Editor:

Dear authors,

thank you for submitting a revised version of your manuscript, which has now been seen again by the two reviewers. As you see, referee 1 still expresses concern about the modelling and benchmarking of microbial biomass. Please address this comment. I have also noticed that Table 5 contains brackets that are not documented in some rows. Please add the required information to the table caption. I look forward to receiving your revised mansucript.

Sincerely,

Chris Folberth

Dear Chris Folberth,

Thank you for the overall positive assessment and for spotting the omission in Table 5. We have added the clarification: "Data rows in brackets were not used in the calculation of the overall model AIC." We also address the concern of reviewer 1 below and added further text to highlight the issue.

We feel strongly that a measure of microbial biomass must be included in SAMM to adhere to our goal of being a measurable model with structural identity. In our opinion, taking out this measure would invalidate the main goal of the paper to connect microbial growth dynamics with aggregate formation in a measurable way. In the absence of data on dormancy, we felt that the best way to address this was in stating the limitation (that ideally, dormancy would be included) in the discussion. We hope that these modifications are acceptable to the reviewers and you.

Thanks a lot in advance,

The authors

Reviewer1:

The revised version of the manuscript submitted by Laub et al is much better and clearer than the previous version.

I nevertheless still have one issue on the microbial biomass. The authors acknowledge that comparing the biomass of the model with the CFE data is not ideal. I understood their arguments that the total biomass is not directly linked with aggregate dynamic and I agree with them but I would suggest to remove the biomass comparison in Fig 5, 6 and Table 5 since CFE data are not directly comparable with the model outputs.

Thank you for the overall positive assessment. We can understand your concern and agree that ideally, we would include a pool of dormant microbes and a pool of active microbes as in the MEND model (Wang et al., 2015). However, our credo was full measurability of pools and we simply had no measurements of microbial dormancy because it is actually very difficult to assess with any available measurement techniques (i.e. the closest estimate is with RNA based methods that are not straightforward in soils). Furthermore, microbial metabolic states are a continuum and defining dormancy in a binary way (dormant vs active) is thus difficult and a large oversimplification of reality (McDonald et al, 2023). It would thus add complexity without a measurable counterpart. As you stated earlier, CFE microbial biomass is representative of all alive microbes, whether dormant or not, and our single MIC pool thus comprises the full CFE microbial biomass, since all $LMW_{C/N}$ that is taken up by microbes and that is not respired ends up in the MIC pool. Hence, we think that the presentation of model outputs together with measured microbial biomass in Fig 5, 6 and Table 5 is appropriate in our case where total microbial biomass was measured and modelled. We agree that the microbial activity factor (a_{MIC}) should ideally be a function of active microbes only and thus we added a section to the limitations to address this issue (as shown below). Since the half saturation constant of the reverse Michaelis Menten kinetics that influences a_{MIC} is a calibrated parameter (K_{MMIC}), we do not see a major issue for model behavior due to this discrepancy. However, we acknowledge that in cases where data on microbial dormancy would be available, it would be worth to consider two MIC pools. It is also reasonable to believe that for field scale modeling variable model structures (with or without splitting of microbial biomass into active and dormant fraction) could successfully describe SOM dynamics (see e.g. Sulman et al., 2018).

some other models include (Wang et al., 2015; Blagodatsky and Richter, 1998). In fact, the estimation of microbial biomass via chloroform fumigation extraction does not separate between dormant and active microbes. While Wang et al. (2015) suggested
390 that a model that includes dormancy can better represent the total magnitude of microbial biomass, an important concept of SAMM was the measurability of all pools and the inclusion of dormancy would thus need data on dormancy, which was not available in this trial. Ideally, only the non-dormant microbes should be considered in the microbial activity factor (a_{MIC}). Since $K_{M_{MIC}}$, which determines a_{MIC}, is a calibrated parameter, this discrepancy does not drastically alter model behavior. However,

it means that the microbial activity factor of SAMM cannot be directly compared to measurements of microbial activity, and it
395 implicitly assumes that the fraction of dormant microbes is constant. Since the water and temperature rate modifiers indirectly account for differences in microbial activity between optimal and poor conditions, the use of chloroform fumigation extraction data is most likely, in the absence of data on dormancy, the best way to represent a single microbial biomass pool while maintaining structural identity.

References

McDonald, M.D., Owusu-Ansah, C., Ellenbogen, J.B., Malone, Z.D., Ricketts, M.P., Frolking, S.E., Ernakovich, J.G., Ibba, M., Bagby, S.C., Weissman, J.L., 2023. What is microbial dormancy? Trends in Microbiology. https://doi.org/10.1016/j.tim.2023.08.006

Sulman, B.N., Moore, J.A.M., Abramoff, R., Averill, C., Kivlin, S., Georgiou, K., Sridhar, B., Hartman, M.D., Wang, G., Wieder, W.R., Bradford, M.A., Luo, Y., Mayes, M.A., Morrison, E., Riley, W.J., Salazar, A., Schimel, J.P., Tang, J., Classen, A.T., 2018. Multiple models and experiments underscore large uncertainty in soil carbon dynamics. Biogeochemistry. https://doi.org/10.1007/s10533-018-0509-z

Wang, G., Jagadamma, S., Mayes, M.A., Schadt, C.W., Megan Steinweg, J., Gu, L., Post, W.M., 2015. Microbial dormancy improves development and experimental validation of ecosystem model. The ISME Journal 9, 226–237. https://doi.org/10.1038/ismej.2014.120