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Edited by

Germano Leão Demolin-Leite

INNOVATIVE CONSERVATION TECHNIQUES AND PERSPECTIVES:
Global Biome Conservation and Global Warming Impacts on Ecology and Biodiversity

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Zoonoses and pandemic potential

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1 Introduction

Over the past decade, much has been learned about the emergence of diseases, including pandemics (Zanella, 2016; Zanella and Zanella, 2023). Furthermore, this has demonstrated the importance of these problems to the health of all living organisms on the planet. Global health mainly includes human health and the integration of health approaches (Gruetzmacher et al., 2020). The core of this umbrella contains the definition of One Health, which considers the integration between human, animal, and environmental health, considering the inseparability between them, mainly for the understanding of disease emergence drivers, the development and adoption of effective public policies for the prevention and control of diseases (Adisasmito et al., 2022). Leaving aside species comes the environmental health approach, which deals with ecological and social interactions. Above all, planetary health is about human civilization and the state of natural systems (Gruetzmacher et al., 2020). But what do all these "healths" have to do with what we are living today, and further, what are the current problems indicating? First, we should think less about species and more about systems (Mettenleiter et al., 2023). We should not work in silos or treat each problem separately. Everything is connected and complex. Worse, we have not been trained on all the necessary aspects. Thus, it is essential to work multisector and multidiscipline (Mettenleiter et al., 2023).

It is well acknowledged that up to 75% of newly discovered or emerging infectious diseases (EIDs) and 60% of recognized infectious illnesses in the last century are zoonoses, diseases caused by agents transmitted from animals to humans (Brown, 2004; Cleaveland et al., 2001; Jones et al., 2008; Taylor et al., 2001). Worldwide, zoonoses cause 2.7 million human fatalities and 2.5 billion episodes of disease in people each year (Jones et al., 2008). Although zoonotic diseases are at the nucleus of this concern, the drivers for spillovers between species are primarily anthropogenic, caused explicitly by human behavior (Meadows et al., 2023; OHHLEP et al., 2023). Of these drivers, the increase in the human population, urbanization, migration, climate change, pollution, deforestation, and intensification of agriculture and livestock production, among others, stand out (Zanella, 2016; OHHLEP et al., 2023).

As the world recovers from the Coronavirus Disease 2019 (COVID-19) pandemic caused by the new coronavirus (SARS-CoV-2), it is crucial to acknowledge the growing crisis of climate change (CLIMADE, 2023). Systematized analyses, especially reviews published after 2015, synthesized five categories of climate impacts. The reviews covered 10 categories of health outcomes; the three most common were (1) infectious diseases, (2) mortality, and (3) respiratory, cardiovascular, or neurological outcomes (Rocque et al., 2021). Indeed, extreme weather events cause widespread distress, necessitating efforts to control wildfires, rebuild infrastructure, and adapt to a hotter environment (CLIMADE, 2023). Climate change, influenced by industrial pollution and anthropogenic factors, may increase zoonoses incidence (Šantić et al., 2021). Despite eradication campaigns, tropical infectious diseases have increased in the late 20th century (Ebert and Fleischer, 2005). With global warming expected to reach 1.4–5.8 °C by 2100, vector-borne tropical diseases are expected to spread (Ebert and Fleischer, 2005).

Still, this complex relationship between climate change and infectious diseases is often overlooked, but science has revealed that climate change could aggravate over 50% of known human pathogens. This pressing reality needs immediate attention (CLIMADE, 2023). While preventive solutions, such as timely detection and epidemiological interventions, may not necessarily reduce zoonoses, it is crucial to consider the potential for climate change to create preconditions for different routes of zoonosis transmission and spread, potentially leading to a global environmental issue (Šantić et al., 2021).

A new report on climate change and epidemics was released at COP28, compiled by over 100 scientists and policymakers (CLIMADE, 2023). The report highlights how climate change is fueling new epidemics globally, particularly in countries from the Global South (CLIMADE, 2023). These countries contribute less than 10% of

greenhouse gas emissions but are likely to suffer the most significant health impacts from climate change due to their less adaptive capacity and preparedness to respond to these threats (CLIMADE, 2023). The report emphasizes the need to build capacity to protect and support health, especially in underserved and underrepresented communities (CLIMADE, 2023).

Agriculture and livestock are essential sectors for many countries' economies, and family farming is often the sole protein source for people (Bank, 2021). The World Bank estimates that zoonotic diseases affect more than two billion people worldwide, causing more than two million deaths every year, resulting in outbreaks with significant impacts on public health and the economy (Bank, 2021). Also, animal diseases still account for 20% of the losses in animal protein chains. Therefore, international organizations such as the Food and Agriculture Organization (FAO), the World Animal Health Organization (WAHO—OIE), and the World Health Organization (WHO) make efforts with the purpose of member countries to prevent animal diseases to ensure food supply, maintain household income, health, and preserve the future.

This chapter will focus on zoonosis emergencies driven by climate change and their potential for pandemics. In addition, it will discuss One Health's approaches, considering the role of international organizations and leadership to implement policies to mitigate climate change outcomes in disease emergence. Mainly, One Health is not just a concept but a way of life, an action that all countries must implement.

2 Zoonotic diseases and emerging pandemics

Zoonoses are infectious diseases transmitted between humans and nonhuman animal species, causing a significant burden of disease at the local, regional, and global levels (Brown, 2004; Thal and Mettenleiter, 2023). WHO defines pandemics as "the global spread of a pathogen or variant that infects human populations with limited or no immunity through sustained and high transmissibility from person to person, overwhelming health systems with severe morbidity and increased mortality, and causing social and economic disruptions, all of which require effective national and global collaboration and coordination for its control" (The World Bank, 2022; WHO, 2021).

The critical question of emerging infectious diseases (EIDs) as a global health concern has been investigated by many scientists. A study analyzing 335 EID events between 1940 and 2004 found nonrandom global patterns, with zoonoses dominating (60.3%), primarily from wildlife (Jones et al., 2008). Bacteria or rickettsia caused 54.3% of EID events (Jones et al., 2008). Another literature review

identified 1415 pathogenic infectious organisms, 61% of which are **zoonotic** and can be transmitted between humans and animals. Out of these, 75% are twice as likely to be associated with emerging diseases than nonzoonotic pathogens. The results indicate that protozoa and viruses are more likely to emerge and helminths less likely to do so (Taylor et al., 2001).

A similar study also identified 58% out of 1407 human pathogen species as zoonotic (Woolhouse and Gowtage-Sequeria, 2005). Out of these, 177 are considered as emerging or reemerging. These pathogens are more likely to have **broad host ranges** and are associated with changes in land use, agriculture, demographics, and societal changes (Woolhouse and Gowtage-Sequeria, 2005). Despite their prevalence, only a small minority have been able to cause major epidemics in the human population, making zoonotic pathogens the most likely source of infectious diseases. This study also showed that **RNA viruses** are 44% of all emerging infectious diseases (Woolhouse and Gowtage-Sequeria, 2005). Another study where a database of disease-causing pathogens in humans and domestic mammals was created revealed that multihost **pathogens** were prevalent (61.6%) in both groups (Cleaveland et al., 2001). A total of 1415 pathogens that cause illness in humans, 616 in animals, and 374 in domestic carnivores were included in the database. In human infections, multihost pathogens were highly abundant (61.6%), and in pathogens affecting **domestic mammals**, they were much more common (livestock 77.3%, carnivores 90.0%). Pathogens able to infect humans, livestock, and wildlife had similar proportions. Again, **RNA viruses** were highly likely to emerge, while helminths and fungi were less likely. The ability to infect multiple hosts was also a risk factor (Cleaveland et al., 2001).

Indeed, in the last century, dozens of infectious or parasitic diseases have emerged or reemerged and, at times, caused pandemics. These include SARS (including MERS-CoV and SARS-CoV-2), Ebola, Dengue, Chikungunya, Zika, Yellow Fever, measles, smallpox, HIV-AIDS, Flu (human, avian, or swine influenza), *Vibrio cholerae*, *Plasmodia parasites*, trypanosomiasis, Marburg, Hendra, Nipah, Mpox, Plague, viral hemorrhagic fevers, e.g., Lassa fever, Rift Valley fever, and Crimean-Congo hemorrhagic fever (Brown, 2004; Chomel et al., 2007; Seleem et al., 2010; Tumpey et al., 2002; CLIMADE, 2023).

In brief, viruses are the most common emerging zoonotic agents, in particular RNA viruses. Another common characteristic is that these viruses that infect various hosts, including domestic or wild animals, and attention should be given to the importance of vectors such as bats. Fig. 22.1 exemplifies recent global zoonotic disease emergencies and vectors and/or reservoirs involved in the epidemiology of those diseases (Gummow, 2010; Onehealthinitiative, 2024).
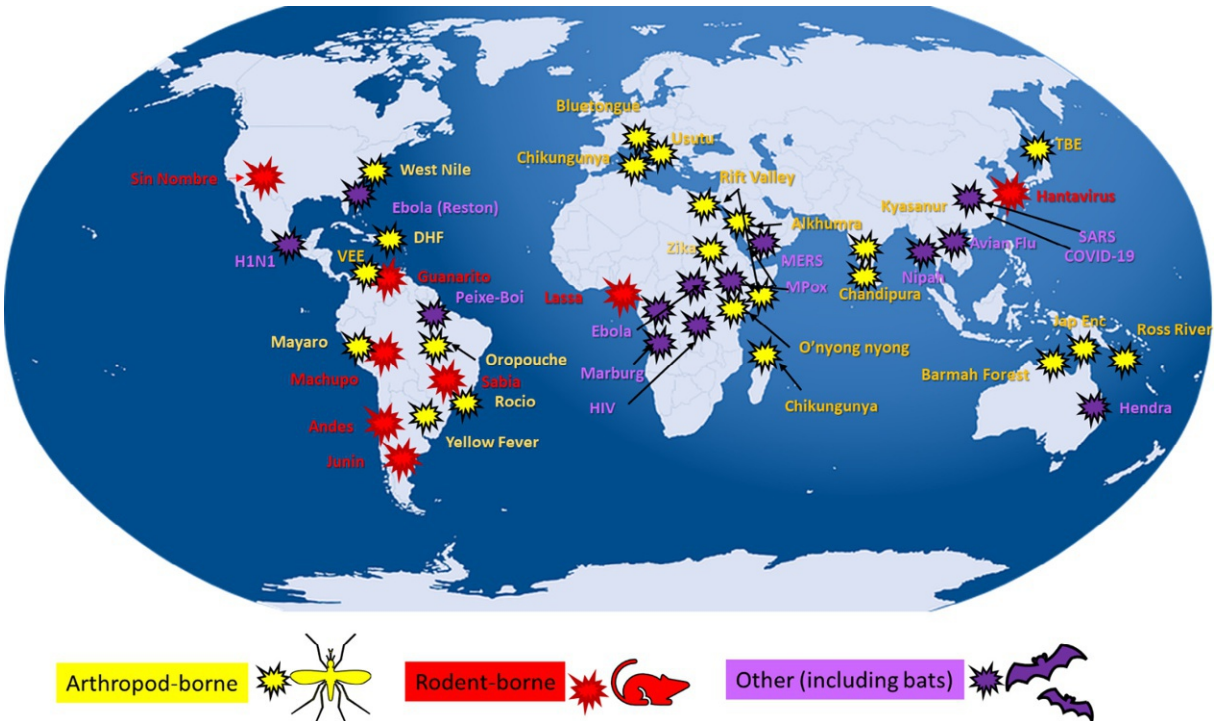
FIG. 22.1 Origin of newly emerging and reemerging zoonosis, along with the intermediary hosts or vectors linked to them (Gummow, 2010; Onehealthinitiative, 2024). Map lines delineate study areas and do not necessarily depict accepted national boundaries. *(Adapted from Gummow, B., 2010. Challenges posed by new and re-emerging infectious diseases in livestock production, wildlife and humans. Livest. Sci. 130, https://doi.org/10.1016/j.livsci.2010.02.009 and https://onehealthinitiative.com/.)*

2.1 Viruses as the most frequent emergent zoonotic pathogen

The International Committee on Taxonomy of Viruses has provided a database with 4958 virus species and 1479 vertebrate virus species and their host ranges (Singh et al., 2022). Viral traits and host ranges were predictors in generalized linear mixed models for confirmed zoonotic, potential zoonotic, and disease emergence outcomes (Singh et al., 2022). Bat- and livestock-adapted viruses posed a high risk, and the risk increased if present in other vertebrates or not reported from invertebrates. The model predicted 39 viruses with never-reported zoonotic potential or potential human virus emergence (Singh et al., 2022). In addition, **RNA viruses** are more frequent emerging pathogens (Woolhouse and Gowtage-Sequeria, 2005; Cleaveland et al., 2001).

2.1.1 WHO priority pathogen list

The World Health Organization's priority pathogen list includes COVID-19, Crimean-Cong hemorrhagic fever, Ebola virus disease, Marburg virus disease, Lassa fever, MERS, SARS, Nipah, henipaviral diseases, Rift Valley fever, Zika, and Disease X (unknown pathogen) (WHO, 2022). The list of priority pathogens will guide global investment in vaccines, tests, and treatments.

A recent study indicates that, besides those, the Ebola-like Machupo virus is also worthy of attention as it poses a significant public health risk (Meadows et al., 2023; Zhong and Huang, 2019). Machupo, also known as "black typhus" and Bolivian hemorrhagic fever, was first isolated in Bolivia in 1959 (Meadows et al., 2023). It is caused by the *Calomys callosus* field mouse, causing symptoms like Ebola-like bleeding, high fever, pain, and rapid death (Meadows et al., 2023). Although there are no licensed vaccines for Machupo, a vaccine for Argentinean hemorrhagic fever may offer protection (Meadows et al., 2023).

Researchers have calculated that the number of viral spillover events of those four viruses (SARS Coronavirus 1, Filoviruses, Machupo virus, and Nipah virus) from animals to humans increased by 5% annually from 1963 to 2019, causing around 1216 deaths in 2020 (Meadows et al., 2023). If the rate continues, four times the number of outbreaks will occur by 2050, causing 12 times the number of deaths, around 15,000 a year (Meadows et al., 2023). Most of the 72 outbreaks were caused by filoviruses in Africa, such as Marburg and Ebola, which caused more than 90% of the 17,000-plus total deaths. Indeed, the

filoviruses family, including Ebola and Marburg, causes hemorrhagic fevers and bleeding from bodily orifices and internal organs (Meadows et al., 2023). Ebola and Marburg kill about 50% of those infected (Meadows et al., 2023). There are no licensed vaccines for all Ebola strains; some are developing for Marburg (Meadows et al., 2023).

The Henipavirus genus, which includes two highly virulent zoonotic viruses, Hendra and Nipah, is primarily bat-borne and has outbreaks in Australia and Southeast Asia (Hernández et al., 2022). Nipah is a lethal paramyxovirus, first identified in Malaysia and Singapore in the 1980s (Bruno et al., 2023; Meadows et al., 2023). Its natural reservoir is fruit bats. Hendra, another henipavirus, was first observed in Australia in 1994 (Meadows et al., 2023). Both cause respiratory illness and flu-like symptoms, potentially leading to encephalitis (Bruno et al., 2023; Meadows et al., 2023). Nipah kills between 45% and 75% of infected individuals. No licensed vaccines exist (Meadows et al., 2023). However, there is limited evidence in the Americas for the circulation of these viruses (Hernández et al., 2022). A novel henipa-like virus was discovered in Brazil from opossums, and the virus was named Peixe-Boi virus (PBV). The study used next-generation sequencing and metagenomic approaches to discover the original evidence of a henipa-like virus genome in Brazil and South America, as well as the first description of a henipa-like virus in marsupial species (Hernández et al., 2022).

The zoonotic origins of coronaviruses, including **SARS-CoV-1**, **MERS**, and **SARS-CoV-2**, which cause large-scale epidemics, are a priority, mainly due to their diversity and the role of **bats** (Beyer et al., 2021). Climate change-driven increase in bat richness in the southern Chinese Yunnan province and neighboring regions in Myanmar and Laos may have played a key role in the evolution of transmission of these two coronaviruses, accounting for an estimated increase of around **100 bat-borne CoVs** across the region (Beyer et al., 2021). In 2002, the first confirmed coronavirus pandemic, SARS-CoV-1, was reported in China and spread to over two dozen countries in North and South America and Europe (Meadows et al., 2023). It originated from bats and spread to civet cats and humans (Meadows et al., 2023). Symptoms include headache, body aches, respiratory symptoms, diarrhea, dry cough, and pneumonia. SARS affected nearly 8100 people and killed just under 10% from 2002 to 2003 (Meadows et al., 2023). There is no licensed vaccine for SARS, but researchers are working on universal coronavirus vaccines (Meadows et al., 2023). There are studies on the effects of climate change on SARS worldwide (Bahrami et al., 2022). A study in Iran showed a positive association between the incidence of SARS and bioclimatic variables by type of climate and gender (Bahrami et al., 2022). This study showed that hospital admissions for climate-related respiratory illnesses in Iran will increase by 36% in 2020–50 (Bahrami et al., 2022). Like the two previous viruses that have caused deadly epidemics during the past 20 years (SARS-CoVs and SARS-CoV-2), MERS-CoVs is also a beta-coronavirus (Zhou et al., 2021). In 2012, a man in Saudi Arabia died of acute pneumonia and renal failure, leading to the isolation of MERS-CoV. Soon enough, 866 confirmed cases were reported, with the majority in Saudi Arabia. MERS-CoVs are closely associated with bats, are derived from camels, and can be transmitted to humans through camels (Zhou et al., 2021).

2.1.2 Recent pandemic or epidemic viruses

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)

Coronaviruses, which cause respiratory infections in humans, have become a significant public health concern in the 21st century. In 2019, SARS-CoV-2 emerged in Wuhan, China, causing unusual viral pneumonia. COVID-19, a highly transmissible virus but less fatal than SARS and MERS-CoV, has rapidly spread worldwide, surpassing SARS and MERS in infected people and epidemic areas (Hu et al., 2021). In December 2019, Wuhan reported clusters of patients with pneumonia of unknown cause, similar to SARS and MERS-CoV. Most cases were linked to Huanan Seafood Wholesale Market, a wet market selling seafood and live animals (Hu et al., 2021). The first known case occurred on December 8, 2019, and Chinese scientists identified a novel betacoronavirus as the causative agent of a severe pneumonia outbreak. The virus spread to other cities in Hubei province and all 34 provinces of China within one month, leading to an increase in confirmed cases. The WHO declared the outbreak a public health emergency of international concern, and the disease was named "SARS-CoV-2" and "COVID-19." As of August 2020, 216 countries reported over 20 million cases and 733,000 deaths, with the United States having the largest number of cases (Hu et al., 2021).

SARS-CoV-2 is a novel betacoronavirus that shares 79% genome sequence identity with SARS-CoV and 50% with MERS-CoV. It is clustered with SARS-CoV and SARS-related coronaviruses found in bats, placing it in the subgenus *Sarbecovirus* genus *Betacoronavirus* (Hu et al., 2021). It is grouped in a distinct lineage with four horseshoe bat coronavirus isolates and novel coronaviruses in pangolins. Bats are significant natural hosts of alphacoronaviruses and betacoronaviruses, with the closest relative being "RaTG13" from Yunnan province, China. Pangolins are another wildlife host likely linked with SARS-CoV-2, with multiple SARS-CoV-2-related viruses identified in tissues of Malayan pangolins smuggled from Southeast Asia into southern China from 2017 to 2019. The animal origin of SARS-CoV-2 is still unclear, but the detection of RaTG13, RmYN02, and pangolin coronaviruses suggests

diverse coronaviruses are circulating in wildlife. Recombination may be involved in the evolution of SARS-CoV-2. Extensive surveillance of SARS-CoV-2-related viruses in China, Southeast Asia, and other regions will help understand its zoonotic origin (Hu et al., 2021).

Monkeypox 2022 (Mpox)

A virus that deserved attention recently was Monkeypox 2022 (Mpox). Mpox, a zoonotic virus similar to smallpox, has rapidly spread outside endemic regions of Africa, with confirmed cases reaching over 3300 in just over a month (Koenig et al., 2022). The transmission mechanisms in animals and the reservoir host remain uncertain, and the spread from humans to wild or domestic animals risks creating new endemic zones (Koenig et al., 2022). Mpox is not considered as a sexually transmitted infection, but anyone with close contact with an infected person, aerosolized infectious material, or contact with fomites or infected animals is at risk (Koenig et al., 2022).

Influenza virus

In the last 100 years, four influenza pandemics have occurred (Webster and Krauss, 2002; Saunders-Hastings and Krewski, 2016; Zanella and Goslar, 2022). Influenza viruses are classified into four types: A, B, C, and D, of which A and B cause seasonal flu epidemics. However, influenza A viruses (IAV) are zoonotic and cause global pandemics when a new, different virus emerges. Introducing swine or avian influenza viruses into the human population can set the stage for a pandemic, with concerns about the Highly Pathogenic Avian Influenza Virus (HPAIV) caused by subtypes (H5 and H7) virus becoming the next pandemic. While pigs are susceptible to several subtypes of IAVs, there is a barrier to infection in pigs. Avian IAVs often undergo reassortment in swine, but there is no evidence of a role for swine in generating pandemic recombinants or transmitting H5N1. The binding type expression profile in the swine upper respiratory tract is an important factor for successfully initiating an AIV infection in this host. However, $\alpha2,3$ receptors are rare in the porcine upper respiratory tract epithelium, and if successful infection progresses to the lower respiratory tract, the more abundant sialic acid $\alpha2,6$-galactose receptors may drive the virus toward greater $\alpha2,6$ binding affinity, potentially favoring subsequent human infections. Control measures include avoiding human virus introduction into pigs and vaccinating pig farming workers.

As was earlier established, four influenza pandemics have occurred in the past century (Webster and Krauss, 2002). The Spanish flu pandemic was one of the largest public health disasters in history, resulting from a highly pathogenic and transmissible strain of the influenza virus (Kilbourne, 2006; Saunders-Hastings and Krewski, 2016). The military context

poor sanitation, overcrowding, and limited health services in Europe accelerated the 1918 outbreak. However, the Spanish flu brought lessons and advances, such as the founding of the WHO and greater cooperation between countries. Besides the discovery of penicillin in 1929, positive pressure ventilators for intensive care units developed in the 1940s prevented another pandemic with a similar fatality rate. The 1968 Hong Kong flu was highly transmissible, driven by Vietnam War veterans returning to the United States and air transport (Saunders-Hastings and Krewski, 2016). Table 22.1 explains the four influenza pandemics.

In March and early April 2009, a new influenza A (HlNl) virus emerged in Mexico and the United States, spreading worldwide to 30 countries through human-to-human transmission (Smith et al., 2009). The new influenza virus, the 2009 H1N1 pandemic virus (H1N1pdm09), became the first influenza pandemic of the 21st century (Garten et al., 2009; Neumann et al., 2009). The virus was derived from several viruses circulating in swine, and the initial transmission to humans occurred several months before the outbreak was recognized (Garten et al., 2009).

A phylogenetic estimate of gaps in genetic surveillance indicates a long period of unsampled ancestry before the H1N1pdm09 outbreak, suggesting that the reassortment of swine lineages may have occurred years before emergence in humans (Smith et al., 2009; Garten et al., 2009). The unsampled history of the epidemic means that the nature and location of the genetically closest swine viruses reveal little about the immediate origin of the epidemic. The results highlight the need for systematic surveillance of influenza in swine and provide evidence that mixing new genetic elements in swine can result in the emergence of viruses with pandemic potential in humans (Smith et al., 2009).

3 Drivers or factors for zoonose emergency and spillover

The emergence of zoonoses has increased in recent decades due to anthropogenic influences such as population size, urbanization, climate change, mobility, global trade, intensive livestock farming, agricultural expansion for growing crops, land use changes, habitat fragmentation, and biodiversity loss (Simpson et al., 2021; Mettenleiter et al., 2023; OHHLEP et al., 2023). Moreover, activities such as hunting or capturing wild animals, farming wild (nondomesticated) species of animals, live wild animal trade, and trade of wild animal products contribute to this rise. In addition, other global factors such as changes in the Earth's habitat, pollution, and environmental degradation, social imbalance, population deprived of liberty, and poor vaccine coverage have favored the emergence of agents of zoonotic diseases (Duarte, 2019; Thal and Mettenleiter, 2023; Simpson et al., 2021).

TABLE 22.1   Comparison of influenza pandemics in the last 100 years.

Year and name	Area of origin	Influenza A subtype (animal type) Genetic introduction/ recombination event	Basic reproduction number (R_0)[a]	Estimated fatality (%)	Estimation of mortality worldwide	Age groups mostly affected
1918–20 "Spanish Flu"	Uncertain	H1N1 (uncertain)	1.2–3.0	2–3	40–50 million	Young adults
1957–58 "Asian Flu"	South China	H2N2 (aviary)	1.5	<0.2	1–4 million	All age groups
1968–69 "Hong Kong Flu"	South China	H3N2 (aviary)	1.3–1.6	<0.2	1–4 million	All age groups
2009–10 "Influenza A(H1N1) 2009"	North America	H1N1 (swine)	1.1–1.8	0.02	400–600 K	Children, young adults, pregnant women

[a]*The basic reproduction number (R_0) is the number of secondary cases a susceptible population would produce, influenced by infectious period duration, infection probability, and contact frequency (Dietz, 1993).*

Pandemics of the 20th–21st centuries. Stockholm, European Centre for Disease Prevention and Control. And Reviewing the History of Pandemic Influenza: Understanding Patterns of Emergence and Transmission (Saunders-Hastings, P.R., Krewski, D., 2016. Reviewing the history of pandemic influenza: understanding patterns of emergence and transmission. Pathogens 5, 66.)

Researchers have warned that over the next 50 years, at least 15,000 occurrences of viruses spreading between species will occur due to the climate crisis. As the planet heats up, many animal species will be forced to move into new areas to find suitable conditions, bringing their parasites and pathogens and causing interactions between species (Carlson et al., 2022). A study forecasts the geographic range shifts of 3139 mammal species due to climatic and land use changes until 2070, finding that even under a relatively low level of global heating, there will be at least 15,000 cross-species transmission events of one or more viruses during this time (Carlson et al., 2022). Also, climate plays a significant role in the spatial distribution of vectors and pathogens (Jagadesh et al., 2021). Bats**,** an important mammal vector, will account for most disease spread because of their ability to travel large distances (Carlson et al., 2022).

However, formerly geographically separated animal species will have more opportunities to share viruses due to changes in temperature and land use (Carlson et al., 2022). A recent study predicts that deaths from zoonotic viruses, which spread from animals to humans, are set to increase 12-fold by 2050 due to climate change and habitat encroachment (Meadows et al., 2023; Prater, 2023). Also, a phylogeographical model of the mammal-virus network was used and estimated global range changes for 3139 mammal species under land-use and climate change

scenarios for the year 2070 to simulate probable hotspots of future viral sharing (Carlson et al., 2022). The study forecasted that the species would group in novel ways at high altitudes, in hotspots for biodiversity, and in regions of Asia and Africa with dense populations of humans, leading to an estimated 4000 times increase in the cross-species transmission of their associated viruses (Carlson et al., 2022). Notably, it was suggested that keeping warming below 2°C in the 21st century won't stop viral sharing in the future and that this ecological transformation may already be occurring (Carlson et al., 2022). These results underline the critical need to combine viral surveillance and discovery efforts with biodiversity surveys monitoring species range changes, particularly in tropical regions that are warming faster and harbor the greatest number of zoonoses (Carlson et al., 2022).

3.1   Social, economic, and demographic changes in the human population

Altogether, the most likely factor to explain the recent occurrence of new diseases is the expansion of the **human population** (Panda et al., 2008). Despite concerns about the scarcity of natural resources and the environment, it is estimated that there will be 10 billion people in the year 2050 (Brown, 2004). This estimate is accompanied by a shocking increase in population urbanization from 39% in 1980 to

46% in 1997 and is predicted to be 60% in 2030, which means an increase in human density in urban centers (Cutler et al., 2010). The predicted global population growth will stress the **need for sustainable energy and food** production, increasing the likelihood of future pandemics (Meisner et al., 2022). Researchers have identified high-resolution environmental zones and predicted longitudinal processes related to these challenges using vector comparison methods (Meisner et al., 2022). The results are captured as networks defined by historical climate similarities (Meisner et al., 2022). Markov clustering and a novel *Correlation of Correlations* method provide unprecedented agglomerative and longitudinal views of climatic relationships (Meisner et al., 2022). The research results in the fastest and largest scientific computations, with over 100 quadrillion edges considered for a single climatic network (Meisner et al., 2022).

Due to cultural, genetic, educational, structural, environmental, and socioeconomic diversity, some populations may be more vulnerable than others (Zhong and Huang, 2019). This is due to different degrees of exposure or sensitivity, geopolitics, poverty, conflicts or wars, demographic density, or weakened health systems in different regions of the planet (Zhong and Huang, 2019). Along with all this, the complexity and specificity of the population or each region require particular approaches in the short, medium, and long term (Zhong and Huang, 2019). Strategies should focus on two levels: increasing resilience to disease and mitigating the health impacts of climate change (Zhong and Huang, 2019).

In short, the main factors that provide favorable conditions for the emergence of new and more complex threats to public health are the growth of human and livestock populations, food and water security, climate change, and the globalization of trade (Previsich et al., 2011). However, there is still a lack of research and understanding of the broader sociopsychological impacts of climate change on health (Rocque et al., 2021).

Climate change, war, conflict, and environmental degradation or disasters are causing increased human and animal **displacement** or migration, with significant implications for global health (Braam et al., 2021). The Out-of-Africa migration, the first major **migration** of anatomically modern humans, was the first of many migratory events that have shaped the world and society (van der Walt, 2022). Migration is characterized by the simultaneous movement of large numbers or groups of people away from their original place of living for specific reasons, which is usually unplanned and disrupts socioeconomic structures, health, and well-being, weakening the immune system and increasing susceptibility to infectious diseases (van der Walt, 2022).

Travel migration, on the other hand, involves many unrelated individuals traveling simultaneously across the globe for work, war, or pleasure (van der Walt, 2022; Kilbourne, 2006; Saunders-Hastings and Krewski, 2016). Advances in air and train travel have enabled this, resulting in a highly interconnected world population (van der Walt, 2022). Pathogens that spread through migration include influenza viruses (soldiers, tourists), smallpox virus, human immunodeficiency virus (HIV), and coronaviruses SARS, MERS, COVID-19 (van der Walt, 2022; Kilbourne, 2006; Saunders-Hastings and Krewski, 2016). During the SARS-CoV-2 pandemic, global mobility patterns impacted epidemic waves, suggesting potential human-driven outbreaks (Tegally et al., 2022, 2023). Advanced mapping of global dispersal dynamics reveals pathogens move along well-connected travel hubs and air traffic networks, supporting the simultaneous movement of pathogens and human mobility (Tegally et al., 2022, 2023).

Extreme events, such as floods, contaminate drinking water sources and cause disease outbreaks and displacement of humans and animals (CLIMADE, 2023). Climate migration, driven by droughts and crop failures, leads to food scarcity, causing migration for sustenance and new economic opportunities (CLIMADE, 2023). Climate changes and migration context will be discussed in more detail below.

3.2 Deforestation, urbanization, and habitat fragmentation

Deforestation, altered microclimates, and artificial breeding habitats favor common disease vectors, such as mosquitoes from the *Anopheles*, *Aedes*, and *Culex* genera, causing changes in pathogen prevalence (Loiseau and Sehgal, 2022). Undeniably, **forest clearance** has significantly increased in recent decades, causing millions of hectares of forests to be lost annually for agricultural activities and timber extraction (Loiseau and Sehgal, 2022). Land conversion also increases accessibility to blood meals, with wild, domesticated animals near humans (Loiseau and Sehgal, 2022). Developing areas **close to tropical forests** for rubber exploitation is related to increased **schistosomiasis** (Cutler et al., 2010). Yet it is unknown how many pathogens are transmitted to wildlife by mosquitoes, and many other parasites and undiscovered viruses are still poorly studied (Loiseau and Sehgal, 2022).

Another typical example of **deforestation**, invasion of wild habitat by urban development, and mining activities was the reemergence of rabies, where **bats** transmitted the **rabies** virus to humans in the Amazon Basin in 2004, where 46 people died (Chomel et al., 2007). Another case of a virus transmitted by bats was the Ebola virus emergency in early 2014 in West African countries (Liberia, Sierra Leone, Ghana, and Nigeria), with more than 20 thousand cases since then. In the 2014 epidemic, the index case resulted from exposure to a colony of insectivorous

bats (*Mops condylurus*) (Mari Saez et al., 2014). There are at least five new cases per year of newly discovered coronaviruses and other respiratory viruses that infect humans from **bats and birds**. More than 3200 coronavirus types are thought to already be present in bats and are just waiting for a chance to infect humans (Frutos et al., 2021).

Just as important as bats, **rodents** are the most abundant and diverse living mammals and have been known to contribute to human diseases since the Middle Ages (Ganjeer et al., 2021). However, climate change and ecosystem composition have led to the global spread of rodents and rodent-borne pathogens, making them a threat to public health, with 217 species harboring 66 zoonoses caused by viruses, bacteria, fungi, helminths, and protozoa (Ganjeer et al., 2021). These diseases include salmonellosis, plague, leptospirosis, leishmaniasis, toxoplasmosis, rat-bit fever, taeniasis-like *Capillaria hepatica*, zoonotic babesiosis, Lassa fever, hemorrhagic fever with renal syndrome (HFRS), and the hantavirus cardiopulmonary syndrome (HCPS) (Ganjeer et al., 2021). Rodents may also harbor complex bacteria like *Mycobacterium tuberculosis*, *Mycobacterium microti*, *Escherichia coli*, agents of Tularemia, Tick-borne relapsing fever, Bartonellosis, Listeriosis, Lyme disease, Q fever, and Ehrlichiosis (Ganjeer et al., 2021). A study of r**odent parasites** and their zoonotic potentials in selected areas in Malaysia was carried out (Tijjani et al., 2020). A total of 89 wild rats were captured, and 12 species of intestinal and tissue parasites were recorded (Tijjani et al., 2020). *Taenia taeniaeformis* was the highest infection recorded (28%), followed by *Hymenolepis nana* (19.5%) and *Capillaria hepatica* (19.1%) (Tijjani et al., 2020). Other parasite species included *Cryptosporidium* spp. (21.3%), *Entamoeba histolytica*/*Entamoeba dispar*, *Moniliformis moniliformis* (17.9%), *Angiostrongylus cantonensis* (16.8%), *Hymenolepis diminuta* (16.1%), *Giardia* spp. (14.6%), *Trichuris* spp. (12.3%), and *Sarcocystis* spp. (6.74) (Tijjani et al., 2020).

3.3 Climate change and zoonoses emergency

As zoonotic diseases become more common, humans must consider the larger picture and their connection to climate change (Gehlot, 2022; Gebremichael et al., 2023). These changes affect the survival, reproduction, abundance, and distribution of hosts, pathogens, and vectors such as rodents, bats, ticks, and mosquitoes in urban areas, and the dynamic interaction between humans, animals, and the environment increases the risk of zoonosis outbreaks (CLIMADE, 2023).

As such, direct and indirect elements contribute to the escalation of infectious illnesses brought on by climatic risks (CLIMADE, 2023). Among the three primary elements are (1) gradual temperature rise; (2) extreme events

such as heavy rains, drought, flooding, and strong winds; and (3) climate migration due to the availability of food and water as well as livelihoods (Zhong and Huang, 2019; CLIMADE, 2023).

3.3.1 Gradual temperature rise

The world's temperatures are rising steadily, and it is expected that the global average temperature will rise by 2–5°C in the future, which makes it easier for disease-carrying vectors like mosquitoes, bats, rodents, and ticks to spread, expanding their geographic range. Globally, outbreak-causing viruses and parasites have increased (CLIMADE, 2023). Arboviral outbreaks are becoming identified more often in Africa; Senegal is experiencing simultaneous **dengue and chikungunya** epidemics, while **yellow fever** outbreaks occur more often in other nations. As of 2023, 34 African and 13 Central and South American countries are endemic to **yellow fever virus** (WHO, 2023). In 2022, 12 African countries reported confirmed cases of yellow fever, with eight experiencing transmission from 2021 and four newly reporting cases (WHO, 2023). In contrast, cold weather is less favorable to vector survival and zoonoses transmission, as shown in a study of **leishmania** in Italy (Gradoni et al., 2022). The easternmost region of Friuli-Venezia Giulia is less favorable to L infantum transmission due to its **cold climate** conditions (Gradoni et al., 2022).

The biggest **dengue and chikungunya** epidemics ever recorded happened in South America and South Asia in 2023, and many of these outbreaks are in countries like Uruguay and Paraguay that never had any of these diseases (Crisis24, 2023; Giovanetti et al., 2023). Paraguay, for instance, confirmed more than 120,000 cases of **chikungunya** this year, in conjunction with the highest-ever average temperature in the nation (Giovanetti et al., 2023). Although there had never been a virus-related death in Paraguay, this outbreak claimed the lives of 46 people, including newborns, and severely disrupted the nation's health system as it spread to every province (Giovanetti et al., 2023). In the same way, Vietnam saw one of its deadliest **dengue** epidemics in 2022, with over 360,000 cases recorded and 140 fatalities. In contrast, Vietnam reported 27 fatalities and 72,880 cases in 2021 (Crisis24, 2023). In Peru, a study investigated the increase of **Zika and dengue** cases during the **El Niño Costero** phenomenon in Peru, affecting mainly young women (Reátegui and Falcón, 2021).

Following this pattern, southern Europe is reporting outbreaks of mosquito-borne zoonosis. The tiger mosquito, *Aedes albopicus*, frequently increases in Europe (Head, 2022; Noyce, 2023). In 2023, **dengue** virus outbreaks in France and multiple local transmissions in Italy's Lombardy and Lazio regions were reported, making most southern Europe susceptible to arboviruses (Head, 2022;

Noyce, 2023; Rezza, 2018). Southern Europe's rising temperatures have also been linked to a **chikungunya** epidemic in Italy in 2017, which spread in the Lazio region, and a secondary outbreak in Guardavalle in 2023 (Rezza, 2018).

West Nile virus (WNV), a mosquito-borne zoonosis, has emerged as a disease of public health concern in new regions in Europe and North America (Farooq et al., 2023; McCrimmon, 2023). Mosquitoes spread WNV zoonosis and are mostly asymptomatic, with flu-like symptoms occurring in 20% of cases (Koch et al., 2019). However, the prevalence of neuroinvasive symptoms caused by WNV has increased in **Europe**, including Hungary, due to changes in precipitation and climate (Koch et al., 2019). Today, with machine learning technology, it is possible to delineate potential risk areas and estimate the growth of the population at risk of WNV expansion in climate change scenarios (Farooq et al., 2023). Compared to 2000–20, these studies show a fivefold increase in the risk of WNV for 2040–60 in Europe, depending on the geographical region and climate scenario (Farooq et al., 2023). The proportion of European areas for WNV risk could increase from 15% to 23%–30%, putting 161–244 million people at risk (Farooq et al., 2023). In all scenarios, Western Europe appears to be facing the greatest increase in WNV outbreak risk (Farooq et al., 2023). The increase in risk is not linear but goes through periods of abrupt change ruled by climatic thresholds associated with ideal conditions for WNV vectors (Farooq et al., 2023).

In Europe and North America, the rates of **WNV, dengue, malaria, and Chikungunya** are also rising, with several nations and states reporting the first instances of local transmission of these infections. Climate change increases mosquito frequency, leading to the first **malaria** cases in the United States, including Texas, Florida, Maryland, and Arkansas, despite being away from the equator or at high elevations (ADH, 2023; CDC, 2023). Colorado is facing its worst **WNV** outbreak since 1999, with 11 deaths by September 1, 2023, and one of the deadliest seasons since the illness's arrival in the United States (McCrimmon, 2023).

Regarding parasitic zoonosis, Indonesia, with its high population and livestock density, is at risk of developing **Trypanosoma** sp. outbreaks due to climate change and **high vector** and reservoir populations (Novita, 2019). Surra, caused by *Trypanosoma evansi*, is present in livestock, and the country's **warm environment** and proximity to humans and livestock also contribute to the risk of human Trypanosoma infection (Novita, 2019).

Just as importantly, the increase or expansion conditions for vectors, but also the reduction in the abundance of natural hosts, cause vectors to look for alternative hosts, increasing opportunities for the transmission of diseases, such as the increase in human cases of borreliosis or **Lyme** disease, ehrlichiosis, and anaplasmosis (Cutler et al., 2010).

However, studies on how these changes affect **vector-borne diseases like Lyme** borreliosis have been limited (Goren et al., 2023). Long-term surveillance data from Norway shows a significant change in the timing of Lyme borreliosis cases, with an annual increase in cases (Goren et al., 2023). The seasonal peak in cases is now 6 weeks **earlier** than 25 years ago, surpassing previous predictions (Goren et al., 2023). A retrospective study conducted in Romania found that Lyme disease, a zoonosis transmitted through tick bites, is prevalent among patients in the North-Eastern region (Manciuc et al., 2019). The study found 1257 cases, with 89 suspected cases, mostly from rural areas (Manciuc et al., 2019). The study also noted that climate change and pet ownership have increased the incidence of borreliosis (Manciuc et al., 2019). A study in **Italy** between 2009 and 2018 analyzed 12,928 cases of **Borrelia** spp. and showed that the highest demand was in autumn 2018, agreeing with a regional trend of rising temperature and humidity in Italy (Stroffolini et al., 2021).

The review of 55 publications examines the spread of natural focal diseases in the Arctic region due to global climate change (Malkhazova et al., 2022). It considers the impact of changing environmental factors on disease foci in Russia, Europe, and North America, as well as the northward shift of pathogens, carriers, and vectors (Malkhazova et al., 2022). The analysis identified 18 significant diseases, with **tick-borne** infections likely to move most intensively to the north due to climate change (Malkhazova et al., 2022). New tularemia and anthrax foci outbreaks could also occur due to increased vector numbers (Malkhazova et al., 2022). The most vulnerable groups are those living in remote areas, where adaptation to climate change is most difficult due to insufficient economic support or infrastructure (Malkhazova et al., 2022). A similar study using a systematic literature search found that arthropod vector-borne diseases have the potential to expand their distribution toward Northern latitudes, and **tick-borne** are a growing threat (Omazic et al., 2019).

3.3.2 Extreme climatic events

Frequent and sudden occurrences of extreme events like changes in precipitation (heavy rains or droughts), flooding, strong winds, rising temperatures, and changes in humidity drive the rise in epidemics (CLIMADE, 2023). These extreme climatic events and calamities can occur in days or weeks, leaving areas and nations unprepared. The quick spread of infectious illnesses might exacerbate the repercussions of such tragedies. Accordingly, extreme weather events trigger infectious disease outbreaks due to the disruption of social and environmental conditions (Chabuka et al., 2023). The World Health Organization reports an acute seventh cholera pandemic since mid-2021, characterized by multiple outbreaks, widespread spread to areas

free of cholera, and high mortality rates (Chabuka et al., 2023). In particular, the 2022 and 2023 worldwide cholera epidemics resulted in hundreds of thousands of infections in Pakistan's first outbreak (Chabuka et al., 2023). The strain responsible for Pakistan's outbreak was also linked to Malawi's deadliest cholera epidemic, with over 57,000 confirmed cases and 1733 deaths (Chabuka et al., 2023). The high mortality rate of 3% shocked the international medical community, according to a Médicins Sans Frontières team (Chabuka et al., 2023).

There have been reports of *E. coli* contamination of water following floods in several parts of the world (CLIMADE, 2023). Floods also increase mosquito breeding probabilities, increasing the spread of dengue and malaria worldwide (CLIMADE, 2023; Samarasekera, 2023). In Pakistan, floods in 2020 led to a surge in dengue cases, with 733 reported in the Sindh province (Khan, 2020). The *El Nino* Southern Oscillation has increased the risk of dengue transmission in Peru due to rising temperatures and rainfall patterns (Dostal et al., 2022; Reátegui and Falcón, 2021).

High **precipitations** during summer in Northern Canada have increased Tularemia, a zoonotic disease primarily transmitted by **rodents** and lagomorphs (Buhler et al., 2023). Arctic foxes primarily eat small mammals and can serve as sentinels for the disease (Buhler et al., 2023). Global seroprevalence in foxes in northern Canada was 2% in 2018–19, with high seroprevalence in summers due to **high precipitation**, snow cover, and vole abundance (Buhler et al., 2023).

Other factors, such as wind speed, can also be an explanatory parameter for the occurrence or nonoccurrence of *Aedes albopictus* **in Europe** (Adeleke et al., 2022). A study tested this model and concluded that climatically suitable and monitored areas where *Ae. albopictus* is not established has a significantly higher wind speed than areas where the species is already established (Adeleke et al., 2022). Wind speed hurts the predicted habitat suitability of *Ae. albopictus* (Adeleke et al., 2022).

Increased **salinity** can also affect mosquito-borne illnesses such as the **Ross River virus** (RRV) (Carver et al., 2009). *Aedes camptorhynchus*, the dominant vector, is more abundant in saline areas, and its abundance determines more variation in the RRV transmission potential (Carver et al., 2009). Dryland salinity in the Wheat belt region of Western Australia has been shown to affect the zoonotic potential for RRV transmission (Carver et al., 2009). Dryland salinity is predicted to expand by 2050, and preserving and restoring freshwater ecosystems may mitigate the potential for RRV transmission and human disease incidence (Carver et al., 2009).

Climate may also play a role in food-borne pathogens' prevalence along the food chain (Smith et al., 2019). A study using integrated surveillance data examined associations between weather variables and Campylobacter,

E. coli, and Salmonella contamination in beef, poultry, and swine meat products in Canada (Smith et al., 2019). **Temperature metrics** were correlated with ***Campylobacter*** prevalence, while ***E. coli* and *Salmonella* were correlated with precipitation and temperatures** (Smith et al., 2019). Campylobacter, the most likely food-borne bacteria affected by climate changes in Canada, showed a seasonal trend, with increased prevalence from June or July through November (Smith et al., 2019).

3.3.3 Climate migration and epidemics

Changes in rainfall and temperature patterns can also impact livelihoods and accessibility of food and water. In an increasingly globalized society, the movement of people, goods, and animals might aggravate the issues brought on by illnesses and climate change. The rapid spread of SARS-CoV-2 variants demonstrates that severe travel restrictions may not always prevent highly transmissible illnesses from spreading virulently. This suggests that illnesses can spread silently and produce epidemics under the correct circumstances. Scientists anticipate that 2024 will be an even warmer year due to the El Niño event, which warms the surface waters in the eastern Pacific Ocean. This is likely to cause extreme drought in certain regions of the world, which might cause large-scale temporary and permanent **migrations**.

Population **migration can be attributed to various factors**, but climate changes are among the most important, increasing the risk of pathogen spillover (Reiner et al., 2012; Willett and Sears, 2020). **Extreme weather** events have caused cholera outbreaks in Haiti and Bangladesh and Hepatitis E virus (HEV) outbreaks in displaced persons camps due to unclean water supply, low hygiene, and sanitation (Ahmed et al., 2013; Reiner et al., 2012; Rinaldo et al., 2012). Severe droughts in the Horn of Africa in 2011 exacerbated socioeconomic issues, leading to overcrowded refugee camps in Kenya and Ethiopia, where devastating outbreaks of cholera, shigellosis, and acute HEV occurred (Ahmed et al., 2013; Reiner et al., 2012).

A study in the Indus Delta, Pakistan, found that displacement affected zoonotic disease transmission risk following the 2010 "**superfloods**" in Sindh province (Braam et al., 2021). This study concluded that displaced populations are vulnerable to zoonotic disease due to their precarious conditions (Braam, 2022). Addressing broader political economy issues and providing comprehensive assistance is crucial for preventing further displacement and disease (Braam, 2022).

Climate pressures and **human migration** have also been linked to changes in disease vector distribution, such as the yellow fever virus (YFV) epidemic in Brazil (Faria et al., 2018; Wilder-Smith and Gubler, 2008). Frequent movements to rural and forested areas increase the risk of

acquiring YFV from the sylvatic cycle. Factors like overcrowding and poor sanitation can lead to outbreaks of mosquito-borne and water-borne diseases in the displaced population's destination locations (Chaparro et al., 2013; Goma Epidemiology Group, 1995; Neiderud, 2015). Proximity to vectors and animal populations near temporary shelters may exacerbate the risk of zoonotic spillovers. For example, an elevated risk of visceral **leishmaniasis** near water supplies in northeastern Brazil was found due to sand fly vectors prevalent in drought-driven human settlements (Thompson et al., 2002). Long-term migration events' increased urbanization and population density impact infectious disease transmission dynamics (Neiderud, 2015; Reyes et al., 2013).

Leishmaniasis is endemic in **Mediterranean countries** and is expected to increase due to climate change and migration (Palma et al., 2021). A population-based study in Barcelona between 1996 and 2019 found 177 cases, with 74.6% being Spanish-born (Palma et al., 2021). The highest incidence was in 2017, along with an increase in the population from **foreign countries** (Palma et al., 2021). Although **canine leishmaniosis** (CanL) has been reported in northern continental Italy since the early 1990s, a study monitored the spread of endemic Leishmania from 2018 to 2019 in five regions (Gradoni et al., 2022). This increase was attributed to climatic changes and infected dogs from the southern **Mediterranean** littoral (Gradoni et al., 2022).

3.4 Climate change and animal diseases

Humans have always relied on animals for food, transport, work, and company (Zanella, 2016). Animals can be a source of infectious diseases caused by viruses, bacteria, and parasites, some of which can be transmitted to the human population (Zanella, 2016). However, anthropogenic factors and climate change can also affect animal health. As such, outbreaks of **Rift Valley viral** fever (RVF) in Africa in 1987, 1997–98, and 2006–07 were associated with changes in the **course of the river** and **floods** as a result of dams or torrential rains in the region (Cutler et al., 2010) causing animal disease emergency.

The interaction between **animal production** and climate change is complex, as animal production contributes to climate change (Gebremichael et al., 2023). However, in the opposite and worse situation, climate change also **affects animal health** and production, as it threatens the survival of many animal species, ecosystems, and the sustainability of livestock production systems worldwide (Gebremichael et al., 2023). This disruption of natural ecosystems allows disease-causing pathogens to move into new areas that can harm wildlife, domestic species, and humans (Gebremichael et al., 2023).

A study of the 2010 "superfloods" in Pakistan (Braam et al., 2021) found that **livestock** was often the only movable asset, and crowded locations were avoided to protect human and animal health (Braam et al., 2021). However, livestock was rarely included in the humanitarian response, leading to fragmentation (Braam et al., 2021). The findings have implications for policymakers and humanitarian responders assisting displaced populations dependent on livestock, calling for the integration of **livestock support in humanitarian** policies for health, survival, and recovery (Braam et al., 2021).

Camels are becoming a popular livestock in Kenya due to climate change effects (Muturi et al., 2021). However, their role in the epidemiology of diseases like RVF, brucellosis, and Q fever is poorly understood (Muturi et al., 2021). A study analyzed 120 camel serum samples from northern Kenya, finding high seropositivity rates for *Brucella*, *Coxiella burnetii*, and RVF virus (Muturi et al., 2021). The high rates suggest the endemicity of these pathogens among camel populations and their potential role in zoonotic disease epidemiology (Muturi et al., 2021).

Domestic dogs carry vector-borne pathogens, particularly zoonotic agents influenced by urbanization, trade, movement or travel, and climate change (Springer et al., 2019). A study of canine vector-borne diseases in Costa Rica showed the highest prevalence for *Ehrlichia* spp., followed by *Babesia* spp., *Anaplasma* spp., and *Borrelia burgdorferi* (Springer et al., 2019). Another study in Spain assessing the prevalence and distribution of four major canine vector-borne diseases (*Dirofilaria immitis*, *Leishmania infantum*, *Anaplasma* spp., and *Ehrlichia canis*) found that 22.14% of dogs were positive for one or several diseases, with the highest prevalence for *D. immitis* (Montoya-Alonso et al., 2020). Protection of dogs from disease-transmitting vectors is recommended from an animal welfare and public health perspective (Springer et al., 2019). Moreover, **preventive measures and awareness campaigns should occur among veterinarians and owners**, as well as collaboration between veterinarians, physicians, and health authorities (Montoya-Alonso et al., 2020).

3.5 Impacts of climate changes on ecosystems, habitats, and wildlife behavior

Climate change also influences the survival and distribution of vertebrate or invertebrate vectors. Herein, some examples of how climate change is influencing wildlife disease dynamics are presented.

Eurasian moose are a species adapted for cold climates and are often not ideal hosts for vectors (Malmsten et al., 2019). However, climate change, characterized by warmer temperatures and altered precipitation patterns, has impacted vector distribution and vector-borne diseases (Malmsten et al., 2019). A study of 615 moose in southern Sweden found that they are exposed to and can act as hosts

for some pathogens, including *Anaplasma*, *Borrelia*, *Babesia*, and *Bartonella* (Malmsten et al., 2019). These pathogens can impact animal and human health, emphasizing the need to consider moose as **sentinels for vector-borne pathogens** (Malmsten et al., 2019).

Wild boars, one of Eurasia's oldest species, are spread throughout Europe, Asia, Africa, and North and South America (Jemeršić et al., 2019). Despite their adaptability, hunting ground management, lack of natural enemies, and favorable climate changes, their increasing numbers threaten farmers and the swine industry (Jemeršić et al., 2019). They can be sources of swine infectious diseases such as African swine fever (ASF), classical swine fever (CSF), Aujeszky's disease (AD), and zoonoses such as hepatitis E (HE), leading to interspecies transmission and virus spread (Jemeršić et al., 2019). Hunting, a significant tourist attraction in Europe, also contributes to viral spread (Jemeršić et al., 2019). Wild boars are also important in **Crimean-Congo hemorrhagic fever (CCHF)** epidemiology. CCHF is a widespread tick-borne viral disease (Vatansever, 2019). The adult ticks of *H. marginatum* are hunter-type and actively seek/wait for hosts on the ground, mostly preferring artiodactyls like cattle, sheep/goats, horses, and wild boars, but bite humans when the preferred host is not available (Vatansever, 2019). In Turkey, CCHF epidemics have been associated with **ecological changes and habitat fragmentation**, leading to an increase in wild animals and *H. marginatum* populations (Vatansever, 2019).

The Svalbard **white whale** population, one of the world's smallest, is highly susceptible to climate change and pathogens (Nymo et al., 2023). A monitoring study of health parameters and zoonotic agents of this **vulnerable population** of white whales from 2001 to 2016 in the **Arctic** showed exposure to influenza A virus and *Brucella* spp. (Nymo et al., 2023).

Another example of how climate change affects the distribution and outbreaks of zoonotic diseases comes from the northern high latitudes, particularly in the middle boreal subzone of northern Sweden (Sipari et al., 2022). Long-term monitoring data from Northern Europe shows that early winters are becoming **increasingly wet**, impacting the transmission of *Puumala ortho hantavirus* (PUUV) in the reservoir host population, the **bank vole**, *Myodes glareolus*, a field mouse (Sipari et al., 2022). This study shows a climate change effect on an endemic northern zoonosis, demonstrating that climate change can alter transmission intensity within host populations (Sipari et al., 2022). Rainy early winters may increase human zoonotic risk in the North (Sipari et al., 2022). This study also demonstrates that climate change can alter transmission intensity within host populations, with rainy early winters potentially increasing human zoonotic risk in the North (Sipari et al., 2022).

Flood influence on the **rodent** community composition, population structure, breeding season, temporal and spatial variations in rodent abundance, and environmental factors on islands of the upper Paraná River Delta in Argentina was carried out (Maroli et al., 2022). Over three years, 377 sigmodontine rodents of seven species were captured (Maroli et al., 2022). The study found that seasonality, land use, and vegetation structure did not explain changes in rodent abundance (Maroli et al., 2022). Rodent abundances were mainly affected by **flooding-related factors** and meteorological conditions (Maroli et al., 2022). The recovery of rodent populations after river flooding was species-specific and heterogeneous (Maroli et al., 2022). While the abundance of some rodent species was affected by *El Niño* Southern Oscillation, the *Oligoryzomys flavescens*, the reservoir of hantavirus pulmonary syndrome, also declined after the flood, but its populations were the first to recover and became dominant in the postflood rodent community (Maroli et al., 2022).

Trichinella nematodes indicate a healthy natural ecosystem (Pozio, 2022). Trichinella, a group of zoonotic parasites, primarily infect **wild carnivores**, with most human infections caused by pork consumption (Pozio, 2022). The nematodes complete the natural life cycle within the host organism, with an important phase involving infecting larvae in rotting carcasses (Pozio, 2022). To survive, they develop an anaerobic metabolism and resistance to freezing (Pozio, 2022). Climate changes, such as increasing temperatures and reduced humidity, reduce larvae's survival time (Pozio, 2022).

Climate change affects wildlife disease dynamics, particularly in **polar bears**, vulnerable to sea ice loss due to accelerated **Arctic** warming (Pilfold et al., 2021). A study in Canada analyzed adult polar bears and found a significant increase in the prevalence of zoonotic parasites and bacterial pathogens between 1986 and 1989 and 1995–98, ranging from 6.2% to 20.8% (Pilfold et al., 2021). *Toxoplasma gondii* seroprevalence was higher following wetter summers, while *Trichinella* spp. and *B. bronchiseptica* were positively correlated with hotter summers (Pilfold et al., 2021). The seroprevalence of antibodies to *F. tularensis* increased in the following years, polar bears spent more days on land, and polar bears captured in human settlements were more likely to be seropositive for *Trichinella* spp. (Pilfold et al., 2021).

Wild ungulates in Austria are known hosts for ticks and reservoirs for pathogens like *Babesia* spp. and *Anaplasma phagocytophilum* (Kogler et al., 2021). Human babesiosis is an emerging zoonosis in central Austria (Kogler et al., 2021). A study tested blood of roe deer, red deer, mouflons, and chamois for DNA of tick-borne pathogens, which was detected in 15.5% of these animals, in addition to a new genotype of *Babesia* (Kogler et al., 2021).

3.6 Ecosystem resilience and importance to preserve biodiversity

The environment is crucial for the health and well-being of humans, animals, and plants. Maintaining ecosystem health through conservation helps preserve biodiversity, limit disease transmission, and promote health. Research also shows that contact with nature benefits psychological and physiological health (Valladares, 2023). However, rising demand for resources is putting pressure on the environment, limiting untainted habitats for plants and animals (Huber et al., 2020).

Environmental degradation caused by human activities poses complex health threats, including water, air, and soil pollution, which can lead to noninfectious diseases like cancer and respiratory illness (Valladares, 2023). Pollutants can contaminate the food supply, leading to adverse health outcomes. Air pollution from fossil fuels and other sources also negatively impacts human and animal health, biodiversity, and water quality. Antimicrobial waste enters the environment and water sources, causing drug-resistant organisms and antimicrobial resistance. Unsafe water, poor sanitation, and poor hygiene contribute to mortality and morbidity due to diseases, especially in low-resource countries. Climate change can exacerbate these threats, compromising feed and food security, increasing the spread of infectious diseases, and affecting ecosystem-useful insects like bees (Adisasmito et al., 2022; Mettenleiter et al., 2023).

Climate change threatens the ecosystem balance and resilience, particularly in Arctic and subarctic regions (Huber et al., 2020). Thawing permafrost transforms soil structures, vegetation, and habitats, increasing the risk of zoonotic diseases (Huber et al., 2020). Rising temperatures also expose historic burial grounds, potentially reviving vectors of deadly infections (Huber et al., 2020). However, biodiversity loss in Southern Hemisphere countries such as Brazil and Australia has affected infectious diseases like malaria, hantavirus pulmonary syndrome, yellow fever, and urban arboviruses, and pandemic risk management has to be applied (Duarte, 2019; Pinter et al., 2022; Woolaston et al., 2022). While some may view climate change and epidemics as temporary, there is overwhelming evidence linking climate change to the surge of disease outbreaks and epidemics, making it a question of when the next epidemic will occur (CLIMADE, 2023).

3.7 Climate change and antimicrobial resistance

High temperatures, rising sea levels, and greenhouse gases bring changes that lead to the emergence and reemergence of infectious pathogens, including those that have already developed significant antimicrobial resistance (AMR) (Gudipati et al., 2020). The interactions between climate change and AMRs are studied using honey bees, One Health model organisms, mainly to investigate the context of climate change and environmental pollutants (de Jongh et al., 2022). These studies include hive immunocompetence and multidrug resistance transporter downregulation, susceptibility to pests, especially American foulbrood, and increased hive products (de Jongh et al., 2022). These studies identified three potential links between pollution climate factors and the risk of AMR (de Jongh et al., 2022).

4 Global coordination and governance help the implementation of one health

4.1 Importance of COVID-19 to trigger one health approaches

Even in the current scenario of the evolution of biomedical research, sophistication of methodologies, equipment, state-of-the-art facilities, and the training of technicians, diseases continue to emerge in nature and infect living beings on all continents (Zanella, 2016). The COVID-19 pandemic urged the discussion on the surveillance of emerging diseases by the scientific society, especially in the case of zoonotic diseases.

The COVID-19 pandemic has caused over 4.3 million confirmed cases and 290,000 deaths globally, causing widespread fear, a global health catastrophe, and a decline in the global **economy** (Gehlot, 2022; Nicola et al., 2020). The impact of the COVID-19 pandemic on human health and the world economy was immense, something over 30 trillion dollars (Jackson et al., 2020). Likewise, social distancing, travel restrictions, and reduced workforce have resulted in job losses, school closures, decreased demand for commodities, increased demand for medical supplies, and an impact on human mental health (Holmes et al., 2020; Nicola et al., 2020; Xiong et al., 2020).

Nevertheless, the impact of COVID-19 on the **food supply chain**, specifically the meat chain, was unexpected. The high incidence of COVID-19 in workers in meat processing plants has rapidly evolved to affect human, animal, and environmental well-being in several countries. This has led to the closure of processing plants due to outbreaks, especially in the pork and poultry industries. The reduction in slaughter resulted in the accumulation of animals on farms, which led to the reduction of food for the animals, their euthanasia, and inappropriate disposal of carcasses. This has impacted animal welfare, producer income, supply, and biosecurity (Marchant-Forde and Boyle, 2020).

4.2 One health high-level expert panel (OHHLEP)

During the COVID-19 pandemic, the Alliance for Multilateralism called on the Tripartite (FAO, WAHO, WHO) and

UNEP (United Nations Environment Programme) to create a One Health High-Level Expert Panel (OHHLEP) (OHHLEP, 2022). Launched in May 2021, OHHLEP appointed 26 international experts from 24 countries, representing various disciplines and policy-related sectors (OHHLEP, 2022). The panel is multidisciplinary, with experts from all world regions. The Partners are committed to using the knowledge generated by OHHLEP, including analyzing scientific evidence on zoonotic disease spillover, developing a risk management framework, and proposing an optimized One Health surveillance system. This will help improve systems to prevent, predict, detect, and respond to global health threats at all levels. The OHHLEP is well placed to provide scientific advice to the partners' organizations and beyond. The focus of OHHLEP Terms of Reference (ToR) consists (1) in providing policy-relevant scientific assessment on the emergence of health crises arising from the human-animal ecosystem interface and research gaps and (2) guidance on development of a long-term strategic approach to reducing the risk of zoonotic pandemics, with an associated monitoring and early warning framework, and the synergies needed to institutionalize and implement the One Health approach, including in areas that drive pandemic risk.

Following this mission, OHHLEP established four working groups: (1) One Health implementation (Adisasmito et al., 2023), (2) One Health research and initiatives inventory, (3) One Health surveillance (Hayman et al., 2023; OHHLEP et al., 2023), and (4) One Health risk analysis (OHHLEP et al., 2023). Fig. 22.2 illustrates OHHLEP's definition of One Health (Adisasmito et al., 2022).

One Health is an integrated, unifying approach that aims to sustainably balance and optimize the health of people, animals, and ecosystems. It recognizes the health of humans, domestic and wild animals, plants, and the wider environment (including ecosystems) are closely linked and interdependent.

The approach mobilizes multiple sectors, disciplines, and communities at varying levels of society to work together to foster well-being and tackle threats to health and ecosystems while addressing the collective need for clean water, energy, and air, safe and nutritious food, taking action on climate change, and contributing to sustainable development.

OHHLEP also provided critical input into the ongoing development of the One Health Joint Plan of Action (JPA) (2022–26), a strategic document outlining the way forward for the Partners' successful implementation of the One Health approach to tackle global problems at the human-animal-ecosystem interface (Mettenleiter et al., 2023). This also aligns with key needs to achieve sustainable development goals and as guiding principles for policymakers and scientists alike. The One Health JPA is built around six interdependent action tracks that collectively contribute to achieving sustainable health and food systems, reduced global health threats, and improved ecosystem management.

- Action track 1: Enhancing One Health capacities to strengthen health systems.
- Action track 2: Reducing the risks from emerging and reemerging zoonotic epidemics and pandemics.
- Action track 3: Controlling and eliminating endemic zoonotic, neglected tropical, and vector-borne diseases.
- Action track 4: Strengthening the assessment, management, and communication of food safety risks.
- Action track 5: Curbing the silent pandemic of antimicrobial resistance—AMR.
- Action track 6: Integrating the environment into One Health.

To help achieve these aims in a comprehensive, systematic, and sustainable way in keeping with the underlying principles of the One Health approach, OHHLEP has developed an over-arching Theory of Change (ToC) Change (2022–35). This ToC is designed to guide OHHLEP's work and that of the Quadripartite and provide a conceptual framework for other organizations, agencies, and initiatives working toward similar One Health goals (Mettenleiter et al., 2023).

5 One health approach and healthy ecosystem

The One Health approach is crucial to achieving the Sustainable Development Goals (SDG) and developing effective responses to health threats (Heukelbach, 2020). This approach must address socio-ecological challenges like climate change, habitat destruction, extinction, urbanization, and zoonotic diseases. This multidisciplinary approach includes medical, veterinary, wildlife, biological, agricultural, and social sciences (Heukelbach, 2020; Mettenleiter et al., 2023). Altogether, One Health is transitioning from a zoonoses perspective to a multidisciplinary approach, encompassing topics like climate change, nutritional food, food safety, policy, welfare, antimicrobial resistance, and many other aspects of environmental health (Fasina et al., 2021; Hayman et al., 2023).

A study in sub-Saharan Africa assessed One Health initiatives and found that an imbalance in representations led to hesitation in adopting the One Health approach (Fasina et al., 2021). To ensure a sustainable future, a theory of change, monitoring frameworks, and standardized evaluation tools are needed (Fasina et al., 2021). National roadmaps for One Health implementation and institutionalization are needed, and the One Health approach should proactively address emerging issues like urbanization and poverty (Fasina et al., 2021).

At the same time, the influence of climate change on public health in a One Health approach is important to be known by **local populations** affected by these challenges (DiPietro et al., 2023). A study of nomadic herders in a conservation area (Ikh Nart Nature Reserve in Mongolia) was
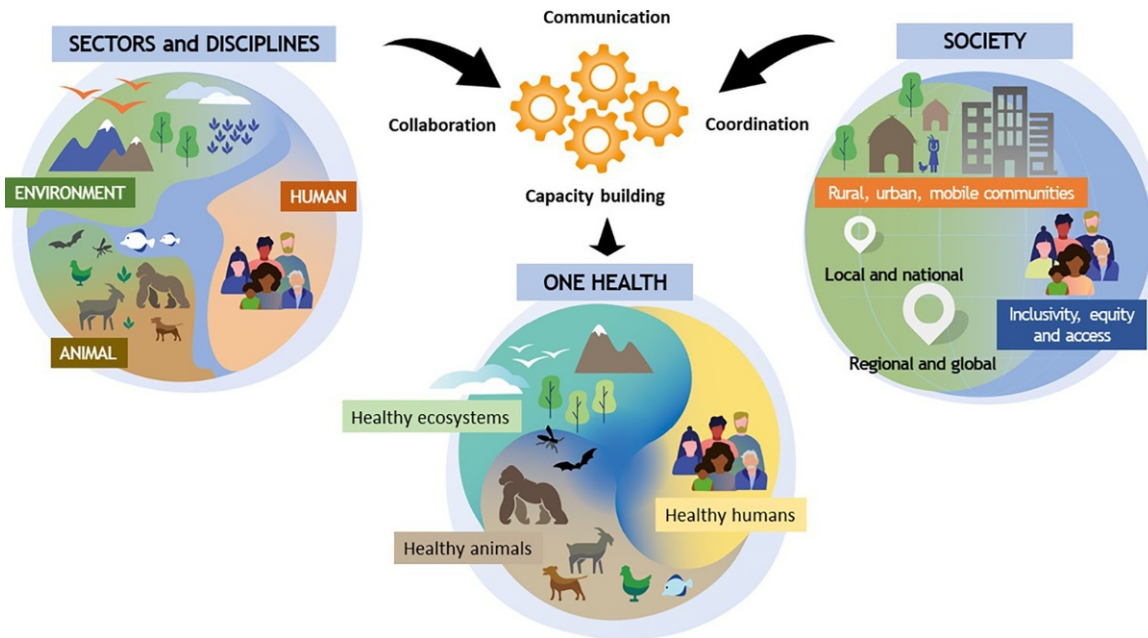
FIG. 22.2 OHHLEP's definition of One Health. *(Reproduced with permission from Adisasmito, W.B., Almuhairi, S., Behravesh, C.B., Bilivogui, P., Bukachi, S.A., Casas, N. et al., 2022. One health: a new definition for a sustainable and healthy future. PLoS Pathog. 18.* https://doi.org/10.1371/journal.ppat.1010537.*).*

carried out to verify their understanding of the interconnectedness of environmental, animal, and human health (DiPietro et al., 2023). The model used was the link between human well-being, environmental factors, and outbreaks of foot-and-mouth disease in ungulates, which occur most frequently in Mongolia (DiPietro et al., 2023). Pastoralists understood One Health concepts adequately, revealing that climate change contributes to landscape degradation, declining animal health, and human socioeconomic consequences (DiPietro et al., 2023). This again demonstrates that Indigenous peoples and Local Communities must be actively involved through leadership and contributions in formulating **transdisciplinary** strategies to combat climate change and its effects on animal and human health (DiPietro et al., 2023).

In the same way, understanding populations at **risky workplaces** is crucial for public health policies and practices (Adam-Poupart et al., 2021). In Quebec, 14 zoonoses have been identified as important for climate change adaptation efforts (Adam-Poupart et al., 2021). The 14 zoonoses included campylobacteriosis, cryptosporidiosis, verocytotoxigenic *Escherichia coli*, giardiasis, listeriosis, salmonellosis, Eastern equine encephalitis, Lyme disease, West Nile virus, food botulism, Q fever, avian and swine influenza, rabies, hantavirus pulmonary syndrome (Adam-Poupart et al., 2021). **Occupational health** revealed that enteric zoonoses were the most frequently reported, followed by agriculture, veterinary services, public administration services, and medical and social services (Adam-Poupart et al., 2021; Riccò et al., 2021). Another study in Spain examined human cases of avian influenza, focusing on management,

personal protective equipment, and surveillance programs (Sánchez et al., 2020). As wild waterfowl are the primary reservoir of influenza viruses, various groups exposed to wild birds should be aware of potential infection sources and how to handle protective equipment, adapt activities, and provide information for surveillance programs (Sánchez et al., 2020). The findings will help public health authorities and decision-makers target sectors and occupations at risk for zoonoses, ultimately optimizing public health practices for those responsible for worker health (Adam-Poupart et al., 2021). **Occupational groups** like farmers and forestry workers are at high risk of Hantavirus due to their interaction with rodents (Riccò et al., 2021). A study of 42 articles found a pooled seroprevalence of 3.7% in farmers and 3.8% in forestry workers, with an increased occurrence in both groups compared to the reference population (Riccò et al., 2021). The analysis emphasizes the actual occurrence of hantaviruses in selected occupational groups and calls for improved understanding of preventive measures and further studies on hantavirus infection rates in reservoir host species and virus transmission to humans to prevent future outbreaks (Riccò et al., 2021).

5.1 Pandemic prevention and preparedness response

Pandemic prevention is crucial to addressing future pandemics but is not yet prioritized (OHHLEP et al., 2023). The primary focus should be preventing pathogen spillover and implementing environmental initiatives like the Post-

2020 Global Biodiversity Framework. Prevention of pathogen spillover from animals to humans involves shifting the infectious disease control paradigm from reactive to proactive. This involves addressing ecological, meteorological, and anthropogenic factors that increase spillover risk, reducing the risk of human infection. This includes biosurveillance, understanding pathogen infection dynamics, and implementing intervention activities (OHHLEP et al., 2023). However, demonstrating the impact of changes in policies or practices on cases or events can be challenging due to poor baseline data. Intermediate indicators can help inform systematic risk reduction processes. A One Health approach should be emphasized, considering specific geographic contexts, socioeconomic and cultural backgrounds, and avoiding human rights violations. Spillover prevention should follow a One Health risk reduction approach, recognizing that many anthropogenic behaviors and activities increase environmental changes and socioeconomic factors that increase spillover risk (OHHLEP et al., 2023). Sustainable investment in spillover prevention is needed, and opportunities like the World Bank Pandemic fund, Global Funding facility, and Global Environmental facility are emerging. A larger commitment is overdue to prevent future pandemics (OHHLEP et al., 2023). Fig. 22.3 represents the important steps for the prevention and preparedness of animal-to-human pathogen spillover (OHHLEP et al., 2023).

5.1.1 Prevention—Identify threats and reduce the risk of spillover due to climate change

According to OHHLEP, the prevention of zoonotic spillover's main goal is to lessen the possibility of occurrences of spillover (OHHLEP et al., 2023). The intervention stage is before the transfer from animals to humans and is considered as an upstream or primary prevention. The strategy uses the One Health concept to identify and address risk factors based on the pertinent stakeholders. The integrated actions involve health surveillance to detect threats and inform risk assessment, addressing disease emergence drivers like climate change, land use, wildlife trade, and food systems, and developing risk reduction activities like biosecurity and vaccination for infection prevention (OHHLEP et al., 2023). Next, some ongoing actions to prevent spillovers related to climate change will be discussed.

Multidisciplinary approaches and public policies

Humans can contract zoonoses during **leisure activities**, such as walking, aquatic activities, hunting, pet farms or fairs (Haddad, 2019). Urban populations' preference for outdoor activities and unawareness of wild and domestic animal diseases increase the risk (Haddad, 2019). **Vigilance** is crucial, as knowledge of prevention and control methods

and active participation of target populations are essential for reducing this risk (Haddad, 2019).

Infectious diseases are a significant public health problem in developing countries, such as **Nepal, which is facing** a burden of epidemic zoonotic diseases, with 60 identified as emerging and reemerging (Paudel, 2020). Among those, six zoonoses are particularly concerning: **Taeniosis, Leptospirosis, Hydatidosis, Brucellosis, Toxoplasmosis, and Avian Influenza** (Paudel, 2020). Influenza is the most common outbreak, with nearly half of the population at high risk and a quarter at moderate risk of rabies (Paudel, 2020). According to Paudel (2020), infectious disease trends are declining due to **joint efforts from veterinary and human medical and public health professionals** in Nepal (Paudel, 2020).

Vector-borne diseases (VBDs) significantly cause morbidity and mortality in humans and animals, particularly in the Mediterranean Basin, where climate changes can influence vector abundance and distribution (Tahir et al., 2019). These diseases, including nematode infections in dogs and cats, are caused by parasitic nematodes transmitted by arthropods like mosquitoes, black flies, drosophilids, ticks, and fleas (Tahir et al., 2019). To control and prevent these infections, a **multidisciplinary approach involving health, research, sociology, economics, governments, and citizens is needed** (Tahir et al., 2019).

Another approach to avoid the expansion of zoonotic diseases, such as **Lyme** disease in Canada, Quebec's Multiparty Observatory on Zoonoses and Adaptation to Climate Change, was established in 2015 as part of the Quebec government's Climate Change Action Plan (Germain et al., 2019). The Observatory brings together public policy agencies and experts from human health, animal health, and environmental sciences to share knowledge and build consensus (Germain et al., 2019). Its main objectives are to anticipate and prioritize potential zoonotic disease issues in Quebec, supporting risk management and climate change adaptation (Germain et al., 2019).

Considering the impact of global climate change on human health and illness, including noncommunicable diseases like allergic, respiratory, cardiovascular, and dermatological diseases, the **role of clinicians in educating communities** on climate change's negative health impact and sustainable healthcare policy benefits should be debated (Torpiano, 2019).

Education

The emergence of zoonoses like Ebola has prompted medical educators to recommend **Interprofessional Education** as a tool to familiarize human medicine students with the One Health framework. These initiatives can help students understand the impact of animal and environmental health factors on human health (Roopnarine and Boeren, 2020). A study examined the readiness for interprofessional learning among
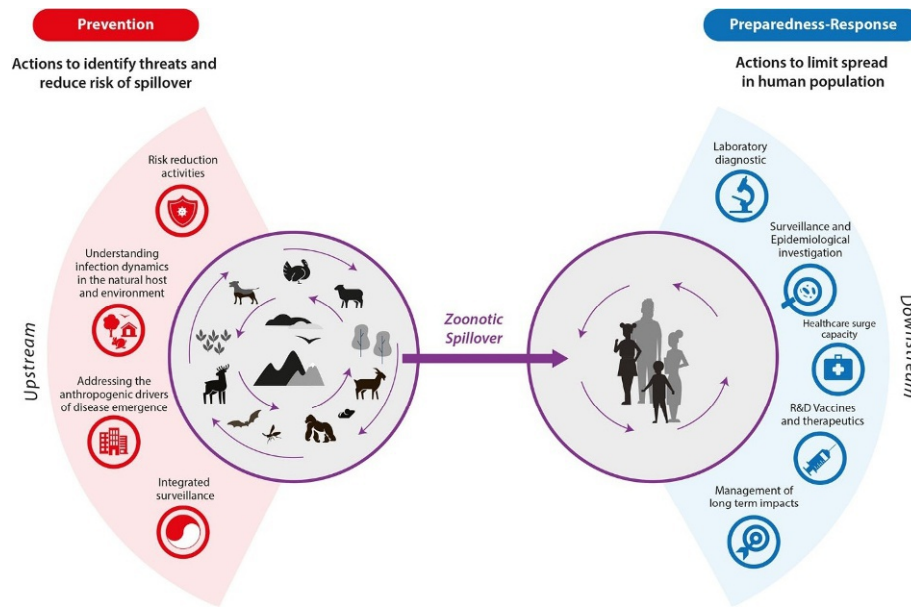
FIG. 22.3 Prevention of pathogen spillover from animals to humans involves shifting the infectious disease control paradigm from reactive to proactive, addressing ecological, meteorological, and anthropogenic factors, biosurveillance, understanding infection dynamics, and intervention activities. *(Reproduced with permission from OHHLEP (Authored by the members of the OHH-LEP), Markotter, W., Mettenleiter, T.C., Adisasmito, W.B., Almuhairi, S., Barton Behravesh, C., et al., 2023. Prevention of zoonotic spillover: from relying on response to reducing the risk at source. PLoS Pathog. 19, e1011504.)*

medical and related human health professionals, including veterinarians and those pursuing dual degrees with a Master of Public Health (Roopnarine and Boeren, 2020). The study concludes that medical curricula should incorporate shared learning and teamwork to increase understanding of the human-animal-environmental spectrum (Roopnarine and Boeren, 2020). A survey of 133 US medical schools found that 56% of programs included OH-related subject matter, primarily in preclinical classroom learning (Docherty and Foley, 2021). This suggests that **OH education efforts in medical schools lag behind those in veterinary schools**, which already include OH as a central part of their curricula (Docherty and Foley, 2021). The study suggests interdepartmental and interdisciplinary collaboration for a holistic approach to health care, considering environmental, wildlife, and domestic animal factors to close educational gaps (Docherty and Foley, 2021). In the same way, as explained by Duarte (2019), the pathology of infectious diseases is crucial for understanding the emergence and reemergence of various diseases (Duarte, 2019). Pathology has been crucial in understanding the history of diseases like tuberculosis, AIDS, Ebola, SARS, and the Zika epidemic (Duarte, 2019).

5.1.2 Preparedness response—Limit the spread of human population due to climate change

Stopping the spread of pathogens in people (also known as secondary or downstream prevention), as proposed by

OHHLEP, is to reduce the effects of spillover-related incidents (OHHLEP et al., 2023). Thus, the intervention stage comes **after** there has been an animal-to-human spillover. Containment is the strategy, which includes preventing spillover from humans to other animal species and inter- and intraspecies transmission. Therefore, the solutions include early human pathogen identification, vaccinations, enhancing health systems, promoting health, altering social and behavioral standards, medications, risk reduction strategies for humans and animals, and hygienic measures (OHHLEP et al., 2023).

Policies and plans

WHO pandemic instrument The International Treaty on Pandemic Prevention, Preparedness and Response (Pandemic Treaty) is a proposed international agreement to strengthen pandemic prevention, preparedness, and response (WHO, 2021). The 194 World Health Organization (WHO) member states agreed in December 2021 to begin negotiations on a global pandemic treaty, aiming for a draft agreement to be finalized by May 2024 for consideration by the 77th World Health Assembly. The central principle of the instrument is equity (WHO, 2021). Experts argue that the COVID-19 pandemic has exposed severe limitations in the International Health Regulations (IHR) and the WHO's institutional capacities (Driece et al., 2023). In response, a special session of the World Health Assembly was convened in November 2021, establishing an intergovernmental negotiating body to draft and

negotiate a WHO convention, agreement, or other international instrument on pandemic prevention, preparedness, and response (WHO, 2021).

The Pandemic Fund supports investments in pandemic prevention, preparedness, and response, focusing on low- and middle-income countries. It provides dedicated resources, incentivizes increased investments, enhances coordination, and serves as a platform for advocacy, highlighting the urgent need for coordinated action (The World Bank, 2022).

As the nature of war changes, **international law to improve food security** and humanitarian legislation must be strengthened to protect civilians (Garcia and Gostin, 2012). Therefore, **refugee laws** play a critical role in protecting the health of intensely exposed people who lack nutrition, housing, and social stability (Garcia and Gostin, 2012). In addition, d**isaster preparedness plans** help prevent the negative impact of infectious diseases, but unforeseen events like the **Ukraine-Russian conflict** and **heavy rain in South Africa** also led to disastrous consequences (van der Walt, 2022). The second example is the heavy rain of April 2022 in the KwaZulu-Natal Province of South Africa, which caused massive destruction of houses and infrastructure, resulting in affected people being **displaced** (van der Walt, 2022).

Multi-institutional, multisectoral, and multidisciplinary approaches

The primary steps to reduce epidemics magnified by climate are listed in the Climate Change and Epidemics 2023 study (CLIMADE, 2023). To address these pressing problems effectively, the study calls for **governments, academic institutions, scientists, public health authorities, private sector businesses, and health organizations** to pool their various skills and resources (CLIMADE, 2023).

International organizations allied with member countries must work on **multisectoral and multidisciplinary approaches** to advise public policies (Zhong and Huang, 2019). An example comes from China, a populous country with a large territorial extension (Zhong and Huang, 2019). Initially, the approach is to estimate how climate change will increase health risks based on geographic distribution (Zhong and Huang, 2019). The acceptable limits of changes in health must also be estimated, and methods for detecting risks must be developed (Zhong and Huang, 2019). Furthermore, it is essential to predict how climate change affects **health systems and infrastructures** and how this entire system could be integrated (Zhong and Huang, 2019).

Research to mitigate climate change and zoonotic spillover

Science is here to help the planet and is done with partnership. Herein, research lines related to mitigating climate change effects on diseases are discussed.

The relationship between **microbiota** and climate change is challenging (Tiedje et al., 2022). On the one hand, microbes produce and consume three important greenhouse gases—carbon dioxide, methane, and nitrous oxide; on the other hand, some microbes cause human, animal, and plant diseases that can be exacerbated by climate change (Tiedje et al., 2022). Thus, knowledge of microbial behavior in the three main ecosystems, terrestrial, oceanic, and urban, will help mitigate the effects of warming and the consequences resulting from heat, drought, and severe storms (Tiedje et al., 2022). These **mitigations** include conducting more controlled studies on the climate impact on microbial processes, system interdependencies, and responses to human interventions, utilizing microbes and their carbon and nitrogen transformations to useful stable products, improving microbial process data for climate models, and adopting the One Health approach to studying microbes and climate change (Tiedje et al., 2022).

Coral reefs are crucial in One Health research due to their sensitivity to ecosystem services and climate change (Sweet et al., 2021). However, understanding these complex systems remains challenging. Integrating coral reef research into the "One World—One Health" framework can improve human and environmental health by enhancing our understanding of ecosystems (Sweet et al., 2021).

Geomatics and satellite remote sensing can be used to understand the relationship between the environment and wildlife-related diseases (Orusa et al., 2020). Research in Italy, specifically on infectious keratoconjunctivitis, a contagious disease for domestic and wild ruminants (Caprinae and Ovinae), used image time series from 2000 to 2019, focusing on climate influence on vegetation in the area (Orusa et al., 2020). Results showed that phenological metrics and evapotranspiration trends significantly changed over the last 20 years, with a continuous progressive tendency (Orusa et al., 2020). The study suggests that remote sensing can effectively support public health and eco-pathological sectors, enabling continuous **monitoring** of the climatic dynamics of wild animals in the Alpine area, including diseases and zoonosis (Orusa et al., 2020). **Based on annual monsoonal rainfall and flooding, Malaysia has also used hydrometeorological variability to predict Leptospirosis emergency** (Jayaramu et al., 2023).

Climatic covariates and the impact of tree cover loss were used to study the species distribution of cutaneous **Leishmaniasis** in French Guiana (Jagadesh et al., 2021). The study showed varied distribution patterns between species and highlighted the impact of tree cover loss and climate on the increasing distribution of *L. braziliensis* in anthropized regions (Jagadesh et al., 2021). This tool allows the detection of high-risk regions for monitoring and active surveillance of the vector and disease distribution (Jagadesh et al., 2021).

Vector distribution was also studied in **Northern regions** (Greenland to Siberia) (Omazic et al., 2019). The research included a systematic literature search from 3 databases for 37 potential climate-sensitive infectious diseases relevant to humans and animals in those regions (Omazic et al., 2019). Results showed that **arthropod vector-borne** diseases have the potential to expand their distribution toward Northern latitudes and are a growing threat, while **tick-borne** encephalitis, borreliosis, midge-borne bluetongue, and fasciolosis can be classified as climate-sensitive (Omazic et al., 2019). The four-climate sensitive infectious diseases identified in this study could be targeted in a systematic surveillance program in Northern regions (Omazic et al., 2019). The spread of **tick-borne** diseases is often overlooked (Le Ng et al., 2022), particularly, **ocular manifestations** of these diseases (Le Ng et al., 2022). Considering significant travel and exposure history, understanding risk factors and control strategies associated with awareness of ocular manifestations of tick-borne diseases will benefit ophthalmologists and generalists in the age of **modern travel** and climate change (Le Ng et al., 2022). Another research developed during the COVID-19 pandemic, influenza, and Mpox was wastewater **surveillance** (Meadows et al., 2023). This wastewater monitoring is less expensive than widespread surveillance and can be used for human or animal health prevention and rapid response in airports or other sites (Meadows et al., 2023).

Another line of research that is evolving is the development of medications. Clinical treatment for epidemics like COVID-19 or influenza can include **nutraceuticals** (probiotics**) and antivirals** (Vinod, 2020). **Antiviral therapy** is currently available for a limited number of zoonotic viral infections. However, further studies are needed to develop more molecules and establish the therapeutic efficacy of nutraceuticals and probiotics in treating viral infections (Vinod, 2020).

Last, but not least, One Health includes sociological studies. The "Mitigation South Africa" study was conducted to identify research priorities for controlling zoonoses due to its complex disease burden and overstretched health system (Simpson et al., 2021). A multidisciplinary group of 18 experts identified 97 research priorities, most focusing on basic epidemiological research and developing new interventions. Seventeen diseases were mentioned, with rabies, TB, brucellosis, Rift Valley fever, and cysticercosis being the top five. Future research should focus on understanding zoonotic burden and risk factors, particularly for **people with limited rural services, immunocompromised individuals, informal settlements, and high-risk occupations** (Simpson et al., 2021).

6 Challenges and future directions

One Health is a way of life and the responsibility of all. Globalization has increased the threat of pandemics and accelerated global transmission but has also facilitated **international cooperation, disease research, and surveillance** (Saunders-Hastings and Krewski, 2016). However, challenges like data gaps, resource limitations, and policy barriers in addressing zoonotic diseases in a changing climate must be addressed. The potential for predictive modeling and research areas that require further exploration must be discussed. There must be interdisciplinary collaboration, policy integration, and the need for continued research.

Zoonotic spillover drivers are known. However, global resources are poorly allocated, with most efforts focused on countries where the next pandemic **is least** likely to originate and not on hotspots (Jones et al., 2008). The 2020 biodiversity objectives set by the Convention on Biological Diversity must be in place, since global temperatures are projected to rise by 2.3–4.1°C by 2100 (Turney et al., 2020). The international community fails to meet the biodiversity targets and prevent global temperature rise (Turney et al., 2020). The COVID-19 pandemic has highlighted the need for a more **integrated global approach**, with the delay in COP meetings providing an opportunity to create coherent policy frameworks across biodiversity, health, food, water, and climate change (Turney et al., 2020). Nature-based solutions and a "Just Transition" approach are essential for **supporting local communities** and addressing the rapidly deteriorating environment (Turney et al., 2020).

Developing countries are more vulnerable to climate disasters and have less adaptive capacity to respond (CLIMADE, 2023). Climate change should be used to build health capacity, especially in underserved communities. Policymakers must swiftly mitigate the public health crisis (CLIMADE, 2023). Governments, academic institutions, scientists, public health officials, private sector industries, and health organizations should collectively address climate-amplified diseases and epidemics (CLIMADE, 2023).

The UN Sustainable Development Goals (**SDGs**) encompass the changes needed to achieve fundamental health (Bhutta et al., 2020). In this way, governments allied with multilateral institutions such as civil society, academia, and the private sector must integrate integrated implementation mechanisms, financing, **and fiscal mechanisms** to catalyze the process (Bhutta et al., 2020).

Indeed, COVID-19 caused 14 million excess deaths globally between 2021 and 2022, hindering progress toward the SDG (Driece et al., 2023; WHO, 2021). The pandemic led to capacity gaps in national prevention, preparedness, response strategies, international collaboration failures, and inequities (Driece et al., 2023). The impacts disproportionately affected **vulnerable populations** and poor access to medical countermeasures, particularly in Africa, exacerbated by vaccine nationalism. The Intergovernmental Negotiating Body (INB) is negotiating for an international instrument on Public Proliferation (PPR) and amending the

International Health Regulations (2005) to address these shortcomings. The Zero Draft of the instrument proposes One Health, a comprehensive approach to prevent disease outbreaks by integrating environmental factors and animal and human health. It focuses on upstream and midstream prevention, with a global watchlist of pathogens with high spillover potential (WHO, 2021). The Zero Draft also suggests strengthening the manufacturing capacity in low- and middle-income countries through technology transfer. It proposes a global mechanism for pathogen access and benefit sharing, incorporating equity principles and a multilateral fund for equitable sharing of benefits (The World Bank, 2022; WHO TEAM One Health Initiative, 2022).

Currently, many tools for One Health implementation are in the study and development phase (Mettenleiter et al., 2023). Nevertheless, many gaps have been identified, such as prioritization of zoonose surveillance, priority species, etc. An example is the Cache Valley virus (CVV), a zoonosis transmitted by mosquitoes (Waddell et al., 2019). Although there are many studies in animals, only six human cases of CVV-associated illness were reported (Waddell et al., 2019). **No research was identified on treatment, societal knowledge, risk perception, economic burden, or predictive models related to climate change impact on CVV** (Waddell et al., 2019). Although it is a zoonosis, small ruminants are the only animals extensively studied on CVV-associated clinical disease (Waddell et al., 2019). It is possible that CVV in humans is not informed or misdiagnosed (Waddell et al., 2019). Future research should focus on CVV infection's impact on human and animal populations (Waddell et al., 2019).

Few studies on species discuss the role of horses and One Health, especially in human and environmental health, highlighting their impact on soil and biodiversity (Lönker et al., 2020). Horses have a long history of service in wars, mines, and developing antidotes for diphtheria (Lönker et al., 2020). They are also involved in animal-assisted therapy, supporting livelihoods, and leisure (Lönker et al., 2020). However, **risk factors like climate change and antimicrobial resistance threaten their health** (Lönker et al., 2020). Therefore, horses are essential for achieving One Health and should be incorporated into any road map (Lönker et al., 2020).

Human activities, urban planning, mental health, and livelihood patterns must be considered as future challenges for One Health and climate change. A review identified 36 studies examining the relationship between emerging zoonotic diseases and global **urban planning** (Murugesan, 2020). Interdisciplinary collaboration, social justice, built environment, climate change adaptation, sustainable urbanization, sanitation, green space, and economic planning should be applied (Murugesan, 2020). Current **livelihood patterns** degrade ecosystems, leading to a cycle of degradation in socio-ecological systems (Everard et al., 2020). This reduces the natural regulating capacities of ecosystem services, limiting disease transfer from animals to humans (Everard et al., 2020). This also undermines natural resource availability, compromising measures like washing and sanitation (Everard et al., 2020). **Human activities** driving this degrading cycle can convert beneficial ecosystem services into disservices, exacerbating zoonotic diseases (Everard et al., 2020). However, protecting or restoring ecosystems can enhance their capacities for human security and opportunity (Everard et al., 2020).

The COVID-19 pandemic has highlighted the potential for environmental challenges and brain health issues in the future (Reis et al., 2021). **Neurological disorders are a challenge, and risk factors** include environmental issues like zoonoses, biodiversity loss, climate change, air pollution, and population and lifestyle factors like transport, urbanization, and migration (Reis et al., 2021). Understanding and responding to these risks can help anticipate, mitigate, and avoid disasters (Reis et al., 2021). Another study examined the role of biodiversity loss in zoonotic emerging illnesses like SARS-CoV-2 (Jaja, 2020). It found that **human activities, such as nonrenewable energy utilization, greenhouse gas production, land use changes, habitat transformation, and species over-exploitation, are linked to biodiversity loss** (Jaja, 2020). This leads to increased zoonotic spillovers and the emergence of previous animal diseases in humans, such as SARS-CoV and SARS-CoV-2, from bat coronaviruses (Jaja, 2020).

Another aspect related to **human activities** is the discussion by Wiebers and Feigin (2020) for measures to limit future zoonoses by **closing live-animal markets**, changing food consumption habits, and reducing habitat destruction (Bergstrom, 2020). These measures would benefit human health, animal welfare, and wildlife conservation (Bergstrom, 2020). Western democracies, such as China, play a significant role in these global problems through consumerism and the illicit wildlife trade (Bergstrom, 2020). Citizens should insist on their government using its **diplomatic soft power** to engage with other nations and global institutions to address species endangerment, habitat destruction, climate change, and emerging infectious diseases (Bergstrom, 2020).

Pandemics affect all food system activities, from production to consumption, and all pillars of food security, but global agri-food systems are also essential for developing emerging diseases (Rivera-Ferre et al., 2021). The pandemic's impacts can be divided into direct and indirect impacts, with vulnerability varying for different types of food systems (Rivera-Ferre et al., 2021). However, avoiding universalizing impacts and responses is crucial, as agri-food systems are diverse and heterogeneous (Rivera-Ferre et al., 2021). There are challenges but opportunities to highlight vulnerabilities and accelerate the transformation toward more sustainable and resilient food systems (Rivera-Ferre et al., 2021).

Pandemics and epidemics are not inevitable but can be mitigated by **reducing risk drivers** like climate change and human interaction with land (Meadows et al., 2023). **Consumers can take actions** to reduce climate change, such as conserving energy and water, switching to renewable energy sources, and rethinking transportation, shopping, and diet (Prater, 2023). Supporting environmentally conscious companies and using your voice can help reduce climate change. Voting for candidates who understand environmental issues and sharing personal changes can inspire others to take action (Prater, 2023).

6.1 COP 28 report and actions (CLIMADE, 2023)

To address climate risks, the Climate Amplified Diseases and Epidemics (CLIMADE) consortium of international scientists is moving quickly to create surveillance systems, information, and appropriate solutions (CLIMADE, 2023).

The CLIMADE report's researchers urge immediate global action by:

1. *Reporting outbreaks promptly: It is critical to declare infectious disease outbreaks clearly and concisely as soon as possible. Governments and medical organizations should pledge to swiftly and transparently disclose outbreaks and provide essential information to pertinent parties. Transparency like this is crucial for international reaction and readiness.*
2. *Strengthen genomic monitoring: To track the emergence and spread of infectious illnesses, governments, educational institutions, and health organizations must invest in and develop genetic surveillance capabilities. This will make it possible to identify new hazards early on and take appropriate action, stopping epidemics before they get out of control.*
3. *Giving priority to vulnerable groups: Infectious illnesses and climate change disproportionately affect the most disadvantaged. These people need to be given priority by governments and the business sector, who should do this by making investments in infrastructure, disaster preparedness, and robust healthcare systems.*
4. *Encouraging climate resilience: To create creative solutions that improve healthcare systems' capacity to withstand climate change, academic institutions and businesses in the private sector should work together. This entails planning infrastructure to endure severe weather conditions and guaranteeing the availability of critical medical supplies in an emergency.*
5. *Devoting sustainable financing: Governments, private sector enterprises, and health organizations must commit to sustainable funding to combat infectious illnesses associated with climate change. This financing should support research, capacity-building, and community involvement to establish a strong defense against these threats.*

7 Conclusions

The importance of climate change in the planet's balance is undeniable. The emergency of diseases such as zoonoses and pandemics have frequently arisen in the last century. Researchers affirm that a new pandemic will certainly occur, but it is unknown when or from where, and prevention must begin quickly. The illnesses may have always existed, hidden far from civilization in untamed and isolated areas. However, until recently, the planet's natural defensive mechanisms were more effective in warding them off.

The importance of the One Health approach in addressing health issues exacerbated by climate change is a priority for international organizations such as the WHO, FAO, WAHO, and UNEP. New tools and policies have been developed with member countries to predict, prevent, and respond to those emergencies. All strategies must be multisectoral, multidisciplinary and have local, regional, and global participation. Developing countries and communities must have investments, and research and actions must be prioritized. Thus, collective action, policy support, and ongoing research to safeguard the health of humans, animals, and ecosystems must occur. It is urgent to take proactive measures to prevent future outbreaks through interdisciplinary collaboration and climate-conscious approaches.

Surveillance of infectious diseases needs to occur, and outbreaks must be reported promptly and transparently to ensure global preparedness and response efforts. Strengthening genomic surveillance is crucial for early detection and response to emerging threats. Vulnerable communities are disproportionately affected by climate change and infectious diseases, so governments and private sector industries must prioritize them by investing in resilient healthcare systems and disaster preparedness measures. Collaboration between academic institutions and private sector industries is essential for developing innovative solutions to enhance climate resilience within healthcare systems. Sustainable funding is also necessary to support research, capacity-building, and community engagement to create a robust defense against climate change-related infectious diseases.

Protecting animals is to preserve our future; controlling zoonotic pathogens in animals is the most effective and economical way to protect people. These must be coordinated at the human-animal-ecosystem interface and applied at national, regional, and global levels through appropriate policies. Human and animal health specialists must build a network for early disease detection at the local, regional, and national levels. Veterinarians are the only public health professionals who oversee both humans and animals. However, all medical specialties must work together and have the appropriate training. This network needs to have diagnostic laboratories (that can be shared), rapid response to disease contingency processes, and reduced risks at the

origin. Research in applied molecular epidemiology must recognize the associations between host and pathogen genotypes.

However, One Health's implementation is much more than zoonoses; it includes nutritional food, food safety, antimicrobial resistance, and many other aspects of environmental health. We need to think more about systems and less about species. We have to face complex problems. More complex than we were originally trained to handle.

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