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ABSTRACT TITLE: Development and Testing the Microbial ENzyme Decomposition (MEND) Model

ABSTRACT: Contemporary models of soil organic carbon simulate C dynamics by determining pool sizes and turnover rates *post hoc* from long term agricultural experiments. This standard representation does not explicitly consider microbial activities, and this lack of quantification means that acclimation of the heterotrophic community and associated exo-enzyme activities to climate change and edaphic conditions are ignored. We created a mechanistic microbial model of enzymatic degradation of measureable pools of soil organic C (OC), the Microbial-ENzyme-mediated Decomposition (MEND) model. The pools consist of soil OC as mineral-associated OC (< 53 µm), particulate OC (> 53 µm), dissolved OC and sorbed dissolved OC, and microbial biomass. Particulate OC is separated into major categories of plant matter (cellulose, lignin) that are attacked by different major classes of microbial enzymes. The activities of extracellular enzymes are considered through the Michaelis-Menten equation, and the model is parameterized by steady-state and dynamic analyses using kinetic parameter values and pool estimates gleaned from an extensive literature search. Lab-scale sorption and incubation experiments using four different ^{14}C labeled substrates (glucose, cellulose, lignin monomer, and fatty acid) and a global selection of soils are being used to calibrate the model. Model sensitivity analysis identified microbial growth efficiency, enzyme production rate, and microbial maintenance rate as targets for current experimental endeavors. Microbial growth efficiency is emerging as an important, temperature-sensitive adjustment of microbial physiology. Several publications predict that growth efficiency decreases as temperature increases, which resulted in lower CO_2 fluxes from the MEND model when compared to constant growth efficiency. Current lab experiments involve testing the growth efficiency under a variety of conditions. For future model testing and field-scale verification, we will choose field sites including tropical, temperate, and arctic ecosystems to determine the functional and phylogenetic composition of the microbial community and its contributions to carbon and nutrient cycling. Eventually, we will link MEND into the Community Land Model (CLM4) and compare performance with the existing model structure. The ultimate outcome is a validated, realistic, globally-relevant mechanistic microbial soil OC model as a robust and mechanistic component of land-surface models in global climate and earth system models.