Biogeosciences
Discussions

Interactive comment on "Modeling microbial exchanges between forms of soil nitrogen in contrasting ecosystems" *by* M. Pansu et al.

M. Pansu et al.

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Thank you for your work on our manuscript, your overall appreciation on our modeling proposition based on quantitative data, and your constructive remarks. We agree to more focus the final paper on the relevant research question of microbial homeostasis. However N cycle is always considered as more complex than C cycle and numerous publications as those explored by Manzoni and Porporato (SBB, 2009) show multiple ways to model N flows, see SIMP, MIT, DIR, MIX and PAR schemes in introduction section. In our mind, the modeling of the N cycle by microbial transformations (MOMOS), in accordance with MIX and PAR schemes, is also a result which should appear in the paper. A previous reviewer for first acceptation in Biogeoscience discussion asked to repeat clearly in discussion section the 3 questions of introduction. We propose to

rewrite the introduction and discussion according to your remark to show more clearly the new insights of the modeling and response to homeostasis question. Concerning this third question we agree that conclusion of this 1st version was not very clear, and was more based on other applications (not published) taking a constant value for C:N ratios of microorganisms. But we propose a way to clarify the proposition from this data, also in accordance with the proposition of the last referee to improve statistical treatments. In this 1st version statistics were applied only at each individual site, we propose to extend the study of predicted vs measured data for the whole results of the 6 sites (as we had done previously for C). In this way we should prove together the robustness of predictions considering the whole of data and the improvement using variable microbial quality in each site. Concerning specific comments We agree to revise again the abstract for a more direct presentation of the key results, Yes we agree that an assumption is not a question and we will try to reformulate this part Indeed the optimized kMB value seems high, it was found increasing with increase of the C:N ratio of substrate (see relation in Table 3), from colleagues microbiologists (eg A. Brauman, D.Masse, comm. Pers.) microbial mortality is difficult to define and range of literature data is very broad, in the MOMOS scheme kMB was named microbial mortality as the 1st process of humification, but probably it does not include only mortality but all transfers of microbial metabolites to SOM during assimilation of plant residues, which constitute a reserve of C and N for microbial functioning even when inputs from plant residues are stopped. From isotopic tracers, the input of labile residues induces high peak of microbial respiration and simultaneously relatively high transfer to SOM, which is modeled in MOMOS by a quadratic function of microbial respiration and high value of kMB. We agree to revise graphs as asked also by another reviewer, they will be presented only in two graphs by figure: evolution of organic 15N forms including living microorganisms (right scale for living organisms, left scale for other organic compartments), and evolution of inorganic forms. This modification induces higher readable graphs and we propose also to reduce the number of graphs, probably with one graph for plain, one for Middle Mountain and one for highest altitude. Also we will add a new

graph representing predicted vs observed values for all sites. This enables to illustrate the robustness of the model predictions in all situations, but perhaps should we maintain line predictions of different hypothesis and assumptions to facilitate discussion relative to homeostasis?

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