

Humans as hosts, vectors and agents of environmental change

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Abstract

COVID-19 has demonstrated that the coordinated actions of individuals and decision makers can make a difference to the outcome of a grave threat to society. This review paper presents a meta-analysis of the literature demonstrating how land use change, environmental degradation and climate change increase the risk of emerging infectious diseases, which can seriously impact human health and society. This paper provides evidence of how a focus on economic growth without **sustainable** production and consumption processes has led to higher risk of future pandemics. While many previous studies have pointed at these risks, we propose that recent experiences with COVID-19 present the potential to turn society toward more socially, economically and environmentally sustainable ways of production, consumption and landscape management.

DEFINITIONS

Disease occurrence from endemic to pandemic level

Most diseases will be present in a community at some base or *endemic* level that is not zero but not high enough to deplete the pool of susceptible people. Occasionally, the number of cases of a disease at a community level may increase, often suddenly, to above what is normally expected for the population in that geographical area, at which point we refer to the disease as an *epidemic*. If the epidemic is restricted to a small geographical area it is called an *outbreak*. When the epidemic spreads to a larger population over several countries or continents, it becomes a *pandemic* (Barreto et al., 2006).

Emerging infectious disease (EIDs)

EIDs are defined as diseases where the incidence in humans has increased within the past two decades or threatens to increase in the near future (van Doorn, 2014). An EID appear in a population for the first time, may have been present previously but was undetected, or has existed previously but is rapidly increasing, either in terms of the number of new cases within a population or in its spread to new geographical areas (WHO, 2014).

Zoonotic disease

This is disease spread from animals to humans. Pathogens (organisms that cause disease) include viruses, bacteria, parasites, fungi and helminth worms. The majority of known human pathogens are transmitted to humans *zoonotically*, i.e. being passed from an animal reservoir to human populations (van Doorn, 2014). Approximately 60% of all infectious diseases, and about 75% of EIDs that have affected people over the past three decades are zoonotic infections (WHO, 2014).

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1. Introduction

People have always had a close relationship with the natural environment given that it provides us with the food, water, air, land and other resources for our various social, economic, cultural, and political activities. Over the centuries, this relationship has become increasingly complex and obscure as we have learnt to reorganise and control the natural environment in ways designed to support economic growth, human life and health. Indeed, in the last 100 years, restructuring of landscapes has accelerated at an unprecedented global scale whereby: 1) industry value chains are distributed across nations according to natural resource endowments, looser regulatory environments, cheap labour, and sites of knowledge and ideation; as well as, 2) a level of urbanisation which now sees a greater number of people living in cities than adjacent rural or remote communities. Increased exploitation of natural habitats has led to widespread environmental degradation, loss of biodiversity, pollution of air, land and water, scarcity of resources and accelerated global climate change.

The global integration of society, economy and governance and the intensifying speed with which it has progressed since the 1970s is the result of ever-faster technological advancements. The result of these global processes has been an increasing **separation of the human self from its environment**, particularly in urban settings. There has been a growing physical and emotional disconnection from the lands, waters and seas that are cultivated, managed and harvested to supply food and other resources. Increasing *per capita* consumption is driving rapid land use change and land degradation in many parts of the world, and the global integration of markets also means that environmental impacts are now economically linked across spatial locations. In the worst-case scenario that COVID-19 has highlighted, the strong economic integration of product value chains can lead to a 'butterfly effect' where a seemingly innocuous consumption choice or action in one small part of the world can lead to devastating consequences at a global level.

“COVID-19, may this moment serve as a wake-up call to our collective capabilities and as an opportunity to renew our understanding of the cost of inaction in the face of our climate crisis”

(Coates et al., 2020)

COVID-19 has shattered the illusion of separation or insulation of people from the global environmental impacts caused by their own local consumption or production patterns. While the circumstances surrounding the emergence of the virus are unclear, it is only the latest in a long line of pathogens that have spilled over from animal to human hosts - facilitated by human activity in both the Global North and the Global South. Experts in public health and environmental conservation have warned that COVID-19 is but *the tip of the iceberg* for the novel viruses that could

emerge under a business-as-usual approach to landscape and wildlife exploitation (Beer, 2020, Vidal, 2020). A recent global synthesis report from the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES) on land degradation provided evidence that transforming natural ecosystems to landscapes dominated by human use increases the risk of novel diseases transmitted between wild animal hosts and people (IPBES, 2018). Outbreaks of COVID-19 in over 200 countries have now **personalised** the impacts of environmental degradation *throughout the world*, potentially providing a turn towards more socially, economically and environmentally sustainable ways of production, consumption and landscape management.

This review paper aims to conduct a comprehensive meta-study of the intersections between land use, environmental degradation and climate change in an era with increasing risk of novel diseases that have the potential for serious consequences on human health and society. It will provide examples of how current, dominant modes of economic growth that deprioritise environmental protection have led to higher risk of future pandemics, highlighting and recommending the urgent need for change within our everyday environments.

2. Steps in the ‘zoonotic spillover’ process

The factors and mechanisms that affect the emergence and persistence of zoonotic diseases, and the transmission of pathogens from animals to humans (or *zoonotic spillover*) are complex and still poorly understood (Karesh et al., 2012, Plowright et al., 2017). In this section, we summarise the best available evidence of the various stages of zoonotic spillover, which provides information on potential critical intervention points to prevent future disease outbreaks. The majority of EIDs originate in animals, mostly wildlife, and their emergence often involves dynamic interactions among species of wildlife, livestock, and people within rapidly changing environments (Wolfe et al., 2007).

The major hosts¹ of zoonotic diseases transmittable to people include bats, primates, rodents, insects, snails, and domesticated animals. Generalist species that thrive in human-modified habitats (such as rats, mice and many species of mosquitoes) can be an important source of zoonotic pathogen transmission (Becker et al., 2015, Johnson et al., 2020, Mendoza et al., 2020). Bats host a particularly diverse range of viruses (including coronaviruses), and their ability to fly has aided in rapid virus dispersal (Morse et al., 2012, Philbey et al., 2008, Plowright et al., 2008). Primates and humans share substantial genetic similarities, facilitating zoonotic spillover. Mammal species with large global populations (for example, common and domesticated species) pose a higher risk of virus spillover into human populations than rarer species (Johnson et al., 2020). The hunting and trade of wild animals, and loss of habitat have increased opportunities for animal–human interactions and in turn facilitate zoonotic disease transmission.

¹ Disease host animals are also known as vectors.

There are multiple barriers impeding the flow of a pathogen from a reservoir host to a recipient host. Spillover can only occur when gaps align in each successive barrier within an appropriate window in space and time (Plowright et al., 2017). Ecological, epidemiological, and behavioural factors influence the exposure of pathogens to human populations. There are also several factors affecting an individual's susceptibility to infection. Understanding the barriers and changing environmental or social conditions through the stages of disease emergence could lead to substantial reductions in the risk of zoonotic disease progressing to a pandemic (Plowright et al., 2017).

Figure 1 illustrates how a spillover event can transition to local disease emergence and through to a pandemic. In the **pre-emergence phase**, a pathogen is still in its natural reservoir (Morse et al., 2012). Interactions between *pathogen diversity* or 'richness' (Brierley et al., 2016) and *pathogen pressure* (the amount of pathogen available to the human host at a given point in space and time (Plowright et al., 2017), will affect opportunities for zoonotic spillover. In the **localised emergence phase**, opportunities for transmission to humans depend on the extent of *pathogen exposure* due to an initial spillover of a wildlife or livestock pathogen to humans. This is a function of the likelihood, route, and dose of exposure of human, host and vector behaviour (Plowright et al., 2017). Exposure can occur through handling, preparation and consumption of butchered wildlife, exposure into wildlife markets or livestock farms, and through vectors such as mosquitoes. Once exposure has occurred, the *probability of infection* will depend on genetic, physiological and immunological attributes of the recipient human host (Plowright et al., 2017). Together exposure and probability of infection determine localised establishment. Finally, sustained person-to-person transmission and large-scale spread may lead to the **pandemic emergence phase** due to global air travel or international trade.

Figure 1: Emergence of pandemic zoonotic disease



Stage 1 is a pre-emergence state, where microbes are transmitted between animal reservoirs. Disturbances to the ecology of these populations (e.g. due to land use changes) shift the dynamics of microbial transmission, heightening the risk of pathogen spillover to other non-human wildlife or livestock hosts. Stage 2 is localised emergence in the human population through self-limiting spillover events. Stage 3 enters sustained person-to-person outbreaks, international or global spread, and the emergence of a true pandemic. The size, spread, and potential effects of spillovers increase from stage 1 to stage 2, but their falling frequency means pandemics are rare. A more structured approach to pandemic prevention is possible by analysing this process and underlying drivers of spillovers and spread. The ultimate goal of pandemic prevention is to remain in stage 1.

Source: Adapted from Morse et al. (2012)

Disturbing areas of high biodiversity (and hence potentially high levels of virus richness) increases the risk of pathogen exposure and EID transmission because they serve as a source pool for new pathogens (Gibb et al., 2020, Keesing et al., 2010). As such, land use changes and encroachment on natural habitats has meant human contact occurs with previously undisturbed pathogen pools (Murray and Daszak, 2013, White and Razgour, 2020). This may drive new patterns of infectious disease exposure by: (1) altering habitats, which affects either the density or presence of pathogens²; (2) altering exposure pathways; (3) changing the genetics of pathogens; (4) changing life cycles of pathogens and vectors; and, (5) affecting species composition within a community of organisms (Myers and Patz, 2009). Additionally, growth in livestock populations allows further opportunities for zoonotic spillover. Finally, the increased potential for interactions among species that have previously not been in contact modifies the dynamics of pathogen transmission among wildlife, promotes cross-species transmission, and increases the risk of endemic infections (Patz et al., 2004).

The threat of zoonotic spillover will increase as human populations continue to expand into pristine and potentially virus-rich habitats, particularly in tropical hotspots (Brierley et al., 2016). Therefore, reducing anthropogenic activity and resource exploitation in regions of high biodiversity will mitigate zoonotic disease risks. The transmission path of Ebola is an example of how spillover can occur in disturbed, biodiverse habitats (see Figure 2, and Appendix 1).

Figure 2: The transmission path of Ebola virus



Source: Adapted from CDC (2016). From <https://www.cdc.gov/vhf/ebola/resources/virus-ecology.html>

² A clear example of altering habitats is the creation of bodies of standing water through irrigation and reservoirs, which can harbour water-borne disease and promote mosquito breeding.

3. Climate change and emerging infectious diseases

Climate change has complex effects on the three elements required for the transmission of EIDs: pathogens, hosts, and the environment. Climate change, along with land use and societal change, is an important driver for the emergence of some parasitic and vector-borne diseases (Short et al., 2017, Sweil et al., 2020) (see Table 1 for some selected examples). Climate change can influence EIDs over timescales ranging from days to decades, from one extreme weather event, through to long-term shifts in the geographic distribution of pathogens and their hosts. Climate change compounds the risks associated with EIDs and challenges global populations on how to mitigate EID outbreaks and transmissions.

Global climate change is expected to increase the frequency and magnitude of tropical cyclones, floods and droughts in many regions of the world (Seneviratne et al., 2012). Flooding and cyclones have been linked to local outbreaks of cholera, typhoid, filariasis, leptospirosis, malaria, Ross River virus, and dengue fever (Wu et al., 2016). Heatwaves and droughts have been linked with outbreaks of Hantavirus, St Louis encephalitis, Chikungunya fever and West Nile virus (Wu et al., 2016). As climate change accelerates, increasingly frequent and severe natural hazards will magnify the potential for infectious disease transmission.

Climate change is altering seasonal patterns and extremes in temperature, rainfall, humidity, wind and sunshine. In turn, these changes can affect the survival, dispersal and reproduction of pathogens (Wu et al., 2016). Diseases hosted by cold-blooded animals such as insects and snails respond to climatic conditions. For example, warmer weather in New Caledonia led to an outbreak of dengue fever as female mosquitoes carrying dengue virus drew more blood to fuel their reproductive cycle, which had been accelerated by higher temperatures (Teurlai et al., 2015). Ebola outbreaks have been associated with rapid changes in humidity at the end of wet season (Alexander et al., 2015). On the other hand, increased temperature and heavy rainfall associated with climate shifts have also led to decreased survival of the mosquitoes that host dengue fever, malaria, yellow fever and West Nile fever in specific locations (Wu et al., 2016). There will be substantial variation (and uncertainty) around how the effects of climate change play out for different EIDs in different regions of the globe. This is in part because there are complex temperature-driven processes that affect the population dynamics and survival of both pathogens and hosts (Lafferty and Mordecai, 2016, Mordecai et al., 2019).

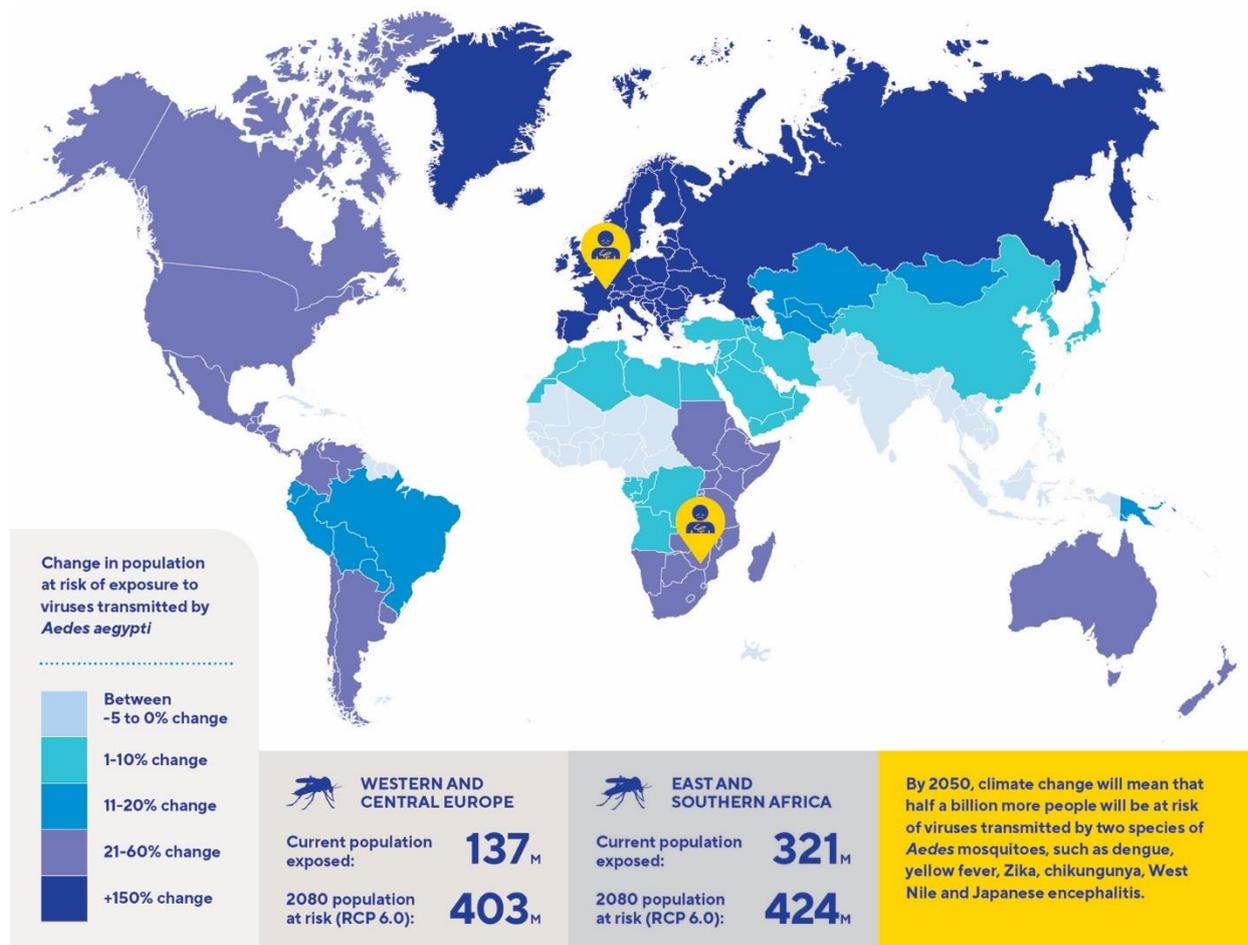
Climate change will alter the geographic distribution of pathogens and hosts. This may increase the areas affected by particular diseases, putting people at greater risk of contracting an EID - as has been shown by expansion of the range of West Nile Virus with increased temperatures in Europe and North America (Paz, 2015). Indeed, vector-borne diseases such as malaria, African trypanosomiasis, Lyme disease, tick-borne encephalitis, yellow fever, and dengue fever have expanded ranges with increased temperatures (Nava et al., 2017). *Aedes* mosquitoes are temperature sensitive, and carry viruses that cause diseases including dengue and yellow fever. Recent modelling has indicated that two *Aedes* species will greatly expand their range under global climate change scenarios, putting at risk half a billion more people by 2050 (Ryan et al., 2019; see also Figure 3).

Table 1: Selected examples of disease outbreaks linked with land use change and/or climate change

Disease and transmission	Relationship to land use change and climate change
<p>Buruli ulcer Caused by environmental bacteria <i>Mycobacterium ulcerans</i>, entering the body through skin puncture such as insect bite</p>	Deforestation coupled with agricultural or urban intrusion linked with greater Buruli ulcer disease occurrence in French Guiana (Morris et al., 2016). Nutrient enrichment in coastal developments caused a surge in disease occurrence in coastal Victoria and Queensland, Australia (Johnson et al., 2007, Veitch et al., 1997).
<p>Ross River virus Alphavirus hosted by marsupials, other mammals and birds, transmitted to humans via mosquitoes</p>	Land degradation (through dry land salinity) increases the vector-borne risk for Ross River virus in south west Western Australia (Carver et al., 2009). Creation of wetlands, reclamation or incorporation of coastal wetlands into residential developments is associated with the disease moving into urban areas (Brokenshire et al., 2000) and involving urban adapted wildlife hosts (Boyd et al., 2001).
<p>Ebola virus Filovirus thought to be hosted by fruit bats, transmitted to humans via infected animals, meat or contaminated fruit</p>	Ebola virus disease outbreaks linked with bushmeat consumption (Alexander et al., 2015), deforestation (Fahr et al., 2006), and land use change (Wallace et al., 2014). Ebola outbreaks are correlated with a sharply dry end to the rainy season, potentially leading to increased infections within reservoir species or greater human contact with reservoir species (Pinzon et al., 2004).
<p>Dengue fever Flavivirus hosted by humans, transmitted principally by mosquito <i>Aedes aegypti</i></p>	An association between increased temperature and higher incidence of dengue fever noted in New Caledonia (Teurlai et al., 2015), Thailand (Watts et al., 1987) (Watts et al., 1987), and Brazil (Barcellos and Lowe, 2014). El Niño Southern Oscillation (ENSO) events have been linked with dengue outbreaks in several countries (Morin et al., 2013). Increased incidence of dengue fever was associated with flooding and higher river levels in Bangladesh (Hashizume et al., 2012).
<p>West Nile virus Flavivirus hosted by birds, transmitted to humans by mosquitoes, principally <i>Culex</i> species</p>	Increased incidence of West Nile virus is associated with dry weather and drought (Wang et al., 2010). Low rainfall enhances the infection rate of West Nile virus (Paz, 2015).
<p>Zika Flavivirus hosted by humans and other primates, transmitted to humans via mosquitoes, principally <i>Aedes aegypti</i></p>	Zika virus outbreaks in Brazil have been associated with urbanization or deforestation, which likely favour the habitat of the mosquito vector (Ali et al., 2017).
<p>Hantavirus Hantavirus hosted by rodents, transmitted to humans via aerosolisation of rodent droppings, urine and saliva</p>	Hantavirus outbreaks have been linked to increased contact between rodent reservoirs and people in rapidly urbanizing and deforested rural areas (Pinto Jr et al., 2014).
<p>Hendra virus Paramyxovirus hosted by fruit bats (also known as flying foxes), transmitted to humans via horses)</p>	Horse farms established in fruit bat habitat. Changed virus ecology following urbanisation of fruit bats as natural habitat degraded and lost (Plowright et al., 2008, Field et al., 2001).
<p>Menangle virus Paramyxovirus hosted by fruit bats, transmitted to humans via pigs</p>	Intensive piggery established in fruit bat habitat. Urban acclimation of fruit bats, and deforestation may play a role (Philbey et al., 2008).

Source: Adapted from Wu et al. (2016) and Nava et al. (2017)

Figure 3: Regional increase in population exposure to viral diseases carried by *Aedes* mosquitoes under one future climate change scenario



The map models change in the proportion of population exposed to *Aedes aegypti* using global climate projections under Representative Concentration Pathway (RCP) 6.0. RCP 6.0 is the higher of two mid-range projections developed by the Intergovernmental Panel on Climate Change (IPCC) in 2014. RCP 6.0 assumes emissions continue to rise until around 2060 and then decline. Text in the yellow box refers to combined exposure to *Aedes aegypti* and *Aedes albopictus*. Regions are the same as those used in the Global Burden of Disease Study (<https://www.thelancet.com/gbd>).

Source: Adapted from Ryan et al. (2019)

Climate change will shift the distribution of many mammals, increasing the chances of first encounters between different mammal species that have not previously shared viruses (Carlson et al., 2020). Novel viruses crossing between species (for example, from bats to primates, civets, or horses) is associated with the emergence of diseases such as Ebola, SARS-CoV, and Hendra virus (see Appendices 1, 2 and 3).

Climate change will compound the effects of pandemic diseases. With millions of individuals infected worldwide, COVID-19 has already overwhelmed healthcare infrastructure in several countries, disproportionately affecting already-vulnerable people (Coates et al., 2020). Compound risks from climate change will exacerbate the unfolding economic crisis and long-standing socioeconomic and racial disparities, both within countries and across regions, putting specific marginalised populations at heightened risk and compromising recovery (Phillips et al., 2020).

The impacts of climate change could result in mass migration to regions of lower risk, exacerbating population pressure and habitat degradation of natural habitats in regions experiencing an influx of people. For example, the World Bank has estimated that 143 million people may be forced to move within their own countries by 2050 in South Asia, Sub-Saharan Africa and Latin America due to slow-onset climate impacts (Rigaud et al., 2018). Such internal and even international movements may, in turn, prompt domestic policy responses that would further widen the gap between communities with diverse experiences of the impact of climate change.

4. Land use change and EIDs

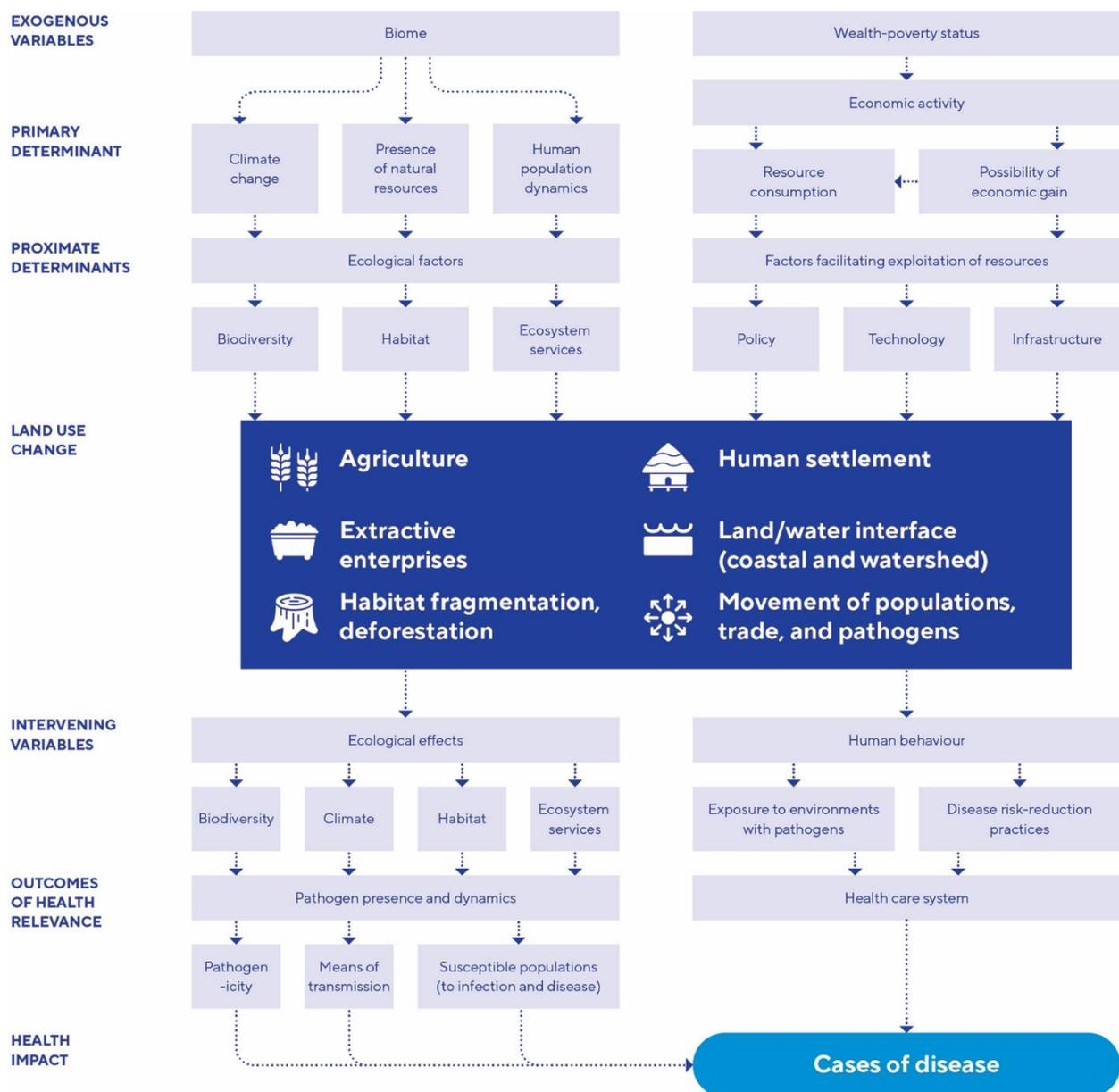
Large-scale, unprecedented human-induced and ecological factors have driven the accelerating deterioration of the natural environment (Reid et al., 2005). The subsequent depletion of ecosystems that occurs as a result is a major threat to public health[‡] (Gibb et al., 2020, Myers and Patz, 2009, Frumkin et al., 2008). Climate change and land-use change are major drivers of this depletion process, acting independently and in concert to increase EID risks. Table 1 provides a number of detailed examples linking particular EIDs with land use change and climate change.

The links between land use change, climate change, and disease emergence are typically complex, with multiple interactions and feedbacks. For example, a network of cascading events from global to local scale influenced the emergence of the Hendra virus in Brisbane, as depicted in Figure 4 (see Appendix 3 for detailed case study). Land clearing for agricultural and urban expansion not only led to habitat loss for fruit bats, but it also increased the availability of exotic fruit in urban areas and peri-urban areas, which attracted hungry bats into areas that were also home to domesticated animals. Hendra virus was transmitted to horses via bats, and then to humans, leading to an outbreak of Hendra virus in the City of Brisbane, Australia (Mahalingam et al., 2012, Marsh and Wang, 2012).

The Hendra virus is an interesting example of how disease outbreak occurs not just in the typified area of deforestation and agricultural encroachment, but in the everyday suburbs of a large metropolitan city in a wealthy economy. It solidifies the urgency to better understand the impact of human activity as a global whole, in that disease outbreaks are not limited to 'other' places with limited health infrastructure, limited regulation of industry practices or lower wealth. Patz et al. (2004) outlined a useful model in visualising the complex ways in which land use change, climate change and socio-economic factors and human behaviour can influence disease transmission (see Figure 5).

[‡] Major threats to public health linked with ecosystem degradation include emerging infectious diseases, food scarcity, water scarcity, natural disasters, and population displacement (Myers and Patz, 2009).

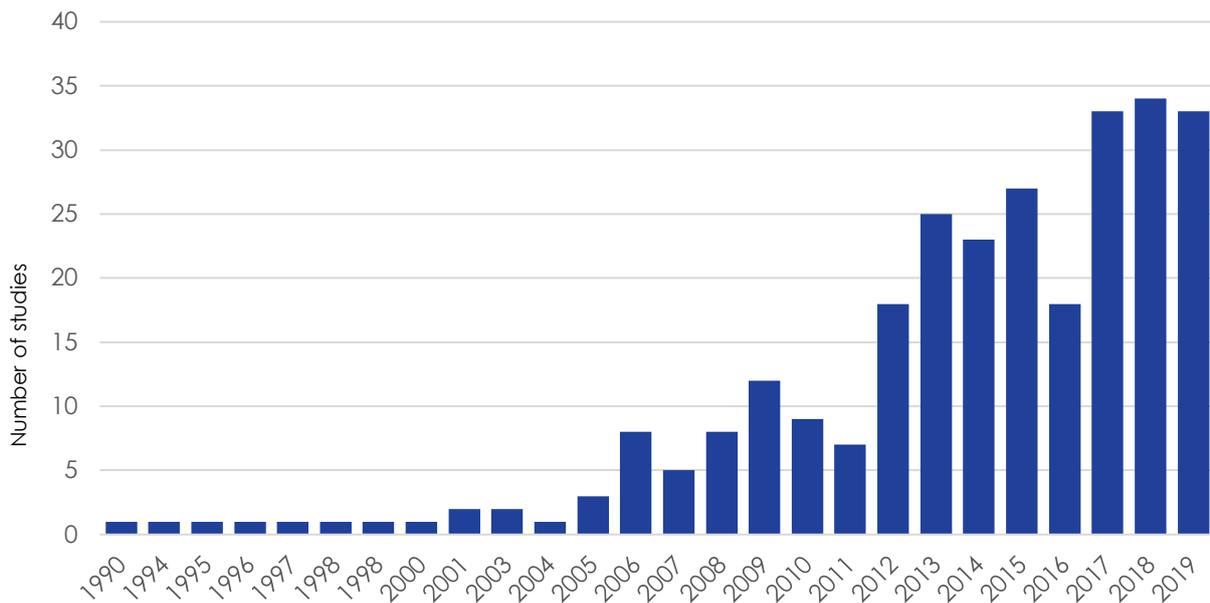
Figure 5: Environmental, social and economic drivers of cases of infectious diseases



Source: Adapted from Patz et al. (2004)

Researchers have devoted increasing attention to the ways in which land use change is driving the emergence of infectious diseases (see Figure 6), with exponential growth in publications on this topic since the turn of the millennium. Spikes of research interest occur in 2006 (aligning with H5N1 or avian influenza outbreak), 2012-2015 (aligning with Ebola outbreak), and then in 2017-2019 (aligning with a variety of more severe influenza viruses; see Mackay and Arden, 2017). The COVID-19 pandemic has thrust some of this research into the global media spotlight, highlighting the clear links between the degradation of natural habitats and the rise of novel diseases.

Figure 6: Annual increase in peer-reviewed publications on land use change and zoonotic disease spread, 1990-2019



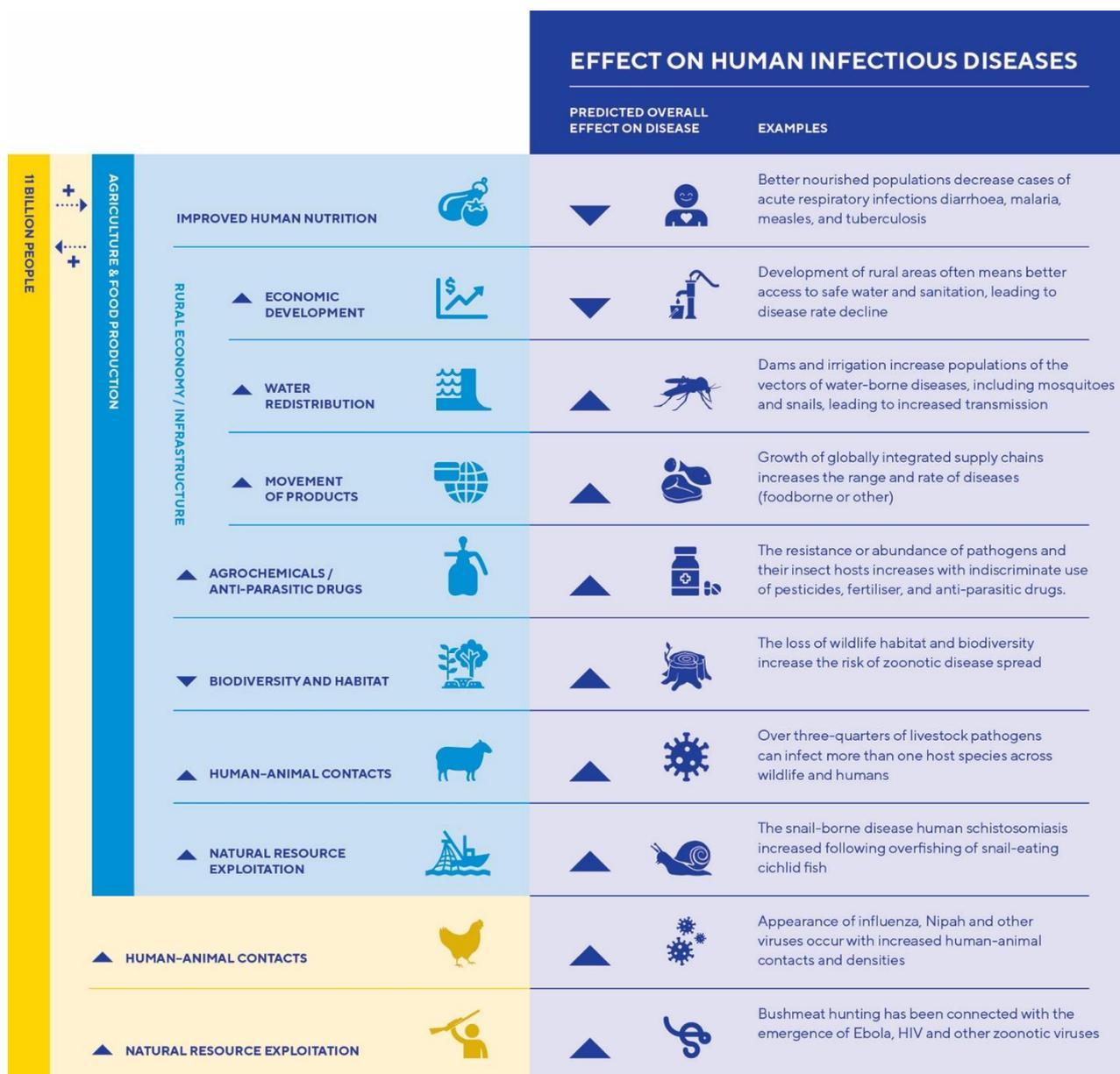
Source: Adapted from White and Razgour (2020)

A comprehensive review by White and Razgour (2020) showed that most of the studies on land use change and zoonotic disease emergence were undertaken in areas where urbanisation drives conversion of natural habitat. In urban areas, rodents, carnivores and birds were among the most commonly named disease vectors. Specifically focussing on land use change, research on agricultural intensification was largely associated with domestic livestock as disease reservoirs, while research on deforestation highlighted links with arthropods, rodents, primates, bats and other species as zoonotic disease vectors. A recent meta-analysis by Gibb et al. (2020) demonstrated that areas with substantial human presence (such as agricultural and urban areas) have higher disease host species richness and abundance than nearby undisturbed habitats.

The locations where deforestation occurs, and where exotic zoonotic diseases emerge might appear to the average city dweller as removed from where they live, and distant from their lives. In reality, the drivers for land use change are complex and often intertwined with consumer demand and production networks stretching across the globe. For example, the extensive clearing of tropical forests in Indonesia for oil palm plantations is the result of global demand for palm oil which is used in items ranging from chocolate to cosmetics to biofuel[§]. Fragmentation of tropical forest habitat puts pressure on wildlife, which may come into more frequent contact with humans and livestock – all factors that may amplify the potential for spillover of a novel or emerging disease. Such perturbations are not limited to any particular agricultural land use. Figure 7 provides a graphical overview of the complex interactions between population health and agriculture.

[§] See [information on palm oil products](#).

Figure 7: Example of the complex interaction of factors impacting EIDs, agricultural and food production industry



Source: Adapted from Rohr et al. (2020)

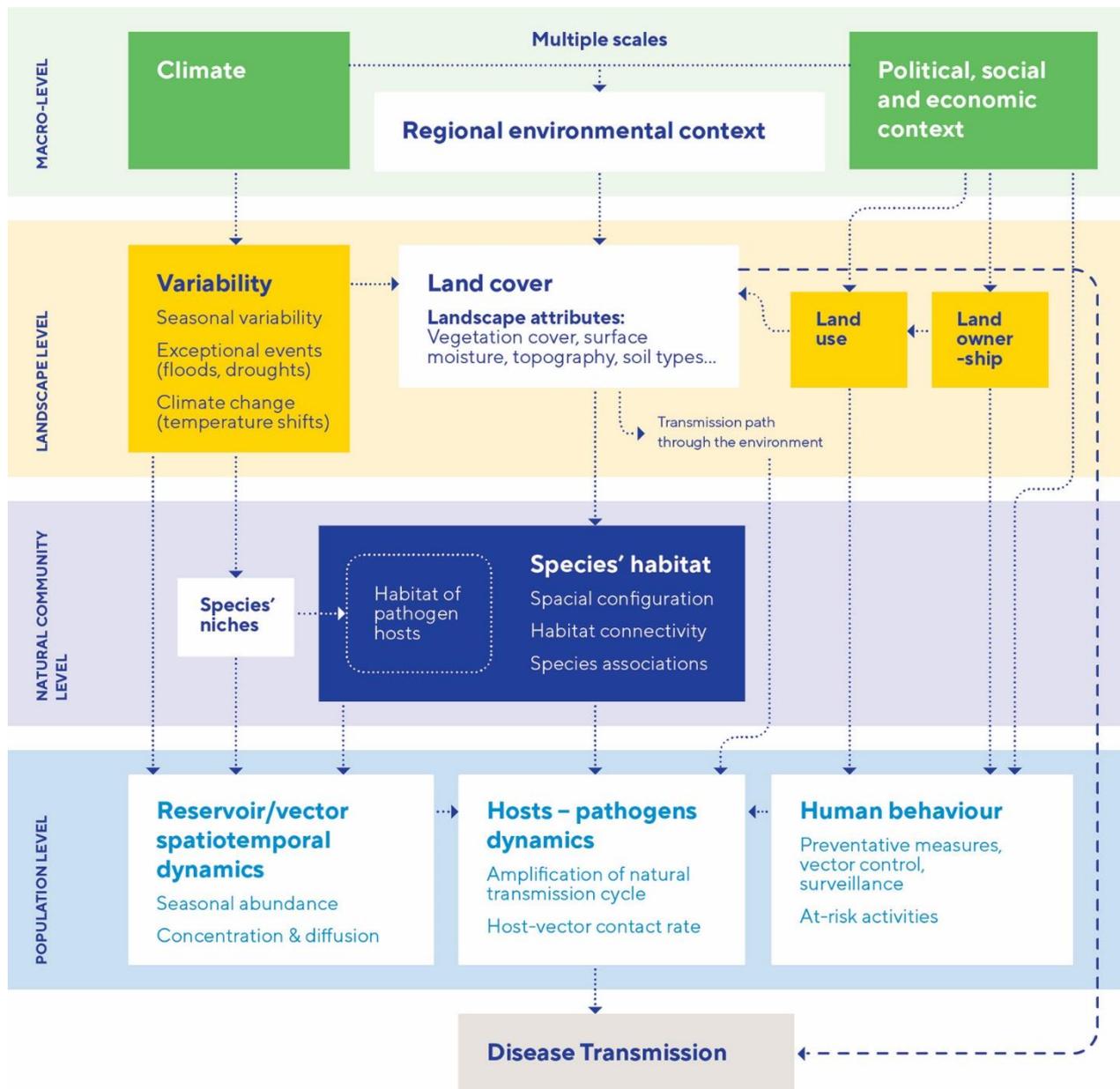
5. Spatial patterns in EIDs and disease transmission

Geography helps to explain the spatial patterns associated with disease emergence and spread, particularly in relation to climate and land use change. For example, the linkages between biodiversity loss and EIDs are apparent in regions where there are relatively large areas of intact vegetation cover. Studies examining disease transmission through animals identified tropical regions as risk hotspots (Allen et al., 2017), particularly where wildlife biodiversity is high. This risk is elevated where there are many mammal species. Many of these regions are also experiencing intense land-use change and increasing human activity (Carlson et al., 2020), a primary factor in accelerating the rate of animal and human interactions.

Identifying regions that are at high risk of EIDs due to particular combinations of wildlife biodiversity, habitat fragmentation and loss, land use, human population density, and economic activities is pivotal in order to alter land management practices or limit exposure for high-risk populations (Allen et al., 2017). This is not simply a problem to be dealt with only by people living in these at-risk regions, given the strong relationship of land use changes (e.g. deforestation for wood or to plant alternative crops) in tropical areas with global supply chain demand. Indeed, places where new diseases emerge appear to have particular vulnerabilities, such as loose environmental regulatory frameworks and limited access to health care services, which may work to inhibit disease transmission. This increases the likelihood of disease outbreaks and the potential for global transmission. Nonetheless, there are many cases where outbreaks have occurred but are not transmitted regionally or globally (such as Hendra virus outbreaks in Australia, see Section 4 and Appendix 3). As such, the occurrence of a disease outbreak does not mean there will be an epidemic or a pandemic. We can understand areas of particular vulnerability by looking firstly at the spatial patterns of EIDs, and then patterns of disease spread.

National and/or regional governance systems are a key determinant of the capacity of different jurisdictions to contain or dampen disease spread once an outbreak has occurred, as has been highlighted with the varying national and intra-national responses to COVID-19. Nonetheless, mitigation of a combination of factors across different spatial levels decreases the likelihood of a pandemic for highly infectious diseases. Lambin et al. (2010) related disease transmission to four spatial levels (individual population, larger community, environmental landscape, and macro or global spatial levels) in their conceptualisation of pathogenic landscapes. As adapted in Figure 8, their model highlights the complex interactions across and between spatial levels for disease emergence and transmission, highlighting the influence of unique individual national, regional and local contexts.

Figure 8: Determinants of disease transmission at various spatial levels



Source: Adapted from Lambin et al. (2010)

Research has attempted to better understand which regions of the world are most vulnerable to EIDs, either because they are impacted by climate change or where it is most likely that either disease hosts, or novel combinations of potential disease hosts, will be in contact with human beings. Using a modelling approach based on climate change projections, the hotspots of potential future cross-species virus transfer are concentrated in areas of high biodiversity, high human population density, and high elevation, and include southeast Asia, southern China, and the Caribbean region (including southeastern USA) (Carlson et al., 2020). Rodents, bats, and birds are among the common disease hosts that also tend to be more abundant in agricultural, urban, and disturbed habitats (Gibb et al., 2020).

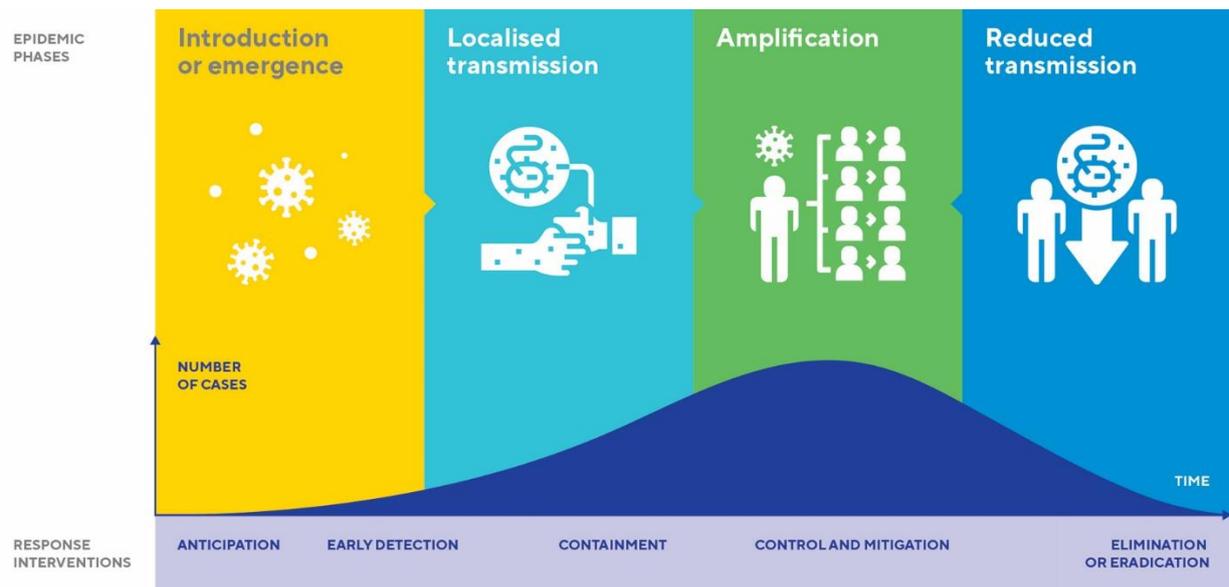
As such, the geographic spatial patterns of EIDs can be largely related to regions of the world where humans come in close contact with wild animals (cf. Carlson et al., 2020). This is driven by three key factors. Firstly, climate change where significant changes in wild animal habitat means species move to new areas. Secondly, land use changes where animal habitats are destroyed in favour of industry or urbanisation, leading populations to search out new habitats. Thirdly, human transportation of wild species into urban areas, where consumer demand (e.g. for medicinal or other purposes) brings new species together in marketplaces. The bringing together of species presents new and novel opportunities for viral sharing, the emergence of new disease strains, and facilitates disease transmission to humans.

The spread of EIDs depends largely on a complex range of human driven factors, producing local vulnerabilities which are exacerbated by climate change. These local vulnerabilities relate to the incumbent socio-economic and governance systems (Lindgren et al., 2012). For example, the degree to which regional public health systems are equipped both to prevent and/or dampen the emergence and transmission of disease, including levels of antimicrobial resistance, health care capacity, animal health, and food safety. Social and demographic factors also play a role in avoiding and/or containing outbreaks, and include factors such as population aging, inequality, poverty, and life-styles (Lindgren et al., 2012). Indeed, disease and infections often have a greater toll on elderly persons, while socially disadvantaged cohorts of a community may have lower to no access to health or social services (Quinn and Kumar, 2014).

As such, some parts of the community may be more severely affected by disease outbreaks than others, including individuals who work in occupations that put them at higher risk of exposure. Further, communities where there is a lack of governance and coordination across government and community sectors will also be at greater risk. The way in which the current COVID-19 pandemic has unfolded in the United States of America, Brazil and India (ABC News, 2020) exemplifies this point. Figure 9 illustrates the phases and responses of disease intervention, which if not properly carried out at any stage place regions at risk of disease outbreaks.

Disease transmission or containment can be largely contributed to lifestyles which connect far places to a greater extent and more intensively than ever (Parodi and Liu, 2020). For example, travel, migration, and global trade (Lindgren et al., 2012) made Italy a hot spot for Chikungunya Fever in 2007, being initially endemic to western Africa and later found in tropical and subtropical regions. The outbreak reported in Northern Italy was a result of international travel from Southeast Asia and Indian Ocean Islands (Spengler et al., 2012, Rezza et al., 2007). Similarly, international travel was linked to the first local transmissions of dengue fever in France and Croatia in 2010, and SARS in Canada in 2003 (Schaffner et al., 2013). Figure 10 highlights the rapid global distribution of cases and deaths occurring over an eight month period across 2002 and 2003. Whereas the spread of H5N1 avian influenza to the western hemisphere was more connected to global trade in poultry (with subsequent spread through migratory birds; Plowright et al., 2008).

Figure 9: Epidemic phases and response interventions



Source: Adapted from WHO (2018)

Figure 10: Global distribution of SARS cases, November 2002 to July 2003

774 deaths reported | November 2002 – July 2003



Source: Adapted from Agence France-Press (2020), source data from World Health Organisation.

H1N1 swine fever has received special attention from the European Commission given the outbreaks in the European Union in 2014 (See Appendix 4). Within the European region, the disease first emerged in Russia and Belarus and continued to spread. By the end of 2019, the disease was present in nine EU countries. A risk assessment on the potential spread of the disease in southeastern countries of Europe including all disease free countries revealed that the estimated probability of spread within one year to be very high (66% - 100%). The identified potential risk factors were related to domestic pig populations, wild boar populations, connectedness of the area in terms of trade of pigs and pig products, societal context including consumption of pork and the disease preparedness and response activities (Nielsen et al., 2019).

6. Conclusion

Current global evidence overwhelmingly shows that changes in land use, land degradation, and climate change heighten the risks of emerging infectious diseases. In a connected world, the consumption and production decisions in one region have potentially devastating consequences for everyone, everywhere. The COVID-19 pandemic has demonstrated how global linkages, both in terms of consumption impacts and the spread of EIDs, and mismanagement of the environment can lead to dire outcomes for humanity. While the pandemic is a tragedy, it has provided pause for humankind to consider the link between individual consumption decisions, economic structures, and environmental and health consequences. It has raised questions regarding future pathways of socio-economic interaction and planetary governance. In the context of strong evidence of connections between climate change, environmental degradation, land use change and zoonotic spillovers, we much learn from the impact of COVID-19 to shift to a new trajectory.

7. References

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APPENDICES

APPENDIX 1: Case study 1 – EVD (Ebola virus disease)

The Ebola virus was first identified in 1976 in two simultaneous outbreaks, in Nzara, South Sudan, and in Yambuku, Democratic Republic of Congo (DRC) (WHO, 2020a). Ebola cases have been reported in Central Africa (principally DRC, Congo, Gabon, Uganda and South Sudan), and West Africa (principally Guinea, Sierra Leone and Liberia). A large outbreak occurred in 2014-2016 in West Africa, killing more than 11,000 people (CDC, 2019). Estimates of economic losses for the three countries most affected by the 2014-2016 epidemic ranged between US\$2.8 to \$32.6 billion (CDC, 2016). The virus spread to seven more countries: Italy, Mali, Nigeria, Senegal, Spain, the United Kingdom and the United States. There have been 10 outbreaks in the DRC, most recently 2018-2020 (CDC, 2020).

The virus is transmitted to people from wild animals and spread through human-to-human transmission (WHO, 2020a). The initial case for the 2014-2016 outbreak was an 18-month-old boy from a small remote village in Guinea. The toddler was seen playing near a hollow tree and was believed to have been infected by bats. Humans are infected with Ebola either through contact with bodily fluids of infected animals or humans, or through other means such as consumption of bushmeat, caring for patients, or preparing the deceased for burial.

Ebola outbreaks are linked with human activity, deforestation and forest fragmentation which brings humans into close contact with fruit bats and other infected mammals. The main drivers for forest clearance in the Central African Congo basin are small scale agriculture and large scale logging (Tyukavina et al., 2018). In the Guinean forests of West Africa, palm oil, cocoa and rubber plantations were the reasons for rapid deforestation (Carr et al., 2015). Recent research highlighted five species of fruit bats particularly attracted to human activities, such as agriculture and habitat fragmentation. Four of these species have been serologically linked with the Ebola virus (Olivero et al., 2020). Therefore, preventing loss of forests could reduce the likelihood of future outbreaks.

Apart from the availability of an effective vaccine, disease containment within Africa was challenging due to the high mobility of people, difficulty in identifying in the early-stage disease patients, locals' reluctance to seek support due to mistrust, lack of decentralised health support systems and regional violence due to civil conflict (Drake, 2019). The 2018-2020 Ebola outbreak in DRC was contained with a coordinated effort led by the DRC Government and Ministry of Health, the World Health Organization (WHO) and partners, donors, UN partner agencies, national and international NGOs and research networks (WHO, 2020b).

APPENDIX 2: Case study 2 - SARS (severe acute respiratory syndrome)

SARS is an acute respiratory illness that emerged in November 2002 in Guangdong province, China and quickly spread to 29 other countries through international travel. SARS is caused by the SARS-associated coronavirus (SARS-CoV). There were large SARS outbreaks in Hong Kong, Taiwan, Singapore, Hanoi, Vietnam, and Canada (CDC, 2004). The virus killed 774 people between November 2002 and July 2003, most of whom were over 65 years old.

Coronaviruses are a family of viruses that infect a range of mammals and birds, and include the viruses that cause SARS, Middle East Respiratory Syndrome (MERS), and COVID-19. SARS-CoV is thought to have crossed from animals to humans through close contact, butchering, or eating undercooked meat in parts of Southern China. The suspected animal hosts of SARS are bats and civets (horseshoe bats in particular harbour SARS-related coronaviruses), although the natural animal reservoir of the virus remains uncertain (Hu et al., 2017, Li et al., 2005).

The outbreak was contained in 2003, following a policy of isolating people suspected of having the condition and screening all passengers travelling by air from affected countries for signs of the infection. The lessons from successful management of SARS have been invaluable in shaping epidemic control. The key lessons included transparent disease reporting, issuing of timely global alerts, global co-operation in international travel, collaboration of multidisciplinary scientific teams both at national and global level, identification of weaknesses in the health systems, and communication of accurate and unambiguous disease information to the public (Heymann and Rodier, 2004).

APPENDIX 3: Case study 3 – Hendra virus

The Hendra virus is endemic to Australia and spread by *pteropid* fruit bats (flying foxes). Hendra was the first recorded zoonotic viral respiratory infection transmitted from bats to horses to humans (Marsh and Wang, 2012). The bat-borne paramyxovirus was first identified in 1994 in a horse stable in the Brisbane suburb of Hendra, Queensland, killing thirteen horses (Mahalingam et al., 2012, Marsh and Wang, 2012). The majority of outbreaks impacted Australia's \$6 billion equine industry, with 104 recorded horse fatalities. An equine vaccine against Hendra virus was released in 2012, but is not widely used by horse owners because of its high cost, the perceived low likelihood of Hendra virus associated disease, and anecdotal reports of impacts on horse performance (Manyweathers et al., 2017).

Despite many pathology studies on Hendra virus, there is limited knowledge on its spillover drivers (Mahalingam et al., 2012). The natural habitat and food resources of *pteropid* fruit bats has been declining due to vegetation clearing, leading them to be drawn to urban and peri-urban areas and increasing opportunities for zoonotic spillover to humans (McFarlane et al., 2011, Plowright et al., 2011). Horses are likely to become infected through contact with pasture or feed that is contaminated with flying fox urine, faeces, birthing products, or spats (Mahalingam et al., 2012). Horse-to-horse transmission has been recorded in several spillover events, with human transmission occurring after direct close contact with infected horses. Other domesticated animals such as dogs and cats can also serve as viral hosts, providing additional spillover opportunities from flying foxes to horses.

Humans can become infected after contact with infected horses, and its high case fatality rate of significant threat to human health. Of the seven known human cases of Hendra virus outbreaks in Australia between August 1994 and July 2009, four resulted in death (Marsh and Wang, 2012). The Hendra virus causes flu-like symptoms like fever, myalgia, lethargy, headaches and vomiting. The disease then progresses to encephalitis with multi-organ failure. Hendra, and viruses of the same *Henipavirus* genus like Nipah virus**, are particularly concerning as no effective treatment is currently available (Mahalingam et al., 2012).

** Nipah virus outbreaks have been recorded throughout South-East Asia including Malaysia, Singapore, India, and Bangladesh and human-to-human transmission has occurred.

APPENDIX 4: Case Study 4 - H1N1 pandemic (swine flu)

Swine flu (H1N1) is a highly contagious respiratory infection caused by a type of influenza A virus. The H1N1 pandemic persisted for around 19 months over 2009-10. In March and April of 2009, H1N1 emerged in Mexico and the United States of America (USA). The virus was eventually responsible for killing approximately 12,000 people in the USA (Shrestha et al., 2011), and 151,700 to 575,400 people worldwide (Dawood et al., 2012). Following emergence, the virus spread rapidly, reaching 30 countries within a few weeks. In the USA, nearly 90% of deaths occurred in people under 65 years of age (Shrestha et al., 2011).

The virus was derived from several viruses circulating in pigs, and the initial transmission to humans had occurred several months before recognition of the outbreak (Smith et al., 2009). The sudden emergence of the virus provided additional evidence for the role of domestic pigs in spreading the virus and the need for systematic swine surveillance in the future (Girard et al., 2010). The development of a vaccine and improvements in surveillance systems and treatment infrastructure were the major focus of the USA during the pandemic. USA investment in global health to enhance surveillance and preparedness of other countries also helps the national interest, reducing the risk by giving forewarning of outbreaks (CSIS, 2010).

Scientists have discovered a new type of swine flu in China that is capable of becoming a pandemic, named G4 EA H1N1 (Sun et al., 2020). The G4 virus is genetically descended from the H1N1 strain that caused a pandemic in 2009 (Sun et al., 2020). Although there is no evidence of human to human transmission, the G4 virus has already passed from pigs to human and it could potentially adapt to become transmissible between humans. Therefore researchers suggest controlling G4 viruses in pigs and close monitoring in human populations, especially the workers in the swine industry, to be urgently implemented (Sun et al., 2020).