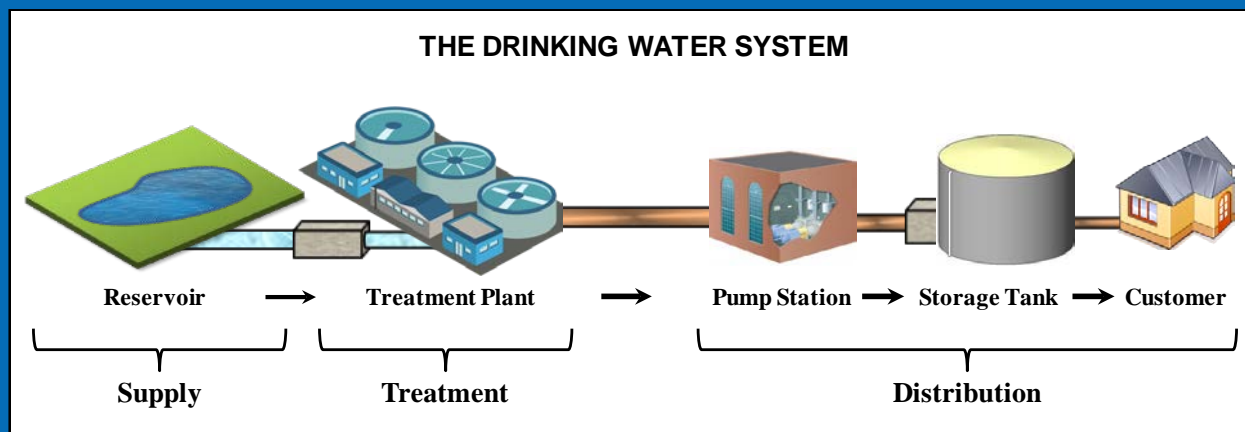
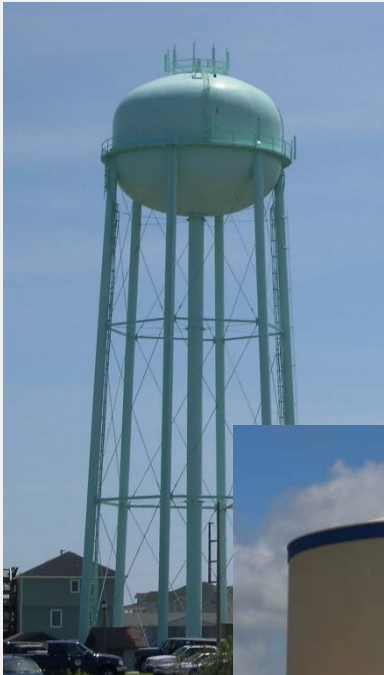


Microbial Community Analysis in Water Storage Tank Sediment Exposed to Monochloramine

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Drinking Water Storage Tanks in Distribution Systems



Storage tanks (or *floating reservoirs*) maintain an adequate supply of water for distribution and provide the system with stable water pressure.



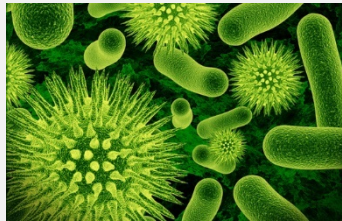
Water storage tanks
accumulate
sediment over time



Sediment accumulation in water storage facilities causes:



Water Quality Degradation



Biological Growth



Disinfectant Decay

Disinfectant penetration within water storage tank sediments is largely uncharacterized

Overall Research Objectives

- **Use microelectrodes to evaluate disinfectant & water quality within a drinking water tank sediment**
 - ❑ monochloramine & free chlorine penetration profiles over time
 - ❑ impact of switching disinfectants (monochloramine → free chlorine → monochloramine)
 - ❑ results presented at **WQTC 2016**

- **Investigate relationship between disinfectant penetration & microbial communities** [Current Presentation]
 - ❑ correlate the previously obtained chemical profiles with the microbial community structure present in the sediment

➤ **Microelectrodes were used to determine chemical variability within a drinking water tank sediment**

- ❑ complete monochloramine or free chlorine penetration was not obtained and evidence of biological activity remained
- ❑ monochloramine penetrated farther (7,000 µm) than free chlorine (500 µm)
- ❑ disinfectant penetration similar to previous research with nitrifying biofilm
- ❑ ammonia was released and converted to nitrate and some nitrite
- ❑ oxygen was fully consumed (12,500 - 14,000 µm)
- ❑ minor pH changes occurred (8.0 → 7.7 - 7.8)

➤ **Disinfectant switching**

- ❑ measurable ammonium, nitrite, & nitrate during free chlorine application
- ❑ nitrification resumed upon a switch back to monochloramine

Findings support removal of sediments

Experimental Approach: Disinfectant Application Scenario

➤ Sediment source

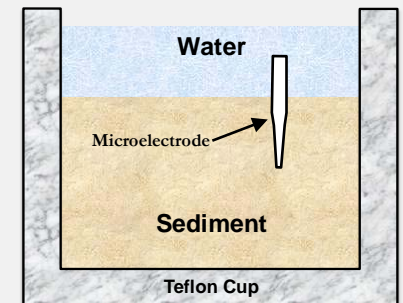
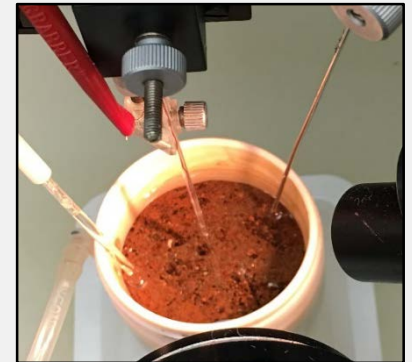
- ❑ a chloramine system storage tank

➤ 5 cm diameter x 4 cm deep teflon cup

- ❑ 2.0 cm (20,000 $\mu\text{m} \approx 0.8''$) sediment depth
- ❑ 0.5 cm (5,000 $\mu\text{m} \approx 0.2''$) water depth over sediment

➤ 5 mL/min flowrate (2 min hydraulic residence time)

- ❑ 4 mg Cl_2/L monochloramine (4:1 $\text{Cl}_2:\text{N}$) or free chlorine
- ❑ pH 8.0 at room temperature (21 - 23° C)
- ❑ no additional amendments (e.g., organic C, phosphorous)

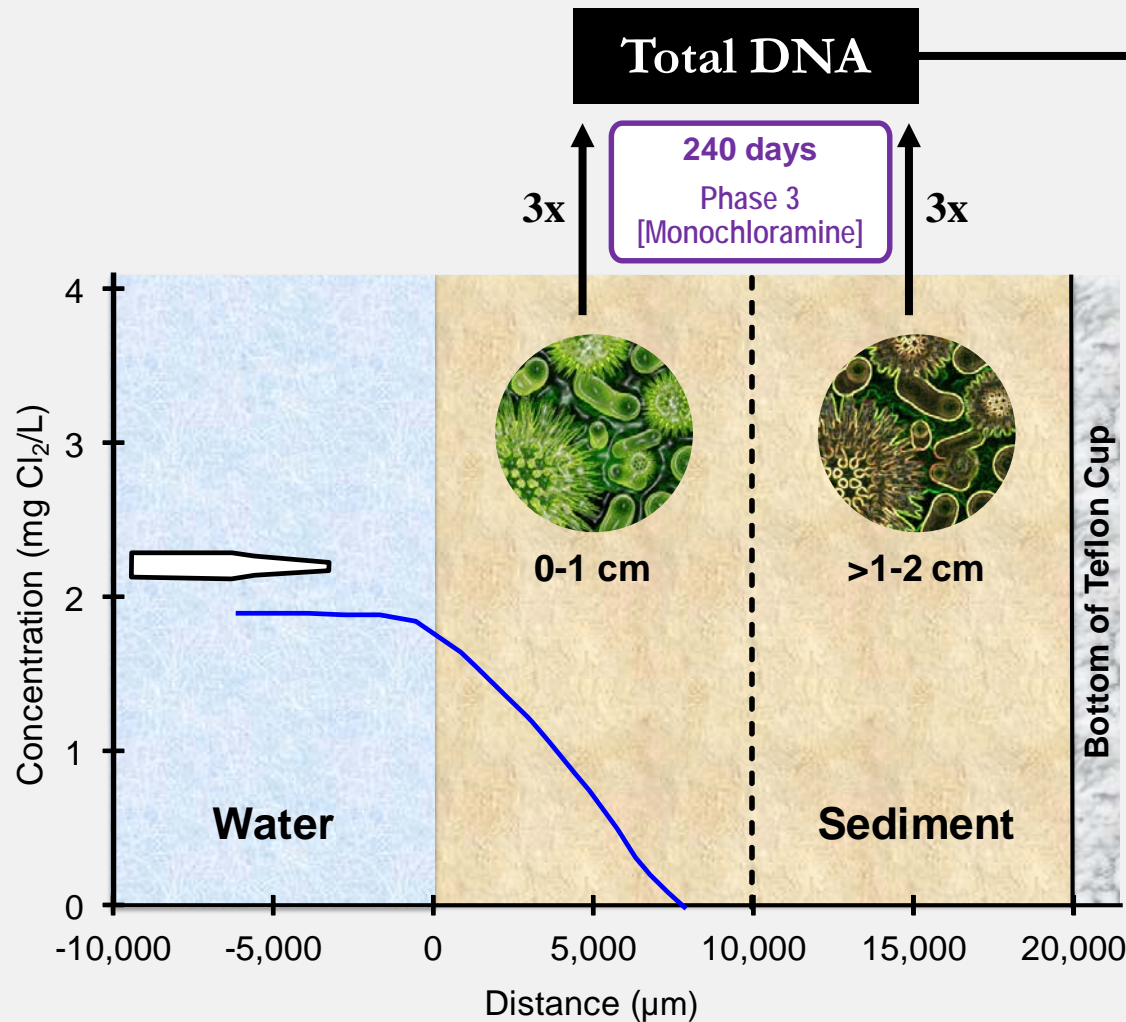


Phase 1 (120 days):
Monochloramine

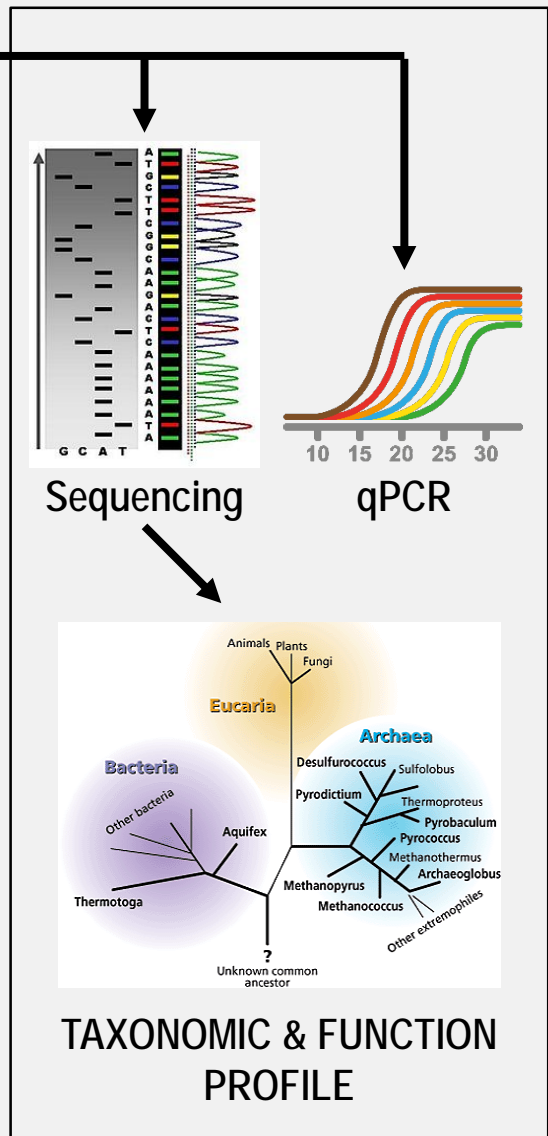
Phase 2 (60 days):
Free chlorine

Phase 3 (60 days):
Monochloramine

Experimental Approach: Microbial Community Analysis



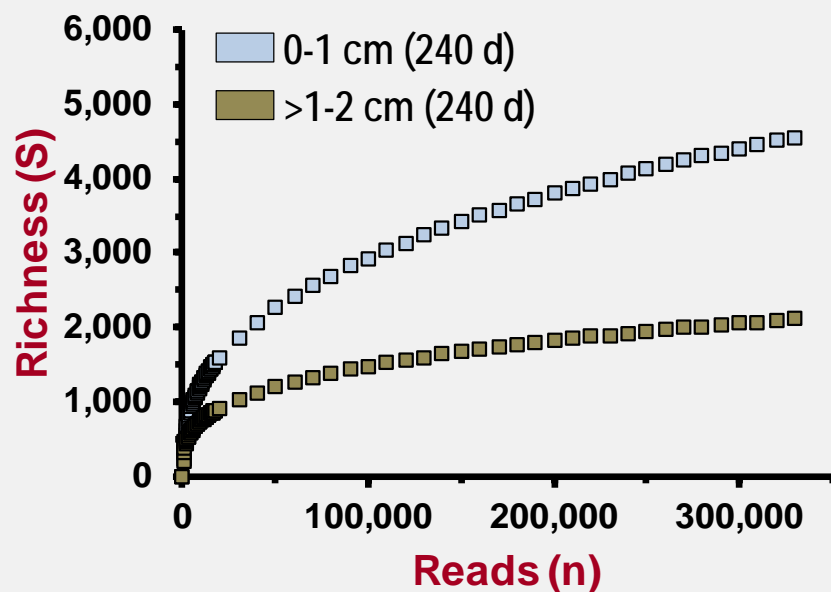
METHODS



Results: Community Diversity

Diversity Indices

Rarefaction

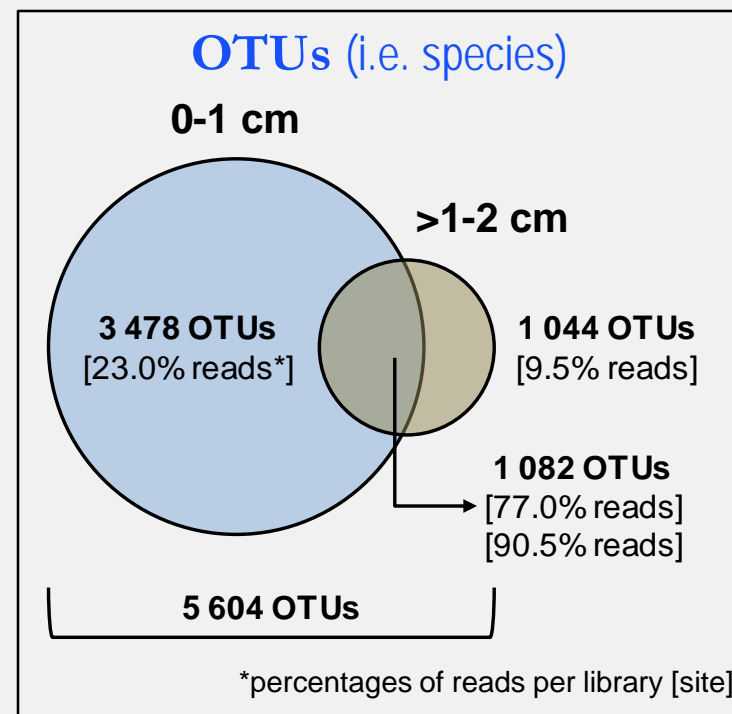


Top section (0-1 cm) is more diverse and contains more species (OTUs).

Source [§]	S [‡]	Richness Estimators		Diversity
		ChaoI	S _{ACE}	Shannon (<i>H</i>)
Sample (depth)				
0 - 1 cm	4 560	6 738 ± 291	7 927 ± 239	6.12 ± 0.01
>1 - 2 cm	2 126	3 018 ± 193	3 387 ± 142	5.70 ± 0.01

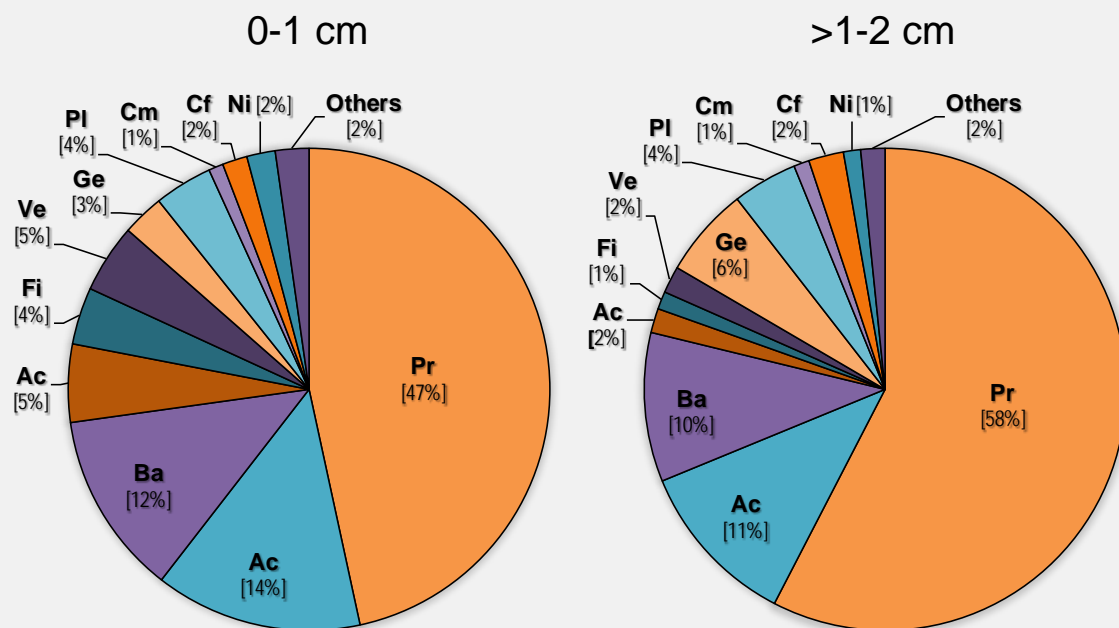
[§]Libraries were normalized to 335 000 reads per sample.

[‡]Richness is the total number of species (defined as aligned sequences with ≥97.0% similarity).



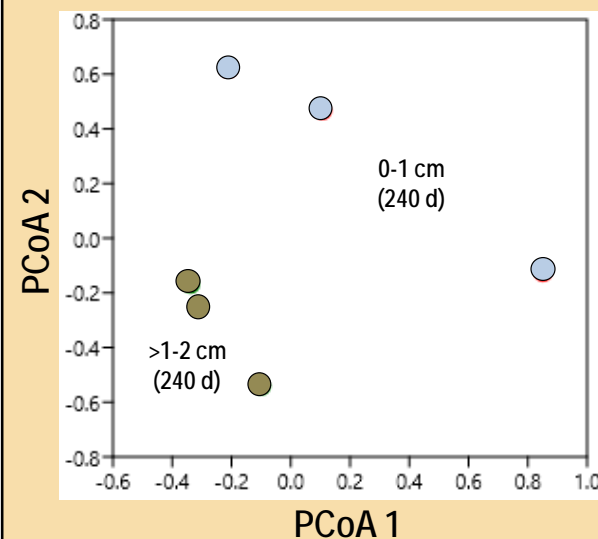
Results: Community Composition

Taxonomic Composition



Legend [phylum]: Proteobacteria (Pr), Acidobacteria (Ac), Bacteroidetes (Ba), Actinobacteria (Ac), Firmicutes (Fi), Verrucomicrobia (Ve), Gemmatimonadetes (Ge), Planctomycetes (PI), Chlamydiae (Cm), Chloroflexi (Cf), Nitrospirae (Ni), and Others <1% (Others).

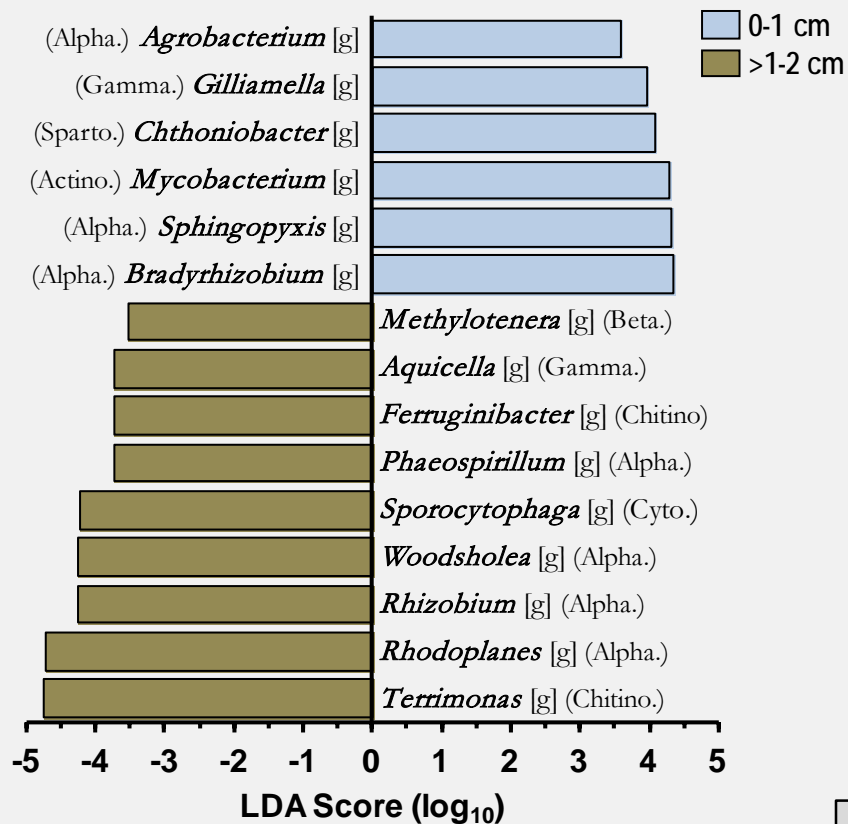
Exploratory Analysis (PCoA)



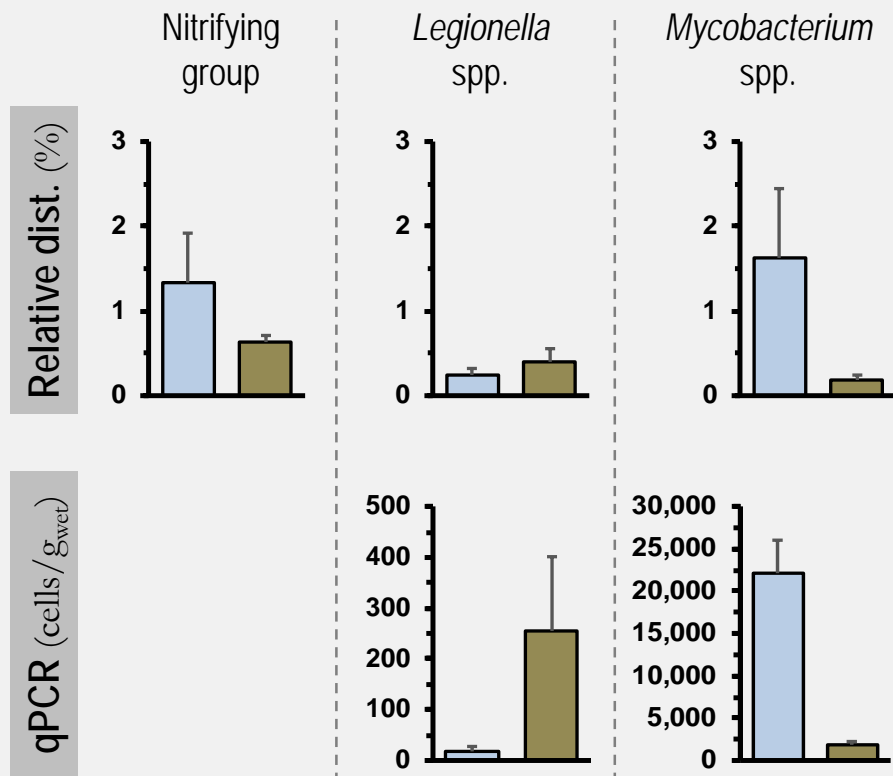
The bacterial community structure of top (0-1 cm) and bottom (>1-2 cm) sections were dissimilar.

Results: Community Structure

Community Structure



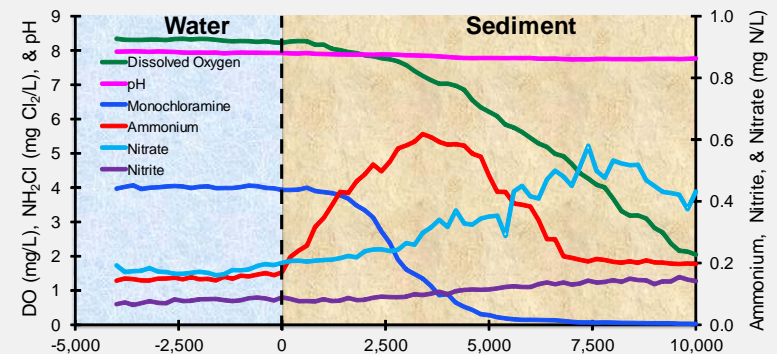
Bacterial Populations



Analysis revealed both an enrichment and depletion of various bacterial populations associated with depth.

Conclusions

- 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).
- The majority of the total diversity was associated with the phylum Proteobacteria (50%) and Acidobacteria (15%), with additional contributions from 29 phyla.
- Community analysis 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. peaked at 1-2 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.



THANK YOU
FOR
YOUR
ATTENTION!
ANY QUESTIONS?