## Microbial contamination in drinking water

Sophie Jones\*

Jones S. Microbial contamination in drinking water. J Environ Geol. 2021;5(2):1.

## EDITORIAL

A small collection of reference virus, bacterial, and protozoan pathogens tends to be sufficient for assessing microbial risks and informing system-based drinking water management. Nonetheless, there are data discrepancies, such as human enteric viruses causing endemic infection levels if disinfection and/ or delivery processes are ineffective, and fungi threats. Cryptosporidiosis is the most likely enteric disease to be detected during waterborne outbreaks where disinfection is the only cure and/or filtration is low, although non-human-infectious genotypes are usually present in the absence of human or calf fecal contamination. During large fecal infection incidents that are ineffectively treated, enteric bacteria can be the most dangerous bacteria. The use of culture-based techniques exaggerates treatment effectiveness while limiting our ability to classify pathogens/indicators; however, next-generation sequencing and polymerase chain reaction approaches are on the verge of changing that. Chemical micro pollutant degradation of water sources is a subject of constant concern and is still being investigated.

Microbial pollution, while being at the root of several outbreaks of gastrointestinal diseases and public health issues, is seldom considered, notwithstanding the fact that several researches have shown a consistent and important connection between heavy rainfall events and waterborne disease outbreaks, as well as climate change implications. Despite the existence of a regulatory mechanism, microbial quality is frequently a source of drinking water supply enforcement issues, especially for Small Scale Water Systems (SSWS) and private water sources. Furthermore, increased microbial contamination is known to impact water quality under severe

weather conditions (climate change), necessitating more rigorous research. The monitoring targets consist of specifically targeting the causes of infection using clear and rapid markers, with a particular emphasis on fecal bacteria (E. coli or Enterococci). Due to the identification limits of widely used techniques, enteric viruses, which play a significant role in waterborne diseases, are poorly investigated. Analytical methods have been used for several years to enhance our understanding of the role and origins of microorganisms. The US Environmental Protection Agency (EPA) has documented over 500 waterborne pathogens of potential concern in drinking water through its candidate contaminant list. The amount of enteric virus in drinking water must be less than one per million liters, a concentration much beyond the capacities of modern measuring techniques. When enteric virus concentrations were about one genomic copy per liter, epidemiology studies found a 30% rise in gastrointestinal danger. Several recent studies have demonstrated the importance of an ecological approach (the role of sediment and aquatic plants). PCR is commonly used in microbial source tracking, but due to its targeted approach for specific microbial genera or species, it has not found widespread application in microbial monitoring programs. The literature is well-documented on MST tools suggested for identifying the source of fecal waste. Aside from these and traditional bacterial culture, there are several other options, such as approaches focused on exploiting the optical properties of water by the optical effects of microorganisms that are often adsorbed on colloids or particles. Bacteria or viruses can be detected using the interaction of light and matter, either as free particles or attached to organo-mineral complexes capable of altering the optical properties of surfaces.

Editorial Board office, Singapore

Correspondence: Sophie Jones, Editorial office, Singapore Received: December 15, 2020, Accepted: January 02, 2021, Published: January 25,2021

This open-access article is distributed under the terms of the Creative Commons Attribution Non-Commercial License (CC BY-NC) (http:// creativecommons.org/licenses/by-nc/4.0/), which permits reuse, distribution and reproduction of the article, provided that the original work is properly cited and the reuse is restricted to noncommercial purposes. For commercial reuse, contact reprints@pulsus.com