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Impact of climate change on the spread of infectious diseases - review

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ABSTRACT

Advances in sanitation, broader access to healthcare, and developments in preventive and clinical medicine have contributed to reducing mortality and morbidity from many infectious diseases. Nevertheless, recent outbreaks of emerging infectious diseases (EIDs) have caused significant health losses, and their frequency is likely to increase due to the impact of climate change on pathogens, the environment, and populations. Extreme or prolonged changes in temperature, precipitation, humidity, and air pollution resulting from climate change can, for example, expand the range of EID reservoirs, increase host–pathogen and cross-species interactions, and degrade the health of susceptible populations, thereby promoting new EID outbreaks.

It is therefore crucial to establish global strategies for tracking and modeling potential EID responses to predict their future behavior and guide research on early detection, diagnostics, and vaccine development. Multi-disciplinary, intercontinental collaborations are essential to develop effective surveillance and modeling platforms that leverage artificial intelligence to mitigate the effects of climate change on EID outbreaks. In this article I discuss how climate change elevates the risk of EIDs, present novel approaches to enhancing the surveillance of emerging pathogens that pose epidemic threats, analyze both existing and new measures to contain or reduce the risk of future EID outbreaks, and describe advanced methods for tracking EIDs during outbreaks to limit their transmission.

Keywords: emerging infectious diseases, climate change, transmission, outbreak, early diagnosis

Introduction

EIDs are cases where more people suddenly get sick due to microorganisms that are either brand new or ones we already know about but have grown more dangerous. These germs might be new because they've never caused illness before, or they could be familiar ones that have changed to spread more easily or do more damage. Either way, these shifts turn them into a bigger issue, affecting more people than they used to [1].

There are several reasons why pandemics seem more likely these days. The world's population keeps growing, and with people traveling and moving around so much, it's easier for diseases to spread from one place to another. On top of that, climate change is shaking things up—altering ecosystems in ways that make it simpler for illnesses to hop from animals to humans. Pollution and the general wear and tear on the environment aren't helping either, creating conditions that favor disease outbreaks. Plus, as more people around the globe get older, there's a bigger group of folks who are naturally more at risk of getting seriously sick. Over the last few decades, we've seen a handful of emerging infectious diseases pop up—EIDs, they call them. Most of these flare-ups haven't turned into long-term problems, fading away after a while. But SARS-CoV-2, the virus that kicked off COVID-19, is different—it's settled in and looks like it's not going anywhere anytime soon. The process typically begins with a zoonotic spillover, where a pathogen jumps from an animal host to a human. For the pathogen to establish sustained transmission, it must adapt to the human host, enabling efficient person-to-person spread—potentially through bodily fluids or respiratory droplets. HIV-1 and SARS-CoV-2 both pulled this off, adapting well enough to stick around. Now, these diseases have caused plenty of havoc, but they haven't wiped people out as fast as the 1918 flu did. That one was a monster, taking millions of lives in no time flat. HIV-1 and SARS-CoV-2 haven't hit that level of rapid destruction, and that's partly because of the way they work and partly because we're better equipped these days. Medicine's come a long way—we're quicker at spotting diseases, keeping tabs on them, and stopping them from spreading as much as they could. Even so, the toll is still massive. Just look at SARS-CoV-2: over 772 million people have caught it, and more than 6.98 million have died. That's a huge blow to health across the planet, and it's still an issue we're wrestling with. HIV-1's no small matter either, touching millions of lives globally and showing no signs of disappearing. All in all, while we've gotten smarter about handling diseases, the challenges aren't going away. With more people, a shifting climate, and an aging world, the odds of facing more pandemics down the road feel higher than ever [2].

Recent outbreaks of emerging infectious diseases, including the 2003 SARS episode, the 2012 MERS event, the 2009 swine flu pandemic, the 2013–2016 Ebolavirus crisis, the 2014 chikungunya surge in the Western Hemisphere, and the 2015 Zika virus epidemic, have revealed considerable levels of morbidity, mortality, and expansive geographic distribution. These occurrences highlight the possibility of even graver consequences arising from future outbreaks. Beyond these examples, various other pathogens, such as Escherichia coli O157:H7, hantavirus, dengue virus, and West Nile virus, are acknowledged as having the potential to initiate outbreaks of emerging infectious diseases. Similarly, conditions like malaria, tuberculosis, cholera, and influenza are frequently viewed as reemerging threats capable of sparking renewed epidemic activity. Innovative approaches, such as rapid point-of-care diagnostic tools and advanced vaccine development techniques, offer potential to curb the dissemination of future outbreaks of emerging infectious diseases, provided they are integrated with comprehensive disease prevention and control frameworks. Nevertheless, despite these technological advancements and broader availability of enhanced sanitation, hygiene practices, and healthcare services, emerging infectious diseases persist as a pressing public health challenge, often resulting in significant mortality. This ongoing vulnerability is partly due to the heightened exposure of immunologically unexposed populations to pathogens responsible for emerging infectious diseases, a phenomenon driven by population growth and migratory shifts linked to climate change [3].

Climate change poses a grave threat to public health

Climate change is widely recognized by the World Health Organization as a pressing concern for global public health. Sustained modifications in environmental factors—such as temperature, precipitation levels, humidity, and the quality of air and water—are already exerting a significant and detrimental effect on human well-being, contributing to elevated rates of illness and death across populations worldwide. These climatic shifts are particularly alarming due to their role in facilitating the proliferation of infectious diseases transmitted through food, water, and vectors, such as mosquitoes. By altering the duration and geographical scope of conditions conducive to pathogen survival and transmission, climate change amplifies the risk of outbreaks, affecting both newly emerging and previously controlled diseases. This heightened vulnerability stems from the influence of changing environmental dynamics on the vitality, reproduction, and mobility of pathogens and their hosts [4, 5].

Climate change is anticipated to exacerbate the global burden of infectious diseases, with projections suggesting an increase in both mortality and morbidity as a result of shifting environmental conditions. The relationship between climatic influences and fungal infections has been thoroughly explored in prior analyses, which highlight a clear connection between changing weather patterns and the prevalence of fungi-related outbreaks. This examination seeks to clarify the processes through which climate change modifies the patterns and distribution of Emerging Infectious Diseases (EIDs). At a worldwide level, various approaches that either have been employed or might be considered to reduce the occurrence and spread of transmission events are presented. Additionally, attention is given to the development of innovative technologies designed to strengthen surveillance frameworks, enabling more timely and effective responses to potential EID outbreaks [6].

The impact of climate change on the spread of EID

The occurrence and spread of emerging infectious diseases can be shaped by a multitude of factors. Modifications in the genetic makeup of pathogens, such as novel mutations or processes like viral recombination and reassortment, can influence their ability to infect different species. Additionally, shifts in the geographical distribution of environmental pathogens or animal vectors can create new risks. Furthermore, patterns of human migration and activities that lead to habitat destruction can facilitate interactions between human populations and pathogens or their vectors in previously unexposed regions [7].

Environmental shifts resulting from climate change can widen the extent of pathogen reservoirs or the populations of their hosts, potentially modifying or broadening their spatial distribution through ecological degradation. These changes may elevate the probability of pathogens transferring between species, thereby increasing the potential for outbreaks by compromising the vitality of host groups and facilitating successful disease emergence. Additionally, climate change can heighten pathogen presence by fostering conditions that enhance the persistence and proliferation of pathogens or their hosts within current ecological settings or by increasing the scope, scale, or fertility of these settings across both familiar and newly reached territories. Fluctuations in temperature, moisture levels, and precipitation can reshape the scale and placement of pathogen and host communities, affecting their maturation, reproduction, and endurance [8].

Environmental changes triggered by climate change can lead to an increase in the range of pathogen reservoirs or their host populations, potentially modifying or expanding their geographic distribution through ecosystem degradation. Such transformations can increase the likelihood of overflow events associated with the emergence of new infectious diseases, while weakening the health of host populations, which promotes the effective transmission of diseases and the emergence of epidemics. Climate change can also contribute to pathogen abundance by creating conditions more favorable for their survival and reproduction within existing ecological niches or by expanding the number, size or reproductive potential of these niches within both existing and newly accessible areas. Fluctuations in temperature, precipitation and humidity can affect the size and distribution of pathogen populations and their hosts, affecting their development, replication and survival processes [9].

Research conducted by Mordecai EA and associates has established that pathogens carried by mosquitoes achieve their most favorable transmission conditions within a temperature window of 23 to 29 degrees Celsius. Outside this span, the ability of these pathogens to spread decreases markedly, halting completely when temperatures drop below a range of 9 to 23 degrees Celsius or exceed 32 to 38 degrees Celsius. This investigation utilized the basic reproduction number, known as R0, to assess how temperature influences the biological mechanisms underlying pathogen transmission. Such analysis offers clear insights into the ways in which climate change might alter the patterns of diseases transmitted by ectothermic vectors and parasites. These findings emphasize the significant implications of environmental temperature shifts for the epidemiology of mosquito-borne illnesses, suggesting a need for enhanced surveillance and responsive health policies to address emerging challenges [10]. It has been noted that pronounced increases in temperature may elevate the potential for outbreaks of emerging infectious diseases among human populations. A relevant illustration of this effect can be seen in the marked rise of SARS-CoV-2 infections observed across the globe during the summer of 2022. This uptick seemed to be associated, at least to some extent, with the inclination of people to gather in cooled indoor spaces, such as shopping centers, especially in regions where air conditioning in homes was not a common feature [11].

Climate change exerts a profound influence on the dynamics of disease transmission by altering the ecological conditions that govern pathogen prevalence within animal populations serving as disease reservoirs. Shifts in climatic factors, such as pronounced changes in temperature and precipitation, can enhance the availability of resources critical to these species, thereby triggering substantial increases in their numbers. Such rapid population growth often exceeds the capacity of natural predators to maintain balance, leading to an expansion in both the spatial distribution and density of these reservoir populations. This, in turn, heightens the potential for disease transmission to human communities by facilitating greater contact, whether through new encounters or intensified existing interactions. A striking illustration of this phenomenon is the Hantavirus outbreak that occurred in the southwestern United States during the 1990s, which was precipitated by a significant surge in the deer-mouse population. This increase was driven by climate-related variations that enriched their food resources while simultaneously weakening the regulatory effects of their predators. Should ongoing climate trends continue to foster environments conducive to such interactions between disease-carrying species and human populations, unchecked by sufficient predatory control, the frequency and scope of similar disease spillover events could escalate considerably over time [12].

Climate change can profoundly influence the spatial distribution of species that serve as reservoirs for pathogens, potentially leading to an expansion or reconfiguration of their habitats. Such transformations may stem from variations in the availability of essential resources, alterations in the balance of predator-prey interactions, or other ecological disturbances. When natural environments undergo degradation, it may become necessary for host populations or their predators to explore new regions to secure sustenance or evade intensified competition or predation pressures. These shifts can result in a greater prevalence of infected individuals, heightened pathogen concentrations within those individuals, and an increased probability of encounters with human populations or those living in close association with humans. Comparable effects may also manifest in human communities and domestic animals, which can act as conduits for disease transmission. In either scenario, the intensified interactions between a compromised host population and a vulnerable one can elevate the risk of contacts conducive to pathogen spillover. A notable instance of this process occurs when elevated temperatures and changing weather patterns, driven by climate change, diminish the availability of surface water through reduced rainfall or enhanced evaporation. This scarcity can prompt wildlife to seek out water sources typically avoided due to their use by humans or livestock, thereby fostering opportunities for direct or indirect interactions between these groups [13].

Climate change is increasingly recognized as influencing variations in the El Niño Southern Oscillation (ENSO), which subsequently play a role in shaping the geographic patterns of endemic cholera. This connection does not primarily arise from elevated rainfall or flooding events. Rather, the impact of ENSO on the spread of cholera reflects a broader interplay of environmental factors, suggesting that shifts in climate patterns may affect disease dynamics through indirect and intricate pathways. Such insights emphasize the need to explore the complex relationships between global climatic shifts and public health challenges, beyond straightforward associations with precipitation changes [14].

The diversity of species associated with EIDs tends to grow as one moves from polar regions toward the equatorial zone. It is posited that this trend is influenced by environmental conditions prevalent at lower latitudes, such as elevated temperatures and greater precipitation, which are thought to facilitate the transmission of pathogens. These climatic factors are considered key contributors to the observed increase in pathogen variety, highlighting the role of geographic and ecological gradients in shaping the distribution of infectious disease risks across the globe [15]. A notable illustration of this phenomenon can be observed in the recent COVID-19 pandemic, during which it is suggested that a precursor to the SARS-CoV-2 virus, likely originating from horseshoe bats (genus Rhinolophus) in Southeast Asia, was transmitted to human populations. This transmission is believed to have occurred via an intermediary host species, the identity of which remains undetermined. Such an event underscores the complex pathways through which zoonotic diseases can emerge and spread, reflecting the intricate interplay between environmental conditions and pathogen dynamics [16].

Diseases transmitted by blood-feeding arthropods, including mosquitoes, ticks, and fleas, contribute significantly to global morbidity and mortality through the spread of illnesses such as malaria, dengue, West Nile virus, and Lyme disease. These conditions collectively represent a considerable proportion of emerging infectious disease incidents worldwide. The arthropod vectors responsible for these transmissions exhibit a pronounced sensitivity to environmental shifts driven by climate change, such as alterations in precipitation, temperature fluctuations, and the occurrence of extreme weather phenomena. This susceptibility underscores the potential for changing climatic conditions to influence the prevalence and distribution of these vector-borne diseases, amplifying their public health impact [17]. Variations in temperature have been shown to influence the duration of transmission or the developmental pace of insect vectors and their associated pathogens. This effect is evident in the mosquito-mediated spread of diseases such as dengue fever and Plasmodium falciparum malaria, where thermal conditions play a critical role in shaping the dynamics of both the vector populations and the pathogens they harbor. Such temperature-driven changes can significantly alter the epidemiological patterns of these diseases, highlighting the intricate relationship between climatic factors and vector-borne disease transmission [18].

The safety of drinking water constitutes a critical determinant in the transmission of EIDs. Climate change can exacerbate this issue by intensifying precipitation and flooding events, which may compromise the integrity of water sources utilized by human populations or those in close proximity to them. Such contamination heightens the likelihood of outbreaks of waterborne diseases (WBDs) driven by enteric pathogens, including bacteria and parasites like Salmonella and Cryptosporidium. These environmental disruptions underscore the vulnerability of water systems to climatic shifts and their subsequent impact on public health risks [19].

Climatic influences have the potential to aggravate air pollution levels, and the combined impact of these conditions can detrimentally affect the immune system of hosts, often in a synergistic manner. Such effects may amplify the spread of respiratory illnesses by prolonging the viability of airborne droplets and the pathogens they transport, while also compromising the integrity of respiratory mucosa and immune defenses in susceptible groups. Prolonged exposure to polluted air is known to trigger inflammation and oxidative stress, weakening immune responses and thereby elevating the prevalence of infectious respiratory conditions. This burden is particularly pronounced among vulnerable demographics, including young children, the elderly, and those with pre-existing respiratory ailments. Notably, heightened exposure to fine particulate matter, such as PM2.5, can intensify the adverse respiratory consequences of climate change by modifying immune functionality and worsening the progression of underlying respiratory diseases [20].

The relationship between heightened disease risk and the interplay of air pollutants and weather-related variables can exhibit considerable complexity. Research has demonstrated that the elevated risk of tuberculosis (TB) is accentuated by increased levels of nitrogen dioxide (NO2) and greater wind speeds, while it diminishes in association with higher ozone (O3) concentrations, elevated temperatures, and increased relative humidity. Conversely, no discernible connection has been observed between TB risk and factors such as PM2.5 or sulfur dioxide (SO2) concentrations, or the duration of sunlight exposure. These findings highlight the intricate and multifaceted nature of environmental influences on disease susceptibility, underscoring the need for nuanced approaches to understanding such interactions [21].

Technological advances in fighting EIDs

Insights gained from managing the COVID-19 pandemic underscore the critical role played by coordinated genomic surveillance systems at both national and global levels. The initial emergence of this previously unrecognized pathogen was identified through a cluster of unexplained pneumonia cases reported in Wuhan, China, toward the end of December 2019. Within weeks, by January 2020, the causative agent was determined to be a newly discovered coronavirus, designated SARS-CoV-2, with its complete genetic sequence made publicly available shortly thereafter. By mid-2020, a systematic nomenclature grounded in phylogenetic analysis was introduced, enabling the classification and monitoring of the expanding array of SARS-CoV-2 genetic variants as they evolved. These developments illustrate the importance of rapid genomic characterization and tracking in addressing the challenges posed by novel infectious agents [22, 23, 24]. This approach facilitated the identification and monitoring of multiple SARS-CoV-2 variants of concern (VOCs), which exhibited characteristics such as enhanced transmissibility or the ability to circumvent immune responses. Such findings emphasized the vital role of genomic sequencing and surveillance data in informing the development of vaccines and shaping public health strategies. The capacity to track these variants underscored the significance of integrating genetic insights into efforts to mitigate the spread and impact of the virus, ensuring that interventions remained responsive to its evolving nature [25].

Genomic surveillance data, when combined with additional datasets, offers valuable perspectives on the origins, temporal progression, and pathways of transmission for EIDs. A pertinent case is the Zika virus outbreak in 2016, during which genetic sequences were extracted from both infected individuals and Aedes aegypti mosquitoes in the United States. This analysis, employed for epidemiological monitoring, indicated that the outbreak likely began several months prior to the identification of the initial cases in Florida in March 2016. Such findings illustrate the utility of genomic information in reconstructing the dynamics of disease emergence and spread, enhancing the understanding of outbreak timelines and sources [26].

Genomic surveillance data serves as a cornerstone in shaping the development, production, and implementation of vaccines and therapeutic agents. Beyond this, studies involving the genetic modification of host cell genomes provide an additional avenue for deepening the understanding of infection mechanisms and pinpointing novel treatment possibilities. In one instance, researchers applied a genome-wide CRISPR-based loss-of-function screening approach to uncover genes and pathways that, when disrupted, imparted resistance to SARS-CoV-2 infection. The validity of these observations was subsequently corroborated through the use of RNA interference techniques and small-molecule inhibitors targeting the identified elements, highlighting the potential of such methods to inform therapeutic innovation [27].

Epidemiological surveys are frequently utilized to discern the primary pathways of disease dissemination during an outbreak, often through detailed contact tracing initiatives. These investigations typically seek to gather comprehensive data, including histories of contacts and possible exposures, basic demographic details, recent records of clinical symptoms, and timelines documenting symptom onset and disease progression. When optimally executed, such data can construct precise chronologies that connect the initial case to subsequent infections via their proximate interactions, while also shedding light on the attributes necessary for transmission to occur. These tracing methodologies may prove equally beneficial in the context of endemic diseases. For instance, a recent prospective epidemiological study conducted among tuberculosis patients in rural China employed whole genome sequencing of cultured specimens to group individuals into distinct genomic clusters. The findings revealed that the predominant mode of transmission was through social interactions, underscoring the utility of integrating genomic and epidemiological approaches in understanding disease spread [28].

Geographic Information Systems (GIS) are employed as an essential framework for gathering and organizing data that is referenced both spatially and temporally. This functionality supports the mapping and examination of elements tied to the emergence and EIDs. Additionally, GIS enables the construction of simulations that project potential influences on the incidence and dissemination of these diseases, thereby contributing to a deeper comprehension of their underlying patterns and behaviors [29].

Technologies such as satellite imaging and remote sensing offer a sophisticated means of detecting regions where interactions between pathogen reservoirs and vulnerable host populations might precipitate disease spillover. These tools enable the identification of critical zones by analyzing environmental factors that could signal heightened risks. Additionally, data gathered from satellites can play a pivotal role in anticipating potential infectious disease outbreaks or spillover occurrences. This is achieved through the ongoing observation of ecological markers—such as shifts in vegetation patterns, changes in water systems, or variations in atmospheric conditions—that are associated with these events, thereby supporting efforts in surveillance, health resource allocation, and outbreak containment. This approach marks a notable departure from earlier mapping strategies, which were traditionally utilized to chart the progression of diseases like cholera and influenza in order to study their spread. In contrast, contemporary methods harness advanced analytical techniques to enhance the interpretation, visualization, and recognition of disease trends. A significant focus within current GIS research in the health domain is now directed toward the spatial depiction of infectious diseases, reflecting the growing importance of these innovative tools in understanding and managing public health challenges [30, 31].

Surveillance systems designed to monitor EIDs are expected to integrate a variety of sophisticated functionalities to address the multifaceted nature of these public health challenges. Among these capabilities is the utilization of geospatial information, satellite-derived imagery, and data gathered from remote sensing technologies. Such resources are instrumental in constructing predictive models that forecast potential epidemic events, enabling health authorities to anticipate and prepare for outbreaks before they intensify. A further critical aspect of these systems involves the centralized aggregation and reporting of diagnostic test outcomes. This mechanism significantly enhances the precision and speed with which cases are documented, thereby facilitating detailed epidemiological assessments. Through these analyses, patterns of disease transmission can be discerned, providing essential evidence to guide the formulation of effective public health responses and containment strategies. The widespread infrastructure of cellular networks has also proven advantageous in establishing more unified and efficient frameworks for infection surveillance. With their extensive geographical coverage, these networks support the real-time collection and exchange of data across diverse populations, including those in isolated or resource-limited areas. This connectivity ensures that critical information can be transmitted promptly, strengthening the ability of health systems to react swiftly to nascent threats [32, 33, 34, 35].

In response to the heightened risk of EID driven by climate change, there is an escalating need for innovative diagnostic tools that are swift, cost-effective, and accessible for analyzing diverse sample types. These tools must possess the ability to detect pathogens with a high likelihood of triggering widespread outbreaks with both precision and sensitivity. Considerable resources have been directed toward the creation of advanced technologies and instruments tailored to meet these demands. Among the promising developments are biosensors, which integrate a bioreceptor—comprising biological elements such as cells, antibodies, enzymes, aptamers, or nucleic acid probes capable of recognizing specific targets—with a detection mechanism, such as an electrochemical, optical, or mass-sensitive transducer. This combination enables the identification of interactions between the target pathogen and the bioreceptor, demonstrating significant potential for effective diagnostic applications in this context [36].

The capacity to swiftly and precisely identify infectious diseases at healthcare facilities plays an essential role in reducing their spread. These diagnostic tools deliver prompt results, enabling medical personnel to make immediate decisions regarding patient management, including the initiation of treatment and the application of isolation protocols. Such an approach mitigates the difficulties tied to delayed test outcomes, notably the challenges of locating individuals for subsequent care or quarantine instructions. The development of these rapid diagnostic examinations has been advanced through the use of biological markers unique to specific illnesses, including COVID-19, Lyme disease, and malaria [37].

Conclusion

The escalating interplay between climate change and EIDs poses a profound threat to global public health, necessitating an urgent and multifaceted response. Rising temperatures, shifting precipitation patterns, and disrupted ecosystems are fundamentally altering the incidence, prevalence, and geographic distribution of EIDs, while simultaneously undermining the immunity of human and human-adjacent species. These environmental shifts increase the likelihood of more frequent and severe epidemics, as pathogens exploit new opportunities for transmission and adaptation. The SARS-CoV-2 pandemic exemplifies this challenge, with its rapid global spread and the emergence of variant strains highlighting the critical need for a cohesive, worldwide framework to detect, prevent, and treat infectious diseases. This framework must leverage cutting-edge technologies to address the evolving risks posed by climate change.

A cornerstone of this response lies in the deployment of innovative tools for disease surveillance and management. Genomic sequencing has emerged as a powerful method for monitoring pathogen evolution, providing essential data to track transmission dynamics and guide the development of vaccines and therapeutics. Complementing this, rapid diagnostic technologies deployed at the point of care can enable early detection and containment, curtailing the spread of outbreaks before they escalate. Geographic information systems (GIS) and epidemiological tracing further enhance these efforts by mapping disease patterns and identifying high-risk areas, offering a clearer picture of how climate variables influence EID behavior. Together, these advancements form a technological foundation for tackling the growing burden of infectious diseases in a warming world.

However, technological innovation must be paired with sophisticated forecasting to anticipate future challenges. Models that integrate historical epidemic data with climate projections are indispensable for predicting the trajectories of specific EIDs under varying environmental scenarios. Such tools allow researchers and policymakers to identify potential hotspots, prioritize early detection strategies, and allocate resources effectively. Establishing global strategies to track and model the responses of candidate EIDs to altered climate conditions is equally vital. These strategies should inform the development of targeted diagnostics and vaccines, ensuring that interventions keep pace with the shifting landscape of infectious threats. AI and remote sensing can amplify these efforts, enabling real-time monitoring of zoonotic spillover risks and facilitating the creation of intercontinental surveillance platforms.

Addressing this complex issue demands more than technical solutions—it requires robust interdisciplinary and international collaboration. Environmental scientists, public health experts, and policymakers must work in tandem to bridge knowledge gaps and devise holistic strategies. Multi-disciplinary partnerships are essential for building surveillance and modeling systems that span continents, integrating data from host reservoirs to human populations. Success hinges on coordinated action across all levels, from community-driven initiatives to national and global coalitions. Policymakers, healthcare providers, and businesses must commit to providing adequate funding and resources, ensuring that innovations are accessible and that local communities are empowered to participate in disease prevention efforts.

In closing, the convergence of climate change and EIDs calls for a proactive, technology-driven, and collaborative global response. As environmental conditions continue to evolve, the urgency of establishing resilient systems for detection, prevention, and treatment grows ever more apparent. Through sustained investment, interdisciplinary cooperation, and a commitment to equity, the international community can mitigate the rising threat of climate-driven infectious diseases. The path forward requires not only vigilance and innovation but also a unified resolve to protect public health in an increasingly uncertain future.

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References:

1. Jones KE, Patel NG, Levy MA, et al. Global trends in emerging infectious diseases. Nature. 2008;451(7181):990.
2. WHO. 2023. Available from: https://covid19.who.int/.
3. Zhang XX, Jin YZ, Lu YH, et al. Infectious disease control: from health security strengthening to health systems improvement at global level. Glob Health Res Policy. 2023;8(1):38.
4. Neira M, Erguler K, Ahmady-Birgani H, Al-Hmoud ND, Fears R, Gogos C, Hobbhahn N, Koliou M, Kostrikis LG, Lelieveld J, Majeed A, Paz S, Rudich Y, Saad-Hussein A, Shaheen M, Tobias A, Christophides G. Climate change and human health in the Eastern Mediterranean and Middle East: Literature review, research priorities and policy suggestions. Environ Res. 2023 Jan 1;216(Pt 2):114537.
5. Semenza JC, Paz S.. Climate change and infectious disease in Europe: impact, projection and adaptation. Lancet Reg Health Eur. 2021;9:100230.
6. Seidel D, Wurster S, Jenks JD, Sati H, Gangneux JP, Egger M, Alastruey-Izquierdo A, Ford NP, Chowdhary A, Sprute R, Cornely O, Thompson GR 3rd, Hoenigl M, Kontoyiannis DP. Impact of climate change and natural disasters on fungal infections. Lancet Microbe. 2024 Jun;5(6):e594-e605.
7. Morens DM, Folkers GK, Fauci AS.. The challenge of emerging and re-emerging infectious diseases. Nature. 2004;430(6996):242–249.
8. Tidman R, Abela-Ridder B, de Castaneda RR.. The impact of climate change on neglected tropical diseases: a systematic review. Trans R Soc Trop Med Hyg. 2021;115(2):147–168.
9. Li Y, Reeves RM, Wang X, et al. Global patterns in monthly activity of influenza virus, respiratory syncytial virus, parainfluenza virus, and metapneumovirus: a systematic analysis. Lancet Glob Health. 2019;7(8):e1031–e1045.
10. Mordecai EA, Caldwell JM, Grossman MK, et al. Thermal biology of mosquito-borne disease. Ecol Lett. 2019;22(10):1690–1708.

11. Lian X, Huang J, Li H, et al. Heat waves accelerate the spread of infectious diseases. Environ Res. 2023;231(Pt 2):116090.
12. Wenzel RP. A new hantavirus infection in North America. N Engl J Med. 1994;330(14):1004–1005.
13. Lau CL, Smythe LD, Craig SB, et al. Climate change, flooding, urbanisation and leptospirosis: fuelling the fire? Trans R Soc Trop Med Hyg. 2010;104(10):631–638.
14. Moore SM, Azman AS, Zaitchik BF, et al. El Nino and the shifting geography of cholera in Africa. Proc Natl Acad Sci U S A. 2017;114(17):4436–4441.
15. Guernier V, Hochberg ME, Guegan JF.. Ecology drives the worldwide distribution of human diseases. PLoS Biol. 2004;2(6):e141.
16. Becker DJ, Albery GF, Sjodin AR, et al. Optimising predictive models to prioritise viral discovery in zoonotic reservoirs. Lancet Microb. 2022;3(8):e625–e637.
17. Rocklöv J, Dubrow R.. Climate change: an enduring challenge for vector-borne disease prevention and control. Nat Immunol 2020;21(5):479–483.
18. Franklinos LHV, Jones KE, Redding DW, et al. The effect of global change on mosquito-borne disease. Lancet Infect Dis. 2019;19(9):e302–e312.
19. Levy K, Smith SM, Carlton EJ. Climate Change Impacts on Waterborne Diseases: Moving Toward Designing Interventions. Curr Environ Health Rep. 2018 Jun;5(2):272-282.
20. Tran HM, Tsai F-J, Lee Y-L, et al. The impact of air pollution on respiratory diseases in an era of climate change: a review of the current evidence. Sci Total Environ. 2023;898:166340.
21. Sun S, Chang Q, He J, et al. The association between air pollutants, meteorological factors and tuberculosis cases in Beijing, China: a seven-year time series study. Environ Res 2023;216:114581.
22. Zhu N, Zhang DY, Wang WL, et al. A novel coronavirus from patients with pneumonia in China, 2019. N Engl J Med. 2020;382(8):727–733.
23. Novel 2019 coronavirus genome. 2023. Available from: https://virological.org/t/novel-2019-coronavirus-genome/319.
24. Rambaut A, Holmes EC, O'Toole A, et al. A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. Nat Microbiol. 2020;5(11):1403–1407.
25. Gangavarapu K, Latif AA, Mullen JL, et al. Outbreak.info genomic reports: scalable and dynamic surveillance of SARS-CoV-2 variants and mutations. Nat Methods. 2023;20(4):512–522.
26. Grubaugh ND, Ladner JT, Kraemer MUG, et al. Genomic epidemiology reveals multiple introductions of Zika virus into the United States. Nature. 2017;546(7658):401.
27. Daniloski Z, Jordan TX, Wessels HH, et al. Identification of required host factors for SARS-CoV-2 infection in human cells. Cell. 2021;184(1):92–105.

28. Li M, Guo MC, Peng Y, et al. High proportion of tuberculosis transmission among social contacts in rural China: a 12-year prospective population-based genomic epidemiological study. Emerg Microbes Infect. 2022;11(1):2102–2111.
29. Boulos MN, Roudsari AV, Carson ER.. Health geomatics: an enabling suite of technologies in health and healthcare. J Biomed Inform. 2001;34(3):195–219.
30. Lyseen AK, Nohr C, Sorensen EM, et al. A review and framework for categorizing current research and development in health related geographical information systems (gis) studies. Yearb Med Inform. 2014;9(1):110–124.
31. Boulos MN. Location-based health information services: a new paradigm in personalised information delivery. Int J Health Geogr. 2003;2:2.
32. De Souza MLM, Lopes GA, Branco AC, et al. Leprosy screening based on artificial Intelligence: development of a cross-platform app. JMIR Mhealth Uhealth. 2021;9(4):e23718.
33. Keutzer L, Wicha SG, Simonsson US.. Mobile health apps for improvement of tuberculosis treatment: descriptive review. JMIR Mhealth Uhealth. 2020;8(4):e17246.
34. Sharpe JD, Kamara MT.. A systematic evaluation of mobile apps to improve the uptake of and adherence to HIV pre-exposure prophylaxis. Sex Health. 2018;15(6):587–594.
35. Pascucci M, Royer G, Adamek J, et al. AI-based mobile application to fight antibiotic resistance. Nat Commun. 2021;12(1):1173.
36. Patel SK, Surve J, Parmar J, et al. Recent advances in biosensors for detection of COVID-19 and other viruses. IEEE Rev Biomed Eng. 2023;16:22–37.
37. Tran NK, Albahra S, Rashidi H, et al. Innovations in infectious disease testing: leveraging COVID-19 pandemic technologies for the future. Clin Biochem 2023;117:10–15.