



Incorporating microbial ecology concepts into soil mineralization models to improve regional predictions of carbon and nitrogen fluxes

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Large-scale predictions of soil carbon (C) and nitrogen (N) fluxes become increasingly needed, as current concerns about climate change and human impacts on ecosystems urge robust estimates of greenhouse gas emissions and nutrient loadings on national to global scales. Large-scale soil organic matter (SOM) models play a pivotal role in such predictions, yet the existing models applicable for a large spatial scale typically have simple structure and thus limited ability to reflect small-scale processes. Benefiting from the recent advances in microbial knowledge, we evaluated critical assumptions on microbial processes in large-scale SOM models. To that aim, we simulated soil respiration rates (C_{min}) and N mineralization rates (N_{min}) in a range of settings using the framework of the CENTURY model, and validated them with incubated soil data ($N=154$ for C_{min} , $N=45$ for N_{min}).

Predicted C_{min} was sensitive to microbial biomass, and improved when using site-specific microbial biomass data. Model sensitivity and model fit were less affected by the mathematical formulation of substrate consumption by microbes. The responses of C_{min} to increasing soil N fertility were idiosyncratic and depended on the assumed mechanism of microbial C:N stoichiometry effects. Model validation showed that C overflow upon N-limitation (due to decreased microbial yield efficiency) is the likely mechanism, indicating a direct control of substrate N richness on soil fluxes of C and N via a microbial feedback. Microbial C:N ratio itself did not have a strong influence on model sensitivity or model fit.

Our study thus identified two important ways to improve predictions of regional fluxes of soil C and N: the use of site-specific input values of microbial pool, and better formulations of microbial processes, particularly those related to the effects of C:N stoichiometry. This highlights the need for better global estimates of microbial biomass and for a reevaluation of C-N interactions. By doing so, SOM models will become more robust and better suited for global change predictions.