

## **Integrating Genomics, Physiology and Genetics of the Oak Ridge Field Research Site Microbiome**

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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.**

Over many years of isolation efforts, ENIGMA has leveraged a network of groundwater wells at the Oak Ridge Field Research Site in which multi-dimensional gradients of inorganic ion contaminants are a complex combinatorial constraint on the microbiome to amass a large culture collection. The microbial isolates in this collection represent a significant percentage of the culturable microbial populations from this contaminated aquifer. Genome sequencing of hundreds of these isolates has revealed both macro and microdiversity, and the isolates display a range of phenotypes with respect to metal resistance, energy metabolism and nutrient utilization. We are using this phenotypic variation to infer the probable niche and range of the various sub-populations. Comparison of laboratory phenotypic characterization with field survey data enables the inference of probable selective pressures acting on the microbiome in the field. Through streamlining genetics and scaling gene function discovery in our isolates, we are linking specific genetic mechanisms of survival or sensitivity to field relevant selective pressures. The observations and tools developed through these efforts are being propagated through publicly available web interfaces and KBase to facilitate new discoveries from across the scientific community.

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