Journal of Water & Health

Journal of Water and Health Vol 22 No 10, 1911 doi: 10.2166/wh.2024.210

From bibliography to understanding: water microbiology and human health

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ABSTRACT

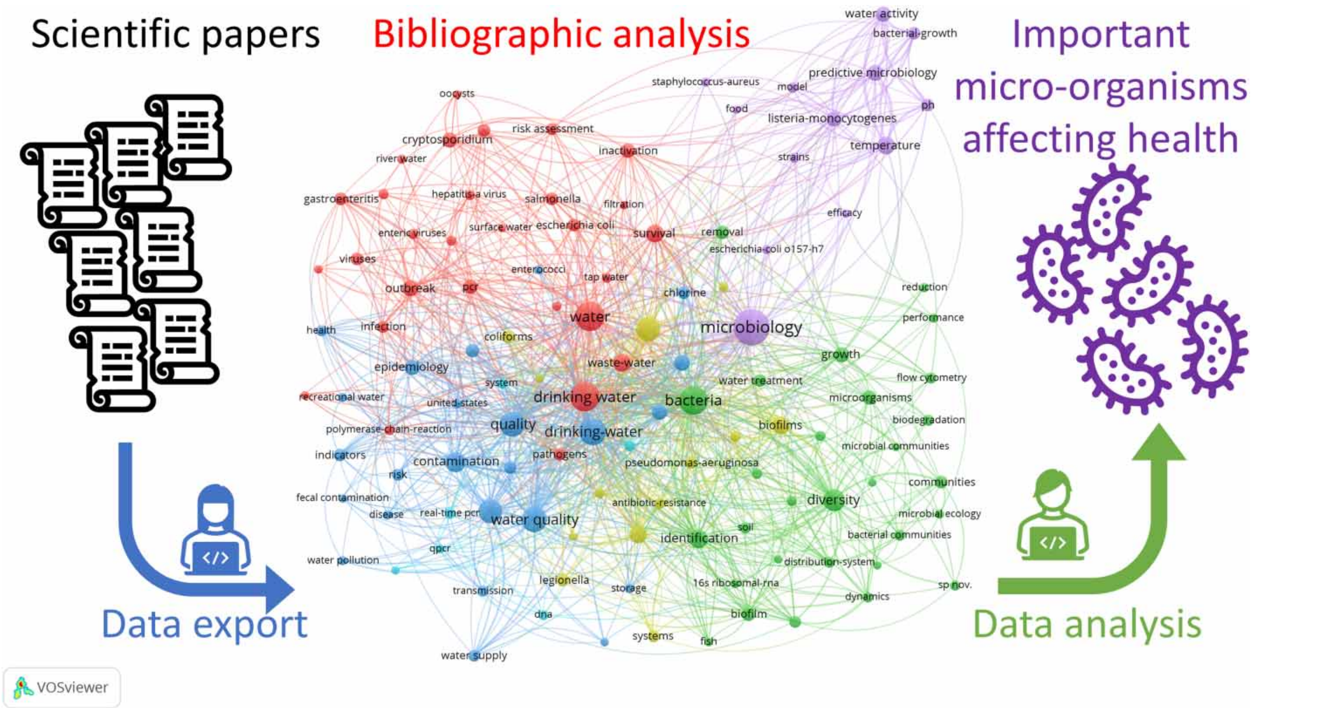
Water is crucial for human health, yet its microbial composition bears significant ecological and health implications. This research utilizes bibliographic methodology, amalgamating data from the Web of Science, and the VOSviewer software to scrutinize a selection of 1,000 seminal articles. It comprehensively delineates (1) the pivotal microorganisms prevailing in aquatic settings, (2) the intricate mechanisms through which microorganisms wield influence over water quality, and (3) the multifaceted repercussions on human health and well-being stemming from these microorganisms. Through this scholarly exploration, the paper illuminates the intricate interplay between water, microorganisms, and human health, providing valuable insights for policymakers, researchers, and health practitioners. Understanding these dynamics is of paramount importance for maintaining both the ecological balance of aquatic systems and safeguarding the health of communities reliant on these resources. This study thus contributes to a deeper comprehension of the intricate relationship between water quality, microorganisms, and human health.

Key words: bibliography study, human health, microbiology, VOSviewer, water

HIGHLIGHTS

- Innovative bibliographic approach.
- Identification of key microorganisms.
- Mechanistic insights.
- Human health implications.
- Policy and practical applications.

GRAPHICAL ABSTRACT



1. INTRODUCTION

Water is unequivocally a fundamental resource for human survival and well-being (Serwecińska 2020; Uddin *et al.* 2024). Beyond its vital role in quenching thirst and supporting various physiological functions, water also serves as an essential component of food production, sanitation, and hygiene (Bishoge 2021). However, the quality of water, particularly in terms of its microbial composition, has far-reaching implications for human health and the ecosystems in which it is found (Danielopol *et al.* 2003; Uddin *et al.* 2021). This paper embarks on a comprehensive exploration of the intricate relationship between water, microorganisms, human health, and the environment (Tao *et al.* 2012).

Microorganisms, including bacteria, viruses, algae, and protozoa, are ubiquitous inhabitants of water bodies, ranging from oceans and rivers to lakes and groundwater (Jacquet *et al.* 2010). While many of these microorganisms are harmless, others can be pathogenic, causing a wide range of waterborne diseases (Leclerc *et al.* 2002). Moreover, microorganisms in water can significantly influence the overall quality and safety of this precious resource (Naidoo & Olaniran 2014). Therefore, understanding the microbial composition of water and its consequences for both human health and ecosystems is of paramount importance (Sentenac *et al.* 2022).

The present research takes a bibliographic approach to this complex issue, aiming to provide a holistic perspective by amalgamating data from the Web of Science and the VOSviewer software. By scrutinizing a carefully selected set of 1,000 articles, we delve into three crucial aspects:

(1) *Pivotal microorganisms in aquatic settings*: A foundational aspect of our study is the identification and characterization of the key microorganisms found in aquatic environments. These microorganisms play a pivotal role in shaping the ecological dynamics of aquatic systems. They are instrumental in nutrient cycling, the decomposition of organic matter, and the overall stability of these ecosystems. Understanding the diversity and functions of these microorganisms is essential for comprehending the intricate web of life in aquatic settings.

(2) *Mechanisms of microbial influence on water quality*: Microorganisms in water have a profound impact on its quality. Their metabolic activities can either improve or degrade water quality. For instance, certain microorganisms can aid in the removal of pollutants through biodegradation processes, thus contributing to water purification. Conversely, some microorganisms can lead to water contamination by releasing harmful toxins or promoting the growth of harmful algal

blooms. A detailed examination of the mechanisms through which microorganisms influence water quality is crucial for effective water resource management.

(3) *Repercussions on human health and well-being*: Water is a direct route for microorganisms to interact with the human population. Contaminated water can serve as a pathway for waterborne diseases, such as cholera, dysentery, and various gastrointestinal infections. In addition to causing acute illnesses, microorganisms in water can have long-term health effects, such as exposure to carcinogenic compounds produced by certain microbial species. Furthermore, the quality of drinking water can influence the overall well-being of communities, particularly those in resource-limited regions where access to clean water is a challenge. Investigating the multifaceted repercussions of waterborne microorganisms on human health and well-being is a critical component of this research.

The interplay between water, microorganisms, human health, and the environment is complex and multifaceted. The objective of this study is to unravel this complexity by employing a bibliographic approach to identify and analyze the most significant articles exploring the relationship between water quality, microorganisms, and human health. By examining these relationships and discussing the most important microorganisms, the study provides valuable insights that can inform policy decisions, guide further research, and assist health practitioners in managing and safeguarding this crucial resource. As we delve deeper into this subject, we contribute to a broader understanding of the intricate connections between water quality, microorganisms, and human health.

2. METHOD

2.1. Data collection and retrieval

The bibliographic analysis methodology employed in this study builds upon established approaches (Chen & Ding 2023a, b, c) with slight modifications to comprehensively investigate the microbial composition of water and its implications for human health and ecosystems. The research commenced by accessing the Clarivate Web of Science database, a widely recognized repository of academic publications, to ensure reliability and accuracy. The protocol involved a systematic two-step process:

Database query: To initiate our exploration, we conducted a targeted search using the keyword 'water microbiology'. This deliberate query aimed to retrieve a substantial and diverse dataset of academic publications relevant to the study of microorganisms in water, encompassing various associated topics. The search resulted in a comprehensive collection of 42,762 records from across all time periods, providing the foundation for our in-depth analysis.

Data export: Following the database query, we extracted a selection of the top 1,000 full articles related to the keyword, as defined by the default sorting order of the Web of Science. These records were exported in a plain text file format, ensuring unfettered access to the complete body of literature essential for conducting a thorough and nuanced analysis. This meticulous approach allowed us to delve into the intricacies of water microbiology, laying the groundwork for insightful conclusions and contributions to the existing body of knowledge.

2.2. Data analysis and processing

Upon obtaining the extensive dataset, we undertook a series of analyses to glean insights and trends within the field of water microbiology, with a particular focus on co-occurrence patterns, co-authorship networks, and affiliations. These analyses were executed using the VOSviewer software, a powerful tool for bibliographic analysis. The following steps outline our approach:

(1) *Co-occurrence analysis*: We selected a 'co-occurrence and keywords' analysis within the VOSviewer software to identify the most prevalent keywords in the retrieved literature. To ensure that the selected keywords were highly representative of the research landscape, we set a criterion of a 'minimum number of occurrences of a keyword' to be no less than 10 occurrences.

(2) *Co-authorship and country analysis*: In addition to keyword analysis, we delved into the collaborative aspects of the research domain. This was achieved through a 'co-authorship and countries' analysis, where we aimed to identify key countries involved in water microbiology research. We set a threshold of 'minimum number of documents of a country' to be at least five documents, ensuring the inclusion of major contributors in this field.

(3) *Co-authorship and organization analysis*: Furthermore, we conducted an analysis of 'co-authorship and organizations' to identify prominent institutions and organizations involved in water microbiology research. We applied a minimum threshold of '2 documents of an organization' to capture the entities with significant contributions.

By employing these bibliographic analyses, we sought to gain a holistic understanding of the state of research, the major players, and the overarching themes within the realm of water microbiology. This methodology allowed us to explore and synthesize a broad range of literature, enabling a comprehensive investigation into pivotal microorganisms, mechanisms influencing water quality, and the far-reaching consequences on human health and well-being. The systematic and data-driven approach undertaken in this research provides a rigorous foundation for our subsequent findings and conclusions.

3. RESULTS

In Figure 1, we delve into the intricate realm of water microbiology through a detailed examination of the main keywords associated with this field. This comprehensive keyword analysis has unearthed a plethora of fascinating insights that provide a nuanced understanding of the domain. Among the diverse range of keywords identified, a significant focus emerges on various microbiological species, including well-known names such as *Pseudomonas aeruginosa*, *Staphylococcus aureus*, and *Escherichia coli*. Furthermore, the analysis illuminates a distinct cluster of keywords intricately tied to microbiological processes. These encompass a spectrum of terms, such as growth, contamination, dynamics, biodegradation, removal, and reduction, unveiling the intricate web of activities that govern microbiological interactions within water systems. The presence of these keywords underscores the complexity and diversity of microbial processes at play in aquatic environments. A notable aspect of the keyword landscape is the prominence of terms related to research targets, highlighting the multifaceted nature of investigations within water microbiology. Key subjects such as health, risk assessment, water quality, and the security of water supply form a significant part of the identified keywords. This emphasis on research targets not only reflects the breadth of topics encompassed by water microbiology but also emphasizes the critical role this field plays in

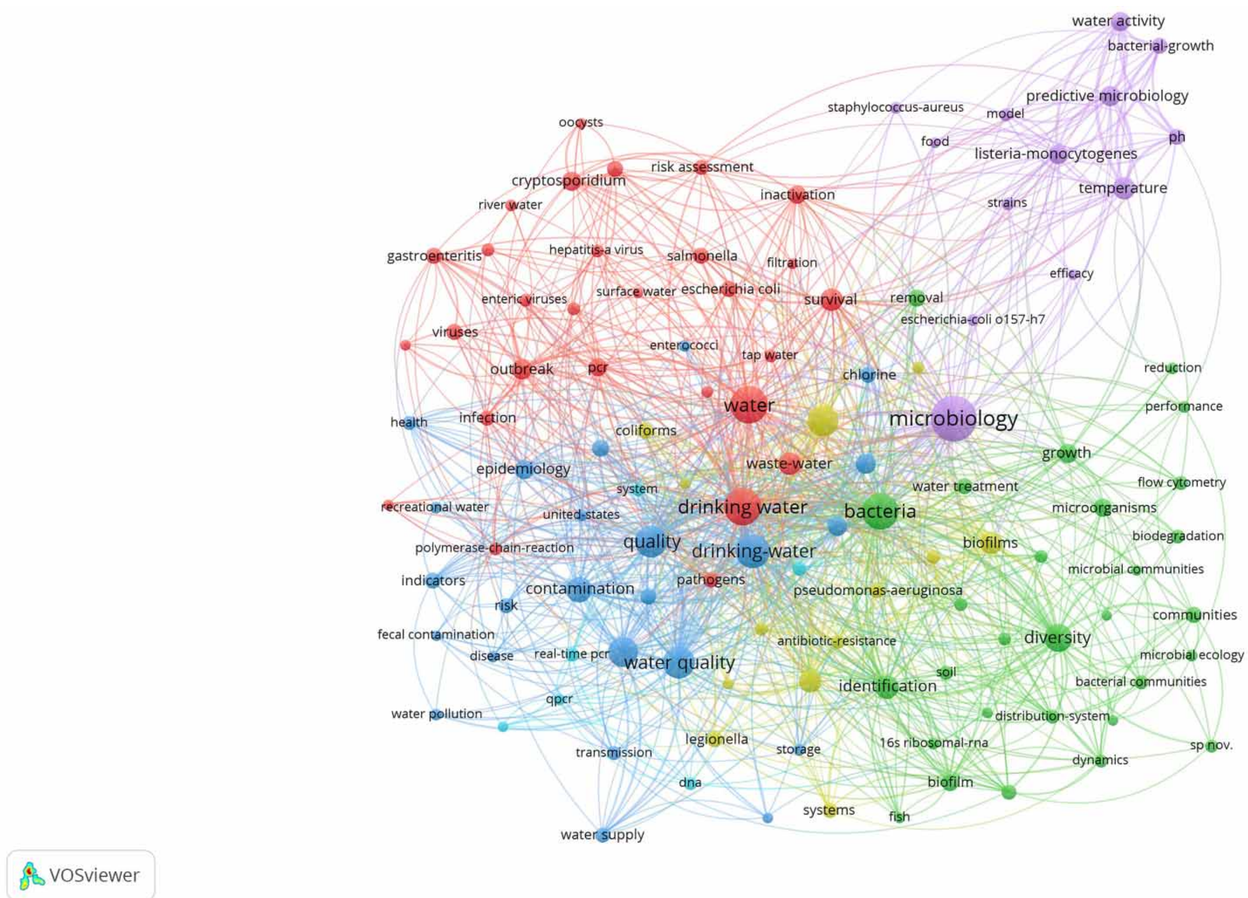


Figure 1 | Thematic keyword clusters unveiled. VOSviewer identifies thematic clusters through the analysis of keyword co-occurrence. The colors represent distinct thematic groups formed by frequently associated keywords.

addressing broader concerns related to public health, environmental safety, and sustainable water management. In essence, the diverse array of keywords presented in Figure 1 paints a vivid picture of the rich and multifaceted landscape within the realm of water microbiology. Beyond the exploration of microbiological species and processes, these keywords delve into specific research endeavors, unveiling the far-reaching implications of microbiology on various aspects of our lives, from the health of ecosystems to the safety of our water supply. This comprehensive understanding is pivotal in guiding future research initiatives, fostering advancements in knowledge, and addressing the myriad challenges associated with water microbiology in a holistic manner.

Figure 2 provides a comprehensive overview of the primary organizations actively engaged in the field of water microbiology. Through a detailed analysis, several institutions emerge as central players in shaping the landscape of water microbiology research. Notably, Delft University of Technology, Michigan State University (MSU), University of Pretoria (UP), and the U.S. Environmental Protection Agency (U.S. EPA) stand out as pivotal contributors to advancements in this field. Beyond these core institutions, a diverse range of entities also plays a significant role in the realm of water microbiology. Institutions such as the University of Helsinki, Medical University of Vienna (MedUni Vienna), University of Calgary, Chinese Academy of Sciences (CAS), The University of Texas at Austin, University of Colorado, and Cornell University all contribute substantially to the collective effort in advancing water microbiology research. In addition to the main institutions shown in the figure, we should also specifically mention the University of North Carolina (contributing nine articles) and the University of Arizona (contributing six articles), which also deserve consideration. This analysis dispels the notion that the pursuit of knowledge in this field is confined to a select a few prestigious universities like Harvard or Stanford. Instead, it underscores the truly global nature of water microbiology research, with numerous institutions worldwide actively engaged in collaborative efforts. The collaboration among these diverse institutions is indicative of a concerted global effort to deepen our understanding of water microbiology. This cooperative approach, involving institutions across different continents, highlights the interdisciplinary and interconnected nature of research in this field. By pooling their expertise and resources, these institutions contribute to a more holistic comprehension of water microbiology, thereby benefiting society at large. The significance of this collaborative effort is underscored by the collective impact of institutions working in tandem to unravel the complexities of water microbiology, ultimately contributing to advancements in scientific knowledge and the betterment of water-related practices.

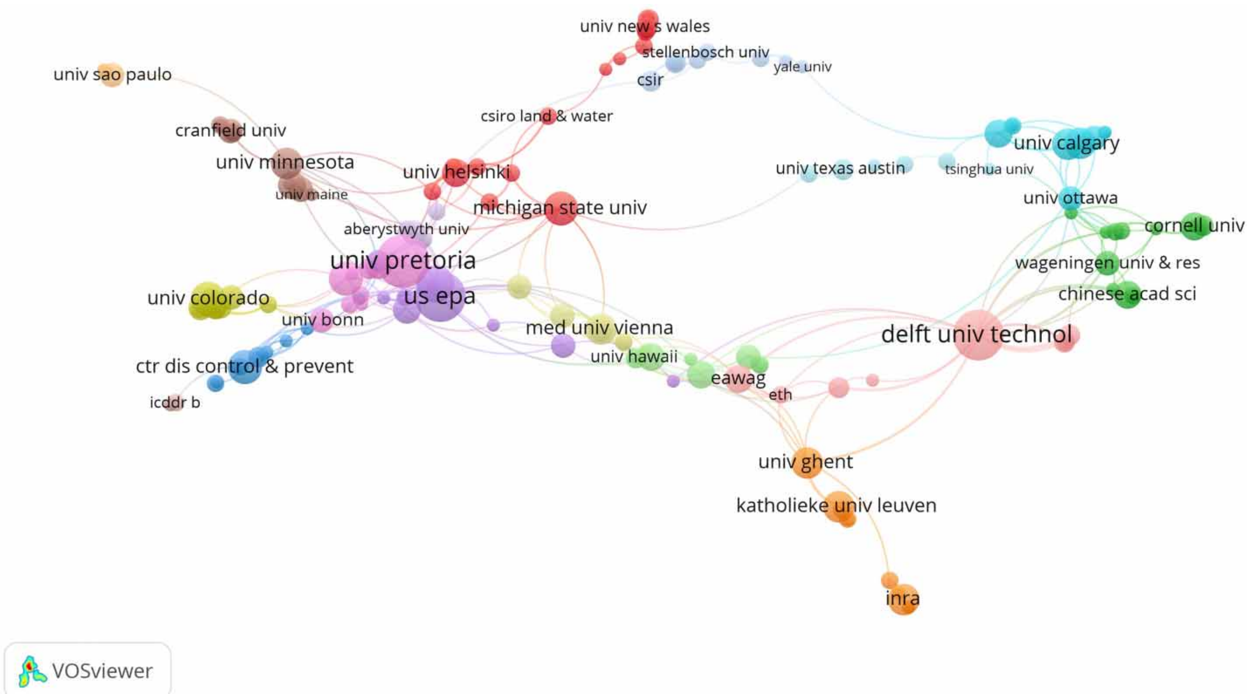


Figure 2 | Collaboration networks, pinpointing thematic clusters among organizations. The colors within these networks signify diverse collaborative clusters among connected institutions.

In Figure 3, a comprehensive depiction of the primary countries or regions actively engaged in the field of water microbiology unfolds, revealing a diverse and globally distributed landscape of research endeavors. Notably, the United States and the United Kingdom emerged as pivotal players, assuming central roles in the advancement of water microbiology studies. Beyond these key contributors, a multitude of countries, including Brazil, Canada, China, Mexico, Finland, Spain, France, Netherlands, Australia, and South Africa, feature prominently as significant players in the ongoing exploration of water microbiology. The prominence of both developed and developing nations in this analysis underscores the collaborative and inclusive nature of research within the water microbiology field. While the United States and the United Kingdom showcase their research prowess, it is equally noteworthy that countries such as Brazil, China, Mexico, and South Africa actively contribute to the collective understanding of water microbiology. This collaborative effort transcends geographical and developmental boundaries, emphasizing the shared commitment to advancing knowledge in this vital field. The involvement of a diverse array of countries in water microbiology research signifies a global collaboration that goes beyond traditional distinctions between developed and developing nations. These findings highlight the mutual engagement and knowledge exchange among nations, collectively contributing to the comprehensive understanding of water microbiology. This collaborative ethos not only enriches the research landscape but also underscores the shared responsibility of the global community in addressing the challenges and complexities associated with water microbiology. As we delve into the intricacies of Figure 3, it becomes evident that the collaborative spirit among countries, irrespective of their developmental status, plays a pivotal role in advancing water microbiology research on a global scale. This shared commitment not only fosters a more inclusive and holistic approach to understanding water microbiology but also holds the potential to yield solutions and innovations that can benefit diverse communities worldwide.

4. DISCUSSION

4.1. Microbial diversity in water environments: an overview

In the expansive realms of rivers, lakes, and seas, thriving within aqueous landscapes, highly diverse and intricate microbial communities form a rich tapestry (Roth Rosenberg *et al.* 2021). This intricate tapestry comprises an extensive array of various microorganisms, each playing a unique and vital role in shaping the dynamic ecosystems of aquatic environments (Lauro

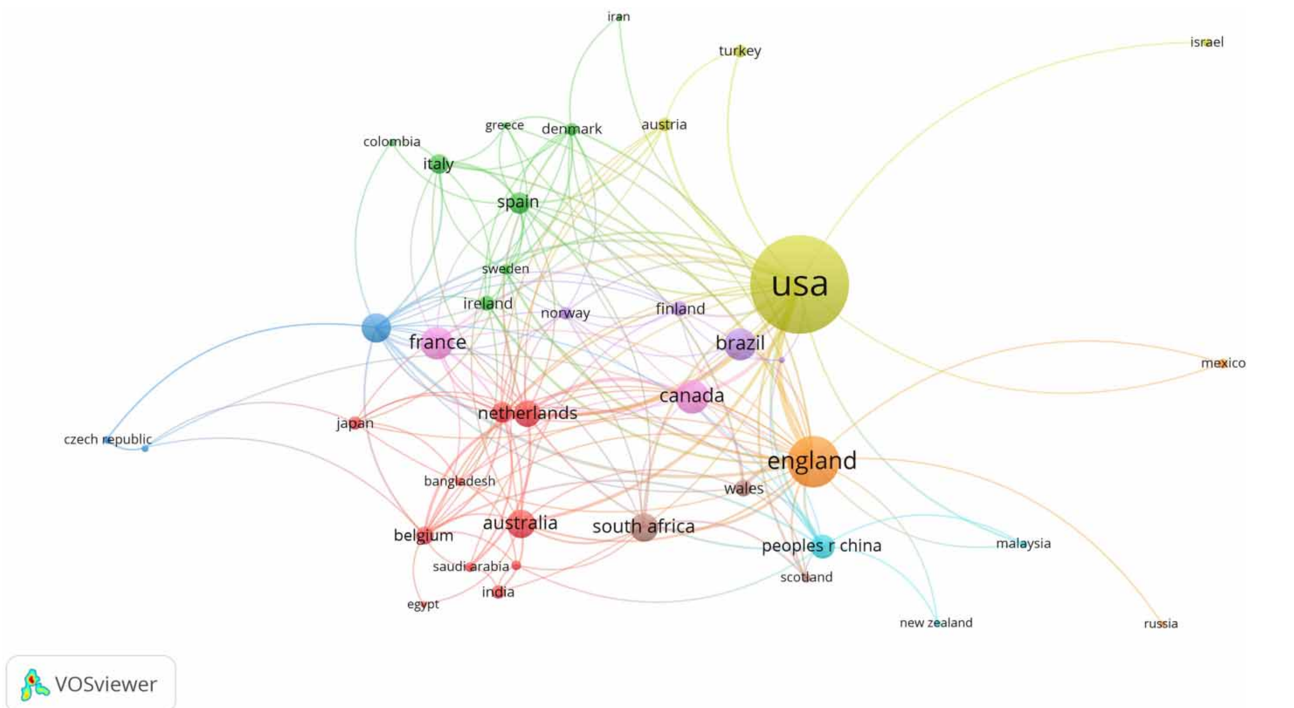


Figure 3 | Collaborative network analysis to identify thematic clusters among different countries and regions. The colors in these networks signify diverse collaborative clusters connecting different countries and regions.

et al. 2009). From the flowing waters of rivers to the vast expanses of lakes and the boundless depths of seas, these microbial communities contribute significantly to the complex web of life that defines the aquatic realm (Karl 2007). This paper discusses main categories such as bacteria, fungi, protozoa, and viruses (Ashbolt 2015).

(1) Bacteria

Table 1 shows a compilation showcasing key bacteria and their respective roles in the field of water microbiology. In the intricate ecosystems of aquatic environments, a diverse array of bacteria, encompassing notable species such as *P. aeruginosa*, *S. aureus*, *E. coli*, *Shewanella oneidensis*, *Bacillus halodurans*, and *Comamonas testosteroni*, thrive. These bacteria coexist within water bodies, forming a dynamic microbial community that extends beyond its ecological implications to potentially pose challenges to environmental integrity and public health. *Shewanella oneidensis*, with its unique characteristics and significant role in microbial communities, particularly stands out amidst this rich bacterial tapestry. *P. aeruginosa*, *S. aureus*, and *E. coli*, well-known bacterial species, contribute to the intricate dynamics of aquatic environments. Their presence, alongside *Shewanella oneidensis*, underscores the multifaceted interactions and dependencies within water bodies. *Legionella pneumophila* is closely linked to water quality and human health, as poor water quality can facilitate bacterial proliferation and increase the risk of Legionellosis, a serious respiratory illness. *B. halodurans*, known for its adaptability to saline environments, and *C. testosteroni*, distinguished by its diverse metabolic capabilities, further enrich the microbial landscape within aquatic ecosystems. This diverse congregation of bacteria not only contributes to the complexity of microbial interactions in water bodies but also represents a potential reservoir of waterborne pathogens. The implications of such microbial diversity extend beyond environmental considerations to public health concerns. The inclusion of these bacteria in the discussion emphasizes the need for comprehensive studies to unravel the intricate dynamics at play within aquatic ecosystems. Assessing the potential impact of this diverse microbial community becomes imperative to safeguard environmental integrity and ensure the well-being of human populations that rely on these vital water resources. As we delve deeper into the complexities of microbial diversity in aquatic environments, the interconnected roles of *P. aeruginosa*, *S. aureus*, *E. coli*, *Shewanella oneidensis*, *B. halodurans*, and *C. testosteroni* highlight the importance of a holistic approach in understanding and managing the intricate web of life within water bodies.

(2) Fungi

Among the diverse inhabitants of water bodies, an array of fungi establishes its presence, with notable examples including water molds and blue-green molds (Zaghloul *et al.* 2020). These fungi play a crucial and multifaceted role in the intricate processes of decomposing organic matter within aquatic environments (Grossart *et al.* 2019). The intricate hyphal networks of

Table 1 | A compilation showcasing key bacteria and their respective roles in the field of water microbiology

Bacteria species	Main findings	References
P. aeruginosa	*P. aeruginosa*, a prevalent bacterium in water, plays a significant role in aquatic ecosystems and can have implications for both environmental health and public well-being.	Mena & Gerba (2009) and Serwecińska (2020)
S. aureus	*S. aureus*, a bacteria commonly found in water environments, poses potential risks to both aquatic ecosystems and human health, emphasizing the need for comprehensive water quality assessments.	Harris *et al.* (2012) and Amarasiri *et al.* (2020)
E. coli	*E. coli*, commonly found in water, serves as an indicator of water quality due to its association with fecal contamination and requires removal through human technology.	Hamdany *et al.* (2021)
Shewanella oneidensis	The presence of *Shewanella oneidensis* in water contributes to the reduction of heavy metals, such as Cr(VI).	Ding *et al.* (2014)
B. halodurans	In aquatic environments, *B. halodurans* can fulfill diverse roles, including functions such as repairing cracks in cement.	Zhang *et al.* (2019)
L. pneumophila	The relationship between *L. pneumophila* and water quality is crucial for accurate detection, as water quality variables like total organic carbon and heterotrophic bacteria significantly impact the performance of detection methods.	Donohue *et al.* (2023)
C. testosteroni	In water environments, *C. testosteroni* may play a role in the biofilm-based biodegradation process of 3-chloroaniline.	Wu *et al.* (2015)

water molds, for instance, facilitate the breakdown of complex organic compounds, contributing to nutrient cycling and promoting the recycling of essential elements (Guhra *et al.* 2022). Similarly, blue-green molds, known for their diverse enzymatic capabilities, engage in the degradation of organic materials, further influencing the dynamics of nutrient availability (Alegbeleye *et al.* 2022).

The involvement of these fungal organisms extends beyond mere decomposition; their activities actively contribute to the maintenance of the delicate ecological balance inherent in aquatic ecosystems (Bull *et al.* 2000). By participating in the breakdown of organic matter, fungi release nutrients back into the water, fostering a nutrient-rich environment that supports the growth of other aquatic organisms (Knicker 2004). Additionally, the interactions between fungi and other microorganisms contribute to the overall biodiversity and stability of aquatic ecosystems (Ratzke *et al.* 2020).

In recognizing the multifaceted contributions of water molds and blue-green molds, it becomes evident that these fungi are integral components of the intricate web of life within water bodies (Corning 1995). Their ecological roles extend beyond decomposition, shaping the nutrient cycling, biodiversity, and overall health of aquatic environments (Benbow *et al.* 2019). The intricate dance of these fungal organisms underscores the interconnected nature of life in water bodies and emphasizes the importance of studying their contributions for a comprehensive understanding of aquatic ecosystems (Celermajer *et al.* 2020).

(3) Protozoa

At the heart of the intricate aquatic food chain lies the crucial presence of protozoa and microzooplankton, two groups of microorganisms whose roles extend far beyond their microscopic size (Kazmi *et al.* 2022). These organisms, though often overlooked, play a pivotal role in the dynamic tapestry of aquatic ecosystems, contributing to the delicate balance that defines the interactions and dependencies within the broader microbial community (Celermajer *et al.* 2020).

Protozoa, unicellular eukaryotic organisms, and microzooplankton, tiny zooplankton comprising various microscopic animals, collectively constitute a vital link in the food web. Their activities encompass predation of bacteria, algae, and other small organisms, thereby influencing the abundance and distribution of these microorganisms. This predation not only regulates population dynamics within the microbial community but also has cascading effects on higher trophic levels, including small fish and other invertebrates (Polazzo *et al.* 2022).

Moreover, the nutrient cycling facilitated by protozoa and microzooplankton is indispensable for maintaining the health and productivity of aquatic ecosystems. Through their feeding activities, these microorganisms release essential nutrients back into the water, contributing to the availability of nutrients for primary producers like algae. This, in turn, influences the entire food web, shaping the distribution and abundance of organisms at various trophic levels (Zhu *et al.* 2023).

The intricate dynamics established by protozoa and microzooplankton extend beyond their immediate ecological functions. Their interactions with other microorganisms, including bacteria and phytoplankton, create a web of dependencies that further shape the overall structure and resilience of aquatic ecosystems. Understanding the multifaceted roles of protozoa and microzooplankton is not only key to comprehending the complexities within these ecosystems but also underscores their significance in sustaining the overall health and functionality of aquatic environments (Sweat *et al.* 2021).

(4) Viruses

In the vast expanse of aquatic environments, the notable presence of waterborne viruses adds an additional layer of complexity to the intricate web of microbial interactions (Garner *et al.* 2021). These viruses, though microscopic in size, wield significant influence due to their potential to exert diverse effects on both aquatic organisms and human health (Zhang *et al.* 2022). The dynamic nature of these interactions underscores the multifaceted role that waterborne viruses play in shaping the delicate balance within water bodies (Thakur & Kumar 2023).

Waterborne viruses, often originating from various sources such as human and animal waste, agricultural runoff, or other contaminated sources, can affect the health and vitality of aquatic ecosystems. Their impact on aquatic organisms ranges from altering the behavior and physiology of microorganisms to influencing the health of fish and other aquatic life forms. The intricate relationships between viruses and their host organisms contribute to the overall biodiversity and stability of the aquatic environment (Harrison *et al.* 2019).

Furthermore, the potential transmission of waterborne viruses to humans through contaminated water sources emphasizes the interconnectedness of aquatic ecosystems with public health. Contaminated water can serve as a pathway for the spread of waterborne diseases, highlighting the importance of understanding the dynamics of viral presence in water bodies. The complex interplay between waterborne viruses, aquatic organisms, and human health necessitates a comprehensive approach to studying and monitoring these interactions (Huang *et al.* 2023).

As we delve deeper into the intricacies of waterborne viruses within aquatic environments, it becomes apparent that their presence is not merely a biological phenomenon but a critical factor in the broader ecological and public health context. Research endeavors aimed at elucidating the mechanisms of viral influence and developing strategies for mitigating potential risks are imperative for safeguarding the integrity of aquatic ecosystems and ensuring the well-being of human populations that rely on these vital water resources (Wikumpriya *et al.* 2023).

4.2. Beyond boundaries: big data and machine learning reshaping water microbiology

In the contemporary landscape, the rapid and remarkable evolution of big data and machine learning has transcended technological boundaries. Their applications have permeated diverse domains, spanning from the revolutionary implementation of autonomous driving technology to the sophisticated prediction of biological species distribution (Chen & Ding 2022) and the nuanced assessment of educational outcomes (Chen & Ding 2023a, b, c). As we gaze into the future, it becomes increasingly conceivable that the intricate field of water microbiology could reap substantial benefits from the seamless integration of big data and machine learning (Wheatley *et al.* 2020).

A compelling application of this integration revolves around the creation of an extensive database, a repository of knowledge encapsulating information about the types and concentrations of microorganisms thriving in water bodies globally. Expanding its scope, this comprehensive database could also incorporate data on the concentrations of pollutants, including hazardous heavy metals known to pose severe threats to human health. This expansive dataset forms the foundation for the development of a sophisticated machine-learning model, a complex black-box system adept at predicting the timing and locations of potential water pollution outbreaks (Deng *et al.* 2021).

The potential of this predictive model for the field of water microbiology is immense, offering policy makers and researchers an unprecedented ability to anticipate and prepare for pollution outbreaks with unparalleled accuracy. Armed with this invaluable information, policy makers can strategically plan and execute targeted preventive measures, thereby safeguarding human life and well-being. The integration of big data and machine learning into water microbiology not only presents an innovative and forward-thinking approach to pollution prevention but also underscores the pivotal role of proactive strategies in environmental protection and public health (Prescott *et al.* 2021).

Envisioning the future of water microbiology, we see a harmonious synergy between cutting-edge technologies and the intricate dynamics of microbial ecosystems. By harnessing the power of big data and machine learning, we stand at the cusp of a new era marked by precision in predicting, preventing, and mitigating waterborne health threats. This visionary integration holds the promise of contributing to a safer and more sustainable coexistence between humanity and the aquatic environment, underlining the transformative potential of scientific advancements in shaping the future of water research and management (Herrfahrdt-Pähle *et al.* 2020).

5. CONCLUSION

Based on the bibliographic method, this study delves into the diverse microbial communities thriving in aquatic environments, creating a rich tapestry that shapes the dynamic ecosystems of rivers, lakes, and seas. Examining bacteria, fungi, protozoa, and viruses, the research highlights their intricate roles and potential implications for environmental and public health. Notable bacterial species like *P. aeruginosa*, *S. aureus*, *E. coli*, *Shewanella oneidensis*, *B. halodurans*, *L. pneumophila*, and *C. testosteroni* are explored, emphasizing the complex microbial interactions within water bodies. Fungi, protozoa, and microzooplankton contribute to the delicate ecological balance, influencing nutrient cycling and the overall dynamics of aquatic ecosystems. The study acknowledges the complexity introduced by waterborne viruses, impacting both aquatic organisms and human health. Looking ahead, the integration of big data and machine learning emerges as a transformative avenue, promising precise anticipation and the prevention of water pollution outbreaks. Overall, this research provides crucial insights for policymakers and researchers, emphasizing the intricate relationship between water quality, microorganisms, and human health in aquatic environments.

DATA AVAILABILITY STATEMENT

All relevant data are included in the paper or its Supplementary Information.

CONFLICT OF INTEREST

The authors declare there is no conflict.

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First received 22 May 2024; accepted in revised form 22 September 2024. Available online 28 September 2024