From Community Structure to Functions: Metagenomics-Enabled Predictive Understanding of Microbial Communities to Climate Warming in Alaskan Tundra

Edward A.G. Schuur[1] (tschuur@ufl.edu)**, Jizhong Zhou**[2], Liyou Wu[2], Kai Xue[2], Lei Cheng[2], Mengting Yuan[2], Jin Zhang[2], Ye Deng[2], Joy D. Van Nostrand[2], **Zhili He**[2], Ryan Penton[3], Jim Cole[3], **James M. Tiedje**[3], Rosvel Bracho-Garrillo[1], Chengwei Luo[4], **Konstantinos Konstantinidis**[4], Xia Xu[2],Dejun Li[2], and **Yiqi Luo**[2]

[1]Department of Biology, University of Florida, Gainesville, FL; [2]Institute for Environmental Genomics and Department of Botany and Microbiology, University of Oklahoma, Norman, OK; [3]Center for Microbial Ecology, Michigan State University, East Lansing, MI; [4]Center for Bioinformatics and Computational Genomics and School of Biology, Georgia Institute of Technology, Atlanta, GA

Determining the responses, adaptations and feedback mechanisms of biological communities to climate change is critical to project future states of the earth and climate systems, but poorly understood for microbial communities. We have carried out our studies at two contrasting long-term experimental facilities, a tundra ecosystem in Alaska (this poster) and a grassland ecosystem in Oklahoma (Poster led by Zhou et al).

Effects of experimental and natural warming of deep soil and permafrost on ecosystem carbon balance in Alaskan tundra. Approximately 1670 Pg (billion tons) of soil carbon are stored in the northern circumpolar permafrost zone, more than twice as much carbon than currently contained in the atmosphere. Permafrost thaw, and the microbial decomposition of previously frozen organic carbon, is considered one of the most likely positive feedbacks from terrestrial ecosystems to the atmosphere in a warmer world. Here we report results from two experimental systems that examine this question: **1)** a natural gradient of permafrost thaw where *minimal*, *moderate*, and *extensive* permafrost degradation has been observed over a decadal time scale, and **2)** a new ecosystem warming manipulation —the Carbon in Permafrost Experimental Heating Research (CiPEHR) project—where we increased air and soil temperature, and degraded the surface permafrost. Within these experiments, net ecosystem C exchange and the radiocarbon age of ecosystem respiration were measured to determine the influence of old C loss on ecosystem C balance. By partitioning respiration sources across the thaw gradient, we determined that areas that thawed over the past 15 years had 75% more annual losses of old C compared to minimally thawed areas, but had overall net ecosystem C uptake as increased plant growth offset these losses. In contrast, sites that thawed decades earlier lost an additional 25% more old C annually, which contributed to overall net ecosystem C release despite increased plant growth. These findings were mirrored by the warming experiment where increased plant uptake appears to compensate for microbial release of carbon, at least in the three years of warming that we have observed. Together, these data document significant losses of soil C with permafrost thaw that, over decadal time scales, overwhelms increased plant C uptake at rates that could make permafrost a large biospheric C source in a warmer world, similar in magnitude to current C fluxes from land use change.

Patterns of permafrost thaw influence on tundra microbial communities. Microbial communities from the permafrost thaw gradient were analyzed by Geochip 4.0. Six cores were

taken from each of the minimal, moderate and extensive permafrost thaw sites; each core contained 6-7 sections by depth (2-3 organic and 3-4 mineral fractions). Various statistical analyses (detrended correspondence analysis, dissimilarity tests and multiple regression tree) all showed that the thaw gradient (sites) was more important than depth in influencing soil microbial community structure, though both had significant impacts. The Simpson diversity index was significantly different across the sites, with the highest value at minimal thawing site and lowest at moderate thawing site. For genes involved carbon degradation, there was no consistent trend across the thaw gradient, though significant differences were observed in some genes. Both methane production and oxidation genes were significantly affected by permafrost thaw, with highest abundances at minimal site and lowest at moderate site. For nitrogen cycling, the abundance of denitrification genes was generally higher at minimal site with only one exception of *narG*, likely due to a more anaerobic condition at minimal site. The genes in assimilatory nitrogen reduction were generally higher at the moderate thaw site, though *nasA* did not differ among three sites, indicating high plant and microbes activity at the moderate site.

Laboratory determination of microbial temperature sensitivity. To determine the temperature sensitivity of microbial respiration (Q_{10}) in soils with different mixtures of labile versus recalcitrant carbon, we are conducting soil incubations of soils from different depths at two constant temperatures (15°C & 25°C). These soils came from a warming experiment in a tundra ecosystem in Alaska and a warming experiment in a grassland in Oklahoma. Three different layers were incubated from Alaska: two surface soils (0 – 15 cm & 15 – 25 cm with high carbon content) and a horizon deeper (>50 cm) within the surface permafrost. From the Oklahoma site, we used soils from control and warmed plots combined with a root exclusion treatment that had kept new root inputs out over the 8 years of the experiment. Instantaneous Q_{10} was measured by exposing soils to 6 different temperatures ranging from 5 to 30°C while measuring CO_2 flux over this range. For Alaskan soils, warmed soils from 0 – 15 cm layer had a slightly higher, but not significant, average Q_{10} than the control plots. No other differences in average Q_{10} were detected for different soil layers or treatments. However, carbon fluxes in the first 15 cm were 10 and 35 times higher than fluxes at 15 – 25cm or from the permafrost soil, respectively.

Modeling integration and development. A new model was developed based on the soil C dynamics model developed at the early stage of the project. The main objectives of the model are to calculate Q_{10} using a data-model fusion technique, and to evaluate dynamics of Q_{10} with recalcitrance of soil organic C (SOC). Q_{10} and turnover rates for different C pools (labile, slow and passive pools) and fraction of each C pool can be optimized using Bayesian probability inversion and a Markov chain Monte Carlo (MCMC) technique. This approach generates posterior probability density functions of model parameters. A previously published dataset using three incubation temperatures (15, 25 and 35 °C) and an incubation period of 588 days was used to test the model. Preliminary results show that Q_{10} values for labile and slow C pools can be constrained very well at temperature regimes of both 15-25 °C and 25-35 °C, but only the Q_{10} value at 25-35 °C can be well constrained for the passive pool. Based on the dataset, Q_{10} values increase with recalcitrance of SOC. This preliminary result also indicates that longer incubation studies are needed in order to assess the temperature sensitivity of slower turnover pools, especially at low temperature regimes. Further work will push towards integrating microbial community into an ecosystem modeling framework.