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Integrating microbial diversity in soil carbon dynamic models parameters

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Faced with the numerous concerns about soil carbon dynamic, a large quantity of carbon dynamic models has been developed during the last century. These models are mainly in the form of deterministic compartment models with carbon fluxes between compartments represented by ordinary differential equations. Nowadays, lots of them consider the microbial biomass as a compartment of the soil organic matter (carbon quantity). But the amount of microbial carbon is rarely used in the differential equations of the models as a limiting factor. Additionally, microbial diversity and community composition are mostly missing, although last advances in soil microbial analytical methods during the two past decades have shown that these characteristics play also a significant role in soil carbon dynamic. As soil microorganisms are essential drivers of soil carbon dynamic, the question about explicitly integrating their role have become a key issue in soil carbon dynamic models development. Some interesting attempts can be found and are dominated by the incorporation of several compartments of different groups of microbial biomass in terms of functional traits and/or biogeochemical compositions to integrate microbial diversity. However, these models are basically heuristic models in the sense that they are used to test hypotheses through simulations. They have rarely been confronted to real data and thus cannot be used to predict realistic situations.

The objective of this work was to empirically integrate microbial diversity in a simple model of carbon dynamic through statistical modelling of the model parameters. This work is based on available experimental results coming from a French National Research Agency program called DIMIMOS. Briefly, 13C-labelled wheat residue has been incorporated into soils with different pedological characteristics and land use history. Then, the soils have been incubated during 104 days and labelled and non-labelled CO_2 fluxes have been measured at ten sampling time in order to follow the dynamic of residue and soil organic matter mineralization. Diversity, structure and composition of microbial communities have been characterized before incubation time. The dynamic of carbon fluxes through CO_2 emissions has been modelled through a simple model. Using statistical tools, relations between parameters of the model and microbial diversity indexes and/or pedological characteristics have been developed and integrated to the model.

First results show that global diversity has an impact on the models parameters. Moreover, larger fungi diversity seems to lead to larger parameters representing decomposition rates and/or carbon use efficiencies than bacterial diversity. Classically, pedological factors such as soil pH and texture must also be taken into account.