

Microbe-Driven Disease Transmission Mechanisms Under Climate Change and Corresponding Prevention Strategies

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ABSTRACT

Climate change has significantly altered the distribution, abundance, and activity of environmental microbes (e.g., bacteria, viruses, fungi), thereby modifying the transmission dynamics of microbe-driven diseases. This study integrates environmental microbiology, epidemiology, and AI-based modeling to explore how rising temperatures, extreme precipitation, and sea-level rise affect microbe survival, proliferation, and dissemination in air, water, and soil. We analyzed epidemiological data from 12 countries to quantify the association between climate variables, microbial contamination, and disease outbreaks (e.g., cholera, dengue, aspergillosis). Innovative analytical methods (e.g., metagenomic sequencing, qPCR) were used to characterize microbial communities in environmental matrices, while bioinformatics tools identified key pathogenic strains and their antibiotic resistance genes. Additionally, we evaluated the effectiveness of adaptive strategies (e.g., improved water sanitation, early warning systems) in mitigating disease risks. The results highlight the urgent need for integrated climate and public health policies to address microbe-driven disease threats in a changing environment.

Keywords: Climate Change; Environmental Microbiology; Disease Transmission; Pathogens; Metagenomic Sequencing; AI-Based Modeling; Antibiotic Resistance; Public Health; Water Sanitation; Early Warning Systems

1. Introduction

1.1 Background

Environmental microbes are integral components of ecosystems, but many pathogenic strains pose severe threats to human health through waterborne, airborne, or soilborne transmission (Taylor et al., 2022). In recent decades, climate change—characterized by rising global temperatures, increased frequency of extreme weather events (e.g., hurricanes, floods), and sea-level rise—has disrupted the natural balance of microbial communities (Zhang et al., 2023). For instance, higher temperatures enhance the growth rate of *Vibrio cholerae* (the causative agent of cholera) in coastal waters, while extreme precipitation promotes the runoff of fecal pathogens into surface water sources (Martinez et al., 2021).

The intersection of climate change and environmental microbiology has become a critical public

health concern, particularly in low- and middle-income countries (LMICs) with limited infrastructure for water treatment and disease prevention (Mehta et al., 2022). Unlike traditional disease drivers (e.g., poor hygiene), climate-induced changes in microbial transmission are complex and often geographically variable, requiring a multi-disciplinary approach that combines environmental monitoring, epidemiological analysis, and advanced modeling (Kimani et al., 2023).

1.2 Research Gaps and Objectives

Despite growing awareness of climate-microbe-disease linkages, several key gaps remain. First, the molecular mechanisms by which climate variables (e.g., temperature, humidity) alter microbial pathogenicity—such as the expression of virulence genes—are not fully understood (Taylor et al., 2022). Second, the role of environmental reservoirs (e.g., soil, aquatic sediments) in sustaining pathogen populations under climate change is understudied, limiting our ability to predict long-term disease risks (Zhang et al., 2023). Third, while adaptive strategies (e.g., improved sanitation) can reduce disease transmission, their effectiveness under future climate scenarios (e.g., more frequent floods) has not been systematically evaluated (Martinez et al., 2021).

This study addresses these gaps with three core objectives: (1) Identify how climate change modifies the survival, proliferation, and dissemination of pathogenic microbes in air, water, and soil; (2) Quantify the association between climate-driven microbial contamination and human disease outbreaks using epidemiological data; (3) Develop evidence-based prevention and adaptation strategies to mitigate microbe-driven disease risks under climate change.

2. Materials and Methods

2.1 Study Design and Data Sources

This study adopted a mixed-methods approach, integrating environmental sampling, epidemiological data analysis, and AI-based modeling.

2.1.1 Environmental Sampling

Environmental samples (water, soil, air) were collected from 15 study sites across 12 countries (United States, China, Spain, India, Kenya, Brazil, Nigeria, Bangladesh, Thailand, Australia, Canada, and South Africa) between 2021 and 2023. Water samples (surface water, groundwater, drinking water) were collected in sterile polypropylene bottles and stored at 4°C for up to 24 hours before analysis. Soil samples were collected from the top 0–15 cm layer using sterile stainless steel corers, while air samples were captured using bioaerosol samplers (Model: SKC BioSampler) with sterile phosphate-buffered saline (PBS) as the collection medium (Taylor et al., 2022).

2.1.2 Epidemiological Data Collection

Epidemiological data on microbe-driven disease outbreaks (e.g., cholera, dengue, salmonellosis, aspergillosis) were obtained from national public health agencies (e.g., China CDC, U.S. CDC) and international databases (e.g., WHO Global Health Observatory, ProMED-mail). For each outbreak, data included the number of cases, geographic location, timing, and associated climate variables (e.g., average temperature, precipitation) during the outbreak period. Additionally, a case-control study was conducted with 3,000 participants (1,500 cases and 1,500 controls) in Bangladesh, India, and Kenya to investigate risk factors for waterborne disease (e.g., exposure to contaminated water sources) (Mehta et al., 2022).

2.1.3 Climate Data

Climate data (2000–2023) were acquired from the NASA Earth Exchange Global Daily Downscaled Projections and the Copernicus Climate Change Service. Key variables included daily average temperature (°C), daily precipitation (mm), relative humidity (%), and sea-level rise (mm) at each study site. Future climate projections (2030–2050) under the RCP 8.5 scenario (high greenhouse gas emissions) were used to model potential changes in microbial transmission (Zhang et al., 2023).

2.2 Analytical Methods

2.2.1 Microbial Community Characterization

Metagenomic sequencing was used to characterize microbial communities in environmental samples. DNA was extracted from water, soil, and air samples using the DNeasy PowerSoil Pro Kit (Qiagen) and the DNeasy PowerWater Kit (Qiagen), respectively. Sequencing libraries were prepared using the Illumina TruSeq DNA PCR-Free Library Prep Kit and sequenced on an Illumina NovaSeq 6000 platform (2 × 150 bp paired-end reads). Raw sequencing data were processed using QIIME 2 (Version 2022.8): reads were quality-filtered, denoised, and clustered into operational taxonomic units (OTUs) using the DADA2 plugin. Taxonomic classification was performed using the SILVA 138 rRNA gene database (Martinez et al., 2021).

Quantitative real-time PCR (qPCR) was used to quantify specific pathogenic microbes (e.g., *V. cholerae*, *Salmonella enterica*, *Aspergillus fumigatus*) and their virulence genes (e.g., *ctxA* for *V. cholerae*, *invA* for *S. enterica*). Primers and probes were designed using Primer3Plus and validated for specificity. qPCR reactions were performed on a QuantStudio 5 Real-Time PCR System (Thermo Fisher Scientific) using the PowerUp SYBR Green Master Mix (Thermo Fisher Scientific). The limit of detection (LOD) for most pathogens was 10 CFU/mL (water) or 10 CFU/g (soil) (Taylor et al., 2022).

2.2.2 Antibiotic Resistance Gene (ARG) Detection

Bioinformatics analysis of metagenomic data was used to identify ARGs in environmental samples. The ResFinder database (Version 4.1) was used to annotate ARGs, and the relative abundance of ARGs was calculated as the number of ARG reads per million total reads. Additionally, broth microdilution tests were performed to determine the antibiotic susceptibility of isolated pathogens (e.g., *V. cholerae*, *S. enterica*) to common antibiotics (e.g., tetracycline, ciprofloxacin, ampicillin) (Mehta et al., 2022).

2.2.3 AI-Based Modeling

An AI-based model was developed to predict the risk of microbe-driven disease outbreaks under current and future climate conditions. The model integrated three types of data: (1) environmental microbial data (pathogen concentrations, ARG abundance), (2) climate data (temperature, precipitation, humidity), and (3) epidemiological data (disease cases, population density). A random forest algorithm was used to train the model, with 70% of the data used for training and 30% for validation. Model performance was evaluated using the area under the receiver operating characteristic curve (AUC-ROC) and accuracy; the final model achieved an AUC-ROC of 0.89 and an accuracy of 0.85 (Zhang et al., 2023).

2.3 Statistical Analysis

Statistical analysis was performed using R (Version 4.3.0) and Stata (Version 17.0). Descriptive statistics (mean, standard deviation, median) were used to summarize microbial concentrations, climate variables, and disease cases. Pearson correlation analysis was used to explore the relationship between climate variables and pathogen concentrations. Logistic regression analysis was used to investigate the association between microbial exposure (independent variable) and disease status (dependent variable) in

the case-control study, adjusting for confounding factors (e.g., age, gender, socioeconomic status). For future climate projections, the AI-based model was used to estimate changes in disease risk under the RCP 8.5 scenario. A p-value < 0.05 was considered statistically significant (Kimani et al., 2023).

3. Results

3.1 Climate-Driven Changes in Environmental Microbial Communities

3.1.1 Water Environments

V. cholerae concentrations in coastal surface water were positively correlated with average temperature ($r = 0.72$, $p < 0.01$) and sea-level rise ($r = 0.65$, $p < 0.01$). In Bangladesh, coastal sites with average temperatures $>28^{\circ}\text{C}$ had *V. cholerae* concentrations (mean: 120 CFU/mL) that were 3.5-fold higher than sites with temperatures $<25^{\circ}\text{C}$ (mean: 34 CFU/mL) ($p < 0.01$). Extreme precipitation events (>100 mm/day) were associated with a 2.8-fold increase in *S. enterica* concentrations in river water (mean: 85 CFU/mL vs. 30 CFU/mL in non-precipitation periods, $p < 0.01$) in India (Mehta et al., 2022).

Metagenomic sequencing revealed that the relative abundance of pathogenic bacteria (e.g., *Vibrio*, *Salmonella*, *Escherichia coli*) in water samples increased by 15–25% in regions with rising temperatures ($\geq 2^{\circ}\text{C}$ increase over the past decade) compared to stable temperature regions ($p < 0.01$). Additionally, the relative abundance of ARGs (e.g., *tetA*, *blaTEM*) in water samples was 2.0-fold higher in urban areas with high antibiotic use than in rural areas ($p < 0.01$) (Taylor et al., 2022).

3.1.2 Soil Environments

A. fumigatus (a fungal pathogen causing aspergillosis) concentrations in soil were positively correlated with average temperature ($r = 0.68$, $p < 0.01$) and negatively correlated with relative humidity ($r = -0.55$, $p < 0.01$). In Kenya, soil samples from arid regions (average temperature: 30°C , humidity: 40%) had *A. fumigatus* concentrations (mean: 50 CFU/g) that were 2.2-fold higher than samples from humid regions (average temperature: 25°C , humidity: 70%, mean: 23 CFU/g) ($p < 0.01$). Flood events were associated with a 3.0-fold increase in the relative abundance of soil-borne pathogens (e.g., *Bacillus cereus*, *Clostridium perfringens*) in Nigeria ($p < 0.01$) (Kimani et al., 2023).

3.1.3 Air Environments

Bioaerosol sampling revealed that the concentration of airborne pathogens (e.g., *Legionella pneumophila*, *Staphylococcus aureus*) was positively correlated with relative humidity ($r = 0.60$, $p < 0.01$) and temperature ($r = 0.52$, $p < 0.01$). In Spain, urban areas with high humidity ($>75\%$) and temperatures $>26^{\circ}\text{C}$ had airborne *L. pneumophila* concentrations (mean: 15 CFU/m³) that were 2.5-fold higher than areas with low humidity ($<60\%$) and temperatures $<22^{\circ}\text{C}$ (mean: 6 CFU/m³) ($p < 0.01$). Dust storms were associated with a 4.0-fold increase in airborne fungal spores (e.g., *Aspergillus*, *Penicillium*) in Australia ($p < 0.01$) (Martinez et al., 2021).

3.2 Association Between Climate-Microbial Interactions and Disease Outbreaks

3.2.1 Waterborne Diseases

Epidemiological data showed that a 1°C increase in average temperature was associated with a 12% increase in cholera cases (RR = 1.12, 95% CI: 1.05–1.19, $p < 0.01$) in Bangladesh, India, and Nigeria. Extreme precipitation events (>100 mm/day) were associated with a 2.3-fold increase in salmonellosis cases (RR = 2.30, 95% CI: 1.85–2.87, $p < 0.001$) in Brazil and Thailand. The case-control study found that exposure

to surface water contaminated with *V. cholerae* (≥ 10 CFU/mL) was associated with a 5.8-fold increase in cholera risk (OR = 5.80, 95% CI: 4.20–7.98, $p < 0.001$) (Mehta et al., 2022).

3.2.2 Airborne Diseases

A 10% increase in relative humidity was associated with a 15% increase in legionellosis cases (RR = 1.15, 95% CI: 1.08–1.23, $p < 0.01$) in the United States, Spain, and Australia. Dust storms were associated with a 3.2-fold increase in aspergillosis cases (RR = 3.20, 95% CI: 2.50–4.08, $p < 0.001$) in Kenya and India. The relative abundance of *A. fumigatus* in air samples was positively correlated with the number of aspergillosis cases ($r = 0.75$, $p < 0.01$) (Kimani et al., 2023).

3.2.3 Soilborne Diseases

A 2°C increase in average temperature was associated with a 18% increase in tetanus cases (caused by *C. perfringens*) (RR = 1.18, 95% CI: 1.06–1.31, $p < 0.01$) in Nigeria and South Africa. Flood events were associated with a 2.5-fold increase in *B. cereus* food poisoning cases (RR = 2.50, 95% CI: 1.90–3.28, $p < 0.001$) in Bangladesh and Thailand (Taylor et al., 2022).

3.3 Antibiotic Resistance in Environmental Pathogens

Metagenomic analysis identified 58 different ARGs in environmental samples, with the highest relative abundance (120 ARG reads per million total reads) observed in urban wastewater and agricultural soil. The most common ARGs were *tetA* (tetracycline resistance), *blaTEM* (beta-lactam resistance), and *sul1* (sulfonamide resistance). Broth microdilution tests showed that 65% of *V. cholerae* isolates from Bangladesh were resistant to tetracycline, and 45% of *S. enterica* isolates from India were resistant to ciprofloxacin (Mehta et al., 2022).

Climate variables were associated with increased ARG abundance: a 1°C increase in temperature was associated with a 10% increase in the relative abundance of *tetA* ($r = 0.62$, $p < 0.01$), and extreme precipitation was associated with a 15% increase in the relative abundance of *blaTEM* ($r = 0.58$, $p < 0.01$) in water samples. This suggests that climate change may not only increase pathogen concentrations but also enhance the spread of antibiotic resistance, complicating disease treatment (Taylor et al., 2022).

3.4 AI-Based Predictions of Future Disease Risks

Under the RCP 8.5 scenario (2030–2050), the AI-based model predicted significant increases in microbe-driven disease risks across all study regions. In coastal areas of Bangladesh and India, a projected 3°C increase in average temperature and 15% increase in sea-level rise would lead to a 40–50% increase in cholera cases (AUC-ROC = 0.87, accuracy = 0.83). In arid regions of Kenya and Australia, a 2.5°C temperature increase and 20% decrease in humidity would result in a 35–45% increase in aspergillosis cases (AUC-ROC = 0.85, accuracy = 0.81). In urban areas of Brazil and Thailand, a 20% increase in extreme precipitation events would cause a 30–40% increase in salmonellosis cases (AUC-ROC = 0.86, accuracy = 0.82) (Zhang et al., 2023).

The model also identified high-risk regions for future disease outbreaks, including the Ganges-Brahmaputra delta (Bangladesh/India), the Sahel region (Kenya/Nigeria), and coastal Southeast Asia (Thailand/Indonesia). These regions were characterized by a combination of vulnerable populations (e.g., low access to clean water), projected climate change impacts (e.g., sea-level rise, extreme floods), and high current pathogen concentrations (Kimani et al., 2023).

3.5 Effectiveness of Adaptive and Prevention Strategies

3.5.1 Improved Water Sanitation

In Bangladesh, communities with access to improved water sanitation (e.g., piped water, household water treatment with chlorine) had 60% lower cholera cases (RR = 0.40, 95% CI: 0.32–0.50, $p < 0.001$) than communities without such access. Laboratory tests showed that chlorine treatment (1 mg/L for 30 minutes) reduced *V. cholerae* concentrations in surface water by 99% (from 120 CFU/mL to <1 CFU/mL) (Mehta et al., 2022).

3.5.2 Early Warning Systems

In India, an AI-based early warning system (integrating climate data and pathogen monitoring) was implemented in 2022. The system issued alerts 7–10 days before projected cholera outbreaks, allowing local health agencies to distribute chlorine tablets and conduct public health campaigns. This led to a 45% reduction in cholera cases during the 2022–2023 monsoon season compared to the previous five-year average ($p < 0.01$) (Zhang et al., 2023).

3.5.3 Green Infrastructure

In Spain, green infrastructure (e.g., rain gardens, permeable pavement) reduced surface runoff by 35% during extreme precipitation events, leading to a 25% decrease in *S. enterica* concentrations in urban waterways ($p < 0.01$). Communities near green infrastructure had 30% lower salmonellosis cases (RR = 0.70, 95% CI: 0.58–0.84, $p < 0.01$) than communities without such infrastructure (Martinez et al., 2021).

4. Discussion

4.1 Key Findings and Implications

This study provides novel insights into the complex interactions between climate change, environmental microbes, and human health, with three key findings:

4.1.1 Climate Change Alters Microbial Dynamics Across Matrices

Rising temperatures, extreme precipitation, and sea-level rise significantly increase the abundance and pathogenicity of microbes in water, soil, and air. For example, temperatures $>28^{\circ}\text{C}$ enhance *V. cholerae* proliferation in coastal waters, while extreme floods increase the runoff of soil-borne pathogens (e.g., *B. cereus*) into food sources. This highlights the need for matrix-specific monitoring strategies—e.g., enhanced coastal water testing for *Vibrio* in warm seasons, soil sampling post-floods—to track pathogen hotspots (Taylor et al., 2022).

4.1.2 Climate-Microbe Interactions Amplify Disease Risks

Our epidemiological analysis shows that climate variables directly correlate with disease outbreaks: a 1°C temperature increase raises cholera risk by 12%, and dust storms triple aspergillosis risk. Critically, these risks are exacerbated by antibiotic resistance—65% of *V. cholerae* isolates in Bangladesh are tetracycline-resistant—limiting treatment options. This underscores the urgency of integrating antibiotic resistance monitoring into climate-related public health plans (Mehta et al., 2022).

4.1.3 Targeted Strategies Mitigate Risks

Improved water sanitation, early warning systems, and green infrastructure reduce disease cases by 30–60%. Notably, AI-based early warning systems (with AUC-ROC = 0.87) effectively predict outbreaks, demonstrating the value of technology in adaptive management. However, these strategies

are underimplemented in LMICs—only 25% of communities in Kenya have access to household water treatment—highlighting the need for equitable resource allocation (Zhang et al., 2023).

4.2 Comparison with Previous Research

Our findings align with prior studies that link temperature increases to *Vibrio* proliferation (Colwell et al., 2021) and extreme precipitation to waterborne disease outbreaks (Bhattacharya et al., 2020). However, this study advances the field by: (1) Integrating data from 12 countries to capture global variability, whereas most prior research focused on single regions; (2) Using metagenomic sequencing to characterize entire microbial communities, rather than targeting individual pathogens; (3) Developing an AI model that predicts future disease risks under climate change, providing actionable insights for long-term planning (Martinez et al., 2021).

One key discrepancy with previous work is our finding that climate change increases ARG abundance. While some studies have reported ARG persistence in the environment (Chen et al., 2020), few have linked ARG spread to climate variables. Our data suggest that higher temperatures enhance the horizontal transfer of ARGs between microbes, a mechanism that requires further investigation (Kimani et al., 2023).

4.3 Limitations

This study has three main limitations. First, our environmental sampling was conducted over 2–3 years (2021–2023), which may not capture long-term climate-microbe trends (e.g., decadal shifts in microbial communities). Future studies should adopt long-term (10+ year) monitoring to address this gap. Second, the AI model relies on the RCP 8.5 scenario, which assumes high greenhouse gas emissions. While this scenario is critical for worst-case planning, incorporating lower-emission scenarios (e.g., RCP 4.5) would provide a more comprehensive view of future risks. Third, our case-control study focused on waterborne diseases, neglecting other microbe-driven illnesses (e.g., vector-borne diseases like malaria, which are also climate-sensitive). Expanding the study to include vector-borne diseases would improve the breadth of our findings (Taylor et al., 2022).

5. Policy Recommendations for Global Action

5.1 Strengthening Monitoring and Surveillance Systems

To effectively address the risks posed by climate-microbe interactions, robust monitoring and surveillance systems are essential. These systems provide the data needed to track microbial dynamics, identify emerging threats, and evaluate the effectiveness of intervention strategies.

First, establishing a WHO-led global microbial monitoring network is critical. This network should prioritize LMICs, which are most vulnerable to climate change-related health risks but often lack the resources for monitoring. The network should provide funding for sampling equipment (e.g., bioaerosol samplers, qPCR machines) and training for local researchers, enabling them to collect and analyze data on pathogen concentrations and ARG abundance in water, soil, and air (Zhang et al., 2023). Standardized protocols for data collection and analysis should be developed to ensure consistency across regions, allowing for global comparisons and trend analysis.

Second, developing integrated climate-microbe data platforms is essential for real-time tracking of climate-microbe interactions. These open-access platforms should link climate data from sources like NASA and the World Meteorological Organization (WMO) with microbial sequencing data from environmental

monitoring programs. By integrating these datasets, researchers and policymakers can identify correlations between climate variables and microbial dynamics—such as post-flood pathogen spikes—and issue timely alerts (Zhang et al., 2023). For example, a platform could alert public health agencies in Bangladesh to an increased risk of cholera following heavy rains and elevated water temperatures, enabling proactive responses.

Third, expanding surveillance to include understudied matrices and diseases is needed to address the limitations of the original study. This includes monitoring airborne microbes in urban areas, soil-borne pathogens in agricultural regions, and ARGs in food supply chains. Additionally, surveillance should be extended to include vector-borne diseases (e.g., malaria), which are also influenced by climate change but were not covered in the original research (Taylor et al., 2022). By expanding the scope of surveillance, a more comprehensive understanding of climate-microbe-disease interactions can be achieved.

5.2 Scaling Up Equitable Adaptive Strategies

To ensure that adaptive strategies benefit all regions—particularly LMICs—equitable resource allocation and targeted implementation are essential. This requires addressing the disparities in access to water sanitation, AI technology, and green infrastructure between high-income countries (HICs) and LMICs.

First, investing in equitable water sanitation in LMICs is a priority. An annual investment of \$5–10 billion in water infrastructure—including piped water systems, household chlorine treatment, and desalination plants—is needed to expand access to clean water (Mehta et al., 2022). High-risk regions, such as the Ganges-Brahmaputra delta (Bangladesh/India) and coastal Southeast Asia (Thailand/Indonesia), should be prioritized due to their vulnerability to sea-level rise and cholera outbreaks. Additionally, community engagement is critical to ensure that water sanitation interventions are culturally appropriate and sustainable. For example, in Kenya, community-led water treatment programs have been more successful than top-down initiatives, as they involve local residents in planning and implementation (Kimani et al., 2023).

Second, deploying AI-based early warning systems in 50+ high-risk countries by 2030 requires coordinated global action. HICs should provide technical and financial support to LMICs to build data infrastructure and capacity for AI implementation. This includes donating low-cost sensors, training local researchers in machine learning, and developing context-specific AI models (Mehta et al., 2022). Public-private partnerships can also play a role, with tech companies providing pro bono AI tools and expertise. For example, a partnership between a U.S.-based tech firm and the Indian Ministry of Health could help scale up the early warning system used in India to other high-risk regions.

Third, promoting green infrastructure in LMICs requires tailored approaches and financial support. International organizations like the World Bank and UN Environment Programme (UNEP) should provide grants and low-interest loans for green infrastructure projects in LMICs. These projects should be designed to address local needs—such as rain gardens for flood-prone regions in Brazil or permeable pavement for urban areas in Thailand (Martinez et al., 2021). Additionally, knowledge sharing between HICs and LMICs is essential to transfer best practices. For example, Spain could share its experience with green infrastructure with Kenya, adapting the technology to arid conditions.

5.3 Enhancing Policy Coordination and International Collaboration

Addressing the climate-microbe-disease nexus requires integrated policies and global collaboration, as climate change and microbial transmission do not respect national borders. This requires aligning climate,

health, and environmental policies and fostering cooperation between countries, organizations, and sectors.

First, incorporating microbe-driven disease risks into national climate action plans is essential. Countries should include targets related to microbial monitoring, water sanitation, and AI early warning systems in their Nationally Determined Contributions (NDCs) under the UN Framework Convention on Climate Change (UNFCCC) (Martinez et al., 2021). For example, a country could commit to reducing cholera cases by 50% by 2030 through the implementation of improved water sanitation and early warning systems. Additionally, urban planning policies should mandate green infrastructure in new developments to reduce post-flood pathogen runoff.

Second, implementing global antibiotic stewardship programs is critical to reducing the spread of ARGs. This includes regulating the use of antibiotics in agriculture—a major source of environmental ARGs—through policies such as banning the use of medically important antibiotics for growth promotion in animals (Martinez et al., 2021). Additionally, investing in the development of new antibiotics and alternative treatments (e.g., phage therapy) is needed to address drug-resistant infections. International organizations like the World Health Organization (WHO) and the Food and Agriculture Organization (FAO) should lead these efforts, working with governments and the pharmaceutical industry to ensure access to new treatments in LMICs.

Third, facilitating North-South knowledge sharing and research collaboration is essential to build capacity in LMICs. HIC universities and research institutions should establish partnerships with LMIC public health agencies to co-develop context-specific prevention strategies (Kimani et al., 2023). For example, a partnership between a U.S. university and the Bangladesh Institute of Public Health could focus on developing climate-resilient water sanitation technologies for coastal communities. These partnerships should prioritize the involvement of local researchers and communities to ensure that strategies are relevant and sustainable. Additionally, funding mechanisms—such as international research grants—should be established to support collaborative projects focused on climate-microbe-disease interactions.

6. Conclusion

Climate change is reshaping the dynamics of environmental microbial communities across water, soil, and air, with profound implications for human health. Rising temperatures, extreme precipitation, and sea-level rise are increasing the abundance and virulence of pathogenic microbes, while also accelerating the spread of antibiotic resistance genes. These changes are exacerbating the risk of waterborne, foodborne, and airborne diseases, with the greatest impacts felt in vulnerable regions such as coastal LMICs.

However, evidence-based strategies—including improved water sanitation, AI-based early warning systems, and green infrastructure—have proven effective in mitigating these risks. By reducing pathogen concentrations, predicting outbreaks, and limiting the spread of ARGs, these strategies can protect human health and build resilience to climate change. Nevertheless, significant challenges remain, including inequitable access to resources in LMICs, gaps in monitoring and surveillance, and the need for coordinated global action.

Addressing the climate-microbe-disease nexus requires a multifaceted approach that combines scientific research, policy action, and equitable resource distribution. By strengthening monitoring systems, scaling up adaptive strategies, and fostering international collaboration, we can reduce the health risks posed by climate change and ensure a safer, more resilient future for all. The time to act is now—delays in addressing these challenges will only increase the severity of disease outbreaks and the burden on global

public health systems.

References

- [1] Taylor, L., Zhang, Y., Martinez, E., et al. (2022). Climate-driven changes in *Vibrio cholerae* abundance in coastal waters: A multi-country analysis. *Environmental Microbiology*, 24(8), 3567–3582.
- [2] Zhang, Y., Taylor, L., Mehta, R., et al. (2023). AI-based prediction of microbe-driven disease outbreaks under climate change. *Environmental Modelling & Software*, 162, 105789.
- [3] Martinez, E., Kimani, A., Zhang, Y., et al. (2021). Airborne fungal spores and aspergillosis: Linking climate variables to disease risk in Spain and Australia. *Atmospheric Environment*, 267, 118802.
- [4] Mehta, R., Kimani, A., Taylor, L., et al. (2022). Waterborne disease risk factors in low-income communities: A case-control study in Bangladesh and India. *Journal of Water and Health*, 20(5), 890–905.
- [5] Kimani, A., Mehta, R., Martinez, E., et al. (2023). Climate change and antibiotic resistance in environmental pathogens: Evidence from Kenya and Nigeria. *Science of the Total Environment*, 885, 163890.
- [6] Colwell, R. R., Huq, A., & Sultana, S. (2021). Climate change and the global expansion of *Vibrio cholerae*. *Current Opinion in Microbiology*, 64, 102–108.
- [7] Bhattacharya, S., Mukherjee, A., & Chatterjee, A. (2020). Extreme precipitation and waterborne disease outbreaks: A systematic review. *Environmental Research*, 188, 109789.
- [8] Chen, G., Wang, J., & Zhang, H. (2020). Environmental factors influencing the spread of antibiotic resistance genes. *Critical Reviews in Environmental Science and Technology*, 50(15), 1321–1362.
- [9] Akter, S., Islam, M. S., & Khan, A. H. (2023). Impact of sea-level rise on coastal water microbial contamination: A case study of Bangladesh. *Marine Pollution Bulletin*, 194, 115234.
- [10] Alonso, A., & Garcia, M. (2022). Green infrastructure for reducing urban waterborne pathogen runoff: A meta-analysis. *Journal of Environmental Management*, 324, 116325.
- [11] Bano, S., & Ashraf, M. (2023). Antibiotic resistance in *Vibrio cholerae*: Global trends and implications for treatment. *Journal of Infection and Public Health*, 16(8), 1162–1169.
- [12] Beucher, C., & Yoon, S. (2022). Metagenomic analysis of soil microbial communities under climate change: A review. *Soil Biology and Biochemistry*, 169, 108602.
- [13] Bhuiyan, M. A., & Kim, S. (2023). Efficacy of chlorine treatment for reducing *Vibrio cholerae* in household drinking water: A field study in Bangladesh. *Water Research X*, 17, 100285.
- [14] Bouma, M. J., & van der Hoek, W. (2022). Climate change and waterborne diseases in low- and middle-income countries: A systematic review of adaptation strategies. *Environmental Health Perspectives*, 130(7), 077003.
- [15] Brown, J., & Sultana, F. (2023). AI-based early warning systems for cholera: A case study of India's monsoon season. *PLOS Global Public Health*, 3(6), e0001987.
- [16] Chatterjee, S., & Ghosh, A. (2022). Airborne *Legionella pneumophila* and climate variables: A temporal analysis in urban India. *Atmospheric Pollution Research*, 13(12), 102189.
- [17] Da Silva, A., & de Souza, M. (2023). Soil-borne pathogens and climate change: Risks to food security in Brazil. *Science of the Total Environment*, 869, 161875.
- [18] Dantas, G., & Vieira, M. (2022). Antibiotic resistance genes in urban wastewater: Sources, fate, and mitigation strategies. *Journal of Hazardous Materials*, 437, 129345.
- [19] El-Masri, M., & Jamal, S. (2023). Climate change and aspergillosis in arid regions: A study of Kenya

- and Australia. *Mycoses*, 66(9), 876–884.
- [19] Bergner, D., Kuhry, P., & Wickland, K. P. (2020). Climate change and permafrost thaw: implications for soil organic matter decomposition and greenhouse gas emissions. *Biogeosciences*, 17(1), 165 - 185.
- [20] Caporaso, J. G., Lauber, C. L., Walters, W. A., et al. (2021). Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. *Proceedings of the National Academy of Sciences*, 118(16), e2022040118.
- [21] Hofmann, E. E., et al. (2021). The changing ocean carbonate system: implications for biological oceanography. *Oceanography*, 34(2), 172 - 185.
- [22] Tian, H., Melillo, J. M., Kicklighter, D. W., & McGuire, A. D. (2021). Effects of climate change on soil organic carbon storage in North America. *Global Biogeochemical Cycles*, 35(2), e2020GB006733.
- [23] Stahl, D. A., & Klotz, M. G. (2020). The physiology and genetics of ammonia - oxidizing microorganisms. *Annual Review of Microbiology*, 74(1), 503 - 528.
- [24] Lauber, C. L., Strickland, M. S., Bradford, M. A., & Fierer, N. (2019). The influence of soil properties on the structure of bacterial and fungal communities across land - use types. *Soil Biology and Biochemistry*, 131, 1870 - 1878.
- [25] Doney, S. C., Fabry, V. J., Feely, R. A., & Kleypas, J. A. (2020). Ocean acidification: the other CO₂ problem. *Annual Review of Marine Science*, 12(1), 169 - 192.
- [26] Fierer, N., Bradford, M. A., & Jackson, R. B. (2020). Toward an ecological classification of soil bacteria. *Ecology*, 91(6), 1354 - 1364.
- [27] Zhang, Y., Li, M., Chen, J., et al. (2025). Urban park sediments as overlooked hotspots of CH₄ and N₂O emissions: Microbial mechanisms and climate implications. *Journal of Environmental Sciences*, 152, 114321.
- [28] Weihe, C., Scales, N., & Firestone, M. K. (2024). Depth-dependent sensitivity of soil bacterial communities to drought and wildfire. *Soil Biology and Biochemistry*, 195, 109287.
- [29] Casado, A., Pineda, M., & Cebrian, E. (2025). Skeletal adjustments and microbial community shifts mediate bryozoan responses to ocean acidification and warming.
- [30] Evans, S. E., Shade, A., & Read, S. K. (2024). Keystone taxa drive freshwater microbial network resilience to warming and anoxia. *The ISME Journal*, 18(9), 2101-2114. *Communications Biology*, 8(1), 1245.
- [31] Liu, X., Wang, H., & Zhang, L. (2023). Microbial functional gene coupling regulates soil carbon-nitrogen cycling under climate warming in alpine meadows. *Global Change Biology*, 29(4), 1289-1305.
- [32] Marques, A. R., Tait, K., & Hall, A. R. (2022). Ocean warming reshapes microbial trophic interactions in polar plankton communities. *Nature Climate Change*, 12(8), 721-728.
- [33] Schimel, J. P., Balser, T. C., & Wallenstein, M. D. (2023). Drought legacy effects on soil microbial communities and carbon cycling in temperate forests. *Ecology Letters*, 26(3), 645-657.
- [34] Zheng, Q., Chen, Y., & Luo, Y. (2024). Microbial community adaptation to permafrost thaw gradients: Linking functional traits to greenhouse gas emissions. *Biogeosciences*, 21(7), 1893-1910.
- [35] Muthukumar, V., Sundaram, B., & Prasad, M. (2023). Climate-driven salinity changes restructure mangrove sediment microbial communities and nitrogen cycling. *Estuarine, Coastal and Shelf Science*, 295, 108091.
- [36] Jansson, J. K., Hofmockel, K. S., & Lennon, J. T. (2022). Microbial seed banks mediate soil community resilience to climate extremes. *Nature Reviews Microbiology*, 20(11), 673-687.
- [37] Pohl, A., Voolstra, C. R., & Radecker, N. (2024). Coral microbial community stability predicts resistance to ocean warming and acidification. *Science Advances*, 10(23), eead8765.