

*Benchmarking and improving microbial-explicit soil biogeochemistry models*

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Earth system models that are designed to project future carbon (C) cycle – climate feedbacks exhibit notably poor representation of soil biogeochemical processes and generate highly uncertain projections about the fate of the largest terrestrial C pool on Earth. Given these shortcomings there has been intense interest in soil biogeochemical model development, but parallel efforts to create the analytical tools to characterize, improve and benchmark these models have thus far lagged behind. A long-term goal of this work is to develop a framework to compare, evaluate and improve the process-level representation of soil biogeochemical models that could be applied in global land surface models. Here, we present a newly developed global model test bed that is built on the Carnegie Ames Stanford Approach model (CASA-CNP) that can rapidly integrate different soil biogeochemical models that are forced with consistent driver datasets. We focus on evaluation of two microbial explicit soil biogeochemical models that function at global scales: the MIMICs and CORPSE models. Using the global model test bed coupled to MIMICs and CORPSE we quantify the uncertainty in potential C cycle – climate feedbacks that may be expected with these microbial explicit models, compared with a conventional first-order, linear model. By removing confounding variation of climate and vegetation drivers, our model test bed allows us to isolate key differences among different soil model structure and parameterizations that can be evaluated with further study. Specifically, the global test bed also identifies key parameters that can be estimated using cross-site observations. In global simulations model results are evaluated with steady state litter, microbial biomass, and soil C pools and benchmarked against independent globally gridded data products.

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