Journal of Environmental Quality SPECIAL SECTION

MICROBIAL WATER QUALITY—MONITORING AND MODELING

# Microbial Water Quality: Monitoring and Modeling

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## Abstract

Microbial water quality lies in the nexus of human, animal, and environmental health. Multidisciplinary efforts are under way to understand how microbial water quality can be monitored, predicted, and managed. This special collection of papers in the *Journal of Environmental Quality* was inspired by the idea of creating a special section containing the panoramic view of advances and challenges in the arena of microbial water quality research. It addresses various facets of health-related microorganism release, transport, and survival in the environment. The papers analyze the spatiotemporal variability of microbial water quality, selection of predictors of the spatiotemporal variations, the role of bottom sediments and biofilms, correlations between concentrations of indicator and pathogenic organisms and the role for risk assessment techniques, use of molecular markers, subsurface microbial transport as related to microbial water quality, antibiotic resistance, real-time monitoring and nowcasting, watershed scale modeling, and monitoring design. Both authors and editors represent international experience in the field. The findings underscore the challenges of observing and understanding microbial water quality; they also suggest promising research directions for improving the knowledge base needed to protect and improve our water sources.

## Core Ideas

- Environmental factors are known to control microbial water quality in natural systems.
- This collection of papers presents a panoramic view of microbial water quality research.
- With this special section, the editors hope to stimulate interdisciplinary efforts in the field.

A STAGGERING NUMBER of people in the world are becoming ill and dying every year due to the microbial contamination of waters used for drinking, recreation, irrigation, and aquaculture (Cabral, 2010; Pandey et al., 2014). Detection, monitoring, prediction, and management of pathogenic contamination of water sources remain the focus of considerable research effort.

Microbial water quality is a measure of the microbiological conditions of water related to human and animal health requirements. Research into microbial water quality addresses it as a multifaceted issue. It involves selection and evaluation of microbial water quality metrics, which currently include the prevalence and concentrations of pathogenic microorganisms, microbial indicators of potential pathogen contamination, and certain genetic material, such as Shiga toxin-related genes and antibiotic resistance genes. Other important aspects of this research include identifying the sources of microorganisms that are detected to derive microbial water quality metrics and elucidating processes that control the release, transport, and survival of organisms and genetic material that are of interest for microbiological conditions of water.

Monitoring and modeling are intertwined activities in microbial water quality research and applications. Substantial advances have been made in these areas (Fujioka et al., 2015; Oliver et al., 2016; Bentzon-Tilia et al., 2016; Lothrop et al., 2018). Yet, many gaps in our knowledge remain. The complexity of microbial populations and their habitats, multiplicity and heterogeneity of transport pathways, multiplicity of controls, and multiscale nature of microbial water quality call for an interdisciplinary research effort to address this public health issue that is of paramount importance.

Environmental factors are known to control microbial water quality in natural systems. Thus, microbial water quality appears to be an organic part of environmental quality in general. This explains the motivation of the *Journal of Environmental Quality* to create and publish a collection of research reports focused on problems and methods in this vibrant and fast-developing field.

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**Abbreviations**: ARG, antibiotic resistance gene.

This special collection focuses mostly on surface water. The 22 papers in this section have been written by an international group of authors from 11 countries. For convenience, we have grouped the content of these papers under 10 subject headings: (i) spatiotemporal variability of microbial water quality, (ii) predictors of spatiotemporal variations, (iii) role of border ecosystems, such as in bottom sediments and biofilms, (iv) correlations between concentrations of indicators and pathogenic organisms and role for risk assessment techniques, (v) molecular markers, (vi) subsurface microbial transport and microbial water quality, (vii) antibiotic resistance, (viii) real-time monitoring and nowcasting, (ix) watershed-scale modeling, and (x) monitoring design. Most of the papers, perhaps not surprisingly, include material relevant to multiple headings. Under each subject heading, we provide a brief introduction of the research topic, along with examples of the research on this topic given in the special collection of papers; we also highlight some research avenues that these papers suggest. An overview of current trends and research needs concludes this introduction.

## Spatiotemporal Variability of Microbial Water Quality

Understanding and quantifying the spatiotemporal variability of microbial water quality are necessary for successful monitoring and management. High spatial variability of microbial water quality metrics is commonly encountered. An example of this is presented in the large baseline study that focuses on fecal indicator organisms and Shiga toxin-related genes across large irrigation districts in California and Washington (Partyka et al., 2018). Median concentrations of generic *Escherichia coli* decreased from May to October in both states. The regulatory threshold for *E. coli* was exceeded, and/or samples containing Shiga toxin-producing *E. coli* were found in about 10% of all samples, while *Salmonella* was detected in about 50% of samples. Microbiological outcomes were highly irrigation district-specific. The authors concluded that the true risk of contamination in irrigation water supplies remains unknown, and monitoring strategy needs to be developed for detecting actual food safety risks.

Observation scale may manifest itself in spatiotemporal variations in the results of microbial water quality monitoring. Spatial scales in microbial water quality studies are most often defined by the order of the stream, the area from which runoff and/or drainage occurs, or in terms of the plot–field–watershed hierarchical sequence. Temporal scales are defined either by the duration of water-sample collection or by the duration of the time interval between water samplings. Change in spatial scale, such as catchment size, was shown to affect average concentrations of indicator organisms in agricultural landscapes (Harmel et al., 2010). A regional study toward this end was done by Rafi et al. (2018), who analyzed *E. coli* data from 743 monitoring stations in the Central Great Plains, Cross Timbers, and South Central Plains ecoregions of Texas and Oklahoma. The analysis of data from "all sites," including least-impacted watersheds and those impacted by wastewater outfalls and urban areas, shows a weak negative relationship between *E. coli* concentrations and stream order/watershed size, with *E. coli* generally decreasing with increasing stream order/watershed size.

Observations at coarser scales can reveal emerging patterns or properties that are not detectable at finer scales. Stocker et al. (2018) studied *E. coli* concentration changes in the stream-bottom sediment after high-flow events and reported that growth of the *E. coli* population was pronounced at the stream-reach scale but could be easily missed with the monitoring at the "single-sample" scale.

Rare but strong sources may have a disproportionally strong influence on coarse-scale measurements. On the other hand, dilution effects may be more pronounced at coarser scales. Scale is a factor that needs to be taken into account in the interpretation and application of microbial water quality–monitoring results. Microbial fate and transport parameters for a specific application, for example, planning the mitigation of microbial pollution such as Total Maximum Daily Load, must be derived from monitoring data obtained at the scale similar to the application scale.

Knowledge of the variability of indicator concentrations at fine time scales of minutes, hours, and days is needed to evaluate the uncertainty of the results from a one-off grab sample intended to represent the daily or weekly values. Such variability was studied by Muirhead and Meenken (2018) for baseflow conditions in three New Zealand rivers in summer and winter seasons. The variability of *E. coli* concentrations at the above three time scales increased with time scale and exceeded the laboratory replication variability at all scales. Currently, information on this type of variability remains very scarce. More needs to be learned given the common practice of using a single daily sample to calibrate and evaluate predictive microbial water quality models.

Comprehensive studies have demonstrated the temporal stability of indicator organism patterns across freshwater sources. One example was given in a study of irrigation ponds (Pachepsky et al., 2018). The authors found that *E. coli* concentrations were consistently lower than the pond average in some parts of the ponds and consistently higher in other parts of ponds. Establishing temporal stability in spatial patterns of indicator concentrations can be beneficial for the microbial water quality–monitoring design, as it allows the number of samples to be reduced without compromising the accuracy of evaluating the average indicator concentration across the water body under observation. Interesting questions for future research are uncovering the mechanisms controlling the temporal stability and seeing whether the temporal stability patterns are preserved for several years.

## Predictors of Spatiotemporal Variations

Environmental and management factors can explain a substantial proportion of the variation in microbial water quality (Rochelle-Newall et al., 2016). For example, precipitation is known to be a powerful controller of microbial water quality (Signor et al., 2005), and there are many other controls. Each control can be characterized by several parameters that may serve as microbial water quality predictors. There is often a need to select and compare statistical techniques that can reduce the number of predictors and create more-robust predictive models (Singh et al., 2004; Truchado et al., 2018). One such technique—canonical correlation analysis—was applied as the input-selection procedure for a machine learning model in the work of Gilfillan et al. (2018), aimed at identifying potential drivers of the impairment of microbial water quality using *E. coli* and F+ and somatic bacteriophages as indicators in the mixed-use stream in East Tennessee. The input selection led the authors to the conclusion that *E. coli* impairment is driven by run-off and erosion, whereas bacteriophage detection is inhibited by high levels of coliforms in sediment.

Microbial water quality databases may combine data collected in conditions with different dominant controls. In such cases, different predictors will be influential in different parts of the database, and classification and regression tree-based data analysis methods may be of interest (Mohammed et al., 2018). Also, an improvement in the interpretation of the observed concentration variations can be expected if the spatiotemporal nature of microbial water quality is explicitly taken into account, such as with the use of empirical orthogonal functions (Hong et al., 2018a).

## Role of Bottom Sediments and Other Border Ecosystems

Water columns in all types of water sources are in direct contact with bottom sediment and periphyton that contains large populations of fecal indicator organisms. These organisms can be released during high-flow events and storm-related mixing due to sediment resuspension (Ribolzi et al., 2016; Kim et al., 2017). The base-flow conditions in creeks also appear to be conducive for fecal indicator bacteria release to the water column (Grant et al., 2011), and the release rates can be sufficient to keep *E. coli* concentrations in exceedance of recreation water standards (Park et al., 2017). Release of fecal indicators from the bottom sediment habitat complicates the evaluation of land-based measures taken to improve microbial water quality, yet information about microbial communities of bottom sediments remains scarce. Concentrations of *E. coli* in water and sediments for creeks in California and Iowa were compared by Pandey et al. (2018). They found that streambed *E. coli* concentrations in bed sediment were higher than in water column for both streams.

Sediment *E. coli* populations can grow between high-flow events. The rate of such growth was studied by Stocker et al. (2018) in highly detailed sampling of streambed sediment across the stream reach before and after artificial and natural high-flow events during 1 mo. The authors show that the increase of *E. coli* in sediment across the reach did occur, but this increase was due to high growth rate in several locations with elevated clay and organic matter contents. The remaining sampling locations with sandy texture exhibited a small increase or decrease in *E. coli* concentrations that did not have much effect on the reach-average streambed sediment *E. coli*. Such heterogeneity obviously complicates surveying and monitoring concentrations of microorganisms in streambed sediment. Mass balance–based measurements at the reach scale (Pachepsky et al., 2017) may be more efficient for assessing microbial exchange between bottom sediments and water columns. Also, the role of periphyton in microbial quality water quality waits to be researched.

Other ecosystems bordering water may alter microbial water quality. In irrigated agriculture, biofilms in hydraulic equipment are another medium that is in direct contact with water used in irrigation, produce processing, and household activities. Microbial communities in biofilms can alter the microbial composition of water (Shelton et al., 2014). At a larger scale, riparian zones may serve both as source and sink of pathogens and indicators. It has been noted that contradictions may arise between the goals of keeping pathogens away from irrigation water by removing buffer strips that harbor wildlife populations and preserving water resources from impairment due to runoff and erosion (Crohn and Bianchi, 2008), and these may need to be reconciled.

## Correlations between Concentrations of Indicators and Pathogenic Organisms and Role for Risk Assessment Techniques

Both high and low correlations between fecal indicator bacteria concentrations and concentrations or prevalence of other water quality metrics have been found in the previous studies (e.g., Pachepsky et al., 2016). This special section also presents a variety of results of correlations development. McConnell et al. (2018) observed significant correlations between *E. coli* and antibiotic resistance gene contents in rural watershed in Canada, whereas pathogens were not associated with exceedance of the regulatory threshold in rural areas of the western United States (Partyka et al., 2018).

The absence of correlations between concentrations of pathogens and indicators complicates establishing microbial water quality standards. The regulatory standards for recreational waters were established not by using correlations between pathogens and indicators but rather by using epidemiological studies on the probabilities of enteric illnesses as functions of *E. coli* concentrations in recreational waters. In the absence of such epidemiological studies for other water uses such as irrigation, aquaculture, and so on, using solely fecal indicator concentrations to establish the microbial water quality standards appears to be problematic (Pachepsky et al., 2016). The plausible direction of microbial water quality evaluation consists in applying risk-assessment methodology and assessing the level of public health threat using probabilities rather than rigid numbers of water quality standards. A multinational group of authors (Hamilton et al., 2018) presents an example of how a database suitable for risk assessment can be assembled from various sources and used to generate the probabilistic description of the human health risk associated with the presence of *Cryptosporidium* and *Giardia*. With this approach, the probabilistic description is developed not only for the dose–response relationship but also for the value of the dose itself. Microbial water quality modeling can serve as another source of statistics to treat the dose as a random value (Whelan et al., 2014)

## Molecular Markers

Substantial improvements in understanding site-specific microbial water quality formation can be achieved using various markers to complement data on fecal indicator organisms. Microbial source tracking relies on various genetic markers; environmental transport of the markers can be affected by hydrological conditions, land use specifics, and possibilities of subsurface transport. Nshimyimana et al. (2018) developed a comprehensive example of regional analysis of animal markers to elucidate transport patterns and mechanisms of different types of animal manures for Michigan's Lower Peninsula. The occurrence of bovine and porcine markers were lowest during base flow, highest during snowmelt for porcine, and highest during the summer rains for bovine. Interestingly, bovine and porcine markers varied with land use and land cover but not with the presence or absence of the riparian buffer zone. Streamflow was the strongest predictor of bovine and porcine marker concentrations in snowmelt periods and bovine marker in baseflow, whereas nutrients were the strongest predictors in summer rains. Rieke et al. (2018) provide another instructive example of using molecular markers to understand environmental pathways of pathogens in agroecosystems. The authors report on the use of 16S rRNA gene sequencing to detect pathogenic bacteria in the agriculturally dominated South Fork Iowa River Watershed, Iowa. DNA sequences from water samples were matched with sequences from known pathogens, and the likely transport pathways for specific pathogens were identified. The authors found that *Enterobacter* concentrations in surface waters were influenced mainly by artificial drainage, whereas *Clostridium sensu stricto* was primarily transported to surface waters by runoff. Recreation environments can also benefit from combining the monitoring of fecal indicator bacteria and molecular markers. Nevers et al. (2018) sought to identify sources of microbial contamination and evaluate a short-term management solution to decrease beach closings by deterring gulls. During 2015 (partial) and 2016 (season-long), dogs were used to deter gull presence. Results indicated that gull, dog, and human sources of contamination were present, with gulls being the dominant source. *Escherichia coli* was highly correlated with the number of gulls, the presence of one of the gull markers, and turbidity. Full-season gull deterrence in 2016 resulted in lower *E. coli* concentrations and fewer beach closings.

Further developments in using molecular markers will rely on standardization and cross-validation of markers and related methods. Little is currently known about the prevalence of different serotypes, serogroups, and strains of pathogens in natural waters. This information may be useful in further development of molecular markers. Concentrations of markers reflect not only sources but also microbial transport conditions (García-Aljaro et al., 2017). Using molecular markers to study *E. coli* transport in epikarst in in western Kentucky, Bandy et al. (2018) successfully detected bacteria in a cave and demonstrated that attenuation was greater for a bacterial isolate with high attachment efficiency compared with an isolate known to have low attachment efficiency. The fate and transport of molecular markers continues to be a significant topic to explore in the field of microbial water quality.

## Subsurface Microbial Transport and Microbial Water Quality

Microbial transport in variably saturated subsurface water and groundwater is controlled by hydrological regime, pore arrangement and connectivity, and surface properties of microorganism and soil solids (Gerba et al., 2015). Full saturation of soil with water is conducive to microbial transport, but subsurface travel distances are usually limited. This is illustrated by Weldeyohannes et al. (2018), who applied naturally occurring *E. coli* in secondarily treated wastewater to the soil surface under seasonally changing conditions in central Alberta, Canada. When the vadose zone increased from 0.4 to 0.9 m, *E. coli* levels in the monitoring wells decreased dramatically despite continued high surface application. Interestingly, *E. coli* travel times corresponded to piston flow, indicating that the retention of *E. coli* was affected not by sorption but rather by straining, that is, immobilization in fine dead-end pores.

Surface properties of the porous media can exert strong control on microbial transport if straining is not a leading process. Irreversible attachment was the dominant mechanism of virus retention during transport through saturated sand-packed columns in the work of Sasidharan et al. (2018). The fractions of two viruses under study that still could pass the columns were affected by temperature. Modeling showed that the rate of inactivation in the sand surfaces was much larger than in liquid phase. The difference between the two rates depended on the virus type.

Transport in soils and groundwater apparently should remain a concern if microbial water quality can be compromised by the influx of very small concentrations of suspended microorganisms. Various aspects of this phenomenon were recently discussed in a special section of the *Journal of Environmental Quality* on microbial transport and fate in the subsurface environment (Bradford et al., 2015, and references therein).

## Antibiotic Resistance

Antibiotic resistance genes (ARGs) are not usually referred to in microbial water quality standards, but there is consensus about the potential dangers of their presence (WHO, 2014), prompting fast-growing research on their sources and spatiotemporal variability in waters that can affect human health. In exemplary research, a river system in rural Nova Scotia, Canada, served as natural laboratory for determining ARG sources (McConnell et al., 2018). The authors confirmed the tertiary-level wastewater treatment plant as a point source and land use activities as a nonpoint source. Concentrations of many ARGs remained above detection limits in headwater river samples, which suggested their ubiquitous presence in this watershed in the absence of obvious pollution sources. Rich information on ARG in surface waters can be obtained from the whole genome analysis. Taggar et al. (2018) assessed antimicrobial resistance in *E. coli* recovered from untreated surface-water sources of dairy farms. Their whole-genome analysis of multidrug-resistant isolates identifies multiple ARGs, including blaCMY-2 and blaCTX-M-1, that confer resistance to the critically important extended-spectrum cephalosporins, as well as a variety of plasmids and class 1 integrons.

Elucidating seasonality in ARG generation appears to be essential for designing and implementing ARG monitoring. An instructive example of such seasonality is presented by Son et al. (2018) for two reservoirs in South Korea, which are located near drinking-water treatment plants. The measured total ARG concentrations reached up to $2.5 \times 10^7$ copies mL$^{-1}$. Sulfonamides, β-lactam antibiotics, and tetracycline resistant genes were the most abundant genes. During the August-to-January observation campaign, the highest ARG abundance was observed in January, which was unexpected given the decreased microbial activity due to lower temperatures, limited nutrients, and increased oxygen levels.

Microbial water quality evaluations currently lack metrics related to ARG, and it remains to be seen how the concentrations and prevalence of various antibiotic resistance genes can be used as the microbial water quality characteristics, as well as how it is linked to animal and human health. Several critical questions need to be answered in that respect (Durso and Cook, 2018). We need to find out whether the antibiotic resistance in actual pathogens increases the risk of disease complications or results in higher treatment cost. It is not known if the presence of ARG in fecal indicators signifies increasing risk of ARG transfer to pathogens. Finally, the role of ARG in environments in the emergence of new pathogens is still to be assessed. The current accumulation of information on ARG will lead to the elucidation of environmental factors that drive resistance and eventually may lead to the construction of conceptual models for how resistance emerges and is disseminated (Bengtsson-Palme et al., 2017).

## Real-Time Monitoring and Nowcasting

Real-time monitoring and nowcasting modeling of microbial water quality are most in demand for recreation waters where beach managers encounter the risk of large outbreaks caused by microbial contamination and beach closures. Speeding up microbial analysis of water is a relevant research direction. Gene detection via quantitative polymerase chain reaction provides a faster alternative to traditional growth-based methods for determining concentrations of fecal indicators enterococci and *E. coli* used in recreational water quality standards. Byappanahalli et al. (2018) compare the two methods on a large number of beach-water and river-water samples in Empire, MI. Results from both methods correlated statistically significantly overall but not always at individual locations. Further work may be of interest in order to improve correlations by accounting for site-specific conditions and evaluate the found correlations considering the variability in epidemiological data used to develop the microbial water quality standards.

Nowcasting—forecasting based on current environmental data—is valuable for recreational site management. Applying regressions to relate concentrations of regulated microorganisms to environmental covariates may not necessarily be accurate since regression imposes a specific type of relationship (linear, polynomial, etc.) that may have not enough flexibility to simulate complex natural relationships. Using more flexible machine learning models may be beneficial in this case. This approach is represented by the work of Park et al. (2018), who developed and compared two types of such models—artificial neural network (ANN) and support vector machine—to simulate *E. coli* and enterococci concentrations in waters of beaches of Busan, South Korea. Input variables included tidal level, air and water temperature, solar radiation, wind direction and velocity, precipitation, discharge from the wastewater treatment plant, and suspended solid concentration in beach water. Only precipitation, discharge from the wastewater treatment plant, and wind direction had a significant effect on the predicted concentrations. The two types of models did not differ much in accuracy, but support vector machines provided more explicable results than ANN when sensitivity analysis was applied.

Improvements in prediction accuracy with machine learning do not diminish the need to analyze prediction reliability, which is possible only with additional systematic data accumulation. The search for best inputs for nowcasting should continue in parallel with a comparison of predictive tools. Selection of best inputs is needed for other types of water with regulated microbial water quality, such as irrigation or shellfish production. It is quite possible that the best input choice may be site- and water use-specific.

## Watershed-scale Modeling

Watershed-scale modeling is a powerful instrument for forecasting changes in microbial water quality under diverse environmental and management scenarios (Islam et al., 2018). As K. Kim et al. (2018) note, watershed-scale modeling can help answer such questions as, What are the major microbial sources? What practices contribute to contamination at the receptor location? What land use types influence contamination at the receptor location? Under what conditions do these sources manifest themselves? The authors describe a loosely configured software infrastructure that has been used in microbial source-to-receptor modeling by focusing on animal- and human-impacted mixed-use watersheds. The system automates, as much as possible, the manual process of accessing and retrieving data and completes input data files of the models. The workflow considers land-applied manure from domestic animals; direct shedding (excretion) on undeveloped lands by domestic animals and wildlife; pastureland, cropland, forest, and urban or engineered areas; sources that directly release to streams from leaking septic systems; and shedding by domestic animals directly to streams. Point sources are also simulated. This system is suited to work for data-rich environments. Data-poor environments can still benefit from watershed-scale modeling. The example given by M. Kim et al. (2018) for a watershed in Laos shows how the Soil and Water Assessment Tool (SWAT) model can assess microbial water quality in a watershed experiencing fast-changing land use. Additional flexibility of SWAT is advocated to improve simulations of microbial water quality in tropical landscapes.

The dependence of the variability and uncertainty in microbial concentrations on the temporal scale of data collection (e.g., Muirhead and Meenken, 2018) creates a conundrum for evaluating the performance of environmental microbial fate and transport simulations. In such simulations, both model calibration and validation commonly do not account for the uncertainty of measured values at the scale of simulated values. A single measured and a single simulated concentration value for a day represent, in fact, different temporal scales and should be compared in a statistical sense rather than by direct subtraction to obtain the daily residual. Several measurements within the day should be made if simulations are done with the daily time step. In the absence of such multiple daily measurements, it has been suggested that model performance be evaluated using statistical tests to compare cumulative distribution of residuals (Baffaut and Benson, 2003; Bougeard et al., 2011; Hong et al., 2018b). Much more information is needed to determine and use scale-dependent commensurate uncertainties of measured and simulated concentrations of microorganisms in watershed-scale modeling.

Watershed-scale modeling serves as the major tool for establishing Total Maximum Daily Loads, that is, plans for restoring impaired waters that identify the maximum amount of a pollutant that a body of water can receive and still meet water quality standards (Benham et al., 2006). Since contradictions may exist between management practices addressing different goals of restoration measures (Crohn and Bianchi, 2008), it is of paramount importance that interactions between different processes and controls of microbial water quality are reflected in the models. Quantifying such interactions should be a research priority (Oliver et al., 2016).

## Monitoring Design

Existing monitoring design schemes are mostly based on the phased approach to monitoring microbial water quality (NRC, 2004). The first phase includes screening, which identifies the potential problem; the second phase involves more-detailed studies to confirm a public health risk and support management decisions; and the third phase involves studies to determine sources of microbial contamination so that the health risk can be abated through a variety of engineering and policy solutions.

What, where, when, and how to sample remain the cardinal questions in microbial water quality monitoring given the multiplicity of factors and the dynamic character of microbial water quality metrics. Both sampling location and sample size depend on the monitoring purpose. A change in sample size from 1 to 2 L doubled the prevalence of *Salmonella* in the multisite survey in the western United States (Partyka et al., 2018). One could expect that samples of recreation and irrigation water should be taken at different distances from the banks. Hydrological conditions can radically change microbial water quality metrics. This is well traced by the work of Aslan et al. (2018) for tidal systems, where routine monitoring is conducted once during the day while tides can be at either ebb or flood conditions, causing a variability in bacterial concentrations and misinterpretation of the illness risk associated with human activities. The occurrence and levels of enterococci and human and avian molecular markers were determined in samples collected during flood- and ebb tide conditions (May–September) from a tidal river used for recreational activities. Contrary to the general assumption that ebb tide flow in a river would likely carry runoff from the land, the microbial contaminants in this case were transported from upstream via ocean water to the river during the flood tide. Such results suggest that hydrology and land use patterns must be considered in sampling design when conducting future microbial water quality monitoring programs. Watershed-scale modeling can efficiently generate massive databases of microbial water quality for various weather and water-use scenarios (Hong et al., 2017). Such synthetic datasets may be used for establishing better microbial water quality monitoring schedules during the intended water use.

Management of microbial water quality is done with measures and technologies applied to the water body, to known sources of microorganisms that may be delivered to water sources, and at the pathways of microorganism delivery from the sources to water bodies. Low microbial water quality continues to be a daunting public health issue in developing countries (Boithias et al., 2016). Okaali and Hofstra (2018) analyzed the effect of changes in sanitation on concentrations of Rotavirus and the indicator organism *E. coli* in surface water in Uganda using modeling and scenario analysis. The authors show that a plausible set of measures may substantially decrease pathogen and indicator emissions.

Common wastewater reclamation practices do not remove or completely inactivate human enteric viruses, creating food safety concerns when this water is used to irrigate produce. The presence and/or concentration of microorganisms in irrigation water does not determine the ability of these microorganisms to internalize, that is, enter via stomata or wounds and survive in plant tissues. Therefore, evaluation of the microbial quality of irrigation water in the food safety arena must also account for microorganism and plant properties. López-Gálvez et al. (2018) analyzed chloride dioxine treatments to remove human noroviruses and astroviruses from secondary effluent of a wastewater treatment plant in Murcia, Spain. Although the applied treatment did not substantially decrease the concentrations of viruses, no viruses were detected in lettuce grown in a greenhouse under irrigation with the treated water.

## Evaluation of Current Trends in Microbial Water Quality

The focus of microbial water quality research has moved historically from drinking water to recreational water and now to irrigation water. Currently, the quality of reused water is attracting growing attention because of both the growing volumes of this irrigation water source and the oft-needed storage of this water before use in irrigation. Concentrations of viruses and antibiotic-resistant genes in reused waters currently are not regulated. It appears to be both an urgent and an exciting direction of research to determine whether there is a need and feasibility of addressing these components of microbial water quality. Reused waters apparently require a different approach to the selection of water quality metrics and thresholds that would constitute microbial water quality.

Most modern microbial water quality studies are not limited to the measurement of the indicator-organism concentrations used in microbial water quality standards. More and more studies include various methods to characterize the microbial communities present in water bodies of interest, measurements of concentrations of some pathogens, companion measurements of molecular markers, and so on. This complementary information may create the foundation of multi-metrics evaluation of waters rather than relying on a single indicator concentration.

New broad monitoring-related themes emerge geared to understanding the relationships between the microbial water quality metrics and other metrics of water quality. Various algae present an essential opportunity here. The relationships between populations of algae and fecal indicators and pathogens are not known and appear to be complex. Nevertheless, there is promise in studying these relationships. Unlike microorganisms, some algae populations, as well as the most influential water quality parameters, can be assessed using remote sensing (Giardino et al., 2015). This opens the opportunity to classify a surface-water body into several zones with different microbial water quality conditions.

## Concluding Remarks

This special collection of papers on microbial water quality presents a panoramic view on the state-of-the-art research but of course does not comprehensively cover this incredibly broad and diverse interdisciplinary field. Microbial water quality is rightly recognized as a public health issue, regulated at different administrative levels; it attracts medical professionals and is of concern for citizen groups. It must be viewed as an essential element of the "one health" integrative effort of multiple disciplines working locally, nationally, and globally to attain optimal health for people, animals, and the environment (Atlas and Maloy, 2014). Better representation of environmental factors in one health–related work is imperative (Barrett and Bouley, 2015; Durso and Cook, 2018). Microbial monitoring and modeling will have an important part to play in establishing and linking different microbial populations and habitats through environmental transfers. As editors, we hope that this collection of papers will stimulate such interdisciplinary advances in microbial water quality research.

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