

151. Identifying Microbial Resource Use with Chip-SIP

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Project Goals: The LLNL Biofuel SFA investigates systems biology of complex microbial communities relevant to bioenergy production. To understand nutrient cycling and potential biofuel production in complex microbial communities we employ an integrated analysis of energy flow using multi-scale approaches including biogeochemical, stable isotope probing, metagenomic/transcriptomic, proteomic/metabolomic and computational analyses. Our ultimate goal is the development of multi-scale models that can predict ecological and biochemical relationships within multi-trophic microbial systems.

One of the key challenges in microbial ecology is determining the ecophysiology of microorganisms in situ complex communities. Stable isotope probing is a technique that identifies taxa that consume specific substrates labeled with rare isotopes in complex assemblages. As part of the LLNL Biofuel SFA, our group developed Chip-SIP, a method which combines NanoSIMS isotope imaging with phylogenetic microarrays to determine the isotopic enrichment of specific populations in the microbial community¹. Recently, we have made a number of recent advances to facilitate the application of Chip-SIP by the greater scientific community. First, we have developed an automated probe design pipeline to accelerate the design of custom Chip-SIP arrays from next-generation sequencing datasets. This process allows researchers to target populations that are specific to their studies. The pipeline clusters taxa into OTUs, generates OTU-specific probes, and then validates the specificity of those probes in-silico using the SILVA database. Second, we have expanded the repertoire of isotopes that can be detected simultaneously by Chip-SIP to include ¹⁸O, in addition to ¹³C and ¹⁵N. Isotopically-labeled water (H₂¹⁸O) is an ideal substrate to identify active populations in many different environments, as all known organisms consume water. Third, we've developed a tool to rapidly detect isotopic enrichment (¹³C, ¹⁵N, ¹⁸O) in picogram quantities of RNA using NanoSIMS, which can quickly identify samples that are suitable for further analysis. Finally, we will report on several recent applications of Chip-SIP: to detect substrate preference in the rhizosphere, and cellulose-degrading communities in the beetle hindgut. These advances highlight the utility of this method to identify specific metabolisms within complex microbial communities, and should facilitate use of the Chip-SIP approach by other research groups working independently or in collaboration with the LLNL Biofuels SFA.

Publications

1. Mayali, X., P.K. Weber, E.L. Brodie, S. Mabery, P. D. Hoeplich, J. Pett-Ridge. (2012). High-throughput isotopic analysis of RNA microarrays to quantify microbial resource use. ISME Journal 6: 1210-1221.

This research was supported by the U.S. Department of Energy Office of Science, Office of Biological and Environmental Research Genomic Science program under the LLNL Biofuels SFA, FWP SCW1039 and collaborative research projects on microbial carbon cycling (with B. Hungate---FWP SCW 1424 and M.K. Firestone---FWP SCW 1421). Work at LLNL was performed under the auspices of the U.S. Department of Energy under Contract DE-AC52-07NA27344. Work at LBNL was performed under the auspices of the U.S. Department of Energy under Contract DE-AC02-05CH11231.