Review #1

This manuscript presents evolution of terrestrial carbon including SOC, microbial biomass carbon etc. from 1901 to 2016 using CLM-Microbe model. The CLM- Microbe model was first validated against various data set. The changes of carbon fluxes and pools in different regions and at global scale were then investigated. The results providing insights about the dynamics of terrestrial carbon pools. However, the write of the paper need improve (e.g reduce repeat of sentences with similar meanings). The paper may discuss more about the implication or meanings of results as a scientific research paper. Besides, the author mentioned in the last paragraph of the introduction that they investigated the effects of environment change on temporal trend of variables related to soil, vegetation, microbes etc., but the author actually did is check the correlations between variables, there are quantitatively effects that are assessed and not summarized in the abstract. I do not mean that evaluation of effects of environment change is necessary, as other part of work has already been enough for a paper published here and consistent with the title, but the author needs reorganize the languages in related sections of the paper. I suggest a minor revision before it can be published in this journal.

Response: Thanks for your positive comments. We appreciate those comments and suggestions. To address the concerns, we have improved the writing by removing repeated sentences and reorganizing the contents to make the manuscript more science-focused. Also, we have summarized the effects of environmental change on the temporal trend of soil, vegetation, and microbial variables in the abstract. Please see the details below.

Specific comments

Abstract: The abstract presented the major results of research, but what are their implication and significance? Especially, the authors said they evaluated the effects of environment change on temporal trend of variables such as NPP, GPP etc., however, these are not presented in the abstract.

Response: Thanks for your comment. We have summarized environmental change on variations of soil, vegetation, and microbial variables in the abstract. See the Abstract section for details.

Line 15: 2901-2016?

Response: Typo corrected.

Line 20-22: This is not a complete sentence, please rephrase it.

Response: Rephrased as requested.

Line 39-47: Huang et al also developed an microbial model named ORCHIMIC, and tried to reproduce the global microbial biomass and soil organic carbon etc.. You may need to add 1 sentence to summarized advantages and disadvantages of this model.

Huang, Y., Guenet, B., Wang, Y.L., Ciais, P., 2021. Global Simulation and Evaluation of Soil Organic Matter and Microbial Carbon and Nitrogen Stocks Using the Microbial Decomposition Model ORCHIMIC v2.0. Global Biogeochemical Cycles 35, e2020GB006836. https://doi.org/10.1029/2020GB006836

Huang, Ye, Guenet, B., Ciais, P., Janssens, I.A., Soong, J.L., Wang, Y., Goll, D., Blagodatskaya, E., Huang, Yuanyuan, 2018. ORCHIMIC (v1.0), a microbe-mediated model for soil organic matter decomposition. Geoscientific Model Development 11, 2111–2138. https://doi.org/10.5194/gmd-11-2111-2018

Response: Thank you for your suggestions. We have read related papers on ORCHIMIC model, and we did not include it for summary in those lines but included papers on ORCHIMIC model in our discussion. This is because our summary is focused on studies investigating carbon cycle responses to climate change, while the ORCHIMIC model does not fit into it. The discussion on comparing microbial models in capturing SOC spatial variables is a good match. Please see L.476-477 for details.

Line 51: delete on of "He et al., 2021"
Response: Sorry for the confusion; we have differentiated them as He et al., 2021a; He et al., 2021b.

Line 49-57: This paragraph has some logical problems. Please rephrase it. For example, the third sentence has already included in the first sentence.
Response: Thanks for pointing it out. We have removed redundant information and rephrased them for clarity. Please see L. 59-67 for details.

Line 78: "the same with" should be "same as"
Response: Corrected as suggested.

Line 92-101: Please unified the format of all equations, not just here. Maybe make all "equation (?)" be left-aligned.
Response: Thank you for your recommendation. We have now formatted all equations left-aligned. Please see them for details.

Line 133: what's your mean by "by column"? or it should be "by layer"
Response: Thank you for your question. We did not mean by layer; layer is for classifying vertical distribution along the soil profile, while we meant to define microbial processes across space. Column is one type of data structure, which includes PFT, column, land unit, and grid. We represented fungi- and bacteria-mediated processes at the column level because soil fluxes and state variables were defined at the column level.

Line: 179: Is 1200 years enough for spin-up? You may provide a plot for this showing the change of soil carbon.
Response: Thank you for your recommendation. We have assessed the SOC dynamics in grid cells from low-, mid-, and high-latitude regions and plotted those temporal variations from initial cold-start (assigned small values for major C/N pools) over a 1200-year spin-up. This information is now provided in Fig. S2.

Line 275-285: which year of model results were used in validation and comparison? If results after the spin up were used, then the change of NPP and SR should be similar if your model had really reached its steady state.
Response: Thank you for the question. We used the output of ten-year averages during 2000-2009 for validation and comparison, and we have clarified this in the main text. Vegetation was closely associated with soil respiratory fluxes; we did observe similar changing trends between NPP, HR, and SR.

Line 458-459: This sentence partially duplicates the previous one. Besides, many sentences are presenting similar results in this paragraph.

Response: These results are different with respect to the area-weighted averaged at the global scale and spatial pattern at the grid scale. We have rearranged the result to make it clear in delivery. Please see L. 428-431 for details.

In section 4.1: Incorporation of microbes into the model may help improve modelling SOC and other variables, but I think it is hard to improve SR as SR is more or like controlled by input (NPP). Of course, if the model runs long enough, it may change SR through change the soil properties (moisture, temperature) by changing soil SOC content (this will change conductivity and porosity etc.)

Response: Thanks for your comment. At the steady state, changes in SR are more likely to be controlled by NPP, but its variations can still be altered by soil microbial processes since HR contributes to about two-thirds of SR and is regulated by the soil microbial community.

Line 542 558: Could the overestimation of microbial biomass in top 1m soil be attributed to O2?

Response: Thanks for the question. The oxygen might be a reason, but we did not modify hydrological processes in the model, which is the same as those in default clm4.5. Therefore, we did not consider it as a reason for overestimated microbial biomass.

Review #2

I have read the study of He and colleagues twice but cannot recommend its publication. The authors provide a manuscript which is mainly descriptive. They show transient model runs with the CLM-Microbe model, compare their results to machine-learning-based upscaled products of SOC, bacterial, fungal biomass, microbial biomass, DOC, GPP, NPP, and soil respiration. They then describe trends in different world regions and where the model performs well. The respective sections in results and discussion are verbose but do not provide new scientific insights. The analysis of drivers of trends is purely statistical, although it would be possible to perform experiments with the mechanistic model to understand the importance of different processes.

In the manuscript, we get a lot of metrics and descriptions of trends, stocks, and fluxes in different regions, but no essential scientific advances are made.

The study design is flawed since the authors have calibrated model parameters (Line 206-214) using the datasets (GPP, SOC, NPP, DOC, FBC, BBC), which are later used to evaluate the model performance. First, it is unclear how this optimization was performed; second, this is not an independent model evaluation against independent datasets.

The CLM-Microbe model is not sufficiently described. Do microbes control the decomposition of litter and SOC pool? Does bacterial and fungal biomass appear in the equations of litter and SOC decomposition for example, in a Michaelis-Menten term? How do microbes in the model affect GPP and NPP? Is there a nutrient competition between plants and microbes implemented? Why do we still need the e-folding factor for decomposition in a microbial explicit model? Koven *et al.* (2013) described this e-folding factor as accounting for unresolved processes such as priming effects (which should be covered in a microbial model) and microscale anoxia or mineral stabilization (are these still unresolved?).

These questions should be answered to gain scientific insights. This manuscript does not provide many relevant scientific insights but is a verbose description of model outputs.

Response: Thanks for your time and thought in making critical comments. We respectfully disagree with the reviewer on those comments. We believe our paper makes important contributions.

First, the reviewer stated that our manuscript is mainly descriptive. As we stated, this manuscript's goal is to provide novel information on model improvement (compared to CLM4.5) and its application at the global scale for simulating major carbon variables and microbial variables. Therefore, this work lays the foundation for future model applications to address specific scientific questions. The novelty of this study is that the CLM-Microbe model represents the first attempt to simulate bacterial and fungal dynamics at the global scale over a century scale. This is important because the CLM-Microbe model can improve our understanding of microbial impacts (e.g., soil microbial community structural change) in carbon cycle at multiple scales. Our unique findings are 1) the CLM-Microbe model can capture variations in soil microbial community (fungi and bacteria) across space; 2) both fungal and bacterial communities grow from 1901 to 2016 at the global scale; and 3) those growing communities are due to enhanced vegetation productivity and changes in soil moisture and temperature. Additionally, this work lays the foundation for future model applications to address additional scientific questions. Take Koven et al. (2013), cited by the reviewer, as an example, there was not much significant scientific advance of that paper; but it has not been prevented from publication, because (Koven et al., 2013) made significant improvements to the CLM4 in terms of

biogeochemistry cascade. Therefore, the publication of (Koven et al., 2013) proved to be an important stepping stone for further development of the CLM4.5 model.

Second, the reviewer questioned the introduction of the equation for microbial controls on GPP, NPP, and other carbon processes. The major improvements in the bacterial and fungal biomass C and N pools have been introduced by He et al. (2021b). On the one hand, the reviewer questioned the scientific focus of this study; on the other hand, the reviewer asked us to provide a more detailed introduction of processes in the biogeochemistry cascade. Those fall in two ends of the story; as we stated, this manuscript mainly focuses on model structure and the brief introduction of model application to support the model introduction. More insightful analyses of model applications are in progress.

Below are our answers to the questions listed by the reviewer.
The CLM-Microbe model is not sufficiently described.
Response: We have added additional details about validation data, experimental design (e.g., model parameterization), and model structure. Please see L. 233-287 for details. Additionally, some of the model structure has been published in He et al. (2021b) and Xu et al. (2014), which we refer to in the manuscript.

Do microbes control the decomposition of litter and SOC pool?
Response: Yes, soil microbes control the decomposition of litter and SOC by regulating litter/SOM breakdown (reflected as fungal and bacterial biomass pool sizes) and microbial carbon use efficiency (the separation of carbon among litter/SOM, soil microbial pools, and the atmosphere).

Does bacterial and fungal biomass appear in the equations of litter and SOC decomposition for example, in a Michaelis-Menten term?
Response: No, bacteria and fungi did not appear in the MM equation; rather, they are represented as parameters (k_fungi and $k\_bacteria$) in soil organic matter breakdown (influenced by microbial biomass) and carbon allocation by microbial carbon use efficiency (determined both by substrate and microbial biomass carbon to nitrogen ratio).

How do microbes in the model affect GPP and NPP?
Response: Soil microbes affect nutrient cycling through the processes of immobilization and mineralization, which is controlled by carbon to nitrogen ratio of soil microbial biomass and substrates for decomposition. They are also in direct competition with plants for nutrients and hence, expected to affect GPP and NPP.

Is there a nutrient competition between plants and microbes implemented?
Response: Yes, nutrient competition between plant and microbes are represented as plant nitrogen uptake and microbial immobilization for inorganic nitrogen in our model. Same as the CLM4.5, the CLM-Microbe model fully coupled carbon and nitrogen dynamics in land components. Microbial immobilization of nitrogen during decomposition steps depends on carbon to nitrogen ratio of organic materials for decomposition, the carbon to nitrogen ratio of fungal and bacterial biomass, and microbial carbon use efficiency. The sum of potential immobilization over all immobilization in the biogeochemistry cascade is used to estimate microbial demand of mineral nitrogen. For each time

step, such microbial mineral nitrogen demand is in competition with the total plant nitrogen demand of all plant functional types on a soil column.

Why do we still need the e-folding factor for decomposition in a microbial explicit model? Koven *et al.* (2013) described this e-folding factor as accounting for unresolved processes such as priming effects (which should be covered in a microbial model) and microscale anoxia or mineral stabilization (are these still unresolved?).

Response: The mechanisms of soil organic matter decomposition along the soil profile were not represented well in the community land models; therefore, the e-folding factor was introduced. For example, gradual declining oxygen and changing molecular structure of the carbon along the soil profile. These are complex molecular-scale processes that are not automatically included in a microbial model (including our own). See (Koven et al., 2013) for more details, which holds true in the CLM-Microbe model.

I point out some mistakes:
- Figure 4 e,f: SOC has units of fluxes (kg m-2 yr-1)
- Abstract: "2901-2016" is an interesting time-period for simulation

Response: Thank you for pointing those out; the typos have been corrected. Figures and periods in the abstract have been updated. Please see L. 15 and updated Figure 4 for details.

Koven CD, Riley WJ, Subin ZM *et al.* (2013) The effect of vertically resolved soil biogeochemistry and alternate soil C and N models on C dynamics of CLM4. Biogeosciences, **10**, 7109-7131.

Review #3

This paper presents CLM-Microbe simulated results of terrestrial carbon fluxes and pools from 1901 to 2016. The study evaluates the model's performance against observational data derived from MODIS, SRDB, etc., and suggests that the model captures the historical dynamics of the terrestrial carbon cycle (e.g., GPP, NPP, HR, SR, MBC, etc.). This is an important study towards incorporating microbial processes into CLM4.5 at the global scale. However, it's quite disappointing how the authors describe the model and organize the results. Here are several of my main concerns:

Response: Thank you for your kind words regarding the significance of our work and comments and suggestions for further improvements; we really appreciate that. To address the concerns, we have improved the writing by providing additional explanations behind our reported patterns or correlations, highlighting the significance of this study, and providing more detailed about the model structure of the representation of fungi- and bacteria-mediated processes on decomposition. Also, we have updated the figures and made other revisions as suggested; please see the details below.

1. Please enhance scientific writing. Most of the context in the results section simply describes patterns or correlations but fails to provide explanations behind them.

Response: Thank you for pointing it out. The temporal and spatial patterns of soil, microbial, and vegetation variables are the results we focused on, and we have now provided additional explanations to corroborate the observed patterns. Owing to the correlations between soil, microbial, and vegetation variables and environmental factors were used to explain the observed patterns, we did not provide further explanations behind those correlations.

2. The authors stated that they investigated the effects of environmental change (climate change, N deposition, rising CO2, and aerosols) on the temporal trend of variables related to soil, vegetation, microbes, etc. But they didn't conduct any analysis regarding that. Please either include some causal analysis or remove this statement.

Response: Thank you for the suggestion; we now avoid highlighting the statement about environmental change (climate change, N deposition, rising CO_2, and aerosols) in the Introduction section. Please see L. 38-42 for details.

3. Abstract – The authors listed lots of results with specific numbers in the abstract but failed to highlight their contributions and significant findings concisely. Please consider rewriting the abstract thoroughly.

Response: Thank you for your suggestion. We have added sentences to highlight our contributions and significant findings of this study in the Abstract. Please see L. 26-28 for details.

4. Model details – Very vague and unclear. The current description makes the CLM-Microbe an implicit representation of fungi and bacteria, not explicit at all.

Response: We agree with the Reviewer that our statement lacked clarity. We have now added specific descriptions on the representation of fungi- and bacteria-related processes such as microbial respiration, lysis, microbial carbon assimilation, carbon use efficiency, etc., in the CLM-Microbe model. Please see L. 99-104 and 128-160 for more details.

5. Figures: Please consider the following modifications:
a. Combine Fig. 1 and Fig. 2

Response: Thank you for the suggestions. If possible, we would keep Figures1 and 2 separated, because: 1) Figures 1 and 2 were obtained from two distinct models: CLM-Microbe and CLM4.5, respectively. The current display is consistent with Figures 3 and 4, for the sake of comparing between current and previous model versions to help the audience understand our contributions; 2) if combining Fig.1 and 2, the combining of Fig.3 and 4 to be consistent would make it difficult to contrast the CLM-Microbe model and CLM4.5. Therefore, we did not combine them into one.

b. Fig. 3 and Fig. 4 – I don't believe some of the r (e.g., for FBC and BBC) is not quite low, given the sparse spread of the scatters. Also, what is the temporal scale for the comparison? You might want to check the comparison at a coarse temporal scale, i.e., monthly or even annually.

Response: Thank you for the question and suggestions. Yes, r should not be high considering the dot distribution in scatter plots. The r in this study is r_s, i.e., Spearman's rank correlation coefficient, since the distribution of the variables did not follow a normal distribution. We, therefore, performed Spearman's rank correlation to test the consistency between observational and simulated values. We have provided information about our statistical approach used in this study, please see L. 290-299 for details.

The Reviewer is correct that a coarse temporal scale should have been performed. Indeed, we performed such a comparison, considering the fact that observational data are long-term averages. The temporal scale for the comparison is the simulations of ten-year averages (2000-2009), which we have clarified in the Statistical analysis section. Please see L. 302-305 for more details.

c. Fig. 5 and Fig. 6 – are the two figures based on the global scale?

Response: Thank you for the questions. Yes, those figures are about the global trend of fluxes and pools from 1901 to 2016.

d. Fig. 7 – why is there minimal change for the high-latitude?

Response: Thank you for the question. By looking into Fig. 9 and 13, the tiny changing trends of grids at high latitudes and no changes in Greenland can explain the small latitude change at high latitudes. Please see Fig. 9 and 13 for more information.

e. Figures 11 and 12 – please consider changing the color scheme to enhance the contrast.

Response: Thank you for the suggestion. We have now replaced the green gradient with a more contrasting purple-white-green color scheme for appropriate comparison. Please see Fig. 8, 11, and 12 for more details.

f. Figure 14 – Again, please consider changing another color scheme.

Response: Thank you for the suggestion. We have replaced the color gradient with a more contrasting dark blue-white-dark red color scheme for comparison. Please see Fig. 14 for more details.

6. The manuscript is way too long. Please consider shortening some unnecessary descriptions, e.g.,

removing those long descriptions about regional patterns, since the Discussion section repeated some of these descriptions again.

Response: Thank you for the suggestion. We have shortened the manuscript by removing unnecessary details about regional patterns of absolute and relative changes of decadal averages in some specific regions as well as changes by continent as well as changing rates from 1901 to 2016. Please see L. 374-425 for details.

Specific comments:

Line 15: It should be 1901, not 2901.

Response: Corrected as recommended.

Line 24: Please be specific about the enhanced understanding.

Response: Thank you for the comment. We have now clarified that this study lays the foundation of enhancing our understanding of microbial role in carbon cycle. Please see L. 26-28 for more details.

Line 32: Please explain/define nitrogen deposition first before mentioning it.

Response: Thank you for the suggestion. We have removed N deposition and aerosols in the Introduction section following the previous suggestion as we did not focus on those analyses; please see L. 38-42 for more details.

Line 33: I bet "influence" or "affect" or "impact" reads better than "disrupt".

Response: Changed as recommended: "disrupted" to "impacted," please see Line 41 for details.

Lines 40-41: This statement is quite vague. Could you please provide more details on the key distinctions between implicit and explicit model representation? Additionally, it would be helpful to specify the types of processes that explicit models can represent but implicit models cannot. Simply adding three additional carbon pools (i.e., fungi, bacterial, and DOM) does not suffice for achieving explicit representation.

Response: Thank you for the comment. We have specified how microbial processes were implicitly represented in conventional models, assuming that respired CO_2 is proportional to the soil C stock and microbial role in decomposition processes is overlooked, and what microbial processes were represented in microbial explicit models, soil microbial respiration, and activities in decomposition processes. Please see L. 47-52 for more details.

Line 51: What do you mean by "at fine scales"? This study didn't conduct validation at find scales either. Or, do you mean validating fungi and bacteria biomass separately?

Response: Thank you for the question. The fine scales were set to provide contrast at the global budget or biome averages, which we validated the model at grid level, along with longitude, and global budget. To avoid misunderstanding, we have clarified that it is relative to coarse scales of validation at global budget or biome averages when mentioning fine scales (grid-level comparison). Please see L. 55-57 and 62-64 for more details.

Line 52: This is just a repetition of the 1st sentence of this paragraph.

Response: We have removed that sentence according to the recommendation.

Lines 60-62: I believe that the mechanistic representations of microbial processes within CLM-Microbe have many fundamental strengths compared to other models (e.g., CLM4.5 itself), and differentiating fungal and bacterial representations is a higher-level capability. The way this sentence was written undermined the mechanistic modeling capability of CLM-Microbe greatly.

Response: Thank you for the positive words on the model development and strengths. We have provided additional details about the advantages and strengths of mechanistically representing microbial mechanisms of soil carbon cycling and differentiating the physiology of two major microbial functional groups (i.e., fungi and bacteria) in the CLM-Microbe model in mechanistically modeling microbe-mediated processes and revealing microbial role in carbon cycling. Please see L. 69-73 for details.

Line 78: Replace "with" with "as".

Response: Replaced as suggested.

Line 86: You don't need to provide the full git hash. Indeed, I suggest shortening lines 85 to 87 by simply providing Xu et al. (2022) and moving the URL into the code availability section. Same thing for the data description section. Please do not include URLs in the context but provide them in the data availability section.

Response: Shortened the sentence by removing the GitHub Hash and moving the URL to the data availability section. Please see L. 95-97 and 717-719 for details, thanks.

Line 90: Any representations of microbe growth and metabolism?

Response: Yes. Fungal and bacterial growth, carbon assimilation, respiration, and death were represented in the model. We have provided more details in the Model Representation of Fungal and Bacterial Biomass section. Please see L. 84-174 for details.

Lines 89 to 92: This description is completely unclear. Does the "carbon input" mean microbial assimilation of SOC?

Response: Sorry for the unclearness. Yes, carbon input from substrates means microbial carbon assimilation from substrate uptake. Carbon input and loss are descriptions regarding the flow of carbon fluxes between pools. We have added details to clarify; please see L. 99-103 for details.

Lines 120 to 131: Again, not clear at all. This is not a mechanistic representation but rather an implicit form.

Response: Thank you for the comment. From available evidence, microbial cell death occurs as a first order rate phenomena (Verhoff et al., 1972). Therefore, death and lysis of microbial biomass was represented by a first-order kinetics. Those processes are modified by environmental scalars such as moisture and temperature, the presentation of microbial lysis considering the rate constant and environmental influence still holds. To avoid uncertainty, we have removed mechanistic from the sentence, please see L. 147-160 for details.

Lines 147 to 148: This approach implies that PFT controls soil microbial communities and their associated properties. Although vegetation characteristics, diversity, and composition can significantly impact soil microbial activities, biomass, enzyme activity, and community composition, this direct association between PFT and microbial properties is still highly uncertain.

Response: We represent fungal- and bacterial-mediated processes by column considering the dominant PFT on the column because our previous work on parametrizing the CLM-Microbe model suggests that soil fungal and bacterial processes varied by biome. The initial parameters of the CLM-Microbe model are biome specific, and soil fluxes and state variables were defined at the column level; we thus represent fungal- and bacterial-mediated processes by column at the global-scale simulation.

Line 183: please elaborate more on the initialization procedure.

Response: We have added additional details on the initial procedure for simulation. Specifically, we assigned the same microbial parameters for PFTs found in the biome as their initial setting since our previous parametrization for microbial processes was biome-specific (He et al., 2021b). For example, broadleaf-evergreen-tree-tropical and broadleaf-deciduous-tree-tropical, belonging to the biome of Tropical/Subtropical forests, parameter set for Tropical/Subtropical forests were adopted for broadleaf-evergreen-tree-tropical and broadleaf-deciduous-tree-tropical in initial simulations. Please see L. 225-231 for details.

Lines 209 to 214: Did you calibrate the model step by step against different observations? Or did you apply a multi-objective calibration strategy? If it is the latter, what is your cost function? Also, not clear to me when the calibration period and the validation period are. Are the two periods the same or different?

Response: Thank you for the questions. We have calibrated the CLM-Microbe model step by step against different observational datasets. Also, the calibration period and the validation period are different, depending on the sampling time of the observational dataset. The parameterization of fungal and bacterial biomass was based on time-series observational data of fungal and bacterial biomass carbon from nine natural biomes (He et al., 2021b). Soil and microbial respiration fluxes were parameterized using the observational data of soil and microbial respiration fluxes from nine natural biomes (He et al., 2021a). In addition, we compared the simulated DOC in the top 30 cm and 1 m with observational data from natural biomes, with at least two data points from each biome (Table 2-3; Fig.S3). Before those comparisons, we guaranteed reasonable soil organic carbon density and vegetation productivity (GPP and NPP) at each site. We have clarified such procedures in the Methods section; please see L. 267-287 for more details.

Line 218: Why use GSWP3v1? If the forcing for CLM4.5 is different from what is used for CLM-Microbe, you cannot compare the two model simulations; at least, you cannot associate model performance discrepancy with model differences because you must exclude the differences caused by different climate forcings.

Response: Thank you for the question. The CLM-Microbe model was forced using the CRUNVEP dataset, but we used the results of CLM4.5 forced using GSWP3v1 for comparison because: 1) the shared output of CLM4.5 to the community is forced using GSWP3v1, we thus only have access to such outputs; 2) the CLM4.5 output forced using GSWP3v1 or other meteorological data are optimized to their observational data, we therefore assumed the CLM4.5 output forced using GSWP3v1 could reflect the capability of capturing the spatial variations in terrestrial carbon cycle variables.

Lines 305 to 306: better than what?

Response: Thank you for the question. We have clarified it by changing the sentence to "Overall,

both the CLM-Microbe model and CLM4.5 performed better at simulating GPP and NPP than simulating soil and/or microbial variables."

Line 364: why these negative changes?
Response: Thank you for the question. We investigated the external environmental factors on GPP, NPP, HR, and SR based on our results. The decreases in GPP and NPP are because of the rising mean annual temperature considering the negative correlation of GPP and NPP with mean annual temperature (Fig. 15, Fig. S5). The decrease in HR and SR can be explained by decreases in GPP and NPP in regions where vegetation C fixation is the major C source for ecosystems (Figures 8a-8f). We have explained that in the Discussion section, please see L. 597-599 and 617-619 for details.

Lines 369 to 370: again, why? You must provide an explanation following these statements.
Response: Thank you for the question. Those results have been discussed in the Discussion section. After investigating the external environmental factors on GPP, NPP, HR, and SR, we found that decreases in GPP and NPP are because of the rising mean annual temperature considering the negative correlation of GPP and NPP with mean annual temperature (Fig. 15, Fig. S5). The decrease in HR and SR can be explained by decreases in GPP and NPP in regions where vegetation C fixation is the major C source for ecosystems (Figures 8a-8f). Please see L. 597-599 and 617-619 for details.

Lines 375 to 376: ok, but why?
Response: Thank for the question. The larger increases resulted from the rapidly increasing rates of GPP, NPP, HR, and SR in eastern Asia, central and northern South America, and southern Europe across space. We have explained that in the Discussion section. please see L. 585-597 for details.

Lines 372 to 454: In my opinion, these descriptions of regional spatial patterns are not informative unless you can associate these spatial patterns with climate change patterns. Alternatively, you can analyze these patterns by vegetation types, but simply describing these patterns by region without exploring the reasons is not scientifically meaningful.
Response: Thank you for the suggestion. We have removed unnecessary details on regional patterns, since we do not focus on regional changes in specific areas and exploring their underlying reasons. Please see L. 395-425 for more details.

Lines 464 to 469: again, why are these negative correlations? Please consider rewriting both sections 3.4 and 3.5 throughout.
Response: Thank you for the question. The negative correlations report the potential mechanisms for changes in carbon cycle fluxes and pools. The reason they are negative or positive is not what we focused on in this study since this manuscript is already quite long, as mentioned above. The relationship between temperature and carbon sequestration has been found to be either positive or negative (Fernández-Martínez et al., 2019). We have rewritten sections 3.4 and 3.5 by teasing out unnecessary details and rearranging the contents. Please see L. 405-466 for details.

Line 511: Not really. For example, I can see that CLM4.5 simulated SOC performs much better than CLM-Microbe simulations, i.e., Fig. 2 vs Fig. 1.

Response: Thank you for your comment. The CLM4.5 underestimated SOC at all latitudes, while the simulations of the CLM-Microbe model can better capture SOC variations along latitude, especially at the top 30 cm (Fig. 1-2). Also, the simulated SOC at the top 30 cm and 1 m by the CLM-Microbe model were better matched with observational data than by CLM4.5 (Table 1). Specifically, the CLM4.5 underestimated SOC (0-30 cm) by 22.4%, while the CLM-Microbe model underestimated it at a much smaller rate of 8.5%.

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