

Development of novel approaches to target microbial drivers of C cycling in soil aggregates

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Abstract: We propose to develop approaches that target metabolically active microorganisms and functions that drive carbon cycling in soils from bioenergy cropping systems. Albeit critically important, soil microbiology cannot yet be incorporated into biogeochemical models due to fundamental knowledge gaps and limited data for parameterization. To address this gap in understanding, we propose an experimental system that examines C cycling microorganisms in reduced systems that are relevant to in situ soil conditions. With the combined expertise and support of the EMSL Cell Isolation and Systems Analysis group and the JGI metagenomics program, we aim to employ metatranscriptomics, genome sequencing, carbon metabolite labeling, cell sorting, and cell isolation methods to access the key organisms involved in soil C cycling (e.g. cellulose) in soil aggregate fractions. As this exploratory collaboration aims to develop novel labeling and cell sorting approaches in a complex community, sequencing will be used to both evaluate and improve our experimental methods and concurrently provide information on the structure and function of C-cycling microbial communities within soil aggregates from bioenergy fields. The proposed project will enable the identification of key soil carbon cycling taxa, and their relationship with other community members and soil characteristics. The proposed research will build upon our current ecosystem scale Carbon Cycling Science USDA-NASA grant and will compliment work submitted to DOE BER Genomic Science panel.