

## 147. Microhabitat-dependent responses of bacterial and fungal communities to experimental nitrogen additions in arid ecosystems

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**Project Goals:** Anthropogenic N deposition is a chronic and increasing condition in temperate regions that may strongly influence C cycling dynamics. One major theme of our Science Focus Area is to determine the influence of chronic N deposition on microbial C cycling processes in two major biomes of Earth's temperate regions, forests and arid grass/shrublands. In both biomes fungal and bacterial biomass is concentrated in shallow surface soil strata where C and N cycling are major processes. The goals of this project are to (a) correlate the resident fungal and bacterial communities, enzyme activities, and local geochemistry across shallow strata of strongly stratified forest soils and biocrust dominated soils of arid grass/shrub lands, (b) determine the impacts of chronic N amendment across multiple forest and arid grass/shrubland biomes using a suite of long-term field experiments, and (c) compare the ability of phylogenetic rRNA gene surveys, soil enzyme assays, and metatranscriptome surveys to detect shifts in community structure and concomitant changes in C cycling processes in response to altered N conditions. Achieving these goals will provide an understanding of the active and responsive components of arid land soils that contribute to carbon cycling, their collective responses to environmental change, and development of efficient molecular tools for broad-scale soil monitoring. This poster focuses on our recent results from two arid land N deposition experiments.

Research on microbial communities, both in terms of surveying resident communities and quantifying response to environmental perturbations, has largely ignored arid ecosystems.

However, drylands cover ~40% of the terrestrial surface of the earth, and are expanding in many regions as a result of desertification. Historical inputs of nitrogen to drylands are generally low, but are increasing due to human activities. The climatic conditions and nutrient cycles in these ecosystems differ dramatically from well-studied mesic systems; they are characterized by highly variable environmental conditions due to sporadic precipitation events, extreme temperature fluctuations and UV radiation stresses, as well as low productivity, patchy distributions of biotic resources (microhabitats) and atypical sources of nutrient inputs. Given these unique characteristics, it is unlikely that responses seen in mesic forests and grasslands will apply in drylands.

We are using high throughput sequencing methods to target the soil bacterial and fungal communities, which together are responsible for the majority of nutrient cycles, including the N and C cycles. These studies were conducted at experimental N deposition field experiments located in an arid shrubland (Nevada) and an arid grassland (Utah) in the Southwestern US. We are applying multivariate statistical approaches to examine shifts in the phylogenetic structure of these communities. In an effort to predict the functional effects of community shifts, we are simultaneously measuring relative microbial biomass, soil chemistry and enzyme assays to link specific environmental shifts to community responses and their functional consequences.

Community surveys indicate that microbial community responses differed between the two sites. In the arid grassland, we found no evidence for community changes in either bacteria or fungi. In the shrubland, however, community composition results found divergent responses of the bacterial and fungal communities, shifts that are dependent upon microhabitat and soil depth. Unlike responses commonly

seen in temperate systems, we found limited response in the fungal community, but strong shifts in richness, community composition and overall relatedness in the bacterial community. We also documented increased fungal and bacterial biomass (qPCR), elevated photosynthetic activity in biocrusts, and shifts toward enzymes linked to phosphorus acquisition in the N plots. There is thus evidence for shifts toward fungal-dominated nutrient cycling in response to nitrogen additions. By combining sequence-based community analyses with soil and enzyme activity measures, we may identify key responsive community members with relevance as indicators of community change and with utility for modeling soil processes.

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