Editorial: Wastewater and microbial contamination of water courses

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Editorial on the Research Topic
Wastewater and microbial contamination of water courses

1 Introduction

Water is a vital component of the environment and essential for human survival on Earth. It is expected that global water usage will increase by 55% from 2000 to 2050, primarily due to increased domestic consumption (Osei-Owusu et al., 2023). As the demand for freshwater continues to grow, concerns about both its quantity and quality are increasingly becoming central to efforts to address water scarcity (Saxena and Bhattacharya, 2024). The United Nations has declared access to safe water for home and personal use as a fundamental human right (Kandjou and Nkwe, 2024). However, nearly 1 billion people receive their drinking water from an intermittent water supply (IWS), which is subject to persistent interruptions and often brings with it microbial contamination. The prevalence of IWS is expected to grow owing to factors such as urbanization, water shortages driven by climate change, and postponed infrastructure investments (Bivins et al., 2021). Microbial contamination in water is a significant global health concern that demands urgent attention. Unsanitary and irregular practices contribute to the introduction of microbial pollutants such as algae, bacteria, fungi, protozoa, and viruses into the water supply. Primary sources of waterborne pathogens include the disposal of fecal matter, industrial runoff, hospital waste, and other organic materials like manure and household waste. These pathogens can cause a range of illnesses from mild symptoms like fever, headaches, and diarrhea, to severe diseases such as cholera, typhoid, polio, and even cancer following the consumption of contaminated water (Rani et al., 2024).

Motivated by the critical necessity to monitor and eliminate microbial contamination in water sources, this Research Topic, titled "*Wastewater and microbial contamination of water courses*," seeks to explore urgent issues and advocate for effective strategies and policies.

2 An overview of the Research Topic

For this specific Research Topic, we have received numerous review and research papers. Each submission has been subject to a thorough peer-review process, resulting in the selection of eight original research and review papers that concentrate on different aspects of microbial contamination in water. The studies presented in this Research Topic cover the following themes:

Various human activities, including the discharge of wastewater, contribute to the introduction of microbial contaminants into aquatic environments. The detection of these microbes are crucial for assessing water quality and the potential health risks associated with waterborne pathogens. Such data are essential for informing and shaping effective environmental policies and management strategies to safeguard public health and maintain ecological balance. The study by Fluke et al. investigated how riverbed sediments affect the spatiotemporal variability of *E. coli* in the Rio Grande near Albuquerque, New Mexico. It finds that fine sediments downstream enhance E. coli survival, significantly affecting urban areas. High *E. coli* concentrations in downstream sediments correlate with increased loads in river water, leading to frequent water quality standard violations. The study suggests incorporating sediment management in strategies aimed at controlling microbial pollution in urban waterways to effectively address public health risks associated with waterborne pathogens. Another study by Brumfield et al. utilized metagenomic sequencing and quantitative real-time PCR (qPCR) to assess fecal pollution in an urban watershed. Traditional monitoring using culture methods only targets specific fecal indicator bacteria (FIB) like *E. coli* and *enterococci*, offering limited taxonomic data. This study integrates host-associated qPCR and metagenomic DNA sequencing with traditional methods to enhance understanding of microbial communities and pollution sources in an urban watershed. After rainfall, significant increases in FIB, enteric microorganisms, and antibiotic resistance genes were observed, demonstrating the effectiveness of a multi-assay approach in identifying diverse sources of fecal contamination. An investigation conducted by Arreola-Serrano et al. quantifies pollutants discharged into the Southern California Bight from Tijuana and Rosarito over 2011–2020. It reveals that only 53% of water samples met Mexican water quality standards, with issues primarily related to high levels of fecal coliforms, total suspended solids, and chemical and biochemical oxygen demands. The study emphasizes the urgent need for improved wastewater management and to include citizen participation and develop learning among the political community to embrace water management processes.

Monitoring microbial populations in water sources is a critical practice that aids in ensuring water safety and public health. By regularly assessing the levels and types of microbes, such as bacteria and viruses, authorities can prevent potential outbreaks of waterborne diseases. Furthermore, this data helps in evaluating the effectiveness of water treatment processes and in making informed decisions about water management practices. De Lorenzi et al. examines the bacterial community in the Lambro River, Italy, using 16S rRNA gene analysis. Findings show a decrease in microbial diversity as the river flows through urban areas, likely due to chemical or physical contaminants selectively impacting bacterial species. Additionally, agricultural regions showed a significant increase in *Bacteroidetes*, indicative of fecal contamination. However, no markers specific to human, dog, cat, cattle, or pig waste were detected, except for a suspected case of swine contamination in a less populated area. This suggests efficient urban wastewater treatment, as no human fecal pollution markers were found. Galvão et al. assessed the potential contamination of SARS-CoV-2 in environmental waters and wastewaters in the Algarve region, Southern Portugal. Despite high fecal contamination levels, SARS-CoV-2 was not detected in surface waters or treated wastewater, indicating effective removal by wastewater treatment processes. The virus was found in untreated sewage on several occasions, with the highest viral load recorded at Faro-Aeroporto WWTP during a peak in regional COVID-19 cases. This study highlights the effectiveness of wastewater treatments and the importance of continuous monitoring to assess public health risks. Mbang Tambe et al. conducted a study in Northern South Africa from January 2021 to May 2022, used wastewater-based genomic surveillance to analyze 487 samples for SARS-CoV-2 RNA. Using qRT-PCR and whole genome sequencing, 75% of samples tested positive, predominantly for the Delta and Omicron variants, identified as early as January and February 2021. Notably, the study highlighted the early detection of these variants compared to other regional reports, underscoring the utility of population-based genomic surveillance over individual testing. This approach also facilitates tracking viral evolution, enhancing public health responses, and guiding vaccine development strategies. Another study by de Ponte Rodrigues et al. investigated dissolved organic matter (DOM) in freshwater ecosystems using fluorescence spectroscopy, particularly in the Paris metropolitan area, including two watercourses, two stormwater outlets, and a wastewater treatment plant effluent. The study aimed to characterize DOM fluorescence components, assess the impact of local rainfall, and identify potential microbial contamination signatures. Using a PARAFAC model with specific fluorescence indices, protein-like components C6 (280/352 nm) and C7 (305/340 nm) were linked to microbial contamination. Notably, C6 levels were higher during wet weather, correlating positively with fecal indicator bacteria (FIB). This suggests that monitoring C6 could enhance detection and management of fecal contamination in urban rivers. In addition, a study by Cutrupi et al. proposes a global model for antimicrobial resistance (AMR) surveillance in aquatic environments, stressing the urgency due to AMR's widespread environmental dissemination. Recognizing water bodies as significant pathways for AMR spread, the paper underscores the need for improved monitoring systems integrating sustainability, enhancing global coordination, and extending monitoring capabilities. It suggests establishing centralized labs and creating a technical committee to develop policies and manage data effectively. This approach aims to standardize methods, ensuring consistent and reliable data crucial for tackling the global threat of AMR in water resources effectively.

In conclusion, this Research Topic (RT) has significantly advanced our understanding of microbial contamination in water sources, highlighting innovative approaches and critical findings that reshape our management and policy strategies. The collective

contributions of the selected studies not only deepen our grasp of microbial dynamics in diverse aquatic environments but also reinforce the urgency of sustained, multidisciplinary efforts in monitoring and mitigation. By integrating cutting-edge research and practical solutions, this RT offers invaluable perspectives that enhance our ability to safeguard public health and preserve ecological integrity. The insights derived here will undoubtedly influence future research directions and foster improved water quality management practices globally.

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