We appreciate the supportive comments from Dr. Wutzler. In our revisions we have provided greater detail to the methodology and assumptions to clarify the interpretations and conclusions drawn from our results. Dr. Wutzler is correct; the paper highlights differences from a first-order model. Accordingly, we have also removed unnecessary value assessments on "improvements" made with MIMICS simulations. For clarity specific reviewer comments are numbered for each reviewer and placed in brackets, our response follows each comment. Specific changes in the revised manuscript are also noted with the same numbering scheme to clearly note how we incorporated reviewers' suggestions.

R1.1 [My biggest concern is that due to the multitude of the objectives and simulations, each of the simulations/objective lacks detail. Methods and assumptions are not sufficiently clear. Therefore, I cannot follow several of the interpretations and conclusions.]

We have tried to clarify specific areas of concern, especially in sections 2.2 and 2.3 of the paper, please see comments below.

R1.2 [One of the main conclusions is that representing microbial diversity by traits in SOM dynamic models is important and improves predictions. However, the model was never compared to a microbial explicit model without this diversity, e.g. with a lumped microbial biomass that influences litter and SOM decomposition. The conclusion that can be drawn is that predictions from this microbial explicit model differ from classical models. But as the paper says: "we already know that ..." (p 2024 L 24). The step from microbial non-explicit to trait based is too big for properly relating observed difference in model predictions to microbial diversity. There are too many causes so that differences in results can be attributed to several features in addition to microbial diversity.]

For the most part we agree. The step from microbial implicit to microbial explicit model structures is likely more significant if soil C models are used to model for numbers- that is to make (hopefully accurate) projections about the fate of C in response to environmental change. If, however, these models are used to model for insight, we argue that models considering microbial diversity can generate testable hypotheses that may provide greater insight into soil biogeochemical dynamics. (See the discussion around Fig. 3). Other results present in the paper, however, do not depend on potential shifts in community composition. Thus, our claims of 'improvements' made by representing microbial diversity are not supported and have been removed from the revised manuscript.

R1.3 [Method Section 2.2 is hard to follow, because several experiments are lumped into this single section. This is similar for the corresponding results section. Many details of are not sufficiently described: The model simulates microbial biomass to increase with litter inputs - why were they kept constant (p. 2017 L23)? How were the litter inputs distributed across depths? And how specifically were the parameters adjusted for depth (p2018 L13)? What varied in the bootstrap analysis (p. 2019 L2ff)?]

We appreciate this feedback and aim to clarify these lengthy methods and results section focusing on cross-site simulations into subsections focusing on Leaf litter decomposition (now section 2.1.1), and belowground response to N enrichment (now 2.1.2). These same numbering conventions are used for Results and discussion to further clarify results. To address specific concerns:

R1.3.1   **We assume that in the real world, litterbag studies effectively operate as passive tracers that are used to quantify rates of litter mass loss. The addition of the litterbag itself does not change rates of leaf litter decomposition. This may be not true in MIMICS (especially in sites with low productivity or small standing litter stocks). In particular, increasing litter inputs builds more microbial biomass and alters rates of litter decomposition. For this reason, we held microbial biomass constant in our LIDET simulations to avoid introducing unintended treatment effects from 'litterbag' additions into our analysis. We feel text in the manuscript adequately and honestly communicates this detail without belaboring the point.**

R1.3.2   **Currently MIMICS lacks representation of vertically resolved soil profiles. Thus litter inputs (gC/m2) were 'evenly' distributed throughout the soil profile (mgC/cm^3) being represented (here 0-30 cm). But whereas LIDET simulations (2.2.1) focused on leaf litter decomposition, our response to N enrichment simulations (2.2.2) focus on soil C stocks, and belowground responses. These parameter modifications were described in Appendix A2, but not referenced in the main text. We have modified this in the revised manuscript.**

R1.3.3   **Variation is generated by among-site responses to increase litter inputs. In MIMICS this was generated by differences in litter quality, soil texture, and their interaction via microbial functional groups.**

R1.4 [Similar for Methods 2.3: E.g. How did you adjust parameter values to account for the 1m (p2019 L18)? Did you adjust litter inputs as well for the 1m constraint?]

Modifications to model parameters are described in Appendix A3, this point is clarified in the text. Litter inputs (gC/m2) were distributed throughout the top meter of soil to generate pools calculating volumetric C concentration (mgC/cm^3)

R1.5 [At several places, ad-hoc adjustments of the model parameters were necessary to match the results (e.g. p 2021 L 18ff). First, these parameter adjustments are described in the results section instead of the methods section and appendices. When reading the methods section first, I was confused about what had been done. In the results section the different adjustment are motivated and discussed. Nevertheless, they are quite ad-hoc and the specific values seem quite arbitrary tunings. I suggest to integrate such adjustments in a proper sensitivity study.]

We appreciate this feedback, and acknowledge that the presentation of these ideas is unnecessarily confusing. To reduce this confusion, we better introduce the motivation for potential parameter changes in the appropriate methods section(s). Upon reflection, the analysis and discussion surrounding Fig. 3 is a complicated story. In our revisions we've tried to simplify our message, placing rationale in the methods, narrowly describing results, and providing interpretation and discussion of the observational and theoretical basis for our findings in the methods and expanded Appendix A of the revised manuscript. At this point, we feel that an additional sensitivity analysis would actually obscures the message that MIMICS offers a tool to begin generating testable hypotheses that may provide greater insight into soil biogeochemical dynamics. For what's already a complicated paper with multiple analyses at different spatial and temporal scales, a proper sensitivity study on one aspect of the manuscript seems unwarranted.

R1.6 [The adjustments were mainly necessary to modify the ratio of biomass in different microbial groups. For a trait-based model I would expect that those ratios arise because of competitions or some other emergent effect of the model instead of prescribing parameters.]

This is a fair assessment, and Dr. Wutzler is correct that competition (in this case for C) structures the relative abundance of different microbial functional groups. If environmental changes drive concurrent physiological changes (i.e., parameters) this will shift the competitive balance and relative abundance of microbial functional groups. These analyses were intended to demonstrate the general applicability of MIMICS to both evaluate and generate testable hypotheses that may provide greater insight into soil biogeochemical dynamics. The exercise also may help focus efforts to develop empirical functions that describe microbial physiological response to environmental change.

R1.7[A big part of the discussion on copiotrophic:oligotrophic ratio (p2021 14ff) is based on the N-addition scenario. However, the described corresponding scenario is an increase in soil litter input carbon (ANPP) instead (p2018 L25). The same scenario could result from increased CO2 with opposite arguments to the litter quality and resulting parameters and stoichiometric effects on microbial groups.]

The logic here is difficult for us to follow, however, we've tried to clarify aspects of the methodology to avoid confusion on our end. Yes, both cross-site and global simulations look at projected changes in soil C following increases in productivity-from N enrichment and elevated CO2, respectively. We only looked at changes in microbial physiology in the cross-site simulations (section 2.1.2). We did not explore potential changes in microbial physiology in the global simulations and tried to make this clear in the text (p2018 L26, of the discussions paper, now in section 2.2.2 of the revised section), which stated "We did not modify our parameterization of MIMICS in transient global simulations because we lack the process-level understanding to guide potential microbial responses to elevated [CO2]." Dr. Wutzler is correct, exploring potential microbial physiological changes to elevated

CO2 is an exciting possibility with MIMICS, but one we don't explore in this manuscript.

R1.8 [There are a number of features in the global runs that only appear in the discussion rather than methods or results, which have a great influence: Specifically: 1) Litter quality parameters of lower and higher latitudes have been set differently 2) Parameterization partitioning of the different SOM pools (related to clay content) differs between low and high latitudes.]

Neither of these specific concerns are accurate. Parameterizations in global runs are <u>identical</u> to those in the LIDET simulation, except for modifications to turnover, the total fraction of metabolic inputs (fmet), and a parameter related to physical protection of SOM (pscalar). This is stated in the methods (now section 2.2.1), with details provided in Appendix A3. The spatial pattern that are presented (section 3.2.2) and discussed (section 4.2), emerge from the biogeographical differences in litter quality, soil texture, and their interactions via microbial community composition. Specifically, high-quality litter inputs and finely textured soils being more common in the tropics, favoring physical protection of SOM (Supplementary Fig. 2) and accumulation of soil C under elevated CO2 (Fig. 6, Supplementary Fig. 3), and low-quality litter inputs and more coarsely textured soils more common at high latitudes.

R1.9 [Again there are many causes of observed differences, and to my opinion it takes more scenarios or specific work to tease apart which of all those assumptions help/hinder the model fit.]

We are unclear what part of the paper to which this comment refers?

Specific comments

R1.10 [Labels of equations A1 to A10 are difficult to follow. I suggest more semantics in Names e.g. dec_LIT_m (A1)]

These changes have been made

R1.11 [I would appreciate some more discussions in Appendix A1 on model features. E.g. Under which conditions is it viable to separate microbial uptake from different portions in the DOM, i.e. different LIT and SOM sources? (There are several completely independent Michaelis-Menten equations for the update.) What is the rationality of applying MM kinetics twice in the breakdown and uptake of SOM_c?

The model structure employed here assumes that the breakdown and assimilation of chemically protected SOM is a two-step process involving depolymerization (eq. A10) and assimilation (eq. A3 & A7). This approach has been used by other microbial explicit (Allison et al. 2010; Wang et al. 2013), and theoretically applies to each pool and flux represented in MIMICS. Here, we simplify assumptions to omit

such dynamics from microbial decomposition of litter pools, focusing on microbial interactions and the breakdown of chemically protected SOM, as a means to potentially simulate priming of "recalcitrant" SOM (Kuzyakov   2010). Parameter values chosen here reflect the greater enzymatic capacity for depolymerization in oligotrophic communities (higher Vmax and lower Km), but copiotropic communities possess a greater enzymatic capacity for assimilation. [This text has been added to Appendix A1.]

R1.12 [How were the empirical relationships clay content and Km or the partitioning of microbial turnover derived?]

We assume that size and chemistry of copiotrophic microbial residues may favor physicochemical stabilization in finely textured soils (Grandy and Neff 2008; Spence et al. 2011). We also assume that finely textured soils will restrict enzyme access to available C substrates, here represented by increasing the half saturation constant (Km) of available SOM with increasing clay content (Zimmerman and Ahn 2011). We stress these empirical relationships for partitioning for microbial residues and modifications to microbial kinetics based on clay content that are used here are based on this theoretical understanding, and the numerical constraints of building plausible SOM and microbial biomass pools with co-existence of both microbial functional types across wide biogeographic and edaphic gradients. These simple equations, however, are not constrained by observational estimates, and ignore potentially important influences in soil mineralogy on SOM stabilization. [These texts has been added to Appendix A1.]

Comment [WW5]: Other / or better refs?

R1.13[P 2017L 18 typo proscribed? Table B1: typo desorbsion rate?]

These have been corrected. Thank you.

R1.14[When trying to the run the Git-Hub source-code, I could not find function quartz() (though it worked without it)]

This syntax is specific to running the R script on a Macintosh operating system. Windows systems use windows(), and Unix platforms use X11().

Reference:
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Kuzyakov, Y.: Priming effects: Interactions between living and dead organic matter, Soil Biology and Biochemistry, 42, 1363-1371, 2010.

Spence, A., Simpson, A.J., McNally, D.J., Moran, B.W., McCaul, MV, Hart, K, Paull, B., and

Kelleher BP. 2011"The degradation characteristics of microbial biomass in soil" Geochimica et cosmochimca Acta 75: 2571-2781

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