Metagenomics-Enabled Predictive Understanding of Microbial Communities to Climate Warming: Results from Long Term Soil Incubations and Modeling Simulations

Elaine Pegoraro[1], Junyi Liang[4], **Edward A.G. Schuur[1]*** (Ted.Schuur@nau.edu), Rosvel Bracho[2], Susan Natali[3], Ji Chen[4], Chang Gyo Jung[4], Wenting Feng[4], Mengting Yuan[4], Xue Guo[4], Lauren E. Hale[4], **Liyou Wu**[4], Jiajie Feng[4], Cong Wang[4], Xishu Zhou[4], **Zhili He**[4], Jim Cole[5], **James M. Tiedje**[5], **Konstantinos Konstantinidis**[6], Katherine Todd-Brown[4], **Yiqi Luo**[4] **and Jizhong Zhou**[4]

[1]Center for Ecosystem Science and Society, Northern Arizona University, Flagstaff, AZ; [2]School of Forest Resources & Conservation, University of Florida, Gainesville, FL; [3]Woods Hole Research Center, Falmouth, MA; [4]Institute for Environmental Genomics and Department of Botany and Microbiology, University of Oklahoma, Norman, OK; [5]Center for Microbial Ecology, Michigan State University, East Lansing, MI; [6]Center for Bioinformatics and Computational Genomics and School of Biology, Georgia Institute of Technology, Atlanta, GA.

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Project goal: 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 carbon (C) cycling processes. The main objectives of this integrative project are to (i) determine the responses of microbial community structure, functions and activities to an increased input of easily decomposable C substrates to soil (priming effects); (ii) determine the extent to which priming enhances mineralization of native soil C; (iii) determine what proportion of the increased mineralization of native soil C is old C; (iv) determine if substrate input with different C quality distinctively affects microbial activity and soil organic matter decomposition; and (v) develop integrated bioinformatics and modeling approaches to scale information across different organizational levels. This study focuses on using laboratory incubations of soil as an isolated system to understand the influence of microbial processes on the release of C, and their response to changes in easily decomposable C substrate inputs.

Warming of tundra ecosystems due to climate change is predicted to thaw permafrost and increase plant biomass and litter input to soil. Additional input of easily decomposable carbon (C) can alter microbial activity by providing a much needed energy source to microbes, thus accelerating soil organic matter decomposition. This phenomenon, known as the priming effect, can increase CO_2 flux from soil to the atmosphere; however, the extent to which it could decrease soil C stocks in the Arctic is unknown. This project investigates priming effects on permafrost soil. We hypothesized that priming would increase and change microbial activity and composition, thus increasing mineralization of old and slowly decomposing C. We are conducting a long-term (> 1 year) incubation experiment that started in July 2015. Soil cores were collected in 2013 from a moist acidic tundra site in Healy, Alaska, from surface (0-15 and 15-25 cm) and deep permafrost layers (45-55, 65-75, and 75-85 cm). Samples were incubated aerobically, at 15 ℃. We amended soil samples with uniformly ^{13}C labeled glucose and cellulose to quantify changes in C mineralization rates attributable to the added substrates. Carbon dioxide flux and $^{13}CO_2$ measurements were coupled and measured every 24 hours for the first 5 days, every 35 hours for 8 days, and every couple of weeks for 4 months. We also sampled $^{14}CO_2$ at days 0, 15, and 105 of incubation to identify the age of respired C. Data shows that substrate

additions resulted in higher respiration rates in amended soils; however, priming was only observed in deep layers amended with glucose, where on average 22%, 29%, and 10% more soil C was respired at 45-55, 65-75, and 75-85 cm, respectively. This suggests that microbes in deep layers are limited in energy due to greater fractions of slowly decomposing C; therefore, additional input of easily decomposable C increases native organic matter decomposition. Glucose and cellulose will be added every 4 months to simulate field input of root exudates, new root biomass, and dissolved organic C leachate, and the same measurements will be performed until Fall 2016. Microbial composition, structure, and dynamics will be measured during the second substrate amendment at days 7, 15, and 65 of incubation using two techniques: the functional gene structure analysis, GeoChip and phylogenetic composition using 16S rRNA gene sequencing on Miseq.

In the same time, model-data assimilation is used to explore effects of possible microbial activity change by long-term field warming on soil C dynamics. Soils were sampled from a long-term warming experiments. In each treatment of both control and warming, two soils, bulk soil and soil from a deep collar, which was inserted in 2000, were sampled. Totally, there are four field treatments, bulk soil at control, deep collar at control, bulk soil at warming, deep collar at warming. Each treatment has 6 replicates. After pre-treatment in lab, the soil samples were incubated at 15 ℃ for 406 days and 25 ℃ for 365 days. A three-pool model, with active, slow, and passive pools, is used to simulate the soil C dynamics during incubation. A Markov Chain Monte Carlo (MCMC) technique is applied to do the model-data assimilation. Results show that CO_2 emission is different among treatments, indicating long-term field warming may change soil microbial activity, which determines soil C dynamics. In addition, long-term field warming significantly increased the decay rates of slow and passive pools. Our results suggest that the changed microbial activity by long-term field warming can accelerate the decomposition of soil C pools with relatively long residence time, which can potentially affect the feedback to long-term climate change. During the incubation, microbial composition, structure, and dynamics were measured at 2 weeks, 3 months, and 9 months using GeoChip. We are analyzing these data to explore the effects of the functional genes on soil C dynamics.

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