

233. 'Species Filter' Effects on Sediment Biofilms and Groundwater Source Diversity

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Project Goals: The goal of Ecosystems and Networks Integrated with Genes and Molecular Assemblies (ENIGMA) is to push the frontier of knowledge on the impact of microbial communities on ecosystems and to elucidate microbial assembly rules. As part of this, we must link genetic capacities to ecological function (e.g., heavy-metal- and radionuclide-contaminated groundwater in DOE sites of interest). In these sites, the microbial communities are often predominantly attached to sediment particles as a biofilm. We have characterized temporal dynamics of bacterial groundwater communities and compared to the establishment of particle-associated bacterial communities on native sediments incubated down-well. In pursuing this goal, inter-laboratory collaboration facilitated by ENIGMA has led to the identification of aquifer population distributions between the liquid/solid boundaries in situ.

Understanding the factors that determine microbial assembly, composition, and function in subsurface environments are critical to assessing contributions to biogeochemical processes such as carbon cycling and bioremediation. However, these factors are still not fully understood. In this study, surrogate sediment samples were incubated for 3 months in 3 wells (FW301, FW303, FW305) within the background site of the Oak Ridge Field Research Center in Oak Ridge, TN. Local sediment biofilm communities were compared to those of the groundwater (source diversity). Groundwater samples from each well were collected approximately 3 times a week. Multiple sediment samples (n=12) were used per well to determine inter- and intra-well variation. Spatial and temporal community analysis of local and source samples via ss-rRNA paired-end sequencing and distribution-based clustering revealed higher richness, diversity, and variability in source groundwater communities compared to sediment-associated communities. Ordination analysis grouped the newly formed local communities as more similar to those of the groundwater than to those of the original parent sediment. The predominant groundwater sequences per well were *Curvibacter*, *Delftia*, and *Acidovorax* for FW- 301, *Aquabacterium*, *Oleiphilus*, and *Bradyrhizobium* for FW---303, and *Acidovorax*, *Curvibacter*, *Caulobacter*, and *Elusimicrobium* for FW-305. Other sequences displayed transitory predominance for different wells. The community composition was different between wells, and FW-305 (a younger well) showed more diversity over time. In sediment samples, 20-40% of the communities consisted of populations that were abundant at less than 5% of the total sampled diversity. The sediment biofilms from each well were also distinct from each other. Intra-well sediment biofilms showed much less variability, with the exception of FW-305. Sediment biofilm communities were distinct from corresponding groundwater communities, with some populations becoming predominant in the biofilm (e.g. *Aquabacterium*, *Perluclidibaca*, and *Paraperluclidibaca*); however, different OTUs were respective to each well. These results indicate a shift in local community structure that is influenced by the available source community as well as hydrology.

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