An Acad Bras Cienc (2022) 94(Suppl. 3): e20211530 DOI 10.1590/0001-3765202220211530
Anais da Academia Brasileira de Ciências | *Annals of the Brazilian Academy of Sciences*
Printed ISSN 0001-3765 I Online ISSN 1678-2690
www.scielo.br/aabc | www.fb.com/aabcjournal

BIOMEDICAL SCIENCES

Synthesizing the connections between environmental disturbances and zoonotic spillover

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Abstract: Zoonotic spillover is a phenomenon characterized by the transfer of pathogens between different animal species. Most human emerging infectious diseases originate from non-human animals, and human-related environmental disturbances are the driving forces of the emergence of new human pathogens. Synthesizing the sequence of basic events involved in the emergence of new human pathogens is important for guiding the understanding, identification, and description of key aspects of human activities that can be changed to prevent new outbreaks, epidemics, and pandemics. This review synthesizes the connections between environmental disturbances and increased risk of spillover events based on the One Health perspective. Anthropogenic disturbances in the environment (e.g., deforestation, habitat fragmentation, biodiversity loss, wildlife exploitation) lead to changes in ecological niches, reduction of the dilution effect, increased contact between humans and other animals, changes in the incidence and load of pathogens in animal populations, and alterations in the abiotic factors of landscapes. These phenomena can increase the risk of spillover events and, potentially, facilitate new infectious disease outbreaks. Using Brazil as a study model, this review brings a discussion concerning anthropogenic activities in the Amazon region and their potential impacts on spillover risk and spread of emerging diseases in this region.

Key words: Amazon Forest, biodiversity, disease ecology, outbreak, spillover, zoonosis.

INTRODUCTION

A robust set of evidence shows that conservation of biodiversity and of balance in ecosystems and food webs reduces the risk of emergence and spread of infectious diseases of zoonotic origin, in addition to contributing to human well-being in general (Ostfeld 2009, Keesing et al. 2010, Pecl et al. 2017, IPBES 2020). From a practical point of view, limiting anthropogenic activity in environments with high abundance and diversity of species contributes to the maintenance of human and environmental health, containing emerging infectious diseases by multiple ecological mechanisms. On the other hand, anthropogenic disturbances (e.g., deforestation, habitat fragmentation, intensive agricultural practices, unplanned urbanization) indeed affect this balance, facilitating the emergence of new pathogens and the spread of diseases (Ellwanger et al. 2020, IPBES 2020). On a global scale, land-use change was the major driver of more than 30% of new emerging infectious-disease events since 1960 (IPBES 2020).

Currently, there are more than 7.7 billion humans on Earth. Projections indicate that the world population will reach 9.4 to 10.2 billion people by 2050 (Boretti & Rosa 2019). Economic, political, social, and cultural factors dictate human activities in the natural environment, many of which cause damage and disturbances to the environment and to animal populations. The food, water, and consumption demands of the global population are putting great pressure on nature and triggering a range of environmental problems, with expected exacerbation of this scenario in the near future due to the growing world population (Conijn et al. 2018, Boretti & Rosa 2019, Pastor et al. 2019).

The connections between environmental disturbances and infectious diseases are increasingly worrying because efforts to contain deforestation, climate change, and other environmental impacts are still very modest. Globally, habitat loss and extinction rates are on the rise (Ceballos et al. 2015, Newbold et al. 2016, Powers & Jetz 2019), and the detrimental effects of climate change on the human population and other species are increasingly evident (Beyer et al. 2021, Ma & Yuan 2021). Concomitant with this scenario of environmental neglect, the number of emerging infectious disease events per decade is increasing (Jones et al. 2008). Table I shows several examples of infectious disease outbreaks associated with anthropogenic pressures on the environment and animal populations. Also, the economic impacts and losses of human lives related to Coronavirus Disease 19 (COVID-19), which is a zoonotic disease, make clear the magnitude and severity of the situation and the need to understand how to reduce the risks of new pandemics (Dobson et al. 2020, Holmes et al. 2021). As of February 2, 2022, COVID-19 had caused more than 381 million infection cases and 5,688,009 deaths worldwide (Dong et al. 2020, Johns Hopkins University 2022). It is increasingly clear that when a pathogen emerges in a given human population after an event of zoonotic spillover, even in a remote location, the pathogen can quickly spread globally by international air travel and other transport systems, especially in situations of high connectivity between remote regions and large urban centers.

Zoonotic spillover is a phenomenon characterized by the transfer of pathogens between different species (usually non-human animals to humans), which may result in new infectious diseases if biological and demographic conditions are conducive to the adaptation of the pathogen in the new species population. Spillover events are among the initial steps towards the emergence of new human infectious diseases, outbreaks, and epidemics (Plowright et al. 2017, Ellwanger et al. 2019). Most of the pathogens (~60%) that affect humans are derived from microbial strains that previously circulated only in non-human animals (Jones et al. 2008), such as HIV (Keele et al. 2006), influenza A viruses (Krammer et al. 2018), Zika virus (Wikan & Smith 2016), Ebola virus (Leroy et al. 2005, Saéz et al. 2015), rubella virus (Bennett et al. 2020), *Echinococcus multilocularis*, *Trypanosoma cruzi* (Thompson 2013), hepatitis B virus (Rasche et al. 2016), MERS-CoV, SARS-CoV (Cui et al. 2019) and SARS-CoV-2 (Andersen et al. 2020), among many others (Montgomery & Macdonald 2020). Considering adenoviruses, phylogenetic analyses indicate that at least 16 B-type human adenoviruses (HAdV) had their original reservoir in great apes, some of them causing severe human disease. Also, it was proposed that the HAdV-B76 strain, which is associated with a human fatality in 1965, arose from recombination of a virus that infected humans, chimpanzees, and bonobos

Table I. Examples of connections among human-related environmental disturbance, animal populations and infectious diseases.

Anthropogenic pressures on the environment and animal populations*	Effect or association with disease emergence or dissemination	References
Habitat loss, deforestation, industrial agriculture, monoculture practices, mining, and other types of land-use changes	Forest fragmentation, fires and other disruptions of natural habitats of bats resulted in outbreaks of Nipah and Hendra viruses in Australasia	Field et al. (2001), Chua (2003), Epstein et al. (2006)
	Deforestation and road expansion were associated with increased human-biting rate of *Anopheles darlingi* (primary malaria vector) in the Peruvian Amazon	Vittor et al. (2006)
	Habitat fragmentation and biodiversity loss were associated with a higher prevalence of *Trypanosoma cruzi* infection among small mammals in an Atlantic Rain Forest landscape of Brazil	Vaz et al. (2007)
	Increasing of land cultivated for sugarcane and high annual mean temperature were associated with hantavirus pulmonary syndrome incidence in the Neotropics	Prist et al. (2016)
	Forest loss triggered increased risk of Kyasanur Forest disease (tick-borne viral hemorrhagic fever) in India	Walsh et al. (2019a)
	Habitat changes of putative wild rodent reservoirs and agriculture-related activities were associated with fatalities from Sabiá virus infection (two in 1990 decade and one in 2020), São Paulo State, Brazil	Ellwanger & Chies (2017), Malta et al. (2020)
	Land-use (e.g., habitat degradation) was associated with changes in parasite richness and prevalence, as well as co-infection patterns, of avian parasites	Reis et al. (2021)
	Agricultural and irrigation practices were associated with mosquito proliferation, with increases in Japanese encephalitis cases	Keiser et al. (2005)
	Deforestation for agriculture and cattle pasture was associated with development and dissemination of antibiotic resistance in the Amazonian soil microbiome	Lemos et al. (2021)
	Anthropogenic deforestation associated with the shortage of fruiting due to drought-triggered movement of fruit bats to livestock areas, infecting pigs and then humans with Nipah virus in Malaysia	Chua et al. (2002), Looi & Chua (2007)
	Colonial practices in Indigenous areas had a major impact on the health of Indigenous populations, who were exposed to various infectious diseases transmitted by European colonizers and explorers in American and African continents, for example	Valeggia & Snodgrass (2015), Owers et al. (2017)
	Mining, logging, illegal land grabbing and other types of land-use changes in Indigenous lands favors the transmission of SARS-CoV-2, malaria, sexually transmitted infections, and other infectious diseases in Amazonian Indigenous populations	Ellwanger et al. (2020), Vittor et al. (2021)
	In Brazil, political changes permissible to illegal activities (e.g., logging, mining, fires, weakening of Indigenous leaders) on Indigenous Lands (*Terras Indígenas*) exposed Indigenous and traditional communities to multiple infectious diseases, including COVID-19	Brancalion et al. (2020), Ferrante et al. (2020)
	Mining and other types of land-use changes were associated with Buruli ulcer (caused by *Mycobacterium ulcerans* infection) in southwestern Ghana	Wu et al. (2015)
	Agricultural practices exacerbated the risks of many infectious and parasitic diseases (hookworm, malaria, scrub typhus, spotted fever group diseases, schistosomiasis, *Trichuris trichuria* infection) in Southeast Asia	Shah et al. (2019)
	Mining related practices favored emerging infectious disease events in Africa, including Ebola outbreaks, with mining-associated political interests exacerbating such outbreaks	Wallace et al. (2016), Guégan et al. (2020), Ostergard Jr (2021)
	Monoculture and other current food systems practices expose populations to various health issues, including infectious and parasitic diseases (in some cases derived from malnutrition) and multi-resistant microbes at a global scale	Pradyumna et al. (2019), Everard et al. (2020)
	Gold mine workers are highly exposed to hantavirus infection, malaria and leishmaniasis in South America	Rotureau et al. (2006), Terças-Trettel et al. (2019)
	Agricultural systems bring some bat species (e.g., *Desmodus rotundus* vampire bat) closer to humans and domestic animals, increasing the risk of bat-borne infections, including rabies outbreaks	Rosa et al. (2006), Kuzmin et al. (2011)
	Infectious diseases events were associated with changes in forest cover and oil palm expansion at a global scale	Morand & Lajaunie (2021)
	Sugar cane monoculture favors some opportunistic rodents, favoring hantavirus infection in humans	Figueiredo et al. (2010)
	Gold mining-associated activities and settlements favor the spread of infectious diseases (e.g., tuberculosis, HIV/AIDS and other sexually transmitted infections, rabies, vector-borne diseases) in Australia, Africa, North America, and South America	Ogola et al. (2002), Eisler (2003)
	Anthropogenic disturbances (e.g., crop plantation, removal of vegetation cover for cattle raising) lead to simplification of ecosystems (biodiversity loss) and thus favor populations of opportunistic/generalist animal species that can transmit hemorrhagic fever viruses to humans	Mills (2006)
	Co-circulation of Araraquara and Juquitiba hantaviruses in rodents was detected in the Brazilian Cerrado biome, with agricultural practices increasing the risk of human hantavirus infection	Guterres et al. (2018)

Table I. Continuation.

Climate change and extreme weather events	Climatic anomalies (with heavy rainfall and eventually flooding after periods of drought) and increase in air and sea surface temperatures triggered outbreaks of Rift Valley Fever in Africa	Anyamba et al. (2001), Martin et al. (2008)
	Fossil fuel-related climate change associated with air pollution favor the occurrence of respiratory infections (e.g, pneumonia, fungal infection, Hantavirus respiratory disease), especially in children	Mirsaeidi et al. (2016), Brugha & Grigg (2014)
	An increase in coccidioidomycosis cases in Arizona from 1998 to 2001 was associated with climatic and environmental changes such as wind, mean temperature, dust and rainfall because these factors affect the abundance of fungal arthrospores of *Coccidioides* species in the air	Park et al. (2005)
	Extreme weather events, in association with de-urbanization, were associated with higher risk of flood-related non-cholera diarrhea in lower hygiene and sanitation groups in a post-flood period in Dhaka, Bangladesh. Rotavirus, *Escherichia coli*, *Campylobacter* and *Aeromonas* were the most common pathogens causing non-cholera diarrhea episodes	Hashizume et al. (2008)
	Climate change was associated with increased human cases of Lyme disease	Germain et al. (2019)
	Fossil fuel-related climate change will change the distribution patterns of zoonotic and vector-borne diseases in the world in a way difficult to accurately predict, but in general favoring the spread of these diseases on a global scale	Wilkinson et al. (2007), Greer et al. (2008), Dantas-Torres (2015), Wilke et al. (2019b)
	Climate change and land-use change were associated with an increased risk of acute gastrointestinal diseases	Brubacher et al. (2020)
	Climate abnormalities and melting of permafrost released *Bacillus anthracis*, the etiological agent of the anthrax disease, infecting reindeer, cattle, and humans	Timofeev et al. (2019), Maksimović et al. (2017), Stella et al. (2020)
	Temperature rise alters the distribution, optimal conditions for breeding, growth and survival of *Schistosoma*-related snails, and such conditions were associated with increased risk of spread and transmission of schistosomiasis	Kalinda et al. (2017)
Hunting, industrial livestock production, bushmeat practices, and other types of wildlife exploitation	Bushmeat-related practices triggered the SARS-CoV emergence and outbreak in Asia in 2003 and 2004	Tu et al. (2004), Kan et al. (2005), Wang et al. (2006)
	Pervasive contact with wildlife (e.g., hunting, bushmeat-related practices), in association with forest fragmentation and loss, triggered Ebola virus disease outbreaks in Africa	Judson et al. (2016), Olivero et al. (2017), Rulli et al. (2017)
	Coccidioimycosis cases resulted from armadillo hunting	Costa et al. (2001), Brillhante et al. (2012), Capellão et al. (2015)
	Poultry and livestock are sources of multiresistant *E. coli* isolates with clinical importance in China	Yassin et al. (2017)
	Livestock and poultry are sources of antimicrobial resistance genes of *Enterococcus* spp. isolates in Lithuania	Ruzauskas et al. (2009)
	An animal-based agriculture river system was associated with antimicrobial resistance of *Salmonella* sp. in Brazil, with multi-resistance found in 18% of isolates	Palhares et al. (2014)
	Poultry and food products (e.g., retail meat, sushi, ready-to-eat foods) are sources of multi-resistant and methicillin-resistant *Staphylococcus aureus* isolates in Europe	Nemati et al. (2008), Li et al. (2019)
	A swine production system was associated with anti-microbial resistance in *Campylobacter* spp., *E. coli* and *Enterococcus* spp. in Australia	Hart et al. (2004)
	Antimicrobial resistance and virulence genes of *Streptococcus* and *Salmonella enterica* were detected in isolates obtained from dairy cows in Asian countries	Chuanchuen et al. (2010), Ding et al. (2016)
	Animals raised for consumption (e.g., chickens, pigs, cattle) use the majority (73%) of antimicrobials sold in the world, and these animals are major sources of multiple multi-resistant microbes, especially in developing countries and emerging economies, such as India, China, Brazil and Iran	Van Boeckel et al. (2019)
	Hunting, cleaning and eating of armadillos were associated with the development of Hansen's disease (*Mycobacterium leprae* infection) in humans	Capellão et al. (2015), Van Vliet et al. (2017), da Silva et al. (2018)
	Human-promoted elephant-livestock interface increased anthrax transmission risk in India	Walsh et al. (2019b)
	The wildlife exploitation through hunting and trade of threatened wildlife species favors close contact between humans and wildlife, which are contributing factors of spillover events	Johnson et al. (2020)
	Human interaction with animal species (wildlife exploitation, animal trade, livestock industry?) triggered the SARS-CoV-2 emergence and the related COVID-19 pandemic	Lam et al. (2020), Zhang & Holmes (2020), Zhang et al. (2020), Holmes et al. (2021)
	Livestock/agro-pastoral activities were associated with occurrence of zoonotic diseases, such as brucellosis, Q-fever, and Rift Valley fever, affecting both humans and livestock in Ethiopia	Ibrahim et al. (2021)
	Hunting, bushmeat and related activities caused the HIV spillover from wild primates to humans in Africa (around 1920 or before), later (around 1960) spreading around the world as a result of road expansion and globalization, among other social and economic factors	Hahn et al. (2000), Gray et al. (2009), Faria et al. (2014), Gryseels et al. (2020)
	Reassortment of different influenza viruses in swine creates new subtypes of influenza, the causative agent of the Spanish flu (1918) and the swine flu (2009); Influenza reassortment events are facilitated by livestock practices	Tomley & Shirley (2009), Shi et al. (2014)

Table I. Continuation.

Urbanization, de-urbanization, and environmental changes due to infrastructure expansion	The construction of the Binational Itaipu Reservoir contributed to the proliferation of *Anopheles* mosquitoes and the increase in *Plasmodium vivax* malaria cases in the region of the Paraná River (Brazil)	Falavigna-Guilherme et al. (2005), Leandro et al. (2021)
	In Fiji, the presence of *Leptospira* antibodies was associated with different environmental and socio-demographic variables such as living in villages, lack of access to treated water, working outdoors, living in rural areas, high poverty rates, contact with animals, among other factors	Lau et al. (2016)
	The construction of dams was associated with malaria transmission in sub-Saharan Africa	Lautze et al. (2007), Kibret et al. (2019)
	Poorly planned urbanization, presence of waste, and precarious sanitation conditions were linked to the proliferation of *Aedes aegypti* mosquitoes and circulation of urban arboviruses (e.g., dengue, chikungunya and zika)	Almeida et al. (2020)
	Poor housing conditions in association with loss of habitat and food sources favor the infestation of human dwellings by triatomine bugs, transmitters of *T. cruzi* (Chagas disease agent)	Starr et al. (1991), Schofield et al. (1999), Lima et al. (2012), Crocco et al. (2019)
	Human contact with wildlife that resulted from mining and entering caves promoted Marburg virus outbreaks in Africa (infection source linked to bats in caves and mines)	Bausch et al. (2003), Paweska et al. (2018), Amman et al. (2020)
	Higher risk of schistosomiasis infection due to the construction of dams (water blockage) in Africa	Sokolow et al. (2017)
	Overcrowding, environmental contamination, exposure to disease vectors and lack of public health infrastructure favors the transmission of infectious and parasitic diseases in Indigenous populations in many countries	Gracey & King (2009)
	Marginalized and Indigenous peoples in the United States and Brazil experience disproportionate burdens of COVID-19 (both morbidity and mortality) due to social injustice, lack of vaccines and public health infrastructure, and political weakening of Indigenous leaders	Santos et al. (2020), Costa et al. (2021), Hiraldo et al. (2021)
	Infrastructure problems, water contamination and poverty favor infectious and parasitic diseases in Indigenous populations of the Arctic	Hotez (2010)

***Many types of anthropogenic pressures on the environment and on animal populations have been grouped by categories for better organization of the table. However, we stress that in many examples, different categories of anthropogenic actions are acting in association to favor the emergence or spread of disease. At the global level, intensive causes/practices of land-use changes (e.g., logging, mining, industrial livestock production, fossil fuel extraction, deforestation) certainly have a much greater impact as drivers of spillover and emerging infectious disease events than individual practices of consumption and behavior.**

(Hoppe et al. 2015, Dehghan et al. 2019, Kremer 2021).

In this article, the expression 'zoonotic spillover' will be used to refer to the introduction of a pathogen into the human population from a different animal species. However, it is essential to emphasize that spillover is a complex phenomenon. There are different pathways of spillover events. For example, a pathogen can be transmitted from one species (source host) to another (recipient host) directly, without an intermediate species. Alternatively, some spillover events involve an intermediate species (intermediary host) that acts as a 'bridge' for the transmission of the pathogen between the source host and the recipient host. The intermediary host can be a vertebrate species or an invertebrate animal (e.g., mosquito, tick). More than one intermediate host may be involved in the spillover event. Also, the spillover can involve the environment. In this case, the recipient host is infected by the pathogen that has been released into the environment by the source or intermediate host (Borremans et al. 2019, Ellwanger & Chies 2021).

The association between anthropogenic activity and emerging infectious diseases has been increasingly recognized by the scientific community and by the general population since the beginning of the COVID-19 pandemic, with some positive impact on public concern and awareness about nature and environmental issues (Rousseau & Deschacht 2020, Severo et al. 2021). A search on the PubMed database using in association the terms "environmental change" and "pandemic" resulted in 1974 documents published in 2021, a huge increase compared to the 64 documents published in 2019 (https://pubmed.ncbi.nlm.nih.gov/; search performed on February 2, 2022). However, the connections and ecological mechanisms linking environmental disturbance and increased risk of zoonotic spillover events are not always explored in scientific publications. Synthesizing the sequence of basic events involved in the emergence of new human pathogens is important to guide the understanding, identification, and description of key aspects of human activities that can be changed to prevent new outbreaks, epidemics, and pandemics. This knowledge is critical for researchers from different fields. Thus, the main aim of this review is to synthesize the principal connections between environmental disturbances and increased risk of spillover events. In this article, 'environmental disturbance' refers to disturbance, damage or imbalance caused by human activity on natural landscapes, urban and rural areas, animal populations, or ecosystems.

Considering the multiple dimensions surrounding the association between anthropogenic activity and infectious diseases, this article was written with the collaboration of authors from multiple fields, a strategy aligned with the One Health perspective. In the first part of this article, we briefly discussed the relationship between biodiversity and spillover risk. Subsequently, the connections between environmental disturbances and spillover events are reviewed. Considering the authors' expertise on tropical ecosystems in the Brazilian context, this review also brings a discussion concerning anthropogenic activities in the Amazon region and their potential impacts on spillover risk and spread of emerging infectious diseases in this region. This article therefore differs from the literature on emerging diseases because it brings together basic information on anthropogenic activities that facilitate zoonotic spillover events in different contexts and countries, and it provides an analysis focused on a specific highly biodiverse biome - the Amazon Forest.

BIODIVERSITY AND SPILLOVER RISK

Biodiversity can be associated with an increased risk of infectious diseases in some situations. For example, this can occur by adding new infectious agents or carriers to the environment (biodiversity as a 'source' of pathogens), or through the incorporation of new (host) species into a given environment, or by increasing food sources for disease vectors and thus contributing to their proliferation (Keesing et al. 2006). A good discussion regarding the complex influences of biodiversity on infectious diseases can be found in Rohr et al. (2020). Although on some occasions biodiverse environments can be associated with increased risk of infectious diseases, biodiversity *per se* is not the *cause* of emerging infectious diseases. On the contrary, biodiversity usually confers protection to human health.

High-biodiversity ecosystems 'dilute' the density of reservoir hosts and competent vectors, minimizing the contact between reservoir hosts and vectors and reducing the prevalence or load of pathogens in these hosts and vectors, thus decreasing the risk of zoonotic infections. Greater richness and diversity of predators and competitors can also contribute to the control of species that are both adapted to human-modified environments and have the potential to transmit zoonotic pathogens (Schmidt & Ostfeld 2001, Keesing et al. 2006, Ostfeld 2009, Pongsiri et al. 2009, Civitello et al. 2015, Kilpatrick et al. 2017). The phenomenon in which high species diversity reduces the risk of infectious diseases is called the 'dilution effect' (Keesing et al. 2006).

A good example of the dilution effect can be found in Lyme disease, which is caused by the *Borrelia burgdorferi* infection and is transmitted by ticks in the genus *Ixodes*. Different mammals are natural hosts of *B. burgdorferi* in nature, including the white-footed mouse (*Peromyscus leucopus*), a highly competent reservoir. The disease affects human populations living in the USA, Canada, and European nations, among other countries. In the presence of a great diversity of reservoir hosts in nature (white-footed mouse plus other hosts), ticks feed on the blood of different hosts with varied competence for *Borrelia* transmission (many with a low reservoir competence), thus 'diluting' the number of infected ticks and consequently the risk of Lyme disease (LoGiudice et al. 2003, Ozdenerol 2015, Keesing & Ostfeld 2021). In brief, high host diversity including poor competent hosts dilutes the infection risk exerted by the few highly competent hosts. On the other hand, the risk of disease increases as the diversity of *Borrelia* hosts declines and the density of competent reservoir hosts increases in a particular area (LoGiudice et al. 2003, Keesing & Ostfeld 2021).

The impact of host diversity on the disease risk was observed in other models beyond Lyme diseases. The risk of human infection by West Nile virus and Hantavirus decreases as the diversity of their hosts (wild birds and rodents, respectively) increases. The opposite correlation can also occur, with the risk of human infection increasing as host diversity decreases (Mills 2006, Allan et al. 2009, Ostfeld 2009). These two additional examples highlight the dilution effect, indicating how biodiversity can 'dilute' the risk of zoonotic spillover events, protecting human health.

The dilution effect is strongly related to the number and relative abundance of taxa, namely taxonomic diversity (Naeem et al. 2012), which is the kind of "biodiversity" discussed above. However, it is essential to consider that other forms of biodiversity exist, with varied impacts on disease risk. According to Naeem et al. (2012), biodiversity can be classified on the basis of several dimensions, including taxonomic, phylogenetic, genetic, functional, spatial or temporal, interaction, and landscape diversities. These other dimensions of biodiversity can also affect spillover events and the spread of pathogens. For example, genetic diversity has contributed to the emergence of new pathogens or variants, as observed in the SARS-CoV-2 and HIV pandemics, facilitating the transmission and spread of the viruses to different countries (Faria et al. 2014, Andersen et al. 2020). Also, interaction diversity (e.g., competition, predation, parasitism) has an important influence on the risk of emergence and spread of zoonotic diseases (Vourc'h et al. 2012) because it modulates the contact between species, host immunity, transmission of pathogens and food webs.

It is also fundamental to stress that the dilution effect does not apply to all types of zoonotic diseases, being more closely related to diseases borne by vectors such as arthropods and rodents, as indicated by the examples mentioned above. Furthermore, the dilution effect may be scale dependent. The protective role of biodiversity on disease risk observed at the local scale may not be observed when the effect of biodiversity is analyzed at the global scale. Also, the ecological history of each disease is different and, in some cases, is either weakly dependent on the degree or dimension of biodiversity or its effect is only indirect (Rohr et al. 2020). Some diseases of zoonotic origin, but that are currently highly specialized on the human host (e.g., measles, tuberculosis, pneumonia), have a weak relation with measures of biodiversity (Rohr et al. 2020).

Other factors (e.g., demography, social issues) also increase the complexity of the relation between biodiversity and zoonotic risk. Globally, countries with high biodiversity are often precisely those where the burden of zoonotic diseases can be observed most intensely. For example, Brazil is classically affected by multiple types of zoonotic vector-borne diseases (Magalhaes et al. 2020), despite being one of the most biodiverse countries in the world. Inadequate sanitary conditions and precarious public health systems, which are frequently observed in tropical developing countries, can override the dilution effect associated with high biodiversity, facilitating the emergence and spread of diseases in these countries (Ellwanger et al. 2021). In brief, the connections between biodiversity and zoonotic spillover are multiple and complex. Although some generalizations are possible, such as the dilution effect and the connections that will be discussed later in this article, each pathogen and spillover event must be analyzed according to its natural history and the context of its occurrence.

ALIGNMENT OF CONDITIONS CONDUCIVE TO ZOONOTIC SPILLOVER

Role of animal groups

An increased risk of spillover events is usually associated with particular animal orders, including Chiroptera and Rodentia, which are composed of species with supposed high 'zoonotic potential'. Also, anthropogenic modifications in landscapes favoring human contact with rodents and bats are usually associated with increased risk of zoonotic infection. However, some criticism concerning these aspects is needed. Some animal species can indeed host a high load or diversity of zoonotic pathogens due to intrinsic biological characteristics (e.g., immune system factors, genetic proximity to humans) or due to ecological characteristics, such as the sharing of a habitat with humans or livestock. However, a greater load and variety of pathogens in certain reservoir hosts can be circumstantial and is not necessarily an intrinsic characteristic of a specific animal group. Bats and rodents are often considered highly competent in transmitting pathogens to humans because they harbor a great diversity of zoonotic pathogens, reproduce quickly and often inhabit human-related environments. Chiroptera and Rodentia are the most numerous orders of placental animals, which can increase the opportunity for the emergence of potential zoonotic agents from these animals (Luis et al. 2013, Han et al. 2016). Canidae and Felidae are families in the order Carnivora that also pose risks to the human population in terms of zoonotic spillover because their members (e.g., dogs, foxes, cats) host different zoonotic pathogens and frequently circulate in human-dominated areas (Han et al. 2021).

Stray dogs and cats find favorable conditions to proliferate in areas where urbanization has taken place in a disorderly way, and these animals are transmitters of zoonotic diseases in urban centers, especially due to soil contamination with the eggs and oocysts of parasites (*Toxocara*, *Trichuris*, *Toxoplasma*, *Cystoisospora* and *Taenia* genera, among others) released into the environment through animal feces. This is a particularly important problem for children because they come into greater contact with the soil in public squares and parks; this affects populations in China, South America, highly developed European nations, and elsewhere (Szwabe & Błaszkowska 2017, Montoya et al. 2018, Fu et al. 2019, Saldanha-Elias et al. 2019). Moreover, leishmaniasis is a major zoonotic disease in several Latin American countries. This disease is caused by *Leishmania* parasites, which have dogs as common reservoirs. The disease is transmitted by phlebotomine sandflies that proliferate in areas with a lack of environmental sanitation and an abundance of domestic animals, thus affecting people living in urban and peri-urban areas (Teodoro et al. 1999, Marcondes & Day 2019). These cases exemplify the role of the order Carnivora as an additional source of zoonotic pathogens.

Mammals in the order Rodentia were initially classified as the animal group with the highest number of zoonotic hosts, with ~11% of species having zoonotic potential. Highly competent rodent reservoirs show a fast life history profile, reaching sexual maturity and producing offspring at higher rates earlier in life as compared to non-reservoir rodents. Also, highly competent rodent reservoirs usually thrive in areas with high human population densities (Han et al. 2015, 2016). Similar to rodents, bats are usually considered to be of special zoonotic concern because they have high longevity, the colonies are numerous, and the share of viruses between different bat species is increased due to sympatry (Luis et al. 2013). Bats have immune systems with unique adaptations that allow these animals to harbor many viruses without themselves becoming sick, which contributes to making these animals of special concern regarding zoonotic risk (Hayman 2019, Subudhi et al. 2019).

However, it is necessary to consider some points regarding the role of the orders Rodentia and Chiroptera (especially bats) as disproportionate zoonotic reservoirs. Limited inflammatory responses, high population densities and gregarious social behaviors observed in some bat species may indeed facilitate pathogen transmission among bats, especially viruses, contributing to the zoonotic potential of this group (Brook & Dobson 2015, Streicker & Gilbert 2020). On the other hand, the lack of knowledge about the immunity of other animal groups, including their ability to harbor pathogens asymptomatically, may currently be biasing the conclusion that bats or rodents are especially competent in harboring and transmitting zoonotic pathogens. There is also high immunological variation among bat species, making generalizations about the ability of bats to transmit zoonosis a complicated task. Beyond bats and rodents, other animal groups can be of great importance for the transmission of zoonotic pathogens to humans, although they have been less considered and sampled in studies involving zoonotic diseases (Streicker & Gilbert 2020). A recent study by Mollentze & Streicker (2020) reported that the viral zoonotic risk was homogenous among mammalian and avian species when reservoir hosts of 415 RNA and DNA viruses were considered, this being the largest dataset to date. Bats and rodents were considered unexceptional zoonotic hosts, with the proportion of zoonotic viruses varying minimally across the taxonomic orders of the reservoirs that were analyzed (Mollentze & Streicker 2020).

Still concerning bats, human activity has effects beyond those expected from human-triggered changes in the sizes and population structures of these animals. Bats are highly sensitive to anthropogenic activity, which generates physiological stress in these animals. These physiological changes impact infection severity and pathogen shedding in bats, affecting their associated viral populations and risk of spillover events. For example, Plowright et al. (2008) observed that reproduction and nutritional stress in little red flying foxes (*Pteropus scapulatus*) increases the risk of Hendra virus infection in these animals, potentially increasing the risk of human infection when these conditions occur. Pregnant and lactating female bats showed higher Hendra virus infection rates, and animals under nutritional stress showed higher infection prevalence, a result potentially derived from factors such as poor immune defense or greater contact with other animals while sharing food (Plowright et al. 2008). Furthermore, recent data have shown that the ecological conditions of the flying fox hosts of Hendra virus influence the timing, magnitude, and cumulative intensity of virus shedding, thus affecting the spillover risk (Becker et al. 2021). Based on these findings, changes in bat immunity derived from human-associated environmental disturbances (e.g., habitat loss, food shortages) can be considered a mechanism by which human activity can increase the risk of spillover events and zoonotic diseases, since these immunological changes can increase infection severity, viral shedding and infection rate in reservoir host populations. Moreover, this information indicates that the zoonotic risk attributed to a given host is *circumstantial* and not necessarily *intrinsic* to a specific animal group, with human-related interference on these hosts influencing the circumstantial zoonotic risk.

Host-associated factors, pathogen characteristics and the environmental context

Several host-associated factors can increase or reduce the risks of spillover events, including pathogen load in the source or intermediate host, immunity or nutritional status of recipient host, similarity of pathogen receptors in the different hosts, and genetic/evolutionary distance between species. Spillover risk is also modulated by ecological conditions (e.g., habitat sharing by different species, changing patterns disease in reservoir populations, changing reservoir species behavior) and environmental factors (e.g., landscape characteristics, environmental sanitary conditions, abiotic factors: temperature, humidity, rainfall). Adding more complexity to spillover risk, characteristics of the pathogens (e.g., virulence, transmissibility, viral family, host range) and human behavior (e.g., interaction with other species, invasion of habitats) also affect the spillover risk. The dose and route of human exposure to pathogens also determine the chances of a pathogen crossing the species barrier. After a pathogen successfully reaches a new host, other factors will affect the outcome of the spillover. Not all spillover events result in an epidemic outbreak, and many spillover events go unnoticed, without medical or epidemiological importance. An outbreak or epidemic only occurs when the pathogen, after crossing the barriers between species, finds favorable conditions for its dissemination in the new population. These conditions are usually population agglomeration, unplanned urbanization, and a large number of susceptible hosts (Plowright et al. 2017, Becker et al. 2019, Borremans et al. 2019, Ellwanger & Chies 2021, Grange et al. 2021, Nandi & Allen 2021).

The human immunological status at the time of contact with a new zoonotic pathogen influences the outcome of a spillover event. Immunosuppressed individuals can be infected by viruses, fungi, parasites, and bacteria much more easily than individuals with fully competent immune systems (Raychaudhuri et al. 2009, Vanichanan et al. 2018). Both the maintenance of a pandemic status and the raising of new pathogenic variants are conditions affected by the human immunological status, as can be seen in the current COVID-19 pandemic dynamics. Similarly, HLA alleles and variants in immune-system genes (e.g., single nucleotide polymorphisms in Toll-like receptor, cytokine and chemokine receptor genes, complement system) can either increase or decrease the risk of infection by different pathogens in human populations, in addition to affecting the progression of infection and the host's pathogen load, and, consequently, disease spread in the population (Burgner et al. 2006, Chang et al. 2008, Pine et al. 2009, Ferguson et al. 2011, Adriani et al. 2013, van den Broek et al. 2020, de Vries et al. 2020, Sánchez-Luquez et al. 2021), indicating the importance of host genetics as a determinant of spillover risk and outcome. Therefore, this information makes it clear that when a new pathogen reaches a human being due to favorable ecological conditions (e.g., contact between species sharing the same habitat, land-use changes), the outcome of the spillover event will also be conditioned to a series of other biological factors.

CONNECTIONS BETWEEN ENVIRONMENTAL DISTURBANCES AND ZOONOTIC SPILLOVER

Human behavior and demography

Human behavior and demographic changes are critical modulators of risk and outcome of spillover events. Keeping animals in captivity for decorative or entertainment purposes, the frequent and close contact with wild species, as well as human entry into wild environments, facilitate spillover events because they put humans in close contact with different species. For example, tourist activities involving cave exploration in Africa facilitated Marburg infection cases in past years. Caves are usually visited by numerous animals, including fruit bats (*Rousettus aegyptiacus*) that act as Marburg reservoir hosts; caves are places where animal deficate and associated pathogens are found in abundance (Johnson et al. 1996, CDC 2009, Amman et al. 2012). Also related to human behavior, the use of wild or exotic animals as pets can facilitate the introduction of new pathogens into the human population (Chomel et al. 2007), in addition to being a conservation problem affecting wild species.

Human migratory flows can also change the epidemiology of infectious diseases through the introduction of known and unknown pathogens into new areas, by overburdening health systems, or by exposing non-vaccinated migrants to new pathogens and precarious health conditions. These problems are particularly important in cases of forced migration due to war, political instability and climate change. This indicates that the global political instability associated with the disparity in terms of access to healthcare directly or indirectly affects populations worldwide concerning control and prevention of infectious diseases (Gushulak & MacPherson 2004, Castelli & Sulis 2017, Berry et al. 2020, Ibáñez et al. 2021). Recent measles outbreaks in Brazil and Colombia due to Venezuelan migration demonstrated failures in the vaccination and access to health services by Venezuelans (Hotez et al. 2020). The number of 'climate refugees' will increase as climate change intensifies, contributing to both the exposure of migrants to new reservoir hosts and related pathogens, and to the change in the profile of infectious diseases in many countries (McMichael 2015). However, we stress that the effect of migratory flows on infectious disease burden on migrants and refugees is greater than the effect on the population of the country that receives the immigrants, especially in Europe (Castelli & Sulis 2017).

Exploitation of wildlife

Hunting, wildlife trafficking, animal trade in 'wet markets,' and 'bushmeat' consumption are classic driving forces of spillover events, since these practices put humans in close contact with pathogens in the meat, blood and other biofluids from a wide range of animal species (Karesh et al. 2005, Smith et al. 2012, Johnson et al. 2020, Magouras et al. 2020, Zhang & Holmes 2020). The expression 'wet markets' refers to places where different live animal species are sold in close contact, sometimes sharing a same cage. Some wet markets sell endangered species (Zhang & Holmes 2020, Peros et al. 2021). Wet markets are frequently associated with bushmeat. The expression 'bushmeat' refers to the meat of hunted wild animals sold in popular or wet markets (Pangau-Adam et al. 2012), in some situations in the absence of adequate sanitary standards according to regulatory agencies (Naguib et al. 2021, Peros et al. 2021, Saylors et al. 2021, WHO 2021). Sanitary requirements may vary depending on the sanitary regulations of each country, and traditional food markets can be considered safe when operating in accordance with health regulations (WHO 2021).

Different from 'bushmeat' (hunted meat for income purposes), 'wild meat' refers to the meat of wild animals killed for consumption by hunters and their families. As bushmeat products usually come from systematic hunting activities, including frequent handling of animal carcasses, blood and viscera without sanitary control or inspection, bushmeat is associated with increased spillover risk (Wolfe et al. 2005, Pangau-Adam et al. 2012, Peros et al. 2021). For these reasons, wet markets and bushmeat consumption are recognized as important drivers of zoonotic spillover, unlike markets or fairs where meat products are sold under sanitary inspection, which reduces the risk of transmission of pathogens to humans (Wolfe et al. 2005, Karesh & Noble 2009, Zhang & Holmes 2020, Naguib et al. 2021, Peros et al. 2021). In these places, spillover risk also exists [as indicated by human outbreaks of food-borne diseases in high-income nations like the UK (Public Health England 2018)], but the risk is lower due to sanitary control.

Land-use changes and exploitation of Indigenous lands

Other human-mediated activities also facilitate spillover events, including deforestation, industrial livestock, monoculture farming, and mining, among other types of human alterations on land. These changes are commonly unified in the expression 'land-use changes.' Land-use changes lead to host exposure to a new array of pathogens (Murray & Daszak 2013). The construction of roads in wild landscapes (e.g., Amazon rainforest), besides causing damage to ecosystems (Ferrante & Fearnside 2020a), increases the contact of humans with forest-associated animal species and the risk of spillover. Although the human presence can scare away some animal species, when humans invade forest environments to build roads or to perform mining and logging activities, among other reasons, the contact with animal species increases, especially contact with mosquitoes and other blood-sucking insects that benefit from the human presence that provides an additional food source. This closer and more frequent interaction between humans and anthropophilic insects favors spillover events mediated by invertebrate intermediate hosts (Ellwanger et al. 2020).

Extensive land-use changes and associated spillover risk are also a major issue for Indigenous populations. Due to limited contact with non-indigenous populations, indigenous peoples have weak or no natural/protective immunity to pathogens that emerged outside Indigenous areas. Such populations also have limited access to vaccines and healthcare facilities. These factors exacerbate the burden related to emerging pathogens in Indigenous populations. This is a problem observed in several situations and in various parts of the world, from the colonization of the Americas and Africa by Europeans to the ongoing COVID-19 pandemic in Brazil, among other situations (Valeggia & Snodgrass 2015, Ferrante & Fearnside 2020b). Of particular concern is a proposed law in Brazil (PL191/2020) opening Indigenous lands to mining, logging, agriculture and other activities by non-indigenous people (Villén-Pérez et al. 2021). The risk is clear in a project that is already moving ahead to grow corn (maize) to feed pigs in an Indigenous area in association with a food and biofuel company (Ferrante et al. 2021). Land-use activities in the Indigenous areas expose both Indigenous peoples and workers to a new range of potential exotic pathogens.

Similarly, human contact with other animal species is facilitated by habitat fragmentation (Wilkinson et al. 2018). For example, the transmission of zoonotic parasitic diseases such as leishmaniasis and Chagas disease is facilitated in areas with fragmented vegetation due to the increased human contact with the vectors of *Leishmania* and *Trypanosoma* parasites (phlebotomine sandflies and triatomine bugs, respectively), and changes in the composition and infectious status of wild hosts (Vaz et al. 2007, Roque et al. 2008, Curi et al. 2014, Zaidi et al. 2017, Cardozo et al. 2021). In a general sense, the maintenance of habitat core/solidity reduces the habitat perimeter, diminishing the human contact with other species and, consequently, the spillover risk. On the other hand, habitat fragmentation increases the habitat perimeter and contact zones where pathogen transmissions may occur between non-human animals and humans (Wilkinson et al. 2018, Borremans et al. 2019, Bloomfield et al. 2020). Specifically, there are examples showing that habitat fragmentation in Africa was associated with increased human contact with non-human primates, bats, and potentially the zoonotic pathogens found in these animals (Rulli et al. 2017, Bloomfield et al. 2020). A recent study reported that the risk of SARS-related coronavirus outbreaks in China is higher in areas with forest fragmentation and concentrations of livestock and humans (Rulli et al. 2021). Habitat fragmentation is strongly associated with loss of ecosystem functions, reduced landscape connectivity, and biodiversity loss (Haddad et al. 2015), which impairs the dilution effect and increases the risk of zoonotic diseases through this additional mechanism (Allan et al. 2003, Keesing et al. 2006). These factors act in synergy with the proliferation of species adapted to human-modified environments and an increase in the load of pathogens hosted by these species, thus creating favorable conditions for the transmission of relatively new zoonotic pathogens to humans.

Livestock industry and antimicrobial resistance

The large scale of the livestock industry for the production of meat and other animal products leads to the confinement of a large number of animals in small areas, usually with frequent contact with humans and other species. As previously described, environments with low species richness can limit the dilution effect, favoring the spread of pathogens. In addition, the movement of livestock within and between countries with little or no sanitary inspection poses a threat to the dissemination of infectious diseases if these animals carry pathogens with zoonotic potential, such as Rift Valley fever virus, as seen in East-African countries that export livestock (Anyamba et al. 2001, Martin et al. 2008, Taylor et al. 2016).

Animals from livestock production also act as intermediate hosts for the adaptation of pathogens from wildlife before they are introduced into the human population. For example, swine (e.g., domestic pigs) are considered to be ‘mixing vessels’ where strains of influenza A viruses from wild birds can undergo genetic recombination or reassortment with other viruses present in pigs, originating new influenza strains that will then be transmitted to the human population. This occurs because pigs have cell receptors recognized by avian and human influenza viruses, in addition to sharing the environment with different species of birds and humans (Ma et al. 2008, Ellwanger & Chies 2021). The role of pigs as mixing vessels for the reassortment of influenza viruses has already been shown by various studies, confirming that pigs can act as intermediate hosts for the adaptation of animal influenza viruses before being introduced into the human population (Zhou et al. 1999, Urbaniak et al. 2017, Zell et al. 2020). In a study performed in Egypt, Gomaa et al. (2018) found evidence of infection with avian (H9N2, H5N1), human (pandemic H1N1), and swine influenza viruses in pigs. Ganti et al. (2021) recently showed that mallard ducks also have the potential to act as mixing vessels for the reassortment of influenza A viruses.

Animals from livestock production (e.g., cattle, swine, poultry) also pose a zoonotic risk to human populations considering diseases caused by parasites, especially when these animals are raised in inadequate facilities and with poor hygiene conditions. Infection by *Fasciola hepatica*, *Schistosoma japonicum*, *Trichinella spiralis*, among other parasitic infections, can affect humans due to problems in the practices of breeding, confinement and sanitary inspection of livestock animals and derived products (Gortázar et al. 2007, Rist et al. 2015). Livestock can act as bridges (intermediate hosts) for the transmission of parasites from wild hosts to humans (Gortázar et al. 2007, Wiethoelter et al. 2015).

Finally, it is possible that the introduction (spillover) of SARS-related viruses (SARS-CoV, MERS-CoV) to the human population from bats, source hosts for both SARS-related viruses, has the participation of intermediate hosts, specifically palm civets for SARS-CoV and camels for MERS-CoV. However, the direct bat-human transmission of these viruses cannot be ruled out (Letko et al. 2020). Some farmed species such as minks, red foxes, and raccoon dogs, potentially acted as intermediary hosts in the SARS-CoV-2 spillover into the human population, but this represents an open question (Koopmans et al. 2021, Lytras et al. 2021). The large number of animals observed in industrial livestock production and the frequent contact with other animal species create numerous opportunities for the adaptation of new pathogens before reaching the human population.

The intensive use of antimicrobial drugs in the livestock industry creates ideal conditions for the selection of microorganisms resistant to multiple drugs and for the emergence of new pathogenic microbial strains, reinforcing opportunities for spillover events (Ye et al. 2016, He et al. 2020, Magouras et al. 2020). Drug-resistant pathogens were responsible for ~20% of all emerging infectious-disease events reported since 1940, a phenomenon stemming from the pervasive use of antimicrobial drugs (Jones et al. 2008). Inappropriate intensive use of antimicrobials in human medicine (e.g., azithromycin as a supposed COVID-19 treatment) will contribute to the emergence of multiresistant strains (Afshinnekoo et al. 2021). The role of drug resistance in the emergence of outbreaks and epidemics is expected to gain greater attention in the coming decades, along with anthropogenic pressures on the environment and animal species.

Fires and other drivers of unusual movement pattern of animals

Fires, deforestation, and habitat loss induce wild animals to assume unusual movement patterns and alternative spatial distributions because these animals need to leave their natural habitats to obtain food, water and shelter, or to escape fire, among other reasons (Johnson et al. 1992, Hadley & Betts 2009, Niebuhr et al. 2015, Nimmo et al. 2019, Ramos et al. 2020). In response to such events, animals often supply their needs in forest-city borders and in urban and peri-urban areas (e.g., migration of non-human primates from wild areas to cities), especially when urban settings are established in areas previously occupied by forests. For instance, in the Brazilian cities of Rio de Janeiro and Porto Alegre, non-human primates share forest fragments with the human population (Cunha et al. 2006, Corrêa et al. 2018). Also in Brazil, non-human primates (howler monkeys) and forest-dwelling mosquitoes found in city-forest interfaces (as a consequence of urbanization, habitat loss and forest fragmentation) can act as bridges between the sylvatic and urban cycles of yellow fever, as well as bridges for the spillover of new human pathogens from wildlife (Cardoso et al. 2010, Almeida et al. 2012, Couto-Lima et al. 2017).

In addition to inducing animals to explore new environments due to habitat loss, fires can favor the occurrence of arboviral diseases. In Brazil, studies have associated fires with outbreaks of Dengue, Zika, Chikungunya and Yellow fever, especially in areas where fires have an anthropogenic origin and are associated with the expansion of agriculture and livestock production (Torres et al. 2019, Moreno et al. 2021). The increase in fire outbreaks recently observed in Brazil and other countries (Pivello et al. 2021) will potentially increase the risk of spillover events involving arboviruses.

Animal trafficking and the domestication of wild animals also contribute to changes in the geographical distribution of animal species and pathogens with zoonotic potential. These processes can put human populations into contact with new pathogens from exotic animals that have been artificially moved to new areas and environments. For example, zoonotic *Salmonella* outbreaks were associated to animal trafficking and exotic pets (e.g., Amazon parrots) (Marietto-Gonçalves et al. 2010, Saidenberg et al. 2021). Also, Kovalev & Mazurina (2022) recently evaluated Omsk hemorrhagic fever, an endemic disease from Western Siberia and associated with muskrats (*Ondatra zibethicus*). Since the Omsk hemorrhagic fever virus (OHFV) is closely related to the tick-borne encephalitis virus (TBEV), considering genetic and ecological characteristics, the authors suggested that the OHFV originated directly from the TBEV (Far Eastern subtype) in a spillover event involving the transmission of the virus from *Ixodes persulcatus* ticks to muskrats after the human introduction of *O. zibethicus* to Western Siberia in the second half of the 1930s. The introduction of *O. zibethicus* in this new region was motivated by the potential use of muskrat's valuable fur (Kovalev & Mazurina 2022).

Unusual animal movement patterns are also of epidemiological concern when they involve domestic animals with competence for the transmission of zoonoses, potentially increasing the risks of zoonotic spillover or creating conditions for these animals to act as bridges to pathogen hosts. Dogs that circulate between urban and forest areas can facilitate the spillover and spillback (human-to-animal transmission) of many pathogens, increasing the infectious-disease risk for both human and animal populations (Martinez et al. 2013, Ellwanger & Chies 2019).

Biotic and abiotic environmental changes

Studies performed with mosquitoes are critical to comprehend how human disturbance of the environment can lead to an increased risk of spillover events mediated by vectors (as intermediary hosts). Environments with high biodiversity tend to have a greater variety and abundance of predators of disease vectors. These predators include bats, birds, amphibians and larvivorous fishes that feed on mosquitoes at different stages of development. Reduction of the diversity of predators due to anthropic action can benefit the survival and proliferation of mosquitoes. Also, abiotic factors (e.g., sunlight, wind patterns, temperature, moisture, and the pH of water in breeding sites) are altered in degraded landscapes and can affect vector distribution and proliferation (Burkett-Cadena & Vittor 2018, Almeida et al. 2019, Franklinos et al. 2019). For example, lower temperatures in the forest can slow the larval development of mosquitoes while the opposite can occur when forests are cleared, resulting in warmer temperatures, greater light intensities, and increased availability of nutrients in water pools, thus benefitting the larvae of some mosquito species (Burkett-Cadena & Vittor 2018, Franklinos et al. 2019). Consequently, these ecological and abiotic changes benefit mosquito populations and increase the risk of spillover events mediated by vectors (Burkett-Cadena & Vittor 2018, Ellwanger & Chies 2018, Almeida et al. 2019, Franklinos et al. 2019). From a global perspective, it is very likely that climate change in the coming decades, including a 1.0–3.5ºC increase of global temperature and more frequent climatic anomalies (e.g., El Niño, droughts, floods), will lead to an increased burden of vector-borne diseases and more zoonotic spillover events mediated by arthropod vectors (Githeko et al. 2000, Watts et al. 2019, Wilke et al. 2019b).

Finally, it is essential to consider that disease cycles are often complex, being influenced by factors that go beyond the abiotic sphere, such as biological aspects of vertebrate hosts (immunity, genetics, and other characteristics, as discussed previously), arthropod resistance to insecticides, and stresses on communities of vectors (Guedes et al. 2017, Pavlidi et al. 2018). Therefore, the impact of climate change on vector-borne and other zoonotic diseases will be affected by these other factors, making it difficult to accurately predict the intensity of impacts and distribution of pathogens and diseases in a changing world. Considering these uncertainties, the precautionary principle must be considered (Mahrenholz 2008) and anthropogenic changes in the environment must be controlled in order to reduce zoonotic risks to the human population.

ANTHROPOGENIC ACTIVITIES IN THE AMAZON REGION AND THEIR POTENTIAL IMPACTS ON SPILLOVER EVENTS

The Amazon Forest is one of the most biodiverse regions in the world, with 70% of the Amazon basin located within Brazil (Kirby et al. 2006). Due to its high biodiversity combined with a diversity of anthropogenic activities in the region, the Amazon Forest is a hotspot for the emergence of new pathogens (Val 2020). Indeed, there are numerous potential new pathogens in the Amazon Forest that could pose a risk to human populations. However, it is the intense human activity in the region that is the main driver of potential spillover events in the Amazon Forest, not the biodiversity *per se*.

Degradation of tropical forests, including the Amazon Forest, is strongly derived from economic activities linked to the exploitation of minerals, oil, and timber, in addition to industrial livestock and monoculture production. Globalization and economic connections between developed and developing countries mean that the triggers of environmental degradation in any given part of the world can be derived from demands of distant countries or even other continents. For instance, land-use changes in the Amazon Forest, including the increasing deforestation rate in the region (see Figure 1, panel a, for more data), are partially triggered by the demand for

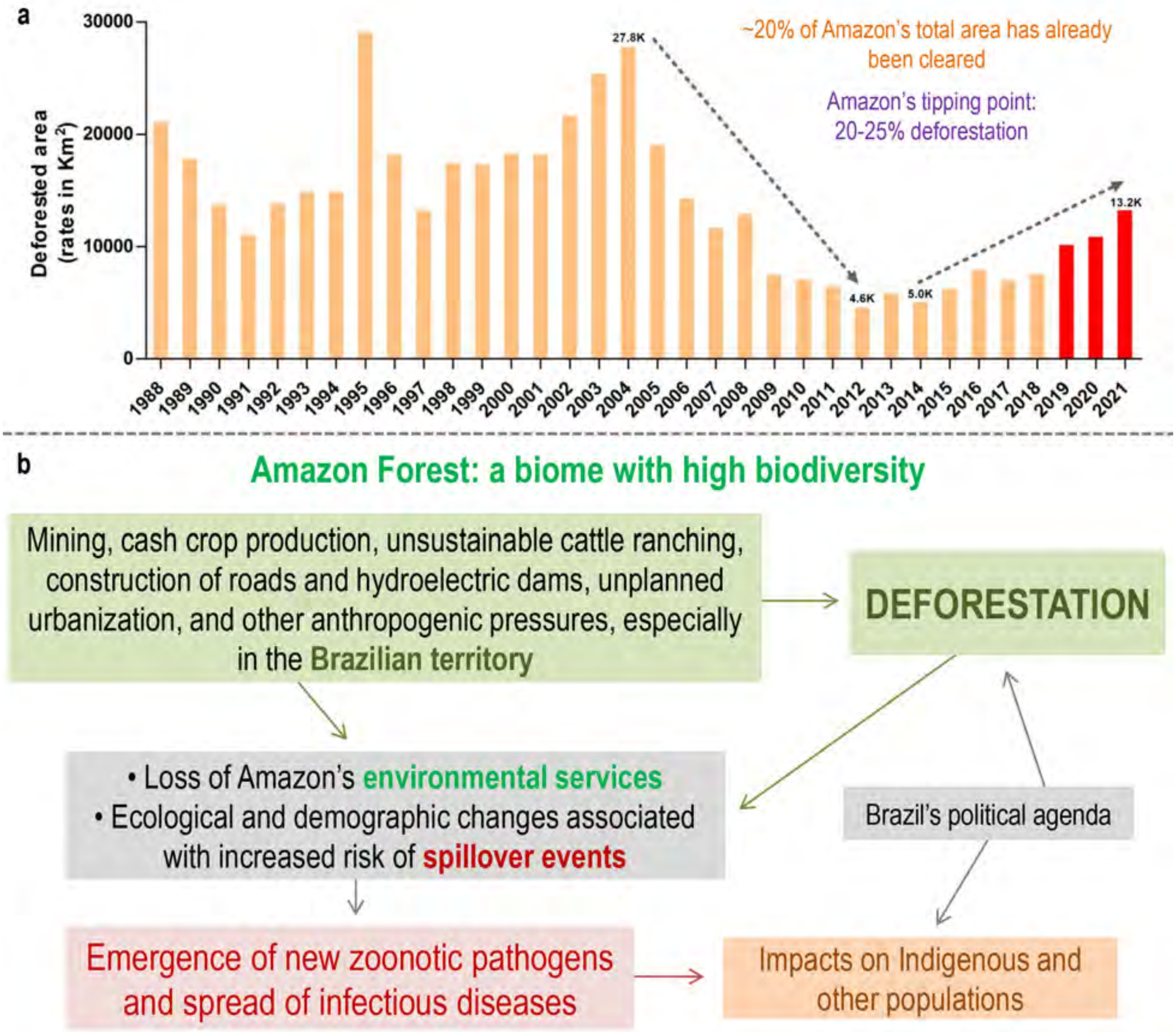

Figure 1. Deforestation rate in Brazilian Amazon Forest (Legal Amazon) between 1988 and 2021 and connections between anthropogenic pressures on Amazon Forest and spillover risk. Panel a: between 2004 and 2012, deforestation in the Amazon underwent a significant reduction, partly as a result of the strengthening of policies for controlling illegal activities. From 2014 onwards there have been increases in deforestation rates, with alarming results in 2019, 2020 and 2021, reflecting the weakening of the regulation of illegal activities in the region. Tipping point: the point at which the Amazon Forest stops properly providing its environmental services (e.g., hydrological cycle, maintenance of carbon stocks), losing many rainforest characteristics and enters into a self-perpetuating decline. Data (deforestation rate by year collected on February 1st, 2022) obtained from TerraBrasilis - *Programa de Cálculo do Desflorestamento da Amazônia* (PRODES), *Instituto Nacional de Pesquisas Espaciais* (INPE); data under CC BY-SA 4.0 license (INPE 2022). The graph was plotted using GraphPad Prism. Additional information was obtained from Aguiar et al. (2016), Lovejoy & Nobre (2018), and Ferrante & Fearnside (2019). Panel b: deforestation and other anthropogenic pressures on Amazon Forest are closely connected activities. These pressures facilitate spillover events, the emergence of pathogens and the spread of infectious diseases, affecting populations living inside and outside the Amazon region.

beef and agricultural commodities by China and European countries (Fearnside et al. 2013, Fuchs et al. 2019, Pendrill et al. 2019), by the bovine leather industry in Europe (Mammadova et al. 2020), among other economic drivers. These human activities in the Amazon region facilitate the risk of zoonotic spillover events and the spread of infectious diseases in multiple ways (Figure 1, panel b).

A recent study performed in the Amazon rainforest showed that anthropogenic pressure on the natural landscape, specifically forest fragmentation, decreases mosquito diversity and increases the abundance of malaria vectors such as *Anopheles (Nyssorhynchus) darlingi* mosquitoes (Chaves et al. 2021). Human occupation in forest areas causes loss and fragmentation of habitat. In association with this, there is an increase in the availability of human hosts and a blockage of water flow, thus facilitating the dispersion and proliferation of human-associated mosquito species with medical importance, like *An. (Ny.) darlingi* (Chaves et al. 2021). These data reinforce the concept that diversity of species is important for the prevention of vector-borne diseases. Furthermore, the same study (Chaves et al. 2021) demonstrates that anthropogenic actions favor the abundance of medically important mosquitoes not only in urban environments but also in tropical forests. In accordance with the information described above, Prist et al. (2022) recently showed that the construction of roads and the associated increase in forest fragmentation and forest edges facilitate yellow fever virus dispersion. Road construction and associated environmental degradation have been a threat to the Amazon biome from the 1970s to the present (Barni et al. 2015, Ferrante & Fearnside 2020a).

The construction of hydroelectric dams in tropical forest areas can result in population explosions of some mosquito species, as occurred in Brazil's Tucuruí Dam for *Mansonia* species (Tadei et al. 1991, Fearnside 1999) and at the Samuel Dam for *Culex* species (Fearnside 2005). In the first years after dam construction, large areas of the reservoirs were covered by aquatic plants (macrophytes) that provide breeding grounds for *Mansonia* mosquitoes (Fearnside 2001). Potential spillover events involving mosquito-borne pathogens are therefore a major concern in the Amazon region.

Hunting and commercialization of wild animals in the Amazon region is very intense, with a bushmeat market reaching up to 6.49 kg per person/year in the central Amazon (quantity varies by Amazon region) (van Vliet et al. 2014, El Bizri et al., 2020). These data suggest that spillover events derived from bushmeat practices are a recurrent possibility in the Amazon region, similar to what happens in other countries with high biodiversity (Ellwanger & Chies 2021).

In addition to habitat fragmentation, construction of water reservoirs and bushmeat practices, logging, mining, and other exploitative (and often illegal) economic activities in the Amazon region trigger a number of ecological and demographic changes, including migratory flows, habitat loss, unplanned urbanization, prostitution, pollution, climate change, and extreme weather events (Ellwanger et al. 2020). As discussed earlier in this article, these conditions directly or indirectly favor the occurrence of spillover events and the spread of emerging pathogens. For this reason, deforestation in the Amazon Forest and other anthropogenic activities in the region create the "perfect storm" of infectious diseases in the Amazon region (reviewed in Ellwanger et al. 2020).

The potential emergence of pathogens in the Amazon Forest may affect populations living in the region as well as people living outside the Amazon region. As exemplified by the COVID-19 pandemic, emerging pathogens can spread across the world very easily and quickly. Thus, conserving the Amazon Forest is critical not only to protect biodiversity and associated ecosystem services (e.g., water cycling, carbon stock maintenance); protecting the Amazon biome is a global public health measure (Fearnside 2008, Ellwanger et al., 2020).

Combating deforestation, mining and other types of land-use change is difficult to achieve, but this is not an impossible task. In Brazil, deforestation in the Amazon region declined greatly (~70%) between 2005 and 2012 (Figure 1, panel a), in part due to government policies (West et al. 2019, Dobson et al. 2020, West & Fearnside 2021). These policies have ended under Brazil's presidential administration that took office in January 2019 (Ferrante & Fearnside 2019, 2020b), but the potential for controlling deforestation through government policies remains an essential lesson. A recent study (Dobson et al. 2020) pointed out that the costs of mitigating a pandemic such as the COVID-19 are much greater (estimated at US$8.1 to US$15.8 trillion) than the amount that would have to be invested to prevent the main drivers of emerging infectious disease events, estimated at US$17.7 to US$26.9 billion per year. Of note, the prevention costs for 10 years would represent ~2% of the costs of the COVID-19 pandemic (Dobson et al. 2020). In other words, conservation actions protect the environment, limit the spread of infectious diseases, and are cheaper than bearing the burden of emerging infectious disease events. Also, in Brazil, the demarcation of Indigenous lands (*Terras Indígenas*) is an effective way of limiting the exploitation of natural resources and land-use changes while protecting traditional communities. The contribution of protected areas governed by local communities and Indigenous peoples in the field of biodiversity conservation is widely recognized (Corrigan et al. 2018). Considering that Brazil holds most of the territory of the Amazon Forest and has strong political and economic powers, the country needs to take the lead in the conservation of the region, contributing to the reduction of the risks of potential spillover events in the Amazon Forest.

CONCLUSION

This article synthesized the main connections between human-related environmental disturbances, ecological modifications, and increased risk of spillover events (Figure 2), primarily based on examples and models from different world regions. In brief, anthropogenic disturbances in the environment lead to changes in ecological niches, reduction of the dilution effect, increased contact between humans and other animals, changes in the incidence and load of pathogens in animal populations, and alterations in the abiotic factors of landscapes, among other ecological changes. These alterations can increase the risk of spillover events, facilitating new infectious disease outbreaks. In addition to our interpretation of the issues addressed in this paper, we emphasize that other models also explain the relationship between human activity, environmental disturbances, and emerging infectious diseases (e.g., Wolfe et al. 2007, Parrish et al. 2008, Karesh et al. 2012, Morse et al. 2012, Murray & Daszak 2013, Faust et al. 2018, Glidden et al. 2021). These interpretations are generally not mutually exclusive, and in most cases are complementary. Above all, it is important to keep in mind that generalist explanations for the emergence of infectious diseases will always be incomplete (Jones et al. 2013). Each outbreak, epidemic, pandemic, or small-scale zoonotic event has its specific characteristics and triggers that are inherent to the place and

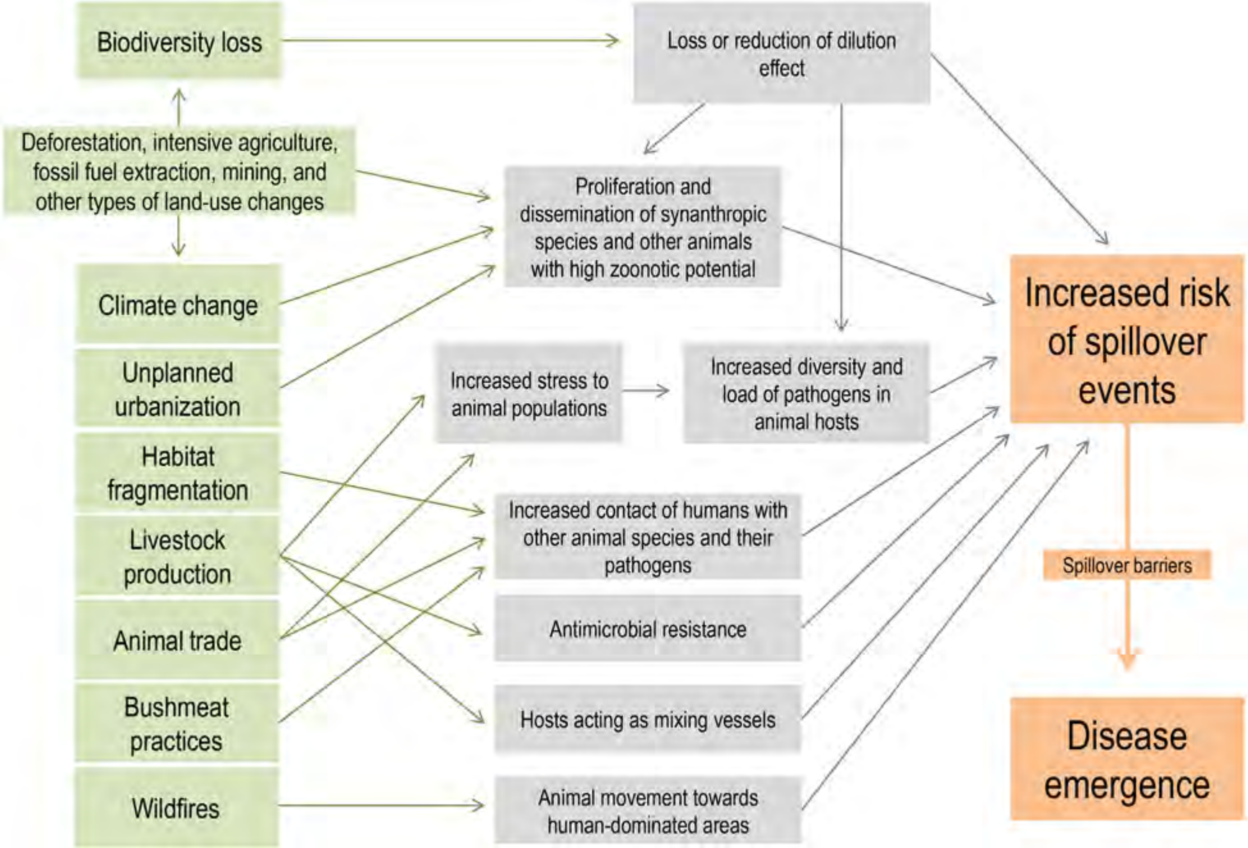

Figure 2. Connections between human-related environmental disturbances, ecological modifications and increased risk of zoonotic spillover events. Spillover barriers are factors that facilitate or hinder the transmission of pathogens between different species/populations. They can be biological (e.g., genetic proximity between hosts, immunological and genetic factors), demographic (e.g., overcrowding), ecological (e.g., habitat sharing), cultural (e.g., bushmeat practices), and associated with pathogens (e.g., virulence, survival in the environment). These barriers affect both spillover risk and the outcome of spillover events. More information concerning spillover barriers can be found in Plowright et al. (2017) and Ellwanger & Chies (2021).

context in which it occurred. Considering the specificities of each environment, our review brought a discussion specifically focused on the Amazon rainforest, showing that increasing anthropogenic damage in the region may also increase the risk of zoonotic spillover events and spread of infectious diseases, impacting the Amazon populations and potentially populations elsewhere (Figure 1). Finally, conservation efforts lead to benefits to different global spheres in an integrated manner, as they help to contain anthropic activities on the environment and to reduce the risk of zoonotic spillover events.

Acknowledgments

We thank the agencies that funded the authors of this article. **Joel Henrique Ellwanger** receives a postdoctoral fellowship from Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (Programa Nacional de Pós-Doutorado – PNPD/CAPES, Brazil). **Philip Martin Fearnside** receives a research fellowship from Conselho Nacional de Desenvolvimento Científico e Tecnológico (Bolsa de Produtividade em Pesquisa - Nível 1A, CNPq, Brazil). **Marina Ziliotto** receives a fellowship from CAPES (Brazil). **Ana Beatriz Gorini da Veiga** receives a research fellowship from CNPq (Bolsa de Produtividade em Pesquisa - Nível 2, CNPq, Brazil) and has research project funded by FAPERGS (Brazil). **Gustavo Fioravanti Vieira** receives a research fellowship from CNPq (Bolsa de Produtividade em Pesquisa - Nível 2, CNPq, Brazil). **Evelise Bach** receives a postdoctoral fellowship from

CAPES (Brazil). **Nícolas Felipe Drumm Müller** receives a fellowship from CNPq (Brazil). **Gabriel Lopes** receives a postdoctoral fellowship from CAPES (Brazil). **Bruna Kulmann-Leal** receives a doctoral fellowship from CAPES (Brazil). **Valéria de Lima Kaminski** receives a postdoctoral fellowship from Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP, Brazil). **Etiele de Senna Silveira** receives a doctoral fellowship from CAPES (Brazil). **Fernando Rosado Spilki** receives a research fellowship from CNPq (Bolsa de Produtividade em Pesquisa - Nível 1B, CNPq, Brazil) and has research project funded by Financiadora de Inovação e Pesquisa do Ministério da Ciência, Tecnologia e Inovações (Finep-MCTI; Brazil). **José Artur Bogo Chies** receives a research fellowship from CNPq (Bolsa de Produtividade em Pesquisa - Nível 1A, CNPq, Brazil) and has research project funded by FAPERGS (Brazil) and CAPES ("Prevenção e combate a surtos, endemias, epidemias e pandemias" CAPES AUXPE 686/2020; Brazil).

REFERENCES

ADRIANI KS, BROUWER MC, GELDHOFF M, BAAS F, ZWINDERMAN AH, PAUL MORGAN B, HARRIS CL, VAN DER ENDE A & VAN DE BEEK D. 2013. Common polymorphisms in the complement system and susceptiblity to bacterial meningitis. J Infect 66: 255-262.

AFSHINNEKOO E ET AL. 2021. COVID-19 drug practices risk antimicrobial resistance evolution. Lancet Microbe 2: e135-e136.

AGUIAR AP ET AL. 2016. Land use change emission scenarios: Anticipating a forest transition process in the Brazilian Amazon. Glob Chang Biol 22: 1821-1840.

ALLAN BF ET AL. 2009. Ecological correlates of risk and incidence of West Nile virus in the United States. Oecologia 158: 699-708.

ALLAN BF, KEESING F & OSTFELD RS. 2003. Effect of forest fragmentation on Lyme disease risk. Conserv Biol 17: 267-272.

ALMEIDA LS, COTA ALS & RODRIGUES DF. 2020. Sanitation, arboviruses, and environmental determinants of disease: impacts on urban health. Cien Saude Colet 25: 3857-3868.

ALMEIDA MAB, DOS SANTOS E, CARDOSO JC, DA FONSECA DF, NOLL CA, SILVEIRA VR, MAEDA AY, DE SOUZA RP, KANAMURA C & BRASIL RA. 2012. Yellow fever outbreak affecting *Alouatta* populations in southern Brazil (Rio Grande do Sul State), 2008-2009. Am J Primatol 74: 68-76.

ALMEIDA MAB, DOS SANTOS E, CARDOSO JC, DA SILVA LG, RABELO RM & BICCA-MARQUES JC. 2019. Predicting yellow fever through species distribution modeling of virus, vector, and monkeys. Ecohealth 16: 95-108.

AMMAN BR ET AL. 2020. Isolation of Angola-like Marburg virus from Egyptian rousette bats from West Africa. Nat Commun 11: 510.

AMMAN BR ET AL. 2012. Seasonal pulses of Marburg virus circulation in juvenile *Rousettus aegyptiacus* bats coincide with periods of increased risk of human infection. PLoS Pathog 8: e1002877.

ANDERSEN KG, RAMBAUT A, LIPKIN WI, HOLMES EC & GARRY RF. 2020. The proximal origin of SARS-CoV-2. Nat Med 26: 450-452.

ANYAMBA A, LINTHICUM KJ & TUCKER CJ. 2001. Climate-disease connections: Rift Valley Fever in Kenya. Cad Saude Publica 17: 133-140.

BARNI PE, FEARNSIDE PM & GRAÇA PM. 2015. Simulating deforestation and carbon loss in Amazonia: impacts in Brazil's Roraima state from reconstructing Highway BR-319 (Manaus-Porto Velho). Environ Manage 55: 259-278.

BAUSCH DG ET AL. 2003. Risk factors for Marburg hemorrhagic fever, Democratic Republic of the Congo. Emerg Infect Dis 9: 1531-1537.

BECKER DJ, EBY P, MADDEN W, PEEL AJ & PLOWRIGHT RK. 2021. Ecological conditions experienced by bat reservoir hosts predict the intensity of Hendra virus excretion over space and time. Available at: https://doi.org/10.1101/2021.08.19.457011. Accessed on February 1st, 2022.

BECKER DJ, WASHBURNE AD, FAUST CL, PULLIAM JRC, MORDECAI EA, LLOYD-SMITH JO & PLOWRIGHT RK. 2019. Dynamic and integrative approaches to understanding pathogen spillover. Philos Trans R Soc Lond B Biol Sci 374: 20190014.

BENNETT AJ ET AL. 2020. Relatives of rubella virus in diverse mammals. Nature 586: 424-428.

BERRY IM, RUTVISUTTINUNT W, SIPPY R, BELTRAN-AYALA E, FIGUEROA K, RYAN S, SRIKANTH A, STEWART-IBARRA AM, ENDY T & JARMAN RG. 2020. The origins of dengue and chikungunya viruses in Ecuador following increased migration from Venezuela and Colombia. BMC Evol Biol 20: 31.

BEYER RM, 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. Sci Total Environ 767: 145413.

BLOOMFIELD LSP, MCINTOSH TL & LAMBIN EF. 2020. Habitat fragmentation, livelihood behaviors, and contact between people and nonhuman primates in Africa. Landscape Ecol 35: 985-1000.

BORETTI A & ROSA L. 2019. Reassessing the projections of the World Water Development Report. npj Clean Water 2: 15.

BORREMANS B, FAUST C, MANLOVE KR, SOKOLOW SH & LLOYD-SMITH JO. 2019. Cross-species pathogen spillover across ecosystem boundaries: mechanisms and theory. Philos Trans R Soc Lond B Biol Sci 374: 20180344.

BRANCALION PHS ET AL. 2020. Emerging threats linking tropical deforestation and the COVID-19 pandemic. Perspect Ecol Conserv 18: 243-246.

BRILLHANTE RSN ET AL. 2012. Coccidioidomycosis in armadillo hunters from the state of Ceará, Brazil. Mem Inst Oswaldo Cruz 107: 813-815.

BROOK CE & DOBSON AP. 2015. Bats as 'special' reservoirs for emerging zoonotic pathogens. Trends Microbiol 23: 172-180.

BRUBACHER J, ALLEN DM, DÉRY SJ, PARKES MW, CHHETRI B, MAK S, SOBIE S & TAKARO TK. 2020. Associations of five food- and water-borne diseases with ecological zone, land use and aquifer type in a changing climate. Sci Total Environ 728: 138808.

BRUGHA R & GRIGG J. 2014. Urban air pollution and respiratory infections. Paediatr Respir Rev 15: 194-199.

BURGNER D, JAMIESON SE & BLACKWELL JM. 2006. Genetic susceptibility to infectious diseases: big is beautiful, but will bigger be even better? Lancet Infect Dis 6: 653-663.

BURKETT-CADENA ND & VITTOR AY. 2018. Deforestation and vector-borne disease: Forest conversion favors important mosquito vectors of human pathogens. Basic Appl Ecol 26: 101-110.

CAPELLÃO RT, LAZAR A & BONVICINO CR. 2015. Infecção natural por agentes zoonóticos em tatus (Mammalia: Cingulata) na América do Sul. Bol Soc Bras Mastozool 73: 23-36.

CARDOSO JC ET AL. 2010. Yellow fever virus in *Haemagogus leucocelaenus* and *Aedes serratus* mosquitoes, southern Brazil, 2008. Emerg Infect Dis 16: 1918-1924.

CARDOZO M, FIAD FG, CROCCO LB & GORLA DE. 2021. Effect of habitat fragmentation on rural house invasion by sylvatic triatomines: A multiple landscape-scale approach. PLoS Negl Trop Dis 15: e0009579.

CASTELLI F & SULIS G. 2017. Migration and infectious diseases. Clin Microbiol Infect 23: 283-289.

CDC - CENTERS FOR DISEASE CONTROL AND PREVENTION. 2009. Imported case of Marburg hemorrhagic fever - Colorado, 2008. MMWR Morb Mortal Wkly Rep 58: 1377-1381.

CEBALLOS G, EHRLICH PR, BARNOSKY AD, GARCÍA A, PRINGLE RM & PALMER TM. 2015. Accelerated modern human-induced species losses: Entering the sixth mass extinction. Sci Adv 1: e1400253.

CHANG LY ET AL. 2008. HLA-A33 is associated with susceptibility to enterovirus 71 infection. Pediatrics 122: 1271-1276.

CHAVES LSM, BERGO ES, CONN JE, LAPORTA GZ, PRIST PR & SALLUM MAM. 2021. Anthropogenic landscape decreases mosquito biodiversity and drives malaria vector proliferation in the Amazon rainforest. PLoS ONE 16: e0245087.

CHOMEL BB, BELOTTO A & MESLIN FX. 2007. Wildlife, exotic pets, and emerging zoonoses. Emerg Infect Dis 13: 6-11.

CHUA KB. 2003. Nipah virus outbreak in Malaysia. J Clin Virol 26: 265-275.

CHUA KB, CHUA BH & WANG CW. 2002. Anthropogenic deforestation, El Niño and the emergence of Nipah virus in Malaysia. Malays J Pathol 24: 15-21.

CHUANCHUEN R, AJARIYAKHAJORN K, KOOWATANANUKUL C, WANNAPRASAT W, KHEMTONG S & SAMNGAMNIM S. 2010. Antimicrobial resistance and virulence genes in *Salmonella enterica* isolates from dairy cows. Foodborne Pathog Dis 7: 63-69.

CIVITELLO DJ ET AL. 2015. Biodiversity inhibits parasites: Broad evidence for the dilution effect. Proc Natl Acad Sci USA 112: 8667-8671.

CONIJN JG, BINDRABAN PS, SCHRÖDER JJ & JONGSCHAAP REE. 2018. Can our global food system meet food demand within planetary boundaries? Agric Ecosyst Environ 251: 244-256.

CORRÊA FM, CHAVES ÓM, PRINTES RC & ROMANOWSKI HP. 2018. Surviving in the urban-rural interface: Feeding and ranging behavior of brown howlers (*Alouatta guariba clamitans*) in an urban fragment in southern Brazil. Am J Primatol 80: e22865.

CORRIGAN C, BINGHAM H, SHI Y, LEWIS E, CHAUVENET A & KINGSTON N. 2018. Quantifying the contribution to biodiversity conservation of protected areas governed by indigenous peoples and local communities. Biol Conserv 227: 403-412.

COSTA ACS, AHMAD S & ESSAR MY. 2021.Vaccination: Brazil fails Indigenous people again with two-tier scheme. Nature 593: 510.

COSTA FAM, REIS RC, BENEVIDES F, TOMÉ GS & HOLANDA MA. 2001. Coccidioidomicose pulmonar em caçador de tatus. J Pneumologia 27: 275-278.

COUTO-LIMA D, MADEC Y, BERSOT MI, CAMPOS SS, MOTTA MA, SANTOS FBD, VAZEILLE M, VASCONCELOS PFDC, LOURENÇO-DE-OLIVEIRA R & FAILLOUX AB. 2017. Potential risk of re-emergence of urban transmission of Yellow Fever virus in Brazil facilitated by competent *Aedes* populations. Sci Rep 7: 4848.

CROCCO L, NATTERO J, LÓPEZ A, CARDOZO M, SORIA C, ORTIZ V & RODRIGUEZ CS. 2019. Factors associated with the presence of triatomines in rural areas of south Argentine Chaco. Rev Soc Bras Med Trop 52: e20180357.

CUI J, LI F & SHI ZL. 2019. Origin and evolution of pathogenic coronaviruses. Nat Rev Microbiol 17: 181-192.

CUNHA AA, VIEIRA MV & GRELLE CEV. 2006. Preliminary observations on habitat, support use and diet in two non-native primates in an urban Atlantic forest fragment: The capuchin monkey (*Cebus* sp.) and the common marmoset (*Callithrix jacchus*) in the Tijuca forest, Rio de Janeiro. Urban Ecosyst 9: 351-359.

CURI NHA, PASCHOAL AMO, MASSARA RL, MARCELINO AP, RIBEIRO AA, PASSAMANI M, DEMÉTRIO GR & CHIARELLO AG. 2014. Factors associated with the seroprevalence of leishmaniasis in dogs living around Atlantic Forest fragments. PLoS ONE 9: e104003.

DA SILVA MB ET AL. 2018. Evidence of zoonotic leprosy in Pará, Brazilian Amazon, and risks associated with human contact or consumption of armadillos. PLoS Negl Trop Dis 12: e0006532.

DANTAS-TORRES F. 2015. Climate change, biodiversity, ticks and tick-borne diseases: The butterfly effect. Int J Parasitol Parasites Wildl 4: 452-461.

DE VRIES RD, DE JONG A, VERBURGH RJ, SAUERHERING L, VAN NIEROP GP, VAN BINNENDIJK RS, OSTERHAUS ADME, MAISNER A, KOOPMANS MPG & DE SWART RL. 2020. Human paramyxovirus infections induce T cells that cross-react with zoonotic henipaviruses. mBio 11: e00972-20.

DEHGHAN S, SETO J, LIU EB, ISMAIL AM, MADUPU R, HEIM A, JONES MS, DYER DW, CHODOSH J & SETO D. 2019. A zoonotic adenoviral human pathogen emerged through genomic recombination among human and nonhuman simian hosts. J Virol 93: e00564-19.

DING Y, ZHAO J, HE X, LI M, GUAN H, ZHANG Z & LI P. 2016. Antimicrobial resistance and virulence-related genes of *Streptococcus* obtained from dairy cows with mastitis in Inner Mongolia, China. Pharm Biol 54: 162-167.

DOBSON AP ET AL. 2020. Ecology and economics for pandemic prevention. Science 369: 379-381.

DONG E, DU H & GARDNER L. 2020. An interactive web-based dashboard to track COVID-19 in real time. Lancet Infect Dis 20: 533-534.

EISLER R. 2003. Health risks of gold miners: a synoptic review. Environ Geochem Health 25: 325-345.

EL BIZRI HR ET AL. 2020 Urban wild meat consumption and trade in central Amazonia. Conserv Biol 34: 438-448.

ELLWANGER JH & CHIES JAB. 2017. Keeping track of hidden dangers - The short history of the Sabiá virus. Rev Soc Bras Med Trop 50: 3-8.

ELLWANGER JH & CHIES JAB. 2018. Wind: a neglected factor in the spread of infectious diseases. Lancet Planet Health 2: e475.

ELLWANGER JH & CHIES JAB. 2019. The triad “dogs, conservation and zoonotic diseases” - An old and still neglected problem in Brazil. Perspect Ecol Conserv 17: 157-161.

ELLWANGER JH & CHIES JAB. 2021. Zoonotic spillover: Understanding basic aspects for better prevention. Genet Mol Biol 44: e20200355.

ELLWANGER JH ET AL. 2020. Beyond diversity loss and climate change: Impacts of Amazon deforestation on infectious diseases and public health. An Acad Bras Cienc 92: e20191375.

ELLWANGER JH, KAMINSKI VL & CHIES JAB. 2019. Emerging infectious disease prevention: Where should we invest our resources and efforts? J Infect Public Health 12: 313-316.

ELLWANGER JH, VEIGA ABG, KAMINSKI VL, VALVERDE-VILLEGAS JM, FREITAS AWQ & CHIES JAB. 2021. Control and prevention of infectious diseases from a One Health perspective. Genet Mol Biol 44: e20200256.

EPSTEIN JH, FIELD HE, LUBY S, PULLIAM JRC & DASZAK P. 2006. Nipah virus: impact, origins, and causes of emergence. Curr Infect Dis Rep 8: 59-65.

EVERARD M, JOHNSTON P, SANTILLO D & STADDON C. 2020. The role of ecosystems in mitigation and management of Covid-19 and other zoonoses. Environ Sci Policy 111: 7-17.

FALAVIGNA-GUILHERME AL, SILVA AM, GUILHERME EV & MORAIS DL. 2005. Retrospective study of malaria prevalence and *Anopheles* genus in the area of influence of the Binational Itaipu Reservoir. Rev Inst Med Trop São Paulo 47: 81-86.

FARIA NR ET AL. 2014. The early spread and epidemic ignition of HIV-1 in human populations. Science 346: 56-61.

FAUST CL, MCCALLUM HI, BLOOMFIELD LSP, GOTTDENKER NL, GILLESPIE TR, TORNEY CJ, DOBSON AP & PLOWRIGHT RK. 2018. Pathogen spillover during land conversion. Ecol Lett 21: 471-483.

FEARNSIDE PM. 1999. Social impacts of Brazil's Tucuruí Dam. Environ Manage 24: 483-495.

FEARNSIDE PM. 2001. Environmental impacts of Brazil's Tucuruí Dam: Unlearned lessons for hydroelectric development in Amazonia. Environ Manage 27: 377-396.

FEARNSIDE PM. 2005. Brazil's Samuel Dam: Lessons for hydroelectric development policy and the environment in Amazonia. Environ Manage 35: 1-19.

FEARNSIDE PM. 2008. Amazon forest maintenance as a source of environmental services. An Acad Bras Cienc 80: 101-114.

FEARNSIDE PM, FIGUEIREDO AMR & BONJOUR SCM. 2013. Amazonian forest loss and the long reach of China's influence. Environ Dev Sustain 15: 325-338.

FERGUSON R, RAMANAKUMAR AV, RICHARDSON H, TELLIER PP, COUTLÉE F, FRANCO EL & ROGER M. 2011. Human leukocyte antigen (HLA)-E and HLA-G polymorphisms in human papillomavirus infection susceptibility and persistence. Hum Immunol 72: 337-341.

FERRANTE L, BARBOSA RI, DUCZMAL L & FEARNSIDE PM. 2021. Brazil's planned exploitation of Amazonian indigenous lands for commercial agriculture increases risk of new pandemics. Reg Environ Change 21: 81.

FERRANTE L & FEARNSIDE PM. 2019. Brazil's new president and 'ruralists' threaten Amazonia's environment, traditional peoples and the global climate. Environ Conserv 46: 261-263.

FERRANTE L & FEARNSIDE PM. 2020a. The Amazon's road to deforestation. Science 369: 634.

FERRANTE L & FEARNSIDE PM. 2020b. Protect Indigenous peoples from COVID-19. Science 368: 251.

FERRANTE L, STEINMETZ WA, ALMEIDA ACL, LEÃO J, VASSÃO RC, TUPINAMBÁS U, FEARNSIDE PM & DUCZMAL LH. 2020. Brazil's policies condemn Amazonia to a second wave of COVID-19. Nat Med 26: 1315.

FIELD H, YOUNG P, YOB JM, MILLS J, HALL L & MACKENZIE J. 2001.The natural history of Hendra and Nipah viruses. Microbes Infect 3: 307-314.

FIGUEIREDO GG, BORGES AA, CAMPOS GM, MACHADO AM, SAGGIORO FP, SABINO JÚNIOR GS, BADRA SJ, ORTIZ AAA & FIGUEIREDO LTM. 2010. Diagnosis of hantavirus infection in humans and rodents in Ribeirão Preto, State of São Paulo, Brazil. Rev Soc Bras Med Trop 43: 348-354.

FRANKLINOS LHV, JONES KE, REDDING DW & ABUBAKAR I. 2019. The effect of global change on mosquito-borne disease. Lancet Infect Dis 19: e302-e312.

FU Y ET AL. 2019. Prevalence and potential zoonotic risk of hookworms from stray dogs and cats in Guangdong, China. Vet Parasitol Reg Stud Reports 17: 100316.

FUCHS R, ALEXANDER P, BROWN C, COSSAR F, HENRY RC & ROUNSEVELL M. 2019. Why the US-China trade war spells disaster for the Amazon. Nature 567: 451-454.

GANTI K, BAGGA A, DASILVA J, SHEPARD SS, BARNES JR, SHRINER S, KOELLE K & LOWEN AC. 2021. Avian influenza A viruses reassort and diversify differently in mallards and mammals. Viruses 13: 509.

GERMAIN G ET AL. 2019. Quebec's multi-party observatory on zoonoses and adaptation to climate change. Can Commun Dis Rep 45: 143-148.

GITHEKO AK, LINDSAY SW, CONFALONIERI UE & PATZ JA. 2000. Climate change and vector-borne diseases: A regional analysis. Bull World Health Organ 78: 1136-1147.

GLIDDEN CK ET AL. 2021. Human-mediated impacts on biodiversity and the consequences for zoonotic disease spillover. Curr Biol 31: R1342-R1361.

GOMAA MR, KANDEIL A, EL-SHESHENY R, SHEHATA MM, MCKENZIE PP, WEBBY RJ, ALI MA & KAYALI G. 2018. Evidence of infection with avian, human, and swine influenza viruses in pigs in Cairo, Egypt. Arch Virol 163: 359-364.

GORTÁZAR C, FERROGLIO E, HÖFLE U, FRÖLICH K & VICENTE J. 2007. Diseases shared between wildlife and livestock: a European perspective. Eur J Wildl Res 53: 241-256.

GRACEY M & KING M. 2009. Indigenous health part 1: determinants and disease patterns. Lancet 374: 65-75.

GRANGE ZL ET AL. 2021. Ranking the risk of animal-to-human spillover for newly discovered viruses. Proc Natl Acad Sci USA 118: e2002324118.

GRAY RR ET AL. 2009. Spatial phylodynamics of HIV-1 epidemic emergence in east Africa. AIDS 23: F9-F17.

GREER A, NG V & FISMAN D. 2008. Climate change and infectious diseases in North America: the road ahead. CMAJ 178: 715-722.

GRYSEELS S, WATTS TD, KABONGO MPOLESHA JM, LARSEN BB, LEMEY P, MUYEMBE-TAMFUM JJ, TEUWEN DE & WOROBEY M. 2020. A near full-length HIV-1 genome from 1966 recovered from formalin-fixed paraffin-embedded tissue. Proc Natl Acad Sci USA 117: 12222-12229.

GUEDES RNC, WALSE SS & THRONE JE. 2017. Sublethal exposure, insecticide resistance, and community stress. Curr Opin Insect Sci 21: 47-53.

GUÉGAN JF, AYOUBA A, CAPPELLE J & DE THOISY B. 2020. Forests and emerging infectious diseases: unleashing the beast within. Environ Res Lett 15: 083007.

GUSHULAK BD & MACPHERSON DW. 2004. Globalization of infectious diseases: the impact of migration. Clin Infect Dis 38: 1742-1748.

GUTERRES A, DE OLIVEIRA RC, FERNANDES J, MAIA RM, TEIXEIRA BR, OLIVEIRA FCG, BONVICINO CR, D'ANDREA PS, SCHRAGO CG & DE LEMOS ERS. 2018. Co-circulation of Araraquara and Juquitiba Hantavirus in Brazilian Cerrado. Microb Ecol 75: 783-789.

HADDAD NM ET AL. 2015. Habitat fragmentation and its lasting impact on Earth's ecosystems. Sci Adv 1: e1500052.

HADLEY AS & BETTS MG. 2009. Tropical deforestation alters hummingbird movement patterns. Biol Lett 5: 207-210.

HAHN BH, SHAW GM, DE COCK KM & SHARP PM. 2000. AIDS as a zoonosis: scientific and public health implications. Science 287: 607-614.

HAN BA, CASTELLANOS AA, SCHMIDT JP, FISCHHOFF IR & DRAKE JM. 2021. The ecology of zoonotic parasites in the Carnivora. Trends Parasitol 37: 1096-1110.

HAN BA, KRAMER AM & DRAKE JM. 2016. Global patterns of zoonotic disease in mammals. Trends Parasitol 32: 565-577.

HAN BA, SCHMIDT JP, BOWDEN SE & DRAKE JM. 2015. Rodent reservoirs of future zoonotic diseases. Proc Natl Acad Sci USA 112: 7039-7044.

HART WS, HEUZENROEDER MW & BARTON MD. 2004. Antimicrobial resistance in *Campylobacter* spp., *Escherichia coli* and enterococci associated with pigs in Australia. J Vet Med B Infect Dis Vet Public Health 51: 216-21.

HASHIZUME M, WAGATSUMA Y, FARUQUE AS, HAYASHI T, HUNTER PR, ARMSTRONG B & SACK DA. 2008. Factors determining vulnerability to diarrhoea during and after severe floods in Bangladesh. J Water Health 6: 323-332.

HAYMAN DTS. 2019. Bat tolerance to viral infections. Nature Microbiol 4: 728-729.

HE Y, YUAN Q, MATHIEU J, STADLER L, SENEHI N, SUN R & ALVAREZ PJJ. 2020. Antibiotic resistance genes from livestock waste: occurrence, dissemination, and treatment. NPJ Clean Water 3: 4.

HIRALDO D, JAMES K & CARROLL SR. 2021. Case Report: Indigenous sovereignty in a pandemic: Tribal codes in the United States as preparedness. Front Sociol 6: 617995.

HOLMES EC ET AL. 2021. The origins of SARS-CoV-2: A critical review. Cell 184: 4848-4856.

HOPPE E ET AL. 2015. Multiple cross-species transmission events of human adenoviruses (HAdV) during hominine evolution. Mol Biol Evol 32: 2072-2084.

HOTEZ PJ. 2010. Neglected infections of poverty among the Indigenous peoples of the Arctic. PLoS Negl Trop Dis 4: e606.

HOTEZ PJ, NUZHATH T & COLWELL B. 2020. Combating vaccine hesitancy and other 21st century social determinants in the global fight against measles. Curr Opin Virol 41: 1-7.

IBÁÑEZ AM, ROZO SV & URBINA MJ. 2021. Forced migration and the spread of infectious diseases. J Health Econ 79: 102491.

IBRAHIM M, SCHELLING E, ZINSSTAG J, HATTENDORF J, ANDARGIE E & TSCHOPP R. 2021. Sero-prevalence of brucellosis, Q-fever and Rift Valley fever in humans and livestock in Somali Region, Ethiopia. PLoS Negl Trop Dis 15: e0008100.

INPE - INSTITUTO NACIONAL DE PESQUISAS ESPACIAIS. 2022. TerraBrasilis, Programa de Cálculo do Desflorestamento da Amazônia (PRODES). Taxas de desmatamento - Amazônia Legal - Estados. Available at: http://terrabrasilis.dpi.inpe.br/app/dashboard/deforestation/biomes/legal_amazon/rates [data under Attribution-ShareAlike 4.0 International (CC BY-SA 4.0) license]. Accessed on February 1st, 2022.

IPBES - WORKSHOP REPORT ON BIODIVERSITY AND PANDEMICS OF THE INTERGOVERNMENTAL PLATFORM ON BIODIVERSITY AND ECOSYSTEM SERVICES. DASZAK P ET AL. 2020. IPBES secretariat, Bonn, Germany. doi: 10.5281/zenodo.4147317.

JOHNS HOPKINS UNIVERSITY. 2022. COVID-19 DASHBOARD BY THE CENTER FOR SYSTEMS SCIENCE AND ENGINEERING (CSSE) AT JOHNS HOPKINS UNIVERSITY. Available at: https://coronavirus.jhu.edu/map.html. Accessed on February 2, 2022.

JOHNSON AR, WIENS JA, MILNE BT & CRIST TO. 1992. Animal movements and population dynamics in heterogeneous landscapes. Landscape Ecol 7: 63-75.

JOHNSON CK, HITCHENS PL, PANDIT PS, RUSHMORE J, EVANS TS, YOUNG CCW & DOYLE MM. 2020. Global shifts in mammalian population trends reveal key predictors of virus spillover risk. Proc Biol Sci 287: 20192736.

JOHNSON ED, JOHNSON BK, SILVERSTEIN D, TUKEI P, GEISBERT TW, SANCHEZ AN & JAHRLING PB. 1996. Characterization of a new

Marburg virus isolated from a 1987 fatal case in Kenya. Arch Virol Suppl 11: 101-114.

JONES BA ET AL. 2013. Zoonosis emergence linked to agricultural intensification and environmental change. Proc Natl Acad Sci USA 110: 8399-8404.

JONES KE, PATEL NG, LEVY MA, STOREYGARD A, BALK D, GITTLEMAN JL & DASZAK P. 2008. Global trends in emerging infectious diseases. Nature 451: 990-993.

JUDSON SD, FISCHER R, JUDSON A & MUNSTER VJ. 2016. Ecological contexts of index cases and spillover events of different Ebolaviruses. PLoS Pathog 12: e1005780.

KALINDA C, CHIMBARI M & MUKARATIRWA S. 2017. Implications of changing temperatures on the growth, fecundity and survival of intermediate host snails of schistosomiasis: A systematic Review. Int J Environ Res Public Health 14: 80.

KAN B ET AL. 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. J Virol 79: 11892-11900.

KARESH WB & NOBLE E. 2009. The bushmeat trade: increased opportunities for transmission of zoonotic disease. Mt Sinai J Med 76: 429-434.

KARESH WB ET AL. 2012. Ecology of zoonoses: natural and unnatural histories. Lancet 380: 1936-1945.

KARESH WB, COOK RA, BENNETT EL & NEWCOMB J. 2005. Wildlife trade and global disease emergence. Emerg Infect Dis 11: 1000-1002.

KEELE BF ET AL. 2006. Chimpanzee reservoirs of pandemic and nonpandemic HIV-1. Science 313: 523-526.

KEESING F & OSTFELD RS. 2021. Dilution effects in disease ecology. Ecol Lett 24: 2490-2505.

KEESING F ET AL. 2010. Impacts of biodiversity on the emergence and transmission of infectious diseases. Nature 468: 647-652.

KEESING F, HOLT RD & OSTFELD RS. 2006. Effects of species diversity on disease risk. Ecol Lett 9: 485-498.

KEISER J, MALTESE MF, ERLANGER TE, BOS R, TANNER M, SINGER BH & UTZINGER J. 2005. Effect of irrigated rice agriculture on Japanese encephalitis, including challenges and opportunities for integrated vector management. Acta Trop 95: 40-57.

KIBRET S, LAUTZE J, MCCARTNEY M, NHAMO L & YAN G. 2019. Malaria around large dams in Africa: effect of environmental and transmission endemicity factors. Malar J 18: 303.

KILPATRICK AM, SALKELD DJ, TITCOMB G & HAHN MB. 2017. Conservation of biodiversity as a strategy for improving human health and well-being. Philos Trans R Soc Lond B Biol Sci 372: 20160131.

KIRBY KR, LAURANCE WF, ALBERNAZ AK, SCHROTH G, FEARNSIDE PM, BERGEN S, VENTICINQUE EM & COSTA C. 2006. The future of deforestation in the Brazilian Amazon. Futures 38: 432-453.

KOOPMANS M ET AL. 2021. Origins of SARS-CoV-2: window is closing for key scientific studies. Nature 596: 482-485.

KOVALEV SY & MAZURINA EA. 2022. Omsk hemorrhagic fever virus is a tick-borne encephalitis virus adapted to muskrat through host-jumping. J Med Virol 94: 2510-2518.

KRAMMER F ET AL. 2018. Influenza. Nat Rev Dis Primers 4: 3.

KREMER EJ. 2021. What is the risk of a deadly adenovirus pandemic? PLoS Pathog 17: e1009814.

KUZMIN IV, BOZICK B, GUAGLIARDO SA, KUNKEL R, SHAK JR, TONG S & RUPPRECHT CE. 2011. Bats, emerging infectious diseases, and the rabies paradigm revisited. Emerg Health Threats J 4: 7159.

LAM TT ET AL. 2020. Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins. Nature 583: 282-285.

LAU CL, WATSON CH, LOWRY JH, DAVID MC, CRAIG SB, WYNWOOD SJ, KAMA M & NILLES EJ. 2016. Human leptospirosis infection in Fiji: An eco-epidemiological approach to identifying risk factors and environmental drivers for transmission. PLoS Negl Trop Dis 10: e0004405.

LAUTZE J, MCCARTNEY M, KIRSHEN P, OLANA D, JAYASINGHE G & SPIELMAN A. 2007. Effect of a large dam on malaria risk: the Koka reservoir in Ethiopia. Trop Med Int Health 12: 982-989.

LEANDRO AS, LOPES RD, MARTINS CA, RIVAS AV, DA SILVA I, GALVÃO SR & MACIEL-DE-FREITAS R. 2021. The adoption of the One Health approach to improve surveillance of venomous animal injury, vector-borne and zoonotic diseases in Foz do Iguaçu, Brazil. PLoS Negl Trop Dis 15: e0009109.

LEMOS LN, PEDRINHO A, VASCONCELOS ATR, TSAI SM & MENDES LW. 2021. Amazon deforestation enriches antibiotic resistance genes. Soil Biol Biochem 153: 108110.

LEROY EM, KUMULUNGUI B, POURRUT X, ROUQUET P, HASSANIN A, YABA P, DÉLICAT A, PAWESKA JT, GONZALEZ JP & SWANEPOEL R. 2005. Fruit bats as reservoirs of Ebola virus. Nature 438: 575-576.

LETKO M, SEIFERT SN, OLIVAL KJ, PLOWRIGHT RK & MUNSTER VJ. 2020. Bat-borne virus diversity, spillover and emergence. Nat Rev Microbiol 18: 461-471.

LI H, ANDERSEN PS, STEGGER M, SIEBER RN, INGMER H, STAUBRAND N, DALSGAARD A & LEISNER JJ. 2019. Antimicrobial resistance and virulence gene profiles of methicillin-resistant and -susceptible *Staphylococcus aureus* from food products in Denmark. Front Microbiol 10: 2681.

LIMA AFR, JERALDO VLS, SILVEIRA MS, MADI RR, SANTANA TBK & MELO CM. 2012. Triatomines in dwellings and outbuildings in an endemic area of Chagas disease in northeastern Brazil. Rev Soc Bras Med Trop 45: 701-706.

LOGIUDICE K, OSTFELD RS, SCHMIDT KA & KEESING F. 2003. The ecology of infectious disease: effects of host diversity and community composition on Lyme disease risk. Proc Natl Acad Sci USA 100: 567-571.

LOOI LM & CHUA KB. 2007. Lessons from the Nipah virus outbreak in Malaysia. Malays J Pathol 29: 63-67.

LOVEJOY TE & NOBRE C. 2018. Amazon tipping point. Sci Adv 4: eaat2340.

LUIS AD ET AL. 2013. A comparison of bats and rodents as reservoirs of zoonotic viruses: are bats special? Proc Biol Sci 280: 20122753.

LYTRAS S, XIA W, HUGHES J, JIANG X & ROBERTSON DL. 2021. The animal origin of SARS-CoV-2. Science 373: 968-970.

MA F & YUAN X. 2021. Impact of climate and population changes on the increasing exposure to summertime compound hot extremes. Sci Total Environ 772: 145004.

MA W, KAHN RE & RICHT JA. 2008. The pig as a mixing vessel for influenza viruses: Human and veterinary implications. J Mol Genet Med 3: 158-166.

MAGALHAES T, CHALEGRE KDM, BRAGA C & FOY BD. 2020. The endless challenges of arboviral diseases in Brazil. Trop Med Infect Dis 5: 75.

MAGOURAS I, BROOKES VJ, JORI F, MARTIN A, PFEIFFER DU & DÜRR S. 2020. Emerging zoonotic diseases: Should we rethink the animal-human interface? Front Vet Sci 7: 582743.

MAHRENHOLZ P. 2008. Climate change and adaptation needs. Parasitol Res 103(Suppl 1): S139-S146.

MAKSIMOVIĆ Z, CORNWELL MS, SEMREN O & RIFATBEGOVIĆ M. 2017. The apparent role of climate change in a recent anthrax outbreak in cattle. Rev Sci Tech 36: 959-963.

MALTA FM ET. 2020. Sabiá virus-like mammarenavirus in patient with fatal hemorrhagic fever, Brazil, 2020. Emerg Infect Dis 26: 1332-1334.

MAMMADOVA A, MASIERO M & PETTENELLA D. 2020. Embedded deforestation: the case study of the Brazilian-Italian bovine leather trade. Forests 11: 472.

MARCONDES M & DAY MJ. 2019. Current status and management of canine leishmaniasis in Latin America. Res Vet Sci 123: 261-272.

MARIETTO-GONÇALVES GA, DE ALMEIDA SM, DE LIMA ET, OKAMOTO AS, PINCZOWSKI P & FILHO RLA. 2010. Isolation of *Salmonella enterica* serovar enteritidis in blue-fronted Amazon parrot (*Amazona aestiva*). Avian Dis 54: 151-155.

MARTIN V, CHEVALIER V, CECCATO P, ANYAMBA A, DE SIMONE L, LUBROTH J, DE LA ROCQUE S & DOMENECH J. 2008. The impact of climate change on the epidemiology and control of Rift Valley fever. Rev Sci Tech 27: 413-426.

MARTINEZ E, CESÁRIO C, DE OLIVEIRA E SILVA I & BOERE V. 2013. Domestic dogs in rural area of fragmented Atlantic Forest: potential threats to wild animals. Cienc Rural 43: 1998-2003.

MCMICHAEL C. 2015. Climate change-related migration and infectious disease. Virulence 6: 548-553.

MILLS JN. 2006. Biodiversity loss and emerging infectious disease: An example from the rodent-borne hemorrhagic fevers. Biodiversity 7: 9-17.

MIRSAEIDI M, MOTAHARI H, KHAMESI MT, SHARIFI A, CAMPOS M & SCHRAUFNAGEL DE. 2016. Climate change and respiratory infections. Ann Am Thorac Soc 13: 1223-1230.

MOLLENTZE N & STREICKER DG. 2020. Viral zoonotic risk is homogenous among taxonomic orders of mammalian and avian reservoir hosts. Proc Natl Acad Sci USA 117: 9423-9430.

MONTGOMERY RA & MACDONALD DW. 2020. COVID-19, health, conservation, and shared wellbeing: details matter. Trends Ecol Evol 35: 748-750.

MONTOYA A ET AL. 2018. Implications of zoonotic and vector-borne parasites to free-roaming cats in central Spain. Vet Parasitol 251: 125-130.

MORAND S & LAJAUNIE C. 2021. Outbreaks of vector-borne and zoonotic diseases are associated with changes in forest cover and oil palm expansion at global scale. Front Vet Sci 8: 661063.

MORENO GS, SANTANA LON, NUVOLONI FM & LOPES EFN. 2021. Incêndios, queimadas e arboviroses: relações emergentes na pré e pós pandemia. Revista Científica ANAP Brasil 14: 1-14.

MORSE SS, MAZET JA, WOOLHOUSE M, PARRISH CR, CARROLL D, KARESH WB, ZAMBRANA-TORRELIO C, LIPKIN WI & DASZAK P. 2012. Prediction and prevention of the next pandemic zoonosis. Lancet 380: 1956-1965.

MURRAY KA & DASZAK P. 2013. Human ecology in pathogenic landscapes: two hypotheses on how land use change drives viral emergence. Curr Opin Virol 3: 79-83.

NAEEM S, DUFFY JE & ZAVALETA E. 2012. The functions of biological diversity in an age of extinction. Science 336: 1401-1406.

NAGUIB MM, LI R, LING J, GRACE D, NGUYEN-VIET H & LINDAHL JF. 2021. Live and wet markets: food access versus the risk of disease emergence. Trends Microbiol 29: 573-581.

NANDI A & ALLEN LJS. 2021. Probability of a zoonotic spillover with seasonal variation. Infect Dis Model 6: 514-531.

NEMATI M, HERMANS K, LIPINSKA U, DENIS O, DEPLANO A, STRUELENS M, DEVRIESE LA, PASMANS F & HAESEBROUCK F. 2008. Antimicrobial resistance of old and recent *Staphylococcus aureus* isolates from poultry: first detection of livestock-associated methicillin-resistant strain ST398. Antimicrob Agents Chemother 52: 3817-3819.

NEWBOLD T ET AL. 2016. Has land use pushed terrestrial biodiversity beyond the planetary boundary? A global assessment. Science 353: 288-291.

NIEBUHR BBS, WOSNIACK ME, SANTOS MC, RAPOSO EP, VISWANATHAN GM, DA LUZ MGE & PIE MR. 2015. Survival in patchy landscapes: the interplay between dispersal, habitat loss and fragmentation. Sci Rep 5: 11898.

NIMMO DG ET AL. 2019. Animal movements in fire-prone landscapes. Biol Rev Camb Philos Soc 94: 981-998.

OGOLA JS, MITULLAH WV & OMULO MA. 2002. Impact of gold mining on the environment and human health: a case study in the Migori Gold Belt, Kenya. Environ Geochem Health 24: 141-157.

OLIVERO J ET AL. 2017. Recent loss of closed forests is associated with Ebola virus disease outbreaks. Sci Rep 7: 14291.

OSTERGARD JR RL. 2021. Ebola and the pestilence of corporate and governmental corruption in Guinea: Did mining interests exacerbate the largest Ebola outbreak in history (2014-2016)? Extr Ind Soc 8: 316-330.

OSTFELD RS. 2009. Biodiversity loss and the rise of zoonotic pathogens. Clin Microbiol Infect 15: 40-43.

OWERS KA, SJÖDIN P, SCHLEBUSCH CM, SKOGLUND P, SOODYALL H & JAKOBSSON M. 2017. Adaptation to infectious disease exposure in indigenous Southern African populations. Proc Biol Sci 284: 20170226.

OZDENEROL E. 2015. GIS and remote sensing use in the exploration of Lyme disease epidemiology. Int J Environ Res Public Health 12: 15182-15203.

PALHARES JCP, KICH JD, BESSA MC, BIESUS LL, BERNO LG & TRIQUES NJ. 2014. *Salmonella* and antimicrobial resistance in an animal-based agriculture river system. Sci Total Environ 472: 654-661.

PANGAU-ADAM M, NOSKE R & MUEHLENBERG M. 2012. Wildmeat or Bushmeat? Subsistence hunting and commercial harvesting in Papua (West New Guinea), Indonesia. Hum Ecol 40: 611-621.

PARK BJ ET AL. 2005. An epidemic of coccidioidomycosis in Arizona associated with climatic changes, 1998-2001. J Infect Dis 191: 1981-1987.

PARRISH CR, HOLMES EC, MORENS DM, PARK EC, BURKE DS, CALISHER CH, LAUGHLIN CA, SAIF LJ & DASZAK P. 2008. Cross-species virus transmission and the emergence of new epidemic diseases. Microbiol Mol Biol Rev 72: 457-470.

PASTOR AV, PALAZZO A, HAVLIK P, BIEMANS H, WADA Y, OBERSTEINER M, KABAT P & LUDWIG F. 2019. The global nexus of food-trade-water sustaining environmental flows by 2050. Nat Sustain 2: 499-507.

PAVLIDI N, VONTAS J & VAN LEEUWEN T. 2018. The role of glutathione S-transferases (GSTs) in insecticide resistance in crop pests and disease vectors. Curr Opin Insect Sci 27: 97-102.

PAWĘSKA JT, VAN VUREN PJ, KEMP A, STORM N, GROBBELAAR AA, WILEY MR, PALACIOS G & MARKOTTER W. 2018. Marburg virus infection in Egyptian rousette bats, South Africa, 2013-20141. Emerg Infect Dis 24: 1134-1137.

PECL GT ET AL. 2017. Biodiversity redistribution under climate change: Impacts on ecosystems and human well-being. Science 355: eaai9214.

PENDRILL F, PERSSON UM, GODAR J, KASTNER T, MORAN D, SCHMIDT S & WOOD R. 2019. Agricultural and forestry trade drives large share of tropical deforestation emissions. Glob Environ Change 56: 1-10.

PEROS CS, DASGUPTA R, KUMAR P & JOHNSON BA. 2021. Bushmeat, wet markets, and the risks of pandemics: Exploring the nexus through systematic review of scientific disclosures. Environ Sci Policy 124: 1-11.

PINE SO, MCELRATH MJ & BOCHUD PY. 2009. Polymorphisms in toll-like receptor 4 and toll-like receptor 9 influence viral load in a seroincident cohort of HIV-1-infected individuals. AIDS 23: 2387-2395.

PIVELLO VR ET AL. 2021. Understanding Brazil's catastrophic fires: Causes, consequences and policy needed to prevent future tragedies. Perspect Ecol Conserv 19: 233-255.

PLOWRIGHT RK, FIELD HE, SMITH C, DIVLJAN A, PALMER C, TABOR G, DASZAK P & FOLEY JE. 2008. Reproduction and nutritional stress are risk factors for Hendra virus infection in little red flying foxes (*Pteropus scapulatus*). Proc Biol Sci 275: 861-869.

PLOWRIGHT RK, PARRISH CR, MCCALLUM H, HUDSON PJ, KO AI, GRAHAM AL & LLOYD-SMITH JO. 2017. Pathways to zoonotic spillover. Nat Rev Microbiol 15: 502-510.

PONGSIRI MJ, ROMAN J, EZENWA VO, GOLDBERG TL, KOREN HS, NEWBOLD SC, OSTFELD RS, PATTANAYAK SK & SALKELD DJ. 2009. Biodiversity loss affects global disease ecology. BioScience 59: 945-954.

POWERS RP & JETZ W. 2019. Global habitat loss and extinction risk of terrestrial vertebrates under future land-use-change scenarios. Nature Clim Change 9: 323-329.

PRADYUMNA A, EGAL F & UTZINGER J. 2019. Sustainable food systems, health and infectious diseases: Concerns and opportunities. Acta Trop 191: 172-177.

PRIST PR ET AL. 2022. Roads and forest edges facilitate yellow fever virus dispersion. J Appl Ecol 59: 4-17.

PRIST PR, URIARTE M, TAMBOSI LR, PRADO A, PARDINI R, D'ANDREA OS & METZGER JP. 2016. Landscape, environmental and social predictors of Hantavirus risk in São Paulo, Brazil. PLoS ONE 11: e0163459.

PUBLIC HEALTH ENGLAND. 2018. Zoonoses Report UK 2017. Available at: https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/918089/UK_Zoonoses_report_2017.pdf. Accessed on October 26, 2021.

RAMOS DL, PIZO MA, RIBEIRO MC, CRUZ RS, MORALES JM & OVASKAINEN O. 2020. Forest and connectivity loss drive changes in movement behavior of bird species. Ecography 43: 1-12.

RASCHE A, SOUZA BFCD & DREXLER JF. 2016. Bat hepadnaviruses and the origins of primate hepatitis B viruses. Curr Opin Virol 16: 86-94.

RAYCHAUDHURI SP, NGUYEN CT, RAYCHAUDHURI SK & GERSHWIN ME. 2009. Incidence and nature of infectious disease in patients treated with anti-TNF agents. Autoimmun Rev 9: 67-81.

REIS S, MELO M, COVAS R, DOUTRELANT C, PEREIRA H, LIMA R & LOISEAU C. 2021. Influence of land use and host species on parasite richness, prevalence and co-infection patterns. Int J Parasitol 51: 83-94.

RIST CL, GARCHITORENA A, NGONGHALA CN, GILLESPIE TR & BONDS MH. 2015. The burden of livestock parasites on the poor. Trends Parasitol. 31: 527-530.

ROHR JR, CIVITELLO DJ, HALLIDAY FW, HUDSON PJ, LAFFERTY KD, WOOD CL & MORDECAI EA. 2020. Towards common ground in the biodiversity-disease debate. Nat Ecol Evol 4: 24-33.

ROSA ES ET AL. 2006. Bat-transmitted human rabies outbreaks, Brazilian Amazon. Emerg Infect Dis 12: 1197-1202.

ROTUREAU B, JOUBERT M, CLYTI E, DJOSSOU F & CARME B. 2006. Leishmaniasis among gold miners, French Guiana. Emerg Infect Dis 12: 1169-1170.

ROQUE AL, XAVIER SC, DA ROCHA MG, DUARTE AC, D'ANDREA OS & JANSEN AM. 2008. *Trypanosoma cruzi* transmission cycle among wild and domestic mammals in three areas of orally transmitted Chagas disease outbreaks. Am J Trop Med Hyg 79: 742-749.

ROUSSEAU S & DESCHACHT N. 2020. Public awareness of nature and the environment during the COVID-19 crisis. Environ Resour Econ (Dordr) 12: 1-11.

RULLI MC, D'ODORICO P, GALLI N & HAYMAN DTS. 2021. Land-use change and the livestock revolution increase the risk of zoonotic coronavirus transmission from rhinolophid bats. Nature Food 2: 409-416.

RULLI MC, SANTINI M, HAYMAN DTS & D'ODORICO P. 2017. The nexus between forest fragmentation in Africa and Ebola virus disease outbreaks. Sci Rep 7: 41613.

RUZAUSKAS M, VIRGAILIS M, ŠIUGŽDINIENĖ R, SUŽIEDĖLIENĖ E, ŠEPUTIENĖ V, DAUGELAVIČIUS R, ZIENIUS D, ŠENGAUT J & PAVILONIS A. 2009. Antimicrobial resistance of *Enterococcus* spp. isolated from livestock in Lithuania. Vet Arhiv 79: 439-449.

SAÉZ AM ET AL. 2015. Investigating the zoonotic origin of the West African Ebola epidemic. EMBO Mol Med 7: 17-23.

SAIDENBERG ABS ET AL. 2021. *Salmonella* Newport outbreak in Brazilian parrots: confiscated birds from the illegal pet trade as possible zoonotic sources. Environ Microbiol Rep 13: 702-707.

SALDANHA-ELIAS AM, SILVA MA, SILVA VO, AMORIM SLA, COUTINHO AR, SANTOS HA, GIUNCHETTI RC, VITOR RWA & GEIGER SM. 2019. Prevalence of endoparasites in urban stray dogs from Brazil diagnosed with *Leishmania*, with potential for human zoonoses. Acta Parasitol 64: 352-359.

SÁNCHEZ-LUQUEZ K ET AL. 2021. Impact of *TLR7* and *TLR9* polymorphisms on susceptibility to placental infections and pregnancy complications. J Reprod Immunol 146: 103342.

SANTOS RA, SEVERO DO & HOEFEL MGL. 2020. Bolsonaro's hostility has driven Brazil's Indigenous peoples to the brink. Nature 584: 524.

SAYLORS KE ET AL. 2021. Market characteristics and zoonotic disease risk perception in Cameroon bushmeat markets. Soc Sci Med 268: 113358.

SCHMIDT KA & OSTFELD RS. 2001. Biodiversity and the dilution effect in disease ecology. Ecology 82: 609-619.

SCHOFIELD CJ, DIOTAIUTI L & DUJARDIN JP. 1999. The process of domestication in Triatominae. Mem Inst Oswaldo Cruz 94: 375-378.

SEVERO EA, DE GUIMARÃES JCF & DELLARMELIN ML. 2021. Impact of the COVID-19 pandemic on environmental awareness, sustainable consumption and social responsibility: Evidence from generations in Brazil and Portugal. J Clean Prod 286: 124947.

SHAH HA, HUXLEY P, ELMES J & MURRAY KA. 2019. Agricultural land-uses consistently exacerbate infectious disease risks in Southeast Asia. Nat Commun 10: 4299.

SHI Y, WU Y, ZHANG W, QI J & GAO GF. 2014. Enabling the 'host jump': structural determinants of receptor-binding specificity in influenza A viruses. Nat Rev Microbiol 12: 822-831.

SMITH KM ET AL. 2012. Zoonotic viruses associated with illegally imported wildlife products. PLoS ONE 7: e29505.

SOKOLOW SH ET AL. 2017. Nearly 400 million people are at higher risk of schistosomiasis because dams block the migration of snail-eating river prawns. Philos Trans R Soc Lond B Biol Sci 372: 20160127.

STARR MD, ROJAS JC, ZELEDÓN R, HIRD DW & CARPENTER TE. 1991. Chagas' disease: risk factors for house infestation by *Triatoma dimidiata*, the major vector of *Trypanosoma cruzi* in Costa Rica. Am J Epidemiol 133: 740-747.

STELLA E, MARI L, GABRIELI J, BARBANTE C & BERTUZZO E. 2020. Permafrost dynamics and the risk of anthrax transmission: a modelling study. Sci Rep 10: 16460.

STREICKER DG & GILBERT AT. 2020. Contextualizing bats as viral reservoirs. Science 370: 172-173.

SUBUDHI S, RAPIN N & MISRA V. 2019. Immune system modulation and viral persistence in bats: Understanding viral spillover. Viruses 11: 192.

SZWABE K & BLASZKOWSKA J. 2017. Stray dogs and cats as potential sources of soil contamination with zoonotic parasites. Ann Agric Environ Med 24: 39-43.

TADEI WP, SCARPASSA VM & RODRIGUES IB. 1991. Evolução das populações de *Anopheles* e de *Mansonia*, na área de influência da Usina Hidrelétrica de Tucuruí (Pará). Ciência e Cultura 43: 639-640.

TAYLOR D, HAGENLOCHER M, JONES AE, KIENBERGER S, LEEDALE J & MORSE AP. 2016. Environmental change and Rift Valley fever in eastern Africa: projecting beyond HEALTHY FUTURES. Geospat Health 11: 387.

TEODORO U, BALDUÍNO J, THOMAZ-SOCCOL V, BARBOSA OC, FERREIRA MEMC, LOZOVEI AL, VERZIGNASSI TG & ROBERTO ACBS. 1999. Environmental sanitation and peri-domiciliar organisation as auxiliary practices for the control of phlebotomines in Paraná state, southern Brazil. Braz Arch Biol Technol 42: 307-314.

TERÇAS-TRETTEL ACP ET AL. 2019. Malaria and hantavirus pulmonary syndrome in gold mining in the Amazon region, Brazil. Int J Environ Res Public Health 16: 1852.

TIMOFEEV V, BAHTEJEVA I, MIRONOVA R, TITAREVA G, LEV I, CHRISTIANY D, BORZILOV A, BOGUN A & VERGNAUD G. 2019. Insights from *Bacillus anthracis* strains isolated from permafrost in the tundra zone of Russia. PLoS ONE 14: e0209140.

TOMLEY FM & SHIRLEY MW. 2009. Livestock infectious diseases and zoonoses. Philos Trans R Soc Lond B Biol Sci 364: 2637-2642.

THOMPSON RC. 2013. Parasite zoonoses and wildlife: One Health, spillover and human activity. Int J Parasitol 43: 1079-1088.

TORRES RG, MOREIRA VM, MOREIRA PF & NEVES RA. 2019. Análise da distribuição espacial dos casos de febre amarela no estado de Goiás, 2007 – 2017. RBMC 5: 35-41.

TU C ET AL. 2004. Antibodies to SARS coronavirus in civets. Emerg Infect Dis 10: 2244-2248.

URBANIAK K, MARKOWSKA-DANIEL I, KOWALCZYK A, KWIT K, POMORSKA-MÓL M, FRĄCEK B & PEJSAK Z. 2017. Reassortment process after co-infection of pigs with avian H1N1 and swine H3N2 influenza viruses. BMC Vet Res 13: 215.

VAL AL. 2020. Biodiversity - the hidden risks. An Acad Bras Cienc 92: e20200699.

VALEGGIA CR & SNODGRASS JJ. 2015. Health of Indigenous peoples. Annu Rev Anthropol 44: 117-135.

VAN BOECKEL TP, PIRES J, SILVESTER R, ZHAO C, SONG J, CRISCUOLO NG, GILBERT M, BONHOEFFER S & LAXMINARAYAN R. 2019. Global trends in antimicrobial resistance in animals in low- and middle-income countries. Science 365: eaaw1944.

VAN DEN BROEK B, VAN DER FLIER M, DE GROOT R, DE JONGE MI & LANGEREIS JD. 2020. Common genetic variants in the complement system and their potential link with disease susceptibility and outcome of invasive bacterial infection. J Innate Immun 12: 131-141.

VAN VLIET N, MORENO J, GÓMEZ J, ZHOU W, FA JE, GOLDEN C, ALVES RRN & NASI R. 2017. Bushmeat and human health: Assessing the evidence in tropical and sub-tropical forests. Ethnobio Conserv 6: 3.

VAN VLIET N, QUICENO-MESA MP, CRUZ-ANTIA D, DE AQUINO LJN, MORENO J & NASI R. 2014. The uncovered volumes of bushmeat commercialized in the Amazonian trifrontier between Colombia, Peru & Brazil. Ethnobio Conserv 3: 7.

VANICHANAN J, UDOMKARNJANANUN S, AVIHINGSANON Y & JUTIVORAKOOL K. 2018. Common viral infections in kidney transplant recipients. Kidney Res Clin Pract 37: 323-337.

VAZ VC, D'ANDREA PS & JANSEN AM. 2007. Effects of habitat fragmentation on wild mammal infection by *Trypanosoma cruzi*. Parasitology 134: 1785-1793.

VILLÉN-PÉREZ S, ANAYA-VALENZUELA L, CRUZ DC & FEARNSIDE PM. 2021. Mining threatens isolated indigenous peoples in the Brazilian Amazon. Glob Environ Change 72: 102398.

VITTOR AY, GILMAN RH, TIELSCH J, GLASS G, SHIELDS T, LOZANO WS, PINEDO-CANCINO V & PATZ JA. 2006. The effect of deforestation on the human-biting rate of *Anopheles darlingi*, the primary vector of Falciparum malaria in the Peruvian Amazon. Am J Trop Med Hyg 74: 3-11.

VITTOR AY, LAPORTA GZ, SALLUM MAM & WALKER RT. 2021. The COVID-19 crisis and Amazonia's indigenous people: Implications for conservation and global health. World Development 145: 105533.

VOURC'H G, PLANTARD O & MORAND S. How does biodiversity influence the ecology of infectious disease? In: MORAND S ET AL. (Eds). New Frontiers of Molecular Epidemiology of Infectious Diseases. Springer Science and Business Media B.V. 2012.

WALLACE RG, KOCK R, BERGMANN L, GILBERT M, HOGERWERF L, PITTIGLIO C, MATTIOLI R & WALLACE R. 2016. Did neoliberalizing West African forests produce a new niche for Ebola? Int J Health Serv 46: 149-165.

WALSH MG, MOR SM & HOSSAIN S. 2019b. The elephant-livestock interface modulates anthrax suitability in India. Proc Biol Sci 286: 20190179.

WALSH MG, MOR SM, MAITY H & HOSSAIN S. 2019a. Forest loss shapes the landscape suitability of Kyasanur Forest disease in the biodiversity hotspots of the Western Ghats, India. Int J Epidemiol 48: 1804-1814.

WANG LF, SHI Z, ZHANG S, FIELD H, DASZAK P & EATON BT. 2006. Review of bats and SARS. Emerg Infect Dis 12: 1834-1840.

WATTS N ET AL. 2019. The 2019 report of The Lancet Countdown on health and climate change: ensuring that the health of a child born today is not defined by a changing climate. Lancet 394: 1836-1878.

WEST TAP, BÖRNER J & FEARNSIDE PM. 2019. Climatic benefits from the 2006–2017 avoided deforestation in Amazonian Brazil. Front For Global Change 2: 52.

WEST TAP & FEARNSIDE PM. 2021. Brazil's conservation reform and the reduction of deforestation in Amazonia. Land Use Pol 100: 105072.

WHO - World Health Organization, OiE - World Organisation for Animal Health, UN Environment Programme. 2021. Reducing public health risks associated with the sale of live wild animals of mammalian species in traditional food markets. Available at: https://www.who.int/publications/i/item/WHO-2019-nCoV-Food-safety-traditional-markets-2021.1. Access on January 30, 2022.

WIETHOELTER AK, BELTRÁN-ALCRUDO D, KOCK R & MOR SM. 2015. Global trends in infectious diseases at the wildlife-livestock interface. Proc Natl Acad Sci USA. 112: 9662-9667.

WIKAN N & SMITH DR. 2016. Zika virus: History of a newly emerging arbovirus. Lancet Infect Dis 16: e119-e126.

WILKE ABB, BEIER JC & BENELLI G. 2019b. Complexity of the relationship between global warming and urbanization - an obscure future for predicting increases in vector-borne infectious diseases. Curr Opin Insect Sci 35: 1-9.

WILKE ABB, CHASE C, VASQUEZ C, CARVAJAL A, MEDINA J, PETRIE WD & BEIER JC. 2019a. Urbanization creates diverse aquatic habitats for immature mosquitoes in urban areas. Sci Rep 9: 15335.

WILKINSON DA, MARSHALL JC, FRENCH NP & HAYMAN DTS. 2018. Habitat fragmentation, biodiversity loss and the risk of novel infectious disease emergence. J R Soc Interface 15: 20180403.

WILKINSON P, SMITH KR, JOFFE M & HAINES A. 2007. A global perspective on energy: health effects and injustices. Lancet 370: 965-978.

WOLFE ND, DASZAK P, KILPATRICK AM & BURKE DS. 2005. Bushmeat hunting, deforestation, and prediction of zoonoses emergence. Emerg Infect Dis 11: 1822-1827.

WOLFE ND, DUNAVAN CP & DIAMOND J. 2007. Origins of major human infectious diseases. Nature 447: 279-283.

WU J, TSCHAKERT P, KLUTSE E, FERRING D, RICCIARDI V, HAUSERMANN H, OPPONG J & SMITHWICK EAH. 2015. Buruli ulcer disease and its association with land cover in Southwestern Ghana. PLoS Negl Trop Dis 9: e0003840.

YASSIN AK ET AL. 2017. Antimicrobial resistance in clinical *Escherichia coli* isolates from poultry and livestock, China. PLoS ONE 12: e0185326.

YE X, FAN Y, WANG X, LIU W, YU H, ZHOU J, CHEN S & YAO Z. 2016. Livestock-associated methicillin and multidrug resistant *S. aureus* in humans is associated with occupational pig contact, not pet contact. Sci Rep 6: 19184.

ZAIDI F, FATIMA SH, JAN T, FATIMA M, ALI A, KHISROON M, ADNAN M & RASHEED SB. 2017. Environmental risk modelling and potential sand fly vectors of cutaneous leishmaniasis in Chitral district: a leishmanial focal point of mount Tirich Mir, Pakistan. Trop Med Int Health 22: 1130-1140.

ZELL R, GROTH M, KRUMBHOLZ A, LANGE J, PHILIPPS A & DÜRRWALD R. 2020. Novel reassortant swine H3N2 influenza A viruses in Germany. Sci Rep 10: 14296.

ZHANG T, WU Q & ZHANG Z. 2020. Probable pangolin origin of SARS-CoV-2 associated with the COVID-19 outbreak. Curr Biol 30: 1346-1351.

ZHANG YZ & HOLMES EC. 2020. A Genomic perspective on the origin and emergence of SARS-CoV-2. Cell 181: 223-227.

ZHOU NN, SENNE DA, LANDGRAF JS, SWENSON SL, ERICKSON G, ROSSOW K, LIU L, YOON KJ, KRAUSS S & WEBSTER RG. 1999. Genetic reassortment of avian, swine, and human influenza A viruses in American pigs. J Virol 73: 8851-8856.

How to cite

ELLWANGER JH ET AL. 2022. Synthesizing the connections between environmental disturbances and zoonotic spillover. An Acad Bras Cienc 94: e20211530. DOI 10.1590/0001-3765202220211530.

Manuscript received on November 24, 2021;
accepted for publication on March 3, 2022

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