Response letter to comments (egusphere-2025-5037)

The following is a point-by-point response to the two reviewers' comments.

Here are our detailed responses to editor and two reviewers. Please note that the comments from the reviewers are in ***italics*** followed by our responses in **regular** text.

Reviewer #1:

This work addresses a critical question in models: how different model structures simulate soil carbon responses to drought. The integration of long-term experimental data from the Tiantong Forest with a multi-model comparison and traceability analysis is a clear strength of the manuscript. Below, I offer some feedback aimed at further strengthening the scientific novelty and rigor of this manuscript.

[Response] Thank you for the positive assessment and constructive feedback. We carefully revised the whole manuscript accordingly to your comments. As a consequence, our manuscript has been considerably improved. Hopefully you will find our revision satisfactory.

First, the introduction effectively establishes the problem but could more sharply define the specific knowledge gap that this study uniquely fills. It stated that models have limited capability and studies are scarce, but what is the conceptual novelty? I think the authors need to convey the message: how does this comparison of different model structure actually contribute to our capability to more accurately/realistically simulate SOC responses to drought?

[Response] Thanks for the comments. We agree that the conceptual novelty needs to be sharpened. In the revised version, we stated that while previous model comparisons have focused on parametric uncertainty or single-model improvements, the core knowledge gap is the structural uncertainty, i.e., how fundamentally different assumptions about carbon stabilization (three-pool partitioning, measurable physical fractions, vs. microbial enzyme kinetics) lead to qualitatively divergent predictions of SOC responses to decadal drought. We further clarify that this comparison contributes to predictive capability not by identifying a single "best" model, but by revealing that the direction of drought effect on SOC (accumulation vs. loss) is structurally contingent, and that explicit representation of enzyme-mediated decomposition (SM3) is required to capture drought-induced reductions in MAOC and POC decomposition—a mechanism absent in SM1 and SM2. This message has been added to the end of the Introduction and summarized in the Conclusions in Lines 135 - 152.

Second, is it possible to illustrate some details of the vegetation model? It does seem that coupling of the vegetation model with the three different soil modules is a significant undertaking worths of highlighting. The flexibility of this vegetation model is a strength. So I would recommend some brief text about the coupling.

[Response] Thanks for your suggestion. We agree that the coupling between the vegetation model and the three soil modules is a key strength of our modeling framework. In the revised manuscript, we revised the Figure 1 (Fig R1) and added description in Section 2.2 (Model description) as "All three soil modules share a common vegetation submodule that simulates photosynthesis using the FBEM model driven by leaf area index, photosynthetically active radiation, air temperature, and relative humidity, detailed information can be found in Wu et al (2009). Net primary productivity is allocated to foliage, fine roots, and wood pools. Carbon transfers from these vegetation pools enter two litter pools (metabolic and structural), which then provide identical carbon inputs to the three soil modules. This unified coupling ensures that differences in simulated soil carbon dynamics arise solely from the structural differences among SM1, SM2, and SM3, rather than from variations in vegetation or litter inputs." We believe this addition appropriately highlights the flexibility and modularity of the vegetation model while reinforcing the rigor of the model comparison.

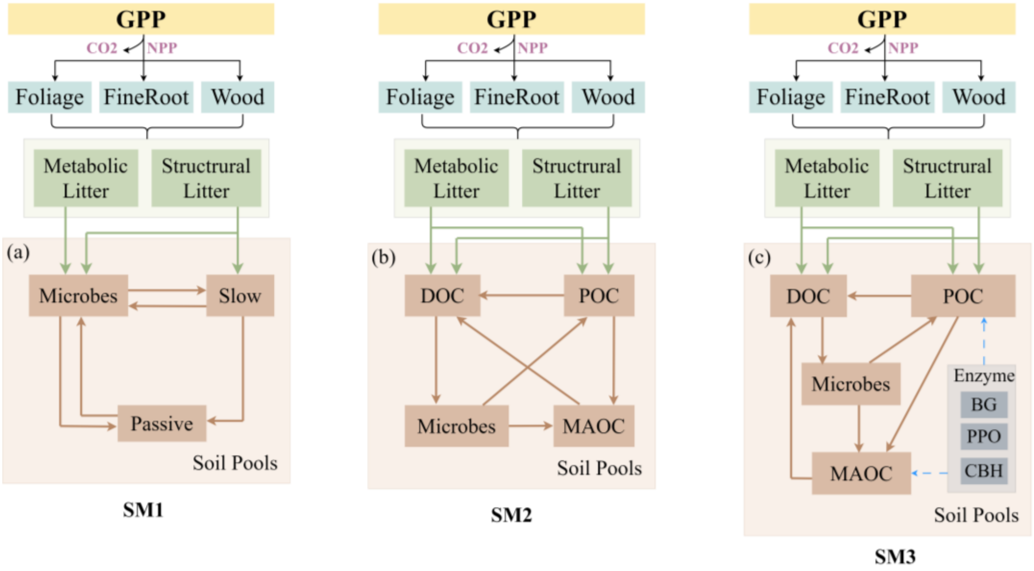

Fig. R1 Conceptual diagram of the soil biogeochemical models with three schemes. **(a)** conventional three-pool partitioning scheme (SM1), **(b)** mineral and particulate- associated carbon partitioning scheme (SM2), and **(c)** Michaelis-Menten regulated carbon-stabilization scheme (SM3). All pools (boxes) and fluxes (arrows) represent C process. BG, β-1, 4-glucosidase, PPO, polyphenol oxidase, CBH, cellobiohydrolase.

Third, the differences between models are clear qualitatively. Is it possible to add a simple metric to quantitatively underscore the magnitude of model-structure-induced uncertainty? This could be a powerful summary statistic.

[Response] Thanks very much for your suggestion. To quantitatively underscore the magnitude of model-structure-induced uncertainty, we added a simple but informative metric in Section 3.2 and a box plot in Figure 3j. Specifically, we calculated the coefficient of variation (CV) of the predicted total organic carbon (TOC) in 2100 across the 1,000 parameter sets for each model, and then compared the range between the median predictions of the three models relative to their pooled uncertainty. The key finding is that the difference between the highest and lowest median TOC predictions among the three models (SM1: 5.2 kg C m^{-2}, SM2: 4.1 kg C m^{-2}, SM3: 3.8 kg C m^{-2}) is approximately 2.5 times larger than the average within-model parametric uncertainty (standard deviation ~0.6 kg C m^{-2}). This indicates that model structural uncertainty dominates parametric uncertainty in projecting long-term SOC responses to drought. We also added this metric to the Results section and a brief interpretation in the Discussion.

Fourth, in the discussion sections, is it possible to discuss what these divergences imply for future model development and large-scale projections? Should all terrestrial models move towards SM2/SM3 structures for drought simulation? What are the trade-offs (complexity, data needs, computational cost)?

[Response] Thanks for your comments. In the revised manuscript, we expanded the discussion to explicitly address the implications for future model development and large-scale applications. While SM2 and SM3 improve simulation accuracy for specific carbon pools and capture nonlinear drought responses, we do not advocate that all terrestrial models should adopt these more complex structures. The appropriate model choice depends on research objectives, data availability, and computational constraints. Specifically, (1) SM1 remains suitable for large-scale simulations and long-term carbon budget assessments where only total SOC data are available, as it is parsimonious and computationally efficient; (2) SM2 is preferable when the goal is to investigate dynamics of measurable carbon fractions (POC, MAOC, DOC) and when corresponding observational data exist for model calibration; (3) SM3 is essential for exploring nonlinear ecosystem responses to extreme climate events (e.g., decadal drought, warming) where microbial enzyme activities play a mediating role. Importantly, the advantages of SM2 and SM3 are contingent upon data availability. Without sufficient constraints (e.g., enzyme activities, DOC, POC, MAOC), increased complexity can lead to higher parametric uncertainty and reduced robustness. Therefore, future model development should adopt a balanced strategy—introducing additional process representations only when supported by data and justified by the targeted application. We integrated that discussion into the revised manuscript in Lines 710 - 796.

Reviewer #2:

This study focuses on the scientific issue of divergent model simulations of soil carbon dynamics under drought stress in subtropical forests. The research findings provide guidance for improving climate-carbon coupling projections. While the results are innovative and meaningful, several points need to be further modified before publication. Below please find my concerns.

[Response] Thank you for the positive assessment and constructive feedback. We have carefully revised the manuscript according to your suggestions. All comments have been addressed point by point, and the corresponding revisions have been made in the manuscript. As a consequence, our manuscript has been considerably improved. Hopefully you will find our revision satisfactory. Detailed responses to each comment are provided below.

First, although the discussion identifies carbon pool partitioning and enzyme-catalyzed processes as key factors underlying the simulation differences, it provides only a general mechanistic explanation for how drought regulates carbon inputs and mean residence times of different carbon pools via plant-microbe-mineral interactions. It lacks targeted analyses incorporating the ecological characteristics of the study area, such as the mineral composition of red and yellow soils, the carbon allocation strategies of evergreen tree species, and the fungal-dominated shift in microbial communities under drought.

[Response] Thanks for your comments. We agree that a general mechanistic explanation is insufficient in Discussion section and that targeted analysis incorporating site-specific ecological characteristics are essential to interpret the divergent model simulations. Accordingly, we added three targeted mechanistic discussions in Section 4.2, including (1) role of red-yellow soil mineralogy in regulating carbon residence time; (2) carbon allocation strategies of evergreen broadleaf trees under drought; and (3) drought-induced shift toward fungal-dominated microbial communities. Please see detail in Lines 480 – 512 and Lines 636 - 694. We believe these additions will substantially strengthen the mechanistic depth, site-specific relevance, and logical rigor of Discussion.

In addition, the consistent result of increased particulate organic carbon (POC) under drought across all three models is not thoroughly explained in terms of its ecological mechanisms and model representation.

[Response] Thanks for your comment again. We agree that the consistent increase in POC under drought across all three models—despite their divergent projections of total SOC—deserves a more thorough explanation, both in terms of underlying ecological mechanisms and how each model structurally represents POC dynamics. Accordingly, in revised version, we added a dedicated paragraph that systematically elaborates on the multiple ecological mechanisms driving POC accumulation and how these mechanisms are represented across the three model structures. Please see detail in Lines 480 - 512.

Second, SM3 incorporated β-1,4-glucosidase (BG), polyphenol oxidase (PPO), and cellobiohydrolase (CBH), but does not clarify the basis for enzyme parameter values (Vmax.enzy, fenzy, KM.enzy)-for example, whether they were calibrated using in-situ measured enzyme activity data from the research station or directly adopted from published literature. The rationale for selecting these three enzymes is not provided, nor is it explained why other enzymes potentially involved indirectly in carbon decomposition were not included.

[Response] Thanks for your comment. In SM3, the kinetic parameters for β-1,4-glucosidase (BG), polyphenol oxidase (PPO), and cellobiohydrolase (CBH) were directly calibrated using in-situ measured enzyme activity data from the research station (2014–2022). These measurements were conducted using microplate enzyme assays (Saiya-Cork et al., 2002; Su et al., 2020) and expressed as substrate conversion per gram of dry soil per hour. The parameters were then estimated using the MCMC data assimilation framework, with prior ranges derived from both published literature (e.g., Allison et al., 2010; Moorhead & Sinsabaugh, 2006) and site-specific constraints. Therefore, the parameters are not arbitrarily adopted but are empirically constrained by local observations.

These three enzymes were selected because they represent the major functional pathways in soil organic carbon decomposition. BG and CBH are responsible for the depolymerization of cellulose and other labile carbon compounds, and PPO is involved in the oxidation of recalcitrant, lignin-like substrates. Together, they capture the decomposition of both labile and more resistant carbon pools, providing a minimal yet functionally representative set of enzymatic processes. This parsimonious choice avoids overparameterization, which critical given the limited number of observational constraints.

We acknowledge that other enzymes (e.g., acid phosphatase, N-acetyl-glucosaminidase, peroxidase) may indirectly contribute to soil carbon decomposition. However, including them would substantially increase model complexity and parameter dimensionality, leading to potential non-identifiability and greater uncertainty—especially given the available data. Our current approach prioritizes process realism balanced with parameter tractability, as also noted in the Discussion (Section 4.2). We have now clarified this rationale in Lines 230 - 249 and 699 - 704.

Line 48: You can cite a more recent version of the IPCC here.

[Response] Done as suggestions.

Line 145: You may consider providing a clear definition of "decadal drought".

[Response] Thanks for your suggestion. In this study, "decadal drought" refers to describe a prolonged drought event lasting approximately one decade. To avoid ambiguity, we have now provided a clear definition in the revised manuscript as "a continuous reduction in natural rainfall by approximately 70%, sustained for over ten years (i.e., 2014–2024 in this study)", This definition (Su et al., 2020) is consistent with the long-term drought manipulation experiment established at the Tiantong Forest Ecosystem Research Station in 2013, which serves as the observational basis for our model evaluation. We have clarified this definition in the Lines 137 - 138.

Lines 186-189: Please pay attention to the subscripts here.

[Response] Thanks for pointing out our mistakes. we have checked and corrected all subscript issues.

Reference

Allison, SD., Wallenstein, MD., and Bradford, MA.: Soil-carbon response to warming dependent on microbial physiology, Nature Geoscience, 3, 336-340, 2010.

Du, Z.G., Zhou, X.H., Shao, J.J., Yu, G.R., Wang, H.M., Zhai, D.P., Xia, J.Y., Luo, Y.Q.: Quantifying uncertainties from additional nitrogen data and processes in a terrestrial ecosystem model with Bayesian probabilistic inversion, J. Adv. Model. Earth Syst, 9 (1), 548–565, https://doi.org/10.1002/2016MS000687, 2017.

Fan, XL., Gao, DC., Zhao, CH., Wang, C., Qu, Y., Zhang, J., Bai, E.: Improved model simulation of soil carbon cycling by representing the microbially derived organic carbon pool, ISME JOURNAL, 15(8), 2248 – 2263, https://doi.org/10.1038/s41396-021-00914-0, 2021.

Moorhead, D.L. and Sinsabaugh, R.L.: A theoretical model of litter decay and microbial interaction. Ecological Monographs, 76, 151-174. https://doi.org/10.1890/0012-9615(2006)076[0151:ATMOLD]2.0.CO;2, 2006.

Saiya-Cork, KR., Sinsabaugh, RL., and Zak, DR.: The effects of long term nitrogen deposition on extracellular enzyme activity in an Acer saccharum forest soil, Soil Biol Biochem, 34(9), 1309-1315, https://doi.org/10.1016/S0038-0717(02)00074-3, 2002.

Su, X. L., Su, X., Zhou, G. Y., Du, Z. G., Yang, S. C., Ni, M. Y., Qin, H., Huang, Z. Q., Zhou, X. H., and Deng, J.: Drought accelerated recalcitrant carbon loss by changing soil aggregation and microbial communities in a subtropical forest, Soil Biol Biochem., 148, https://doi.org/10.1016/j.soilbio.2020.107898, 2020.

Wu, XW., Luo, YQ., Weng, ES., Luther, White., Ma, Y., Zhou, XH.: Conditional inversion to estimate parameters from eddy-flux observations, Journal of plant ecology, 2(2), 55 – 68, https://doi.org/10.1093/jpe/rtp005. 2009.