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Climate-driven changes in aquatic pathogen distribution and emerging human infectious disease risks

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Received: April 2025 Accepted: July 2025

Abstract

Climate change is altering aquatic ecosystems and influencing the distribution of waterborne pathogens, creating potential threats to human health. Rising temperatures and changing rainfall patterns may increase environmental conditions favourable for infectious microorganisms. Studies of climate-driven changes in aquatic pathogens have been conducted previously but there is little comparative evidence across bacterial and protozoan species. This study aims to fill this gap by exploring climate-driven pathogen suitability and potential human exposure under different environmental conditions. A computational simulation was performed for Vibrio cholerae, *Vibrio vulnificus* and *Cryptosporidium* spp. for 12 aquatic monitoring sites and four climate scenarios. Under the highest-change scenario, the percentage of suitable habitat-days for V. cholerae increased from 79.42% to 99.08%, and for *V. vulnificus* from 53.52% to 76.17%. The results show opposing pathogen responses to warming and changes in precipitation. These results provide a basis for improving climate-sensitive aquatic surveillance, environmental monitoring, and public health preparedness strategies.

Keywords: Climate change, Aquatic pathogens, Waterborne infectious diseases, Environmental suitability, Human exposure assessment

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Introduction

Climate change is an important environmental factor influencing the distribution and behaviour of microorganisms in aquatic ecosystems. Rising water temperatures, changes in rainfall, flooding, and variations in salinity can affect the survival, movement, and environmental persistence of waterborne pathogens. Rivers, reservoirs, coastal waters and estuaries all contain different microbial communities, including organisms that can cause human infectious diseases. Environmental changes can influence the seasonal availability of suitable habitats and affect opportunities for human exposure via drinking water, recreation and seafood consumption. Climate-driven changes in the aquatic environment have been linked to shifts in the geographical distribution of pathogenic Vibrio species (Archer *et al*., 2023). But the relationship between climate conditions and pathogen occurrence is not consistent among aquatic ecosystems. But pathogens respond to environmental change through different biological and ecological mechanisms, so pathogen-specific assessments are needed to understand potential public health consequences.

Bacterial pathogens belonging to the genus Vibrio are particularly important in discussions of climate-sensitive aquatic infectious diseases. Vibrio cholerae occurs in freshwater and brackish environments, although only certain toxigenic strains cause epidemic cholera. Temperature, salinity, nutrient availability and aquatic ecological conditions may affect its environmental abundance. Studies of V. cholerae in estuarine environments have shown temperature to be an important factor related to bacterial abundance but relationships with other environmental variables vary with sampling location (Leard *et al*., 2023). Another important bacterium for the environment is *Vibrio vulnificus*. It is usually found in coastal and brackish waters and can cause serious infections if a wound comes into contact with it or if contaminated seafood is eaten. Warming of coastal waters may improve the environmental conditions of this organism and may also affect its geographic distribution. Seasonal cholera patterns in Kolkata have also been studied and found to be influenced by temperature and rainfall through different environmental processes (Shackleton *et al*., 2023). These findings highlight the need to study bacterial responses across different climate scenarios rather than assuming a general increase in environmental suitability with temperature.

The protozoan pathogens are associated with various environmental and public health problems. *Cryptosporidium* species can be found in surface water contaminated by human sewage, livestock waste, agricultural runoff and storm water. They produce oocysts which are resistant to the environment and can be transmitted under conditions other than those that support the growth of aquatic bacteria. Increased rain can wash contaminated materials into rivers and reservoirs. Heavy precipitation can affect water treatment systems and increase exposure

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potential for humans. Climate-based modeling of cholera infection risk in Bangladesh has shown the importance of incorporating environmental changes in evaluating potential disease transmission patterns (Kruger *et al*., 2023). Prediction modeling of *V. vulnificus* abundance has also provided information on its environmental distribution and factors affecting suitable aquatic conditions (Riedinger *et al*., 2022). Similarly, ecological niche modeling of human-associated *Cryptosporidium* has been used to study habitat suitability and potential outbreak risk under climate change conditions (Wang *et al*., 2023). The results indicate that climate-driven infectious disease risks depend not only on the survivability of microbes but also on the pathways of contamination, human activities and the quality of water management systems. Therefore, models that take into account different environmental responses and exposure routes are required to compare bacterial and protozoan pathogens.

The study develops a computational framework to explore climate-driven changes in the distribution of aquatic pathogens and the potential for human exposure. Three representative pathogens, *V. cholerae*, *V. vulnificus* and *Cryptosporidium* spp. are discussed across estuarine, coastal and fresh waters. The simulation includes seasonal water temperature, variation of rainfall, salinity and environmental suitability functions for pathogens. Four climate scenarios are used to assess how increasing temperature and rainfall may influence suitable habitat availability, seasonal distribution, and relative environmental exposure. Investigations of climate-related environmental conditions associated with *V. vulnificus* in coastal communities have highlighted the importance of understanding pathogen responses to local climate variability (Jamal *et al*., 2024). The investigation uses repeated annual simulations to quantify variability and compare responses between pathogens. Unlike approaches that assume all aquatic microorganisms respond similarly to climate change, the proposed framework represents separate environmental conditions and response functions for each pathogen. The main objective is to identify differences in climate sensitivity and examine how environmental changes may influence opportunities for human exposure to aquatic infectious agents.

Methodology

The study applies a computational simulation design to explore the response of aquatic pathogens to changing climate conditions. The simulation environment included 12 virtual monitoring sites representing three types of aquatic habitat: four estuarine sites for V. cholerae, four coastal sites for *V. vulnificus*, and four freshwater sites for *Cryptosporidium* spp. These are hypothetical locations not related to specific geographical sampling stations. For each simulated location, daily environmental data for water temperature, rainfall, and habitat characteristics were provided for a 365-day period. Research *on V. vulnificus* in tropical estuarine environments has

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shown that freshwater impacts can influence the abundance and environmental distribution of the bacteria (Nigro *et al*., 2022). Studies of environmental factors associated with the occurrence of pathogenic Vibrio also support the incorporation of temperature and other water quality conditions in assessments of aquatic pathogens (Brumfield *et al*., 2023). The study looks at four climate scenarios which include a baseline condition and three scenarios with increasing temperature and rainfall. Thirty independent annual simulations are conducted for every pathogen and scenario, providing 1,460 site-day observations per annual simulation. The resulting framework allows changes in environmental suitability to be compared across pathogens under controlled climate conditions.

The environmental variables are generated using seasonal functions and reproducible random variation. Baseline mean water temperatures are set at 23.5°C for estuarine environments, 21.0°C for coastal environments, and 18.0°C for freshwater environments. Seasonal temperature variation is modeled as sinusoidal annual cycles with amplitudes of 5.0, 6.0 and 5.5°C, respectively. Variability is further affected by temperature differences at a site and by daily fluctuations. Rainfall conditions are produced from a gamma distribution that is parameterized to reflect seasonal precipitation patterns and sporadic high rain events. Studies in the Baltic Sea have identified temperature, salinity and sediment resuspension as relevant environmental factors related to the prevalence of *V. vulnificus* (Fernández-Juárez *et al*., 2024). Moreover, studies of bacterial growth in the Baltic Sea have investigated the effect of eutrophication and algal bloom conditions on the aquatic environment (Riedinger *et al*., 2024). The baseline scenario is compared with three combined climate scenarios representing temperature increases of 1.0°C, 2.0°C, and 3.5°C and corresponding rainfall increases of 10%, 25%, and 40%. These conditions are controlled sensitivity scenarios rather than direct projections from a specific global climate model. The same baseline weather realization is used across the four scenarios within each simulation run, ensuring that differences arise from the defined climate changes rather than unrelated random weather sequences.

Pathogen-specific environmental suitability is estimated using mathematical response functions relating climate variables to favourable aquatic conditions. For *V. cholerae*, temperature suitability is represented by a Gaussian response centred at 28°C, with an assumed thermal spread of 7°C. Salinity suitability is calculated around a reference value of 10 practical salinity units, allowing environmental conditions to influence the predicted suitability of estuarine habitats. A similar approach is applied to *V. vulnificus*, using a reference temperature of 27°C and salinity of 16 practical salinity units. These parameters represent assumed environmental response conditions rather than universal biological optima. Temperature and salinity suitability values are combined

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with a rainfall-response factor to calculate a bounded environmental suitability index between zero and one. The Gaussian response functions allow suitability to increase as environmental conditions approach the selected reference values and decrease when conditions move further away. This approach provides a consistent numerical representation of the relationships between climate variables and bacterial habitat suitability. The calculated index represents favourable modeled conditions rather than actual bacterial concentrations or confirmed pathogen presence.

For *Cryptosporidium* spp., the simulation uses a different response structure because environmental transport and oocyst persistence are more relevant than multiplication in aquatic water. The thermal suitability function is centred at an assumed reference temperature of 18°C with a broader response width of 11°C. A separate rainfall-runoff function increases the environmental contamination suitability index as precipitation rises, reflecting the modeled movement of oocysts from surrounding land into freshwater systems. Data-driven investigations of riverine *Cryptosporidium* concentrations have demonstrated the usefulness of environmental information for predicting changes in protozoan contamination (Smalley *et al*., 2025). Research examining the seasonal inactivation of *Cryptosporidium parvum* oocysts has also supported the consideration of environmental conditions in pathogen persistence modeling (Thapaliy *et al*., 2025). Unlike the bacterial models, no salinity response is included for the freshwater pathogen. The final index combines the thermal and runoff components and is restricted to values between zero and one. This simplified approach distinguishes rainfall-related contamination processes from bacterial environmental suitability. The principal simulation settings, pathogen-specific parameters, and climate scenarios are summarized in Table 1.

The environmental suitability index is used to calculate the proportion of site-days meeting a defined suitability threshold. A threshold value of 0.42 is applied to the three pathogen-specific indices to maintain consistent computational classification rules. A site-day is classified as environmentally suitable when its modeled suitability equals or exceeds this threshold. The percentage of suitable habitat-days is calculated from the number of suitable observations divided by the total observations for the relevant pathogen and scenario. Research investigating climate-related environmental determinants of Vibrio occurrence has demonstrated the importance of incorporating several ecological variables into predictive risk assessment (Brumfield *et al*., 2025). The use of a common numerical threshold supports within-model comparisons, although the environmental response functions differ between pathogens. The resulting percentages describe simulated habitat availability and must not be interpreted as microbiological detection frequencies. Daily suitability values are also summarized by month to examine

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seasonal changes and identify periods with greater modeled environmental suitability.

Table 1: Climate simulation design, aquatic pathogen characteristics, and environmental modeling parameters.

Component	Parameter	Simulation specification
Aquatic environments	Monitoring locations	12 virtual sites: 4 estuarine, 4 coastal, 4 freshwaters
Climate scenarios	Temperature and rainfall changes	Baseline; +1°C/+10%; +2°C/+25%; +3.5°C/+40%
Bacterial pathogens	Thermal response parameters	V. cholerae: 28°C, spread 7°C; V. vulnificus: 27°C, spread 6°C
Protozoan pathogen	Temperature and runoff response	Cryptosporidium spp.: 18°C reference, spread 11°C; rainfall-dependent runoff function
Simulation duration	Repeated annual experiments	365 days per simulation; 30 independent runs per pathogen and climate scenario
Evaluation parameters	Distribution and exposure measures	Habitat suitability (0-1), suitable habitat-days (%), relative environmental exposure index, 95% simulation confidence intervals

Potential human exposure is examined using a relative environmental exposure index derived from the mean suitability of each pathogen-specific habitat. The baseline annual mean is assigned an index value of one, and the corresponding values under warmer and wetter conditions are expressed relative to that baseline within the same simulation run. This calculation provides a consistent measure of proportional environmental change without assuming actual pathogen concentrations, population contact rates, or infection probabilities. Investigations of cryptosporidiosis and giardiasis have examined relationships between extreme weather conditions and disease occurrence using distributed-lag nonlinear models (Grover *et al.,* 2024). Such findings support the importance of considering environmental variability when interpreting potential waterborne pathogen exposure. Accordingly, the simulation does not convert pathogen suitability directly into predicted clinical cases. A higher exposure index is interpreted as an increase in environmental conditions that could support exposure if viable pathogens and relevant human contact pathways are present. The index is suitable for comparing climate scenarios within each pathogen model but not for ranking the absolute infectious risk of different pathogens.

Statistical evaluation is performed using the outputs of 30 independently generated annual simulations. For each pathogen and climate scenario, mean habitat suitability, suitable habitat-day percentage, and relative environmental exposure are calculated. Variability across simulation runs is summarized using standard deviations and approximate 95% confidence intervals for the simulation mean. The differences between baseline and climate-change scenarios are evaluated using paired simulation outputs, since each run uses a

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shared baseline weather realization across its climate scenarios. Machine learning and explainable artificial intelligence have also been investigated for predicting waterborne cryptosporidiosis and giardiasis, demonstrating the usefulness of computational approaches for supporting environmental health assessments (Ligda *et al*., 2024). The analysis examines monthly changes to identify differences in seasonal response patterns. All calculations use fixed random number generation with seed 20261112, enabling exact reproduction of the reported numerical results. The simulation is implemented in Python using NumPy and Pandas, while Matplotlib is used for scientific visualization. The model is intended to test defined climate-response assumptions and does not claim validation against measured pathogen concentrations or epidemiological records.

Results and discussion

The computational results showed distinct changes in environmental suitability among the three aquatic pathogens under increasing temperature and rainfall conditions. Figure 1 compares the percentage of suitable habitat-days across the four climate scenarios. For V. cholerae, suitable habitat-days increased from 79.42% under baseline conditions to 88.33% under the first warming scenario, 94.98% under moderate warming, and 99.08% under the highest-change scenario. *V. vulnificus* demonstrated a stronger proportional response, increasing from 53.52% to 76.17% between baseline and the highest-change scenario. These results represent an increase of 19.66 and 22.66 percentage points, respectively. In contrast, *Cryptosporidium* spp. showed limited changes, with suitable habitat-days decreasing slightly from 97.29% to 95.78% under the highest-change scenario. This difference occurred because the bacterial models benefited from warmer environmental conditions, while the protozoan model was already close to its assumed suitability threshold across most simulated freshwater observations. The results indicate that climate-driven changes in aquatic pathogen distribution depend strongly on the biological response functions and existing environmental conditions.

Seasonal analysis revealed that warming influenced both the magnitude and timing of favourable environmental conditions. Figure 2 compares monthly suitability under baseline conditions and the highest-change scenario. For V. cholerae, the baseline suitability index reached its highest monthly value of 0.838 during August, while the highest-change scenario produced a peak of 0.852 during October. During January, suitability increased from 0.351 to 0.602, indicating a substantial improvement in conditions during the cooler part of the simulated year. *V. vulnificus* showed a similar seasonal extension, with January suitability increasing from 0.114 to 0.298 and its highest monthly suitability shifting from July to September. In contrast, *Cryptosporidium* exhibited a different response, with baseline suitability reaching 0.725 in October and

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increasing to 0.760 in November under the highest-change scenario. However, its minimum monthly suitability declined from 0.582 to 0.554. These findings suggest that warming may extend favourable seasonal conditions for some aquatic bacteria, while the response of protozoan contamination is more dependent on the interaction between temperature and rainfall-related environmental transport.

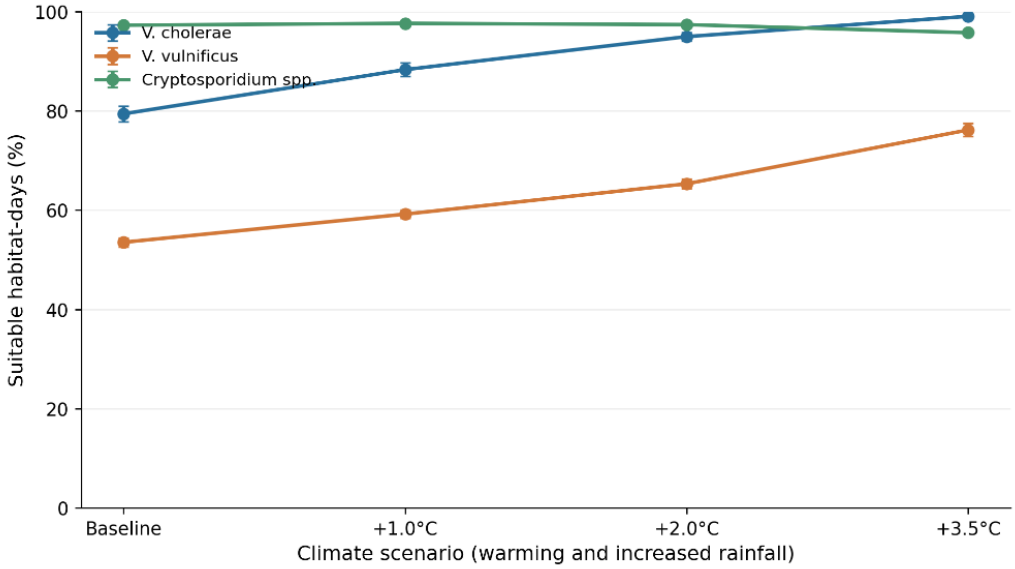


Figure 1: Climate-driven changes in suitable habitat availability across aquatic pathogens and warming scenarios.

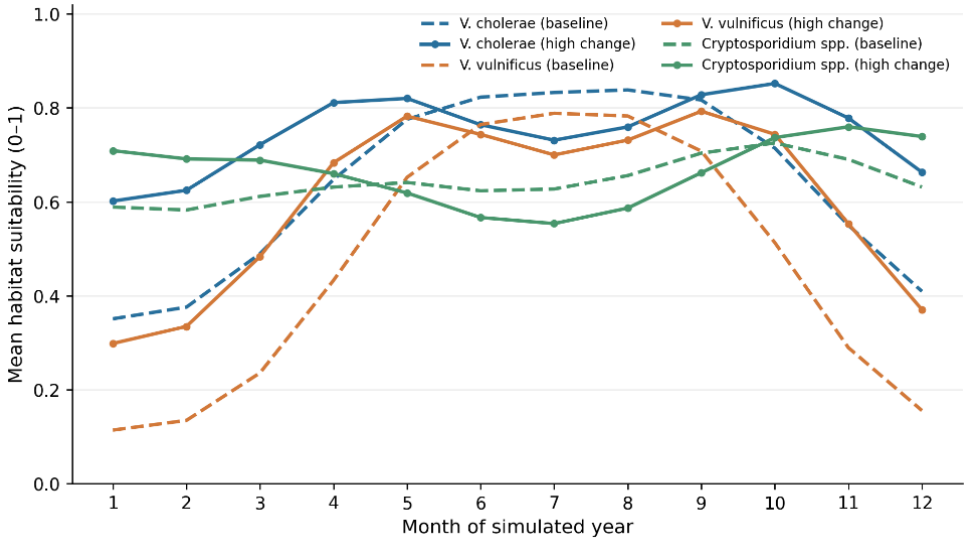


Figure 2: Seasonal variation in aquatic pathogen suitability under baseline and high climate-change conditions.

The relative environmental exposure assessment showed differences in the potential importance of climate changes for the three pathogen groups. Figure 3 presents the exposure index normalized to a baseline value of 1.00 for each

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pathogen. Under the highest-change scenario, the V. cholerae index increased to 1.176, representing a 17.6% increase in modeled environmental exposure opportunity. The greatest proportional increase was *V. vulnificus* with 1.298, equivalent to a 29.8% increase over baseline conditions. Under the lower warming scenarios, the increase was more gradual, with *V. vulnificus* having index values of 1.100 and 1.191 under the first and second climate scenarios respectively. The response of *Cryptosporidium* was smaller and non-linear, increasing to 1.019 and 1.038 and then falling back slightly to 1.034 under the highest-change scenario. This trend is due to the combined effects of increased runoff and decreased thermal suitability in warmer periods. The results indicate possible changes in environmental exposure conditions. These values are not probabilities of infection because the simulation did not include pathogen concentration, virulence, frequency of human contact, and dose-response relationships.

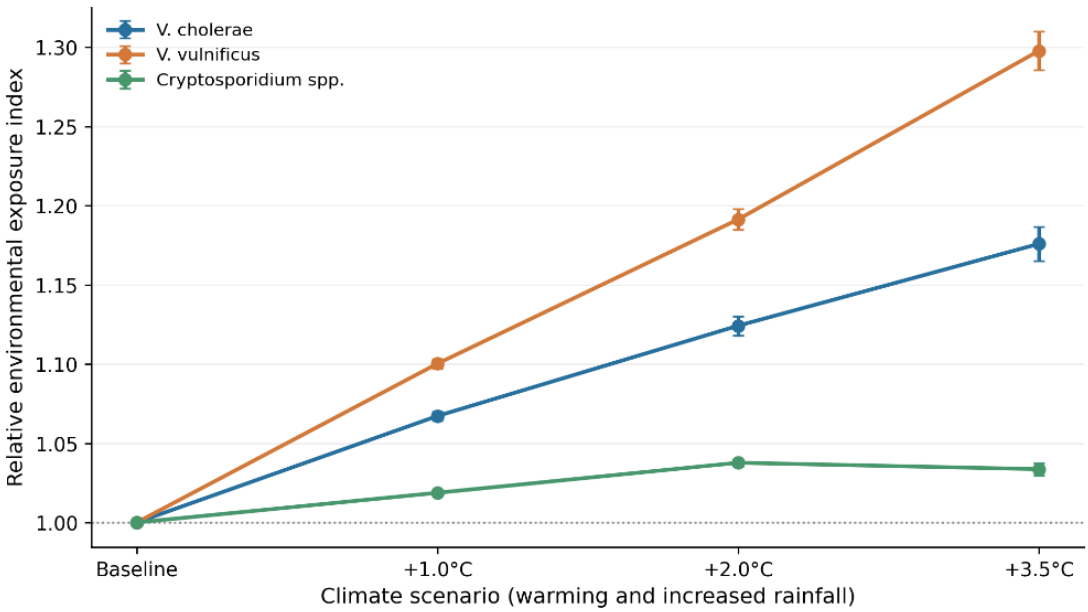


Figure 3: Relative environmental exposure indices of aquatic pathogens under different climate scenarios.

The combined findings demonstrate that aquatic pathogen responses to climate change are not uniform across different environments. The strongest proportional increase in environmental suitability was observed for *V. vulnificus*, suggesting that warming could increase the availability of favourable coastal conditions within the modeled temperature range. *V. cholerae* also showed greater suitability under warmer conditions, although the increase became smaller as the simulated habitat approached its maximum suitability classification. *Cryptosporidium* responded differently because greater rainfall-related transport was partly offset by the effects of increasing temperature.

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The 30 independent simulations showed relatively narrow confidence intervals for scenario means, although these intervals reflect variation within the assumed model rather than uncertainty about real biological responses. The findings support the need for pathogen-specific aquatic monitoring strategies, with particular attention to seasonal warming, coastal exposure, and rainfall-related contamination pathways. However, the simulation does not account for pathogen strain diversity, water treatment, sanitation, population behaviour, or geographical movement between aquatic habitats. Consequently, the results provide a controlled assessment of potential environmental changes rather than predictions of actual infection incidence or the emergence of specific disease outbreaks.

Conclusion

This study investigated the influence of changing climatic conditions on the environmental distribution and potential human exposure implications of three aquatic pathogens using a reproducible computational simulation. The analysis included V. cholerae, *V. vulnificus*, and *Cryptosporidium* spp. at 12 simulated monitoring sites for four temperature and rainfall scenarios. The highest-change scenario showed that suitable habitat-days increased from 79.42% to 99.08% for V. cholerae and from 53.52% to 76.17% for *V. vulnificus*. The relative environmental exposure indices increased by 17.6% and 29.8%, respectively, while *Cryptosporidium* showed a smaller and non-linear response. Seasonal analysis also revealed changes in the timing and duration of favourable environmental conditions. These results demonstrate that pathogen-specific climate sensitivity is important when evaluating potential changes in aquatic environmental contamination and associated human exposure opportunities.

The main contribution of this research is a comparative simulation framework that integrates seasonal climate variability, characteristics of aquatic habitats, pathogen-specific suitability functions and relative exposure assessment. The results suggest that warming and changing precipitation conditions may affect aquatic pathogens in different ways, depending on their ecological needs and how they are transported in the environment. The study is limited by the use of assumed biological response parameters, hypothetical monitoring locations, and the lack of measured pathogen concentrations or epidemiological validation. Thus, shifts in environmental suitability cannot be directly interpreted as shifts in human infection rates. Future studies should integrate observed microbial monitoring data, regional climate projections, pathogen-specific dose-response relationships, and information on human exposure to improve the accuracy of predictions. Combining these approaches with long-term environmental surveillance could support earlier identification of climate-sensitive aquatic contamination and more effective public health preparedness.

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