Poster #98

Linking Meta-omics with the Microbial ENzyme Decomposition Model
TES Early Career Award

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Microbes are increasingly included in soil carbon decomposition models, but it is widely recognized that one functional group may be insufficient to represent the diversity of substrates. Microbial metagenomics, metaproteomics, metatranscriptomics, and other related techniques provide important insight into microbial genes and activities, but it remains unclear how to include such detailed information in models of any scale. We provide a solution to this complex problem and demonstrate its application using a pilot study from the Gigante Fertilization Experiment near Barro Colorado Island, Panama. Soils were collected from control and phosphorus (P) addition plots and analyzed for metagenomics, metaproteomics, phosphatase enzyme activities, and CO_2 production during incubation experiments. Fertilized soils exhibited around 30% more CO_2 release than control soils and had greater microbial biomass than control soils. Control soils exhibited greater monophosphoesterase and diphosphoesterase activities, and had significantly more genes coding for the production of phytase, phospholipase, and exoribonuclease phosphomonoesterase than P addition soils. We also observed differences in genes for carbon decomposition and the reduction of nitrogen and sulfur, and results were consistent between metagenomic and metaproteomic analyses. We incorporated the enzyme functions, the P cycle (Yang et al. 2013, 2016), and a continuum carbon decomposition scheme into the Microbial ENzyme Decomposition model (Wang et al. 2013, 2014, 2015). Model results were able to match the patterns of CO_2 evolution in control and P addition soils, indicating the improved model provides a reasonable pathway for including meta-omic information into soil nutrient cycling models. Future work will focus on including anaerobic decomposition pathways.