

Mechanism across scales: integrating laboratory and field studies for microbial ecology as illustrated by the ENIGMA SFA

L. M. Lui^{1,*}, E. L-W. Majumder^{2,*}, H.J. Smith^{3,*} (hjsmith12@gmail.com), H. K. Carlson¹, F. v. Netzer⁴, T. N. Nielsen¹, M. Peng⁵, X. Tao⁵, A. Zhou⁵, M. Price¹, J. V. Kuehl¹, A.J. Hendrickson¹, V. Trotter¹, S. Gushgari-Doyle¹, J. Valenzuela⁶, A. Otwell⁴, K. Hunt⁴, A. Carr, K. Walker^{7,8}, E. Dixon^{7,8}, F. Poole⁹, M. Thorgersen⁹, X. Ge⁹, M.W.W. Adams⁹, E.J. Alm¹⁰, N.S. Baliga⁶, J.-M. Chandonia¹, A.M. Deutschbauer¹, D.A. Elias⁷, M.W. Fields³, T. C. Hazen^{7,8}, T.R. Northen¹, A. Mukhopadhyay¹, G.E. Siuzdak¹¹, D.A. Stahl⁴, P.J. Walian¹, J. Zhou¹¹, R. Chakraborty¹, A.P. Arkin^{1,12} and **P.D. Adams¹**

*Contributed equally

¹Lawrence Berkeley National Lab, Berkeley; ²University of Wisconsin, Madison; ³Montana State University, Bozeman; ⁴University of Washington, Seattle; ⁵University of Oklahoma, Norman; ⁶Institute for Systems Biology, Seattle; ⁷Oak Ridge National Lab, Oak Ridge; ⁸University of Tennessee, Knoxville; ⁹University of Georgia, Athens; ¹⁰Massachusetts Institute of Technology, Cambridge; ¹¹Scripps Research Institute, San Diego; ¹² University of California at Berkeley, Berkeley.

<http://enigma.lbl.gov>

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.

Abstract

Over the last century, leaps in technology for imaging, sampling, detection, high-throughput sequencing and ‘omics analyses have revolutionized microbial ecology to enable rapid acquisition of extensive datasets for microbial communities across ever-increasing temporal and spatial scales. The present challenge is capitalizing on our enhanced abilities of observation and integrating diverse data types from different scales, resolutions and disciplines to reach a causal and mechanistic understanding of how microbial communities transform and respond to perturbations in the environment. This type of causal and mechanistic understanding will make predictions of microbial community behavior more robust and actionable in addressing microbially-mediated global problems. To discern drivers of microbial community assembly and function, we recognize the need for coordinated, model-driven experiments that integrate the analysis of genomics data, biogeochemical parameters, and ecological and physical forces to rates of microbial growth at specific locations.

To link processes and factors from the gene scale to the ecosystem scale for subsurface microbiology, ENIGMA, a U.S. Department of Energy Science Focus Area, seeks to understand the biogeochemical and microbial processes in the Oak Ridge Reservation (ORR). To accomplish this, we are using a coordinated inter-laboratory framework to link processes and factors from the gene scale to the ecosystem scale. ENIGMA coordinates multiple studies at the

field scale, mesocosm scale, and molecular/species level and has major research thrusts aimed at field surveys, laboratory and bioreactor studies of isolates, syncoms, enrichments, improved isolation methods, genetic tool development, and bioinformatics analyses and tools. We describe how these ENIGMA efforts are being utilized to characterize and build a predictive understanding of the microbial subsurface communities of ORR and how we are generalizing this integrated approach to be applicable to other study systems and environments.

This material by ENIGMA- Ecosystems and Networks Integrated with Genes and Molecular Assemblies a Science Focus Area Program at Lawrence Berkeley National Laboratory is based upon work supported by the U.S. Department of Energy, Office of Science, Office of Biological & Environmental Research under contract number DE-AC02-05CH11231