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Microbial Water Quality Assessment Using Molecular Diagnostic Tools

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Introduction

Microbial water quality is critical for human, animal and environmental health. Notably, pathogenically polluted water may create major health concerns, such as waterborne epidemics, which have resulted in massive economic and societal losses. In this situation, early identification of microbial contamination is critical for early warning and timely response with appropriate therapies. Recently, molecular diagnostics have been increasingly used for the rapid and robust assessment of microbial water quality implicated by various microbial pollutants, such as waterborne pathogens and antibiotic-resistance genes (ARGs), posing the most serious health threats to humans and the environment.

Description

Continuous technological advancements have resulted in continuous improvements and expansions of molecular methods such as conventional end-point PCR, DNA microarray, real-time quantitative PCR (qPCR), multiplex qPCR (mqPCR), loop-mediated isothermal amplification (LAMP), digital droplet PCR (ddPCR) and high-throughput next-generation DNA sequencing (HT-NGS). These cutting-edge molecular techniques greatly simplify monitoring microbiological water quality in a variety of aquatic systems and wastewater. This study gives an up-to-date summary of the evolution of the primary molecular instruments often used for microbiological water quality evaluation, as well as future perspectives on their usage [1].

End-point convention PCR can determine the presence or absence of target pathogens in water. It has been widely utilised for environmental assessments since the 1990s. In general, PCR comprises three cycle phases to multiply and amplify a specific target DNA sequence: denaturation, annealing and elongation. The target sequence can be exponentially enriched after hundreds of amplification cycles and the produced product can be identified and observed using agarose gel electrophoresis [2].

Water quality is a vital criteria for all living things. Clean water is a critical worldwide need and it is a specified core aim among the 17 United Nations Sustainable Development Goals. Water of poor quality provides major health concerns to humans and animals, either directly through waterborne illnesses and/or indirectly through foodborne sickness caused by microorganisms in reclaimed water used for irrigation/food production. Water polluted with microbiological infections is a huge public health concern across the world, killing over 800,000 people each year. The annual worldwide economic loss is projected to be close to USD 12 billion. Pathogen contaminations have been detected/reported in several types of water, including freshwater, marine water, drinking water, reclaimed water and wastewater [3].

Antimicrobial resistance (AMR) has emerged as a serious public health problem worldwide in recent years. It is estimated that by 2050, this global burden would have resulted in around 10 million fatalities. Aquatic systems have been recognised as the key reservoirs and transmission hubs for antibiotic-resistant bacteria (ARB) and antibiotic resistance genes (ARGs). Pathogenic bacteria are more susceptible to AR development because to persistent selection pressure and widespread dispersion. Antibiotic residues can infiltrate aquatic habitats through a variety of means, including wastewater treatment plant (WWTP) discharge and agricultural runoff (containing livestock manure and organic fertilizers). ARBs and ARGs have been found in a variety of water sources, including groundwater, surface water and drinking-water treatment facilities and distribution networks.

The microarray, also known as a DNA chip or lab-on-chip, was invented in the early to mid-1990s. DNA microarrays are gene chips that include a high density (thousands) of nucleic acid probes (genomic DNA, cDNA, or oligonucleotides) in an organised two-dimensional matrix, allowing the detection of several target genes in a single test. The presence/absence of the microorganism of interest may be probed by assessing the fluorescence signal generated by hybridization between the immobilised particular probe and the target gene encoding the complementary sequence [4].

A DNA microarray was utilised to check for the presence of 941 bacterial pathogens in groundwater. To determine the incidence of waterborne pathogens in a fecally polluted watershed, a multigene target microarray was created. Pathogens discovered in the impaired streams included five viruses, nine bacteria and three eukaryotes. For water microbiological surveillance, Gomes et al. created a DNA microarray with 16 implanted probes targeting P. *aeruginosa*, *Staphylococcus aureus* (S. aureus), *Clostridium perfringens*, *E. coli*, total and faecal coliforms and enterococci. A 21 probe-based microarray was created to investigate common aquatic protozoan diseases and effectively recognised the protozoa *Acanthamoeba castellanii* (A. *castellanii*), *Cryptosporidium parvum* (*C. parvum*) and *Giardia intestinalis* (G. *intestinalis*) [5].

Conclusion

The viability and variety of molecular diagnostic methods used for the surveillance of aquatic microorganisms posing a danger to human and environmental health are highlighted in this study. Ever-evolving molecular technologies provide an increasing number of technical options for the qualitative and quantitative assessment of key components related to aquatic microbial quality, such as waterborne pathogens, ARGs and microbial community dynamics under a variety of anthropogenic and environmental influences. Finally, there is an urgent need to standardise the technical procedures involved (for example, water sample collection and preservation, water concentration/enrichment, DNA/RNA extraction methods, qPCR and NGS data analysis protocols) to facilitate cross-laboratory, cross-country and cross-continent data comparison and technology transfer.

Conflict of Interest

No potential conflict of interest was reported by the authors.

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References

1. Alhamlan, Fatimah S., Ahmed Ali Al-Qahtani and Mohammed N. Ahmed Al-Ahdal. "Recommended advanced techniques for waterborne pathogen detection in developing countries." *J Infect Dev Ctries* 9 (2015): 128-135.
2. Cui, Qijia, Yong Huang, Hui Wang and Tingting Fang. "Diversity and abundance of bacterial pathogens in urban rivers impacted by domestic sewage." *Environ Pollut* 249 (2019): 24-35.
3. Liu, Sheng, Chao Wang, Peifang Wang and Juan Chen, et al. "Variation of bacterioplankton community along an urban river impacted by touristic city: With a focus on pathogen." *Ecotoxicol Environ Saf* 165 (2018): 573-581.
4. Fernandez-Cassi, X.., C. Silvera, S. Cervero-Aragó and M. Rusiñol, et al. "Evaluation of the microbiological quality of reclaimed water produced from a lagooning system." *Environ Sci Pollut Res Int* 23 (2016): 16816-16833.
5. Jahne, Michael A., Nichole E. Brinkman, Scott P. Keely and Brian D. Zimmerman, et al. "Droplet digital PCR quantification of norovirus and adenovirus in decentralized wastewater and graywater collections: Implications for onsite reuse." *Water Res* 169 (2020): 115213.

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