ENIGMA: Core Values: Large-Scale Analysis of Environmental Constraints on Microbial Community Assembly, Activity, and Dispersal in Groundwater and Sediment from a Contaminated Subsurface Aquifer

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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 microorganisms play important roles in mediating major biogeochemical cycles, but only in recent years have studies shed light on their population structure, biogeography, and metabolisms present. The Department of Energy ENIGMA Scientific Focus Area seeks to map the causal interactions that constrain microbial community assembly and dispersal in chemically and physically complex environments. Recently, we initiated a study of microbial communities in the shallow subsurface of a contaminated aquifer at the Oak Ridge Field Research Center, a site of nuclear weapon development during the Manhattan Project.

We hypothesize that strong gradients of pH, heavy metals, nitrate, and other contaminants at the site influence the distribution, structure, and activity of microbial communities. To study community assembly mechanisms, we performed large-scale analysis of two sediment cores and associated groundwater for which we produced depth-index data sets of physical, chemical, bulk biological and sequencing measurements. One core is considered uncontaminated (466 cm), and the other core (815 cm) is contaminated by chemicals from man-made processes. We divided the cores into ~23 cm segments for processing, resulting in 56 segments which allowed us to do a finer-grained analysis of the vertical transect as compared to other subsurface studies.

The contaminated core is much less diverse as 250 exact sequence variants (ESVs) from 16S amplicon sequencing account for 50% of observed reads as compared to 660 from the uncontaminated core, suggesting strong selective pressure from contamination. Initial analysis of ESV location suggests that there is little mixing and dispersal along a core. In general, there is little overlap in ESVs between the two

cores (~300-350 meters apart). Many of the chemical and physical measures are strongly dependent on depth and highly colinear; these colinear groups are strongly predictive of the ESV group distribution and their measured activity although not all observed groups are well predicted. Currently, we are processing shotgun metagenomics data to compare taxonomy and genes to our other data. From the water and sediment data, we have over 50 genomes with >98% completeness and <2% contamination. We are tracking these genomes through the vertical length of the core and analyzing the potential functional roles of these organisms. This study integrates over 12 measures of microbial community composition, activity, and environmental controls to provide new insights into subsurface microbial communities.