

Fungal and Bacterial Communities Vary in their Carbon Cycling Response to Climate

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

<http://allison.bio.uci.edu/projects/controls-over-decomposition.html>

Project Goals: We aim to uncover the genomic and cellular mechanisms that underlie microbial traits important for carbon cycling under climate change. Traits related to drought tolerance, resource acquisition, and growth yield will be measured with molecular and biochemical approaches. In addition, we will quantify the extent to which trait tradeoffs occur across versus within microbial taxa and the consequences of these tradeoffs for litter carbon loss and transformation into microbial residues. Tradeoff relationships will be used to parameterize models that predict microbial community and carbon cycling responses to climate. The predictions will be validated and further refined with data from field measurements of microbial communities and carbon cycling processes.

Microbial communities are the engines of decomposition, a fundamental process in the carbon cycle. While much is understood about how changes in abiotic conditions and substrate quality affect decomposition rates, the role of microbial community composition remains elusive. This knowledge gap may be key for predicting how ecosystems will respond to climate change.

Here, we first surveyed the microbial community composition of decaying leaf litter along an elevation gradient in southern California, USA. The gradient included five sites with precipitation increasing, and temperature decreasing with elevation. To test the importance of climate for microbial composition, we conducted a transplant experiment. We used “microbial cages” to transplant leaf litter communities to different climates while preventing microbial exchange with the environment. We inoculated transplant communities onto a common, irradiated, grassland litter. In contrast with observational data, this manipulation isolates the effects of climatic conditions versus that of microbial composition on litter decomposition. To characterize fungal and bacterial community composition, we extracted DNA from the inoculum, intact litter at sites, and litter in the microbial cages, and amplified and sequenced part of the ITS and 16S rRNA regions. We also analyzed microbial biomass with fungal hyphal abundance counts and bacterial flow cytometry. We investigated the functional consequences of these transplants by measuring decomposition as mass loss and analyzing nutrient content.

We hypothesized that communities from along the climatic gradient would differ in their abundance and composition, and that communities at the extremes of the gradient would be most affected by climate. We found that microbial communities did indeed differ greatly between the

five sites (PERMANOVA; Fungi: $R^2 = 0.58$, $P < 0.01$; Bacteria: $R^2 = 0.61$, $P < 0.01$) with fungi primarily dominated by the Ascomycota. The main axis of community separation appeared to be between the colder and wetter sites versus the hotter and drier sites.

After transplantation, fungal communities retained a strong signature of the inoculum whereas bacteria were quickly influenced by local climate. Inoculum source was the strongest factor influencing fungi ($R^2 = 0.57$, $P < 0.01$), but site was also significant ($R^2 = 0.14$, $P < 0.01$). In contrast, site was the strongest factor affecting bacterial composition ($R^2 = 0.34$, $P < 0.01$), although inoculum source was also significant ($R^2 = 0.16$, $P < 0.01$). A strong site by inoculum interaction effect for both fungi ($R^2 = 0.15$, $P < 0.01$) and bacteria ($R^2 = 0.19$, $P < 0.01$) indicates that the strength of the inoculum effect varied by site, meaning that not all communities responded similarly to the climate gradient. In contrast to our expectation, communities from the extremes of the gradient were not most affected by climate. Instead, intermediate communities had the most significant impacts on decomposition and types of carbon compounds degraded when transplanted. Moreover, significant site by inoculum interactions impacting decomposition lasted a year after transplantation. These results demonstrate that microbial communities affect decomposition, but bacteria will shift more rapidly in response to climate than fungi, with fungi retaining a strong inoculum signal even after 1.5 years.

Publication

1. Glassman, SI, C Weihe, J Li, MBN Albright, C Looby, AC Martiny, KK Treseder, SD Allison, JBH Martiny. 2018. Microbial communities vary in their carbon cycling response to climate. In preparation.

This research was funded by the Genomic Science Program and the US National Science Foundation Ecosystem Studies Program. The Genomic Science Program is part of the Biological System Science Division (BSSD) of Biological and Environmental Research (BER) in the US Department of Energy Office of Science.

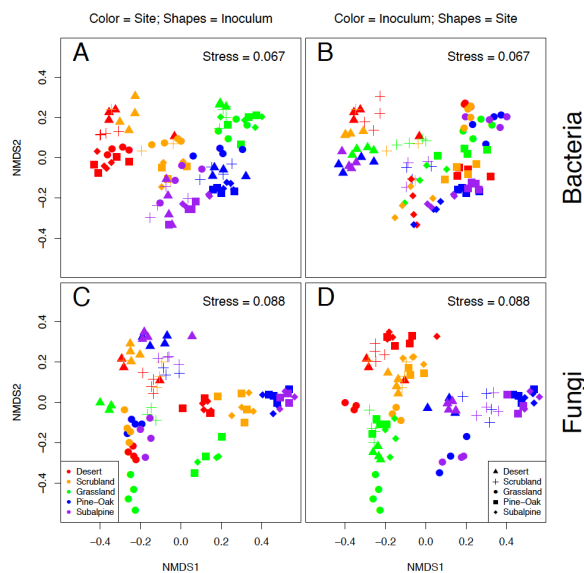


Fig. 1. NMDS of Bray-Curtis microbial community composition at 18 months for A) bacteria (16S) colored by site and shapes by inoculum and B) bacteria colored by inoculum and shapes by site. The bottom two panels are both fungal community composition with either C) colored by site or D) colored by inoculum.