

Trait-based approaches for linking metagenomic data with microbial carbon cycling under drought conditions

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<http://allison.bio.uci.edu/projects/a-trait-based-framework-for/>

Project Goals: A key challenge in microbial ecology is to predict the functioning of microbial communities under changing environmental conditions. Metagenomics and other high-throughput molecular approaches can help address this challenge by revealing the functional potential of microbial communities. We coupled metagenomics with models and experimental manipulations to address microbial responses to drought in a California grassland ecosystem along with the consequences for carbon cycling (Fig. 1). We developed an approach for extracting trait information from metagenomic data and asked: 1) What is the phylogenetic structure of drought response traits? 2) What is the relationship between these traits and those involved in carbohydrate degradation? 3) How do both classes of traits vary seasonally and with precipitation manipulation? 4) How resilient are these traits in the face of perturbation?

We found that drought response traits are phylogenetically conserved at an equivalent of 5-8% ribosomal RNA gene sequence dissimilarity. Experimental drought treatment selected for the genetic potential to degrade starch, xylan, and mixed polysaccharides, suggesting a link between drought response and carbon cycling traits. In addition, microbial communities exposed to experimental drought showed a reduced potential to degrade plant biomass. Particularly among bacteria, seasonal drought had a larger impact on microbial composition, abundance, and carbohydrate-degrading genes compared to experimental drought. Bacterial communities were also more resilient to drought perturbation than fungal communities, which showed legacies of drought perturbation for up to three years (Fig. 2). Altogether, these findings imply that microbial communities exhibit trait diversity that facilitates resilience but with substantial time lags and consequences for carbon turnover. This information is being used to inform new trait-based models that address the challenge of predicting microbial functioning under precipitation change.

Publication

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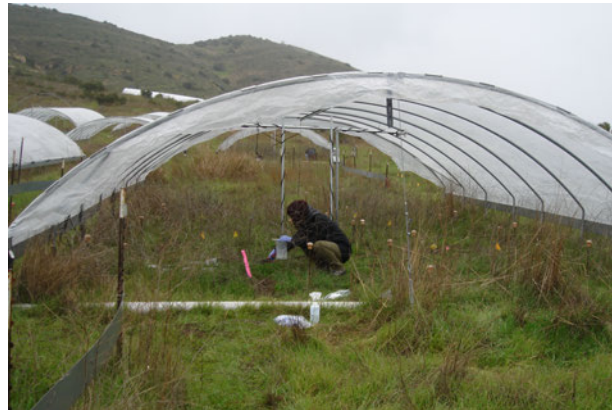


Fig. 1. Drought manipulation

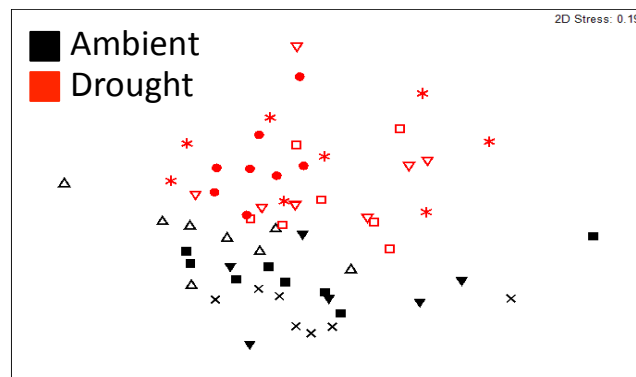


Fig. 2. NMDS ordination of fungal communities four months after transplant