Closing the Nitrogen Cycle: Utilizing Molecular Biological Tools to Address Nitrogen Transformation in Wastewater Treatment

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Background/Objectives. Microorganisms have demonstrated a remarkable ability to bioremediate sites worldwide. They are our most valuable players in preserving the safety of our drinking water as well as water destined for environmental and industrial use. Molecular biological tools (MBTs) such as quantitative polymerase chain reaction (qPCR) can be used to assess the native genetic potential for nitrogen removal at wastewater treatment sites and monitor microbial response to treatment over time. The ability to compare concentrations of key microbial populations spatially, temporally, and even across sites can provide context and influence decision making at wastewater treatment facilities to optimize treatments and maximize cost-savings. With a comprehensive review of pivotal steps in nitrogen cycling such as ammonification, nitrification and denitrification, this work will illuminate the organisms and enzymes involved in nitrogen removal that can be quantified using qPCR and provide their detection frequencies and median concentrations based on a database of qPCR results from over 40,000 environmental samples.

Approach/Activities. Using case studies, we will build a deeper understanding of how MBTs can be utilized to assess a system's potential to cope with high nitrogen loads. This work will illustrate ways qPCR data can be incorporated into routine monitoring plans with the goal of driving better management decisions at wastewater treatment facilities. Drawing from a database of over 40,000 samples, statistical analysis will provide insight into how often relevant microbial groups such as denitrifiers, nitrite oxidizers, nitrogen fixers, and ammonia oxidizers, among others, are detected in water samples and their median concentrations.

Results/Lessons Learned. Through analysis of the database of qPCR results, detection frequencies and median concentrations of key organisms behind pivotal steps in nitrogen cycling such as ammonification, nitrification and denitrification are identified. For example, denitrifying bacteria were detected in 81% of the 734 samples analyzed for this target with a median concentration of 1.06E+07 cells/mL. Nitrite oxidizing bacteria were detected in 26% of water samples analyzed (n=84), and the median concentration was 1.47E+03 cells/mL. Nitrogen fixing bacteria were identified in 74% of samples analyzed (n=76) with a median concentration of 9.40E+05 cells/mL. Ammonia oxidizing bacteria were identified in 91 samples with 22% detection and median of 1.71E+03 cells/mL. Further data will be presented with expanded contextual relevance. Establishing these metrics is beneficial for comparing microbial results between sites and developing context for successful remediation of wastewater for reuse and safe reentry into the environment. While microorganisms involved in the nitrogen cycle do not have to be "better than average" to ensure biotransformation for successful wastewater remediation, this work intends to inform continued investigation of how elucidating the potential for nitrogen transformation via qPCR analysis can be used to enhance system performance at wastewater treatment facilities.