Splitting the Microbiome: High-Throughput Functional Ecology of Microbial Communities

Adam M. Deutschbauer[1,4], Lauren Lui[1], Morgan N. Price[1], Alex Carr[1], Jennifer V. Kuehl[1], Adam P. Arkin[1,3], Hans K. Carlson[1,*]

1Environmental Genomics and Systems Biology Division, Lawrence Berkeley National Laboratory, Berkeley, CA 94720, USA; 2Earth and Environmental Sciences Area, Lawrence Berkeley National Laboratory, Berkeley, CA 94720, USA; 3Department of Bioengineering, University of California, Berkeley, CA 94720, USA; 4Department of Plant and Microbial Biology, University of California, Berkeley, CA 94720, USA

Microorganisms survive, persist and mediate biogeochemical element cycles across spatial and temporal scales in the presence of diverse selective pressures. Only by quantifying the influence of diverse selective pressures on diverse microbial communities can researchers link function and gene content to community structure in an environmental context. We are applying a scalable laboratory-based functional ecology method based on the high-throughput enrichment cultivation of archived and metagenome sequenced microbiomes to quantify the fitness and metabolic traits of genetically diverse microbial sub-populations in selective growth conditions. As an example, we measured the influence of 94 carbon sources on the end-products of microbial nitrate reduction. We enriched for nitrate reducing microbial populations from diverse environments and archived these enrichments by cryopreservation. 16S rRNA amplicon and shotgun metagenome sequencing allowed us to assign gene content to individual microbial sub-populations. By recovering these enrichments with selective carbon sources and measuring the concentration nitrite and ammonium using colorimetric assays, we were able to identify selective carbon sources that favor the growth of microbial sub-populations with increased capacity for ammonium or nitrite accumulation. Isolation of bacterial strains from the enrichments confirmed carbon utilization phenotypes and bioaugmentation confirmed these strains capacity to influence nitrate reduction end-products. Our results add important specificity to the controls on nitrogen cycling and demonstrate important condition-trait-strain-gene linkages to improve our mechanistic models of this process.