

## 82. Functional and taxonomic characterization of Alaskan permafrost and Oklahoma prairie soils using comparative metagenomics: implications for responses to climate change

Konstantinos T. Konstantinidis<sup>1\*</sup> ([kostas@ce.gatech.edu](mailto:kostas@ce.gatech.edu)), Eric R. Johnston<sup>1</sup>, Chengwei Luo<sup>1</sup>, Luis M. Rodriguez-R<sup>1</sup>, Liyou Wu<sup>2</sup>, Shi Zhou<sup>2</sup>, Kai Xue<sup>2</sup>, Zhili He<sup>2</sup>, Mengting Yuan<sup>2</sup>, Yiqi Luo<sup>2</sup>, Edward A.G. Schuur<sup>3</sup>, James R. Cole<sup>4</sup>, James M. Tiedje<sup>4</sup>, Jizhong Zhou<sup>2</sup>

<sup>1</sup>Georgia Institute of Technology, Atlanta, GA 30332, USA; <sup>2</sup>University of Oklahoma, Norman, OK 73019, USA; <sup>3</sup>Northern Arizona University, Flagstaff, AZ 86011, USA; <sup>4</sup>Michigan State University, East Lansing, MI 48824, USA.

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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. Regarding 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 of recalcitrant C decomposition; (iii) To determine the 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.

Under this project, we have investigated microbial communities from Alaskan tundra permafrost (AK) and Oklahoma temperate grassland (OK) soils, both of which have been experimentally warmed 2 to 4°C for five years above ambient temperature in-situ. Our analyses of well-replicated 16S rRNA gene amplicon, meta-transcriptomic, and whole- community shotgun metagenomic datasets from these soils after one year of warming (5- year data are forthcoming) showed small but significant shifts in community composition, gene expression, and functional metabolic potential compared to the control (unwarmed, adjacent communities). The specific microbial populations and gene/pathways enriched by warming were different between AK and OK. Greater taxonomic composition differences were observed at the OK site relative to AK, presumably resulting from longer generation times due to the less optimal conditions for growth at permafrost soils. Analysis of rRNA gene amplicons recovered in the shotgun-metagenomic data revealed no significant shifts in fungal taxa at both sites, but that the ratio of fungi to bacteria decreased with warming, indicating that the warming treatment was more favorable for bacteria, at least in the short term. The most pronounced bacterial taxon shifts observed at OK site, which was somewhat also observed at the AK site, were an increase in abundance of Actinobacteria and a decrease in Planctomycetes, both representing major phyla in soils, particularly involved in C cycling. In terms of functions, the communities of AK warmed plots were enriched in metabolic pathways related to labile carbon mobilization and oxidation whereas fewer of these patterns were observed in the OK communities, indicating that soil C was more vulnerable to microbial respiration at AK. The OK communities were instead enriched in genes involved in heat shock response and cellular surface structures, particularly, trans-membrane transporters for glucosides and ferrous iron. These results, which were consistent with independent physicochemical measurements and process rates determined in-situ, were linked with higher primary productivity of the aboveground plant communities stimulated by warming. By implementing a new contig binning strategy, we recovered large genomic fragments (>500Kbp continuous; 2-8Mbp non-continuous) representing several abundant populations (0.2-2% of the total community) in the AK metagenomes. These populations appeared to be highly conserved across spatial and environmental

gradients at the AK site and apparently played a key role in microbial community response to the warming treatment. Collectively, our findings suggest that microbial communities of grassland soils play important roles in mediating feedback responses of the soil ecosystem to climate change and that even short periods of warming induce significant changes in microbial community function and composition

To enable this research, we have also developed several bioinformatics tools that addressed practical limitations during the comparative analysis of the soil metagenomes such as how to assess the fraction of the community captured by a metagenomic dataset and estimate the sequencing effort required in study design (Nonpareil tool; Rodriguez-R and Konstantinidis, Bioinformatics 2013), how to determine the taxonomic affiliation of a metagenomic sequence (MyTaxa; Luo et al., NAR 2014), how to bin assembled contigs into population genomes based on time-series metagenomes (BinGeR; Luo et al., in preparation), and how to determine differentially present genes between metagenomic datasets (Luo et al., Methods Enzymol. 2013). Altogether, these make up our Microbial Process Toolkit for gene, metagenomic and metatranscriptomic data integration, modeling and visualization. We are in the process of implementing our toolkit in KBase and we will report on these efforts as well.

#### References

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*Funding statement: Our work is supported by the U.S. DOE Office of Science, Biological and Environmental Research Division (BER), Genomic Science Program, Award No. DE-SC0010715.*