

Characterization of Microorganisms Resistant to Multiple Metals from the Contaminated Environment at the Oak Ridge Reservation

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<http://enigma.lbl.gov>

Project Goals: ENIGMA (Ecosystems and Networks Integrated with Genes and Molecular Assemblies) uses 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. The goal of this project is to isolate and characterize microbial strains that are resistant to many different metals at concentrations found in contaminated wells at the Oak Ridge Reservation environment. We will use diverse techniques such as transposon sequencing and global isotope metabolomics to investigate multi-metal resistance in these strains. In addition, the large amounts of characterization data gathered will be aggregated in KBase, where new KBase tools will be used to organize, analyze and distribute results to the public.

Abstract: The metal resistance campaign of ENIGMA is focused on investigating molecular mechanisms of microbial metal resistance. One of the defining characteristics of the Oak Ridge Reservation (ORR) environment is the presence of nitrate and mixed metal industrial waste with concentrations many metals over 1,000 times elevated in contaminated areas compared to pristine groundwater. Several metal centric high throughput anaerobic enrichments from contaminated ORR groundwater and sediment have been conducted including those using media containing a suite of metals at concentrations based on the ORR environment. These isolates are all resistant to metals such as uranium, aluminum, manganese and nickel ($\geq 100 \mu\text{M}$) when grown under nitrate-reducing growth conditions. After high-throughput preliminary screening, isolates that have unusual metal resistance properties indicative of novel mechanisms will be selected for in depth characterization by an array of lab processes and technologies as part of the metal resistance campaign pipeline including; genome sequencing, screening for genetic tractability, random barcode TN-Seq, DNA affinity purification sequencing, and global isotopic metabolomics. All characterization data can then be uploaded to KBase where new tools developed to analyze generic data sets are being used to organize, analyze, and eventually distribute results to the public.

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