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Integrating microbial physiology and enzyme traits in the quality model

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Microbe activity plays an undisputable role in soil carbon storage and there have been many calls to integrate microbial ecology in soil carbon (C) models. With regard to this challenge, a few trait-based microbial models of C dynamics have emerged during the past decade. They parameterize specific traits related to decomposer physiology (substrate use efficiency, growth and mortality rates...) and enzyme properties (enzyme production rate, catalytic properties of enzymes...). But these models are built on the premise that organic matter (OM) can be represented as one single entity or are divided into a few pools, while organic matter exists as a continuum of many different compounds spanning from intact plant molecules to highly oxidised microbial metabolites. In addition, a given molecule may also exist in different forms, depending on its stage of polymerization or on its interactions with other organic compounds or mineral phases of the soil.

Here we develop a general theoretical model relating the evolution of soil organic matter, as a continuum of progressively decomposing compounds, with decomposer activity and enzyme traits. The model is based on the notion of quality developed by Agren and Bosatta (1998), which is a measure of molecule accessibility to degradation.

The model integrates three major processes: OM depolymerisation by enzyme action, OM assimilation and OM biotransformation. For any enzyme, the model reports the quality range where this enzyme selectively operates and how the initial quality distribution of the OM subset evolves into another distribution of qualities under the enzyme action. The model also defines the quality range where the OM can be uptaken and assimilated by microbes. It finally describes how the quality of the assimilated molecules is transformed into another quality distribution, corresponding to the decomposer metabolites signature. Upon decomposer death, these metabolites return to the substrate.

We explore here the how microbial physiology and enzyme traits can be incorporated in a model based on a continuous representation of the organic matter and evaluate how it can improve our ability to predict soil C cycling. To do so, we analyse the properties of the model by implementing different scenarii and test the sensitivity of its parameters.

Agren, G. I., & Bosatta, E. (1998). Theoretical ecosystem ecology: understanding element cycles. Cambridge University Press.