84. Methods for estimating temperature sensitivity of soil organic matter based on incubation data: A comparative evaluation

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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 K-Base.

Abstract: To better understand the temperature sensitivity (Q10) of soil organic matter (SOM) decomposition, we compared several commonly used methods (i.e., one-pool (1P) model, two- discrete-pool (2P) model, three-discrete-pool (3P) model, and time-for-substrate (T4S) Q10 method) plus a new and more process-oriented approach for estimating Q10 of SOM decomposition from laboratory incubation data to evaluate the influences of the different methods and assumptions on Q10 estimation (Liang et al., 2015). The process-oriented approach is a three-transfer-pool (3PX) model that resembles the decomposition sub-model commonly used in Earth system models. The temperature sensitivity and other parameters in the models were estimated from the cumulative CO2 emission using the Bayesian Markov Chain Monte Carlo (MCMC) technique. The estimated Q10s generally increased with the soil recalcitrance, but decreased with the incubation temperature increase. Our results indicated that the 1P model did not adequately simulate the dynamics of SOM decomposition and thus was not adequate for the Q10 estimation. All the multi-pool models fitted the soil incubation data well. The Akaike information criterion (AIC) analysis suggested that the 2P model is the most parsimonious. As the incubation progressed, Q10 estimated by the 3PX model was smaller than those by the 2P and 3P models because the continuous C transfers from the slow and passive pools to the active pool were included in the 3PX model. Although the T4S method could estimate the Q10 of labile carbon appropriately, our analyses showed that it overestimated that of recalcitrant SOM. The similar structure of 3PX model with the decomposition sub-model of Earth system models provides a possible approach, via the data assimilation techniques, to incorporate results from numerous incubation experiments into Earth system models.

However, it is difficult to constrain the transfer parameters between carbon pools based on the soil respiration data alone (Liang et al., 2015). We propose using the change in functional gene quantified over the course of an incubation to further constrain these models. We took soils from a field warming and deep collar experiment in Oklahoma and incubated the cores over 9 months. In addition to traditional bulk soil organic carbon measurements and soil respiration readings, we quantified the DNA associated with 14,000+ genes involved in carbon degradation and metabolism using GeoChip at 2 weeks, 3 months,

and 9 months during the incubation. Genes were selected as 'fast' genes if they did not increase during the incubation and dropped below 50% of their initial expression levels. Fast genes were then averaged and used with CO2 respiration readings to constrain the parameters of the 3PX model. The results showed that each field treatment has a unique microbial community associated with the fast pool. The fast genes were not enriched with labile carbon metabolic genes and instead were roughly proportional to the gene types sampled. Fast pool estimates provided more information on several parameters for the model without resulting in different carbon predictions over 100 years.

References:

1. Liang J, Li D.,Shi Z., Tiedje J.M., Zhou J., Schuur E.A.G., Konstantinidis K.T., Luo Y. (2015) Methods for estimating temperature sensitivity of soil organic matter based on incubation data: A comparative evaluation. Soil Biology & Biochemistry 80: 127-135.

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