ENIGMA Microbiology Physiology: Dissecting the Physiology and Community Interactions of Environmental Bacteria

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Project Goals:

The ENIGMA (Ecosystems and Networks Integrated with Genes and Molecular Assemblies) project aims to elucidate the mechanisms and key processes that enable microorganisms and their communities to function in metal-contaminated soil sites. The ENIGMA Laboratory Component focuses its efforts on uncovering the genetic and biochemical basis of physiology and metabolism in key microbial species in isolation and in laboratory-defined communities. These data are used to develop models of microbial community activity and principles of community organization in an effort to predict the role that microbial species and their interactions play in the dynamics of geochemical transformations in a changing environment.

Abstract:

The mission of the Laboratory Component involves four primary goals that are closely coordinated with the Environmental, Biotechnology, and Computational Components within ENIGMA. Here, we describe these goals and highlight recent progress in these areas with a focus on the biology and interactions of the sulfate-reducing bacterium (SRB) *Desulfovibrio vulgaris* Hildenborough (DvH) in microbial consortia (1). In collaboration with the Environmental Component, we will characterize key microbes and communities enriched directly from metal-contaminated sites and prioritize these systems for deep functional annotation based on physiological properties, interactions among microorganisms, and potential biogeochemical activities. With flexible experimental techniques developed in concert with the Biotechnology component, we will use metabolomics, proteomics, transcriptomics, high-resolution microscopy, and high-throughput mutagenesis/phenotyping approaches to define transcript architecture, signal transduction, gene function, sRNA function, protein interactions and localization, elucidate the structure and function of biofilm formation, the metalloproteome,

metabolism and mechanisms of specific interaction in these key isolates and their relatives (2). With the Computational group, we will use these data to construct predictive models of metabolism and gene regulation, which in turn will be used as drivers for new hypotheses and further experimentation (3). Using key microbial isolates, we will constitute laboratory simulation of enriched and defined assemblages in planktonic and attached states and assess different cellular compositions under varying environmental constraints. As a two species community model system, we have used long-term evolution experiments to map the genetic basis of improved syntrophy between DvH and a methanogen. More recently, transcriptomics and whole-genome mutant fitness profiling have identified key genes and pathways involved in the syntrophy of *Desulfovibrio alaskensis* G20 with a methanogen (4). These form a basis for pilot studies on the molecular dissection of competitive association among multiple SRB and methanogens in common culture. Lastly, we aim to determine how information flows among microbes and to assess the specificity, mutualism, and antagonism among pairs and groups of microbes by application of genetic, biochemical and computational technologies.

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