

ENIGMA: Using in-field bioreactors to monitor microbial community dynamic shifts with geochemical perturbations

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Project Goals: ENIGMA -Ecosystems and Networks Integrated with Genes and Molecular Assemblies use a systems biology approach to understand the interaction between microbial communities and the ecosystems that they inhabit. To link genetic, ecological, and environmental factors to the structure and function of microbial communities, ENIGMA integrates and develops laboratory, field, and computational methods.

Abstract

Subsurface microbial communities mediate the transformation and fate of redox-sensitive compounds including organic matter, metals and radionuclides. Few studies have explored how changing geochemical conditions influence the composition of groundwater microbial communities. As part of the ENIGMA Environmental Ark campaign, we used 1L in-field bioreactors receiving background and contaminated well water from the Department of Energy site at the Oak Ridge Reservation, TN to test the effect of abiotic forces on microbial community structure. (For additional reactor studies see “Dissecting microbial nitrogen cycling in the subsurface using tailored reactor schemes” by Hunt et. al., and “Metabolomics and Transcriptomics for Environmental Systems Biology: Molecular Mechanisms of Reduced Sulfur Caused Growth Inhibition of Field-Isolated Nitrate-Reducing Bacterium” by Majumder et. al.) Planktonic and biofilm microbial communities were initialized with background water to establish communities in triplicate control reactors and triplicate test reactors. All were fed filtered water from the background site for 18 days. On day 18, three reactors were switched to filtered water from a contaminated well, enriched in total dissolved solids relative to the

background site, particularly chloride, nitrate, uranium, and sulfate. Biological and geochemical data were collected throughout the experiment, including planktonic and biofilm DNA for 16S rRNA amplicon sequencing, cell counts, total protein, anions, cations, trace metals, organic acids, bicarbonate, pH, Eh, DO, and conductivity. We observed significant shifts in both planktonic and biofilm microbial communities receiving contaminated water. This included a loss in diversity, especially amongst members of the *Bacteroidetes*, *Acidobacteria*, *Chloroflexi*, and *Betaproteobacteria*, but enrichment in the Fe(III)-reducing *Ferribacterium* and parasitic *Bdellovibrio*. These shifted communities were more similar to the contaminated well community, suggesting that geochemical influences on microbial community structure are substantial.

This material by ENIGMA- Ecosystems and Networks Integrated with Genes and Molecular Assemblies a Scientific Focus Area Program at Lawrence Berkeley National Laboratory is based upon work supported by the U.S. Department of Energy, Office of Science, Office of Biological & Environmental Research under contract number DE-AC02-05CH11231