

Get Your Model Out of the Clouds! Ground-Truthing Assumptions About how the Earth's Tiniest Engines Drive the Carbon Cycle

Grace Pold^{1*} (apold@umass.edu), Seeta Sistla,² Serita D. Frey,³ Kevin Geyer,³ Stuart Grandy,³ and **Kristen M. DeAngelis**⁴

¹University of Massachusetts, Amherst; ²Hampshire College, Amherst, MA; ³University of New Hampshire, Durham

Project Goal: Our long-term goal is to better predict the fate of soil C by developing mathematical and ecosystem models of SOM decomposition that incorporate a genetic and physiological understanding of CUE. Specifically, we propose to define the genomic basis of soil microbial CUE in the context of changing environments, and use this new knowledge to generate more realistic models of SOM decomposition.

Soil microbes are central players in Earth's carbon cycle, yet the diverse physiologies displayed by these organisms are poorly integrated into models of the carbon cycle. Such negligence exists on the one hand due to the ignorance about the role soil microbes play, and on the other hand due to the infeasibility of integrating the entirety of microbial physiology into models. To overcome these shortcomings, we are completing extensive physiology and comparative genomics of bacterial and fungal isolates to identify scalable genomic markers of key steps in microbial processing of soil organic matter. This data will be used to modify the structure and parameterization of soil carbon models working on a number of temporal and spatial scales in order to evaluate how soil carbon stocks may change with climate warming. Preliminary research shows that the efficiency with which bacteria convert soil carbon to additional cell biomass differs between temperatures in a "species"-specific manner. Further work to identify the specific responses of bacteria and fungi to other environmental stressors is expected to greatly expand on the limited existing data currently used to parameterize soil carbon models, and therefore improve their ability to project soil carbon stocks in decades to come.

This work is supported by the University of Massachusetts Graduate School, the University of Massachusetts Graduate Program in Organismic and Evolutionary Biology, and the Office of Biological and Environmental Research in the DOE Office of Science.