



# THE ROLE THAT NATURE CONSERVATION CAN PLAY TO MITIGATE THE SPREAD OF FUTURE INFECTIOUS DISEASES

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## Abstract.

*The emergence of infectious diseases is reviewed highlighting the potential role played by main environmental anthropogenic disturbances as, deforestation, land-use change, human-induced climate change, biodiversity loss and the illegal wildlife trade. Ultimately, it is plausible that the human impact on the biosphere could be the root cause of these emerging diseases, and that economic globalization, population growth and landscape anthropization might increase the likelihood of the emergence of novel zoonoses. This pattern bears similarities to phenomena that occurred during the Neolithic period with the emergence of agriculture and cattle domestication. Still today such phenomena could be accelerated by the vastly increased traffic of people and goods. Finally, we argue in favour of strong policies and actions aiming to mitigate the human impact on natural ecosystems as a key strategy to prevent future zoonoses.*

**Key words:** *biodiversity loss, climate change, coronavirus, deforestation, wildlife trading, zoonosis*

## 1. INTRODUCTION

In December 2019, an unusual pneumonia outbreak was reported in Wuhan, Hubei province, China (Zhou et al. 2020; Wu et al. 2020). The cause of the illness, called Coronavirus Disease 19 (COVID-19), was traced to the virus denominated SARS-CoV-2 (Gorbalenya et al. 2020). At this time (April 2021), about fifteen months after the first case was discovered, SARS-CoV-2 has infected nearly 150 million people in 192 countries, causing more than 3,000,000 deaths (Dong et al. 2020). There is a broad consensus among the scientific community that SARS-CoV-2 has a zoonotic origin, but at the date no animal intermediate host has been identified (Andersen et al. 2020), although some studies suggest that bats of the genus *Rhinolophus* would be acting as natural reservoir and the Malaysian pangolin (*Manis javanica*, Desmarest, 1822) as intermediate host (Lam et al. 2020; Zhou et al. 2020). This lack of knowledge about the necessary intermediate host did not rule out the possibility that appearance of SARS-CoV-2 could be produced by the process of virus growth un-

der laboratory iterations (serial passage; see Sirotkin & Sirotkin 2020).

With its particular genetic and antigenic diversity that makes therapeutic solutions elusive, coronaviruses pose specific challenges (Sheahan & Frieman 2020), but COVID-19 is only the latest of a growing number of emerging infectious diseases of zoonotic origins that affect humans. Zoonotic diseases are responsible for about 2.5 billion cases of infection and 2.7 million deaths every year, with substantial socioeconomic consequences (Gebreyes et al. 2014). Most of the infectious organisms that are pathogenic to humans (e.g. viruses, prions, bacteria, fungi, protozoa and helminths) have zoonotic origins (Jones et al. 2008; Taylor et al. 2001), including, Ebola, SARS, MERS, Hantavirus, HIV, Nipah virus, West Nile virus, Lyme disease and Rift Valley fever. Of all the parasite species listed as pathogenic to humans, at least 60% are zoonotic in origin (Taylor et al. 2001). However, apart from their crucial role in human disease, bacteria and viruses are intimately linked to the origin and functioning of life. Indeed, Earth may be

home to upwards of one trillion microbial species (Locey & Lennon 2016), viral genes outnumber cellular genes in the biosphere (Forterre & Prangishvili 2013), and gene transfers from bacteria and viruses may be essential to shaping multicellular organisms (Callier 2019) and vertebrate immune systems (Broecker & Moelling 2019). Hence, when we look at bacteria and viruses, we are looking at the most ancient and strongest evolutionary forces of genome dissemination in the history of life on Earth. Zoonotic diseases are thus part of human history and evolution, especially following the rise of agriculture and animal domestication and the passage from hunter/gatherer societies to sedentary or pastoralist settlements (Dobson & Carper 1996; D ux et al. 2020; Wolfe et al. 2007). Even if we do not know what was the disease emergence rates before the Anthropocene, in the last decades, as a consequence of the Homogenocene epoch (*sensu* Samways 1999) with its unprecedented globalization of human actions, zoonotic infections seem to increase (Jones et al. 2008; Morand et al. 2014).

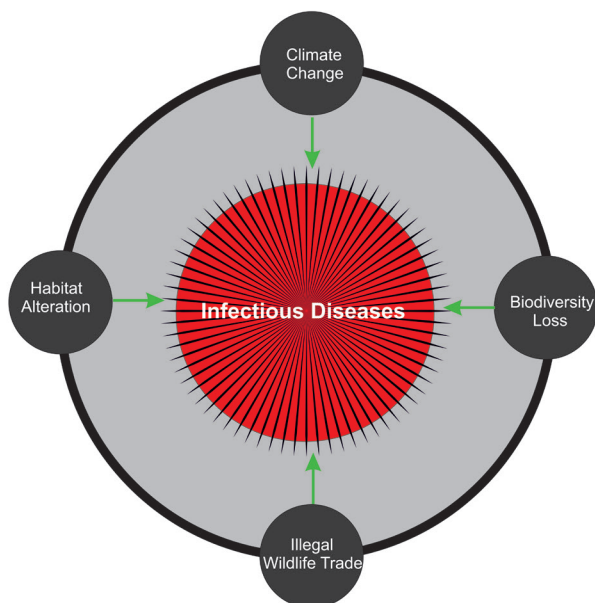
The precise emergence of a disease is impossible to predict since several factors could be involved in its appearance (Plowright et al. 2017), but it is recognized that one of the most critical causal factors is in the anthropogenic impacts on natural ecosystems and the altered human behaviours (Morse 1995; McMichael 2004; Jones et al. 2008; Jones et al. 2013; Allen

et al. 2017). It is acknowledged that many current emerging infectious diseases, such as those related to coronaviruses, are associated with anthropogenic modifications of the environment (Pearce-Duvel 2006; Afelt et al. 2018). These changes in the environment increase the likelihood of contact between wild fauna and humans and their livestock, thus increasing the risk of cross-species infection (Patz et al. 2004). Anthropogenic land use can influence disease transmission by altering vector niches, hosts, and pathogens; by changing community structures (e.g., species diversity or species composition) and the behaviour of hosts and vectors or by increasing direct contact between humans and wildlife reservoirs (Gottdenker et al. 2014). Therefore, analysing infectious diseases in the light of ecological and evolutionary theories is of great importance for understanding mechanisms, patterns, and effects of host-pathogen interactions and the role played by environmental factors (Jankowiak et al. 2020; Sk orka et al. 2020).

Clearly, anthropogenic factors are not mutually exclusive, and their interaction can be complex, with positive, negative or neutral effects on disease emergence (Wood & Lafferty 2013). However, several empirical studies point to a direct link between anthropogenic changes and emerging or re-emerging diseases. In particular, these investigations focus on four main interconnected factors, which ultimately can be viewed as different facets of a single whole: deforestation and changes in land-use, human-induced climate change, biodiversity loss and the illegal wildlife trade.

## 2. DEFORESTATION AND CHANGES IN LAND-USE

It has been estimated that 75% of zoonotic diseases are linked to wildlife (Taylor et al. 2001). Every year, millions of hectares of forest are permanently converted for agriculture, mining or energy infrastructure (Achard et al. 2002; Curtis et al. 2018). Hence, it is not surprising that the majority of emerging infectious diseases arise in forested tropical regions which generally have a high level of mammal diversity and thus can act as disease reservoirs. Indeed, greater host richness increases the pool from which novel pathogens may emerge (Allen et al. 2017; Murray & Daszak 2013); hence, about 15% of all emerging infectious diseases have a direct link to forests (Wilcox & Ellis 2006). Deforestation can alter reservoir species or vector ecology (McMahon et al. 2018; Faust et al. 2018). When human settle-



**Figure 1.** Relationship between four interconnected factors that impact emerging or re-emerging infectious diseases.

ments and activities (i.e. agriculture and livestock production) are located on the edge of the forest, anthropized landscapes can attract animals such as bats, rodent and passerine bird recognized as zoonotic hosts (Despommier et al. 2007; Jones et al. 2013; Kettle & Koh 2014; Gibb et al. 2020). Therefore, the possibility of spatial overlap with pathogen viruses and the risk of spillover can increase significantly (Faust et al. 2018). Although forest habitat alteration and consequent changes in land-use appear to be a necessary but not sufficient factor in contributing to an increased risk of spillover (Hosseini et al. 2017), several examples underscore the role that deforestation can play in exacerbating the threat of spillover.

The Nipah virus is a paramyxovirus whose natural reservoir host is the *Pteropus* spp. fruit bat (Hyatt et al. 2004). The Nipah virus causes encephalitis and respiratory illness and has a mortality rate of about 39% (Chua et al. 2000). It emerged in 1998 in Malaysia, and its emergence is likely related to the intensification of pig farming on the edge of tropical forests where fruit bats live. Deforestation affected the fruit bat population dynamics, and the bats were attracted to the fruit trees planted around the pig farms, infecting the pigs that consumed the fruit contaminated with bat saliva and urine. The pigs, in turn, acted as an amplifier host infecting humans (Daszak et al. 2006). Malaria also shows a strong link with deforestation. In Brazil, a 10% rise in deforestation led to a 3.3% increase in malaria incidence due to the ecological alteration of *Nyssorhynchus (Anopheles) darlingi* (Root, 1926) habitats and breeding site availability (MacDonald & Mordecai 2019; Vittor et al. 2009). Ebola provides another example of how deforestation can have an impact on emerging diseases. The Ebola virus was first identified in Africa in 1976 when it caused about 13,000 deaths, with a fatality rate of about 50% (World Health Organization 2020). At that time, the natural reservoir of the Ebola virus appeared to be fruit bats with apes and monkeys acting as intermediate hosts (Leroy et al. 2005; De Nys et al. 2018; Ayouba et al. 2019). Although the use of bushmeat seems to be the primary direct mechanism in Ebola spillover (Alexander et al. 2015), deforestation also plays an important role in today's epidemics. Deforestation, indeed, can alter the virus ecology by changing the composition, abundance and behaviour of reservoir species, increasing the interface between human and animal populations and thus increasing the likelihood of exposure (Olivero et al. 2017,

2020; Rulli et al. 2017). Another essential change in land use that can act as an infectious disease driver is dam building. Although dam construction aims to increase food security and energy supplies, dams may lead to an increase in the incidence of numerous diseases, especially vector-borne illnesses, which are closely linked to wetlands. Indeed, dam projects have been shown to cause an increased incidence of multiple diseases, namely schistosomiasis, malaria, Rift Valley fever, filariasis, leishmaniasis, dracunculiasis, onchocerciasis and Japanese encephalitis (Myers et al. 2013). In the case of coronaviruses, environmental change has long been recognized as the main risk factor that can lead to new human infections. Indeed, the emergence of recent coronavirus outbreaks in Southeast Asia probably came in the wake of accelerated deforestation and land-use change in the region (Allen et al. 2017; Afelt et al. 2018). Finally, pandemic could be an indirect driver of tropical deforestation as proposed by Brancalion et al. (2020). Indeed, even if the causal linkage has to be confirmed, during COVID-19 pandemic and confinement measures, illegal and opportunistic forest clearing in tropical countries doubled compared to 2019, showing that zoonotic diseases and deforestation could be linked by feedback loops with complex consequences (Brancalion et al. 2020).

### 3. CLIMATE CHANGE ASSOCIATED WITH HUMAN ACTIVITIES

Human activities are the primary drives of global climate change leading to warmer temperatures, increased extreme weather events, the loss of ice and permafrost and changes in the biogeochemical cycles (IPCC 2013). Climate change has a substantial impact on faunal assemblages, their structure and the dispersion of their elements, which in turn can lead to infectious disease outbreaks. Such outbreaks are more likely to occur due to the altered ecophysiology of the host-pathogen interaction as well as the expanded ranges and modified population dynamics of the host (Altizer et al. 2013; Hoberg & Brooks 2015). Using mammal-virus relationships and projections of geographic ranges Carlson et al. (2020) estimate that climate change may lead to alarming population aggregations, which could increase the share of viruses and the risk of exposure to pathogens. An example of how climate change affect disease emergence can be found in the Sin Nombre Virus (SNV), a Hantavirus which causes a severe disease called Hantavirus Car-

diopulmonary Syndrome (HCPS) with a mortality rate of about 35% (Richardson et al. 2013). A natural reservoir of SNV is the deer mouse *Peromyscus maniculatus* (Wagner, 1845), which excretes virus in its urine, faeces and saliva (Childs et al. 1994). El Niño events in 1991–92 and 1997–98 increased the incidence of human infections in the Southwestern USA through an ecological cascade effect. Briefly, increased precipitation resulted in greater trophic and habitat availability for rodents, whose population density grew, producing more frequent virus transmission and host dispersal. These events were followed by a three-year increase in the number of HCPS cases in the Southwestern United States (Klempa 2009; Carver et al. 2015; Dearing & Dizney 2010; Mills et al. 2010). Another disease that is driven by climate is meningococcal meningitis, found in parts of Africa. This infection of the meninges is caused by the bacterium *Neisseria meningitides* (Albrecht & Ghon 1901) Murray, 1929, which, in the so-called African meningitis belt (sub-Saharan Africa, from Senegal to Ethiopia), causes between 7,000 to 180,000 cases annually with a mortality rate ranging between 10% and 20% (Borrow et al. 2017). The bacterium is highly contagious and is transmitted from person to person through the air via respiratory secretions. The climate has a significant effect on this disease. Indeed, upsurges in outbreaks of the disease are reported during the dry season, when hot dry air and dust may create the conditions for disease transmission by damaging the mucosal barrier and inhibiting its immune capacity (Sultan et al. 2005; García-Pando et al. 2014). Another very relevant case is dengue, one of the most important arboviral diseases in the world with an incidence that has increased 30 fold in the last 50 years (e.g. 390 million infections in 2010). Among other factors related to globalization, global warming is the most crucial driver of the current distribution and incidence of the primary dengue vectors *Aedes aegypti* (L. 1762) and *A. albopictus* Skuse, 1895 (Ebi & Nealon 2016). Although there is not a broad consensus on the effect of climate change on disease vectors, due to the complex and nonlinear relationships of the variables involved (Franklinos et al. 2019), climate change may drive arthropod-borne diseases (Patz et al. 1996, 2005). In particular, it could do so by spreading vectors in temperate and high altitude zones, bringing together organisms that were previously separated, and increasing the incidence of arthropod-borne diseases by modifying vector devel-

opment, survival, biting rates, and population density (Ogden & Lindsay 2016; Caminade et al. 2019).

#### 4. BIODIVERSITY LOSS

The current rate of species extinction is about 1000 times the natural background rate (Pimm et al. 2014), and biodiversity loss can increase the risk of pathogen spillover, especially for vector-borne diseases (Pongsiri et al. 2009; Civitello et al. 2015). Generally, vectors feed on a broad range of hosts, some of which are not very pathogen competent. Hence, in highly diverse communities, a reduction in the encounter rate between vectors and the most competent hosts may reduce the risk of disease due to a “dilution effect” (Keesing et al. 2006). On the contrary, a loss of biodiversity could increase the risk of disease due to the increased likelihood of encounters with competent hosts (Keesing et al. 2010; Jones et al. 2013). An example of increased pathogen transmission and disease incidence due to biodiversity loss can be found in the case of the West Nile virus. The West Nile virus is a mosquito-borne disease that can cause severe neurological illness in humans (Petersen et al. 2013). The natural reservoirs for the West Nile virus are birds, and passerines tend to be the most competent hosts compared to non-passerine birds (Komar et al. 2003). Several studies have found that a loss of avian biodiversity (especially non-passerine birds) is related to an increased incidence of West Nile virus in humans in the United States (Allan et al. 2009; Ezenwa et al. 2006; Swaddle & Calos 2008), corroborating the dilution effect hypothesis. Another example of increased human disease risk due to biodiversity loss regards Lyme disease, caused by a spirochete bacterium transmitted by feeding ticks of the genus *Ixodes*. If untreated, Lyme disease can cause arthritis as well as neurological and cardiac symptoms, which can persist for years even after treatments (Franz & Krause 2003). Ticks are ecologically generalist species and feed on several species of vertebrates, but the white-footed mouse (*Peromyscus leucopus* (Rafinesque, 1818)) seems to be the most competent reservoir for the pathogen in eastern North America (Schmidt & Ostfeld 2001). It has been shown that a loss of diversity among vertebrates that are poor reservoirs for the Lyme spirochete could increase tick infection and, consequently, the incidence of Lyme disease due to a loss of dilution hosts (Schmidt & Ostfeld 2001; Ostfeld & Keesing 2000; LoGiudice et al. 2003). Moreover, not only is the

number of species essential for diminishing disease risk, but also the identity of the species could have an important effect on emerging diseases. For example, the loss of predator species may increase disease risk more than the loss of other species (Ostfeld & Holt 2004; Rohr et al. 2015). An example of this ecological process is found in the case of Schistosomiasis in Lake Malawi. Schistosomiasis is a parasitic disease caused by trematodes of the genus *Schistosoma*, affecting over 250 million people in 78 countries around the world and causing about 280,000 deaths each year (LoVerde 2019). Schistosomes require specific freshwater snail species to complete their life cycles, and people are infected when they enter in contact with water containing trematode cercariae (the infective larval stage). In Lake Malawi, overfishing caused a decrease in the Cichlid *Trematocranus placodon* (Regan, 1922), a snail predator, leading to an increase in the snail population, which in turn led a rise in schistosome parasite transmission to humans (Evers et al. 2006; Stauffer et al. 2006). Finally, it was demonstrated that, at a global scale, anthropogenic habitat disturbance has a differential effect on biodiversity composition. Indeed, land-use change increases the abundance and the richness of wildlife hosts of human-shared pathogens and parasites in anthropized areas, which reflect a potential zoonotic hazard (Gibb et al. 2020). Hence, it seems that synanthropic species (e.g. bats, rodents or passerine birds), which increase in diversity as a result of anthropogenic disturbances, are more likely to be pathogenic hosts capable to harbouring a greater number of pathogen species, including those infectious for humans (Beyer et al. 2021; Gibb et al. 2020; Johnson et al. 2020; Ostfeld & Keesing, 2020).

##### 5. THE ILLEGAL ANIMAL TRADE AND BUSHMEAT

The wildlife trade and consumption of bushmeat are already well recognized as a threat to the global conservation of nature (Scheffers et al. 2019). Besides, wildlife trade can increase a direct contact between wildlife and humans, increasing the risk of disease emergence. Dozens of pathogens have been isolated in illegally traded wildlife species (Gómez & Aguirre 2008) with a high risk of spillover and disease spread in new areas (Pavlin et al. 2009). The illegal wildlife trade is one of the largest black markets in the world, second only to drug trafficking (Toledo et al. 2012). From 1998 to 2007 around 30 million animals from 300 CITES-listed species were exported worldwide from Southeast Asia (Nijman 2009), and

it is estimated that the same order of magnitude of individuals and species is sold each year in the wet markets of East and Southeast Asia (Karesh et al. 2005). As reported by Karesh et al. (2005), “these numbers combined suggest that at least some multiple of 1 billion direct and indirect contacts among wildlife, humans, and domestic animals result from the wildlife trade annually”. In several rural areas of the world, bushmeat consumption has played a relevant role for several generations, providing an essential source of protein in people’s diets and supporting local economies (Milner-Gulland et al. 2003). Nevertheless, deforestation and the construction of new roads, as well as the expansion of luxury markets for bushmeat in “developed” countries (Chaber et al. 2010) have made this practice not only detrimental to the conservation of biodiversity (Milner-Gulland et al. 2003), but also a growing threat to global health because of its potential to facilitate the spread of emerging infectious diseases (Swift et al. 2007). An example of how the illegal wildlife trade can cause the emergence and spread of disease is the 2003 monkeypox outbreak in the United States, which led to dozens of human infections (Reed et al. 2004; Di Giulio & Eckburg 2004). The virus was introduced through the importation of several African rodents, which were kept with other mammals, including prairie dogs (Bernard & Anderson 2006). Another example can be found in the 2002 outbreak of Severe Acute Respiratory Syndrome (SARS) caused by the virus SARS-CoV. The virus emerged in Guangdong province (China), with 8422 confirmed cases, 916 deaths and a mortality rate of about 11% (Chan-Yeung & Xu 2003). Although bats of the genus *Rhinolophus* appear to be the natural reservoir of SARS-CoV, the masked palm civet (*Paguma larvata* (C.E.H. Smith, 1827)) probably acted as an intermediate host transmitting the virus to humans at live animal markets (Li et al. 2005; Hu et al. 2017). Finally, the most important virus that traces its origins to bushmeat hunting and consumption is the Human Immunodeficiency Virus (HIV), which causes the Acquired Immune Deficiency Syndrome (AIDS). Over the last four decades, about 60 million people have been infected with HIV, and about 25 million people have died of AIDS (Merson et al. 2008). The virus evolved from the simian immunodeficiency virus (SIV), and there are several pieces of evidence indicating that primate hunting, butchering, and consumption were the principal drivers of HIV emergence (Peeters et al. 2002; Sharp & Hahn 2011).

## 6. CONCLUSIONS

All the examples cited above point to the probable relationship between the increasing human impact on natural environments and emerging and re-emerging diseases. The human population has increased from 4.4 million people in the early Holocene period to around 7,800 million today. Before the industrial revolution, approximately 600 million people populated the Earth and this figure has grown exponentially over the last 300 years registering a 13-fold increase (Goldewijk et al. 2017) linked to the use of high energy fossil fuel. The increase in the land used for grazing and crops has followed similar trends. While 7.3% of the Earth land area was destined for anthropic uses in 1700, the current percentage is close to 37.1% (Goldewijk et al. 2017), taking a heavy toll on the “natural” environment. The consequences of this increase are many, affecting the structure and functioning of the entire Earth system: the concentrations of carbon dioxide and methane and have risen to the point that they are now driving climate change. Many researchers now consider that Earth is presently in its sixth great extinction event (Ceballos et al. 2017) and different environmental problems accumulate (Ripple et al. 2020); fertilizer production from atmospheric nitrogen and fossil fuels exceeds that which is generated by natural processes, human appropriation of the net primary production of potential vegetation is about 25%, and the human contribution to the global production of sediments is more than 24 times higher than the sediments supplied by world’s rivers (Steffen et al. 2007; Krausmann et al. 2013; Cooper et al. 2018).

We are aware that the listed factors are not the only one involved in a zoonotic spillover (Plowright et al. 2017) and there are a context and scale dependency (Hosseini et al. 2017). Indeed, no pandemic has ever been predicted, and more research is needed to understand in deep the factors and the interactions that drive the emergence of zoonosis (Morse et al. 2012). However, the human impact on the biosphere can be counted among the key causes of emerging and re-emerging diseases (Plowright et al. 2008; Morse 1995). It would appear that increased contact between humans and other organisms is a decisive factor, even if not sufficient, in the emergence of pandemics, and the connections facilitating zoonoses could grow with economic globalization, population growth and landscape anthropization. This process is similar to the process related to the emergence of

agriculture and cattle domestication during the Neolithic period (Wolfe et al. 2007), but now could be accelerated by the exponentially increased traffic in people and goods. Ecology and cybernetics have shown us that large networks with many interactions between their components are frequently unstable and fragile (Pasqualetti et al. 2020). Evolution continually fosters systems of relationships between living things that are compartmentalized and adapted to their local conditions. When human actions alter these local systems, globalizing and homogenizing them, the consequence is the invasion of foreign species, the loss of biological diversity and a breakdown in the functionality of ecosystems. It is revealing that the globalized economy, in its constant striving for ever higher productivity, blindly favours systems of relationships between living things which are the opposite of the kinds of relationships fostered by the evolution of natural systems. We know that most zoonoses originate from the domestication of and interaction with wild animals, and that more than 10,000 animal viruses can potentially be transmitted to humans (Carlson et al. 2019). This transmission could be accelerated by the increasing mobility of goods and people, but also by changes in the climate that lead to the dispersal of human and animal populations, as well as the continuous environmental degradation and loss of biodiversity that can facilitate our contact with pathogens. Insisting on a globalized economic strategy to the detriment of local production and consumption networks cannot be said to be a reasonable strategy to avoid future humanitarian and environmental disasters.

Even though anthropogenic impacts on ecosystems can be seen as one of the most important factors in the emergence of human infectious diseases, today scientific and economic efforts to reduce the impacts of pathogens are mainly focused on quarantine strategies and the development of new drugs and vaccines (Pike et al. 2014). In other words, our global strategy attempts to mitigate the impact after a disease has already emerged, but does not include preventive measures aiming to minimize the human impact on natural ecosystems. Every year, only \$6 billion is spent on the management of protected areas around the world (James et al. 2001), a sum which is several orders of magnitude lower than the economic loss caused by infectious diseases and post-emergence investment and costs (World Bank 2012; Pimentel et al. 2001; McKibbin & Sidorenko 2006)

such as the EU fund set up ([https://global-response.europa.eu/index\\_en](https://global-response.europa.eu/index_en)) to ensure universal deployment of diagnostics, treatment and vaccines against COVID-19. If we only take into consideration six major outbreaks of fatal zoonoses in the last few decades (Nipah Virus, West Nile Fever, SARS, HPAI, BSE, Rift Valley Fever), we could have saved an average of \$6.7 billion per year if these outbreaks had been prevented (World Bank 2012). Moreover, vaccine development for each of the principal epidemic infectious diseases could cost a minimum of \$2.8-3.7 billion (Gouglas et al. 2018). In 2003, the SARS outbreak alone caused a worldwide economic loss of about \$40 billion (Lee & McKibbin 2004), the 2014 Ebola outbreak in West Africa caused an economic loss of more than \$50 billion (Huber et al. 2018), and to date, HIV/AIDS may have cost \$500 billion (Greger 2007). Recently, the Asian Development Bank (ADB), using the Global Trade Analysis Project model, estimates that the global economic impact of COVID-19 could reach \$8.8 trillion (9.7% of global GDP) under a 6-month containment scenario (Park et al. 2020). These data underscore the global society's focus on post-emergence pathogen mitigation, and its inability to examine the root causes of the problem.

A shift from a reactive to a preventive strategy is urgently needed to avoid the emergence of future infectious diseases. Nature conservation must be adopted as a fundamental tool alongside health surveillance, medical treatments and vaccine research to avert future global health crises. Furthermore, infectious disease prevention strategies should be integrated into sustainable development plans (Di Marco et al. 2020). It is clear that nature conservation is not just an ethical problem; instead, it is a crucial issue that will determine the future safety of humankind (Costanza et al. 2014) as well as the human physical and psychological well-being (Balmford & Bond 2005; Murawiec & Tryjanowski 2020; Soga et al. 2020). To avert future global health crises politicians and governments around the world should seek to prioritize the conservation of nature and the implementation of green policies (Newell 2019).

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