80. Denitrifying and diazotrophic community responses to artificial warming in permafrost and tallgrass prairie soils

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Project Goals: The overall goal of this project is to advance system-level predictive understanding of the feedbacks of belowground microbial communities to multiple climate change factors and their impacts on soil C cycling processes. Towards this goal, we are pursuing the following objectives: (i) To determine the responses of microbial community structure, functions and activities to climate warming, altered precipitation, soil moisture regime and/or clipping in the tundra and temperate grassland ecosystems; (ii) To determine the temperature sensitivity and substrate priming on recalcitrant C decomposition; (iii) To determine microbiological basis underlying temperature sensitivity of recalcitrant C decomposition; and (iv) To develop integrated bioinformatics and modeling approaches to scale information across different organizational levels towards predictive understanding of ecosystem responses to multiple climate change factors, which will be collaborated and integrated with the KBase.

Increasing air temperatures has been shown to impact soil biogeochemical processes, although the corresponding changes to the underlying microbial functional communities are not well understood. Alterations in the nitrogen (N) cycling functional component are particularly important as N availability can affect microbial decomposition rates of soil organic matter and influence plant productivity. To assess these changes, the composition of the N-fixing (nifH), and denitrifying (nirS, nirK, nosZ) soil microbial communities was assessed by targeted pyrosequencing of functional genes involved in N cycling in Oklahoma (OK) tallgrass prairie and Alaskan (AK) permafrost soils at sites where the experimental effect of climate warming is under investigation. Raw reads were processed for quality, translated with frameshift correction, and a total of 313,842 amino acid sequences were clustered and linked to a nearest neighbor using reference datasets. The number of OTUs recovered ranged from 231 (NifH) to 862 (NirK). The N functional microbial communities of the prairie, which had experienced a decade of experimental warming were the most affected with changes in the richness and/or overall structure of NifH, NirS, NirK and NosZ. In contrast, the AK permafrost communities, which had experienced only one year of warming, showed decreased richness and a structural change only with the nirK-harboring bacterial community. A highly divergent nirK- harboring bacterial community was identified in the permafrost soils, suggesting much novelty, while other N functional communities exhibited similar relatedness to the reference databases, regardless of site. Prairie and permafrost soils also harbored highly divergent communities due mostly to differing major populations. Lastly, in order to capture a higher percentage of functional gene harboring microbial communities, we have implemented a primer design tool. New nosZ primer sets have been designed, capturing >93% of diversity among 1,600 reference
sequences.

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