ENIGMA Biotechnology: Systems approaches to studying microbial communities

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Project goals: Microorganism-based approaches to address DOE mission goals in remediation, carbon sequestration and energy production will require quantitative understanding of biological complexity at multiple scales -- from molecular networks of individual species to the dynamic inter-species interactions within the communities in which they reside. The broad goals of ENIGMA are to understand, at a molecular systems level, the bacterial soil communities at DOE sites contaminated with heavy metals or radionuclides with sufficient detail to predictively model interactions within microbial and community processes that drive complex geochemistry in key environments. In doing so we expect to define biological principles governing selection of microbial community function and composition in given environments.

To ascertain the key processes contributed by an organism to a community and to characterize that process within the organism in molecular detail, it is necessary not only to identify the components of the pathways involved, but to also understand their functional interactions with other processes in the organism of interest. The Biotechnology Component of ENIGMA is developing and applying a suite of technological approaches, from genetics, protein abundance, structure, localization, and metabolism to enable systems-level insights into microbial activity. We have established a flexible experimental pipeline in metal-reducing and sulfate-reducing bacteria (SRB) for (1) high-throughput strain/construct generation, (2) evidence-based annotation of gene function using mutagenesis and extensive phenotyping, (3) evidence-based annotation of transcripts using tiling microarrays and RNAseq (4) protein and protein complex isolation (TEM and x-ray techniques), (5) mass spectrometric based proteomic analysis, (6) Protein and protein complex structural analysis, (7) mass spectrometry based metabolomics analysis (GC-TOF, LC-MS/MS, NIMS), and (8) high resolution imaging (FIB/SEM, SBF/SEM, PALM, STORM). Further technology development will enable us to apply our approaches to environmental isolates rapidly and cost effectively. Additionally, we are exploring the integration of diverse data types including metabolomics and high-throughput genetics to elucidate gene function. Long term, these diverse data will form the foundation for predictive models for a number of key microorganisms from a single environment thereby providing a rich resource for assessing ecological questions relevant to microbial community structure and function.

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