

Linking Genes to Ecosystem Processes: Microbial Nitrogen and Carbon Cycling

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<http://www.lanl.gov/org/padste/adcles/bioscience/bioenergy-biome-sciences/soil-carbon.php>

Project Goals:

Project 1: Identify nitrogen (N) deposition linked molecular markers in a short-term controlled laboratory experiment to develop the capability of monitoring N- responses in more complex field settings.

Project 2: Determine the prevalence of incomplete versus complete N cycling pathways, as well as the distribution of N cycling pathways across sequenced prokaryotic genomes, to inform meta-omic studies using these genetic markers.

Project 3: Describe the spatial distribution of bacteria and fungi on plant litter during decomposition to assess the potential for nutrient exchanges among microbes.

Abstract

The LANL Genomic Science SFA aims to inform climate modeling and enable carbon management. The SFA uses genomics approaches to reveal microbial processes affecting biogeochemical cycling (e.g. C and N cycling) in terrestrial ecosystems. This involves discovery of fundamental principles driving the organization and interactions of soil microbes at multiple scales.

The work presented here addresses BER grand challenge 4.2: define the sphere of influence and key elements of microbial communities in space and time relevant for predicting larger-scale ecosystem phenomena for Earth system understanding. Genomic data needs to be simplified for tractable application in ecosystem models. However, current approaches of consolidation have not been effective. The abundances of functional genes are inconsistently correlated with associated process rates. Moreover, studies routinely find ecosystem-specific responses to environmental perturbations such as N deposition instead of common patterns among ecosystems. Achieving the goal of predictive biology will require new ways of characterizing microbial communities and their functions in terrestrial environments.

Here, we summarize three complementary, but independent projects. The first project focuses on identifying genetic marker response to N addition. Numerous studies have examined the long-term effect of experimental N deposition in terrestrial ecosystems, however N-specific mechanistic markers are difficult to disentangle from responses to other environmental changes. The strongest picture of N-responsive mechanistic markers is likely to arise from measurements over a short (hours to days) timescale immediately after the deposition of inorganic N. To test the hypothesis that N fertilization represses the initial expression of fungal and bacterial genes linked to N-mining from plant litter, we performed a soil meta-transcriptome study in laboratory microcosms. We examined the short-term (3-day) transcriptional response of pine forest

microbial communities in two soil strata to a high dose of N fertilization. **The observed transcriptional response to N deposition was extremely weak, suggesting that direct N repression of microbial functional gene expression is not the principle mechanism for reduced soil respiration immediately after N deposition.**

The second project explores the distribution of N cycle genetic markers across bacterial and archaeal genomes. Attempts to link microbial communities to ecosystem processes regularly use marker genes to represent relevant biochemical pathways. This approach often fails to demonstrate a positive relationship between a gene of interest and the corresponding ecosystem process rate. Inaccurate measurement of marker gene abundance may contribute to failure. In this study, nitrogen metabolism (N-cycling) pathways were mapped in over 6000 complete prokaryotic genomes in the Integrated Microbial Genomes (IMG) database. **The analysis revealed many partial and incomplete N cycling pathways in complete genomes, pointing to a substantial weakness in current marker-gene analyses.**

The third project assesses the potential for nutrient exchanges among microbes on decomposing plant litter. Scanning electron microscopy (SEM) was used to measure the extent of fungal and bacterial colonization of decomposing pine needles. **The observed microbial colonization of pine needles is sparse, with much open space, suggesting ample opportunity for nutrient loss/leaching from decomposing plant litter.** Collectively, this research points towards gaps to address for robust linkage of microbial community composition to ecosystem processes.

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