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Reply on RC2

Weilin Huang et al.

Author comment on "Implementation of mycorrhizal mechanisms into soil carbon model improves the prediction of long-term processes of plant litter decomposition" by Weilin Huang et al., Biogeosciences Discuss., https://doi.org/10.5194/bg-2021-275-AC2, 2021

Response to Reviewer 2

R2.0. This study investigates variation in litter decomposition across ecosystems of varying plant-mycorrhizal associations by adding a mycorrhizal association effect to the Yasso15 soil carbon decomposition model. The model was parameterized using a Markov chain Monte Carlo approach from a large set of litter decomposition measurements. The model changes are a simple but reasonable approach to incorporating site-level effects of mycorrhizal associations. Interactions between mycorrhizal associations and decomposition are an important area of study in biogeochemistry and these model developments represent a valuable step toward incorporating these processes into models. However, I think care needs to be taken not to over-interpret the results. The model formulation is a simple linear function of mycorrhizal association on decomposition rates, and does not address the mechanisms of mycorrhizal-decomposition interactions. The parameters and their effects on decomposition are determined by statistical parameter fitting and are validated only using statistical measures of fit to total decomposition over time, so interpretations of the resulting model in terms of changes in litter composition over the course of decomposition are not very strongly supported. The actual improvement in RMSE and related measures is very small, which undermines the stated value of the model changes. I think the interpretation of the results and the support for the value of the model developments would be more robust if model predictions were compared to specific observed trajectories of decomposition over time from sites with different mycorrhizal associations and similar climates (rather than statistical measures over the whole dataset that could hide other covariates or effects). The interpretations would be greatly strengthened if they could be compared with actual measurements of litter composition or lignin content over time. As it is, much of the interpretation of the results relating to different modes of decomposition and changes in the relative amount of labile and recalcitrant litter fractions over time for different mycorrhizal associations is based purely on a model that was not constrained using measurements of litter chemical composition over time.

Re R2.0: Thank you for providing helpful comments which will serve to improve the reader's experience of the manuscript. Below we address these points one by one following the detailed requests specified by the referee. Our responses are highlighted in bold.

Specific comments:

R2.1. Figure 1: It would be helpful to label the blue CO2 arrows with the percentage that is converted to CO2. This can probably be inferred from the labeled green arrows but it's not immediately straightforward what the respired fraction is because there are several green arrows that need to be added up.

Re R2.1: Thank you for your suggestion, we will add the label for CO_2 arrows.

R2.2. Line 145: What chemical composition data were available? Does this mean that the initial composition of litter (in terms of model pools) was measured for each site and used in model initialization?

Re R2.2: Yes, this is exactly the case. "Chemical composition data" contains the initial composition of litter in terms of WAEN fractions which was measured for each site, and this data together with other environmental data were used for initializing the model. We will modify this sentence by adding "...chemical composition data (WAEN components in the initial litter, during decomposition process and at the end of the decomposition) were supplemented...".

R2.3. Line 149: If plant community composition was available for each site, then why was the map of mycorrhizal associations needed? Wouldn't local measurements of plant community composition be more accurate?

Re R2.3: Thank you for spotting this inconsistency. The text in Line 149 should be "...general ecosystem types of each site were carefully checked for consistency with the map", because the plant community composition information was not available for all sites.

R2.4. Table 1: Are the "a" parameters here the same as the "alpha" parameter in Equation A3?

Re R2.4: Yes, the "alfa" parameters (a_W, a_A, a_E and a_N) in Table 1 are the same terms of "ai" as shown in Equation A3. We will make sure to use one symbol representing "alfa", using "□" throughout the text to keep the consistency and avoid confusion.

R2.5. Line 230: It's not clear what was different about the inputs in Appendix D. Does this mean that the main simulations used measured chemical fractions for each site while the Appendix D simulations used an average chemical fraction? Is there a table or graph somewhere of the chemical fractions from the sites that were used?

Re R2.5: For the comparisons in Appendix D, two sets of initial litter composition data were used for representing two typical types of litter material, i.e. roots (17%-W, 55%-A, 9%-E, and 20%N) and leaves (25%-W, 45%-A, 12%-E, and 18%N). In this comparison, we aimed to demonstrate that the mycorrhizal impacts of AMvsEM dominance are not affected by the initial litter types. These chemical fractions of initial litter from sites are available in the datasets. We

added text to explain that the chemical composition of the initial litter was available, also see reply to R2.2 Line145.

R2.6. Line 237-238 and Table 2: The differences in RMSE seem very small, and in many cases RMSE was higher in the mycorrhizal model than in the original model. Overall it seems like weak evidence supporting new model developments. It's also hard to understand why AIC and BIC decreased for models that had higher RMSE and more parameters than the original model (like V4, which had higher RMSE for all three datasets but a lower AIC). How can the updated model be a better fit than the original if it had higher error? Maybe there is a better way to show model improvement than these statistics which don't present a very strong case.

Re R2.6: Indeed, the improvement of the performance parameters of the model is relatively small. The main reason for it is that the original YASSO model is predicting soil carbon dynamics with high accuracy (ca 90%). Thus, there is actually little opportunity to further improve the predictive capability of the model. However, the original YASSO model does not explicitly account for mycorrhizal impacts. Instead, it accounts for the entire suite of environmental conditions that include activities of mycorrhizal fungi and climate. Yet, these two drivers of decomposability (climate and mycorrhizal impacts) are principally different in the nature of the imposed mechanisms. Thus, though the original YASSO model was parameterized to provide accurate predictions of litter decomposition, it provides these predictions while not separating individual drivers (a feature not unique for YASSO, indicating the relevance of our study). The main advancement of our new model, is the explicit separation of these two drivers, allowing us to account for climate per se versus alterations in mycorrhizal types (which could for instance be the result of land management actions). The examination of formal performance parameters (RMSE, AIC, BIC) has the primary aim of selecting the best model, among the set of alternative models conceptualizing distinct ways of representing the mycorrhizal impact as being mechanistically independent of climate. We will clarify this logic throughout the manuscript by emphasizing this main aim better in the introduction, showing how this separation affects model parameters and subsequently model sensitivity and discussing the consequences of these changes for predictions of litter decomposition.

Yet following the requests to clarify the logic of model selection, we will provide more details on this, accounting for the following aspects: Firstly, the validation dataset was selected as 20% of the time series. We will make it clear in the manuscript in Lines 190-191, "using 80% of data (decomposition time series) randomly drawn from the dataset for calibration and the remaining 20% of the data (decomposition time series) used for validation". Secondly, for Table2, all RMSEs were assessed with the validation dataset containing data not used for calibration. However, the AIC and BIC were based on the performance of the calibrated dataset, which contained 80% of the dataset. We will specify this in methods to avoid confusion, from Line194: "We used root mean square error (RMSE), Akaike information criterion (AIC) and Bayesian information criterion (BIC) as the criteria for comparing relative quality of models based on the 'cross-validation dataset' (RMSE from the 20% validation dataset, AIC and BIC based on the 80% data used for calibration), thereby selecting the optimal model".

Please also note, that our optimal model (V2) had a lower RMSE for all datasets than the original model. Therefore, although differences are not large, we conclude –in combination with the substantially improved BIC and AIC- that the

performance of the mycorrhizal model is (marginally) better. Importantly, in doing so, the model represented more closely the complexity of drivers expressed in the soil environment (as explained above).

R2.7. It would also be helpful to include Pearson's r in Table 2.

Re R2.7: Thank you for the suggestion. We presented the Pearson's r in text in Lines 235-236. However, we did not include it in Table 2 given that Pearson's r does not account for differences in degrees of freedom (in contrast to AIC and BIC). Therefore, we considered it an inferior metric to base model selection on.

R2.8. Figure 8: It's not clear which axis scale (right or left) is used for the bars and which is used for the line

Re R2.8: As explained in the caption of the figure, "Bars represent the relative RMSE differences between Yasso15 and Myco-Yasso per period. The line with dots shows the absolute value of the RMSE differences (Yasso15- Myco)." We will add extra legends on the axes to directly link individual axes to the contents.

R2.9. Figure 9: Showing some measurements from sites of contrasting mycorrhizal associations to compare with the model here would make a much clearer case for whether this model behavior is realistic and whether it represents an improvement compared to the original model. It would also be useful to show the prediction of the original Yasso15 model on these plots to show how the mycorrhizal model compares to the original.

Re R2.9: We agree that it is important to compare the model performance at each site level. That is also the reason why we did cross-validation using 20% data, and this data was not used for calibration (i.e. the other 80% were used for calibration), see current Lines 190-191. This validation dataset contains from contrasting mycorrhizal environments. The prediction of the original Yasso15 compared to the new mycorrhizal model is shown in Fig.C1.

R2.10. Line 339: It seems like "environment of plant litter decomposition" could refer to any number of processes, from microbial community to litter quality to physical and hydrological effects of the litter layer… It is useful to assess the combined effect of factors that are integrated by different mycorrhizal associations, but it doesn't provide much insight about the underlying processes. I think this makes it somewhat inaccurate to call this a "mechanistic" approach.

Re R2.10: Here we are specifically referring to the "mycorrhizal environment of plant litter decomposition". Indeed, mycorrhiza can affect C cycles via three mechanistically distinct pathways of "(1) provisioning dead mycelium as the substrate for decomposition, (2) mediating plant litter quality and amounts, and (3) controlling the environment of plant litter decomposition" (see Lines 337-339). Our work in this paper focused on one pathway "controlling the environment of plant litter decomposition", which refers to a composite decomposition environment with different types of mycorrhizal vegetation and its impact to the litter decomposition process. We explicitly did not specify the

other two pathways because our dataset does not allow examining these pathways. These pathways could not be examined because the decomposition results examined here are from litter bag experiments and thus not products of the local plant community composition. Thus, mycorrhizal impacts on the other two pathways were excluded as litter amount and initial litter types were controlled.

As we explained in the rebuttal to R2.6, the main advancement of our model is an explicit separation of the two drivers of decomposition, climate and mycorrhizas; assessing the integral impacts of mycorrhiza through their effects on decomposition. Therefore, we will remove statements on the "mechanistic accounting for mycorrhizal impacts'', and instead clarify the line of reasoning on the model advances, as we explained in the R2.6.

R2.11. Line 356: It is difficult to measure changes in composition and breakdown of litter components over time, but that does not mean modeling these processes is easy either! In fact, it's often more difficult to model processes that are poorly understood from the observational side because it means there is a weaker theoretical basis for developing a model.

Re R2.11: We agree with this point. We will acknowledge that there are difficulties in the modelling process in the discussion. However, it is also extremely challenging to measure the flow between decomposition pools, which we actually can assess by modelling. We will address this point in the discussion section.

R2.12. Line 357: I would say litter decomposition, not soil C

Re R2.12: We agree that we are looking at the litter decomposition process, and we admit that we did not look into the mineralization process. However, decomposition is an important process within soil C cycling, and particularly during the initial stages of SOM formation. Reviewer 3 also acknowledged this (see under R3.0). We will soften the tone when we mention soil C to make explicit that our study refers to the initial stage of soil C formation.

R2.13. Line 379-381: If mycorrhizal associations are tightly correlated with temperature, wouldn't this also affect the calibrated model? How can we know that the model's results in terms of temperature and mycorrhizae effects are not also driven by large-scale covariation between climate and mycorrhizal association? One way to investigate this would be to show observed patterns of decomposition from sites with similar climates and contrasting mycorrhizal associations compared with the model as in Figure 9.

Re R2.13: We acknowledge that mycorrhizal associations are correlated to climate, like almost all natural processes are correlated to climate. There is no doubt that climate is a factor driving global vegetation distribution, and it could also potentially affect mycorrhizal associations. The original Yasso15 structure only considers climate as a decomposition factor but without potential mycorrhizal impacts, and according to the sensitivity analysis in Fig.6 and Fig.7, we think that potential mycorrhizal impacts were partly accounted for by climate variables in the original Yasso15. In the new model, we account for mycorrhizal impacts separately from climate, while the magnitude of these impacts is scaled to the abundance of mycorrhizal vegetation. Though the latter is undoubtfully

driven by climate, it is accounted for as a separate input parameter of the model, thus model formulation-wise being separated from climate. We agree about the need to run the model for similar climate conditions, and this is exactly how the sensitivity analysis was performed: at global mean climate conditions. To explore these patterns further, we are working on a global estimation of the mycorrhizal impacts, employing the same type of analysis. However, it is not within the scope of this model description paper. We look forward to sharing more interesting findings with you in the future.

R2.14. Line 407-408: The model does not provide mechanistic insights since it just relates decomposition rates to overall site mycorrhizal associations, not to specific underlying processes. And the model addresses litter decomposition, not soil C.

Re R2.14: These two issues seem to be already mentioned and have been addressed within the replies to R2.10 and R2.12. Please see our responses to these points.

R2.15. Line 409-411: The accumulation of recalcitrant compounds and impacts on labile compounds were model results and were not validated with any measurements of compounds such as lignin or soluble C over time, so I would be wary about interpreting this too confidently.

Re R2.15: There seems to be some misunderstanding here. The database used for calibrating the model has information on different recalcitrant compounds over time in terms of WAEN, not only for the initial stage, but over the whole decomposition process till the end of the decomposition. Hence, our model is capable of predicting the differences in recalcitrant compounds at the end of the decomposition stage. Though it has been specified in Appendix B, we feel it is necessary to add more details to describe the database in Line 143 to avoid confusion: 'We calibrated our new model using litter decomposition databases (Appendix B) used in Yasso modelling which included total mass loss and different chemical components variations over time (Tuomi et al., 2009, 2011b, 2011a)'. Also, see reply to R2.17.

R2.16. Line 413: The differences in RMSE from Table 1 and Figure 8 were quite small, so it seems like a stretch to say that it "greatly improves the accuracy." The difference was from RMSE of 19.9 to 19.3, or 10.55 to 10.5, which seems barely significant. Or, according to Figure 8, just a couple of percent of RMSE. If there are alternative metrics that show a clearer improvement, it would be helpful to highlight those. And the model predicted to litter decomposition, not SOM dynamics.

Re R2.16: We agree with these points. Very similar concerns were raised in R2.6 (RMSE) and R2.12 (litter vs SOM). We will modify the text in Line 413, according to the plan proposed under R2.6 and R2.12.

R2.17. Line 443-444: The differences in recalcitrant compounds are purely a model result, not constrained by any measurements of litter composition over time so I would be wary of drawing this conclusion too strongly.

Re R2.17: Please also see the reply to R2.15; our model is capable of predicting the differences in recalcitrant compounds at any decomposition stage, as it is calibrated with data of WAEN during the whole decomposition process and not only at the initial stage. Thus, we draw the conclusion using the words in Lines 443-444.

R2.18. Figure C1: It's hard to tell much difference between the two model versions from this figure. Would color coding the dots by mycorrhizal association of each site help to highlight any improvements from adding mycorrhizal effects to the model?

Re R2.18: The scatter plots and the 1:1 line should be helpful to compare the performance of the two models. Dots that are closer to the 1:1 line indicate that those model predictions are closer to measurement values. From Fig.C1, we can see that blue dots are more constrained to the 1:1 line compared to the grey circles. This already supports that Yasso-Myco has a better performance than the original model. We are afraid that colour-coding of the dots by mycorrhizal association might not help to reflect more information but might add more distractions. The performance of different associations of the site can be found in Fig.4.

R2.19. Fig. D2: I think this caption should say leaf material, not root material

Re R2.19: Thank you for pointing out this error. We will correct the sentence in the caption "The initial WAEN composition of leaf material is 25%-W, 45%-A, 12%-E, and 18%N (typical for plant leaf material)".