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***Linking Proteogenomics, Metabolomics, and Soil Organic Chemistry of Tropical Wetlands to a Soil Nutrient Cycling Model***

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**Abstract:** Our goal is to explicitly link microbial function for decomposition of soil organic matter to substrate organic chemistry to improve process representation in a soil organic carbon and phosphorus (P) cycling model, and thereby better predict the proportion of CO<sub>2</sub> and CH<sub>4</sub> gas fluxes from tropical wetlands. Our Microbial ENzyme Decomposition (MEND) model uses explicit microbes and enzymes to decompose particulate and mineral-associated organic matter. We recently made a major upgrade to MEND by using gene copy numbers from proteogenomic analyses to directly inform the enzyme pools for P acquisition in the model. Further, Electrospray Ionization Fourier Transformed Ion Cyclotron Resonance Mass Spectrometer (ESI-FTICR MS) at EMSL is expected to directly inform the organic matter (SOM) pools in the model using a Rapid Access proposal. This recent work is a huge scientific advancement -- we can now quantitatively include proteogenomic information in a soil carbon cycle model, and we know how to explicitly link the genes to SOM substrates. However, we have only tested the model at one site, and we were mainly focused on genes for phosphorus acquisition and carbon decomposition.

This proposal targets the Biogeochemistry Topical Area of the FICUS call -- specifically, we are linking microbial genes and populations to soil molecular biochemistry. Our model explicitly uses gene copy information to parameterize enzyme functional groups (Specific Aim 1), and uses soil organic chemical composition to develop soil organic matter pools (Specific Aim 2). We will leverage the capabilities at EMSL and JGI to use the -omics analyses and build a broadly-applicable tropical wetland ecosystem model (Specific Aim 3). We will sample phosphorus gradients at two tropical wetland sites. A total of ~90 soil samples will be analyzed using ESI-FTICR MS and GC-MS at EMSL, and 16S rRNA amplicon sequencing. We will use the soil organic chemistry results to prioritize ~12-18 samples for metagenomic, metatranscriptomic, and metaproteomic analyses at JGI. We will focus on genes for extracellular carbon, nitrogen and phosphorus cycling, and as well as redox-sensitive processes including iron, manganese, and sulfur reduction as well as methanogenesis and methanotrophy. Including such a wide range of genes, particularly focusing on redox-sensitive transformations, will enable development of the MEND model to include both aerobic and anaerobic processes and ultimately improve our ability to predict CO<sub>2</sub> and CH<sub>4</sub> gas fluxes from tropical wetlands, which will be tested at select sites using lab incubations. The information gained from the FICUS project will enable us to build the needed connections between SOM chemistry and metagenomic and metaproteomic information to ensure that the model is sufficiently generalizable to apply to tropical wetlands around the globe.