

Microbial Communities Exhibit Resilient Extracellular Enzyme Activity Along a Climate Gradient

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Project Goals: The effects of climate change on litter decomposition rates and carbon cycling are uncertain. Environmental microbes significantly contribute to both processes; however, the physiological constraints faced by the microbes from environmental stress is not fully understood. We aim to understand the cellular mechanisms and biochemical activities of environmental microbes under stressful environmental conditions simulating future climate change. By analyzing microbial community extracellular enzyme activity, we can infer the effects of changing climate on litter decomposition and thereby carbon cycling. The goal is to test the dependency of litter decomposition on microbial communities, and to predict the effects of future climate change on microbial activity.

Understanding the consequences of environmental change for the microbial regulation of carbon and nutrient cycling is a critical need. We collected data on extracellular enzyme activities from an 18-month experiment where microbial communities were reciprocally transplanted along a Southern California elevation gradient with inverse variation¹ in temperature and precipitation. The microbial communities were from desert, scrubland, grassland, pine-oak, and sub-alpine ecosystems. By simulating different temperature and precipitation changes for ecosystem-specific microbial communities, this study was designed to predict microbial community response and resilience to future environmental changes. Our first hypothesis proposed a “home field advantage” (HFA) of enzyme activity and litter decomposition, where microbial communities in their home ecosystem outperform microbial communities transplanted from other ecosystems. Our alternate hypothesis states that transplanted microbial communities will exhibit functional resilience by producing enzymes and decomposing litter at the same rate as native microbial communities when exposed to temperature and precipitation changes. Microbial community extracellular enzyme activities were evaluated with analysis of variance. Enzyme datasets yielding a significant ($p < 0.05$) site by microbial community interaction were further analyzed with Tukey post hoc comparisons within each site to compare the extracellular enzyme activities associated with different microbial communities. Our results partially supported the microbial community resilience hypothesis with respect to extracellular enzyme activity. Significant interaction effects did not support our HFA hypothesis and instead indicated a home field disadvantage, where the transplanted microbial community displayed higher extracellular enzyme activity than the native community. Our findings suggest that transplanted microbes are resilient to climate change, which may be due to their previous adaptations to extreme temperatures and drought. These enzymatic

patterns are consistent with litter decomposition rates, which also did not exhibit home field advantage.

Figure 1: Conceptual diagram of home field advantage (HFA) and functional resilience hypotheses. With HFA, extracellular enzyme (EE) activities of native microbial communities should be significantly greater than those of transplanted microbial communities. Alternatively, our functional resilience hypothesis states that the enzyme activities of all microbial communities are the same, regardless of microbial origin. The x-axis indicates the desert, scrubland, grassland, pine-oak, and sub-alpine microbial communities, respectively. Bold lines within the boxplot are the replicate averages for each microbial community. Boxplots encompassed in a rectangle denote the home field microbial community (desert in this case).

