

## **Large Scale-Analysis of Constraints on Microbial Community Assembly, Activity, and Dispersal in a Contaminated Subsurface Aquifer**

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Subsurface microorganisms play important roles in major biogeochemical cycles, but only in recent years have studies shed light on their population structure, biogeography, and metabolisms. To study the effects of hydrogeology and biogeochemistry on microbial communities, we performed large-scale analysis of two sediment cores (contaminated-815cm, background-466cm) and associated groundwater from the shallow subsurface of the contaminated aquifer at Oak Ridge Field Research Center. We hypothesize that gradients of pH, uranium, nitrate, heavy metals, and other contaminants at the site influence microbial community dispersal, structure, and activity. Both cores have depth-indexed datasets of physical, chemical, bulk biological measurements including basic geochemistry, metabolites, 17 metals, GeoChip, BONCAT, nitrate and sulfate respiration activity, 16S, and metagenomics sequencing. We divided the cores into ~23cm segments, which provides finer-grained analysis of the vertical transect as compared to other subsurface studies. Initial analyses suggest that there is little microbial dispersal along a core and a strong selective pressure from the contamination. Currently we are tracking genomes through the core and water samples and analyzing the effect of the measured parameters on metabolic activity. This study integrates measures of microbial community composition, activity, and environmental controls to provide new insights into subsurface microbial communities.