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ENVIRONMENTAL AND MICROBIOLOGICAL INTERACTIONS OF HADV, *E. FAECALIS*, AND *E. COLI* IN COASTAL WATERS: A SCOPING REVIEW OF EVIDENCE AND RESEARCH GAPS

INTERAÇÕES AMBIENTAIS E MICROBIOLÓGICAS DE HADV, *E. FAECALIS* E *E. COLI* EM ÁGUAS COSTEIRAS: UMA REVISÃO DE ESCOPO DE EVIDÊNCIAS E LACUNAS DE PESQUISA

INTERACCIONES AMBIENTALES Y MICROBIOLÓGICAS DE HADV, *E. FAECALIS* Y *E. COLI* EN AGUAS COSTERAS: UNA REVISIÓN DE ALCANCE DE LA EVIDENCIA Y LAS BRECHAS DE INVESTIGACIÓN

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Abstract

The microbiological quality of coastal environments is a critical determinant of global public health, particularly under increasing anthropogenic pressure and climate change, influencing pathogen persistence in marine ecosystems. This scoping review aimed to map and analyze the scientific evidence on environmental and microbiological aspects of HAdV, *E. faecalis,* and *E. coli* in marine waters, with emphasis on global distribution, influential environmental factors, and public health implications. In addition, knowledge gaps were identified, and evidence-based recommendations for environmental monitoring and public health policies were synthesized. A structured literature search was conducted across PubMed, MEDLINE, Scopus, LILACS, SciELO, and the Cochrane Library using standardized descriptors, focusing on articles published between 2023 and 2025. The review adhered to PRISMA-ScR guidelines and the Joanna Briggs Institute Methodology. Twenty-seven studies were selected that assessed microbiological concentrations, antimicrobial resistance patterns, and environmental variables in coastal regions. Results indicates that HAdV exhibits superior persistence in saline water, detected in up to 60% of analyzed samples; *E. faecalis* displayed multidrug resistance rates of 41–91% among isolates, confirming its role as a vector for resistance genes; and *E. coli* remained present in 58% of recreational water samples, with significantly higher concentrations during elevated temperature periods and storm events. Environmental factors, including salinity, solar radiation, and temperature, directly influence the survival of viruses and bacteria, while anthropogenic activities intensify the coastal microbial load. In conclusion, integrating viral and bacterial indicators into surveillance protocols, developing standardized analytical methodologies, and adopting interdisciplinary One Health approaches are

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crucial for guiding effective public policies that promote environmental protection and prevent waterborne diseases in populations exposed to contaminated marine environments. This scoping review was registered on the Open Science Framework (OSF) platform under registration: https://osf.io/v4zq5 and DOI: 10.17605/OSF.IO/V4ZQ5

Keywords: Human Adenoviruses; Seawater; *Enterococcus faecalis; Escherichia coli*.

Resumo

A qualidade microbiológica dos ambientes costeiros constitui um determinante crítico da saúde pública global, especialmente diante do aumento da pressão antropogênica e das mudanças climáticas, que influenciam a persistência de patógenos nos ecossistemas marinhos. Esta revisão de escopo teve como objetivo mapear e analisar as evidências científicas acerca dos aspectos ambientais e microbiológicos de HAdV, *E. faecalis* e *E. coli* em águas marinhas, com ênfase na distribuição global, nos fatores ambientais influentes e nas implicações para a saúde pública. Além disso, foram identificadas lacunas de conhecimento e sintetizadas recomendações baseadas em evidências para o monitoramento ambiental e a formulação de políticas de saúde pública. Foi realizada uma busca estruturada da literatura nas bases PubMed, MEDLINE, Scopus, LILACS, SciELO e Cochrane Library, utilizando descritores padronizados, com foco em artigos publicados entre 2023 e 2025. A revisão seguiu as diretrizes PRISMA-ScR e a metodologia do Joanna Briggs Institute. Foram selecionados vinte e sete estudos que avaliaram concentrações microbiológicas, padrões de resistência antimicrobiana e variáveis ambientais em regiões costeiras. Os resultados demonstraram que o HAdV apresenta maior persistência em água salina, sendo detectado em até 60% das amostras analisadas; *E. faecalis* apresentou taxas de resistência multidroga entre 41% e 91% entre os isolados, confirmando seu papel como vetor de genes de resistência; e *E. coli* permaneceu presente em 58% das amostras de águas recreacionais, com concentrações significativamente mais elevadas durante períodos de temperaturas altas e eventos de tempestade. Fatores ambientais, incluindo salinidade, radiação solar e temperatura, influenciam diretamente a sobrevivência de vírus e bactérias, enquanto atividades antropogênicas intensificam a carga microbiana costeira. Conclui-se que a integração de indicadores virais e bacterianos aos protocolos de vigilância, o desenvolvimento de metodologias analíticas padronizadas e a adoção de abordagens interdisciplinares fundamentadas no conceito *One Health* são fundamentais para orientar políticas públicas eficazes que promovam a proteção ambiental e previnam doenças de veiculação hídrica em populações expostas a ambientes marinhos contaminados. Esta revisão de escopo foi registrada na plataforma *Open Science Framework* (OSF) sob o registro: https://osf.io/v4zq5e DOI: 10.17605/OSF.IO/V4ZQ5.

Palavras-chave: Adenovírus humanos; Água marinha; *Enterococcus faecalis; Escherichia coli*.

Resumen

La calidad microbiológica de los ambientes costeros constituye un determinante crítico de la salud pública global, particularmente en un contexto de creciente presión antropogénica y cambio climático, que influye en la persistencia de patógenos en los ecosistemas marinos. Esta revisión de alcance tuvo como objetivo mapear y analizar la evidencia científica sobre los aspectos ambientales y microbiológicos de HAdV, *E. faecalis* y *E. coli* en aguas marinas, con énfasis en la distribución global, los factores ambientales influyentes y las implicaciones para la salud pública. Además, se identificaron hiatos de conocimiento y se sintetizaron recomendaciones basadas en evidencia para el monitoreo ambiental y las políticas de salud pública. Se realizó una búsqueda bibliográfica estructurada en PubMed, MEDLINE, Scopus, LILACS, SciELO y la Biblioteca Cochrane utilizando descriptores estandarizados, centrada en artículos publicados entre 2023 y 2025. La revisión se llevó a cabo conforme a las directrices PRISMA-ScR y la metodología del Joanna Briggs Institute. Se seleccionaron veintisiete estudios que evaluaron concentraciones microbiológicas, patrones de resistencia antimicrobiana y variables ambientales en regiones costeras. Los resultados

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demostraron que HAdV presenta una persistencia superior en agua salina, siendo detectado en hasta el 60 % de las muestras analizadas; *E. faecalis* mostró tasas de resistencia multidrogas del 41–91 % entre los aislados, confirmando su papel como vector de genes de resistencia; y *E. coli* permaneció presente en el 58 % de las muestras de aguas recreativas, con concentraciones significativamente mayores durante períodos de temperaturas elevadas y eventos de tormenta. Los factores ambientales, incluidos la salinidad, la radiación solar y la temperatura, influyen directamente en la supervivencia de virus y bacterias, mientras que las actividades antropogénicas intensifican la carga microbiana costera. En conclusión, la integración de indicadores virales y bacterianos en los protocolos de vigilancia, el desarrollo de metodologías analíticas estandarizadas y la adopción de enfoques interdisciplinarios basados en el concepto *One Health* son fundamentales para orientar políticas públicas eficaces que promuevan la protección ambiental y prevengan enfermedades transmitidas por el agua en poblaciones expuestas a ambientes marinos contaminados. Esta revisión de alcance fue registrada en la plataforma *Open Science Framework* (OSF) bajo el registro: https://osf.io/v4zq5y DOI: 10.17605/OSF.IO/V4ZQ5

Palabras clave: Adenovirus humanos; Agua de mar; *Enterococcus faecalis; Escherichia coli*.

1. INTRODUCTION

The marine environment plays a crucial role in human health and well-being by providing essential ecosystem services, including food, biotechnology, recreation, sports activities, tourism, and regulating the global climate. Oceans sustain diverse economic activities that are vital for millions of families (Panequi et al., 2025). However, wastewater pollution represents an emerging public health threat, contributing to the increasing global burden of waterborne and foodborne diseases (Mannion et al., 2024).

Conventional fecal contamination monitoring in coastal waters relies on indicator bacteria such as *E. faecalis* and *E. coli*, which require 24–48 hours for cultivation, resulting in critical delays in implementing public health measures (Good et al., 2024). This concern is global: studies have reported runoff-driven contamination by *E. coli* and *Enterococcus* in coastal waters of Mexico (Curiel-Ayala et al., 2012), China (Zhang et al., 2013), Cuba (Larrea-Murrel et al., 2013), Colombia (Moreno et al., 2019), Italy (Federigi et al., 2017), and the United States (Tilburg et al., 2015).

Polymicrobial infections, involving multiple microorganisms, are particularly concerning as they can cause more severe diseases than single-microorganism infections. This phenomenon, known as polymicrobial synergy, refers to the

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interaction of two or more microbes at an infection site, resulting in enhanced disease severity (Murray et al., 2014).

Although human adenoviruses (HAdV) are not included in the regulatory standards of some countries, such as those in Latin America, they can persist in water even after wastewater treatment, representing a hidden public health risk. The presence of resistant viruses, such as HAdV, that persist in water even after sewage treatment poses a hidden public health risk. Pathogenic viruses, frequently detected in sewage-contaminated marine waters are transmitted via the fecal-oral route and include emerging enteric viruses from *Adenoviridae* (strains 3, 7, 40, and 41), *Caliciviridae*, *Picornaviridae*, and *Reoviridae* families. HAdV types 40 and 41 were recognized as significant gastroenteritis pathogens, representing the second leading cause of childhood gastroenteritis globally (Fongaro et al., 2013). Studies indicate these viral pathogens can cause various infections, from gastrointestinal to respiratory, in individuals exposed to contaminated recreational waters. Furthermore, the prolonged survival of viruses and their nucleic acids in marine environments raises public health concerns, particularly regarding recreational exposure in polluted areas (Griffin et al., 2003).

HAdVs demonstrate remarkable stability in aquatic environments, surviving up to 30 days in saline water, and are associated with disease outbreaks, including conjunctivitis and gastroenteritis, representing a serious public health concern (Owliaee et al., 2024). Analysis of exogenous factors, such as climate change and urbanization, on pathogen prevalence dynamics in marine ecosystems, including HAdV, *E. faecalis,* and *E. coli*, reveals a critical literature gap. Although investigations exist regarding the relationship between these factors and aquatic ecosystem health, a notable scarcity of specific data persists on the interactions among pathogens, environmental variables, and human exposure in urban and climatic contexts (Henninger, 2013). The high detection rate of respiratory viruses and the rapid availability of results (within two hours) have been associated with reduced antibiotic prescriptions and decreased demand for complementary tests (Echavarría et al., 2018).

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The literature suggests that climate change, through increased water temperatures, acidification, and alterations in salinity, may influence the virulence and distribution of marine pathogens. However, most studies focus on specific organisms or isolated ecosystems, lacking comprehensive analyses of interactions among multiple pathogens and human exposure (Semenza et al., 2025). Urbanization significantly impacts coastal water quality, often leading to increased pollutant and pathogen loads. Urban runoff represents a critical source of *E. faecalis* and *E. coli* in marine environments, and these pathogens pose direct risks to human health, particularly for recreational water users and fishing communities. The relationship between urbanization and HAdV prevalence, a virus transmitted through contaminated waters, remains underexplored. The lack of longitudinal data linking urbanization to pathogen prevalence limits our understanding of infection dynamics in both human and marine populations (Freeman et al., 2019).

Furthermore, antibiotic resistance in *E. faecalis* is a growing concern that exogenous factors may exacerbate. The interaction between antibiotic resistance and urbanization, particularly in coastal areas, constitutes a critical research gap. Chemical pollutants and the introduction of antibiotics into marine environments may influence resistance. Still, the lack of integrated data on *E. faecalis* prevalence and resistance under different environmental conditions represents a significant knowledge gap. This resistance affects human health, as infections caused by resistant strains are more challenging to treat (Korajkic et al., 2020).

Human exposure to these pathogens in contaminated marine environments can lead to various health issues, including gastroenteritis, respiratory infections, and other infectious diseases. The lack of regular water quality monitoring in recreational areas, combined with the absence of data on the prevalence of HAdV, *E. faecalis*, and *E. coli*, exacerbates this public health concern (Henninger, 2013). The interaction between marine ecosystem health and human health is complex and requires an integrated approach that considers both environmental and behavioral factors (Byers, 2021).

Quantitative risk assessments have estimated health risks for individuals engaged in aquatic recreation. A key contribution to risk assessment models is the

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rate of water ingestion. However, as no water ingestion estimates were available for everyday limited-contact aquatic activities such as canoeing, fishing, kayaking, motorboating, and rowing, data from a published study estimating water ingestion rates during swimming were utilized. These data were employed to derive translation factors that quantify self-reported estimate volumes. Consequently, fewer than 2% of canoeists and kayakers reported swallowing a teaspoon, and 0.5% reported swallowing a mouthful or more. Swimmers in pools were 25 to 50 times more likely to report swallowing a teaspoon of water than participants in limited-contact recreational activities in surface waters. Mean and high-confidence estimates of water ingestion during limited-contact recreation in surface waters are approximately 3.4 mL and 10.15 mL, respectively (Dorevitch et al., 2011).

In summary, the scarcity of data on how exogenous factors, such as climate change and urbanization, affect the prevalence dynamics of HAdV, *E. faecalis*, and *E. coli* in marine ecosystems, as well as their relationships with human health, underscores a critical gap that requires urgent attention. Conducting interdisciplinary studies integrating microbiology, ecology, climatology, urban planning, and public health is essential to elucidate the complex interactions between these factors and the health of marine ecosystems and human populations. Understanding these dynamics will contribute to the preservation of ecosystems and the protection of public health in coastal regions, where human-marine environment interactions are inevitable.

Given the complexity of these interactions and the knowledge gaps highlighted herein, conducting a critical synthesis of current evidence becomes imperative. Therefore, this scoping review is justified because it integrates dispersed literature data in a structured manner, providing a robust foundation for future research and public policy decisions.

Justification

Human exposure to pathogens in marine environments, including HAdV, *E. faecalis*, and *E. coli*, poses significant public health risks, particularly in recreational and subsistence contexts. The interaction between exogenous factors, such as

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climate change and urbanization, and the persistence of these microorganisms in coastal ecosystems remains poorly understood, with a scarcity of integrated data that simultaneously assesses environmental variables, microbial loads, and health outcomes. Furthermore, conventional monitoring methodologies present temporal and operational limitations, hindering rapid responses to protect vulnerable populations. Quantitative studies, such as those by Dorevitch et al. (2011), reinforce the relevance of aqueous exposure routes even during limited-contact activities, underscoring the urgency for interdisciplinary approaches to inform surveillance policies and coastal management strategies.

Objective

This study aimed: (i) to map and analyze scientific evidence on environmental and microbiological aspects related to HAdV, *E. faecalis*, and *E. coli* in marine waters, with emphasis on global distribution, influential environmental factors, and public health implications; (ii) to identify knowledge gaps and synthesize evidence-based recommendations for environmental monitoring and public health policies.

2. METHODS

The online tool (https://whatreviewisrightforyou.knowledgetranslation.net/) was used to determine the most appropriate knowledge synthesis method for the specific research needs by responding to a series of guided questions (Amog et al., 2022).

A scoping review was selected to map key concepts within the research area, incorporating diverse sources and comprehensive literature coverage to identify gaps in existing knowledge (Arksey and O'Malley, 2005). This study was registered on the Open Science Framework (OSF) platform (https://osf.io/) under registration: https://osf.io/v4zq5 and DOI: 10.17605/OSF.IO/V4ZQ5. A quantitative approach was applied to analyze the number of selected articles, while a qualitative approach guided the discussion of their content (Gil, 2017; Pereira et al., 2018).

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The research question was formulated using the Population, Concept, and Context (PCC) mnemonic framework to structure essential topics:

- **Population/Participants**: Communities and/or individuals exposed to marine waters.
- **Concept**: Environmental and microbiological aspects related to HAdV, *E. faecalis*, and *E. coli*.
- **Context**: Coastal environments or marine recreational water settings.

Integrating these elements, the following guiding question was developed:

"What are the environmental and microbiological aspects, including distribution patterns, persistence mechanisms, antimicrobial resistance profiles, and public health implications, of HAdV, E. faecalis, and E. coli in coastal waters?"

Table 1 Outlines the PCC model used in this study. The search strategy and review process followed the Joanna Briggs Institute (JBI) Methodology for Systematic Reviews (Peters et al., 2020).

Table 1. PCC Framework Applied to the Study

PCC Component	Description
Population	Communities and individuals exposed to marine recreational waters and coastal environments.
Concept	Environmental and microbiological aspects of HAdV, *E. faecalis*, and *E. coli*, including distribution patterns, persistence mechanisms, antimicrobial resistance profiles, and public health implications.
Context	Coastal marine waters and recreational beach environments globally.

Source: Prepared by the authors

A comprehensive search was conducted across the following databases: Cochrane Library, LILACS, MEDLINE, PubMed, SciELO, and Scopus. The initial selection of studies used descriptors from the MeSH (Medical Subject Headings) terms: *Adenoviruses, Human*; *Seawater*; *Enterococcus faecalis;* and *Escherichia coli*. These terms were combined using the Boolean operator "AND" as follows: *Adenoviruses Human* AND *Seawater*, *Adenoviruses Human* AND *Enterococcus faecalis*, *Adenoviruses Human* AND *Escherichia coli*, *Seawater* AND *Enterococcus*

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faecalis, *Seawater* AND *Escherichia coli*, *Enterococcus faecalis* AND *Escherichia coli*. These search strategies were applied uniformly across all databases. The selected databases are recognized for their significance and relevance in health sciences, as the most important journals in these fields are indexed therein. The search covered the period from January 1, 2023, to October 7, 2025. Search Strategy Rationale and Temporal Delimitation

The exclusive use of the AND Boolean operator between specific MeSH terms was deliberately chosen to maintain thematic precision in retrieving studies addressing concurrent environmental interactions among these microorganisms in marine ecosystems. Preliminary exploratory searches using broader strategies (OR operators, single-term searches) yielded over 250,000 results predominantly comprising clinical or terrestrial studies with limited relevance to coastal water contexts. The adopted strategy balanced methodological feasibility with thematic specificity appropriate for scoping review objectives.

The temporal delimitation to 2023-2025 was intentionally selected to capture contemporary methodological advances (including droplet digital PCR, remote sensing integration, and One Health surveillance frameworks) and recent epidemiological patterns following global modifications to wastewater surveillance infrastructure post-COVID-19 pandemic. This temporal focus aligns with the objective of informing current policy and research agendas, positioning this work as a contemporary evidence snapshot rather than exhaustive historical mapping.

Microplastic-pathogen interactions, while referenced in the emergent findings, were not primary search targets. These themes emerged organically during evidence synthesis from included studies (Metcalf et al., 2023; Sun et al., 2025) and are positioned appropriately as secondary findings rather than a priori search objectives.

The PRISMA-ScR extension guided the review protocol, as per Tricco et al. (2018), and is available through the Joanna Briggs Institute (JBI) (Peters et al., 2020). Although health-related review protocols can be registered in the PROSPERO database, it does not currently accept registrations for scoping reviews

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(Centre for Review and Dissemination, 2016). Consequently, this protocol was registered on the Open Science Framework (OSF), accommodating scoping review protocols. The study selection criteria were adapted from Sampaio and Mancini (2007) and included: Studies published between 2023 and 2025, consistent with the study timeframe; Studies in any language; Quantitative and qualitative approaches; Primary and secondary studies, including systematic reviews with meta-analyses and/or meta-syntheses (following an initial search without date restrictions). Exclusion criteria encompassed: Duplicate articles; Gray literature (Open Grey, www.opengrey.eu); Inconclusive studies; Theses, dissertations, monographs; Conference abstracts; Studies irrelevant to the guiding research question. Search results will be presented using a PRISMA flow diagram (Figure 1), following the guidelines of Page et al. (2021).

2.1 METHODOLOGICAL LIMITATIONS AND CONSIDERATIONS

Several methodological limitations inherent to the scoping review design and the specific parameters of this study warrant acknowledgment:

Selection Bias and Temporal Restriction: The deliberate temporal delimitation to 2023–2025, while justified by the objective of capturing contemporary advances, may have excluded foundational studies that provide essential historical context for understanding pathogen dynamics in marine environments. Additionally, restriction to peer-reviewed articles indexed in selected databases introduces potential publication bias, favoring studies with statistically significant or positive findings. The exclusion of gray literature (government reports, technical documentation, conference proceedings) may have omitted practically relevant surveillance data from public health agencies.

Methodological Heterogeneity: Included studies exhibited substantial methodological diversity across multiple dimensions: (i) sample matrices (seawater, sediment, bivalves); (ii) analytical techniques (quantitative PCR, culture-based enumeration, droplet digital PCR, viability-PCR methods); (iii) quantification units (colony-forming units per 100 mL, gene copies per liter, presence/absence); and (iv) detection limits. This heterogeneity precluded formal meta-analytic aggregation and

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constrained the ability to generate unified effect size estimates or establish predictive concentration thresholds. Consequently, findings are synthesized narratively with explicit study attribution, limiting direct quantitative comparisons.

Geographic Representation Bias: Studies were disproportionately concentrated in high-income countries with established coastal monitoring infrastructure (North America, Western Europe, and specific regions of South America and Asia). This geographic imbalance limits the generalizability of findings to under-resourced coastal regions, particularly in sub-Saharan Africa, South Asia, and Pacific island nations, where monitoring capacity may be constrained and pathogen burdens potentially elevated.

Absence of Formal Quality Assessment: Consistent with Joanna Briggs Institute methodology for scoping reviews, formal risk of bias assessment was not conducted. While this approach is methodologically appropriate for exploratory mapping exercises, it implies that included studies of varying methodological rigor contribute equally to the synthesis. Studies with potential limitations in sampling design, analytical validation, or statistical analysis may influence the evidential landscape, potentially leading to overestimation or mischaracterization of effect magnitudes.

Language Bias: Although no explicit language restrictions were applied in database searches, practical constraints related to translation resources may have resulted in underrepresentation of studies published in languages other than English, Spanish, and Portuguese. This limitation may affect the comprehensiveness of evidence from non-Anglophone regions.

Implications for Interpretation: These limitations collectively suggest that findings should be interpreted as representative of contemporary evidence patterns in well-monitored coastal regions rather than definitive global assessments. Future systematic reviews incorporating meta-analysis, formal quality assessment, and broader geographic representation will be essential to validate and extend these preliminary observations.

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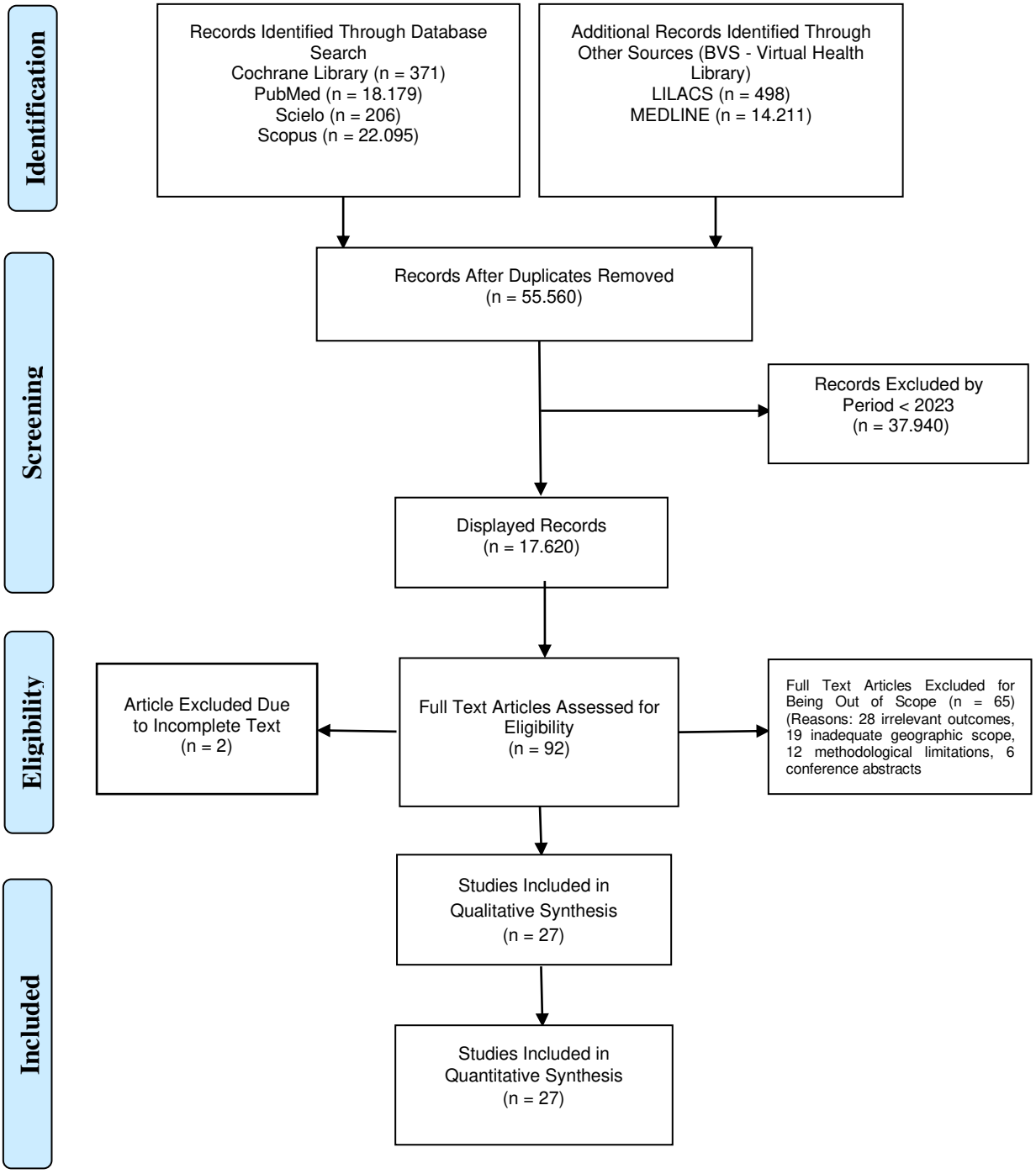

Figure 1. Literature Search Strategy Flow Diagram.

Source: Preferred Reporting Items for Systematic Reviews and Meta-Analysis Protocols (PRISMA-ScR) 2015 Statement (Moher et al., 2016).

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2.1 POTENTIAL STUDY LIMITATIONS

Several limitations and considerations should be acknowledged in this scoping review protocol. The authors acknowledge that the temporal delimitation, exclusion of gray literature, theses, dissertations, monographs, conference abstracts, and the use of synthesis and evaluation methodology may constitute constraints in the present review. Establishing the analysis period from 2023 onward could exclude earlier studies that provide valuable insights.

3. RESULTS AND DISCUSSION

The screening process initially identified 55,560 articles. Of these, 92 underwent full-text eligibility assessment, including 27 studies that met the predetermined criteria. The characteristics of the included studies selected for data extraction are detailed in Table 2.

Table 2. Studies selected for data extraction

STUDY	YEAR	AUTHOR(S)	OBJECTIVE	CONCLUSION
1	2023	Adeniji et al.	Characterize Class 1 Integron and evaluate antimicrobial susceptibility of *Enterococcus* in Kidd's Beach, South Africa.	Aquatic *Enterococcus* exhibits antibiotic resistance via class 1 integrons, indicating horizontal gene transfer.
2	2023	Behera et al.	Quantify abundance and resistance profiles of indicator and pathogenic bacteria along the industrial coast of Visakhapatnam, India.	Industrial discharges elevate loads of multidrug-resistant *E. coli*, exceeding regulatory limits and indicating health risks.
3	2023	Cheng et al.	Assess proliferation and release of *E.coli* from subsurface to coastal waters during storm events.	Storms stimulate growth and export of *E. coli* from groundwater to coastal zones.

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4	2023	De Macena et al.	Monitor microbiological contamination along the coast of Rio de Janeiro, Brazil, following the implementation of submarine outfalls.	Drainage channels are primary sources of intact HAdV (up to 3 log copies/L) in recreational waters.
5	2023	Dos Santos et al.	Investigate viral transmission in surface and wastewater in rural areas with inadequate sanitation.	Anthropogenic and livestock-related water contamination necessitates improved effluent treatment to reduce health risks.
6	2023	Gholipour et al.	Characterize coastal water microbiota and quantify health risks in recreational activities.	Swimming in contaminated water increases the risk of gastroenteritis from *Cryptosporidium* and adenovirus, as well as dermal afflictions.
7	2023	Ghozzi et al.	Identify bacterial, viral, and protozoan contamination along the Tunisian coast.	Tunisian bivalves contaminated with viruses, protozoa, and multidrug-resistant bacteria require advanced monitoring and treatment.
8	2023	Heim et al.	Characterize the distribution and genetic diversity of *Enterococcus* along the Norwegian coast.	*Enterococcus* in bivalves shows genomic diversity; multi-locus surveillance is recommended to assess resistance and contamination.
9	2023	Metcalf et al.	Evaluate the survival of microbial indicators and *Pseudomonas aeruginosa* in microplastic biofilms.	Microplastics transport and perpetuate fecal pathogens in aquatic environments, necessitating regulations for their disposal.
10	2023	Muñoz-Cortés et al.	Detect viral contamination in submarine discharges in the Mexican Caribbean during dry and rainy seasons.	Submarine discharges introduce viral pathogens into the Mexican Caribbean, generating environmental and health risks.
11	2023	Thompson et al.	Investigate variations in water quality and their impact on scallop production in Ilha Grande Bay.	Global warming increases concentrations of *Vibrio spp.* and *E. coli*, impairing scallop cultivation.
12	2023	Zaidi et al.	Assess frequency and genetic diversity of *Enterococcus* in swine within a One Health context.	Tetracycline and macrolide resistance genes persist in *Enterococcus spp* across the One Health continuum.

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13	2024	Denpetkul et al.	Define critical concentration thresholds for enteric pathogens based on microbial risk assessment.	Reverse-QMRA defines critical pathogen concentrations in recreational waters, indicating heightened vulnerability in children.
14	2024	Fehrenbach et al.	Estimate health risks associated with enteric viruses and bacteria in shellfish.	*E. coli* is a limited indicator for enteric viruses in shellfish; an integrated approach across the production chain is essential.
15	2024	Hernández-Zepeda et al.	Analyze fecal pollution and quantify the risk of adenovirus infection in Caribbean lagoons.	Persistent HAdV in tropical lagoons elevates infection risks for snorkelers (>32/1,000 exposures).
16	2024	Lewis et al.	Investigate the effects of beach nourishment on *E. coli* occurrence and sediment granulometry.	*E. coli* persists in sandy beaches; nourishment temporarily alters microbiota.
17	2024	Owliaee et al.	Assess the global distribution of adenoviruses in diverse water bodies.	Wastewater treatment plants show insufficient viral removal; more effective protocols are needed.
18	2024	Park et al.	Examine the distribution of fecal indicators in rivers and coastal zones of Gomso Bay, Korea.	Agricultural and residential activities elevate fecal contamination in coastal waters; geospatial tracking is recommended.
19	2024	Phan et al.	Identify essential genes for uropathogenic *E. coli* survival in human urine.	Uropathogenic *E. coli* (UPEC) indicates increasing antimicrobial resistance and urine-adapted metabolism.
20	2024	Prario et al.	Analyze the annual variation of *E. coli* and *Enterococcus* at Argentine recreational beaches.	Beach sand retains *E. coli* and *Enterococcus* year-round, with risk peaks in summer.
21	2024	Santiago et al.	Investigate the occurrence of resistant *Enterococcus* at beaches in the state of São Paulo, Brazil.	Coastal *Enterococcus spp.* exhibit high multidrug resistance and environmental dissemination potential.

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22	2025	Hafiane et al.	Assess bacterial contamination in water and mussels in the Gulf of Annaba, Algeria.	Mussels exposed to urban effluents harbor pathogenic bacteria, requiring sanitary monitoring.
23	2025	Kevill et al.	Investigate the degradation of enteric viruses in aquatic environments under sunlight.	Summer conditions and urbanization elevate viral and bacterial contamination in mussels and coastal waters.
24	2025	Kong et al.	Verify correlation between remote sensing data and *E. coli* levels in coastal waters.	Remote sensing accurately estimates coastal *E. coli*, aiding pollution alerts.
25	2025	Nirmala et al.	Understand epidemiology and resistance patterns of bacterial infections in northern India.	Seasonal variations and multidrug resistance in Gram-negative bacteria necessitate effective control measures.
26	2025	Ofori et al.	Examine the occurrence and persistence of bacteria in water and oysters from US aquaculture.	Raw oysters pose seasonal microbiological risks, primarily from *Vibrio spp*.
27	2025	Sun et al.	Elucidate nanoplastic transport in porous media under bacterial and salinity influences.	Nanoplastics (<30 nm) have a high potential impact in coastal zones, though their dynamics remain poorly understood.

Source: Prepared by the authors.

Environmental Aspects

Coastal water quality is increasingly threatened by human activities, with sewage discharge contamination posing a significant public health risk (Santiago et al., 2024). These waters constitute essential ecological habitats, primary drivers of the blue economy, and vital public health resources (Kong et al., 2025). The co-circulation of human and animal viruses poses potential environmental impacts from raw sewage discharge from regional communities, posing risks to human and animal health (Dos Santos et al., 2023).

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Environmental factors such as nutrient availability, water temperature, tidal cycles, and contaminant presence determine microbial distribution. The intensification of human activities in coastal areas has increased anthropogenic contaminants, threatening shellfish farms and consumer safety (Fehrenbach et al., 2024). Coastal erosion poses a significant threat to ocean beaches worldwide, prompting management agencies to employ beach nourishment practices that may alter physical beach characteristics and influence microbial communities (Lewis et al., 2024).

Salinity significantly influences viral persistence under low-light conditions, with most viruses surviving longer in seawater than in freshwater. However, sunlight is essential for viral decay in all water types, while elevated temperatures significantly accelerate viral degradation (Kevill et al., 2025). Storms significantly exacerbate fecal pollution of coastal waters, stimulating subsurface bacterial growth and accelerating microbial export to receiving waters (Cheng et al., 2023).

Microplastics are discharged from wastewater treatment plants into aquatic environments. These plastics are rapidly colonized by microbial biofilms, forming distinct plastisphere communities that may include potential pathogens (Metcalf et al., 2023). Small nanoplastics (<30 nm) with high accumulation in biological organisms may interact with bacteria and phosphate, posing potential risks to complex coastal ecosystems (Sun et al., 2025).

Microbiological Aspects Related to Human Adenoviruses (HAdV)

HAdV constitutes the second leading cause of childhood gastroenteritis worldwide. Studies demonstrate viral presence in water resources, with the highest rates in sewage, and treatment plant influent and effluent, indicating weaknesses in viral removal systems (Owliaee et al., 2024).

The submarine sewage outfall in Barra da Tijuca, Rio de Janeiro, Brazil, is not the primary source of pollution for nearby beaches. The channels connecting the lagoon system to the coast represent the primary sources of fecal contamination. Detected and quantified intact HAdV may be a complementary parameter for

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assessing recreational water quality. Molecular characterization of infectious HAdV-A12, -D, -F40, and -F41 viruses, responsible for respiratory, ocular, and gastroenteric diseases, confirms contamination of domestic sewage (De Macena et al., 2023).

Estimated HAdV infection risks for snorkeling activities were approximately 1-2 orders higher than for swimming. Although Mexico lacks recreational water risk parameters, average illness risks for snorkeling exceed the US EPA benchmark of 32/1000 (Hernández-Zepeda et al., 2024). Potential risks of gastrointestinal illness from enteric microorganisms through water ingestion during swimming events exist, primarily from *Cryptosporidium* and *Adenovirus* (Gholipour et al., 2023).

The occurrence of fecal microorganisms, including HAdV genomes was explored in submarine groundwater discharges in the Mexican Caribbean, demonstrating that these constitute significant sources of viral pathogens at the land-sea interface and represent risks for recreational activities (Muñoz-Cortés et al., 2023).

Microbiological Aspects Related to *Enterococcus faecalis*

Enterococci are gram-positive bacteria isolated from diverse environments, including soil, water, plants, and the intestinal tracts of humans and animals. Although considered commensal in humans, *Enterococcus spp*. constitutes important opportunistic pathogens. Due to their presence and persistence in various environments, they are ideal for antimicrobial resistance studies from a One Health perspective (Zaidi et al., 2023).

During 10 months, seawater samples were collected from four beaches in São Paulo state, Brazil. Results revealed the prevalence of *E. faecalis*, *E. faecium*, and *E. hirae*. Of 130 isolates, 118 demonstrated multi-antibiotic resistance, providing evidence of potential antimicrobial resistance transfer in the environment (Santiago et al., 2024).

The marine environment may harbor *Enterococcus*, but its role as an evolutionary niche and dissemination vector remains under investigated. Analyses

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of marine bivalves collected from 86 sites in Norway detected *Enterococcus* in 287 of 471 samples examined, though at low concentrations. Of the positive samples, 479 isolates belonged to 10 different species, with *E. faecium* (n = 247), *E. hirae* (n = 114), and *E. faecalis* (n = 66) being the most frequent. Resistance to one or more antimicrobial agents was observed in 197 isolates (41%) (Heim et al., 2023). The impact of *Enterococcus* related hospital infections and the challenges of antibiotic-resistant treatment are problematic. The ability of *Enterococcus* to acquire resistance genes through natural conjugation transfer suggests that other resistances constitute a critical challenge (Adeniji, Nontongana & Okoh, 2023).

Microbiological Aspects Related to *Escherichia coli*

E. coli constitutes an important indicator of fecal contamination in marine waters. Studies demonstrate its significant presence in various coastal regions worldwide, often associated with antimicrobial resistance. Increasing urbanization and industrialization in the Visakhapatnam region have introduced domestic sewage and industrial wastewater into the coastal ocean. Samples collected from ten different areas revealed the presence of indicator bacteria (*E. coli* and *E. faecalis*) and pathogenic bacteria. Samples collected during industrial discharge periods showed higher bacterial loads, including *E. coli*. Some isolates demonstrated multi-antibiotic resistance (Behera et al., 2023).

E. coli counts were significantly higher during warmer periods, potentially reducing scallop productivity. Results suggest that scallop mariculture collapse results from synergistic adverse effects of global warming and poor seawater quality (Thompson et al., 2023).

Analysis of fecal contamination indicator concentrations and distribution at a recreational beach on Argentina's Atlantic coast demonstrated that 58% of samples exceeded permitted limits. *E. coli* showed higher concentrations in water during summer, with the highest abundance identified during summer months (Prario et al., 2024).

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High numbers of coliform bacteria, including *E. coli*, were detected in mussels and seawater in the Gulf of Annaba, northeastern Algeria, representing a three-order-of-magnitude increase in summer compared to winter. Biochemical analyses identified potentially pathogenic species, including *E. coli*, highlighting serious human health threats (Hafiane et al., 2025). Uropathogenic *E. coli* (UPEC) constitutes the primary cause of urinary tract infections and is increasingly associated with antibiotic resistance. This scenario has been aggravated by the emergence of pandemic UPEC sequence type 131 (ST131), a multidrug-resistant clone associated with extraordinarily high infection rates (Phan et al., 2024).

Considerations on Aquaculture Products and Public Health

Aquaculture products, such as shellfish, scallops, and oysters, constitute the primary vectors for fecal derived pathogens. Somatic and male specific coliphages correlate strongly with human noroviruses, the leading enteric viruses worldwide (Park et al., 2024).

The filter-feeding nature of oysters, anthropogenic activities, and increased agriculture compromise the microbial safety of farmed eastern oysters. Molecular confirmation demonstrated the presence and persistence of eight bacterial species in seawater and oysters, including *Vibrio parahaemolyticus*, *Shiga* toxin-producing *E. coli*, and other pathogenic species (Ofori, Parsaeimehr & Ozbay, 2025).

Fecal indicators, including *E. coli* and *Salmonella spp.*, were detected in shellfish and mussels from Tunisia's coastal region. *Vibrionaceae* species were also recorded in seawater, sediments, fish, and shellfish, with *Vibrio alginolyticus* predominating. The isolation of multidrug resistant bacterial strains demonstrates significant dissemination of antibiotic resistance (Ghozzi et al., 2023).

Public Health Implications and Monitoring

Increasing anthropogenic pressures and climate disturbances present significant challenges for microbial water quality. Using satellite data to estimate concentrations of fecal indicator bacteria linked to human health in coastal waters is

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feasible and may improve the performance of pollution alert systems (Kong et al., 2025).

Quantitative Microbial Risk Assessment (QMRA) determines the critical concentrations of pathogenic microorganisms in recreational waters for regulatory purposes. Pathogens such as norovirus, *C. jejuni*, and *Cryptosporidium* pose a high risk even at low concentrations, requiring continuous monitoring. Given increasing contamination from human and animal waste, concerns exist regarding the exposure of vulnerable groups, particularly children. Current guidelines still lack the complete integration of risk-based criteria, which is essential for optimizing public health protection (Denpetkul et al., 2024).

Antimicrobial resistance constitutes a growing threat to global health. Temperature influences seasonal patterns of bacterial infections, aiding outbreak prediction and prevention. Results emphasize the threat of multidrug resistance, particularly in Gram-negative bacteria, reinforcing the need for enhanced infection control (Nirmala et al., 2025).

4. CONCLUSION

The collective findings of this contemporary scoping review indicate that HAdV exhibits enhanced persistence in marine waters compared to traditional bacterial indicators, with detection frequencies reaching 60% in wastewater samples (Owliaee et al., 2024) and quantifiable concentrations up to 3 log copies/L in coastal drainage channels (De Macena et al., 2023), necessitating sensitive molecular detection methods for accurate water quality assessment in coastal contexts. Molecular characterization of HAdV-A12, -D, -F40, and -F41 serotypes in Brazilian recreational waters evidenced domestic sewage contamination, while international studies confirmed that intact HAdV may serve as a complementary parameter for evaluating recreational water quality. E. faecalis shows high prevalence in marine environments globally, with 41–91% of isolates exhibiting multi-antibiotic resistance (Heim et al., 2023; Santiago et al., 2024), supporting its potential role as a vector for

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antimicrobial resistance gene dissemination. *E. coli* remains a reliable indicator of fecal contamination, though its detection shows significant seasonal variations, with higher concentrations during warmer periods (Thompson et al., 2023; Prario et al., 2024). The synergistic interaction between environmental factors, including temperature, salinity, solar radiation, and anthropogenic activities, directly influences the persistence and virulence of these microorganisms in coastal ecosystems.

Future Perspectives

1. Climate Change Interactions

Future research should prioritize understanding how climate change intensifies pathogen dynamics in marine and coastal environments. Ocean warming is expected to expand the geographical range of thermotolerant pathogens, such as *Vibrio spp*., thereby reshaping host-pathogen interactions and increasing the likelihood of disease outbreaks in previously unaffected regions. Concurrently, ocean acidification, characterized by decreased pH, may disrupt viral capsid integrity and compromise bacterial membrane stability. These conditions could enhance the infectivity of HAdV and facilitate the uptake of antibiotic resistance genes (ARGs) by environmental microbial communities. In addition, synergistic processes associated with sea-level rise and intensified storm surges are projected to exacerbate coastal sewer overflows, creating new pathways for pathogen mobilization and dispersal into estuarine and nearshore systems. Collectively, these climate-driven stressors underline the need for integrative models that link environmental change to microbial risks in the Anthropocene.

2. Mechanistic Insights into Plastic–Pathogen Trojan Horse Dynamics

Our study highlighted the need to characterize plastisphere-associated microbial communities as reservoirs of emerging pathogens and resistance genes, underscoring the importance of holistic approaches to marine environmental health for adequate global public health protection. Understanding the mechanistic pathways through which plastics influence microbial risks requires a detailed investigation of nanoplastics as permeable carriers that can facilitate the

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intracellular delivery of pathogens. Emerging evidence suggests that these nanoscale particles can be internalized by human cells, particularly via phagocytosis in the respiratory and gastrointestinal tracts, potentially serving as vectors that transport bacteria and viruses across epithelial barriers. The photodegradation of larger microplastics can amplify this concern by forming nanoplastics in sunlit surface waters, a process that increases particle abundance, enhances bioavailability, and augments toxicological potential within marine ecosystems. To resolve these interactions with the required spatial precision, synchrotron-based spectroscopic techniques, such as scanning transmission X-ray microscopy (STXM), can be employed to visualize pathogen–nanoplastic associations at submicron scales. Together, these mechanistic insights strengthen the understanding of plastics as active participants in pathogen transmission pathways rather than as passive environmental contaminants.

3. Integrated One Health Risk Modeling:

Advancing a One Health perspective requires developing coupled human–animal–environment risk models that capture the complex interactions among wastewater discharge, agricultural runoff, and contamination across marine food webs. Such integrated frameworks enable a more accurate assessment of how these multifaceted pressures collectively influence the persistence, bioaccumulation, and transmission of pathogens to humans and wildlife. To complement these system-level analyses, agent-based modeling can be employed to simulate individual-level exposure pathways, providing detailed representations of how swimmers, athletes, and coastal communities encounter pathogens under varying environmental and behavioral scenarios. Together, these approaches generate a more comprehensive understanding of risk dynamics and support the design of targeted, evidence-based interventions for coastal public health protection.

4. Mitigation Strategies and Policy Interfaces

Building on the mechanistic evidence of pathogen–plastic interactions, this research also advances mitigation strategies and policy interfaces that bridge

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engineering innovation with global environmental governance. On the technological front, the study explores engineered interventions, such as optimized UV-LED wastewater disinfection systems specifically calibrated to inactivate plastic-associated pathogens, whose surface shielding and biofilm matrices often reduce the efficacy of conventional treatment. At the policy level, it was emphasized that coordinated international governance requires partnerships with organizations, including the UNEP and WHO, to establish harmonized guidelines for reducing microplastic emissions and enhancing pathogen surveillance in coastal environments. These actions are framed within the DAPSI(W)R(M) approach, enabling the translation of scientific evidence into regulatory pathways that address Drivers, Activities, Pressures, States, Impacts, Welfare, Responses, and Management measures. This integrated framework ensures that mitigation solutions are not only technologically sound but also embedded within comprehensive, multi-scale environmental policies.

Recommendations

For Researchers

Future research should prioritize harmonizing analytical methods for monitoring coastal pathogens. Establishing standardized, ISO aligned protocols for detecting HAdV, *E. faecalis*, and *E. coli* supported by ddPCR as the reference quantification tool will enable reliable cross-regional comparisons. Advancements in monitoring should integrate satellite remote sensing with autonomous biosensors and machine-learning models to generate real time, high-resolution forecasts of microbial risks.

Methodological improvements must include viability-focused approaches such as ICC-qPCR, PMA-PCR, and multiplex assays that couple molecular signatures with metabolic activity indicators. Investigations into microplastic–pathogen interactions remain essential, particularly regarding nanoplastic formation, adsorption–desorption behavior, and the role of plastisphere biofilms in facilitating the transfer of antimicrobial resistance genes. Techniques like metagenomics,

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FISH, and synchrotron-based imaging can illuminate these mechanisms at submicron scales.

Lastly, in the long term, ecosystem-based monitoring combining seasonal time series with microbial source tracking will be crucial for clarifying contamination origins, pathogen persistence, and gene transfer dynamics under accelerating environmental change.

For Managers

Implementing integrated monitoring systems combining traditional viral and bacterial indicators is recommended, prioritizing the detection of intact HAdV as a complementary marker of fecal contamination in recreational waters. Managers should establish early alert protocols that integrate meteorological data with viral monitoring to enable a rapid response to water quality fluctuations. Adaptive management strategies that account for seasonal variations in microbial persistence, particularly during heatwaves and storm events that intensify coastal contamination, are essential. Surveillance programs for antimicrobial resistance in marine environments should be prioritized, establishing specific risk assessment criteria based on critical pathogen concentrations identified through QMRA.

Conflict of Interest Statement

The authors declare that there are no potential conflicts of interest regarding the research, authorship, and/or publication of this article.

Statement on the Use of Artificial Intelligence (AI)

The authors declare the use of artificial intelligence tools for specific purposes in support of the writing and technical revision of this manuscript. The automated translation systems Google Translate (utilizing AI-based models Gemini, PaLM 2, and Google Neural Machine Translation - GNMT) were employed to assist with translation into English, and the Grammarly Pro platform was used for spell checking, grammatical adjustments, and textual similarity detection. It is emphasized that the use of these tools was strictly supervised and did not replace

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critical reasoning, interpretive analysis, or the intellectual authorship of the work. The authors assume full responsibility for the integrity, accuracy, and originality of the scientific content presented.

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