



Editorial: Functional Diversity of Aquatic Microorganisms and Their Roles in Water Quality

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Editorial on the Research Topic

Functional Diversity of Aquatic Microorganisms and Their Roles in Water Quality

As an important component of aquatic environments, microorganisms are functionally diverse and play a crucial role in water quality and human health. Through a wide spectrum of biogeochemical processes, they can improve the sustainability and stability of aquatic ecosystems and positively influence water quality (Zinger et al., 2012). For example, many aquatic microorganisms are capable of removing chemical hazards such as heavy metals (Dixit et al., 2015) and petroleum (Zaki et al., 2015), and of catalyzing wastewater treatment processes (Daims et al., 2006). Meanwhile, contamination of agricultural, recreational, and drinking water by human pathogens is of public health concern due to the potential for transmission to humans directly (e.g., through drinking, dermal contact) and indirectly (e.g., through the use of contaminated water to irrigate crops) (Egli et al., 2002). Thus, characterizing the functional diversity of aquatic microorganisms and understanding their impact on water environments represent a key research need. However, despite the importance, aquatic microorganisms in many regions in the world are understudied. As a result, affordable, targeted tools for assessing and managing water quality are limited. This Research Topic aimed to improve the understanding of the distribution, structure, and function of aquatic microbial populations with a specific focus on potential approaches for improving the assessment and management of water quality. We received contributions across a wide range of topics, including microbial dynamics in wastewater and surface water, environmental factors driving the distribution of foodborne pathogens in water, and novel approaches to water quality monitoring and microbial risk assessment. Here, we briefly summarize these contributions by their relevance to three water types—wastewater, agricultural water, and recreational water.

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WASTEWATER

Wastewater treatment and wastewater reuse is essential to the global demand for water in the era of climate change (Yadav et al., 2020). Microorganisms are responsible for biological wastewater treatment processes such as removal of organic matter, toxic metals, odors, nutrients including nitrogen and phosphorus (Wagner et al., 2002; Ferrera and Sanchez, 2016). Therefore, knowledge on the structure and functions of microbial communities and populations in wastewater are crucial for the development and optimization of wastewater treatment systems. Huang et al.

investigated temporal and spatial changes in composition and putative function of bacterial communities in wastewater stabilization ponds (WSP), a commonly used system to treat municipal wastewater in the Canadian Arctic. They identified temperature as a major factor influencing the bacterial community structure and potential removal of nutrients in the WSPs. In a preliminary study, Cruz et al. examined differences in the composition and richness of bacterial communities in treated and untreated wastewater from different sources (e.g., hospitals, fish farming sites, sewage effluents, and surface waters) in Sri Lanka and Philippines.

AGRICULTURAL WATER

Given the central role of water in food production, ensuring and monitoring agricultural water is essential to the maintenance of a safe and secure food supply (Molden et al., 2010). However, contamination of agricultural water by fecal contaminants and human pathogens in agricultural water presents a key human health risk (Rodrigues et al., 2019). To effectively manage health risks associated with contamination of agricultural water, it is important to understand factors that are associated with fecal and pathogen contamination. Murphy et al. showed that weather, especially temperature, was strongly associated with *Salmonella* contamination of north and South Florida agricultural water sources. Bihn et al. found that water specific conductance, pH, and turbidity were slightly associated with fecal indicator bacteria levels in NY and TN, USA and highlighted the importance of using multiple data types (e.g., bacterial, physicochemical) when assessing irrigation water quality. Belias et al. developed machine learning models using water quality parameters, surrounding land-use, weather conditions, and sampling site characteristics as predictors to predict pathogen presence in canals used to source water for produce production in the Southwestern US agricultural water. Belias et al. findings suggest that predictive models could supplement or provide an alternative to current approaches for monitoring agricultural water quality. Smith et al. detected stable spatial and temporal changes in phytoplankton functional groups in two agricultural irrigation ponds in Maryland and found that water quality parameters were associated with certain phytoplankton functional groups.

RECREATIONAL WATER

Exposure to contaminated recreational water represents another pathway for human pathogen transmission (Fewtrell and Kay,

2015). While understanding these infectious agents of concern, including fecal indicator bacteria in recreational water is of great importance, additional information on factors associated with pathogen contamination of recreational waterways and tools for assessing contamination is needed. By analyzing water samples collected along an urban-rural gradient, Weller et al. found that temperature, nutrient, sediment levels, and land use are key factors associated with the levels of fecal indicator bacteria in Upstate New York streams used for both agricultural and recreation. Fernández-Baca et al. developed a rapid, in-field workflow for detecting fecal indicator bacteria in recreation water that takes substantially less time compared to culture-based assays. Tools like that developed by Fernández-Baca et al. can facilitate risk management (e.g., opening and closing of beaches), by providing decision-makers with key data faster. Brooks and Rose compared models for evaluating the long-term persistence of enteric markers in sewage spiked river water and found that log-linear models overestimated the persistence of enteric markers and suggested that best fit models with dynamic decay rates in water quality models are more accurate in evaluating the decay of enteric markers.

CONCLUDING REMARKS

Over the last several decades, efforts in understanding water quality have moved beyond its physical and chemical attributes to biological attributes (Fewtrell et al., 2001). The growing interests in the role of microorganisms in water quality is well reflected by the large number of contributions received in this Research Topic. It is exciting to see active research characterizing the composition, function, diversity of microbial communities, populations, and pathogens in water across different types including wastewater, agricultural water, and recreational water, as well as developing useful tools for water quality monitoring. This Research Topic has provided insights and solutions for both favorable and unfavorable consequences of water quality influenced by microorganisms. With the emerging technologies (e.g., high-throughput sequencing) in profiling microorganisms and broad application of deep learning in the field of environmental microbiology, we are optimistic to a new level of water management and public health improvement.

AUTHOR CONTRIBUTIONS

All authors have made a substantial contribution in writing and revising the editorial. All authors contributed to the article and approved the submitted version.

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