

Microbial Community Analysis in Water Storage Tank Sediment Exposed to Monochloramine

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Sediment accumulation in water storage facilities causes water quality degradation, including enhanced biological growth and more rapid disinfectant decay. The current research evaluated the microbial community composition after a drinking water storage facility's sediment was exposed to monochloramine. A 5 cm diameter teflon reactor with a 4 cm depth was filled with 2 cm of drinking water storage tank sediment. The reactor was continuously fed with a 4 mg Cl_2/L monochloramine solution, resulting in a water depth above the sediment of 0.5 cm. At WQTC 2016, we presented results of microelectrode obtained profiles of DO, pH, monochloramine, ammonium, nitrite, and nitrate penetration into the sediment. Results showed that monochloramine slowly penetrated into the sediment with only 2 mg Cl_2/L monochloramine reaching a depth of 0.25 cm and no monochloramine was measurable at sediment depths greater than 0.5 cm. Likewise, DO never fully penetrated the sediment but progressed inward with time to a maximum depth of 1 cm. Evidence of microbial activity was demonstrated with an increase in nitrate and a concurrent decrease in ammonium with sediment depth and minimal nitrite accumulation, indicating complete nitrification occurred in the sediment. There were minimal changes in pH (range 7.8 to 8.0).

For the current presentation, we desired to correlate the previously obtained chemical profiles with the microbial community present in the sediment. Microbial communities were characterized based on 16S rRNA-encoding gene sequences of triplicate sediment cores, of which two sections were examined (top; 0-1 cm and bottom; 1-2 cm). In addition, we investigated the abundance of bacterial subpopulations using quantitative real-time PCR (qPCR). Overall, the majority of the total diversity was associated with the phylum Proteobacteria (50%) and Acidobacteria (15%), with additional contributions from 29 phyla. Bacterial communities are highly diverse and structured as a function of both environment and depth, being more diverse in the top section (0-1 cm). Linear discriminative analysis (LDA) effect size (LEfSe) revealed both an enrichment and depletion of various bacterial populations associated with depth; with the genus *Mycobacterium* and *Bradyrhizobium* overrepresented, while *Syntrophobacter*, *Rhodoplanes*, and *Terrimonas* underrepresented in the 0-1 cm. Nitrifying bacteria closely related to *Nitrospira* and *Nitrosomonas* (2%) were detected in 0-1 cm, but decreased to <0.7% in 1-2 cm. qPCR results indicated that *Mycobacterium* dominated the 0-1 cm, while environmental *Legionella*-like species peaked at 1-2 cm. Overall, these results provide an ecological insight of the microbial community in storage tank sediment and indicate that even with extended periods of chloramine residual maintained in the bulk water, limited monochloramine penetration occurred into the sediment and biological activity remained.