Point-by-point response to Reviewer 2

> We thank the reviewers for their thorough and positive evaluation of our manuscript and for their valuable comments, which have helped to improve this work substantially. In response, we have implemented comprehensive revisions, which we detail point-by-point below.
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> Please note that we have reorganized the Sections of the manuscript, relocating the content of the former Section 3, and adding a Discussion Section (Section 4). We added new control simulations for the case studies and tables of empirical ranges for parameters, which are relatively extensive. We decided to present these in a separate Supplement to the main text (supplement.pdf). We also moved parameter and notation tables from the main text to the Supplement.

Summary

Lücken and colleagues present a 0D box model of phototroph-heterotroph-DOM-nutrient interactions. The paper is simple and easy to read and understand. The model equations and motivations are well stated. The outcomes are clearly drawn via use cases against some experimental data.

I have minor comments given that the paper is well written, well presented, and doesn't overreach. It is a simple model, and the authors are able to fit/explain some experimental data with phototroph-heterotroph interactions with only simple tweaks to their model parameters. While these explanations are not deeply convincing, it does convince me that the model is useful for exploratory studies.

My only comments are:

- Line 79: Can you please define X and Y sub- super-scripts and what these are referring to exactly. Is X flux in and Y flux out?

Response:

> Thank you for that suggestion. We have modified the Model description section, in particular the initial part, to provide a clearer overview of the model and the notations. Regarding the notation for fluxes, we have changed the notation to $f_{X \rightarrow Y}$ throughout the manuscript. Here, X denotes the source and Y the sink of the flow. We state this unambiguously in the revised manuscript:
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> "For the formal presentation, we use the notation $f_{X \rightarrow Y}$ to denote elemental fluxes, where X is the source and Y the sink of the corresponding flow." (ll. 103-104)

- Line 308: While this is one way to explain the data, it's not super convincing. However, you are also not saying that this result is the ultimate explainer… So, I think that's fine. Perhaps just make a note here that there are other possible processes/mechanisms that could explain this.

Response:

We agree that modeling the accumulation of all inaccessible nitrogen solely as refractory dissolved organic nitrogen (DON) may not fully capture the reality. In our configuration, the refractory DON pool only serves as a conceptual representation for diverse irreversible nutrient losses. We have added a sentence in the revised manuscript to clarify this:

“This pool represents a sink for non-recyclable matter, encompassing not only refractory DON, but all other inaccessible nutrient sinks, e.g., particulate forms.” (ll. 325-326)

- Line 334: by reducing loss rates right?

Response:

Yes, that’s correct. To make this clear, we modified the sentence to:

“For the inhibitory case, metabolite effects increase the phytoplankton loss rate, resulting in a reduced net growth rate.” (ll. 355-356)

- Figure 8, panel f: can you give a more clear explanation of this figure for the reader in the text? It took me some time to figure out exactly what was going on here. Your explanation is already okay, but perhaps too concise to allow for smooth interpretation.

Response:

Thank you for this comment. We included additional explanations for Figure 7(f) [former Figure 8(f)] in the main text:

“The relative averaged abundance over the last ten years of the simulation is reported for each simulation run in Panel (f). In this panel, for each overlap value, two horizontal bar groups are displayed: the top group corresponds to initializations with consortium A dominant, and the bottom group to consortium B dominant. Each group contains 20 stacked bars (one per community), where each bar represents 100% relative abundance. The bars are divided into colored segments: shades of green for species from consortium A and shades of red for consortium B, with segment lengths proportional to species’ average abundances. Starting from different initial states, priority effects appear as systematic differences in the dominant consortium (i.e., predominantly green vs. red segments) between the top and bottom groups for the same overlap. Convergence is indicated when both groups exhibit similar color distributions.” (ll. 418-425)

Further, we extended the description of Panel (f) in the figure’s caption, now reading:

“ (f) Asymptotic relative abundances by consortium (green: A, red: B) for different overlap values and initial states. For each overlap, top bar group: initial A dominance; bottom group: initial B dominance. Each horizontal bar represents one community’s species distribution (n = 20 communities per group).”