Predictions of Microbial Coexistence on Limited Resources

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Project Goals: To develop a set of ecological and evolutionary principles that explains and can predict the distribution of metabolic networks of microbial communities. In a 'bottom-up' strategy, Metabolomics will be used to determine resource usage patterns of diverse environmental microbial isolates, and these patterns will be used to predict and test mixed community compositions to develop simple rules for biochemical ecology. These principles can then be used to design or modify microbial assemblages.

Microorganisms were the first living beings on this planet, rising from an incredibly dynamic environment. Over the past 3.5 billion years, the environments in which these microbes live have changed dramatically and multicellular life has evolved, creating countless new environments that microbes have colonized, forming interdependent microbial communities. Throughout this time, microbes have developed complex and highly regulated metabolic systems to efficiently use resources. However, until recently, microbes have generally been studied as individuals and little is known what role(s) their metabolic systems have in microbial consortia. In order to fill this knowledge gap, we are determining the resource usage kinetics of microbial isolates of every energy source in defined media.

We use this information to predict how the isolates might behave in mixed communities and how to alter the environment to achieve a desired outcome (e.g. causing one species to dominate the culture). We show quantitative differences between usage of resources in three environmental isolates grown on a defined medium of amino acids and glucose, and discuss how these differences affect the outcomes of mixed community experiments. In addition to targeted metabolomics, we have the capability of conducting high-throughput untargeted metabolomics experiments. The targeted mass spectrometry used to analyze the defined media and spent media informs parameters in the Metabolite Atlas platform, including retention time, relative ionization efficiencies, and fragmentation patterns. Metabolite Atlas users can search their raw experimental data (mass spectra) in the context of this information to more confidentially identify and characterize the compounds detected.

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