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Interactive comment on "Diffusion based modelling of temperature and moisture interactive effects on carbon fluxes of mineral soils" *by* Fernando E. Moyano et al.

Fernando E. Moyano et al.

fmoyano@uni-goettingen.de

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We thank T. Wutzler for a constructive review. Below we address each comment individually.

Reviewer comments are quoted followed by the author response and, where relevant, changes to the manuscript.

"Moyano et al. compare several versions of SOM turnover models with a comprehensive set of observations of varying temperature and soil moisture. They show that ex-

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plicitly accounting for diffusion, compared to using empirical formulation of the temperature/moisture rate modifiers, improves fit and understanding of SOM decomposition. This result is interesting to the soil model developers and biogeoscientists studying SOM turnover and consequences at soil core to larger scales. The paper contains a strong validation by a good agreement with independent data. The clarity of the discussion on reasons for the good validation fit, interactions with initial pools, and different resulting temperature sensitivities can be improved. With an extension of discussion and some more clarifications in the discussion, the paper could be published. Nevertheless, I suggest several additional tasks with this model and data, that would help the community."

Please see responses to comments by R. Grant for changes already made to the discussion.

"First, while the paper already contains three different structural versions of decomposition, I suggest including another version of an inverse Michaelis-Menten dynamics for depolymerization (but not for DOM uptake), where the non-linear term is in enzymes instead of the substrate (F = V C_P * C_E/(K + C_E)). This would broaden the application of conclusions of this study, because the inverse formulation is used by many microbial models since suggested by Schimel and Weintraub 2003."

Reverse MM kinetics assume that enzyme concentrations can increase enough that they start to compete for binding sites on SOM and thus saturate at some point. Schimel and Weintraub used this approach to deal with a problem of model instability driven by the dynamics of the microbial pool. However, we think a general saturation of the available SOM by enzymes in soils is unlikely to be the norm, as it would imply a large and likely unsustainable production of enzymes and very rapid decomposition of all polymeric C. We did not have stability issues in our model that would justify using this MM form and find it an unlikely explanation of soil C dynamics. However, we

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will test the effect of using the reverse MM and, if relevant, include information in the revised manuscript.

Changes in manuscript: inclusion of any relevant results following model calibration using reverse-MM and comparison with other versions.

"Second, the study describes a decoupling between depolymerization and microbial uptake at low diffusion rates, I assume by accumulating OM in the dissolved pool. Are the fluxes correlated again for the same treatment, if you aggregate over say two weeks? The decoupling is a challenging fact for upscaling studies, that often assume the DOM pool in quick quasi steady state with decomposition and microbial uptake. For low moisture the decomposed flux was almost not taken up and respired (Fig. 9). Would this also be true with two separate DOM pools after longer time? I would appreciate an extended discussion on this topic."

As well pointed out, Figure 9 shows that for some samples at lower moisture decomposition did not equilibrate with uptake in the 6 months of the simulated incubation. The plot also gives a good idea of how fast soil at higher moisture content return to equilibrium. We kept the model simple where possible. The current form where there is only one DOC pool is a simplification that assumes microbes have access to an amount equivalent to the concentration in the bulk soil times a conductivity value. If conductivity is not 0, this amount will increase if the concentration increases, until the input from decomposition equals output from uptake. The reason this is done differently for enzymes is that enzymes have a decay rate, which means that the pool decreases with time. So even if equilibrium is reached, the flux of enzymes from microbes to the decomposition site will be lower if conductivity is lower, simply because a larger fraction is lost before diffusing. Further analysis of the model could indeed go more into detail looking at such dynamics. We take this as a suggestion future research.

Changes in manuscript: discussion extended under section 7.2 Moisture effects and

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diffusion limitation

“The model used enzyme pools split to locations but a simplified diffusion limited rate multiplier for DOM. What is the reasoning for this decision, and what are the expected consequences for using a rate modifier for enzymes too?”

See response to previous comment.

“There is an interesting differentiation between parameterized temperature sensitivity (E_a) and an apparent predicted one, the latter one also depending on partitioning of the pools (P13l20ff). What are the reasons and consequences here. The paper would profit from an extended discussion here.”

We have extended the discussion on this topic. See also responses to R. Grant.

Changes in manuscript: discussion extended. P.14 L.2-18

“p5l10: The choice of the wording “particulate” suggests to OM floating together with the DOM. I assume instead that C_P comprises litter and residues also sitting on surfaces. When using “polymeric” it conveys a different connotation and still the “P” can be used as acronyms.”

We followed the advice and changed to “polymeric”. (For the record: according to Wikipedia “Particulate organic matter is defined as soil organic matter between 0.053 mm and 2 mm in size”.)

Changes in manuscript: the term “particulate” was changed to “polymeric”

“p7l10: The model assumes enzyme production to be modeled similar to growth respi-

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ration as a fraction of uptake, instead similar to maintenance respiration as determined by microbial biomass. What are the reasons for this formulation ? ”

From a practical side, initial testing of model structure resulted in this approach fitting the data best (data not shown). From a theoretical side, is would be logical that microbes produce enzymes mostly when C becomes available and save resources otherwise. A continued enzyme production would lead to an unnecessary depletion of resources. We now note this in the same paragraph.

Changes in manuscript: text added near P.7 L.10-12

“p8l4ff: The wording here suggests, that all the processes have the same temperature sensitivity, i.e. same E_a. I suggest adding another index to E_a that this parameter varies between processes.”

We followed the suggestion and added a subindex.

Changes in manuscript: E_a in equation 19 changed to E_ap

“P8l10: I assume there is only one set of parameters fitted to the entire data of all temperature and moisture treatments. Would be nice to state that here. Please, also state the number of fitted parameters, and add the initial partitions to Table 1."

That is correct. This is now clarified. Because of space limitations, initial parameter values and their lower and upper bounds were added in a table in the supplementary material.

Changes in manuscript: - text added at P.8 L.10-11. - table with initial parameter values and boundaries added to supplementary material.

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"The fitted parameter vector in a 20 dimension space is quite challenging for a gradient based search. Did you check global convergence by starting from more states, maybe more random distributed as just the one described for p11l30. What are the most important correlations in parameter estimates?"

We agree. A global minima can of course not be guaranteed. In preliminary work we explored parameter spaces manually and using latin hyper square methods. The initial parameter values used here are already the result of these tests. Parameters in such model are often correlated and this was also the case in our study. High, but not very high, correlations occurred between some parameters, e.g. V_U_ref and g_0 (0.89), V_U_ref and E_r (0.83), V_D_ref and g_0 (0.84), f_CD and E_K (0.83) and V_D_ref and V_U_ref (0.8), f_ug and f_ge (0.83). We therefore do not make conclusions on how well constrained our estimates are, as this information is not obtained with gradient or deterministic algorithms. However, we now added these remarks and a correlation plot in the supplementary material for extra information.

Changes in manuscript: - text added in the discussion P.12 L. 13-16 - correlation plot of parameter sensitivities added to the supplementary material

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"P8l10: model calibration open questions: How were enzyme pools initialized? What were the values of fractions for particulate, dissolved and microbial pool, how do they compare to usual concentration of DOM and microbial biomass? I assume they were equal for all moisture and temperature treatments, right?"

As clarified in response to comments by R. Grant, all C pools were initialized by fitting them similarly to other model parameters (as initial steady state was not assumed). Upper and lower bounds were set (see Table S1) to assure they stayed in a realistic range (text added in P.8 L.23-24). The initial values of these fractions are found in Table 1. fM with 0.07 is in particular on the upper range of observed values.

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“P3l20: Citation of the kinetic respiration analysis (Wutzler 2011) is not appropriate in this context. I assume you wanted to refer to: Wutzler T & Reichstein M (2008) Colimitation of decomposition by substrate and decomposers - a comparison of model formulations. Biogeosciences, 5, 749-759 10.5194/bg-5-749-2008”

Thanks for pointing this out.

Changes in manuscript: reference changed to Wutzler T & Reichstein M (2008)

“Fig 4: There seem to be two groups of observations, a higher branch and a lower one. Why is this? Is it ok to fit a single smoother to this data?”

Figure 4 is mainly meant as a visual aid since it is not possible to mark which model point corresponds to which data point. The smooth lines ignore the variability along the y axis, caused mainly by the time effects resulting from two incubation cycles, but they help visualize the general resulting relationship between moisture content and respiration fluxes. We added this clarification in the results section.

Changes in manuscript: added text near P.11 L.2-4

“Technical comments: The grammar of the paper needs to be re-checked, e.g. p9L18, p9L25, p13L19.”

Changes in manuscript: spelling and grammar mistakes were corrected.

Please also note the supplement to this comment:
https://www.biogeosciences-discuss.net/bg-2018-95/bg-2018-95-AC2-supplement.pdf

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