We thank for the editor for the comments and edits. We have addressed the specific comments as follows:

R1) Both reviewers asked for suggestions or guidelines to address the parameterization step. Although I agree with you that a detailed parameterization description is beyond the scope of the article, the request is much simpler than this. Simply provide, based on your experience, a set of recommendations for users about how to address the parameterization problem. For example, what parameters should receive priority, what parameters tend to be correlated among each other, and which ones seem to be less sensitive. This is just to help new users get started with this difficult task.

> We have added the following text on lines 332-338 as initial guidance related to parameterization.
>
> "In general, parameterization efforts are inherently challenging. For Lambda-PFLOTRAN, which models microbially mediated processes, it is recommended to initially focus on constraining biomass parameters (i.e., CC, k_{deg}, and V_h) by measuring temporal changes in biomass concentrations. Further, V_h and μ_{max} are typically highly sensitive and often correlated. However, since V_h represents the theoretical volume accessible to microbes and cannot be directly measured, it is suggested to fix V_h within a range of 1-10 m^3. If these microbial parameters can be adequately constrained, focus can shift to μ_{max}, the maximum microbial growth rate, which significantly influences overall respiration and is expected to exhibit the highest variability across different locations and conditions."

R2) Line 170 (tracked changes version). bias instead of basis?

> We have made this update on line 409 (tracked changes version).

R3) Test case 1 presents a comparison with a 'bulk SOM model' or 'bulk carbon' model, but I don't recall seeing a description of this model. Do you have a description of this model in the previous sections?

We have moved the description of the generic bulk carbon reaction network up to line 274 – 277 (tracked changes version).

R4) Figure 6. Replace 'carbons' for 'C atoms'.

> Updated Figure 6 accordingly.

R5) When clicking on the link https://doi.org/10.15485/2281403 I get a blank page. Can you check whether this is working properly?

> The link is working properly for us. Please let us know if this is still an issue though.

R6) One comment on your method, which I don't expect you to address in a revised version. The fact that the input data doesn't provide information on how the total carbon mass is distributed

among the different lambda bins seems to be as a major limitation of this approach. However, the approach allows you to compute entropies, and you have some entropy formulas in equation 11. Have you thought about using entropy maximization to obtain a plausible distribution of the lambda bins? This seems to me as a good potential approach to this with this limitation of the method.

Thank you for this idea! It is very interesting and worth pursuing.