17. Compartmentalization of metabolic functions in microbial communities

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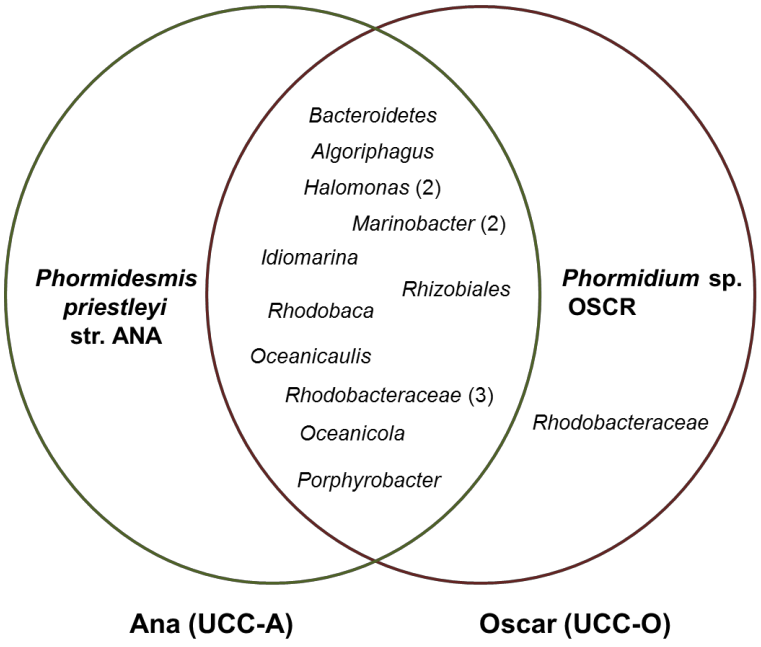
Project Goals:

Microbial mats are laminated biofilm communities of bacteria, archaea, and microeukaryotes embedded in extracellular polymeric substances. The complex and compact spatial structure promotes metabolic networks among community members, leading to efficient energy utilization, nutrient cycling, and obligate mutualistic relationships. Assembly of these communities is driven by a combination of stochastic forces (e.g., colonization order) and deterministic forces (energy acquisition, nutrient availability, resource competition, microbial interactions), while spatial arrangement is constrained by gradients of physical and chemical parameters formed by environmental forces and microbial function. We hypothesize that functional compartmentalization is a mechanism which promotes community diversity and metabolic interaction. These interactions have a stabilizing effect upon diversity, and thereby lead to community resilience to stochastic environmental variation.

To examine niche partitioning and metabolic functional compartmentalization and the effects of key environmental variables upon community composition, we are using metagenomics to study two microbial communities: 1) a laboratory system of two uni-cyanobacterial consortia (UCC-A and UCC-O) derived from the hypersaline Hot Lake phototrophic mat, each containing a single photoautotroph and a stable heterotrophic assemblage, and 2) a field system of low-complexity chemotrophic Fe^{2+}-oxidizing mat communities from geothermal springs. In addition, we have axenic cultures and single-cell genomes (in progress) from each system. The simplified structure of these communities has allowed us to generate near-complete genome sequence for most members of each community. The genomic data is being used to predict the metabolic function of the individual species, which provides a foundation for predicting metabolic interactions. These predictions are subsequently tested through controlled manipulations of community-derived isolates and consortia. Field observations of environmental parameters have been correlated with changes in the community composition, spatial structure and gene content (metabolic potential) to identify key factors driving community assembly and stability.



Metagenomic sequence data collected from the UCC-A and UCC-0 cultures were assembled and segregated into taxonomic bins resulting in 18 distinct, near-complete (est. >90%) genome sequences, 15 of which are shared between the two communities. Each consortium contained a single cyanobacterium that is the sole obligate autotroph, capable of fixing inorganic carbon and N_2. Moreover, each consortium contains a heterotrophic assemblage comprised of members of *Bacteroidetes*, *Gamma-proteobacteria*, and *Alpha-proteobacteria*. Most organisms in the cultures can use urea as a nitrogen source and the gamma-proteobacteria can use cyanate, a by-product of the urea cycle. The alphaproteobacterium *Oceanicola* sp. possesses the most diverse set of carbohydrate catabolic genes and is capable of degrading a range of mono- and di-saccharides, organic acids and sugar alcohols. Conversely, the gammaproteobacterium *Idiomarina* and alphaproteobacterium *Oceanicaulis* spp. are putative amino acid fermenters. Isolate strains were tested for growth on various carbon sources to test these predictions. These predictions highlight examples of potential niche specialization and functional compartmentalization among community members that will be empirically validated using our consortia and isolates of organisms present within them.

Spatial gradients in environmental parameters also promote niche partitioning and functional compartmentalization within microbial mat communities. Within the Yellowstone One Hundred Spring Plain (OSP) Fe^{2+} mats, dissolved O_2 concentrations decrease rapidly with mat depth. As a result of biological consumption O_2 penetration is limited to 700 μm. This gradient correlates with changes in community composition and metabolic potential. The distribution of aerobic (*Hydrogenobaculum, Metallosphaera*) versus anaerobic (*Acidilobales*) populations varies with mat depth, suggesting that O_2 is a critical variable driving community spatial arrangement and stability. Transcript abundance of *Metallosphaera* heme copper oxidases (*foxA*) was higher in the surface layer of OSP mats, and metabolic reconstruction from genome assemblies shows different functional capabilities consistent with the observed spatial compartmentalization.

Together, results from two disparate community types show the importance of metabolic partitioning in promoting microbial interaction. This effect is observed as a function of both time and space and at the resolution of single organisms and entire communities. Our future goal is to develop a mechanistic understanding of niche specialization, spatial and temporal structuring of microbial communities, and individual and community response to changes in environmental variables. Measurement of metabolic potential and/or response in studies of natural communities and isolates/consortia will provide a basis for testing key metabolic interactions as a function of time and space, and how these attributes link with physicochemical properties of environmental systems.