards spillover or introduction into, for example a farm of animals or humans. Improvements in sanitary and welfare conditions or management of critical control points in the wildlife trade supply chains would be beneficial, without doubt and this might include banning certain practices in the value chain, such as live animal markets or particular species identified as "high risk" following disease risk assessment. The general trend based on CITES data shows a shift from wild- to captive-sourced wildlife products but this does not account for non-CITES traded species requiring differential risk assessment.

Human use of the wildlife is a complex and a divisive topic. It cannot be oversimplified nor assessed independently from the context in which it occurs nor by excluding local communities and other relevant stakeholders. Future policies ought to take into account the socio-political, economic, and ecological dimensions in a holistic manner. We would caution against use of *ad-hoc* interventions in the wildlife trade market and other animal translocations to address health risks. Instead, international guidance beyond that provided by FAO, OIE, WHO, WTO is required.

This should include:

a) Implementation of SMART regulation approaches i.e. *"the use of multiple rather than single policy instruments, and a broader range of regulatory actors, will produce better regulation."* (Gunningham & Sinclair, 2017). This appeals to an evidence-based approach to managing trade into the future which is supported by others (Booth et al., 2020a)

b) Implementation of guidance and manuals for wildlife disease risk analysis aimed at live animals and wildlife-derived products generated by IUCN (IUCN 2013; Jakob-Hoff et al. 2014; OIE & IUCN 2014; CI-

TES 2016) and other relevant international organisations (FAO, 2011; European Centre for Disease Prevention and Control., 2019; IATA, 2021) need to be adapted for specific purposes, systems, trades or wildlife movements. Conservation translocations are a special case, usually intensively managed and low risk but illegal wildlife trade, wildlife rehabilitation and confiscations of wildlife, often involving translocations and introductions, (e.g. invasive species) pose a largely unknown but likely, significant risk.

c) Implementation of HACCP principles and existing guidelines to wild meat production and transport systems (FAO, 1998; OIE, 2000; Center for Food Safety and Applied Nutrition, 2020; Biggs et al., 2021; FAO & WHO, 2021; IATA, 2021). A differential targeted risk assessment needs development specifically on traded wildlife species, starting with mammals and birds, with a similar approach to what it is already implemented in domesticated and international livestock trade (e.g. market hygiene, welfare, transport, containment, and quarantine strategies). The findings should be then applied to targeted monitoring for early detection, critical control points along the supply chain, general sanitary, biosecurity measures, and welfare guidelines for prevention, control, and management of diseases.

d) Further research is needed to understand the hazards along the supply chain and characterise practices in accordance to risk mitigation measures (i.e. occupational risk factors). Education, engagement, and behavioural change schemes targeted at populations at risk will likely deliver the most feasible set of actions to improve trade practices.

e) Increased public health research and routine surveillance for zoonosis in medical practice. Case records of zoonotic infections should be tracked back to origins from all medical and public health settings, to establish sources and reservoirs of human pathogens that can be transmitted directly or indirectly. Promote cross sectoral investigation into source with reporting and establishment of national and global burden of zoonoses databases.

f) Future policies ought to include local communities and consider the socio-political context in which the use of wildlife occurs. Moving from classical top-down approaches will facilitate the integration and identification of local preferences and needs. Transdisciplinary and intersectoral collaboration is needed to appropriately identify the type of intervention that could maximise socio-ecological and economic benefits while minimising undesired negative impacts from future regulations.

g) Expansion of existing collaborative regulatory spaces (e.g. WHO, FAO, OIE and UNEP quadripartite) to secure participation of environment and wildlife agencies, CITES, UNDP, national trade regulators, Indigenous peoples and local communities, wildlife producers, traders, and consumers.

7.2.2. Deforestation, landscape change, and intensified agriculture

There remain many uncertainties around precise mechanisms by which deforestation and other land use changes affect the pathogen emergence landscape. There are some clear associations mostly through vector-borne infections, occasional direct spillover from sylvatic cycles into humans or indirectly through domesticated animals or synanthropic species. There are a few convincing epidemiologies and pathways described for particular emergent diseases such as edge effects, ecotone diseases, artificial water sources, development of agricultural landscapes, peridomestic synanthropic species, domesticated species and range.

Intensified crop and animal agriculture are a great attractant to invasive species and pathogens of these systems. Domestication itself, of animals, for companion/pet, draught, security, or animal-based food systems results in the majority of zoonosis incidence, perhaps 99% of such diseases that humans suffer. The role of wildlife species in intensively reared food or fur farms, in terms of zoonosis or EID risk, is still poorly understood. However, there is increasing evidence for coronaviruses that fur farm and untypical food animals, such as racoon dogs, palm civets, mink can acquire virus zooanthropo-notically and can also disseminate virus zoonotically under farm conditions and therefore could have had a core role in the SARS and COVID-19 origins. This would be as an intermediary or proximate source host species and possible modifier/amplifier in the evolution of this pathogen and its introduction into human populations. In some countries, including China, large scale intensive production from wildlife-based food and large domesticated animal (pig and poultry) factory farming systems, is a relatively recent development and coincident with pandemic emergence of viral disease, including the most significant, human or zoonotic influenzas, SARS and COVID-19 in the last twenty years. Given conducive conditions of human population, behaviour, and a landscape with massive growth in animal exploitation and captive wildlife industries, pathogens in these systems can more easily emerge and adapt over time to humans due to their abundance and proximity.

Bringing or attracting wildlife species into human-modified environments or through management (intentional or unintentional synanthropy) is increasing the likelihood of novel EID and will undoubtedly add new zoonosis to the current list of about 900 human zoonotic pathogens. Ecosystem fragmentation, degradation and hard edges between natural ecosystems and domestic landscapes are likely to increase risk of pathogen spillover and naive epidemics in human and domesticated animals from wildlife species.

Humanity has probably reached the limit of exploitation of its environment without risking dire consequences for survival in the long term (WWF, 2020). Efforts need to urgently amplify to recover ecosystems, biodiversity, degrowth current consumption and production patterns driven by an ever-growing human population, and reduce domesticated animal populations; the latter perhaps by 75% in order to achieve this transition and recovery. Use of wildlife species need not be a significant concern where use is proven sustainable but

with perhaps 25% of trade known to be unsustainable, the need for greater controls is obvious but these arguments should not be confused nor mixed with managing disease risk. The biggest threat in this context is not zoonosis risk per se but the expanding human populations, growing demand, and increased global connectivity.

How relevant deforestation is to some of the novel EID, such as coronaviruses, is not clear and until the epidemiology, especially with respect to spillover of these types of virus from bats is clarified, any association is speculative. The risk from sylvatic cycles contrasts with wildlife exploited for commercial use, captive breeding, and mass production where there is greater per-capita risk of EID arising from such industries probably than even from domesticated animals. Investment in or development of any communities or animal or agricultural industries adjacent to forest ecosystems or connected to harvest should take this risk of sylvatic spillover into consideration and as part of land use policy, environment impact assessment and development strategies.

Deforestation in the Republic of the Congo
Photo © Michael D. Kock
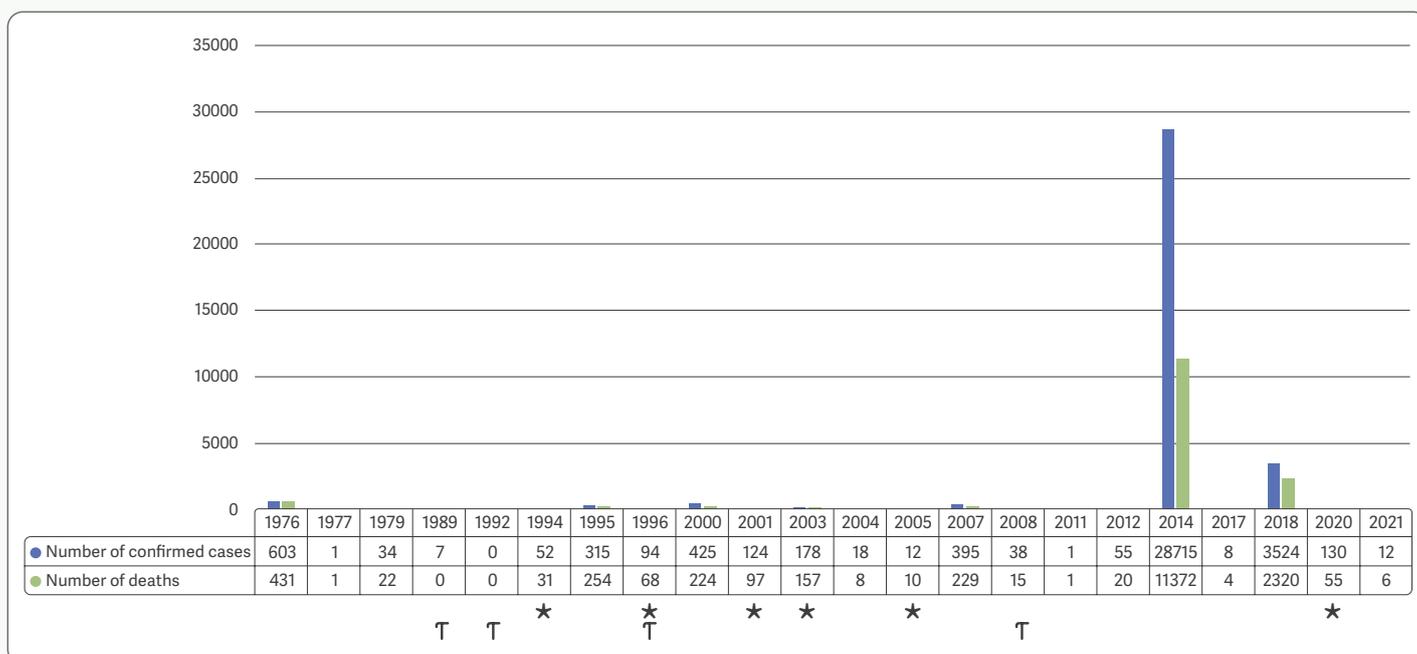
Figure 17. Global Ebola virus (EVD) outbreaks (1976–2021)

This graph represents all the Ebola outbreaks since 1976 in the Democratic Republic of the Congo (formerly Zaire) spillover events (CDC, 2021a). Eight out 48 outbreaks were linked to wildlife hunters (indicated with an asterisk "*" on the year of occurrence) and suspected from epidemiological data from on association with non-human primates (Georges et al., 1999; CDC, 2021a), whilst there is speculation over a number of other possible meat sources (Kümpel et al., 2015). The Reston ebolavirus variant has been detected six times (indicated with the Greek letter Tau "*" on the year of occurrence). The Reston ebolavirus variant is capable of infecting humans but does not cause illness (asymptomatic). Out of the six times it has been detected since 1976, five were from in monkeys in quarantine facilities from the Philippines (three times in the Philippines, twice in the U.S, and once in Italy) and in 2008, it was detected in six pig farm and slaughterhouse workers who developed antibodies against the virus (CDC, 2021a). Nevertheless, the vast majority of cases (>99%) are due to human-to-human transmission (i.e. nosocomial infection, factories, family groups, laboratory infections). This illustrates the important role of secondary epidemiological cycles determined by the secondary host population and its dynamics rather than zoonosis transmission.
Source: Prepared by the report authors using CDC, 2021.

7.2.3. Transport networks

In terms of direct and indirect (vector and food borne) transmitted infections from animals, and associated epidemics and pandemics, there is no doubt that the growth in transport infrastructure, animals, and animal product movements globally, has increased the opportunity for emergence. Indeed, trade is what led to the establishment of OIE, the animal equivalent to the WHO but here the focus was on domesticated animals and not wildlife. OIE has been effective in preventing animal pandemic disease to a great extent originating from the legal trade in domesticated animals and animal products through strict testing and quarantine. Breakdown does occur and animal pandemics such of African Swine Fever and goat plague are contemporary issues. From the perspective of the human host, a sure way to reduce pandemic risk is to reduce the volume of human travel, especially air travel, and instigate control measures

on pathogen and vector movement that are far more effective than currently applied, under international human and animal disease and quarantine regulations, being inclusive of wildlife trade. Effective measures to reduce the environmental and societal impacts of globalisation require combined efforts by governments and the private sector. The new physical and dynamic networks, and largely disconnected political governance of risk, make this extremely difficult to achieve, especially for human movements and increasingly for animals because of sheer volumes. However, as shown with COVID-19 attempts at preventing human movement in the face of novel disease pandemics may be unfeasible, given human attitudes and behaviours, demands of political economy and levels of international collaboration.

Drowned Mopane trees, skeletal like, stand out of the waters of Lake Kariba in Zimbabwe, African buffalo graze quietly along the Matusadona National Park lake shore.
Large tracts of land were submerged in the Zambezi Valley after the construction of Kariba dam in the late 1950s, displacing wildlife, people, and altering established ecosystems.
Photo © Michael D. Kock

7.2.4. Climate change

There is not much evidence to show climate change having very much direct impact on the emergence and rate of emergence of novel pathogens, but a lot is uncertain in this respect. Research on the interrelationships between climate change and infectious diseases requires interdisciplinary and international collaboration (improving infrastructure and training). Climate change has and will influence shifting patterns in disease occurrence in frequency and geography, but it is not clear what its role might be in the emergence of novel pathogens. For example, the effect on mammals and birds and their microbiomes as temperatures exceed the animal's adaptive capacity, could stress populations, and create unusual wildlife disease emergence and potential for spillover. Certainly, climate change has a considerable influence on the spread of pathogens and vectors into previously unaffected landscapes, as temperature and humidity effects change the ecologies of whole geographies, enabling establishment of vectors and changes in seasonal cyclicity of parasites. In general, focus needs to be on vector control in the face of climate shifts and more research is needed in this area to inform policy and interventions. Overall, in the context of health, reversing the current trends in climate will benefit humans by reducing associated disease risks.

7.2.5. Antimicrobial resistance

Antimicrobial resistance (AMR) is considered a major part of the EID complex according to widely used definitions but its relevance to wildlife trade and free ranging wildlife is minimal and for the purposes of this situation analysis is not considered important. AMR is a natural response to antimicrobial use so the logical and only practical response to the rapid growth in AMR globally is to reduce and where possible prevent the use of antimicrobial compounds, except where they are critical. For example, it is not justified to have animal production systems dependent on antibiotics to compensate for the high-disease prevalence of animals, that is associated with the stress of intensive husbandry and the genetic manipulations for desired production characteristics. Breeding programmes should re-establish animal resilience, genetically and immunologically, and modern husbandry practice encourage natural behaviours and use of the environment, even if this is at the cost of production efficiency and economics. In the long term this may be the only sustainable animal-based food system. The parallel approach is to reduce the overall dependency of humans on domesticated animals in favour of plant-based foods, although modern crop production systems are not immune to issues of AMR ■

References

Aguirre, A. A. (2017). Changing Patterns of Emerging Zoonotic Diseases in Wildlife, Domestic Animals, and Humans Linked to Biodiversity Loss and Globalization. *ILAR Journal, 58*(3), 315–318. https://doi.org/10.1093/ilar/ilx035

Ahammed, T., Anjum, A., Rahman, M. M., Haider, N., Kock, R., & Uddin, M. J. (2021). Estimation of novel coronavirus (COVID-19) reproduction number and case fatality rate: A systematic review and meta-analysis. *Health Science Reports, 4*(2), e274. https://doi.org/10.1002/hsr2.274

Albery, G. F., Carlson, C. J., Cohen, L. E., Eskew, E. A., Gibb, R., Ryan, S. J., … Becker, D. J. (2021). *Urban-adapted mammal species have more known pathogens* [Preprint]. Ecology. https://doi.org/10.1101/2021.01.02.425084

Allen, T., Murray, K. A., Zambrana-Torrelio, C., Morse, S. S., Rondinini, C., Di Marco, M., … Daszak, P. (2017). Global hotspots and correlates of emerging zoonotic diseases. *Nature Communications, 8*(1), 1124. https://doi.org/10.1038/s41467-017-00923-8

Alves, R. R. N., & van Vliet, N. (2018). Chapter 10—Wild Fauna on the Menu. In R. R. Nóbrega Alves & U. P. Albuquerque (Eds.), *Ethnozoology* (pp. 167–194). Academic Press. https://doi.org/10.1016/B978-0-12-809913-1.00010-7

Alzahrani, A., Kujawski, S. A., Abedi, G. R., Tunkar, S., Biggs, H. M., Alghawi, N., … Watson, J. T. (2020). Surveillance and Testing for Middle East Respiratory Syndrome Coronavirus, Saudi Arabia, March 2016–March 2019. *Emerging Infectious Diseases Journal - CDC, 26*(7). https://doi.org/10.3201/eid2607.200437

Andersen, K. G., Rambaut, A., Lipkin, W. I., Holmes, E. C., & Garry, R. F. (2020). The proximal origin of SARS-CoV-2. *Nature Medicine, 26*(4), 450–452. https://doi.org/10.1038/s41591-020-0820-9

Anderson, R. M., & May, R. M. (1982). Coevolution of hosts and parasites. *Parasitology, 85* (Pt 2), 411–426. https://doi.org/10.1017/s0031182000055360

Animals Australia. (2011). Kangaroo meat producers weigh chinese market. Retrieved 1 December 2020, from https://www.animalsaustralia.org/media/in_the_news.php?article=2161

Antarctic Treaty. (1959, December 1). The Antarctic Treaty. Retrieved 2 May 2021, from The Antarctic Treaty website: https://www.ats.aq/e/antarctictreaty.html

Apetrei, C., & Marx, P. A. (2004). Simian retroviral infections in human beings. *The Lancet, 364*(9429), 137–138. https://doi.org/10.1016/S0140-6736(04)16620-8

Arnold, K. E., Williams, N. J., & Bennett, M. (2016). 'Disperse abroad in the land': The role of wildlife in the dissemination of antimicrobial resistance. *Biology Letters, 12*(8), 20160137. https://doi.org/10.1098/rsbl.2016.0137

Asogun, D. A., Günther, S., Akpede, G. O., Ihekweazu, C., & Zumla, A. (2019). Lassa Fever: Epidemiology, Clinical Features, Diagnosis, Management and Prevention. *Infectious Disease Clinics of North America, 33*(4), 933–951. https://doi.org/10.1016/j.idc.2019.08.002

Austin, B. J., & Corey, B. (2012). Factors contributing to the longevity of the commercial use of crocodiles by Indigenous people in remote Northern Australia: A case study. *The Rangeland Journal, 34*(3), 239–248. https://doi.org/10.1071/RJ11082

American Veterinary Medical Association (AVMA). (2021). SARS-CoV-2 in animals. Retrieved 8 April 2021, from American Veterinary Medical Association website: https://www.avma.org/resources-tools/animal-health-and-welfare/covid-19/sars-cov-2-animals-including-pets

Ayukekbong, J. A., Ntemgwa, M., & Atabe, A. N. (2017). The threat of antimicrobial resistance in developing countries: Causes and control strategies. *Antimicrobial Resistance & Infection Control, 6*(1), 47. https://doi.org/10.1186/s13756-017-0208-x

Balloux, F., & van Dorp, L. (2017). Q&A: What are pathogens, and what have they done to and for us? *BMC Biology, 15*. https://doi.org/10.1186/s12915-017-0433-z

Banerjee, A., Kulcsar, K., Misra, V., Frieman, M., & Mossman, K. (2019). Bats and Coronaviruses. *Viruses, 11*(1). https://doi.org/10.3390/v11010041

Bar-On, Y. M., Phillips, R., & Milo, R. (2018). The biomass distribution on Earth. *Proceedings of the National Academy of Sciences, 115*(25), 6506–6511. https://doi.org/10.1073/pnas.1711842115

Barrios, G., & Cremieux, J. (2018). *Protocolo de rancheo para cocodrilo de pantano (Crocodylus moreletii) en México*. México: Comisión Nacional para el Conocimiento y Uso de la Biodiversidad (conabio).

Beare, A. S., & Webster, R. G. (1991). Replication of avian influenza viruses in humans. *Archives of Virology, 119*(1), 37–42. https://doi.org/10.1007/BF01314321

Bekiempis, V. (2020). Nearly 10,000 mink dead from Covid-19 outbreak at Utah fur farms. *The Guardian*. Retrieved from https://www.theguardian.com/world/2020/oct/11/utah-10000-minks-dead-from-coronavirus

Bell, J. H. (2002). Anthrax and the Wool Trade. *American Journal of Public Health, 92*(5), 754–757.

Bennett, E. L., Underwood, F. M., & Milner-Gulland, E. J. (2021). To Trade or Not to Trade? Using Bayesian Belief Networks to Assess How to Manage Commercial Wildlife Trade in a Complex World. *Frontiers in Ecology and Evolution, 9*, 587896. https://doi.org/10.3389/fevo.2021.587896

Berners-Lee, M., Kennelly, C., Watson, R., & Hewitt, C. N. (2018). Current global food production is sufficient to meet human nutritional needs in 2050 provided there is radical societal adaptation. Elementa: *Science of the Anthropocene, 6*(52). https://doi.org/10.1525/elementa.310

Berthe, F. (2020). The global economic impact of ASF: -EN- -FR- *Impact économique mondial de la peste porcine africaine -ES- El impacto económico mundial de la peste porcina africana. Bulletin de l'OIE*, 2020(1), 1–2. https://doi.org/10.20506/bull.2020.1.3119

Beyer, R. M., Manica, A., & Mora, C. (2021). Shifts in global bat diversity suggest a possible role of climate change in the emergence of SARS-CoV-1 and SARS-CoV-2. *Science of The Total Environment, 767,* 145413. https://doi.org/10.1016/j.scitotenv.2021.145413

Bezerra-Santos, M. A., Mendoza-Roldan, J. A., Thompson, R. C. A., Dantas-Torres, F., & Otranto, D. (2021). Illegal Wildlife Trade: A Gateway to Zoonotic Infectious Diseases. *Trends in Parasitology.* https://doi.org/10.1016/j.pt.2020.12.005

Biggs, D., Caceres-Escobar, H., Kock, R., Thomson, G., & Compton, J. (2021). Extend existing food safety systems to the global wildlife trade. *The Lancet Planetary Health, 5*(7), e402–e403. https://doi.org/10.1016/S2542-5196(21)00142-X

Biggs, D., Cooney, R., Roe, D., Dublin, H. T., Allan, J. R., Challender, D. W. S., & Skinner, D. (2017a). Developing a theory of change for a community-based response to illegal wildlife trade. *Conservation Biology, 31*(1), 5–12. https://doi.org/10.1111/cobi.12796

Biggs, D., Cooney, R., Roe, D., Dublin, H. T., Allan, J. R., Challender, D. W. S., & Skinner, D. (2017b). Developing a theory of change for a community-based response to illegal wildlife trade. *Conservation Biology, 31*(1), 5–12. https://doi.org/10.1111/cobi.12796

Blaha, T. (2012). One World-One Health: The Threat of Emerging Diseases. A European Perspective: EU Perspective of 'One World-One Health'. *Transboundary and Emerging Diseases, 59,* 3–8. https://doi.org/10.1111/j.1865-1682.2011.01310.x

Bloom, J. D., Chan, Y. A., Baric, R. S., Bjorkman, P. J., Cobey, S., Deverman, B. E., … Relman, D. A. (2021). Investigate the origins of COVID-19. *Science, 372*(6543), 694.1-694. https://doi.org/10.1126/science.abj0016

Bloomfield, L. S. P., McIntosh, T. L., & Lambin, E. F. (2020). Habitat fragmentation, livelihood behaviors, and contact between people and nonhuman primates in Africa. *Landscape Ecology, 35*(4), 985–1000. https://doi.org/10.1007/s10980-020-00995-w

The British Medical Journal (BMJ) Best Practice. (2021). Middle East respiratory syndrome (MERS). Retrieved 30 May 2021, from https://bestpractice.bmj.com/topics/en-us/1301/prevention#reference-Pop87

Bolkovic, M. L., & Ramadori, D. (Eds.). (2006). Manejo de fauna silvestre en la Argentina: Programas de uso sustentable. Buenos Aires: Ministerio de Salud y Ambiente de la Nación. Retrieved from https://09825386066902646259.googlegroups.com/attach/b79ea59.

Bonwitt, J., Kelly, A. H., Ansumana, R., Agbla, S., Sahr, F., Saez, A. M., … Fichet-Calvet, E. (2016). Rat-atouille: A Mixed Method Study to Characterize Rodent Hunting and Consumption in the Context of Lassa Fever. *ECOHEALTH, 13*(2), 234–247.

Booth, H., Arias, M., Brittain, S., Challender, D. W. S., Khanyari, M., Kupier, T., … Milner-Gulland, E. J. (2020). *Managing wildlife trade for sustainable development outcomes after COVID-19.* SocArXiv. https://doi.org/10.31235/osf.io/2p3xt

Booth, H., Pooley, S., Clements, T., Putra, M. I. H., Lestari, W. P., Lewis, S., … Milner-Gulland, E. J. (2020). Assessing the impact of regulations on the use and trade of wildlife: An operational framework, with a case study on manta rays. *Global Ecology and Conservation, 22,* e00953. https://doi.org/10.1016/j.gecco.2020.e00953

Boseret, G., Losson, B., Mainil, J. G., Thiry, E., & Saegerman, C. (2013). Zoonoses in pet birds: Review and perspectives. *Veterinary Research, 44*(1), 36. https://doi.org/10.1186/1297-9716-44-36

Bottrill, M., Cheng, S., Garside, R., Wongbusarakum, S., Roe, D., Holland, M. B., … Turner, W. R. (2014). What are the impacts of nature conservation interventions on human well-being: A systematic map protocol. *Environmental Evidence, 3*(1), 16. https://doi.org/10.1186/2047-2382-3-16

Breman, J. G. (2000). Monkeypox: An Emerging Infection for Humans? In W. Scheld, W. Craig, & J. Hughes (Eds.), *Emerging Infections 4* (pp. 45–67). Washington, DC: ASM Press. https://doi.org/10.1128/9781555816971.ch5

Bueno, I., Smith, K. M., Sampedro, F., Machalaba, C. C., Karesh, W. B., & Travis, D. A. (2016). Risk Prioritization Tool to Identify the Public Health Risks of Wildlife Trade: The Case of Rodents from Latin America. *Zoonoses and Public Health, 63*(4), 281–293. https://doi.org/10.1111/zph.12228

Burridge, M. J., Simmons, L.-A., & Allan, S. A. (2000). Introduction of Potential Heartwater Vectors and Other Exotic Ticks into Florida on Imported Reptiles. *Journal of Parasitology, 86*(4), 700. https://doi.org/10.1645/0022-3395(2000)086[0700:IOPHVA]2.0.CO;2

Butchart, S. H. M., Walpole, M., Collen, B., van Strien, A., Scharlemann, J. P. W., Almond, R. E. A., … Watson, R. (2010). Global Biodiversity: Indicators of Recent Declines. *Science, 328*(5982), 1164–1168. https://doi.org/10.1126/science.1187512

Cáceres-Escobar, H., Broad, S., Challender, D. W. S., Kinnaird, M. F., Keenan, C., Lichtenstein, G., … Kock, R. A. (2020). PROTOCOL: Situation Analysis EGM [Online resource]. https://doi.org/10.6084/m9.figshare.13392275.v2

Cahan, E. & 2020. (2020). COVID-19 hits U.S. mink farms after ripping through Europe. Retrieved 4 December 2020, from Science | AAAS website: https://www.sciencemag.org/news/2020/08/covid-19-hits-us-mink-farms-after-ripping-through-europe

Cai, X., Fry, C. V., & Wagner, C. S. (2021). International collaboration during the COVID-19 crisis: Autumn 2020 developments. *Scientometrics.* https://doi.org/10.1007/s11192-021-03873-7

Campbell Collaboration. (2020). *Guidance for producing a Campbell evidence and gap map.* Campbell Systematic Reviews. Retrieved from https://onlinelibrary.wiley.com/pb-assets/Campbell%20EGM%20guidance%20-%20Consultation-1593530394570.pdf

Cantlay, J. C., Ingram, D. J., & Meredith, A. L. (2017). A Review of Zoonotic Infection Risks Associated with the Wild Meat Trade in Malaysia. *EcoHealth, 14*(2), 361–388. https://doi.org/10.1007/s10393-017-1229-x

Cappelle, J., Zhao, D., Gilbert, M., Nelson, M. I., Newman, S. H., Takekawa, J. Y., … Xiao, X. (2014). Risks of avian influenza transmission in areas of intensive free-ranging duck production with wild waterfowl. *EcoHealth, 11*(1), 109–119. https://doi.org/10.1007/s10393-014-0914-2

Carlson, C. J., Albery, G. F., Merow, C., Trisos, C. H., Zipfel, C. M., Eskew, E. A., … Bansal, S. (2020). Climate change will drive novel cross-species viral transmission. *BioRxiv*, 2020.01.24.918755. https://doi.org/10.1101/2020.01.24.918755

Caron, A., Cappelle, J., Cumming, G. S., de Garine-Wichatitsky, M., & Gaidet, N. (2015). Bridge hosts, a missing link for disease ecology in multi-host systems. *Veterinary Research, 46*(1), 83. https://doi.org/10.1186/s13567-015-0217-9

Carroll, D., Wang, J., Fanning, S., & McMahon, B. J. (2015). Antimicrobial Resistance in Wildlife: Implications for Public Health. *Zoonoses and Public Health, 62*(7), 534–542. https://doi.org/10.1111/zph.12182

Cascio, A., Bosilkovski, M., Rodriguez – Morales, A. J., & Pappas, G. (2011). The socio-ecology of zoonotic infections. *Clinical Microbiology and Infection, 17*(3), 336–342. https://doi.org/10.1111/j.1469-0691.2010.03451.x

Castilho, L. C., De Vleeschouwer, K. M., Milner-Gulland, E. J., & Schiavetti, A. (2019). Hunting of mammal species in protected areas of the southern Bahian Atlantic Forest, Brazil. *Oryx, 53*(4), 687–697. https://doi.org/10.1017/S0030605317001247

Convention on Biological Diversity (CBD). (1993). *Convention on Biological Diversity: Article 2: Use of Terms*. Convention on Biological Diversity. Retrieved from https://www.cbd.int/doc/legal/cbd-en.pdf

Centers for Disease Control and Prevention (CDC) (2018). CDC - Emerging Infectious Diseases—NIOSH Workplace Safety and Health Topic. Retrieved 30 November 2020, from https://www.cdc.gov/niosh/topics/emerginfectdiseases/default.html

CDC (2020a). Bringing an African Rodent into the United States. Retrieved 10 April 2021, from https://www.cdc.gov/importation/bringing-an-animal-into-the-united-states/african-rodents.html

CDC (2020b). Human Rabies. Retrieved 1 May 2021, from https://www.cdc.gov/rabies/location/usa/surveillance/human_rabies.html

CDC (2021a). History of Ebola Virus Disease (EVD) Outbreaks. Retrieved 7 June 2021, from https://www.cdc.gov/vhf/ebola/history/chronology.html

CDC (2021b). Marburg (Marburg Virus Disease). Retrieved 1 December 2021, from https://www.cdc.gov/vhf/marburg/index.html

CDC, National Center for Emerging and Zoonotic Infectious Diseases (NCEZID), & Division of High-Consequence Pathogens and Pathology (DHCPP). (2015, May 11). African Rodent Importation Ban | Monkeypox | Poxvirus. Retrieved 2 December 2020, from https://www.cdc.gov/poxvirus/monkeypox/african-ban.html

CDC, NCEZID, & DHCPP (2018). 2003 United States Outbreak of Monkeypox | Monkeypox | Poxvirus | CDC. Retrieved 2 December 2020, from https://www.cdc.gov/poxvirus/monkeypox/outbreak.html

Center for Food Safety and Applied Nutrition. (2020). HACCP Principles & Application Guidelines. *FDA*. Retrieved from https://www.fda.gov/food/hazard-analysis-critical-control-point-haccp/haccp-principles-application-guidelines

Chaber, A.-L., Allebone-Webb, S., Lignereux, Y., Cunningham, A. A., & Marcus Rowcliffe, J. (2010). The scale of illegal meat importation from Africa to Europe via Paris: Illegal intercontinental meat trade. *Conservation Letters, 3*(5), 317–321. *https://doi.org/10.1111/j.1755-263X.2010.00121.x*

Chai, J.-Y., Darwin Murrell, K., & Lymbery, A. J. (2005). Fish-borne parasitic zoonoses: Status and issues. *International Journal for Parasitology, 35*(11–12), 1233–1254. https://doi.org/10.1016/j.ijpara.2005.07.013

Chakanya, C., Arnaud, E., Muchenje, V., & Hoffman, L. C. (2020). Fermented meat sausages from game and venison: What are the opportunities and limitations? *Journal of the Science of Food and Agriculture, 100*(14), 5023–5031. https://doi.org/10.1002/jsfa.9053

Challender, D. W. S. (2019). Mischaracterization of wildlife trade threat. Response to 'Global wildlife trade across the tree of life'. *Science ELetters, 366*(6461), 71–76.

Challender, D. W. S., Harrop, S. R., & MacMillan, D. C. (2015a). Towards informed and multi-faceted wildlife trade interventions. *Global Ecology and Conservation, 3*, 129–148. https://doi.org/10.1016/j.gecco.2014.11.010

Challender, D. W. S., Harrop, S. R., & MacMillan, D. C. (2015b). Understanding markets to conserve trade-threatened species in CITES. *Biological Conservation, 187*, 249–259. *https://doi.org/10.1016/j.biocon.2015.04.015*

Challender, D. W. S., Heinrich, S., Shepherd, C. R., & Katsis, L. K. D. (2020). Chapter 16—International trade and trafficking in pangolins, 1900–2019. In D. W. S. Challender, H. C. Nash, & C. Waterman (Eds.), *Pangolins* (pp. 259–276). Academic Press. https://doi.org/10.1016/B978-0-12-815507-3.00016-2

Challender, D. W. S., Hinsley, A., Veríssimo, D., & Sas-Rolfes, M. 't. (2020). Coronavirus: Why a blanket ban on wildlife trade would not be the right response. Retrieved 23 July 2020, from The Conversation website: http://theconversation.com/coronavirus-why-a-blanket-ban-on-wildlife-trade-would-not-be-the-right-response-135746

Challender, D. W. S., & MacMillan, D. C. (2014). Poaching is more than an Enforcement Problem: Poaching is more than an enforcement problem. *Conservation Letters, 7*(5), 484–494. https://doi.org/10.1111/conl.12082

Challender, D. W. S., & Waterman, C. (2017). *Implementation of CITES Decisions 17.239 b) and 17.240 on Pangolins (Manis spp.)*. IUCN, International Union for Conservation of Nature. Retrieved from https://cites.org/sites/default/files/eng/com/sc/69/E-SC69-57-A.pdf

Chan, Y. A., & Zhan, S. H. (2020). Single source of pangolin CoVs with a near identical Spike RBD to SARS-CoV-2. *BioRxiv*, 2020.07.07.184374. https://doi.org/10.1101/2020.07.07.184374

Chardonnet, P., Chardonnet, B., Daniel, P., Darroze, S., Feer, F., Forster, M., ... Zorzi, N. (1995). *Faune sauvage africaine: La ressource oubliée. Tome I, Synthèse*. Luxembourg: Commission Européenne. Retrieved from https://agritrop.cirad.fr/327235/

Charity, S., & Ferreira, J. M. (2020). *Wildlife Trafficking in Brazil*. Cambridge, United Kingdom: TRAFFIC International.

Charron, D. F. (2012). Ecosystem approaches to health for a global sustainability agenda. *EcoHealth, 9*(3), 256–266. https://doi.org/10.1007/s10393-012-0791-5

Chaves, L. F., Gottdenker, N., Velasquez Runk, J., Liebman, A., Williams-Guillén, K., Kelley, L., ... Wallace, R. (2021). Dispatch 7: Scientists say land use drives new pandemics. But what if "land" isn't what they think it is? Retrieved 16 April 2021, from PReP Dispatches website: https://drive.google.com/file/d/12cW-PkPU9Z5TtoEMqKuhPnUGs-mOLVp16/view?usp=sharing&usp=embed_facebook

Chaves, W. A., Monroe, M. C., & Sieving, K. E. (2019). Wild Meat Trade and Consumption in the Central Amazon, Brazil. *Human Ecology, 47*(5), 733–746. https://doi.org/10.1007/s10745-019-00107-6

Chaves, W. A., Wilkie, D. S., Monroe, M. C., & Sieving, K. E. (2017). Market access and wild meat consumption in the central Amazon, Brazil. *Biological Conservation, 212,* 240–248. https://doi.org/10.1016/j.biocon.2017.06.013

Cheng, V. C. C., Lau, S. K. P., Woo, P. C. Y., & Yuen, K. Y. (2007). Severe Acute Respiratory Syndrome Coronavirus as an Agent of Emerging and Reemerging Infection. *Clinical Microbiology Reviews, 20*(4), 660–694. https://doi.org/10.1128/CMR.00023-07

Cheng, Y., Gao, Z., & Seale, J. (2015). Changing structure of China's meat imports. *Journal of Integrative Agriculture, 14*(6), 1081–1091. https://doi.org/10.1016/S2095-3119(14)60991-6

Choo, S. W., Zhou, J., Tian, X., Zhang, S., Qiang, S., O'Brien, S. J., ... Sitam, F. T. (2020). Are pangolins scapegoats of the COVID-19 outbreak-CoV transmission and pathology evidence? *Conservation Letters, 13*(6), e12754. https://doi.org/10.1111/conl.12754

Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) (2018). CITES and Livelihoods. Retrieved 12 November 2020, from https://www.cites.org/eng/prog/livelihoods

CITES (2019). *Draft Amendments To Resolution Conf. 11.15 (Rev. Cop 12) On Non-Commercial Loan, Donation Or Exchange Of Museum, Herbarium Speciments And Draft Amendments To Resolution Conf. 12.3 (Rev. Cop17) On Permits And Certificatesand Draft Decisions Of The Conference Of The Parties*. Retrieved from https://cites.org/sites/default/files/eng/com/sc/2020-2021/E-SC2020-02.pdf

CITES (2020a). CITES glossary. Retrieved 30 November 2020, from https://cites.org/eng/resources/terms/glossary.php#

CITES (2020b). *Guidance On The Use Of The Scientific Exchange Exemption And The Simplified Procedures To Issue Permits And Certificates*. Retrieved from https://cites.org/sites/default/files/eng/com/sc/2020-2021/E-SC2020-02.pdf

CITES (2020c). The CITES species. Retrieved 17 November 2020, from https://www.cites.org/eng/disc/species.php

CITES. (2021). CITES Trade Database. Retrieved 30 October 2020, from Full CITES Trade Database download available (version 2020.1) website: https://trade.cites.org/

Civitello, D. J., Cohen, J., Fatima, H., Halstead, N. T., Liriano, J., McMahon, T. A., ... Rohr, J. R. (2015). Biodiversity inhibits parasites: Broad evidence for the dilution effect. *Proceedings of the National Academy of Sciences of the United States of America, 112*(28), 8667–8671. https://doi.org/10.1073/pnas.1506279112

Coad, L., Fa, J. E., Abernethy, K., van Vliet, N., Santamaria, C., Wilkie, D., ... Nasi, R. (2019). *Toward a sustainable, participatory and inclusive wild meat sector*. Center for International Forestry Research (CIFOR). https://doi.org/10.17528/cifor/007046

Coalition to End the Trade (2020). #ENDTHETRADE. Retrieved 2 December 2020, from #ENDTHETRADE website: https://endthetrade.com/

Coconier, E. G., & Lichtenstein, G. (2014). [Loros, gripe aviar y soja: Los alcances de políticas globales sobre proyectos locales]. *AVA Revista de Antropologia.*

Cohen, J. M., Sauer, E. L., Santiago, O., Spencer, S., & Rohr, J. R. (2020). Divergent impacts of warming weather on wildlife disease risk across climates. *Science, 370*(6519). https://doi.org/10.1126/science.abb1702

Coker, R., Rushton, J., Mounier-Jack, S., Karimuribo, E., Lutumba, P., Kambarage, D., ... Rweyemamu, M. (2011). Towards a conceptual framework to support one-health research for policy on emerging zoonoses. *The Lancet Infectious Diseases, 11*(4), 326–331. https://doi.org/10.1016/S1473-3099(10)70312-1

Comisión Nacional para el Conocimiento y Uso de la Biodiversidad (CONABIO) (2018). *Guía informativa para el manejo y aprovechamiento sustentable de caoba en el marco de las disposiciones de la CITES*. Ciudad de México, México: Comisión Nacional para el Conocimiento y Uso de la Biodiversidad. Retrieved from https://cites.org/sites/default/files/ndf_material/S-PC24-Inf-03.pdf

Conrad, K. (2012). Trade Bans: A Perfect Storm for Poaching? *Tropical Conservation Science, 5*(3), 245–254. https://doi.org/10.1177/194008291200500302

Cook, J., Nuccitelli, D., Green, S. A., Richardson, M., Winkler, B., Painting, R., ... Skuce, A. (2013). Quantifying the consensus on anthropogenic global warming in the scientific literature. *Environmental Research Letters, 8*(2), 024024. https://doi.org/10.1088/1748-9326/8/2/024024

Cook, J., Oreskes, N., Doran, P. T., Anderegg, W. R. L., Verheggen, B., Maibach, E. W., ... Rice, K. (2016). Consensus on consensus: A synthesis of consensus estimates on human-caused global warming. *Environmental Research Letters, 11*(4), 048002. https://doi.org/10.1088/1748-9326/11/4/048002

Cooney, R., Kasterine, A., MacMillan, D., Milledge, S., Nossal, K., Roe, D., & 't Sas-Rolfes, M. (2015). *The trade in wildlife: A framework to improve biodiversity and livelihood outcomes*. Geneva, Switzerland: International Trade Centre.

Cooney, R., Roe, D., Dublin, H., & Booker, F. (2018). *Wild life, Wild Livelihoods: Involving Communities in Sustainable Wildlife Management and Combatting the Illegal Wildlife Trade*. Nairobi, Kenya: United Nations Environment Programme. Retrieved from http://wedocs.unep.org/bitstream/handle/20.500.11822/22864/WLWL_Report_web.pdf

Cooney, R., Roe, D., Dublin, H., Phelps, J., Wilkie, D., Keane, A., … Biggs, D. (2017). From Poachers to Protectors: Engaging Local Communities in Solutions to Illegal Wildlife Trade. *Conservation Letters, 10*(3), 367–374. https://doi.org/10.1111/conl.12294

Costard, S., Wieland, B., de Glanville, W., Jori, F., Rowlands, R., Vosloo, W., … Dixon, L. K. (2009). African swine fever: How can global spread be prevented? Philosophical Transactions of the Royal Society of London. *Series B, Biological Sciences, 364*(1530), 2683–2696. https://doi.org/10.1098/rstb.2009.0098

Crosier, A., McVey, D., & French, J. (2015). 'By failing to prepare you are preparing to fail': Lessons from the 2009 H1N1 'swine flu' pandemic. *The European Journal of Public Health, 25*(1), 135–139. https://doi.org/10.1093/eurpub/cku131

Crutzen, P. J. (2002). Geology of mankind. *Nature, 415*(6867), 23–23. https://doi.org/10.1038/415023a

Curseu, D., Popa, M., Sirbu, D., & Stoian, I. (2009). Potential Impact of Climate Change on Pandemic Influenza Risk. *Global Warming*, 643–657. https://doi.org/10.1007/978-1-4419-1017-2_45

Cwynar, P., Stojkov, J., & Wlazlak, K. (2019). African Swine Fever Status in Europe. *Viruses, 11*(4). https://doi.org/10.3390/v11040310

Cyranoski, D. (2017). Bat cave solves mystery of deadly SARS virus—And suggests new outbreak could occur. *Nature, 552*(7683), 15–16. https://doi.org/10.1038/d41586-017-07766-9

Cyranoski, D., & Abbott, A. (2003). Virus detectives seek source of SARS in China's wild animals. *Nature, 423*(6939), 467. https://doi.org/10.1038/423467a

DAISIE (Ed.). (2009). *Handbook of alien species in Europe*. Dordrecht, Netherlands: Springer.

D'Cruze, N., Harrington, L. A., Assou, D., Ronfot, D., Macdonald, D. W., Segniagbeto, G. H., & Auliya, M. (2020). Searching for snakes: Ball python hunting in southern Togo, West Africa. *Nature Conservation, 38*, 13–36. https://doi.org/10.3897/natureconservation.38.47864

Dee, S. A., Niederwerder, M. C., Patterson, G., Cochrane, R., Jones, C., Diel, D., … Sundberg, P. (2020). The risk of viral transmission in feed: What do we know, what do we do? *Transboundary and Emerging Diseases, 67*(6), 2365–2371. https://doi.org/10.1111/tbed.13606

Department of Environmental Affairs, Republic of south Africa. (2019, September 3). Biodiversity Economy—*Game Meat*. Retrieved from https://www.environment.gov.za/sites/default/files/docs/publications/biodiversity2019gamemeat.pdf

Department of Agriculture, Water and the Environment, Australian Government (2020). Australian red meat export statistics. Retrieved 1 December 2020, from https://www.agriculture.gov.au/export/controlled-goods/meat/statistics

Di Marco, M., Baker, M. L., Daszak, P., Barro, P. D., Eskew, E. A., Godde, C. M., … Ferrier, S. (2020). Opinion: Sustainable development must account for pandemic risk. *Proceedings of the National Academy of Sciences, 117*(8), 3888–3892. https://doi.org/10.1073/pnas.2001655117

Diaz, J. H., Warren, R. J., & Oster, M. J. (2020). The Disease Ecology, Epidemiology, Clinical Manifestations, and Management of Trichinellosis Linked to Consumption of Wild Animal Meat. *Wilderness & Environmental Medicine, 31*(2), 235–244. https://doi.org/10.1016/j.wem.2019.12.003

Dobzhansky, T. (1982). *Genetics and the origin of species*. New York, USA: Columbia University Press.

Du, Z., Wang, L., Cauchemez, S., Xu, X., Wang, X., Cowling, B. J., & Meyers, L. A. (2020). Risk for Transportation of Coronavirus Disease from Wuhan to Other Cities in China. *Emerging Infectious Diseases, 26*(5), 1049–1052. https://doi.org/10.3201/eid2605.200146

Duckworth, J. W., Batters, G., Belant, J. L., Bennett, E. L., Brunner, J., Burton, J., … Wirth, R. (2012). Why South-east Asia should be the world's priority for averting imminent species extinctions, and a call to join a developing cross-institutional programme to tackle this urgent issue. *S.A.P.I.EN.S. Surveys and Perspectives Integrating Environment and Society*, (5.2). Retrieved from http://journals.openedition.org/sapiens/1327

Dudley, J. P., Hoberg, E. P., Jenkins, E. J., & Parkinson, A. J. (2015). Climate Change in the North American Arctic: A One Health Perspective. *EcoHealth, 12*(4), 713–725. https://doi.org/10.1007/s10393-015-1036-1

Dunn, R. R., Davies, T. J., Harris, N. C., & Gavin, M. C. (2010). Global drivers of human pathogen richness and prevalence. *Proceedings. Biological Sciences, 277*(1694), 2587–2595. https://doi.org/10.1098/rspb.2010.0340

European Centre for Disease Prevention and Control (ECDC). (2020). *Detection of new SARS-CoV-2 variants related to mink. 19*.

ECDC (2021). Factsheet on A(H5N1). Retrieved 9 April 2021, from European Centre for Disease Prevention and Control website: https://www.ecdc.europa.eu/en/zoonotic-influenza/facts/factsheet-h5n1

Eckstein, S., Ehmann, R., Gritli, A., Ben Yahia, H., Diehl, M., Wölfel, R., … Ben Moussa, M. (2021). Prevalence of Middle East Respiratory Syndrome Coronavirus in Dromedary Camels, Tunisia. *Emerging Infectious Diseases, 27*(7), 1964–1968. https://doi.org/10.3201/eid2707.204873

EcoHealth Alliance. (2019). *Infectious disease emergence and economics of altered landscapes*—IDEEAL (P. Daszak, T. Hughes, C. Zambrana-Torrelio, J. H. Epstein, H. E. Field, A. H. White, … S. Kitchakarn, Eds.). New York, New York, U.S.A.: EcoHealth Alliance. Retrieved from https://www.ecohealthalliance.org/wp-content/uploads/2019/09/IDEEAL_report_final.pdf

Ecojust. (2020). Bushmeat trafficking in Europe: A ticking time bomb? Retrieved 15 November 2020, from https://www.ecojust.eu/bushmeat-trafficking-in-europe-a-ticking-time-bomb/

Edwards, C. E., Yount, B. L., Graham, R. L., Leist, S. R., Hou, Y. J., Dinnon, K. H., … Baric, R. S. (2020). Swine acute diarrhea syndrome coronavirus replication in primary human cells reveals potential susceptibility to infection. *Proceedings of the National Academy of Sciences, 117*(43), 26915–26925. https://doi.org/10.1073/pnas.2001046117

Effiom, E. O., Nuñez-Iturri, G., Smith, H. G., Ottosson, U., & Olsson, O. (2013). Bushmeat hunting changes regeneration of African rainforests. Proceedings. *Biological Sciences, 280*(1759), 20130246. https://doi.org/10.1098/rspb.2013.0246

European Food Safety Authority (EFSA) & ECDC. (2019). The European Union One Health 2018 Zoonoses Report. *EFSA Journal, 17*(12), e05926. https://doi.org/10.2903/j.efsa.2019.5926

El Masry, I., von Dobschuetz, S., Plee, L., Larfaoui, F., Yang, Z., Song, J., … Sumption, K. (2020). *Exposure of humans or animals to SARS-CoV-2 from wild, livestock, companion and aquatic animals*. Rome, Italy: FAO. https://doi.org/10.4060/ca9959en

Ellis, E. C., Kaplan, J. O., Fuller, D. Q., Vavrus, S., Klein Goldewijk, K., & Verburg, P. H. (2013). Used planet: A global history. Proceedings of the National Academy of Sciences, 110(20), 7978–7985. https://doi.org/10.1073/pnas.1217241110

Ellis-Petersen, H. (2015, March 25). Fur trade booming after swing from fashion faux pas to catwalk favourite. Retrieved 10 December 2020, from The Guardian website: http://www.theguardian.com/fashion/2015/mar/25/fur-trade-booming-fashion-catwalks

Eskew, E. A., & Carlson, C. J. (2020). Overselling wildlife trade bans will not bolster conservation or pandemic preparedness. *The Lancet Planetary Health, 4*(6), e215–e216. https://doi.org/10.1016/S2542-5196(20)30123-6

Euronews & Agence France-Presse (AFP) (2020). Lithuania confirms its first coronavirus cases at a mink farm. Retrieved 4 December 2020, from Euronews website: https://www.euronews.com/2020/11/26/lithuanian-authorities-find-first-coronavirus-cases-at-a-mink-farm

European Centre for Disease Prevention and Control (ECDC). (2019). *Operational tool on rapid risk assessment methodology: ECDC 2019*. LU: Publications Office. Retrieved from https://data.europa.eu/doi/10.2900/104938

Evans, T. S., Myat, T. W., Hom, N. S., Ricks, K. M., Maw, M. T., Oo, Z. M., … Thu, H. M. (2021). Seroepidemiologic Survey of Crimean-Congo Hemorrhagic Fever Virus in Logging Communities, Myanmar. *Emerging Infectious Diseases, 27*(6), 1709–1713. https://doi.org/10.3201/eid2706.203223

Everard, M., Johnston, P., Santillo, D., & Staddon, C. (2020). The role of ecosystems in mitigation and management of Covid-19 and other zoonoses. *Environmental Science & Policy, 111*, 7–17. https://doi.org/10.1016/j.envsci.2020.05.017

Fa, J. E., Seymour, S., Dupain, J., Amin, R., Albrechtsen, L., & Macdonald, D. (2006). Getting to grips with the magnitude of exploitation: Bushmeat in the Cross–Sanaga rivers region, Nigeria and Cameroon. *Biological Conservation, 129*(4), 497–510. https://doi.org/10.1016/j.biocon.2005.11.031

Fabreti, L. G., Castro, D., Gorzoni, B., Janini, L. M. R., & Antoneli, F. (2019). Stochastic Modeling and Simulation of Viral Evolution. *Bulletin of Mathematical Biology, 81*(4), 1031–1069. https://doi.org/10.1007/s11538-018-00550-4

Fairhead, J., Leach, M., & Millimouno, D. (2021). Spillover or endemic? Reconsidering the origins of Ebola virus disease outbreaks by revisiting local accounts in light of new evidence from Guinea. *BMJ Global Health, 6*(4), e005783. https://doi.org/10.1136/bmjgh-2021-005783

Food and Agriculture Organization of the United Nations (FAO) (1998). *Food Quality and Safety Systems—A Training Manual on Food Hygiene and the Hazard Analysis and Critical Control Point (HACCP) System*. Rome, Italy: Publishing Management Group, FAO Information Divisio. Retrieved from http://www.fao.org/3/W8088E/w8088e00.htm#Contents

FAO (2011). *A value chain approach to animal diseases risk management: Technical foundations and practical framework for field application*. Rome: Food and Agriculture Organization of the United Nations. Retrieved from http://www.fao.org/3/a-i2198e.pdf

FAO (2019). *The state of the world's biodiversity for food and agriculture* (J. Bélanger & D. Pilling, Eds.). FAO Commission on Genetic Resources for Food and Agriculture. Retrieved from http://www.fao.org/3/CA3129EN/CA3129EN.pdf

FAO. (2020a). *Global Forest Resources Assessment 2020 – Key – Findings*. Rome: FAO. Retrieved from FAO website: http://www.fao.org/documents/card/en/c/ca8753en

FAO. (2020b). Global meat production. Retrieved 1 December 2020, from Our World in Data website: https://ourworldindata.org/grapher/global-meat-production

FAO. (2021). FAOSTAT. Retrieved 11 December 2020, from http://www.fao.org/faostat/en/

FAO, *Centre de Coopération Internationale en Recherche Agronomique pour le Développement* (CIRAD), Center for International Forestry Research (CIFOR), & The Wildlife Conservation Society (WCS). (2020). White paper: Build back better in a post-COVID-19 world – Reducing future wildlife-borne spillover of disease to humans: Sustainable Wildlife Management (SWM) Programme. Rome: FAO. https://doi.org/10.4060/cb1503en

FAO, World Organisation for Animal Health (OIE), & World Health Organisation (WHO). (2006). *Global Early Warning and Response System for Major Animal Diseases, including Zoonoses* (GLEWS).

FAO, OIE, & WHO (2010). The FAO-OIE-WHO Collaboration: A tripartite concept note. Retrieved 30 September 2020, from WHO website: http://www.who.int/foodsafety/areas_work/zoonose/concept-note/en/

FAO, OIE, & WHO (2021). GLEWS — The Global Early Warning System. Retrieved 9 April 2021, from GLEWS+ The Joint FAO–OIE–WHO Global Early Warning System for health threats and emerging risks at the human–animal–ecosystems interface website: http://www.glews.net/

FAO, OIE, WHO, and United Nations Environment Programme (UNEP) (2021). *Joint Tripartite (FAO, OIE, WHO) and UNEP Statement—Tripartite and UNEP support OHHLEP's definition of "One Health". 2.*

FAO & WHO (2001). *Codex alimentarius: Food hygiene basic texts* (2nd ed). Rome: Food and Agriculture Organization of the United Nations : World Health Organization. Retrieved from http://www.fao.org/fao-who-codexalimentarius/en/

FAO & WHO (2021). Codex Alimentarius: International Food Standards. Retrieved from http://www.fao.org/fao-who-codexalimentarius/en/

Farag, E. A. B., Nour, M., El Idrissi, A., Berrada, J., Moustafa, A., Mehmood, M., … Ismail, M. H. (2019). Survey on Implementation of One Health Approach for MERS-CoV Preparedness and Control in Gulf Cooperation Council and Middle East Countries. *Emerging Infectious Diseases, 25*(3). https://doi.org/10.3201/eid2503.171702

Faust, C. L., Dobson, A. P., Gottdenker, N., Bloomfield, L. S. P., McCallum, H. I., Gillespie, T. R., … Plowright, R. K. (2017). Null expectations for disease dynamics in shrinking habitat: *Dilution or amplification? Philosophical Transactions of the Royal Society B: Biological Sciences, 372*(1722), 20160173. https://doi.org/10.1098/rstb.2016.0173

Food and Drug Administration (FDA). (2018). *CVM GFI #245 Hazard Analysis and Risk-Based Preventive Controls for Food for Animals*. Retrieved from https://www.fda.gov/regulatory-information/search-fda-guidance-documents/cvm-gfi-245-hazard-analysis-and-risk-based-preventive-controls-food-animals

Fèvre, E. M., Bronsvoort, B. M. de C., Hamilton, K. A., & Cleaveland, S. (2006). Animal movements and the spread of infectious diseases. *Trends in Microbiology, 14*(3), 125–131. https://doi.org/10.1016/j.tim.2006.01.004

Field, H. E. (2009). Bats and emerging zoonoses: Henipaviruses and SARS. *Zoonoses and Public Health, 56*(6–7), 278–284. https://doi.org/10.1111/j.1863-2378.2008.01218.x

Findell, K. L., Berg, A., Gentine, P., Krasting, J. P., Lintner, B. R., Malyshev, S., … Shevliakova, E. (2017). The impact of anthropogenic land use and land cover change on regional climate extremes. *Nature Communications, 8*(1), 989. https://doi.org/10.1038/s41467-017-01038-w

Findlater, A., & Bogoch, I. I. (2018). Human Mobility and the Global Spread of Infectious Diseases: A Focus on Air Travel. *Trends in Parasitology, 34*(9), 772–783. https://doi.org/10.1016/j.pt.2018.07.004

Fine, A. E., Pruvot, M., Benfield, C. T. O., Caron, A., Cattoli, G., Chardonnet, P., … Meeting Participants. (2020). Eradication of Peste des Petits Ruminants Virus and the Wildlife-Livestock Interface. *Frontiers in Veterinary Science, 7*, 50. https://doi.org/10.3389/fvets.2020.00050

Fischhoff, I. R., Castellanos, A. A., Rodrigues, J. P. G. L. M., Varsani, A., & Han, B. A. (2021). Predicting the zoonotic capacity of mammal species for SARS-CoV-2. *BioRxiv*, 2021.02.18.431844. https://doi.org/10.1101/2021.02.18.431844

Forest Europe. (2015). State of Europe's Forests 2015 Report. Retrieved 1 December 2020, from https://foresteurope.org/state-europes-forests-2015-report/

Forgey, Q. (2020, April 3). 'Shut down those things right away': Calls to close 'wet markets' ramp up pressure on China. Retrieved 29 September 2020, from POLITICO website: https://www.politico.com/news/2020/04/03/anthony-fauci-foreign-wet-markets-shut-down-162975

Freuling, C. M., Breithaupt, A., Müller, T., Sehl, J., Balkema-Buschmann, A., Rissmann, M., … Mettenleiter, T. C. (2020). Susceptibility of Raccoon Dogs for Experimental SARS-CoV-2 Infection—Volume 26, Number 12—December 2020—Emerging Infectious Diseases journal—CDC. *Emerging Infectious Diseases, 26*(12). https://doi.org/10.3201/eid2612.203733

Frutos, R., Serra-Cobo, J., Chen, T., & Devaux, C. A. (2020). COVID-19: Time to exonerate the pangolin from the transmission of SARS-CoV-2 to humans. *Infection, Genetics and Evolution, 84*, 104493. https://doi.org/10.1016/j.meegid.2020.104493

Fukushima, C. S., Mammola, S., & Cardoso, P. (2020). Global wildlife trade permeates the Tree of Life. *Biological Conservation, 247*, 108503. https://doi.org/10.1016/j.biocon.2020.108503

Fur Commission USA. (2020). Global Fur Trade Worth as Much as Wi-Fi. Retrieved 10 December 2020, from Fur Commission USA website: https://furcommission.com/new-research-reveals-the-global-fur-trade-is-worth-as-much-as-wi-fi/

Garnier, J., Savic, S., Boriani, E., Bagnol, B., Häsler, B., & Kock, R. (2020). Helping to heal nature and ourselves through human-rights-based and gender-responsive One Health. *One Health Outlook, 2*(1), 22. https://doi.org/10.1186/s42522-020-00029-0

Garry, R. F. (2021, May 12). Early appearance of two distinct genomic lineages of SARS-CoV-2 in different Wuhan wildlife markets suggests SARS-CoV-2 has a natural origin—SARS-CoV-2 coronavirus. Retrieved 24 May 2021, from Virological website: https://virological.org/t/early-appearance-of-two-distinct-genomic-lineages-of-sars-cov-2-in-different-wuhan-wildlife-markets-suggests-sars-cov-2-has-a-natural-origin/691

Garten, R. J., Davis, C. T., Russell, C. A., Shu, B., Lindstrom, S., Balish, A., … Cox, N. J. (2009). Antigenic and Genetic Characteristics of Swine-Origin 2009 A(H1N1) Influenza Viruses Circulating in Humans. *Science, 325*(5937), 197–201. https://doi.org/10.1126/science.1176225

Garten, Rebecca J., Davis, C. T., Russell, C. A., Shu, B., Lindstrom, S., Balish, A., … Cox, N. J. (2009). Antigenic and Genetic Characteristics of the Early Isolates of Swine-Origin 2009 A(H1N1) Influenza Viruses Circulating in Humans. *Science (New York, N.Y.), 325*(5937), 197–201. https://doi.org/10.1126/science.1176225

Global Burden of Disease (GBD). (2012). *Global Burden of Disease Study 2010 (GBD 2010) Results by Cause 1990-2010* [Data set]. Institute for Health Metrics and Evaluation (IHME). https://doi.org/10.6069/J86D-DZ43

Georges, A.-J., Leroy, E. M., Renaut, A. A., Benissan, C. T., Nabias, R. J., Ngoc, M. T., … Georges-Courbot, M.-C. (1999). Ebola Hemorrhagic Fever Outbreaks in Gabon, 1994–1997: Epidemiologic and Health Control Issues. *The Journal of Infectious Diseases, 179*(Supplement_1), S65–S75. https://doi.org/10.1086/514290

Gibb, R., Redding, D. W., Chin, K. Q., Donnelly, C. A., Blackburn, T. M., Newbold, T., & Jones, K. E. (2020). Zoonotic host diversity increases in human-dominated ecosystems. *Nature*, 1–5. https://doi.org/10.1038/s41586-020-2562-8

Gilbert, M., Newman, S. H., Takekawa, J. Y., Loth, L., Biradar, C., Prosser, D. J., … Xiao, X. (2010). Flying over an infected landscape: Distribution of highly pathogenic avian influenza H5N1 risk in South Asia and satellite tracking of wild waterfowl. *EcoHealth, 7*(4), 448–458. https://doi.org/10.1007/s10393-010-0672-8

Gilbert, M., Xiao, X., Chaitaweesub, P., Kalpravidh, W., Premashthira, S., Boles, S., & Slingenbergh, J. (2007). Avian influenza, domestic ducks and rice agriculture in Thailand. *Agriculture, Ecosystems & Environment, 119*, 409–415. https://doi.org/10.1016/j.agee.2006.09.001

Gogin, A., Gerasimov, V., Malogolovkin, A., & Kolbasov, D. (2013). African swine fever in the North Caucasus region and the Russian Federation in years 2007-2012. *Virus Research, 173*(1), 198–203. https://doi.org/10.1016/j.virusres.2012.12.007

Gong, L., Li, J., Zhou, Q., Xu, Z., Chen, L., Zhang, Y., … Cao, Y. (2017). A New Bat-HKU2–like Coronavirus in Swine, China, 2017. *Emerging Infectious Diseases, 23*(9), 1607–1609. https://doi.org/10.3201/eid2309.170915

Gottdenker, N. L., Streicker, D. G., Faust, C. L., & Carroll, C. R. (2014). Anthropogenic Land Use Change and Infectious Diseases: A Review of the Evidence. *EcoHealth, 11*(4), 619–632. https://doi.org/10.1007/s10393-014-0941-z

Grace, D., Gilbert, J., Randolph, T., & Kang'ethe, E. (2012). The multiple burdens of zoonotic disease and an ecohealth approach to their assessment. *Tropical Animal Health and Production, 44*(1), 67–73. https://doi.org/10.1007/s11250-012-0209-y

Grace, D., Mutua, F., Ochungo, P., Kruska, R., Jones, K., Brierley, L., … Ogutu, F. (2012). *Mapping of poverty and likely zoonoses hotspots: Report to Department for International Development, UK*. ZSL, ILRI, HSPH. Retrieved from https://cgspace.cgiar.org/bitstream/handle/10568/21161/ZooMap_July2012_final.pdf

Grantham, H. S., Duncan, A., Evans, T. D., Jones, K. R., Beyer, H. L., Schuster, R., … Watson, J. E. M. (2020). Anthropogenic modification of forests means only 40% of remaining forests have high ecosystem integrity. *Nature Communications, 11*(1), 5978. https://doi.org/10.1038/s41467-020-19493-3

Greatorex, Z. F., Olson, S. H., Singhalath, S., Silithammavong, S., Khammavong, K., Fine, A. E., … Mazet, J. A. K. (2016). Wildlife Trade and Human Health in Lao PDR: An Assessment of the Zoonotic Disease Risk in Markets. *PLOS ONE, 11*(3), e0150666. https://doi.org/10.1371/journal.pone.0150666

Green, J., Coulthard, E., Norrey, J., Megson, D., & D'Cruze, N. (2020). Risky Business: Live Non-CITES Wildlife UK Imports and the Potential for Infectious Diseases. Animals: *An Open Access Journal from MDPI, 10*(9). https://doi.org/10.3390/ani10091632

Grimm, D. (2021). Major coronavirus variant found in pets for first time. Retrieved 8 April 2021, from Science | AAAS website: https://www.sciencemag.org/news/2021/03/major-coronavirus-variant-found-pets-first-time

Gu, E., & Li, L. (2020). Crippled community governance and suppressed scientific/professional communities: A critical assessment of failed early warning for the COVID-19 outbreak in China. *Journal of Chinese Governance, 5*(2), 160–177. https://doi.org/10.1080/23812346.2020.1740468

Gunningham, N., & Sinclair, D. (2017). Smart regulation. In P. DRAHOS (Ed.), *Regulatory Theory* (pp. 133–148). ANU Press. Retrieved from https://www.jstor.org/stable/j.ctt1q1crtm.16

Haberl, H., Erb, K. H., Krausmann, F., Gaube, V., Bondeau, A., Plutzar, C., … Fischer-Kowalski, M. (2007). Quantifying and mapping the human appropriation of net primary production in earth's terrestrial ecosystems. *Proceedings of the National Academy of Sciences, 104*(31), 12942–12947. https://doi.org/10.1073/pnas.0704243104

Haider, N., Rothman-Ostrow, P., Osman, A. Y., Arruda, L. B., Macfarlane-Berry, L., Elton, L., … Kock, R. A. (2020). COVID-19—Zoonosis or Emerging Infectious Disease? *Frontiers in Public Health, 8*. https://doi.org/10.3389/fpubh.2020.596944

Haider, N., Yavlinsky, A., Chang, Y.-M., Hasan, M. N., Benfield, C., Osman, A. Y., … Kock, R. (2020). The Global Health Security index and Joint External Evaluation score for health preparedness are not correlated with countries' COVID-19 detection response time and mortality outcome. *Epidemiology and Infection, 148*, e210. https://doi.org/10.1017/S0950268820002046

Haider, N., Yavlinsky, A., Simons, D., Osman, A. Y., Ntoumi, F., Zumla, A., & Kock, R. (2020). Passengers' destinations from China: Low risk of Novel Coronavirus (2019-nCoV) transmission into Africa and South America. *Epidemiology & Infection, 148*. https://doi.org/10.1017/S0950268820000424

Hale, V. L., Dennis, P. M., McBride, D. S., Nolting, J. M., Madden, C., Huey, D., … Bowman, A. S. (2021). SARS-CoV-2 infection in free-ranging white-tailed deer. *Nature*. https://doi.org/10.1038/s41586-021-04353-x

Hammerschmidt, F., Schwaiger, K., Dähnert, L., Vina-Rodriguez, A., Höper, D., Gareis, M., … Eiden, M. (2017). Hepatitis E virus in wild rabbits and European brown hares in Germany. *Zoonoses and Public Health, 64*(8), 612–622. https://doi.org/10.1111/zph.12355

Harfoot, M., Glaser, S. A. M., Tittensor, D. P., Britten, G. L., McLardy, C., Malsch, K., & Burgess, N. D. (2018). Unveiling the patterns and trends in 40 years of global trade in CITES-listed wildlife. *Biological Conservation, 223*, 47–57. https://doi.org/10.1016/j.biocon.2018.04.017

Harrington, L. A., Green, J., Muinde, P., Macdonald, D. W., Auliya, M., & D'Cruze, N. (2020). Snakes and ladders: A review of ball python production in West Africa for the global pet market. *Nature Conservation, 41*, 1–24. https://doi.org/10.3897/natureconservation.41.51270

Harrison, R. D., Tan, S., Plotkin, J. B., Slik, F., Detto, M., Brenes, T., … Davies, S. J. (2013). Consequences of defaunation for a tropical tree community. *Ecology Letters, 16*(5), 687–694. https://doi.org/10.1111/ele.12102

Hassell, J. M., Begon, M., Ward, M. J., & Fèvre, E. M. (2017). Urbanization and Disease Emergence: Dynamics at the Wildlife–Livestock–Human Interface. *Trends in Ecology & Evolution, 32*(1), 55–67. https://doi.org/10.1016/j.tree.2016.09.012

Hautefeuille, C., Dauphin, G., & Peyre, M. (2020). Knowledge and remaining gaps on the role of animal and human movements in the poultry production and trade networks in the global spread of avian influenza viruses – A scoping review. *PLOS ONE, 15*(3), e0230567. https://doi.org/10.1371/journal.pone.0230567

Hawley, D. M., & Altizer, S. M. (2011). Disease ecology meets ecological immunology: Understanding the links between organismal immunity and infection dynamics in natural populations. *Functional Ecology, 25*(1), 48–60. https://doi.org/10.1111/j.1365-2435.2010.01753.x

Hay, S. I., Battle, K. E., Pigott, D. M., Smith, D. L., Moyes, C. L., Bhatt, S., … Gething, P. W. (2013). Global mapping of infectious disease. *Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences, 368*(1614), 20120250. https://doi.org/10.1098/rstb.2012.0250

Hess, J., Boodram, L.-L. G., Paz, S., Stewart Ibarra, A. M., Wasserheit, J. N., & Lowe, R. (2020). Strengthening the global response to climate change and infectious disease threats. *BMJ*, m3081. https://doi.org/10.1136/bmj.m3081

Hierink, F., Bolon, I., Durso, A. M., Ruiz de Castañeda, R., Zambrana-Torrelio, C., Eskew, E. A., & Ray, N. (2020). Forty-four years of global trade in CITES-listed snakes: Trends and implications for conservation and public health. *Biological Conservation, 248*, 108601. https://doi.org/10.1016/j.biocon.2020.108601

Hinsley, A., de Boer, H. J., Fay, M. F., Gale, S. W., Gardiner, L. M., Gunasekara, R. S., … Phelps, J. (2018). A review of the trade in orchids and its implications for conservation. *Botanical Journal of the Linnean Society, 186*(4), 435–455. https://doi.org/10.1093/botlinnean/box083

Hinsley, A., & 't Sas–Rolfes, M. (2020). Wild assumptions? Questioning simplistic narratives about consumer preferences for wildlife products. *People and Nature, 2*(4), 972–979. https://doi.org/10.1002/pan3.10099

Holloway, P., Gibson, M., van Doremalen, N., Nash, S., Holloway, T., Letko, M., … Guitian, J. (2021). Risk Factors for Middle East Respiratory Syndrome Coronavirus Infection among Camel Populations, Southern Jordan, 2014–2018. *Emerging Infectious Diseases, 27*(9), 2301–2311. https://doi.org/10.3201/eid2709.203508

Holmes, A. H., Moore, L. S. P., Sundsfjord, A., Steinbakk, M., Regmi, S., Karkey, A., … Piddock, L. J. V. (2016). Understanding the mechanisms and drivers of antimicrobial resistance. *The Lancet, 387*(10014), 176–187. https://doi.org/10.1016/S0140-6736(15)00473-0

Hughes, J. D. (2003). Europe as Consumer of Exotic Biodiversity: Greek and Roman times. *Landscape Research, 28*(1), 21–31. https://doi.org/10.1080/01426390306535

Huong, N. Q., Nga, N. T. T., Long, N. V., Luu, B. D., Latinne, A., Pruvot, M., … Olson, S. H. (2020). Coronavirus testing indicates transmission risk increases along wildlife supply chains for human consumption in Viet Nam, 2013-2014. *PLOS ONE, 15*(8), e0237129. https://doi.org/10.1371/journal.pone.0237129

Hutson, C. L., Lee, K. N., Abel, J., Carroll, D. S., Montgomery, J. M., Olson, V. A., … Regnery, R. L. (2007). Monkeypox zoonotic associations: Insights from laboratory evaluation of animals associated with the multi-state US outbreak. *The American Journal of Tropical Medicine and Hygiene, 76*(4), 757–768.

Hutton, J.M., & Webb, G. (2003). Crocodiles: Legal trade snaps back. In S. Oldfield. *The Trade in Wildlife: Regulation for Conservation* (pp. 108–120). London: Earthscan Publications.

Hutton, Jon M., & Leader-Williams, N. (2003). Sustainable use and incentive-driven conservation: Realigning human and conservation interests | Oryx | *Cambridge Core. 37*(2), 215–226. https://doi.org/10.1017/S0030605303000395

International Air Transport Association (IATA) (2021). *Live Animals Regulations* (LAR) (47th Edition – Effective 1 January-31 December 2021). Retrieved from https://www.iata.org/en/publications/store/live-animals-regulations/

Ibbett, H., Keane, A., Dobson, A. D. M., Griffin, O., Travers, H., & Milner-Gulland, E. J. (2020). Estimating hunting prevalence and reliance on wild meat in Cambodia's Eastern Plains. Oryx, 1–11. https://doi.org/10.1017/S0030605319001455

Institute for Health Metrics and Evaluation (IHME) (2021). Global Burden of Disease. Retrieved 26 July 2021, from Institute for Health Metrics and Evaluation website: http://www.healthdata.org/gbd/2019

Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES) (2018). *The IPBES assessment report on land degradation and restoration*. Zenodo. https://doi.org/10.5281/ZENODO.3237392

IPBES (2019). *Summary for policymakers of the global assessment report on biodiversity and ecosystem services* (Version summary for policy makers). Zenodo. https://doi.org/10.5281/ZENODO.3553579

IPBES (2020). Workshop Report on Biodiversity and Pandemics of the Intergovernmental Platform on Biodiversity and Ecosystem Services. Daszak, P., das Neves, C., Amuasi, J., Hayman, D., Kuiken, T., Roche, B., Zambrana-Torrelio, C., Buss, P., Dundarova, H., Feferholtz, Y., Foldvari, G., Igbinosa, E., Junglen, S., Liu, Q., Suzan, G., Uhart, M., Wannous, C., Woolaston, K., Mosig Reidl, P., O'Brien, K., Pascual, U., Stoett, P., Li, H., Ngo, H. T., Bonn, Germany: IPBES secretariat. https://doi.org/10.5281/zenodo.4147317

Intergovernmental Panel on Climate Change (IPCC) (2014). *Climate change 2014: Impacts, adaptation, and vulnerability: Working Group II contribution to the fifth assessment report of the Intergovernmental Panel on Climate Change* (C. B. Field, V. R. Barros, D. J. Dokken, K. J. Mach, M. D. Mastrandrea, T. E. Bilir, … L. L. White, Eds.). New York, NY: Cambridge University Press.

IPCC (2018). *Global Warming of 1.5°C. An IPCC Special Report on the impacts of global warming of 1.5°C above pre-industrial levels and related global greenhouse gas emission pathways, in the context of strengthening the global response to the threat of climate change, sustainable development, and efforts to eradicate poverty* ([Masson-Delmotte, V., P. Zhai, H.-O. Pörtner, D. Roberts, J. Skea, P.R. Shukla, A. Pirani, W. Moufouma-Okia, C. Péan, R. Pidcock, S. Connors, J.B.R. Matthews, Y. Chen, X. Zhou, M.I. Gomis, E. Lonnoy, T. Maycock, M. Tignor, and T. Waterfield], [Masson-Delmotte, V., P. Zhai, H.-O. Pörtner, D. Roberts, J. Skea, [P.R. Shukla, A. Pirani, W. Moufouma-Okia, C. Péan, R. Pidcock, S. Connors, J.B.R. Matthews, Y. Chen, X. Zhou, M.I. Gomis, E. Lonnoy, & T. Maycock, M. Tignor, and T. Waterfield], Eds.).

International Union for Conservation of Nature (IUCN) (2016). Informing decisions on trophy hunting: *A Briefing Paper regarding issues to be taken into account when considering restriction of imports of hunting trophies.*

IUCN (2017a). Wildlife Trade. Retrieved 5 November 2020, from IUCN website: https://www.iucn.org/commissions/commission-environmental-economic-and-social-policy/our-work/specialist-group-sustainable-use-and-livelihoods-suli/wildlife-trade

IUCN (2017b). The North American Wild Harvest Initiative (WHI). Retrieved 1 December 2020, from IUCN website: https://www.iucn.org/commissions/commission-environmental-economic-and-social-policy/our-work/specialist-group-sustainable-use-and-livelihoods-suli/hunting-and-sustainable-wildlife-management/north-american-wild-harvest

IUCN (2019). *Guidelines for the Management of Confiscated, Live Organisms*. Gland, Switzerland: IUCN. https://doi.org/10.2305/IUCN.CH.2019.03.en

IUCN, Members' Assembly (2021, October 4). Resolution 7.135: *Promoting human, animal and environmental health, and preventing pandemics through the One Health approach and by addressing the drivers of biodiversity loss, WCC 2020 Res 135*. Retrieved 8 December 2021, from IUCN World Conservation Congress 2020 website: https://portals.iucn.org/library/node/49807

IUCN, Members' Assembly (2021). *Addendum to the IUCN Programme 2021–2024: Impacts and implications of the COVID-19 pandemic and health on the IUCN Programme Nature 2030*. Gland, Switzerland: IUCN. Retrieved from https://portals.iucn.org/library/node/49760

IUCN/Species Survival Commission (SSC) (2013). *Guidelines for reintroductions and other conservation translocations*. (Version 1.0). Gland, Switzerland: IUCN Species Survival Commission. Publication ID: 10386. Retrieved from https://www.iucn.org/content/guidelines-reintroductions-and-other-conservation-translocations

Jakob-Hoff, R. M., MacDiarmid, S. C., Lees, C., Miller, P. S., Travis, D., & Kock, R. (2014). *Manual of procedures for wildlife disease risk analysis*. Paris: OIE (World Organisation for Animal Health). CAB-Direct. Retrieved from https://www.cabdirect.org/cabdirect/abstract/20143127643

Jee, Y., Carlson, J., Rafai, E., Musonda, K., Huong, T. T. G., Daza, P., ... Yoon, T. (2018). Antimicrobial resistance: A threat to global health. *The Lancet Infectious Diseases, 18*(9), 939–940. https://doi.org/10.1016/S1473-3099(18)30471-7

Johnson, C. K., Hitchens, P. L., Pandit, P. S., Rushmore, J., Evans, T. S., Young, C. C. W., & Doyle, M. M. (2020). Global shifts in mammalian population trends reveal key predictors of virus spillover risk. *Proceedings of the Royal Society B: Biological Sciences, 287*(1924), 20192736. https://doi.org/10.1098/rspb.2019.2736

Johnson, C. K., Hitchens, P. L., Smiley Evans, T., Goldstein, T., Thomas, K., Clements, A., ... Mazet, J. K. (2015). Spillover and pandemic properties of zoonotic viruses with high host plasticity. *Scientific Reports, 5*, 14830. https://doi.org/10.1038/srep14830

Johnson, P. T. J., & Thieltges, D. W. (2010). Diversity, decoys and the dilution effect: How ecological communities affect disease risk. The Journal of Experimental Biology, 213(6), 961–970. https://doi.org/10.1242/jeb.037721

Johnson, Pieter T. J., Roode, J. C. de, & Fenton, A. (2015). Why infectious disease research needs community ecology. *Science, 349*(6252). https://doi.org/10.1126/science.1259504

Jones, B. A., Grace, D., Kock, R., Alonso, S., Rushton, J., Said, M. Y., ... Pfeiffer, D. U. (2013). Zoonosis emergence linked to agricultural intensification and environmental change. Proceedings of the National Academy of Sciences, 110(21), 8399–8404. https://doi.org/10.1073/pnas.1208059110

Jones, K. E., Patel, N. G., Levy, M. A., Storeygard, A., Balk, D., Gittleman, J. L., & Daszak, P. (2008). *Global trends in emerging infectious diseases. Nature, 451*(7181), 990–993. https://doi.org/10.1038/nature06536

Kan, B., Wang, M., Jing, H., Xu, H., Jiang, X., Yan, M., ... Xu, J. (2005). Molecular evolution analysis and geographic investigation of severe acute respiratory syndrome coronavirus-like virus in palm civets at an animal market and on farms. *Journal of Virology*. https://doi.org/10.1128/JVI.79.18.11892-11900.2005

Karesh, W. B., Cook, R. A., Bennett, E. L., & Newcomb, J. (2005). Wildlife trade and global disease emergence. *Emerging Infectious Diseases, 11*(7), 1000–1002. https://doi.org/10.3201/eid1107.050194

Karesh, W. B., Dobson, A., Lloyd-Smith, J. O., Lubroth, J., Dixon, M. A., Bennett, M., ... Heymann, D. L. (2012). Ecology of zoonoses: Natural and unnatural histories. *The Lancet, 380*(9857), 1936–1945. https://doi.org/10.1016/S0140-6736(12)61678-X

Karesh, W. B., & Noble, E. (2009). The Bushmeat Trade: Increased Opportunities for Transmission of Zoonotic Disease. *Mount Sinai Journal of Medicine: A Journal of Translational and Personalized Medicine, 76*(5), 429–434. https://doi.org/10.1002/msj.20139

Karesh, W., Cook, R., Gilbert, M., & Newcomb, J. (2007). Implications of wildlife trade on the movement of Avian Influenza and other infectious diseases. *Journal of Wildlife Diseases, 43*, S55.

Karesh, William, Kock, R., & Machalaba, C. (2020). It is Time for a Global Wildlife Health Authority [Blog]. Retrieved 22 September 2020, from IUCN website: https://www.iucn.org/crossroads-blog/202009/it-time-a-global-wildlife-health-authority

Kasterine, A., & Lichtenstein, G. (2018). *Trade in Vicuna Fibre: Implications for Conservation and Rural Livelihoods*. GenevaPage: International Trade Centre.

Keesing, F., Belden, L. K., Daszak, P., Dobson, A., Harvell, C. D., Holt, R. D., … Ostfeld, R. S. (2010). Impacts of biodiversity on the emergence and transmission of infectious diseases. *Nature, 468*(7324), 647–652. https://doi.org/10.1038/nature09575

Khanh, N. C., Thai, P. Q., Quach, H.-L., Thi, N.-A. H., Dinh, P. C., Duong, T. N., … Anh, D. D. (2020). Transmission of SARS-CoV 2 During Long-Haul Flight. *Emerging Infectious Diseases, 26*(11), 2617–2624. https://doi.org/10.3201/eid2611.203299

Knight, M. H., Emslie, R. H., Smart, R., & Balfour, D. (2015). *Biodiversity-Management Plan For The White Rhinoceros (Ceratotherium Simum) in South Africa 2015-2020. Pretoria.* South Africa: Department of Environmental Affairs.

Kock, R. (2014). Drivers of disease emergence and spread: Is wildlife to blame? *Onderstepoort Journal of Veterinary Research, 81*(2), 1–4.

Kock, R. A. (2015). Vertebrate reservoirs and secondary epidemiological cycles of vector-borne diseases. *Revue Scientifique Et Technique (International Office of Epizootics), 34*(1), 151–163. https://doi.org/10.20506/rst.34.1.2351

Kock, R. A., Woodford, M. H., & Rossiter, P. B. (2010). Disease risks associated with the translocation of wildlife. *Revue Scientifique Et Technique (International Office of Epizootics), 29*(2), 329–350. https://doi.org/10.20506/rst.29.2.1980

Kock, Richard A., Alders, R., & Wallace, R. (2012). Wildlife, wild food, food security and human society. In Global Conference on Wildlife: Animal Health and Biodiversity - Preparing for the Future & OIE - World Organisation for Animal Health (Eds.), *Animal health and biodiversity: Preparing for the future ; compendium of the OIE Global Conference on Wildlife, 23.-25. February 2011, Paris (France)* (pp. 71–79). Paris: OIE.

Kock, Richard A., Orynbayev, M., Robinson, S., Zuther, S., Singh, N. J., Beauvais, W., … Milner-Gulland, E. J. (2018). Saigas on the brink: Multidisciplinary analysis of the factors influencing mass mortality events. *Science Advances, 4*(1), eaao2314. https://doi.org/10.1126/sciadv.aao2314

Koh, L. P., Li, Y., & Lee, J. S. H. (2021). The value of China's ban on wildlife trade and consumption. *Nature Sustainability, 4*(1), 2–4. https://doi.org/10.1038/s41893-020-00677-0

Kolby, J. E. (2020). To prevent the next pandemic, it's the legal wildlife trade we should worry about. Retrieved 21 September 2020, from National Geographic—Animals website: https://www.national-geographic.com/animals/2020/05/to-prevent-next-pandemic-focus-on-legal-wildlife-trade/

Koopmans, M. (2020). SARS-CoV-2 and the human-animal interface: Outbreaks on mink farms. *The Lancet Infectious Diseases,* S1473309920309129. https://doi.org/10.1016/S1473-3099(20)30912-9

Korber, B., Muldoon, M., Theiler, J., Gao, F., Gupta, R., Lapedes, A., … Bhattacharya, T. (2000). Timing the ancestor of the HIV-1 pandemic strains. *Science (New York, N.Y.), 288*(5472), 1789–1796. https://doi.org/10.1126/science.288.5472.1789

Krishnasamy, K., & Zavagli, M. (2020). S*outheast Asia: At the heart of wildlife trade*. 116.

Kümpel, N., Cunningham, A., Fa, J. E., Jones, J., Rowcliffe, M., & Milner-Gulland, E. (2015). Ebola and bushmeat: *Myth and reality. NWFP Update, 2015.*

Kurpiers, L. A., Schulte-Herbrüggen, B., Ejotre, I., & Reeder, D. M. (2016). Bushmeat and Emerging Infectious Diseases: Lessons from Africa. In F. M. Angelici (Ed.), *Problematic Wildlife: A Cross-Disciplinary Approach* (pp. 507–551). Cham: Springer International Publishing. https://doi.org/10.1007/978-3-319-22246-2_24

Lainé, N., & Morand, S. (2020). Linking humans, their animals, and the environment again: A decolonized and more-than-human approach to 'One Health'. *Parasite (Paris, France), 27,* 55. https://doi.org/10.1051/parasite/2020055

Lambin, E. F., Geist, H. J., & Lepers, E. (2003). Dynamics of Land-Use and Land-Cover Change in Tropical Regions. *Annual Review of Environment and Resources, 28*(1), 205–241. https://doi.org/10.1146/annurev.energy.28.050302.105459

Lambin, E. F., Turner, B. L., Geist, H. J., Agbola, S. B., Angelsen, A., Bruce, J. W., … Xu, J. (2001). The causes of land-use and land-cover change: Moving beyond the myths. *Global Environmental Change, 11*(4), 261–269. https://doi.org/10.1016/S0959-3780(01)00007-3

Lange, M., Siemen, H., Blome, S., & Thulke, H.-H. (2014). Analysis of spatio-temporal patterns of African swine fever cases in Russian wild boar does not reveal an endemic situation. *Preventive Veterinary Medicine, 117*(2), 317–325. https://doi.org/10.1016/j.prevetmed.2014.08.012

Larsen, J., Raisen, C. L., Ba, X., Sadgrove, N. J., Padilla-González, G. F., Simmonds, M. S. J., … Larsen, A. R. (2022). Emergence of methicillin resistance predates the clinical use of antibiotics. *Nature, 1*–7. https://doi.org/10.1038/s41586-021-04265-w

Latinne, A., Hu, B., Olival, K. J., Zhu, G., Zhang, L., Li, H., … Daszak, P. (2020). Origin and cross-species transmission of bat coronaviruses in China. *Nature Communications, 11*(1), 4235. https://doi.org/10.1038/s41467-020-17687-3

Lavine, J. S., Bjornstad, O. N., & Antia, R. (2021). Immunological characteristics govern the transition of COVID-19 to endemicity. *Science, 371*(6530), 741–745. https://doi.org/10.1126/science.abe6522

Laxminarayan, R., Kakkar, M., Horby, P., Malavige, G. N., & Basnyat, B. (2017). Emerging and re-emerging infectious disease threats in South Asia: Status, vulnerability, preparedness, and outlook. *BMJ, 357,* j1447. https://doi.org/10.1136/bmj.j1447

Le Guenno, B., Formenty, P., Formentry, P., Wyers, M., Gounon, P., Walker, F., & Boesch, C. (1995). Isolation and partial characterisation of a new strain of Ebola virus. *Lancet (London, England), 345*(8960), 1271–1274. https://doi.org/10.1016/s0140-6736(95)90925-7

Leclère, D., Obersteiner, M., Barrett, M., Butchart, S. H. M., Chaud-hary, A., De Palma, A., … Young, L. (2020). Bending the curve of te-rrestrial biodiversity needs an integrated strategy. *Nature, 585*(7826), 551–556. https://doi.org/10.1038/s41586-020-2705-y

Lederberg, J., Shope, R. E., & Oaks, S. C. (Eds.). (1992). *Emerging Infec-tions: Microbial Threats to Health in the United States*. Washington (DC): National Academies Press (US). Retrieved from http://www.ncbi.nlm.nih.gov/books/NBK234855/

Lee, J., Hughes, T., Lee, M.-H., Field, H., Rovie-Ryan, J. J., Sitam, F. T., … Daszak, P. (2020a). No Evidence of Coronaviruses or Other Poten-tially Zoonotic Viruses in Sunda pangolins (Manis javanica) Entering the Wildlife Trade via Malaysia. *EcoHealth*. https://doi.org/10.1007/s10393-020-01503-x

Lee, J., Hughes, T., Lee, M.-H., Field, H., Rovie-Ryan, J. J., Sitam, F. T., … Daszak, P. (2020b). No evidence of coronaviruses or other potentially zoonotic viruses in Sunda pangolins (Manis javanica) entering the wildlife trade via Malaysia. *BioRxiv*, 2020.06.19.158717. https://doi.org/10.1101/2020.06.19.158717

Leendertz, S. (2016). Testing New Hypotheses Regarding Ebolavirus Reservoirs. Viruses, 8(2), 30. https://doi.org/10.3390/v8020030
Leibler, J. H., Otte, J., Roland-Holst, D., Pfeiffer, D. U., Soares Magal-haes, R., Rushton, J., … Silbergeld, E. K. (2009). Industrial food animal production and global health risks: Exploring the ecosystems and economics of avian influenza. *EcoHealth, 6*(1), 58–70. https://doi.org/10.1007/s10393-009-0226-0

Leroy, E. M., Epelboin, A., Mondonge, V., Pourrut, X., Gonzalez, J.-P., Muyembe-Tamfum, J.-J., & Formenty, P. (2009). Human Ebola out-break resulting from direct exposure to fruit bats in Luebo, Demo-cratic Republic of Congo, 2007. *Vector Borne and Zoonotic Diseases (Larchmont, N.Y.), 9*(6), 723–728. https://doi.org/10.1089/vbz.2008.0167

Levi, T., Massey, A. L., Holt, R. D., Keesing, F., Ostfeld, R. S., & Peres, C. A. (2016). Does biodiversity protect humans against infectious di-sease? Comment. *Ecology, 97*(2), 536–542. https://doi.org/10.1890/15-354.1

Levitt, T. (2020). Two billion and rising: The global trade in live animals in eight charts. *The Guardian*. Retrieved from https://www.theguar-dian.com/environment/2020/jan/20/two-billion-and-rising-the-glo-bal-trade-in-live-animals-in-eight-charts

Li In Review. (2021). Manuscript submitted for publication (ZPH).
Li, M., Havelaar, A. H., Hoffmann, S., Hald, T., Kirk, M. D., Torgerson, P. R., & Devleesschauwer, B. (2019). Global disease burden of pa-thogens in animal source foods, 2010. *PLOS ONE, 14*(6), e0216545. https://doi.org/10.1371/journal.pone.0216545

Li, W., Shi, Z., Yu, M., Ren, W., Smith, C., Epstein, J. H., … Wang, L.-F. (2005). Bats are natural reservoirs of SARS-like coronaviruses. *Science (New York, N.Y.), 310*(5748), 676–679. https://doi.org/10.1126/science.1118391

Li, X., Zai, J., Zhao, Q., Nie, Q., Li, Y., Foley, B. T., & Chaillon, A. (2020). Evolutionary history, potential intermediate animal host, and cross-species analyses of SARS-CoV-2. *Journal of Medical Virology, 92*(6), 602–611. https://doi.org/10.1002/jmv.25731

Li, Y. (2020). China's Announcement on Wildlife Trade—What's New and What Does It Mean? Retrieved 30 November 2020, from Inter-disciplinary Centre for Conservation Science website: https://www.iccs.org.uk/blog/chinas-announcement-wildlife-trade-whats-new-and-what-does-it-mean

Liang, Z., Appleton, S., & Song, L. (2016). I*nformal Employment in Chi-na: Trends, Patterns and Determinants of Entry* (Working Paper No. 10139). IZA Discussion Papers. Retrieved from IZA Discussion Papers website: http://hdl.handle.net/10419/145273

Lichtenstein, G. (2010). Vicuña conservation and poverty alleviation? Andean communities and international fibre markets. *International Journal of the Commons, 4*(1), 100–121. https://doi.org/10.18352/ijc.139

Lichtenstein, G., & Cowan Ros, C. (2021). Vicuña conservation and community re-creation in the Andes. In *Routledge Studies in Envi-ronment, Culture, and Society Series. Making commons dynamic: Understanding change through commonisation and decommonisa-tion* (pp. 102–122). Routledge.

Lilly, A. A., Mehlman, P. T., & Doran, D. (2002). Intestinal Parasites in Gorillas, Chimpanzees, and Humans at Mondika Research Site, Dzanga-Ndoki National Park, Central African Republic. *Inter-national Journal of Primatology, 23*(3), 555–573. https://doi.org/10.1023/A:1014969617036

Lion Coalition. (2020). Open letter to World Health Organisation. Retrieved 15 October 2020, from Lion Coalition website: https://lion-coalition.org/2020/04/04/open-letter-to-world-health-organisation/

Littlewood, W. (1905). *Cattle Plague in Egypt in 1903*-04-05. 18, 312–321.

Liu, Y.-Y., Wang, Y., Walsh, T. R., Yi, L.-X., Zhang, R., Spencer, J., … Shen, J. (2016). Emergence of plasmid-mediated colistin resistance mecha-nism MCR-1 in animals and human beings in China: A microbiologi-cal and molecular biological study. *The Lancet Infectious Diseases, 16*(2), 161–168. https://doi.org/10.1016/S1473-3099(15)00424-7

Loh, E. H., Zambrana-Torrelio, C., Olival, K. J., Bogich, T. L., Johnson, C. K., Mazet, J. A. K., … Daszak, P. (2015). Targeting Transmission Pathways for Emerging Zoonotic Disease Surveillance and Control. *Vector Borne and Zoonotic Diseases (Larchmont, N.Y.), 15*(7), 432–437. https://doi.org/10.1089/vbz.2013.1563

Longdon, B., Brockhurst, M. A., Russell, C. A., Welch, J. J., & Jig-gins, F. M. (2014). The Evolution and Genetics of Virus Host Shifts. *PLOS Pathogens, 10*(11), e1004395. https://doi.org/10.1371/journal.ppat.1004395

Lyons, J. A., Natusch, D. J. D., & Jenkins, R. W. G. (2017). *A Guide to the application of CITES source codes*. Gland, Switzerland: CITES Secretariat by the International Union for Conservation of Nature (IUCN). Retrieved from https://cites.org/sites/default/files/eng/prog/captive_breeding/E-Souce%20codes%20booklet%20-%20April%2017.pdf

Lyons, J., & Natusch, D. (2012). *Lyons and Natusch (2012) Over-step-ping the Quota? The Trade in Sugar Gliders in West Papua, Indonesia.*

Macdonald, G. (1957). The Epidemiology and Control of Malaria. *The Epidemiology and Control of Malaria*. Retrieved from https://www.cabdirect.org/cabdirect/abstract/19581000237

Machalaba, C., Uhart, M., Kock, R., Diaz, F., & Karesh, W. B. (2020). *Urgent Needs for Global Wildlife Health*. Zenodo. https://doi.org/10.5281/ZENODO.4105126

Machovina, B., Feeley, K. J., & Ripple, W. J. (2015). Biodiversity conservation: The key is reducing meat consumption. *Science of The Total Environment, 536*, 419–431. https://doi.org/10.1016/j.scitotenv.2015.07.022

MacLean, O. A., Lytras, S., Weaver, S., Singer, J. B., Boni, M. F., Lemey, P., … Robertson, D. L. (2021). Natural selection in the evolution of SARS-CoV-2 in bats created a generalist virus and highly capable human pathogen. *PLOS Biology, 19*(3), e3001115. https://doi.org/10.1371/journal.pbio.3001115

Magwedere, K., Hemberger, M. Y., Hoffman, L. C., & Dziva, F. (2012). Zoonoses: A potential obstacle to the growing wildlife industry of Namibia. *Infection Ecology & Epidemiology, 2*. https://doi.org/10.3402/iee.v2i0.18365

Maillard, J.-C., & Gonzalez, J.-P. (2006). Biodiversity and emerging diseases. *Annals of the New York Academy of Sciences, 1081*, 1–16. *https://doi.org/10.1196/annals.1373.001*

Malaiyan, J., Arumugam, S., Mohan, K., & Gomathi Radhakrishnan, G. (2021). An update on the origin of SARS-CoV-2: Despite closest identity, bat (RaTG13) and pangolin derived coronaviruses varied in the critical binding site and O-linked glycan residues. *Journal of Medical Virology, 93*(1), 499–505. https://doi.org/10.1002/jmv.26261

Mallapaty, S. (2020). Animal source of the coronavirus continues to elude scientists. *Nature*. https://doi.org/10.1038/d41586-020-01449-8

Marí Saéz, A., Weiss, S., Nowak, K., Lapeyre, V., Zimmermann, F., Düx, A., … Leendertz, F. H. (2015). Investigating the zoonotic origin of the West African Ebola epidemic. *EMBO Molecular Medicine, 7*(1), 17–23. https://doi.org/10.15252/emmm.201404792

Marsh, S. M. E., Hoffmann, M., Burgess, N. D., Brooks, T. M., Challender, D. W. S., Cremona, P. J., … Roe, D. (2020). Prevalence of sustainable and unsustainable use of wild species inferred from the IUCN Red List. *BioRxiv*, 2020.11.04.367763. https://doi.org/10.1101/2020.11.04.367763

Maxwell, S. L., Fuller, R. A., Brooks, T. M., & Watson, J. E. M. (2016). Biodiversity: The ravages of guns, nets and bulldozers. *Nature News, 536(7615)*, 143. https://doi.org/10.1038/536143a

McCallum, H. I. (2015). Lose biodiversity, gain disease. *Proceedings of the National Academy of Sciences, 112*(28), 8523–8524. https://doi.org/10.1073/pnas.1510607112

McCormick, K. D., Jacobs, J. L., & Mellors, J. W. (2021). The emerging plasticity of SARS-CoV-2. *Science, 371*(6536), 1306–1308. https://doi.org/10.1126/science.abg4493

McEvoy, J. F., Connette, G., Huang, Q., Soe, P., Pyone, K. H. H., Valitutto, M., … Leimgruber, P. (2019). Two sides of the same coin – Wildmeat consumption and illegal wildlife trade at the crossroads of Asia. *Biological Conservation, 238*, 108197. https://doi.org/10.1016/j.biocon.2019.108197

McEwen, S. A., & Fedorka-Cray, P. J. (2002). *Antimicrobial use and resistance in animals. Clinical Infectious Diseases: An Official Publication of the Infectious Diseases Society of America, 34 Suppl 3*, S93–S106. https://doi.org/10.1086/340246

McFarlane, R., Sleigh, A., & McMichael, A. (2013). Land-Use Change and Emerging Infectious Disease on an Island Continent. *International Journal of Environmental Research and Public Health, 10*(7), 2699–2719. https://doi.org/10.3390/ijerph10072699

McMahon, B. J., Morand, S., & Gray, J. S. (2018). Ecosystem change and zoonoses in the Anthropocene. *Zoonoses and Public Health, 65*(7), 755–765. https://doi.org/10.1111/zph.12489

McRae, L., Freeman, R., Geldmann, J., Moss, G. B., Kjær-Hansen, L., & Burgess, N. D. (2020). *A global indicator of utilised wildlife populations: Regional trends and the impact of management* [Preprint]. Ecology. https://doi.org/10.1101/2020.11.02.365031

Meier, R., & Ryser-Degiorgis, M. (2018). Wild boar and infectious diseases: Evaluation of the current risk to human and domestic animal health in Switzerland: A review. *Schweizer Archiv Fur Tierheilkunde, 160*(7–8), 443–460. https://doi.org/10.17236/sat00168

Mendoza, H., Rubio, A. V., García-Peña, G. E., Suzán, G., & Simonetti, J. A. (2020). Does land-use change increase the abundance of zoonotic reservoirs? Rodents say yes. *European Journal of Wildlife Research, 66*(1), 6. https://doi.org/10.1007/s10344-019-1344-9

Microbiology by numbers. (2011). *Nature Reviews Microbiology, 9*(9), 628–628. https://doi.org/10.1038/nrmicro2644

Millennium Ecosystem Assessment. (2005). *Ecosystems and human well-being: Synthesis*. Washington, DC: Island Press. Retrieved from https://www.millenniumassessment.org/documents/document.356.aspx.pdf

Mittermeier, R. A. (2020, April 3). Coronaviruses and the Human Meat Market. Retrieved 8 December 2020, from The Revelator website: https://therevelator.org/coronaviruses-human-meat-market/

Moehrenschlager, A. (2017). Tiptoeing Cautiously Yet Confidently: Health Considerations for Conservation Translocations. *EcoHealth, 14*(1), 167–170. https://doi.org/10.1007/s10393-016-1155-3

Mohd Nor, M. N., Gan, C. H., & Ong, B. L. (2000). Nipah virus infection of pigs in peninsular Malaysia. *Revue Scientifique Et Technique (International Office of Epizootics), 19*(1), 160–165. https://doi.org/10.20506/rst.19.1.1202

Mollentze, N., & Streicker, D. G. (2020). Viral zoonotic risk is homogenous among taxonomic orders of mammalian and avian reservoir hosts. *Proceedings of the National Academy of Sciences, 117*(17), 9423–9430. https://doi.org/10.1073/pnas.1919176117

Molyneux, D., Hallaj, Z., Keusch, G. T., McManus, D. P., Ngowi, H., Cleaveland, S., … Kioy, D. (2011). Zoonoses and marginalised infectious diseases of poverty: Where do we stand? *Parasites & Vectors, 4*(1), 106. https://doi.org/10.1186/1756-3305-4-106

Moran, N. (2021, February 9). Intermediary host species likely introduced SARS-CoV-2 virus, says WHO. Retrieved 10 April 2021, from https://www.bioworld.com/articles/503405-intermediary-host-species-likely-introduced-sars-cov-2-virus-says-who

Morand, S. (2020). Emerging diseases, livestock expansion and biodiversity loss are positively related at global scale. *Biological Conservation, 248*, 108707. https://doi.org/10.1016/j.biocon.2020.108707

Morand, S., Figuié, M., Keck, F., Gilbert, C., Brender, N., Roger, F., & Zylberman, P. (2018). *Emergence of infectious diseases. Risks and issues for societies.* éditions Quae. https://doi.org/10.35690/978-2-7592-2773-0
Morand, S., & Lajaunie, C. (2020). *Outbreaks of Vector-Borne and Zoonotic Diseases Are Associated With Changes in Forest Cover and Oil Palm Expansion at Global Scale* (SSRN Scholarly Paper No. ID 3710299). Rochester, NY: Social Science Research Network. https://doi.org/10.2139/ssrn.3710299

Morcatty, T. Q., Bausch Macedo, J. C., Nekaris, K. A., Ni, Q., Durigan, C. C., Svensson, M. S., & Nijman, V. (2020). Illegal trade in wild cats and its link to Chinese–led development in Central and South America. *Conservation Biology, 34*(6), 1525–1535. https://doi.org/10.1111/cobi.13498

Morens, D. M., Folkers, G. K., & Fauci, A. S. (2004). The challenge of emerging and re-emerging infectious diseases. *Nature, 430*(6996), 242–249. https://doi.org/10.1038/nature02759

Morse, S. S., Mazet, J. A., Woolhouse, M., Parrish, C. R., Carroll, D., Karesh, W. B., … Daszak, P. (2012). Prediction and prevention of the next pandemic zoonosis. *The Lancet, 380*(9857), 1956–1965. https://doi.org/10.1016/S0140-6736(12)61684-5

Morton, W. (2011). Supply and Use of NHP Around The World. In National Research Council (Ed.), *Animal Research in a Global Environment: Meeting the Challenges: Proceedings of the November 2008 International Workshop* (p. 13175). Washington, D.C.: National Academies Press. https://doi.org/10.17226/13175

Moschione, F. N., & Banchs, R. A. (2006). Proyecto Ele: Para el aprovechamiento sustentable del Loro Hablador Amazona aestiva en la Argentina. In M. L. Bolkovic & D. Ramadori (Eds.), *Manejo de Fauna Silvestre en la Argentina. Programas de uso sustentable* (pp. 15–25). Buenos Aires, Argentina: Dirección de Fauna Silvestre, Secretaría de Ambiente y Desarrollo Sustentable.

Munnink, B. B. O., Sikkema, R. S., Nieuwenhuijse, D. F., Molenaar, R. J., Munger, E., Molenkamp, R., … Koopmans, M. P. G. (2020a). Jumping back and forth: Anthropozoonotic and zoonotic transmission of SARS-CoV-2 on mink farms. *BioRxiv*, 2020.09.01.277152. https://doi.org/10.1101/2020.09.01.277152

Munnink, B. B. O., Sikkema, R. S., Nieuwenhuijse, D. F., Molenaar, R. J., Munger, E., Molenkamp, R., … Koopmans, M. P. G. (2020b). Transmission of SARS-CoV-2 on mink farms between humans and mink and back to humans. *Science*. https://doi.org/10.1126/science.abe5901

Murray, C. J. L., Aravkin, A. Y., Zheng, P., Abbafati, C., Abbas, K. M., Abbasi-Kangevari, M., … Lim, S. S. (2020). Global burden of 87 risk factors in 204 countries and territories, 1990–2019: A systematic analysis for the Global Burden of Disease Study 2019. *The Lancet, 396*(10258), 1223–1249. https://doi.org/10.1016/S0140-6736(20)30752-2

Nasi, R., Taber, A., & Van Vliet, N. (2011). Empty forests, empty stomachs? Bushmeat and livelihoods in the Congo and Amazon Basins. *International Forestry Review, 13*(3), 355–368. https://doi.org/10.1505/146554811798293872

National Institutes of Health (US) & Biological Sciences Curriculum Study. (2007). Understanding Emerging and Re-emerging Infectious Diseases. In N*IH Curriculum Supplement Series [Internet]*. National Institutes of Health (US). Retrieved from https://www.ncbi.nlm.nih.gov/books/NBK20370/

Natusch, D. . J. D., & Lyons, J. A. (2016). *Sustainable Management of the Trade in Reticulated Python Skins in Indonesia and Malaysia. A report under the 'Python Conservation Partnership' programme of research. Occasional Paper of the IUCN Species Survival Commission No. 61.* Gland, Switzerland: IUCN Global Species ProgrammeIUCN Species Survival Commission (SSC), Boa and Python Specialist Group. Retrieved from http://dx.doi.org/10.2305/IUCN.CH.2016.SSC-OP.61.en

Newbold, T., Hudson, L. N., Hill, S. L. L., Contu, S., Lysenko, I., Senior, R. A., … Purvis, A. (2015). Global effects of land use on local terrestrial biodiversity. *Nature, 520*(7545), 45–50. https://doi.org/10.1038/nature14324

Niederwerder, M. C. (2021). Risk and Mitigation of African Swine Fever Virus in Feed. *Animals, 11*(3), 792. https://doi.org/10.3390/ani11030792

Nijman, V. (2010). An overview of international wildlife trade from Southeast Asia. *Biodiversity and Conservation, 19*(4), 1101–1114. https://doi.org/10.1007/s10531-009-9758-4

Nunes, A. V., Peres, C. A., Constantino, P. de A. L., Santos, B. A., & Fischer, E. (2019). Irreplaceable socioeconomic value of wild meat extraction to local food security in rural Amazonia. *Biological Conservation, 236*, 171–179. https://doi.org/10.1016/j.biocon.2019.05.010

World Organisation for Animal Health (OIE). (2000). *International animal health code: Mammals, birds and bees.* Paris: OIE. Retrieved from http://catalog.hathitrust.org/api/volumes/oclc/466631168.html

OIE (2013). World Animal Health Information Database (WAHIS) Interface. Retrieved 7 December 2020, from https://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home

OIE (2019a). Aquatic Animal Health Code. Retrieved 7 June 2021, from https://www.oie.int/en/what-we-do/standards/codes-and-manuals/aquatic-code-online-access/?id=169&L=1&htmfile=sommaire.htm

OIE (2019b). *Terrestrial Animal Health Code.*

OIE (2020a). Working Group on Wildlife: OIE - World Organisation for Animal Health. Retrieved 18 March 2021, from https://www.oie.int/en/standard-setting/specialists-commissions-working-ad-hoc-groups/working-groups-reports/working-group-on-wildlife/

OIE (2020b). Preserving our future by protecting wildlife health: OIE - World Organisation for Animal Health. Retrieved 6 April 2021, from https://www.oie.int/en/for-the-media/press-releases/detail/article/preserving-our-future-by-protecting-wildlife-health/

OIE (2021a). African swine fever. Retrieved 29 August 2021, from OIE - World Organisation for Animal Health website: https://www.oie.int/en/disease/african-swine-fever/

OIE (2021b). World Animal Health Information System (WAHIS). Retrieved 9 April 2021, from OIE-WAHIS website: https://wahis.oie.int/#/home

OIE & IUCN (2014). *Guidelines for Wildlife Disease Risk Analysis*. Paris: Published in association with the IUCN and the Species Survival Commission. Retrieved from https://portals.iucn.org/library/sites/library/files/documents/2014-006.pdf

Ojasti, J. (1993). *Utilización de la Fauna Silvestre en América Latina. Situación y Perspectivas para un Manejo Sostenible*. Roma. Retrieved from https://www.fao.org/3/t0750s/t0750s00.htm

Olaitan, A. O., Chabou, S., Okdah, L., Morand, S., & Rolain, J.-M. (2016). Dissemination of the mcr-1 colistin resistance gene. *The Lancet Infectious Diseases, 16*(2), 147. https://doi.org/10.1016/S1473-3099(15)00540-X

Olaitan, A. O., Dandachi, I., Baron, S. A., Daoud, Z., Morand, S., & Rolain, J.-M. (2021). Banning colistin in feed additives: A small step in the right direction. *The Lancet Infectious Diseases, 21*(1), 29–30. https://doi.org/10.1016/S1473-3099(20)30915-4

Oldfield, S. (Ed.). (2003). The trade in wildlife: Regulation for conservation. London, UK; Sterling, VA: Earthscan Publications.
Olival, K. J., Hosseini, P. R., Zambrana-Torrelio, C., Ross, N., Bogich, T. L., & Daszak, P. (2017). *Host and viral traits predict zoonotic spillover from mammals. Nature, 546*(7660), 646–650. https://doi.org/10.1038/nature22975

Olivero, J., Fa, J. E., Real, R., Márquez, A. L., Farfán, M. A., Vargas, J. M., ... Nasi, R. (2017). Recent loss of closed forests is associated with Ebola virus disease outbreaks. *Scientific Reports, 7*(1), 14291. https://doi.org/10.1038/s41598-017-14727-9

Oreskes, N. (2004). The Scientific Consensus on Climate Change. *Science, 306*(5702), 1686–1686. https://doi.org/10.1126/science.1103618

Parkes, M. W., Bienen, L., Breilh, J., Hsu, L.-N., McDonald, M., Patz, J. A., ... Yassi, A. (2005). All Hands on Deck: Transdisciplinary Approaches to Emerging Infectious Disease. *EcoHealth, 2*(4), 258–272. https://doi.org/10.1007/s10393-005-8387-y

Parry, L., Barlow, J., & Pereira, H. (2014). Wildlife Harvest and Consumption in Amazonia's Urbanized Wilderness. *Conservation Letters, 7*(6), 565–574. https://doi.org/10.1111/conl.12151

Paternoster, G., Babo Martins, S., Mattivi, A., Cagarelli, R., Angelini, P., Bellini, R., ... Tamba, M. (2017). Economics of One Health: Costs and benefits of integrated West Nile virus surveillance in Emilia-Romagna. *PloS One, 12*(11), e0188156. https://doi.org/10.1371/journal.pone.0188156

Patterson, E. I., Elia, G., Grassi, A., Giordano, A., Desario, C., Medardo, M., ... Decaro, N. (2020). Evidence of exposure to SARS-CoV-2 in cats and dogs from households in Italy. *Nature Communications, 11*(1), 6231. https://doi.org/10.1038/s41467-020-20097-0

Patz, J. A., Daszak, P., Tabor, G. M., Aguirre, A. A., Pearl, M., Epstein, J., ... Members of the Working Group on Land Use Change Disease Emergence. (2004). Unhealthy Landscapes: Policy Recommendations on Land Use Change and Infectious Disease Emergence. *Environmental Health Perspectives, 112*(10), 1092–1098. https://doi.org/10.1289/ehp.6877

Patz, J. A., & Hahn, M. B. (2012). Climate Change and Human Health: A One Health Approach. In J. S. Mackenzie, M. Jeggo, P. Daszak, & J. A. Richt (Eds.), *One Health: The Human-Animal-Environment Interfaces in Emerging Infectious Diseases (pp. 141–171). Berlin, Heidelberg: Springer Berlin Heidelberg*. https://doi.org/10.1007/978-3-662-45791-7_274

Pavlin, B. I., Schloegel, L. M., & Daszak, P. (2009). Risk of importing zoonotic diseases through wildlife trade, United States. *Emerging Infectious Diseases, 15*(11), 1721–1726. https://doi.org/10.3201/eid1511.090419

Paweska, J. T., Blumberg, L. H., Liebenberg, C., Hewlett, R. H., Grobbelaar, A. A., Leman, P. A., ... Swanepoel, R. (2006). Fatal Human Infection with Rabies-related Duvenhage Virus, South Africa. *Emerging Infectious Diseases, 12*(12), 1965–1967. https://doi.org/10.3201/eid1212.060764

Pernet, O., Schneider, B. S., Beaty, S. M., LeBreton, M., Yun, T. E., Park, A., ... Lee, B. (2014). Evidence for henipavirus spillover into human populations in Africa. *Nature Communications, 5*(1), 5342. https://doi.org/10.1038/ncomms6342

Peters, C. J., Picardy, J., Darrouzet-Nardi, A. F., Wilkins, J. L., Griffin, T. S., & Fick, G. W. (2016). Carrying capacity of U.S. agricultural land: Ten diet scenarios. *Elementa: Science of the Anthropocene, 4*, 000116. https://doi.org/10.12952/journal.elementa.000116

Petersen, E., Petrosillo, N., Koopmans, M., Beeching, N., Caro, A. D., Gkrania-Klotsas, E., ... Storgaard, M. (2018). Emerging infections—an increasingly important topic: Review by the Emerging Infections Task Force. *Clinical Microbiology and Infection, 24*(4), 369–375. https://doi.org/10.1016/j.cmi.2017.10.035

Peterson, A. T. (2014). *Mapping disease transmission risk: Enriching models using biogeography and ecology*. Baltimore: Johns Hopkins University Press.

Petrovan, S., Aldridge, D. C., Bartlett, H., Bladon, A., Booth, H., Broad, S., ... Cunningham, A. A. (2020). Post COVID-19: A solution scan of options for preventing future zoonotic epidemics. OSF. https://doi.org/10.17605/OSF.IO/5JX3G

Phillips, C. A., Caldas, A., Cleetus, R., Dahl, K. A., Declet-Barreto, J., Licker, R., ... Carlson, C. J. (2020). Compound climate risks in the COVID-19 pandemic. *Nature Climate Change*, 1–3. https://doi.org/10.1038/s41558-020-0804-2

Pienkowski, T., Bickersteth, S., & Milner-Gulland, E. J. (2019). *Evidencing Links between Biodiversity and Health: A Rapid Review with a Water Quality Case Study*. 57.

Pienkowski, T., Dickens, B. L., Sun, H., & Carrasco, L. R. (2017). Empirical evidence of the public health benefits of tropical forest conservation in Cambodia: A generalised linear mixed-effects model analysis. *The Lancet Planetary Health, 1*(5), e180–e187. https://doi.org/10.1016/S2542-5196(17)30081-5

Plowright, R. K., Parrish, C. R., McCallum, H., Hudson, P. J., Ko, A. I., Graham, A. L., & Lloyd-Smith, J. O. (2017). Pathways to zoonotic spillover. *Nature Reviews. Microbiology, 15*(8), 502–510. https://doi.org/10.1038/nrmicro.2017.45

Plowright, R., Reaser, J., Locke, H., Woodley, S. J., Patz, J. A., Becker, D., … Tabor, G. M. (2020). A call to action: Understanding land use-induced zoonotic spillover to protect environmental, animal, and human health [Preprint]. *EcoEvoRxiv*. https://doi.org/10.32942/osf.io/cru9w

Possas, C., Lourenço-de-Oliveira, R., Tauil, P. L., Pinheiro, F. de P., Pissinatti, A., Cunha, R. V. da, … Homma, A. (2018). Yellow fever outbreak in Brazil: The puzzle of rapid viral spread and challenges for immunisation. *Memorias Do Instituto Oswaldo Cruz, 113*(10), e180278. https://doi.org/10.1590/0074-02760180278

Pruvot, M., Khammavong, K., Milavong, P., Philavong, C., Reinharz, D., Mayxay, M., … Newton, P. (2019). Toward a quantification of risks at the nexus of conservation and health: The case of bushmeat markets in Lao PDR. *Science of The Total Environment, 676,* 732–745. https://doi.org/10.1016/j.scitotenv.2019.04.266

Pulliam, J. R. C., Epstein, J. H., Dushoff, J., Rahman, S. A., Bunning, M., Jamaluddin, A. A., … Daszak, P. (2012). Agricultural intensification, priming for persistence and the emergence of Nipah virus: A lethal bat-borne zoonosis. *Journal of The Royal Society Interface, 9*(66), 89–101. https://doi.org/10.1098/rsif.2011.0223

Queenan, K. (2017). Roadmap to a One Health agenda 2030. *CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources, 12*(014). https://doi.org/10.1079/PAVSNNR201712014

Rabinovich, J. (2005). Parrots, Precaution and Project Elé: Management in the Face of Multiple Uncertainties. In R. Cooney, B. Dickson, & Fauna Flora International (Eds.), *Biodiversity and the Precautionary Principle: Risk, Uncertainty and Practice in Conservation and Sustainable Use* (pp. 174–188). Earthscan Editions.

Rahalkar, M. C., & Bahulikar, R. A. (2020). Lethal Pneumonia Cases in Mojiang Miners (2012) and the Mineshaft Could Provide Important Clues to the Origin of SARS-CoV-2. *Frontiers in Public Health, 8.* https://doi.org/10.3389/fpubh.2020.581569

Rambaut, A., Holmes, E. C., O'Toole, Á., Hill, V., McCrone, J. T., Ruis, C., … Pybus, O. G. (2020). A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. *Nature Microbiology, 5*(11), 1403–1407. https://doi.org/10.1038/s41564-020-0770-5

Randolph, S. E., & Dobson, A. D. M. (2012). Pangloss revisited: A critique of the dilution effect and the biodiversity-buffers-disease paradigm. *Parasitology, 139*(7), 847–863. https://doi.org/10.1017/S0031182012000200

Rapport, D. J., Böhm, G., Buckingham, D., Cairns, J., Costanza, R., Karr, J. R., … Whitford, W. G. (1999). Ecosystem Health: The Concept, the ISEH, and the Important Tasks Ahead. *Ecosystem Health, 5*(2), 82–90. https://doi.org/10.1046/j.1526-0992.1999.09913.x

Reaser, J., Tabor, G. M., Becker, D., Muruthi, P., Witt, A., Woodley, S. J., … Plowright, R. (2020). Land use-induced spillover: Priority actions for protected and conserved area managers [Preprint]. *EcoEvoRxiv*. https://doi.org/10.32942/osf.io/bmfhw

Reed, K. D., Melski, J. W., Graham, M. B., Regnery, R. L., Sotir, M. J., Wegner, M. V., … Damon, I. K. (2004). The detection of monkeypox in humans in the Western Hemisphere. *The New England Journal of Medicine, 350*(4), 342–350. https://doi.org/10.1056/NEJMoa032299

Regueira, R. F. S., & Bernard, E. (2012). Wildlife sinks: Quantifying the impact of illegal bird trade in street markets in Brazil. *Biological Conservation, 149*(1), 16–22. https://doi.org/10.1016/j.biocon.2012.02.009

Relman, D. A. (2020). Opinion: To stop the next pandemic, we need to unravel the origins of COVID-19. *Proceedings of the National Academy of Sciences, 117*(47), 29246–29248. https://doi.org/10.1073/pnas.2021133117

Reuter, A., Kunen, J., & Roberton, S. (2018). *Averting a Crisis: Wildlife Trafficking in Latin America*. New York: NY: WCS.

Reuters. (2020). Some key facts about the mink industry in Europe. *Reuters*. Retrieved from https://www.reuters.com/article/health-coronavirus-denmark-mink-factbox-idUSKBN27L1KH

Reuters Staff. (2019). China's hog herd may drop by 55% from fatal swine fever: Rabobank. Reuters. Retrieved from https://www.reuters.com/article/us-china-swinefever-hogs-idUSKBN1WH2IG

Reuters Staff (2021). UPDATE 1-Denmark to compensate mink farmers with up to $3.1 bln after nationwide cull. Retrieved 6 April 2021, from https://www.reuters.com/article/healthcoronavirus-denmark-mink-idUSL1N2K021W

Reynolds, M. G., & Damon, I. K. (2012). Outbreaks of human monkeypox after cessation of smallpox vaccination. *Trends in Microbiology, 20*(2), 80–87. https://doi.org/10.1016/j.tim.2011.12.001

Reynolds, M. G., Davidson, W. B., Curns, A. T., Conover, C. S., Huhn, G., Davis, J. P., … Damon, I. K. (2007). Spectrum of infection and risk factors for human monkeypox, United States, 2003. *Emerging Infectious Diseases, 13*(9), 1332–1339. https://doi.org/10.3201/eid1309.070175

Radio France Internationale (**RFI**) (2020a). France culls 1,000 minks after first case of Covid breaks out on farm. Retrieved 4 December 2020, from RFI website: https://www.rfi.fr/en/france/20201122-france-culls-1-000-minks-after-covid-breaks-out-on-farm-coronavirusspread-mutation-denmark

Radio France Internationale (RFI). (2020b). Six countries reported coronavirus on mink farms, WHO…
says. Retrieved 4 December 2020, from RFI website: https://www.rfi.fr/en/wires/20201107-six-countries-reported-coronavirus-mink-farms-who-says

Rights and Resources Initiative (2020). *Rights-Based Conservation: The path to preserving Earth's biological and cultural diversity?* Washington, D.C.: Rights and Resources Initiative.

Ripple, W. J., Wolf, C., Newsome, T. M., Barnard, P., & Moomaw, W. R. (2019). World Scientists' Warning of a Climate Emergency. *BioScience*, biz088. https://doi.org/10.1093/biosci/biz088

Ritchie, H. (2017). 'Meat and Dairy Production'. Published online at OurWorldInData.org. [[Online Resource]]. Retrieved 1 December 2020, from Our World in Data website: https://ourworldindata.org/meat-production

Robinson, J. E., Griffiths, R. A., Fraser, I. M., Raharimalala, J., Roberts, D. L., & St. John, F. A. V. (2018). Supplying the wildlife trade as a livelihood strategy in a biodiversity hotspot. *Ecology and Society, 23*(1), art13. https://doi.org/10.5751/ES-09821-230113

Robinson, J. G., & Bennett, E. L. (2002). Will alleviating poverty solve the bushmeat crisis? *Oryx, 36*(4), 332–332. https://doi.org/10.1017/S0030605302000662

Rocha, R., Aziz, S. A., Brook, C. E., Carvalho, W. D., Cooper–Bohannon, R., Frick, W. F., … Webala, P. W. (2020). Bat conservation and zoonotic disease risk: A research agenda to prevent misguided persecution in the aftermath of COVID–19. *Animal Conservation*, acv.12636. https://doi.org/10.1111/acv.12636

Rock, M., Buntain, B. J., Hatfield, J. M., & Hallgrímsson, B. (2009). Animal-human connections, 'one health,' and the syndemic approach to prevention. *Social Science & Medicine (1982), 68*(6), 991–995. https://doi.org/10.1016/j.socscimed.2008.12.047

Roe, D. (2008). *Trading nature: A report, with case studies, on the contribution of wildlife trade management to sustainable livelihoods and the Millennium Development Goals.* Cambridge, UK : Gland, Switzerland: TRAFFIC International ; WWF-International.

Roe, D., Dickman, A., Kock, R., Milner-Gulland, E., Rihoy, E., & t' Sas-Rolfes, M. (2020). Beyond banning wildlife trade: COVID-19, Conservation and Development. *World Development*, 105121. https://doi.org/10.1016/j.worlddev.2020.105121

Roe, D., & Lee, T. M. (2021). Possible negative consequences of a wildlife trade ban. *Nature Sustainability, 4*(1), 5–6. https://doi.org/10.1038/s41893-020-00676-1

Roger, F., Bonnet, P., Steinmetz, P., Salignon, P., & Peyre, M. (2016). *The One Health Concept to Dovetail Health and Climate Change Policies.* https://doi.org/10.13140/RG.2.1.3488.2002

Rohr, J. R., Barrett, C. B., Civitello, D. J., Craft, M. E., Delius, B., DeLeo, G. A., … Tilman, D. (2019). Emerging human infectious diseases and the links to global food production. *Nature Sustainability, 2*(6), 445–456. https://doi.org/10.1038/s41893-019-0293-3

Rosen, G. E., & Smith, K. F. (2010). Summarizing the evidence on the international trade in illegal wildlife. *EcoHealth, 7*(1), 24–32. https://doi.org/10.1007/s10393-010-0317-y

Rosenthal, S. R., Ostfeld, R. S., McGarvey, S. T., Lurie, M. N., & Smith, K. F. (2015). Redefining disease emergence to improve prioritization and macro-ecological analyses. *One Health, 1,* 17–23. https://doi.org/10.1016/j.onehlt.2015.08.001

Roser, M., & Ritchie, H. (2013). Hunger and Undernourishment. *Our World in Data.* Retrieved from https://ourworldindata.org/hunger-and-undernourishment

Rugarabamu, S., Mboera, L., Rweyemamu, M., Mwanyika, G., Lutwama, J., Paweska, J., & Misinzo, G. (2020). Forty-two years of responding to Ebola virus outbreaks in Sub-Saharan Africa: A review. *BMJ Global Health, 5*(3), e001955. https://doi.org/10.1136/bmjgh-2019-001955

Rushton, J., Viscarra, R., Viscarra, C., Basset, F., Baptista, R., & Brown, D. (2005). *How Important is Bushmeat Consumption in South America: Now and in the Future?* 4.

Sainsbury, A. W., Chantrey, J., Ewen, J. G., Gurnell, J., Hudson, P., Karesh, W. B., … Tompkins, D. M. (2020). Implications of squirrelpox virus for successful red squirrel translocations within mainland UK. *Conservation Science and Practice, 2*(6), e200. https://doi.org/10.1111/csp2.200

Sallard, E., Halloy, J., Casane, D., Decroly, E., & van Helden, J. (2021). Tracing the origins of SARS-COV-2 in coronavirus phylogenies: A review. *Environmental Chemistry Letters, 19*(2), 769–785. https://doi.org/10.1007/s10311-020-01151-1

Sansonetti, P. (2006). [How to define the species barrier to pathogen transmission?]. *Bulletin De l'Academie Nationale De Medecine, 190*(3), 611–622; discussion 623, 625–627.

Schelling, E., Wyss, K., Béchir, M., Moto, D. D., & Zinsstag, J. (2005). Synergy between public health and veterinary services to deliver human and animal health interventions in rural low income settings. *BMJ, 331*(7527), 1264–1267. https://doi.org/10.1136/bmj.331.7527.1264

Schulte–Hostedde, A. I., & Mastromonaco, G. F. (2015). Integrating evolution in the management of captive zoo populations. *Evolutionary Applications, 8*(5), 413–422. https://doi.org/10.1111/eva.12258

Schwarz, D., Newton, D., & Ratzimbazafy, C. (2017). Assessment of the international illicit wildlife trade in the critically endangered Malagasy tortoise species Astrochelys yniphora and Astrochelys radiata. *Salamandra, 53*(1), 163–166.

Segreto, R., Deigin, Y., McCairn, K., Sousa, A., Sirotkin, D., Sirotkin, K., … Zhang, D. (2021). An open debate on SARS-CoV-2's proximal origin is long overdue. *ArXiv:2102.03910 [q-Bio].* Retrieved from http://arxiv.org/abs/2102.03910

Semenza, J. C., & Zeller, H. (2014). Integrated surveillance for prevention and control of emerging vector-borne diseases in Europe. *Euro Surveillance: Bulletin Europeen Sur Les Maladies Transmissibles = European Communicable Disease Bulletin, 19*(13). https://doi.org/10.2807/1560-7917.es2014.19.13.20757

Semenza, Jan C., Lindgren, E., Balkanyi, L., Espinosa, L., Almqvist, M. S., Penttinen, P., & Rocklöv, J. (2016). Determinants and Drivers of Infectious Disease Threat Events in Europe. *Emerging Infectious Diseases, 22*(4), 581–589. https://doi.org/10.3201/eid2204

Shah, H. A., Huxley, P., Elmes, J., & Murray, K. A. (2019). Agricultural land-uses consistently exacerbate infectious disease risks in Southeast Asia. *Nature Communications, 10*(1), 4299. https://doi.org/10.1038/s41467-019-12333-z

Sharp, P. M., & Hahn, B. H. (2011). Origins of HIV and the AIDS pandemic. *Cold Spring Harbor Perspectives in Medicine, 1*(1), a006841. https://doi.org/10.1101/cshperspect.a006841

Sheath, D. J., Castañeda, R. R. de, Bempong, N.-E., Raviglione, M., Machalaba, C., Pepper, M. S., ... Flahault, A. (2020). Precision global health: A roadmap for augmented action. *Journal of Public Health and Emergency, 4*(0). https://doi.org/10.21037/jphe.2020.01.01

Shi, Z., & Hu, Z. (2008). A review of studies on animal reservoirs of the SARS coronavirus. *Virus Research, 133*(1), 74–87. https://doi.org/10.1016/j.virusres.2007.03.012

Siegel. (2011). Kangaroo meat producers weigh Chinese market. Retrieved 1 December 2020, from www.nytimes.com/2011/04/13/business/global/13kangaroo.html

Shriner, S. A., Ellis, J. W., Root, J. J., Roug, A., Stopak, S. R., Wiscomb, G. W., ... DeLiberto, T. J. (2021). SARS-CoV-2 Exposure in Escaped Mink, Utah, USA. *Emerging Infectious Diseases, 27*(3), 988–990. https://doi.org/10.3201/eid2703.204444

Siddiqui, A. H., & Koirala, J. (2020). Methicillin Resistant Staphylococcus Aureus. In *StatPearls [Internet]*. StatPearls Publishing. Retrieved from https://www.ncbi.nlm.nih.gov/books/NBK482221/

Siegert, R., Shu, H. L., Slenczka, W., Peters, D., & Müller, G. (1967a). [On the etiology of an unknown human infection originating from monkeys]. *Deutsche Medizinische Wochenschrift (1946), 92*(51), 2341–2343. https://doi.org/10.1055/s-0028-1106144

Siegert, R., Shu, H.-L., Slenczka, W., Peters, D., & Müller, G. (1967b). Zur Ätiologie einer unbekannten, von Affen ausgegangenen menschlichen Infektionskrankheit. *DMW - Deutsche Medizinische Wochenschrift, 92*(51), 2341–2343. https://doi.org/10.1055/s-0028-1106144

Singh Khadka, S. K. (2020). Coronavirus: China wildlife trade ban 'should be permanent'. BBC News. Retrieved from https://www.bbc.com/news/science-environment-51310786

Sirotkin, K., & Sirotkin, D. (2020). Might SARS-CoV-2 Have Arisen via Serial Passage through an Animal Host or Cell Culture? *BioEssays*, 42(10), 2000091. https://doi.org/10.1002/bies.202000091

Smith, K. F., Behrens, M., Schloegel, L. M., Marano, N., Burgiel, S., & Daszak, P. (2009). Reducing the Risks of the Wildlife Trade. *Science, 324*(5927), 594–595. https://doi.org/10.1126/science.1174460

Smith, K. M., Anthony, S. J., Switzer, W. M., Epstein, J. H., Seimon, T., Jia, H., ... Marano, N. (2012). Zoonotic Viruses Associated with Illegally Imported Wildlife Products. *PLOS ONE, 7*(1), e29505. https://doi.org/10.1371/journal.pone.0029505

Soorae, P. S. (Ed.). (2021). *Global conservation translocation perspectives: 2021*. Case studies from around the globe. Gland, Switzerland: IUCN SSC Conservation Translocation Specialist Group, Environment Agency - Abu Dhabi and Calgary Zoo, Canada. Retrieved from https://portals.iucn.org/library/es/node/49298

Stanford, C. B., Iverson, J. B., Rhodin, A. G. J., Dijk, P. P. van, Mittermeier, R. A., Kuchling, G., ... Walde, A. D. (2020). Turtles and Tortoises Are in Trouble. *Current Biology, 30*(12), R721–R735. https://doi.org/10.1016/j.cub.2020.04.088

Stapleton, P. D., & Taylor, P. W. (2002). Methicillin resistance in Staphylococcus aureus. *Science Progress, 85*(Pt 1), 57–72.

Statistics New Zealand. (2020). At a glance industry statistics | Deer Industry New Zealand. Retrieved 1 December 2020, from https://www.deernz.org/about-deer-industry/nz-deer-industry/deer-industry-statistics/glance-industry-statistics#.X8ZNbGhKiHt

Steffen, W., Broadgate, W., Deutsch, L., Gaffney, O., & Ludwig, C. (2015). The trajectory of the Anthropocene: The Great Acceleration. *The Anthropocene Review, 2*(1), 81–98. https://doi.org/10.1177/2053019614564785
Steinfeld, H., Gerber, P., Wassenaar, T. D., Castel, V., Rosales M., M., & Haan, C. de. (2006). Livestock's long shadow: Environmental issues and options. Rome: Food and Agriculture Organization of the United Nations.

Stephens, T., Wilson, S. C., Cassidy, F., Bender, D., Gummer, D., Smith, D. H. V., ... Moehrenschlager, A. (2018). Climate change impacts on the conservation outlook of populations on the poleward periphery of species ranges: A case study of Canadian black-tailed prairie dogs (Cynomys ludovicianus). *Global Change Biology, 24*(2), 836–847. https://doi.org/10.1111/gcb.13922

Stitt, T., Mountifield, J., & Stephen, C. (2007). Opportunities and obstacles to collecting wildlife disease data for public health purposes: Results of a pilot study on Vancouver Island, British Columbia. *The Canadian Veterinary Journal = La Revue Veterinaire Canadienne, 48*(1), 83–87, 89–90. https://doi.org/10.4141/cjas68-011

Stone, D. A. (2008). Cambios del clima previstos para los años venideros y su repercusión en el estudio de las consecuencias de las enfermedades: -EN- Predicted climate changes for the years to come and implications for disease impact studies -FR- Le changement climatique attendu pour les prochaines années et ses conséquences sur les études d'impact sanitaire -ES-. *Revue Scientifique et Technique de l'OIE, 27*(2), 319–330. https://doi.org/10.20506/rst.27.2.1809

Suzán, G., Marcé, E., Giermakowski, J. T., Mills, J. N., Ceballos, G., Ostfeld, R. S., ... Yates, T. L. (2009). Experimental Evidence for Reduced Rodent Diversity Causing Increased Hantavirus Prevalence. *PLOS ONE, 4*(5), e5461. https://doi.org/10.1371/journal.pone.0005461

Swanepoel, R., Smit, S. B., Rollin, P. E., Formenty, P., Leman, P. A., Kemp, A., ... International Scientific and Technical Committee for Marburg Hemorrhagic Fever Control in the Democratic Republic of Congo. (2007). Studies of reservoir hosts for Marburg virus. *Emerging Infectious Diseases, 13*(12), 1847–1851. https://doi.org/10.3201/eid1312.071115

Symes, W. S., McGrath, F. L., Rao, M., & Carrasco, L. R. (2018). The gravity of wildlife trade. *Biological Conservation, 218*, 268–276. https://doi.org/10.1016/j.biocon.2017.11.007

't Sas-Rolfes, M., Challender, D. W. S., Hinsley, A., Veríssimo, D., & Milner-Gulland, E. J. (2019). Illegal Wildlife Trade: Scale, Processes, and Governance. *Annual Review of Environment and Resources, 44*(1), 201–228. https://doi.org/10.1146/annurev-environ-101718-033253

Takekawa, J. Y., Newman, S. H., Xiao, X., Prosser, D. J., Spragens, K. A., Palm, E. C., … Ji, W. (2010). Migration of waterfowl in the East Asian flyway and spatial relationship to HPAI H5N1 outbreaks. *Avian Diseases, 54*(1 Suppl), 466–476. https://doi.org/10.1637/8914-043009-Reg.1

Taylor, L. H., Latham, S. M., & woolhouse, M. E. J. (2001). Risk factors for human disease emergence. Philosophical Transactions of the Royal Society of London. *Series B: Biological Sciences, 356*(1411), 983–989. https://doi.org/10.1098/rstb.2001.0888

Temmam, S., Davoust, B., Chaber, A.-L., Lignereux, Y., Michelle, C., Monteil-Bouchard, S., … Desnues, C. (2017). Screening for Viral Pathogens in African Simian Bushmeat Seized at A French Airport. *Transboundary and Emerging Diseases, 64*(4), 1159–1167. https://doi.org/10.1111/tbed.12481

Tensen, L. (2016). Under what circumstances can wildlife farming benefit species conservation? *Global Ecology and Conservation, 6*, 286–298. https://doi.org/10.1016/j.gecco.2016.03.007

Terpstra, C., & Wensvoort, G. (1986). [African swine fever in the Netherlands]. *Tijdschrift Voor Diergeneeskunde, 111*(8), 389–392.

The European Commission (2007). New rules for captive bird imports to protect animal health in the EU and improve the welfare of imported birds.

The National People's Congress of The People's Republic of China. (2020, February 24). [Decision on Comprehensive Ban on Illegal Wildlife Trade; Eliminate (the bad habit) of Eating Wildlife (in order to) Ensure Public Health and Safety] (in Chinese). Retrieved 11 December 2020, from http://www.npc.gov.cn/npc/c30834/202002/c56b129850aa42acb584cf01ebb68ea4.shtml

Thiel, P.-P. A. M. van, Bie, R. M. A. de, Eftimov, F., Tepaske, R., Zaaijer, H. L., Doornum, G. J. J. van, … Kager, P. A. (2009). Fatal Human Rabies due to Duvenhage Virus from a Bat in Kenya: Failure of Treatment with Coma-Induction, Ketamine, and Antiviral Drugs. *PLOS Neglected Tropical Diseases, 3*(7), e428. https://doi.org/10.1371/journal.pntd.0000428

Thomas–Walters, L., Hinsley, A., Bergin, D., Burgess, G., Doughty, H., Eppel, S., … Veríssimo, D. (2020). Motivations for the use and consumption of wildlife products. *Conservation Biology,* cobi.13578. https://doi.org/10.1111/cobi.13578

Thorbjarnarson, J. (1999). Crocodile Tears and Skins: International Trade, Economic Constraints, and Limits to the Sustainable Use of Crocodilians. *Conservation Biology, 13*(3), 465–470. https://doi.org/10.1046/j.1523-1739.1999.00011.x

Towner, J. S., Khristova, M. L., Sealy, T. K., Vincent, M. J., Erickson, B. R., Bawiec, D. A., … Nichol, S. T. (2006). Marburgvirus genomics and association with a large hemorrhagic fever outbreak in Angola. *Journal of Virology, 80*(13), 6497–6516. https://doi.org/10.1128/JVI.00069-06

TRAFFIC (2008). *What's Driving the Wildlife Trade? A Review of Expert Opinion on Economic and Social Drivers of the Wildlife Trade and Trade Control Efforts in Cambodia, Indonesia, Lao PDR and Vietnam. Washington*, D.C.: East Asia and Pacific Region Sustainable Development Departmen, World Bank. Retrieved from https://www.traffic.org/site/assets/files/5435/whats-driving-wildlife-trade.pdf

TRAFFIC (2020). Illegal Wildlife Trade. Retrieved 27 November 2020, from https://www.traffic.org/about-us/illegal-wildlife-trade/

Turcios-Casco, M. A., & Cazzolla Gatti, R. (2020). Do not blame bats and pangolins! Global consequences for wildlife conservation after the SARS-CoV-2 pandemic. *Biodiversity and Conservation*, 1–5. https://doi.org/10.1007/s10531-020-02053-y

Turvey, S. T., & Risley, C. L. (2006). Modelling the extinction of Steller's sea cow. *Biology Letters, 2*(1), 94–97. https://doi.org/10.1098/rsbl.2005.0415

United Nations Environment Programme (UNEP) (2016). Frontiers 2016 Report: *Emerging Issues of Environmental Concern*. UN. https://doi.org/10.18356/4392feb8-en

UNEP (2020, December 11). UNEP joins three international organizations in expert panel to improve One Health. Retrieved 10 December 2020, from UN Environment website: http://www.unenvironment.org/news-and-stories/story/unep-joins-three-international-organizations-expert-panel-improve-one-health

UNEP & International Livestock Research Institute (ILRI) (2020). *Preventing the Next Pandemic: Zoonotic diseases and how to break the chain of transmission*. Nairobi, Kenya. Retrieved from https://wedocs.unep.org/bitstream/handle/20.500.11822/32316/ZP.pdf?sequence=1&isAllowed=y

UNEP-World Conservation Monitoring Centre (WCMC) & Joint Nature Conservation Committee (JNCC) (2021). *Zoonotic potential of international trade in CITES-listed species | JNCC Resource Hub*. Retrieved from https://hub.jncc.gov.uk/assets/964ae259-410e-4205-8ec7-e2c54f5c6e3d

United Nations (2019). *World Population Prospects 2019*: Highlights. Retrieved from https://doi.org/10.18356/13bf5476-en

United Nations Office on Drugs and Crime (UNODC) (2020). *World Wildlife Crime Report 2020*. United Nations Office on Drugs and Crime. Retrieved from https://www.unodc.org/documents/data-and-analysis/wildlife/2020/World_Wildlife_Report_2020_9July.pdf

U.S. Department of State. (2021). Joint Statement on the WHO-Convened COVID-19 Origins Study. Retrieved 30 April 2021, from United States Department of State website: https://www.state.gov/joint-statement-on-the-who-convened-covid-19-origins-study/

Van Schepen, M. D., & Kunesh, J. P. (1981). *African swine fever: An overview [Ornithodoros moubata ticks act as virus reservoirs]. 43*(3), 100–107.

Van Velden, J. L., Travers, H., Moyo, B. H. Z., & Biggs, D. (2020). Using scenarios to understand community-based interventions for bushmeat hunting and consumption in African savannas. *Biological Conservation, 248*, 108676. https://doi.org/10.1016/j.biocon.2020.108676

Van Velden, J. L., Wilson, K., & Biggs, D. (2018). The evidence for the bushmeat crisis in African savannas: A systematic quantitative literature review. *Biological Conservation, 221*, 345–356. https://doi.org/10.1016/j.biocon.2018.03.022

Van Vliet, N., Quiceno-Mesa, M. P., Cruz-Antia, D., Tellez, L., Martins, C., Haiden, E., … Nasi, R. (2015). From fish and bushmeat to chicken nuggets: The nutrition transition in a continuum from rural to urban settings in the Colombian Amazon region. *Ethnobiology and Conservation*. https://doi.org/10.15451/ec2015-7-4.6-1-12

Van Vliet, Nathalie, Moreno, J., Gómez, J., Zhou, W., Fa, J. E., Golden, C., … Nasi, R. (2017). Bushmeat and human health: Assessing the Evidence in tropical and sub-tropical forests. *Ethnobiology and Conservation*. https://doi.org/10.15451/ec2017-04-6.3-1-45

Vijaykrishna, D., Bahl, J., Riley, S., Duan, L., Zhang, J. X., Chen, H., … Guan, Y. (2008). Evolutionary Dynamics and Emergence of Panzootic H5N1 Influenza Viruses. *PLoS Pathogens, 4*(9). https://doi.org/10.1371/journal.ppat.1000161

Vliet, N. van, Quiceno, M., Moreno, J., Cruz, D., Fa, J. E., & Nasi, R. (2017). Is urban bushmeat trade in Colombia really insignificant? *Oryx, 51*(2), 305–314. https://doi.org/10.1017/S0030605315001118

Vollset, S. E., Goren, E., Yuan, C.-W., Cao, J., Smith, A. E., Hsiao, T., … Murray, C. J. L. (2020). Fertility, mortality, migration, and population scenarios for 195 countries and territories from 2017 to 2100: A forecasting analysis for the Global Burden of Disease Study. *Lancet (London, England), 396*(10258), 1285–1306. https://doi.org/10.1016/S0140-6736(20)30677-2

Von Grebmer, K., Bernstein, J., Alders, R., Dar, O., Kock, R., Rampa, F., … Fritschel, H. (2020). *2020 Global Hunger Index: One Decade to Zero Hunger—Linking Health and Sustainable Food Systems*. Bonn and Dublin: Bonn: Welthungerhilfe; and Dublin: Concern Worldwide. Retrieved from https://www.globalhungerindex.org/pdf/en/2020.pdf

Vos, T., Lim, S. S., Abbafati, C., Abbas, K. M., Abbasi, M., Abbasifard, M., … Murray, C. J. L. (2020). Global burden of 369 diseases and injuries in 204 countries and territories, 1990–2019: A systematic analysis for the Global Burden of Disease Study 2019. *The Lancet, 396*(10258), 1204–1222. https://doi.org/10.1016/S0140-6736(20)30925-9

Waage, J., & Yap, C. (Eds.). (2015). *Thinking Beyond Sectors for Sustainable Development*. London: Ubiquity Press. https://doi.org/10.5334/bao

Wallace, R. (2020). Dead epidemiologists: *On the origins of covid-19*. New York: Monthly Review Press.

Wallace, R. G., HoDac, H., Lathrop, R. H., & Fitch, W. M. (2007). A statistical phylogeography of influenza A H5N1. *Proceedings of the National Academy of Sciences, 104*(11), 4473–4478. https://doi.org/10.1073/pnas.0700435104

Wallace, Robert G. (2016). *Big farms make big flu: Dispatches on infectious disease, agribusiness, and the nature of science*. New York: Monthly Review Press.

Wallace, Robert G., Bergmann, L., Kock, R., Gilbert, M., Hogerwerf, L., Wallace, R., & Holmberg, M. (2015). The dawn of Structural One Health: A new science tracking disease emergence along circuits of capital. *Social Science & Medicine (1982), 129*, 68–77. https://doi.org/10.1016/j.socscimed.2014.09.047

Wallace, Robert G, Gilbert, M., Wallace, R., Pittiglio, C., Mattioli, R., & Kock, R. (2014). Did Ebola Emerge in West Africa by a Policy-Driven Phase Change in Agroecology? Ebola's Social Context. *Environment and Planning A: Economy and Space, 46*(11), 2533–2542. https://doi.org/10.1068/a4712com

Wallace, Robert G, Kock, R., Bergmann, L., Gilbert, M., Hogerwerf, L., Pittiglio, C., … Wallace, R. (2016). Did Neoliberalizing West African Forests Produce a New Niche for Ebola? *International Journal of Health Services, 46*(1), 149–165. https://doi.org/10.1177/0020731415611644

Wallace, Rodrick, Chaves, L. F., Bergmann, L. R., Ayres, C., Hogerwerf, L., Kock, R., & Wallace, R. G. (2018). *Clear-cutting disease control: Capital-led deforestation, public health austerity, and vector-borne infection*. Retrieved from https://search.ebscohost.com/login.aspx?direct=true&scope=site&db=nlebk&db=nlabk&AN=1716819

Walsh, M. G., Mor, S. M., Maity, H., & Hossain, S. (2019). Forest loss shapes the landscape suitability of Kyasanur Forest disease in the biodiversity hotspots of the Western Ghats, India. *International Journal of Epidemiology, 48*(6), 1804–1814. https://doi.org/10.1093/ije/dyz232

Walzer, C. (2020). COVID-19 and the Curse of Piecemeal Perspectives. *Frontiers in Veterinary Science, 7*, 582983. https://doi.org/10.3389/fvets.2020.582983

Wang, H., Shao, J., Luo, X., Chuai, Z., Xu, S., Geng, M., & Gao, Z. (2020). Wildlife consumption ban is insufficient. *Science (New York, N.Y.), 367*(6485), 1435. https://doi.org/10.1126/science.abb6463

Wang, L.-F., & Eaton, B. T. (2007). Bats, Civets and the Emergence of SARS. In J. E. Childs, J. S. Mackenzie, & J. A. Richt (Eds.), *Wildlife and Emerging Zoonotic Diseases: The Biology, Circumstances and Consequences of Cross-Species Transmission* (pp. 325–344). Berlin, Heidelberg: Springer Berlin Heidelberg. https://doi.org/10.1007/978-3-540-70962-6_13

Wang, N., Li, S.-Y., Yang, X.-L., Huang, H.-M., Zhang, Y.-J., Guo, H., … Shi, Z.-L. (2018). Serological Evidence of Bat SARS-Related Coronavirus Infection in Humans, China. *Virologica Sinica, 33*(1), 104–107. https://doi.org/10.1007/s12250-018-0012-7

Wang, T., Sun, Y., & Qiu, H.-J. (2018). African swine fever: An unprecedented disaster and challenge to China. *Infectious Diseases of Poverty, 7*(1), 111. https://doi.org/10.1186/s40249-018-0495-3

Wardeh, M., Risley, C., McIntyre, M. K., Setzkorn, C., & Baylis, M. (2015). Database of host-pathogen and related species interactions, and their global distribution. *Scientific Data, 2*(1), 150049. https://doi.org/10.1038/sdata.2015.49

Wardeh, M., Sharkey, K. J., & Baylis, M. (2020). Integration of shared-pathogen networks and machine learning reveals the key aspects of zoonoses and predicts mammalian reservoirs. *Proceedings of the Royal Society B: Biological Sciences, 287*(1920). https://doi.

org/10.1098/rspb.2019.2882

Watson, J. E. M., Shanahan, D. F., Di Marco, M., Allan, J., Laurance, W. F., Sanderson, E. W., … Venter, O. (2016). Catastrophic Declines in Wilderness Areas Undermine Global Environment Targets. *Current Biology, 26*(21), 2929–2934. https://doi.org/10.1016/j.cub.2016.08.049

Watts, N., Adger, W. N., Agnolucci, P., Blackstock, J., Byass, P., Cai, W., … Costello, A. (2015). Health and climate change: Policy responses to protect public health. *The Lancet, 386*(10006), 1861–1914. https://doi.org/10.1016/S0140-6736(15)60854-6

Watts, N., Amann, M., Ayeb-Karlsson, S., Belesova, K., Bouley, T., Boykoff, M., … Costello, A. (2018). The Lancet Countdown on health and climate change: From 25 years of inaction to a global transformation for public health. *The Lancet, 391*(10120), 581–630. https://doi.org/10.1016/S0140-6736(17)32464-9

Wildlife Conservation Society (WCS) (2020). S*ummary of WCS Policy and Messaging on COVID-19.* Retrieved from https://c532f75abb9c-1c021b8c-e46e473f8aadb72cf2a8ea564b4e6a76.ssl.cf5.rackcdn.com/2020/04/01/8294efiuzg_COVID_19_Summary_of_WCS_Policies_and_Messaging_March29.2.pdf

Weiss, R., & Sankaran, N. (2022). Emergence of epidemic diseases: Zoonoses and other origins. *Faculty Reviews, 11,* (2). https://doi.org/10.12703/r/11-2

Wells, K., Morand, S., Wardeh, M., & Baylis, M. (2020). Distinct spread of DNA and RNA viruses among mammals amid prominent role of domestic species. *Global Ecology and Biogeography: A Journal of Macroecology, 29*(3), 470–481. https://doi.org/10.1111/geb.13045

White, R. J., & Razgour, O. (2020). Emerging zoonotic diseases originating in mammals: A systematic review of effects of anthropogenic land–use change. *Mammal Review*, mam.12201. https://doi.org/10.1111/mam.12201

Whitmee, S., Haines, A., Beyrer, C., Boltz, F., Capon, A. G., de Souza Dias, B. F., … Yach, D. (2015). Safeguarding human health in the Anthropocene epoch: Report of The Rockefeller Foundation–Lancet Commission on planetary health. *The Lancet, 386*(10007), 1973–2028. https://doi.org/10.1016/S0140-6736(15)60901-1

World Health Organization (WHO) (2014). *A brief guide to emerging infectious diseases and zoonoses*. WHO Regional Office for South-East Asia. Retrieved from https://apps.who.int/iris/handle/10665/204722

WHO (2015). *WHO estimates of the global burden of foodborne diseases*. Geneva, Switzerland: World Health Organization.

WHO (2017). P*reventing noncommunicable diseases (NCDs) by reducing environmental risk factors*. Geneva: World Health Organization. Retrieved from https://apps.who.int/iris/bitstream/handle/10665/258796/WHO-FWC-EPE-17.01-eng.pdf?sequence=1

WHO (2018). *Joint external evaluation tool: International Health Regulations* (2005), second edition (2nd Edition). Geneva, Switzerland: World Health Organization: World Health Organization. Retrieved from https://www.who.int/ihr/publications/WHO_HSE_GCR_2018_2/en/

WHO (2019). *Infection prevention and control during health care for probable or confirmed cases of Middle East respiratory syndrome coronavirus* (MERS-CoV) infection Interim guidance. Retrieved from https://www.who.int/csr/disease/coronavirus_infections/ipc-mers-cov/en/

WHO (2020a). Disease outbreaks. Retrieved 8 December 2020, from WHO website: http://www.who.int/emergencies/diseases/en/

WHO (2020b). Zoonoses. Retrieved 10 November 2020, from https://www.who.int/news-room/fact-sheets/detail/zoonoses

WHO (2020c). Antimicrobial resistance. Retrieved 6 April 2021, from https://www.who.int/news-room/fact-sheets/detail/antimicrobial-resistance

WHO (2021a). Monkeypox. Retrieved 30 May 2021, from https://www.who.int/news-room/fact-sheets/detail/monkeypox

WHO (2021b). Prioritizing diseases for research and development in emergency contexts. Retrieved 26 July 2021, from who.int/activities/prioritizing-diseases-for-research-and-development-in-emergency-contexts

WHO (2021c). *WHO-convened Global Study of Origins of SARS-CoV-2: China Part*. WHO Headquarters (HQ). Retrieved from https://www.who.int/publications/i/item/who-convened-global-study-of-origins-of-sars-cov-2-china-part

WHO (2021d). Zoonoses. Retrieved 27 June 2021, from https://www.who.int/news-room/fact-sheets/detail/zoonoses

WHO (2021e). *COVID-19 Virtual Press conference transcript—9 February 2021 [Press briefing transcript]*. WHO Team Department of Communications. Retrieved from https://www.who.int/publications/m/item/covid-19-virtual-press-conference-transcript---9-february-2021

WHO (2021f). Marburg virus disease. Retrieved 1 December 2021, from https://www.who.int/news-room/fact-sheets/detail/marburg-virus-disease

WHO & Training in Tropical Diseases (TDR) (2012). Research priorities for zoonoses and marginalized infections: *Technical report of the TDR Disease Reference Group on Zoonoses and Marginalized Infectious Diseases of Poverty*. Geneva: World Health Organization.

Williams, K. C., & Burdo, T. H. (2009). HIV and SIV infection: The role of cellular restriction and immune responses in viral replication and pathogenesis. APMIS: Acta Pathologica, *Microbiologica, et Immunologica Scandinavica, 117*(5–6), 400–412. https://doi.org/10.1111/j.1600-0463.2009.02450.x

Wolfe, N. D., Daszak, P., Kilpatrick, A. M., & Burke, D. S. (2005). Bushmeat hunting, deforestation, and prediction of zoonoses emergence. *Emerging Infectious Diseases, 11*(12), 1822–1827. https://doi.org/10.3201/eid1112.040789

Wolfe, N. D., Dunavan, C. P., & Diamond, J. (2007). Origins of major human infectious diseases. *Nature, 447*(7142), 279–283. https://doi.org/10.1038/nature05775

Wong, R. W. Y. (2019). *The illegal wildlife trade in China: Understanding the distribution networks*. Cham: Suisse : Palgrave Macmillan.

Woo, H. J., & Reifman, J. (2014). Quantitative Modeling of Virus Evolutionary Dynamics and Adaptation in Serial Passages Using Empirically Inferred Fitness Landscapes. *Journal of Virology, 88*(2), 1039–1050. https://doi.org/10.1128/JVI.02958-13

Woolhouse, M. E. J., & Gowtage-Sequeria, S. (2005). Host range and emerging and reemerging pathogens. *Emerging Infectious Diseases, 11*(12), 1842–1847. https://doi.org/10.3201/eid1112.050997

Woolhouse, M., Scott, F., Hudson, Z., Howey, R., & Chase-Topping, M. (2012). Human viruses: Discovery and emergence. *Philosophical Transactions of the Royal Society B: Biological Sciences, 367*(1604), 2864–2871. https://doi.org/10.1098/rstb.2011.0354

World Bank (2019). *Illegal Logging, Fishing, and Wildlife Trade*. World Bank, Washington, DC. https://doi.org/10.1596/32806

World Bank (2020). *Air transport, passengers carried*. Retrieved 9 December 2020, from https://data.worldbank.org/indicator/IS.AIR.PSGR

World Wide Fund for Nature (WWF) (2020). *Living Planet Report 2020—Bending the curve of biodiversity loss* (Gland, Switzerland; R. E. A. Almond, Grooten M, & T. Petersen, Eds.). WWF. Retrieved from https://f.hubspotusercontent20.net/hubfs/4783129/LPR/PDFs/ENGLISH-FULL.pdf

Xia, W., Hughes, J., Robertson, D., & Jiang, X. (2021). *How One Pandemic Led To Another: Asfv, the Disruption Contributing To Sars-Cov-2 Emergence in Wuhan*. https://doi.org/10.20944/preprints202102.0590.v1

Xiao, X., Newman, C., Buesching, C. D., Macdonald, D. W., & Zhou, Z.-M. (2021). Animal sales from Wuhan wet markets immediately prior to the COVID-19 pandemic. *Scientific Reports, 11*(1), 11898. https://doi.org/10.1038/s41598-021-91470-2

Xiao, K., Zhai, J., Feng, Y., Zhou, N., Zhang, X., Zou, J.-J., … Shen, Y. (2020). Isolation of SARS-CoV-2-related coronavirus from Malayan pangolins. *Nature, 583*(7815), 286–289. https://doi.org/10.1038/s41586-020-2313-x

Xinhua. (2020). China's legislature adopts decision on banning illegal trade, consumption of wildlife. Retrieved 29 July 2020, from http://www.xinhuanet.com/english/2020-02/24/c_138814139.htm

You, S., Liu, T., Zhang, M., Zhao, X., Dong, Y., Wu, B., … Shi, B. (2021). African swine fever outbreaks in China led to gross domestic product and economic losses. *Nature Food, 2*(10), 802–808. https://doi.org/10.1038/s43016-021-00362-1

Zhang, L., Hua, N., & Sun, S. (2008). Wildlife trade, consumption and conservation awareness in southwest China. *Biodiversity and Conservation, 17*(6), 1493–1516. https://doi.org/10.1007/s10531-008-9358-8

Zhang, S., Qiao, S., Yu, J., Zeng, J., Shan, S., Tian, L., … Wang, X. (2021). Bat and pangolin coronavirus spike glycoprotein structures provide insights into SARS-CoV-2 evolution. *Nature Communications, 12*(1), 1607. https://doi.org/10.1038/s41467-021-21767-3

Zhang, T., Wu, Q., & Zhang, Z. (2020). Probable Pangolin Origin of SARS-CoV-2 Associated with the COVID-19 Outbreak. *Current Biology, 30*(7), 1346-1351.e2. https://doi.org/10.1016/j.cub.2020.03.022

Zhao, L., Abbasi, A. B., & Illingworth, C. J. R. (2019). Mutational load causes stochastic evolutionary outcomes in acute RNA viral infection. *Virus Evolution, 5*(vez008). https://doi.org/10.1093/ve/vez008

Zhou, G., Zhang, W., & Xu, X. (2012). China's meat industry revolution: Challenges and opportunities for the future. *Meat Science, 92*(3), 188–196. https://doi.org/10.1016/j.meatsci.2012.04.016

Zinsstag, J., Schelling, E., Waltner-Toews, D., & Tanner, M. (2011). From 'one medicine' to 'one health' and systemic approaches to health and well-being. *Preventive Veterinary Medicine, 101*(3–4), 148–156. https://doi.org/10.1016/j.prevetmed.2010.07.003

Zinsstag, Jakob, Crump, L., Schelling, E., Hattendorf, J., Maidane, Y. O., Ali, K. O., … Cissé, G. (2018). Climate change and One Health. *FEMS Microbiology Letters, 365*(11). https://doi.org/10.1093/femsle/fny085

Zumla, A., Dar, O., Kock, R., Muturi, M., Ntoumi, F., Kaleebu, P., … Petersen, E. (2016). Taking forward a 'One Health' approach for turning the tide against the Middle East respiratory syndrome coronavirus and other zoonotic pathogens with epidemic potential. *International Journal of Infectious Diseases, 47*, 5–9. https://doi.org/10.1016/j.ijid.2016.06.012

Supplementary information

1. Literature search and scoping review protocol

The initial body of literature (or benchmark literature) was provided by the multiple experts participating in this project and additional communications with several international experts. Following an initial assessment of *key literature*, the core team conducted a non-systematic extensive literature review of both scientific and grey literature using a both backward and forward reference searching to identify relevant literature. The novel coronavirus COVID-19 (and its etiological agent SARS-CoV-2) do not have a MeSH (Medical Subject Headings) assigned to facilitate the search of articles yet. Therefore, the core team conducted a free search in multiple repositories every fifteen days (list below) by using simplified search terms to capture the information regarding SARS-CoV-2/COVID-19, its origin, wildlife connections, and other relevant information to the topics discussed in the situation analysis. As a result, more than 1,500 scientific and grey literature were screened and critically assessed by the team.

Repository name	Website
COVIPENDIUM	https://zenodo.org/record/
OpenAIRE	https://www.openaire.eu/
NCBI SARS-CoV-2 Resources	https://www.ncbi.nlm.nih.gov/sars-cov-2/
Coronavirus (COVID-19)	https://www.nih.gov/coronavirus
Coronavirus Disease 2019 (COVID-19)	https://www.coronavirus.gov/
Coronavirus Library	https://www.en.fondazione-menarini.it/Home/Coronavirus-Library
Coronavirus: Research, Commentary, and News (AAAS)	https://www.sciencemag.org/collections/coronavirus
SARS-CoV-2/COVID-19 TOOLBOX	https://absa.org/covid19toolbox/
Coronavirus Disease Research Community - COVID-19	https://zenodo.org/communities/covid-19?page=1&size=20
COVID-19 Global Research Information & Resources Litcovid	https://covid19.researcher.life/
LitCovid (NCBI NLM NIH)	https://www.ncbi.nlm.nih.gov/research/coronavirus/
Open Access to COVID-19 and related research	https://www.openaccess.nl/en/open-access-to-covid-19-and-related-research
COVID-19 CMMID	https://cmmid.github.io/topics/covid19/
Global research on coronavirus disease (COVID-19)	https://www.who.int/emergencies/diseases/novel-coronavirus-2019/global-research-on-novel-coronavirus-2019-ncov
Coronavirus Research Repository (Elsevier)	https://coronavirus.1science.com/search
Elsevier's Novel Coronavirus Information Center	https://www.elsevier.com/connect/coronavirus-information-center
The Lancet-COVID-19 Resource Centre	https://www.thelancet.com/coronavirus
Coronavirus	https://www.ssrn.com/index.cfm/en/coronavirus/
Nature Collection Coronavirus	https://www.nature.com/collections/hajgidghjb
ResearchGate COVID-19 research community	https://www.researchgate.net/

Additionally, given the initial focus on the role and risks of wildlife trade in the emergence of human infectious disease and zoonoses, the team conducted a systematic search by implementing an Evidence Gap Maps (EGMs). Evidence synthesis approaches, such as EGMs are a useful method to capture, summarise, and critically assess the evidence for a particular topic or field of study (Campbell Collaboration, 2020). The goal is to identify and prioritise research needs and support evidence-based decision making by mapping "what works". Further details on the methodology and search protocol can be found in the online published document (Cáceres-Escobar et al., 2020) https://figshare.com/articles/online_resource/Situation_Analysis_EGM_Protocol_16_12_2020/13392275/2.

2. Emerging infectious disease in context

Emerging infectious diseases (EIDs) are commonly defined as infectious agents that are newly identified in a population or newly evolved, or a known infectious agent or variant that is rapidly increasing in incidence (i.e. re-emerging infectious agents) or expanding geographical range, host (i.e. host-switch) or vector range (*WHO 2014; CDC 2018; Petersen et al. 2018*). This does not account for newly detectable infections due to novel surveillance or diagnostic advances either globally or locally, that give an appearance of emergence. The new detection includes a general assumption which may or may not be true. Some authors also use an arbitrary 20-year timeframe since its first record (*CDC 2018*), but many analyses do not incorporate this temporal component which makes any global statistical interpretation complicated and frequently misleading. To expand from the analysis done by *Jones et al. (2008) and Allen et al. (2017)*, we divided the dataset according four components of EIDs:

1) Evolution of an existing organism

2) New region, increase incidence, range expansion, and reappearance (re-emergence)

3) Drug resistant/increase virulence (variant)

4) New host range

The variability and lack of precision of the definition of EID, which does not distinguish between different types of emergence and re-emergence or whether it is artifact of other influences such as better surveillance or tools, makes it hard to compare the different drivers of EIDs and assess the magnitude in terms of global burden, threat, and origin of the "new" infectious agents.

3. Review of African wild meat and reported zoonoses

Most of the analysis in wildlife is centred around lists of pathogens (i.e. hazards for human health) identified by surveys and described as potential risks for zoonosis. This approach ignores the intrinsic pathogen and host characteristics, environmental conditions, and transmission conditions

	Pathogen	Location
Great Apes (Chimpanzee, Bonobo, Gorilla)		
Pan troglodytes (Common chimpanzee)	Zaire Ebolavirus (V)	Cameroon, Gabon, Republic of Congo
	Tai Forest Ebolavirus (V)	Côte d'Ivoire
	HIV-1/SIVcpz (V)	Cameroon, Democratic Republic of the Congo, Tanzania
	HLTV/SLTV-1 (V)	Central & Eastern Africa
	Simian Foamy Virus (V)	Cameroon, Côte d'Ivoire, Gabon, Republic of Congo, Tanzania
	Strongyloides fulleborni (H)	Gabon
	Entamoeba histolytica (P)	Tanzania
	Balantidium coli (P)	Central African Republic, Tanzania
	Giardia intestinalis (P)	Guinea Bissau
	Bacillus anthracis (B)	Côte d'Ivoire
Pan paniscus (Bonobo)	HTLV/STLV-2, HTLV/STLV-3 (V)	Democratic Republic of the Congo
Gorilla gorilla (Western gorilla)	Zaire Ebolavirus (V)	Cameroon, Gabon
	HIV-1/SIVgor (V)	Cameroon
	HTLV/STLV-1 (V)	Cameroon
	Simian Foamy Virus (V)	Cameroon, Gabon
	Rabies (V)	Central African Republic, Kenya
	Strongyloides fulleborni (H)	Central African Republic
	Entamoeba histolytica (P)	Central African Republic
	Balantidium coli (P)	Central African Republic
	Giardia intestinalis (P)	Central African Republic, Rwanda
Other nonhuman primates		
Colobus angolensis (Angola colobus)	HTLV/STLV-3 (V)	Democratic Republic of the Congo
	Strongyloides fulleborni (H)	Uganda
	Entamoeba histolytica (P)	Uganda
Colobus guereza (Mantled guereza)	Strongyloides fulleborni (H)	Cameroon, Uganda
	Entamoeba histolytica (P)	Uganda
Piliocolobus badius (Western red colobus)	HTLV/STLV-1 (V)	Côte d'Ivoire
Piliocolobus tephrosceles (Ugandan red colobus)	HTLV/STLV-1 (V)	Uganda
	Strongyloides fulleborni (H)	Uganda

	Pathogen	Location
	Entamoeba histolytica (P)	Uganda
Piliocolobus tholloni (Thollon's red colobus)	HTLV/STLV-1, HTLV/STLV-3 (V)	Democratic Republic of the Congo
Lophocebus albigena (Gray-cheeked mangabey)	HTLV/STLV-1, HTLV/STLV-3 (V)	Cameroon
	Strongyloides fulleborni (H)	Cameroon
Lophocebus aterrimus (Black crested mangabey)	HTLV/STLV-3 (V)	Democratic Republic of the Congo
Papio anubis (Olive baboon)	Zaire Ebolavirus (V)	Cameroon
	HTLV/STLV-1 (V)	Ethiopia, Kenya
Papio cynocephalus (Yellow baboon)	HTLV/STLV-3 (V)	Tanzania
Papio hamadryas (Hamadryas baboon)	HTLV/STLV-3 (V)	Eritrea, Ethiopia, Senegal
Papio ursinus (Chacma baboon)	HTLV/STLV-1 (V)	South Africa
	Bacillus anthracis (B)	Namibia
Papio sp. (Baboon sp.)	Rabies (V)	Kenya, Namibia, Zambia
Theropithecus gelada (Gelada)	HTLV/STLV-3 (V)	Ethiopia
Cercocebus agilis (Agile mangabey)	HTLV/STLV-1, HTLV/STLV-3 (V)	Cameroon
	Strongyloides fulleborni (H)	Cameroon
	Entamoeba histolytica (P)	Central African Republic
	Balantidium coli (P)	Central African Republic
Cercocebus atys (Sooty mangabey)	HIV-2/SIVsm (V)	West Africa
	HTLV/STLV-1 (V)	Sierra Leone
Cercocebus torquatus (Collared mangabey)	HTLV/STLV-1, HTLV/STLV-3 (V)	Cameroon
Mandrillus leucophaeus (Drill)	Zaire Ebolavirus (V)	Cameroon
Mandrillus sphinx (Mandrill)	Zaire Ebolavirus (V)	Cameroon
	HTLV/STLV-1 (V)	Cameroon
	Simian foamy virus (V)	Cameroon, Gabon
Allenopithecus nigroviridis (Allen's swamp monkey)	HTLV/STLV-1 (V)	Democratic Republic of the Congo
Miopithecus ogouensis (Gabon talapoin)	HTLV/STLV-1 (V)	Cameroon
	Strongyloides fulleborni (H)	Cameroon
Erythrocebus patas (Patas monkey)	HTLV/STLV-1 (V)	Cameroon, Central African Republic, Senegal
Chlorocebus aethiops (Grivet)	Marburg virus (V)	Uganda
	HTLV/STLV-1 (V)	Ethiopia, Senegal

	Pathogen	Location
Chlorocebus pygerythrus (Vervet monkey)	HTLV/STLV-1 (V)	Kenya
	Leptospira (B)	Botswana
Chlorocebus sabaeus (Green monkey)	HTLV/STLV-1 (V)	Senegal
Chlorocebus tantalus (Tantalus monkey)	HTLV/STLV-1 (V)	Kenya
Cercopithecus albogularis (Sykes' monkey)	HTLV/STLV-1 (V)	Kenya
Cercopithecus ascanius (Red-tailed monkey)	HTLV/STLV-1 (V)	Democratic Republic of the Congo
	Strongyloides fulleborni (H)	Uganda
Cercopithecus cephus (Moustached guenon)	HTLV/STLV-1, HTLV/STLV-3 (V)	Cameroon
	Strongyloidesfulleborni (H)	Cameroon
Cercopithecus lhoesti (L'Hoest's monkey)	Strongyloides fulleborni (H)	Uganda
Cercopithecus mitis (Blue monkey)	Strongyloides fulleborni (H)	Kenya, Uganda
Cercopithecus mona (Mona monkey)	HTLV/STLV-1, HTLV/STLV-3 (V)	Cameroon
	Strongyloides fulleborni (H)	Cameroon
Cercopithecus neglectus (De Brazza's monkey)	Zaire Ebolavirus (V)	Cameroon
	HTLV/STLV-1 (V)	Democratic Republic of the Congo
	Simian Foamy Virus (V)	Cameroon
	Strongyloides fulleborni (H)	Cameroon
Cercopithecus nictitans (Greater spot-nosed monkey)	HTLV/STLV-1, HTLV/STLV-3 (V)	Cameroon
	Strongyloides fulleborni (H)	Cameroon
Cercopithecus pogonias (Crested mona monkey)	HTLV/STLV-1 (V)	Cameroon
	Strongyloides fulleborni (H)	Cameroon
Cercopithecus wolfi (Wolf's mona monkey)	HTLV/STLV-1 (V)	Democratic Republic of the Congo
"Vervet monkey"	Rabies (V)	Zambia
	Strongyloides fulleborni (H)	Uganda
Unspecified primate sp.	Rabies (V)	Ethiopia, Ghana, Kenya, Malawi, Mozambique; Namibia, Sudan, Uganda, Zimbabwe
Bats		
Eidolon helvum (African straw-colored fruit bat)	Zaire Ebolavirus (V)	Ghana
	Lagos bat virus (V)	Ghana, Kenya, Nigeria, Senegal
	Henipaviruses (V)	Cameroon, Ghana, Republic of Congo, Zambia
Hypsignathus monstrosus (Hammer-headed fruit bat)	Marburgvirus (V)	Gabon, Republic of Congo

	Pathogen	Location
	Zaire Ebolavirus (V)	Ghana, Gabon, Republic of Congo
Epomops franqueti (Franquet's epauletted fruit bat)	Marburgvirus (V)	Gabon, Republic of Congo
	Zaire Ebolavirus (V)	Ghana, Gabon, Republic of Congo
Epomophorus gambianus (Gambian epauletted fruit bat)	Zaire Ebolavirus (V)	Ghana
Epomophorus wahlbergi (Wahlberg's epauletted fruit bat)	Lagos Bat Virus (V)	South Africa
Micropteropus pusillus (Peters's lesser epauletted fruit bat)	Marburgvirus (V)	Gabon, Republic of Congo
	Zaire Ebolavirus (V)	Gabon, Republic of Congo
	Lagos Bat Virus (V)	Central African Republic
Rousettus aegyptiacus (Egyptian rousette)	Marburgvirus (V)	Democratic Republic of the Congo, Gabon, Kenya, Republic of Congo, Uganda
	Zaire Ebolavirus (V)	Gabon, Republic of Congo
	Lagos Bat Virus (V)	Kenya
Myonycteris torquata (Little collared fruit bat)	Zaire Ebolavirus (V)	Gabon, Republic of Congo
Nanonycteris veldkampii (Veldkamp's dwarf epauletted fruit bat)	Zaire Ebolavirus (V)	Ghana
Rhinolophus eloquens (Eloquent horseshoe bat)	Marburgvirus (V)	Democratic Republic of the Congo
Miniopterus inflatus (Greater long-fingered bat)	Marburgvirus (V)	Democratic Republic of the Congo
Miniopterus schreibersii (Schreibers's long-fingered bat)	Duvengahe virus (V)	South Africa
Nycteris gambiensis (Gambian slit-faced bat)	Lagos Bat Virus	Senegal
Mops condylurus (Angolan free-tailed bat)	Zaire Ebolavirus (V)	Gabon
Unspecified bat sp.	Duvengahe virus (V)	Kenya
Rodents		
Funisciurus anerythrus (Thomas's rope squirrel)	Monkeypox virus (V)	Democratic Republic of the Congo
Funisciurus sp. (African striped squirrel sp.)	Monkeypox virus (V)	Ghana
Heliosciurus gambianus (Gambian sun squirrel)	Monkeypox virus (V)	Ghana
Paraxerus cepapi (Smith's bush squirrel)	Leptospira (B)	Botswana
Xerus sp. (African ground squirrel sp.)	Monkeypox virus (V)	Ghana
Unspecified squirrel sp.	Rabies (V)	Namibia, Zimbabwe
Lophuromys sikapusi (Rusty-bellied brush-furred rat)	Mokola virus (V)	Central African Republic
Rattus norvegicus (Brown rat)	Leptospira (B)	Botswana
Unspecified "rat species"	Rabies (V)	Namibia
Cricetomys sp. (Giant pouched rat sp.)	Monkeypox virus (V)	Ghana

	Pathogen	Location
Atherurus africanus (African brush-tailed porcupine)	Salmonella (B)	Gabon
Aardvark		
Orycteropus afer (Aardvark)	Leptospira (B)	Botswana
Ungulates		
Equus burchellii (Burchell's zebra)	Bacillus anthracis (B)	Namibia
Phacochoerus aethiopicus (Desert warthog)	Rabies (V)	Namibia
Phacochoerus africanus (Common warthog)	Leptospira (B)	Botswana
Alcelaphus buselaphus (Hartebeest)	Rabies (V)	Namibia
	Bacillus anthracis (B)	Namibia
Connochaetes taurinus (Blue wildebeest)	Rabies (V)	Namibia
	Bacillus anthracis (B)	Namibia, Tanzania
Antidorcas marsupialis (Springbok)	Rabies (V)	Namibia
	Bacillus anthracis (B)	Namibia
	Brucella (B)	Namibia
Syncerus caffer (African buffalo)	Bacillus anthracis (B)	Tanzania
	Brucella (B)	Botswana, Mozambique
Taurotragus oryx (Common eland)	Rabies (V)	Namibia, Zimbabwe
	Bacillus anthracis (B)	Namibia
Tragelaphus strepsiceros (Greater kudu)	Rabies (V)	Namibia, Zimbabwe
Cephalophus sp. (Duiker sp.)	Zaire Ebolavirus (V)	Gabon
Sylvicapra grimmia (Bush duiker)	Rabies (V)	Zimbabwe
Hippotragus niger (Sable antelope)	Rabies (V)	Zimbabwe
Oryx gazelle (Gemsbok)	Rabies (V)	Namibia
Unspecified "oryx," "antelope," "duiker"	Rabies (V)	Namibia
*Due to its length, this is a summarised version of the complete table. The complete table will be included in a digital format		