The Ecophysiological Determinants of Mineral-Associated Carbon in Agricultural Soil

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Project Goals

Our project aims to develop understanding of the ecological determinants of microbially-processed soil carbon (C) fated to become mineral-associated C (MAC). We aim to identify ecological traits and genomic signatures of bacteria that are predictive of the quantity and/or quality of MAC. We study the trade-offs between growth rate and metabolite production / carbon utilization efficiency in bacteria common to agricultural soils, where management favors fast-growing, ruderal organisms and the gradual loss of MAC. By linking ecology, metabolite production and MAC, our research tests the ecophysiological controls on MAC formation and identifies where such information can be used to improve C-cycle modeling and management practices.

Abstract

Microbiota in cropland soils experience punctuated changes in physical, chemical and biological properties at varying frequency and intensity depending on management practices. Disturbances favor organisms that respond rapidly, and often transiently, to new conditions (i.e. 'zymogenous' species), while negatively affecting those with competitive strategies favored by periods of stability (i.e. late-stage or 'climax' species). While members of these groups broadly differ in their metabolic capabilities, we hypothesize that the general trade-offs necessary for rapid growth may exert an overarching influence on the quality and quantity of MAC produced, stemming from limits to the richness of an organism's metabolome and/or carbon utilization efficiency (CUE). We selected cosmopolitan soil bacteria isolates representing each ecological group based upon physiological, genomic and environmental characterizations with pairings obtained from seven major phylogenetic groups found in soil (belonging to *Actinobacteria*, *Alphaproteobacteria* and *Firmicutes*). We then characterized CUE and exometabolite profiles (i.e. low molecular weight extra-cellular metabolites) of each during exponential growth (replete conditions) and during maintenance growth (limiting conditions) in a soil-defined media. Exometabolite samples were then filtered through a set of common minerals, representing end-members for hydrophilicity (Montmorillonite, Kaolinite, Illite and Hematite) and hydrophobicity (Pyrophyllite and Talc), to characterize MAC-forming potential. While this work is on-going, we will present an overview of isolate selection and highlight genomic signatures that define the ecological groups. These signatures offer potential parameters for microbe-explicit C-cycling models.