

Towards a more explicit representation of soil microbial communities in soil carbon and nitrogen dynamics models: a review

Benjamin P. Louis^{*,1,2,3}, Valérie Viaud^{2,1,3}, Philippe Leterme^{1,2,3}, Pierre-Alain Maron⁴ and Safya Menasseri-Aubry^{1,2,3}

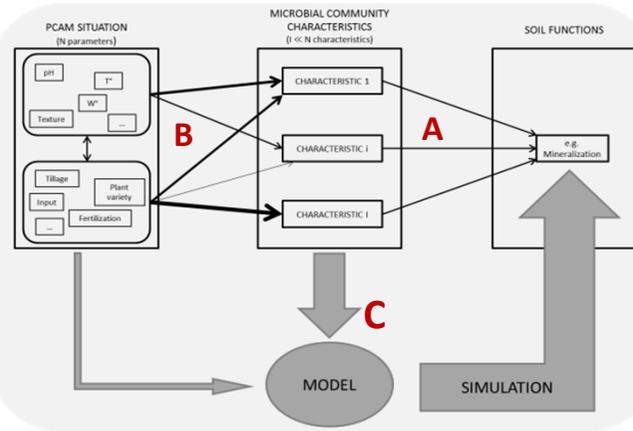
¹AGROCAMPUS OUEST, UMR 1069 SAS, F-35042 Rennes, France, ²INRA, UMR 1069 SAS, F-35042 Rennes, France, ³Université européenne de Bretagne, France, ⁴INRA, Université de Bourgogne, UMR 1229 Microbiologie du Sol et de l'Environnement, Dijon Cedex, France

*benjamin.louis@agrocampus-ouest.fr

Context : Last advances in research about soil microbial community emphasize the question about their role in C and N dynamics models

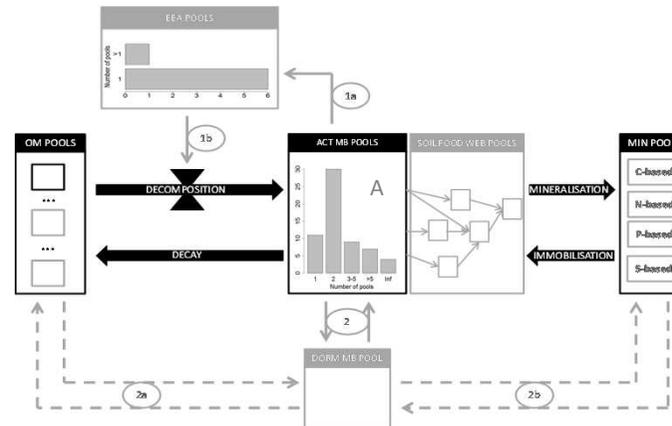
Objective : To review the role and representations of soil microbial communities in C and N dynamics models

Role in C and N dynamics



- **A** : Soil microbial communities affect soil C and N dynamics [1] through :
 - their diversity : changes in functions such as mineralization or denitrification are observed with a change in microbial diversity
 - their activity : microorganisms produce exoenzymes which control organic substrates decomposition but all microorganisms are not active in the soil
- **B** : Microbial diversity and activity are hardly regulated by a combination of **Pedo-Climatic factors and Agricultural Management practices (PCAM)**
- C** : Thus, a **better representation of soil microbial communities**, as well as their role in the PCAM-Microbial Community-Soil Functioning continuum, in C and N dynamics models **could improve the quality of models' predictions** [2]

Current representation in models



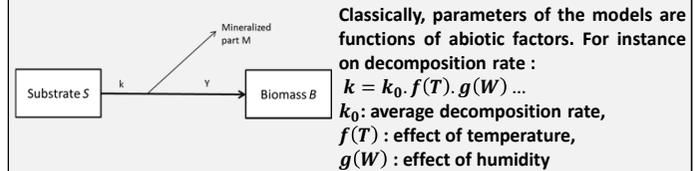
- **Microbial diversity** is often represented through the **multiplication of theoretical compartments (A)** of active microbial biomass with different functional traits and/or taxonomic meanings → **Increase of model's complexity** [3]
- **Microbial activity** is often represented through **enzymes content pools** which drives decomposition (arrows 1) or through a compartment of **dormant pool** which interacts differently with organic and mineral pools (arrows 2) → **Lack of knowledge** lead to **theoretical assumptions** about enzymes and dormant pools

Overall, models representing explicitly microbial diversity or activity are mainly **theoretical models testing hypothesis** due either to a lack of knowledge or to the increase of model's complexity. Yet, there is a clear **lack of predictive models with explicit representation of the role of microbial communities**

Proposal for future researches

Microbial diversity to adjust models' parameters :

An alternative of multiplying microbial compartments is to **integrate a function for models' parameters adjustment** as it is classically done for abiotic factors (e.g. temperature, humidity) :



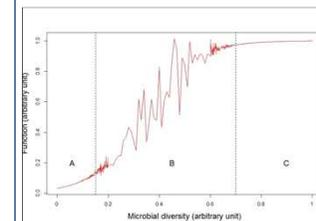
We can add metric(s) of microbial diversity (θ) through a function h to adjust the value of models' parameters : $k = k_0 \cdot f(T) \cdot g(W) \cdot h(\theta) \dots$

Two steps are important to do it :

1. Identifying relevant microbial diversity metric(s)

It is not clear, in literature, **which metrics of microbial diversity metrics (θ) is relevant** to explain C and N dynamics in soil and thus to integrate in models. There is a strong need to find these metrics through experiments and explorative statistical learning.

2. Quantifying the relation



Hypothesis can be made about the microbial diversity – soil function relation h :
A : at very low level of diversity, soil functions are hardly affected
B : at intermediate levels, functions change differently according to the community composition and the environmental conditions (idiosyncrasy)
C : from a level of diversity, there is a functional redundancy in the relation

This **relation** between soil functions and previously identified microbial community **must be quantified**. Statistical modelling should be a useful tool to do it.

Références :

- [1] Maron, P.-A.; Mougel, C. & Ranjard, L. 2011. Soil microbial diversity : Methodological strategy, spatial overview and functional interest. *Comptes Rendus Biologies*
 [2] You, Y., Wang, J., Huang, X., Tang, Z., Liu, S. and Sun, O.J. 2014. Relating microbial community structure to functioning in forest soil organic carbon transformation and turnover. *Ecology and Evolution* 4(5), 633-647
 [3] Manzoni, S. and Porporato, A. 2009. Soil carbon and nitrogen mineralization: Theory and models across scales. *Soil Biology & Biochemistry* 41, 1355-1379

PCAM : Pedoclimatic and Agricultural Management factors
 OM : Organic Matter
 MB : Microbial Biomass

ACT : Active
 DORM : Dormant
 MIN : Mineral

