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Original Research Paper

Epidemiology

CLIMATE CHANGE, ENVIRONMENTAL PERSISTENCE, AND THE EMERGING PUBLIC HEALTH THREAT OF ENTEROVIRUSES: A SYSTEMATIC REVIEW

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ABSTRACT

Enteroviruses are a diverse group of non-enveloped RNA viruses causing illnesses like hand, foot, and mouth disease (HFMD), meningitis, and respiratory infections, primarily impacting children under five. A systematic review of 20 studies (1979–2026) indicates that climate change may be reshaping enterovirus epidemiology, though effects vary by region. While enteroviruses can persist in soil and water under favorable conditions, temperature and humidity are frequently tied to seasonal HFMD peaks. Flooding increases waterborne transmission risks, especially in low- and middle-income countries, while wastewater epidemiology shows promise for early-warning surveillance. However, because the reviewed studies were observational, geographically concentrated, and varied in design, direct comparisons remain difficult. Ultimately, these shifting patterns underscore the need for standardized wastewater monitoring, stronger surveillance, and further high-quality research.

KEYWORDS : Enterovirus Infections; Climate Change; Wastewater-Based Epidemiology; Hand, Foot and Mouth Disease; Waterborne Transmission; Environmental Surveillance

INTRODUCTION

Enteroviruses (EVs), which belong to the Picornaviridae family, are some of the most widespread human pathogens globally but are underrepresented in national disease surveillance systems in many low- and middle-income countries (LMICs) (Alotaibi et al., 2025). These viruses lack an envelope, which makes them stable in a variety of environmental conditions and allows them to persist in different ecological niches like soil, sediments, surface water, and wastewater (Gerba et al., 1980; Goyal & Gerba, 1979; Lodder & de Roda Husman, 2005; Lodder et al., 2010; Fong & Lipp, 2005). Their impact on public health is significant as they can cause a variety of diseases ranging from hand, foot, and mouth disease (HFMD) to aseptic meningitis, acute flaccid myelitis, and respiratory syndromes (Meijer et al., 2012; Oberste et al., 2004). Although climate change and its impact on infectious diseases are gaining attention from scientists around the world, enteroviruses have largely been ignored when compared to vector-borne pathogens (Baker et al., 2024; Alotaibi et al., 2025). This omission from the literature is critical considering that temperature and humidity have been shown to impact enteroviruses' ability to survive and transmit between hosts (Sattar et al., 1988; Onozuka & Hashizume, 2020; Wang et al., 2023). Additionally, flooding and other extreme precipitation events are known to facilitate the transmission of enteroviruses through contaminated water supplies and the strain they place on sanitation infrastructure (Kraay et al., 2020; Kraay et al., 2018; Tan et al., 2025). Projections of the climate through 2100 indicate that the planet will experience not only rising temperatures but also more extreme precipitation events and increased variability in the availability of water resources. These conditions closely mimic those associated with outbreaks of enteroviruses (Baker et al., 2024; Kraay et al., 2018). How these projected changes in the climate will impact the distribution and burden of enteroviruses around the world remains an important question that has yet to be answered.

Objectives

This systematic review aims to address the gaps in the existing literature by focusing on the following objectives:

1. To synthesize the existing evidence on the relationship between climate variables, environmental conditions, and enterovirus transmission or persistence.
2. To evaluate the role of wastewater-based epidemiology as an early warning surveillance tool.
3. To assess the health system vulnerability, particularly in low- and middle-income countries (LMICs).
4. To generate evidence-based recommendations to support climate-adaptive public health policy and surveillance.

METHODS

Protocol and PRISMA Compliance

This systematic review was conducted and reported in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 guidelines. A protocol was developed a priori to define the research question, eligibility criteria, search strategy, data extraction methods, and quality assessment framework. Due to the diversity in study designs and reported outcomes, a meta-analysis was not performed; instead, a narrative synthesis organised by key themes was undertaken.

Research Question: PECO Framework

- Population: Human populations across all age groups, with particular emphasis on children under five, exposed to enteroviruses in any geographic setting.
- Exposure: Climate variability (including temperature, humidity, precipitation, and seasonality), broader climate change, flooding and extreme weather events, environmental contamination of water and soil, and wastewater or sewage systems.
- Comparator: Geographic regions or time periods with lower environmental exposure, more stable climate conditions, or pre-outbreak baseline settings, where applicable.
- Outcome: Measures of enterovirus transmission, including HFMD incidence, outbreak intensity, detection frequency in wastewater, environmental persistence, and paediatric morbidity burden.

Information Sources and Search Strategy

Systematic searches were conducted in PubMed, Scopus, Web of Science, and Google Scholar. The search covered publications from inception to May 2026. The Boolean search strategy employed was:

("Enterovirus" OR "Non-polio enterovirus" OR "HFMD" OR "Hand foot and mouth disease" OR "Enterovirus D68" OR "Enterovirus A71" OR "Coxsackievirus")

AND

("Climate change" OR "Temperature" OR "Humidity" OR "Precipitation" OR "Flooding" OR "Rainfall" OR "Seasonality" OR "Meteorological factors")

AND ("Wastewater surveillance" OR "Wastewater-based epidemiology" OR "Sewage" OR "Environmental persistence" OR "Waterborne transmission" OR "Water contamination" OR "Microplastics")

Eligibility Criteria
Inclusion criteria comprised peer-reviewed original research, systematic reviews, and meta-analyses examining enteroviruses in relation to climatic, environmental, or wastewater variables, across any geographic setting, and published in English.

Exclusion criteria included studies focused exclusively on polioviruses or rhinoviruses without clear relevance to non-polio enteroviruses; in vitro studies lacking environmental or epidemiological context; conference abstracts, editorials, or other non–peer-reviewed grey literature; and studies with insufficient methodological detail.

Study Selection, Data Extraction and Quality Assessment
Title and abstract screening was followed by a full-text review. Data extraction included key study characteristics such as study design, population, geographic setting, EV serotype(s), climate or environmental variables, outcome measures, and main findings. Study quality was assessed using adapted GRADE criteria, incorporating risk of bias, consistency, directness, and precision of evidence. Laboratory studies were evaluated separately using domain-specific quality checklists.

PRISMA Flow Summary
Database searches yielded 387 records, of which 301 unique records remained after deduplication and were screened by title and abstract. A total of 89 full-text articles were then assessed for eligibility. Following the application of inclusion and exclusion criteria, 20 studies were retained for qualitative synthesis (Figure 1). The most common reasons for exclusion included exclusive focus on poliovirus (n = 24), absence of climatic or environmental variables (n = 19), non–peer-reviewed format (n = 15), and insufficient methodological reporting (n = 11).

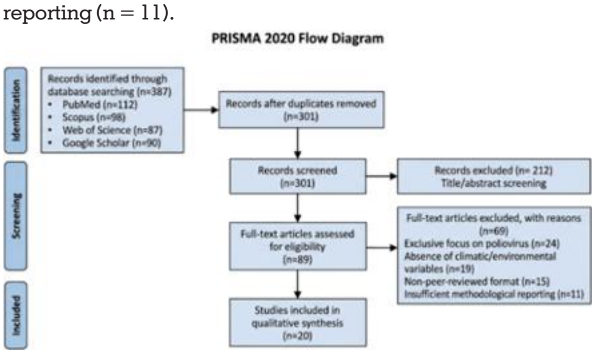

Figure 1: PRISMA 2020 Flow Diagram.

RESULTS
Theme 1: Environmental Persistence and Reservoirs
The environmental persistence of enteroviruses is a key determinant of their epidemiological behaviour. Gerba et al. demonstrated that enteroviruses can adsorb strongly to soil and sediment matrices under flowing water conditions (Gerba et al., 1980). This adsorption is influenced by factors such as ionic strength, organic matter content, and flow velocity (Gerba et al., 1980). Importantly, adsorption not only protects virions from inactivation but also facilitates their subsurface transport into groundwater (Gerba et al., 1980; Fong & Lipp, 2005). Goyal and Gerba further demonstrated differential adsorption patterns between human enteroviruses and animal rotaviruses, with enteroviruses showing a generally higher affinity for soil substrates (Goyal & Gerba, 1979). These findings have direct implications for groundwater contamination dynamics during and after flood events, particularly in unconfined aquifer settings that are common across South Asia (Kraay et al., 2020; Tan et al., 2025).

Surface water contamination pathways have been characterised through sentinel studies conducted in the Netherlands. Lodder and de Roda Husman detected enteroviruses alongside noroviruses in sewage and surface waters, demonstrating that enteric viral loads closely track with faecal contamination indicators (Lodder & de Roda Husman, 2005). A subsequent study by Lodder et al. further showed that source waters used in drinking water production contained detectable enteroviral genomes, underscoring the inadequacy of relying solely on bacterial indicators for water quality assessment (Lodder et al., 2010). Fong and Lipp conducted a comprehensive appraisal of enteric viruses in aquatic environments, concluding that conventional water treatment processes provide inconsistent protection against viral contamination and that enteroviruses remain a credible waterborne risk even in treated water supplies (Fong & Lipp, 2005).

A newly emerging environmental concern is the role of microplastics and nanoplastics as viral carriers. Mija et al. reported that these ubiquitous particles can adsorb enteroviruses, enhance their environmental stability, and facilitate cellular entry, while also modulating host immune responses (Mija et al., 2026). This pathway is particularly concerning given the widespread presence of microplastics in riverine and coastal environments across South and Southeast Asia. It reflects a convergence of two major planetary health challenges—plastic pollution and climate-amplified infectious disease—with potentially synergistic risks that remain poorly quantified (Mija et al., 2026; Alotaibi et al., 2025).

Collectively, the evidence within this theme is strong and methodologically diverse, although most studies on environmental persistence are derived from temperate settings. In contrast, data from tropical and subtropical low-income contexts—where temperature-dependent decay rates and soil properties differ substantially—remain a critical evidence gap.

Theme 2: Climate Drivers of Enterovirus Transmission
Temperature and humidity emerge as the dominant meteorological factors influencing enterovirus transmission, although their effects are nonlinear and context-dependent. Onozuka and Hashizume demonstrated, using distributed lag nonlinear models applied to Japanese HFMD surveillance data, that both variables exert significant lagged effects on transmission dynamics (Onozuka & Hashizume, 2020). Importantly, the study identified clear threshold effects, with temperatures below approximately 10 °C showing a protective association, whereas above 20 °C, increasing temperature was linked to accelerated transmission (Onozuka & Hashizume, 2020). This pattern is consistent with the geographic distribution and spatiotemporal dynamics of HFMD burden observed across tropical and subtropical Asia (Onozuka & Hashizume, 2020; Wang et al., 2023).

Wang et al. extended this analysis across multiple climate zones in China, demonstrating that the meteorological drivers of HFMD vary substantially between regions (Wang et al., 2023). In subtropical southern China, high temperature and humidity were identified as the dominant drivers, whereas in temperate northern regions, humidity alone was more predictive (Wang et al., 2023). This spatial heterogeneity highlights the limitations of universal climate–enterovirus models and underscores the need for region-specific surveillance frameworks. The joint effects of multiple meteorological variables—including temperature, humidity, wind speed, and air pollution—were further analysed by Sun et al. in western China. Their time-series analysis demonstrated synergistic interactions between PM . , SO , and meteorological exposures, suggesting that urban air pollution may amplify climate-related enterovirus risk (Sun et al., 2026). This finding has direct implications for industrially transitioning low- and middle-income countries (LMICs) (Sun et al., 2026; Alotaibi et al., 2025).

At a continental scale, Pons-Salort et al. characterised the seasonality of non-polio enteroviruses in the United States, identifying a summer–autumn dominance pattern linked to temperature-dependent fomite survival and human behavioural factors (Pons-Salort et al., 2018). This work provides a mechanistic framework that can be applied to climate scenario modelling. Building on this, Baker et al., in a landmark *Nature Communications* analysis, integrated climate model outputs with epidemiological data to project that rising temperatures will amplify enterovirus outbreak intensity globally through 2100 (Baker et al., 2024). Their projections identify South and Southeast Asia and sub-Saharan Africa as the highest-risk regions, reflecting both high climate exposure and low adaptive capacity (Baker et al., 2024; Alotaibi et al., 2025). This has important implications for the Indian subcontinent.

Early work by Sattar et al. on Enterovirus 70 provided foundational evidence that temperature and relative humidity influence viral survival on environmental surfaces (fomites), with higher temperatures and lower humidity accelerating inactivation under certain conditions (Sattar et al., 1988). This dual effect—where some temperature ranges may initially enhance transmission but ultimately reduce fomite persistence—highlights the complexity of climate–enterovirus interactions and the limitations of linear extrapolation (Sattar et al., 1988; Onozuka & Hashizume, 2020).

Theme 3: Floods, Extreme Weather, and Waterborne Outbreaks

Flooding represents one of the most operationally acute climate–enterovirus interactions. Kraay et al. conducted a systematic review of faecal contamination and diarrhoeal disease during and after flooding in LMICs, concluding that flood events significantly increase waterborne pathogen transmission through multiple pathways (Kraay et al., 2020). These include overflow of pit latrines and open defaecation areas into surface water, damage to water treatment infrastructure, and submergence of wellheads (Kraay et al., 2020). While the primary focus was on diarrhoeal disease more broadly, these mechanisms are directly relevant to enteroviruses, given their faecal–oral transmission route and environmental persistence (Kraay et al., 2020; Fong & Lipp, 2005).

Tan et al. specifically analysed flood-associated disease outbreaks in Southeast Asia, a region experiencing increasing flood frequency and magnitude due to intensifying monsoon variability and sea-level rise (Tan et al., 2025). Their analysis documented repeated cycles of enteroviral HFMD intensification in the weeks following major flood events, with children under five years bearing the greatest burden (Tan et al., 2025). Importantly, disruption of healthcare systems during floods—including reduced outpatient capacity, interrupted diagnostic cold chains, and displacement of health workers—further compounds infectious disease risk, creating conditions that allow outbreaks to go undetected and amplify (Kraay et al., 2020; Tan et al., 2025).

Kraay et al. also modelled environmentally mediated rotavirus transmission to characterise the role of temperature and hydrological factors (Kraay et al., 2018). Although the analysis focused on rotavirus, the underlying mechanistic framework—linking rainfall intensity, faecal contamination in surface water, and transmission rates—is directly applicable to enteroviruses (Kraay et al., 2018; Fong & Lipp, 2005). Their findings further showed that high-intensity, short-duration rainfall events are more conducive to transmission than sustained moderate rainfall, consistent with projected changes in precipitation patterns under RCP 4.5 and RCP 8.5 climate scenarios (Baker et al., 2024; Kraay et al., 2018).

Janahi et al. demonstrated the presence of detectable enteric viruses in both sewage treatment effluent and shallow coastal waters in Bahrain, highlighting that treatment processes do not consistently eliminate viral contamination and that coastal populations remain at risk of persistent environmental exposure (Janahi et al., 2020). This is particularly relevant for low-lying coastal regions of India, Bangladesh, and the wider Bay of Bengal littoral, where storm surge flooding and inadequate wastewater treatment infrastructure often converge (Tan et al., 2025; Janahi et al., 2020).

Theme 4: Wastewater-Based Epidemiology and Early Warning Surveillance

Wastewater-based epidemiology (WBE) has emerged as one of the most scalable and cost-effective tools for enterovirus surveillance. By detecting viral genomes in sewage before clinical cases become apparent, WBE provides a lead time of days to weeks, which is critical for outbreak prevention rather than response (Raya et al., 2025; Lodder et al., 2010). Raya et al. demonstrated the feasibility of WBE for HFMD-associated enteroviruses in Nepal, a low-resource setting, detecting multiple serotypes—including Enterovirus A71 and Coxsackievirus A variants—in wastewater samples that correlated with community HFMD burden (Raya et al., 2025). This study is particularly significant in showing that WBE is operationally viable in LMIC settings with resource constraints, provided that appropriate molecular infrastructure is in place (Raya et al., 2025; Alotaibi et al., 2025).

Lodder and de Roda Husman, along with the subsequent source water study by Lodder et al., collectively demonstrate that wastewater and surface water monitoring in the Netherlands can detect enteroviral concentrations that track seasonal HFMD trends (Lodder & de Roda Husman, 2005; Lodder et al., 2010). The application of this model to tropical settings, however, requires careful adaptation. Temperature-dependent viral decay in wastewater varies substantially in these settings, and standard genome-based quantification methods may underestimate infectious viral loads under high-temperature conditions (Sattar et al., 1988; Onozuka & Hashizume, 2020).

Alotaibi et al., in a bibliometric analysis of global enteric virus research trends from 1990 to 2024, reported a sharp increase in WBE-related publications following the COVID-19 pandemic, reflecting the expansion of infrastructure and methodological standardisation driven by SARS-CoV-2 wastewater monitoring (Alotaibi et al., 2025). This momentum should be deliberately channelled towards enterovirus surveillance. However, there is currently no globally standardised protocol for quantifying enteroviruses in wastewater, and reported detection thresholds, extraction methods, and molecular assays vary widely across studies (Raya et al., 2025; Alotaibi et al., 2025). This lack of standardisation represents a major barrier to cross-national comparison and effective policy implementation (Alotaibi et al., 2025).

Meijer et al. documented the emergence and epidemic spread of Enterovirus D68 respiratory infections in the Netherlands in 2010, detected through sentinel surveillance of respiratory samples (Meijer et al., 2012). Although not focused on wastewater, this study highlights that novel enterovirus variants can emerge with limited forewarning even within high-income surveillance systems (Meijer et al., 2012; Alotaibi et al., 2025). In LMIC settings, where wastewater-based epidemiology is often absent, such emergence would likely only be detected once a substantial clinical burden has developed (Raya et al., 2025; Alotaibi et al., 2025).

Theme 5: Paediatric Vulnerability and Health-System Burden

Children under five years represent the primary vulnerable population for enterovirus-associated disease, reflecting immunological naivety, greater reliance on environmental play spaces, and lower adherence to hand hygiene (Sun et al., 2026; Alotaibi et al., 2025). Sun et al. reported that meteorological exposures have stronger effects on paediatric HFMD rates than on adult disease rates, consistent with differences in immune competence (Sun et al., 2026). Baker et al. further projected that increased outbreak intensity will be most pronounced in paediatric populations in tropical LMICs, where malnutrition, co-infections, and limited access to healthcare amplify case-fatality risk (Baker et al., 2024; Alotaibi et al., 2025).

The health-system implications are substantial. HFMD outbreaks consistently place a high burden on paediatric emergency departments, particularly in Asia, and are associated with significant productivity losses for caregivers (Sun et al., 2026; Wang et al., 2023). Neurological complications of Enterovirus A71 infections—including brainstem encephalitis and acute flaccid paralysis—result in long-term morbidity and require intensive care resources that often exceed health-system capacity in many LMICs (Meijer et al., 2012; Oberste et al., 2004). Climate change–driven increases in outbreak intensity are therefore likely to impose additional fiscal and capacity pressures on already strained health systems (Baker et al., 2024; Alotaibi et al., 2025), with compounded effects when flood events simultaneously damage infrastructure and increase transmission risk (Kraay et al., 2020; Tan et al., 2025).

Oberste et al.'s characterisation of the complete genome sequences of Enterovirus A species members established the molecular epidemiological framework enabling phylogeographic tracking of outbreak strains (Oberste et al., 2004). This genomic infrastructure is a prerequisite for understanding how climate-amplified transmission alters the evolutionary dynamics of circulating serotypes—a research priority of considerable public health importance (Baker et al., 2024; Oberste et al., 2004).

DISCUSSION

Synthesis of Evidence

This systematic review synthesises a diverse but methodologically heterogeneous body of evidence suggesting that climate change may influence enterovirus transmission risk through multiple environmental and epidemiological pathways. The evidence converges on several key biological mechanisms. These include temperature-dependent acceleration of enterovirus replication in the host intestinal tract and on environmental surfaces; humidity-mediated modulation of aerosol and fomite transmission; precipitation and flooding as pathways for faecal–oral transmission through water contamination; and the emerging role of microplastic vectors in aquatic environments.

Importantly, the relationship between temperature and enterovirus transmission is not monotonic. Some studies suggest that extreme heat may reduce fomite survival while simultaneously accelerating in-host replication and altering human behaviour, such as increased outdoor activity and communal water use. This nonlinearity highlights the limitations of simple linear projections and underscores the need for ensemble modelling approaches that incorporate behavioural, ecological, and biological parameters.

Climate–Enterovirus Transmission Model

A coherent conceptual model of climate–enterovirus interaction can be articulated as follows (Figure 2). Rising temperatures extend the transmission season and increase outdoor human contact that facilitates faecal–oral spread. Changes in precipitation patterns lead to flooding events that mobilise enterovirus-contaminated faecal matter, overwhelm water treatment infrastructure, and introduce infectious viral loads into waterways. Increased humidity under subtropical conditions further enhances droplet and fomite transmission. These direct pathways are compounded by indirect effects, including population displacement into crowded settings during floods, disruption of water and sanitation (WASH) systems, and reduced access to healthcare, all of which amplify transmission risk and case-fatality.

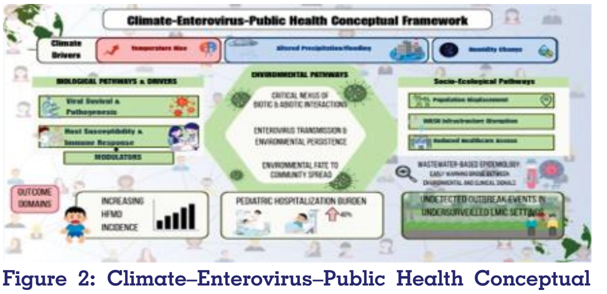

Figure 2: Climate–Enterovirus–Public Health Conceptual Framework.

Comparison with Other Climate-Sensitive Pathogens

Enteroviruses share several climate-sensitivity characteristics with well-studied pathogens. Like cholera, they exploit flood-contaminated water sources; like rotavirus, they exhibit temperature-dependent environmental persistence and paediatric seasonality. In contrast to vector-borne diseases such as dengue and malaria—which have received substantially more climate-attribution research—enteroviruses are transmitted via direct faecal–oral and respiratory routes. As a result, their transmission is less amenable to vector-control interventions but more responsive to improvements in water, sanitation, and hygiene (WASH). The relative neglect of enteroviruses in climate–health literature represents a significant evidence gap and suggests a misalignment in global health research priorities.

LMIC Vulnerability and Environmental Justice

The geography of enterovirus climate risk is highly inequitable. Baker et al.'s projections identify South Asia (including India, Bangladesh, and Pakistan) and sub-Saharan Africa as the highest-burden regions under future climate scenarios (Baker et al., 2024). These regions also have the most limited capacity to implement surveillance, respond effectively to outbreaks, or invest in climate-resilient WASH infrastructure (Baker et al., 2024; Kraay et al., 2020; Alotaibi et al., 2025). India, in particular, faces a convergence of vulnerabilities, including a large under-five population, high population density, intensifying monsoon climate variability, and marked urban–rural disparities in sanitation (Kraay et al., 2020; Alotaibi et al., 2025). These findings should serve as an urgent call to action for Indian public health policy, highlighting the need to align climate adaptation strategies with infectious disease preparedness frameworks under the National Health Mission (Baker et al., 2024; Alotaibi et al., 2025).

Environmental justice analysis indicates that enterovirus risk is concentrated in communities with the least political agency, including informal urban settlements, flood-prone rural areas, and displaced populations. Inadequate WASH infrastructure is not merely a development gap but a structural vulnerability that climate change is likely to intensify. Achieving Sustainable Development Goals 3 (Health and Well-being) and 6 (Clean Water and Sanitation) is therefore a direct prerequisite for climate-adaptive enterovirus control.

One Health Perspective

While enteroviruses are primarily human pathogens, environmental enteroviruses also circulate in animal reservoirs and aquatic ecosystems (Fong & Lipp, 2005). The One Health framework is relevant in two key respects. First, animal enteroviruses present in agricultural runoff can contribute to environmental viral loads in surface waters shared with human communities, particularly in flood-affected settings (Kraay et al., 2020; Fong & Lipp, 2005). Second, climate-driven changes in animal reservoir ecology and geographic range may alter spillover dynamics (Baker et al., 2024; Alotaibi et al., 2025). Goyal and Gerba's comparative adsorption studies further demonstrated distinct adsorption profiles for human and animal enteroviruses, suggesting differences in environmental persistence and transport (Goyal & Gerba, 1979). This distinction is particularly relevant for source attribution in contaminated waterways (Goyal & Gerba, 1979; Fong & Lipp, 2005).

Wastewater Surveillance Integration and Policy

The SARS-CoV-2 pandemic demonstrated that wastewater surveillance can provide actionable public health intelligence at a population scale, even with minimal clinical infrastructure. The evidence reviewed here supports the immediate expansion of existing COVID-19 WBE networks to include enterovirus monitoring, particularly in India and other LMICs where clinical surveillance remains incomplete (Raya et al., 2025; Alotaibi et al., 2025). The Nepal WBE study by Raya et al. provides a clear proof of concept in a resource-constrained setting (Raya et al., 2025). Standardisation of methods is now an urgent priority, including concentration protocols, RT-qPCR primer sets, and reporting thresholds, with a key role for the WHO and regional technical bodies (Raya et al., 2025; Alotaibi et al., 2025).

Importantly, WBE should be integrated into climate-responsive outbreak alert systems rather than functioning as a static monitoring tool. Real-time linkage between meteorological data—such as flood alerts and temperature anomalies—and WBE signals could enable pre-emptive public health responses. These may include school closures during high-risk periods, pre-positioning of oral rehydration supplies, and activation of enhanced hygiene campaigns, implemented days to weeks before clinical outbreak recognition.

Research Gaps and Future Directions

Several critical evidence gaps limit the translation of current findings into policy. First, environmental persistence data are largely derived from temperate settings, while tropical and subtropical conditions—characteristic of the highest-burden regions—remain undercharacterised (Gerba et al., 1980; Lodder & de Roda Husman, 2005; Fong & Lipp, 2005). Second, the microplastic–enterovirus interaction pathway identified by Mija et al. requires urgent mechanistic and epidemiological investigation, given the widespread presence of microplastics in LMICs (Mija et al., 2026). Third, health economic analyses evaluating the integration of WBE into national surveillance systems are lacking, which hinders the development of strong investment cases for policy-makers (Raya et al., 2025; Alotaibi et al., 2025). Fourth, climate-attribution studies that link specific outbreak events to climate anomalies—analogous to event attribution in meteorology—are needed to strengthen the causal evidence base for climate adaptation investment (Baker et al., 2024; Alotaibi et al., 2025). Fifth, integrating genomic epidemiology with climate data could help elucidate how rising temperatures influence the evolutionary fitness of enterovirus serotypes (Baker et al., 2024; Oberste et al., 2004).

CONCLUSION

Systematic reviews have shown that climate change is a driver of enterovirus transmission, environmental persistence, and outbreak severity. Factors like rising temperatures, changed rainfall patterns, flooding, and emerging vectors all contribute to such increases in risks. Enterovirus outbreaks threaten children and the populations of low- and middle-income countries severely, especially in the Indian subcontinent.

Based on the evidence synthesised in this review, three priority actions are recommended:

1. Global Standardization and Policy Integration: The WHO should create standardized protocols for wastewater-based epidemiology (WBE) for enteroviruses. Enteroviruses should also be included in the major climate–health frameworks.
2. Strengthened National and Local Surveillance: Countries should expand hand, foot, and mouth disease (HFMD) programs to include all age groups and create WBE programs. Local diagnostic facilities for pediatric enteroviruses should be enhanced.
3. Climate Adaptation and Pediatric Protection: Enterovirus outbreaks should be part of the national climate adaptation plans, especially concerning the protection of WASH facilities. Public health policies should focus on children, with protocols for school closures and the deployment of EV-A71 vaccines.

Enteroviruses represent an increasingly important climate-sensitive public health threat. Integrating enterovirus preparedness into climate adaptation, surveillance, and public health planning frameworks will be essential to reduce future disease burden, particularly among children and vulnerable populations in low- and middle-income countries.

Table 1: Characteristics of Included Studies (n = 20)

Author (Year)	Study Design	Setting / Country	EV Serotype(s)	Environmental / Climate Variable	Key Outcome Measured	Quality (GRADE)
Sattar et al. (1988)	Experimental	Laboratory (Canada)	EV-70	Temperature, Relative Humidity	Fomite survival rates	Moderate
Goyal & Gerba (1979)	Laboratory	USA	Multiple EVs	Soil type, adsorption conditions	Virus adsorption to soil substrates	Moderate
Gerba et al. (1980)	Experimental	USA	Multiple EVs	Soil/sediment, flow conditions	EV adsorption to sediment matrices	Moderate
Lodder & Husman (2005)	Observational	Netherlands	Multiple EVs	Sewage, surface water	Virus detection in sewage & surface water	Moderate-High
Fong & Lipp (2005)	Review	Global	Multiple EVs	Aquatic environment	EV health risks in water	High
Oberste et al. (2004)	Genomic	Global (USA)	EV-A species	N/A (Genomic characterisation)	Complete genome sequences EV-A	High
Lodder et al. (2010)	Observational	Netherlands	Multiple EVs	Source water quality	EV detection in drinking water sources	Moderate-High
Pons-Salort et al. (2018)	Ecological	USA	Non-polio EVs	Temperature, seasonality	Seasonality patterns, outbreak drivers	High

Kraay et al. (2018)	Modelling	Global	Rotavirus (proxy)	Temperature, hydrology	Env. transmission modelling	High
Meijer et al. (2012)	Surveillance	Netherlands	EV-D68	Seasonal emergence	EV-D68 epidemic occurrence	Moderate-High
Kraay et al. (2020)	Systematic Review	LMICs, Global	Multiple enteric pathogens	Flooding, precipitation	Faecal contamination post-flood	High
Janahi et al. (2020)	Observational	Bahrain	Multiple EVs	Sewage effluent, coastal water	EV in treated wastewater	Moderate
Onozuka & Hashizume (2020)	Time-series	Japan	HFMD EVs	Temperature, humidity	HFMD incidence	High
Wang et al. (2023)	Spatiotemporal	China (multi-zone)	HFMD EVs	Multiple meteorological vars	HFMD spatiotemporal patterns	High
Baker et al. (2024)	Modelling Study	Global	Non-polio EVs	Climate projections RCP 4.5/8.5	Projected outbreak intensity 2024–2100	High
Alotaibi et al. (2025)	Bibliometric	Global	Multiple enteric viruses	Publication trends	Global research trends 1990–2024	Moderate
Tan et al. (2025)	Review	Southeast Asia	HFMD EVs	Flooding, extreme weather	Flood-associated outbreak transmission	Moderate-High
Raya et al. (2025)	WBE Surveillance	Nepal (LMIC)	EV-A71, CVA variants	Wastewater viral load	WBE feasibility for HFMD in LMIC	Moderate-High
Sun et al. (2026)	Time-series	Western China	HFMD EVs	Meteorological + air pollution	Joint effects on HFMD risk	High
Mija et al. (2026)	Review	Global	Multiple EVs	Microplastics/ nanoplastics	Viral carriage, immune modulation	Moderate

Table 2: Climate and Environmental Variables and Associated Enterovirus Outcomes

Climate / Environmental Variable	Direction of Effect	Outcome Measure	Setting / Region	Key Reference(s)	Evidence Quality & Caveats
Elevated temperature (>20°C)	Increased transmission	HFMD incidence, seasonality	Japan, China, USA, Global	Onozuka & Hashizume (2020); Pons-Salort (2018); Baker (2024)	High; nonlinear threshold effects documented
Low temperature (<10°C)	Decreased transmission	HFMD incidence	Japan, China	Onozuka & Hashizume (2020); Wang (2023)	Moderate; varies by climate zone
High relative humidity	Increased EV transmission	HFMD incidence, fomite persistence	Subtropical Asia	Sattar (1988); Onozuka (2020)	Moderate; interacts with temperature
Flooding / intense precipitation	Increased waterborne transmission	EV detection in water; outbreak clusters	LMICs, SE Asia	Kraay (2020)10; Tan (2025)	Moderate-High; lagged effects common
Air pollution (PM2.5, SO2)	Synergistic amplification	HFMD incidence in China	Western China	Sun et al. (2026)	Moderate; single-region study
Soil / sediment adsorption	Prolonged EV persistence	EV survival in soil/water	Laboratory / USA	Gerba (1980); Goyal & Gerba (1979)	Moderate; limited tropical data
Surface / source water contamination	Persistent EV reservoir	EV detection in water supplies	Netherlands, Bahrain	Lodder (2005); Lodder (2010); Janahi (2020)	High; regulatory implications
Microplastic burden in water	Enhanced viral persistence & uptake	Viral adsorption, immune modulation	Global (modelling/lab)	Mija et al. (2026)	Low-Moderate; emerging evidence

Table 3. Wastewater-Based Epidemiology Findings, Research Gaps, and Future Priorities

Domain/Study	Key Findings	Current Limitations	Future Priority
Lodder & Husman (2005)	EVs detected in sewage and surface water year-round; correlated with seasonal disease patterns	Temperate-setting only; limited LMIC applicability	Expand surveillance studies in tropical LMIC settings
Lodder et al. (2010)	EV genomes detected in drinking-water source waters	Lack of correlation with disease incidence	Evaluate treatment efficacy and health outcomes
Janahi et al. (2020)	Enteric viruses detected in treated effluent and coastal waters	Cross-sectional design	Longitudinal monitoring in coastal LMIC regions
Raya et al. (2025)	Demonstrated feasibility of WBE in Nepal; correlated with HFMD burden	Cold-chain and standardisation challenges	Develop standardised LMIC-compatible WBE protocols
Alotaibi et al. (2025)	Rapid growth of WBE research following COVID-19	No globally harmonised protocol	WHO-led standardisation initiatives
Environmental Persistence	Limited tropical/subtropical persistence data	Geographic evidence gaps	Longitudinal environmental sampling studies
Microplastic Vectors	Uncertain quantitative risk estimates	Limited mechanistic evidence	Experimental and epidemiological studies
Climate Attribution	Lack of outbreak-specific attribution studies	Weak causal evidence	Climate-attribution modelling
Genomic Epidemiology	Limited understanding of climate effects on EV evolution	Sparse genomic-climate datasets	Integrated phylogeographic analyses
Health Economics	No cost-effectiveness studies of WBE implementation	Insufficient policy evidence	Decision-analytic modelling

Paediatric Burden	Underestimated disease burden in LMICs	Incomplete hospitalisation data	Multi-centre paediatric surveillance
One Health	Animal contributions poorly characterised	Limited integrated datasets	One Health surveillance programmes

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