

Biogeosciences Discuss., author comment AC2
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Reply on RC2

Samu Elovaara et al.

Author comment on "Contrasting patterns of carbon cycling and dissolved organic matter processing in two phytoplankton–bacteria communities" by Samu Elovaara et al.,
Biogeosciences Discuss., <https://doi.org/10.5194/bg-2021-220-AC2>, 2021

Dear referee

Thank you for your kind and constructive comments! Please find embedded in your comment our initial suggestions for improving the issues pointed out and answers to your questions.

The manuscript determined the carbon cycling and subsequent effect on bacterial community composition using an experimental approach based on monoculture of two common phytoplankton species in the Baltic Sea, *A. malmogiense* and *R. marina*. The manuscript found the clear differences in carbon cycling including the DOM composition and degradability which cause predominance of different bacterial species. The conclusion was derived from comprehensive experimental data, i.e., carbon cycling with ¹⁴C tracer experiments, DOM degradability with its composition, bacterial community composition etc. This manuscript is novel and contains some very exciting results that I think will be of interest to readers of Biogeosciences. However, I have some major comments which will improve the manuscript.

(1) The discussion, conclusion, and implication to natural environments are generally well written based on the experimental results. However, I do have one concern about this point. The authors added natural bacterial inoculum to phytoplankton incubations. However, the major bacteria in the DOM consumption experiments was derived from non-axenic phytoplankton cultures but not from natural seawater inoculum. In this case, what is the source of bacteria in non-axenic phytoplankton cultures? Furthermore, is the production and degradation of DOM by these bacteria comparable to the bacterial community in natural seawater? The authors should describe/discuss these issues in the revised manuscript.

Authors: The bacteria in the cultures originate from sea water from when the cultures were first established (lines 98-100). These bacteria end up dominating the bacterial communities even after adding the inoculum of sea water bacteria, and so they are likely responsible for most of the DOM processing we observed. The small contribution of the added bacteria to the bacterial processing of DOM is already discussed (lines 607-619), but we will expand the discussion. This experiment used phytoplankton cultures with higher concentration than in natural waters to better detect the studied processes. The volume related production rates in the experiment are therefore assumed to be different than in the natural experiments, but cell specific production rates could be much closer.

We anyway tried to avoid comparing the rates in the experiment with rates in the natural environment. Instead we assumed, that the differences in rates between the two phytoplankton species would be similar also in the natural environment. We will make sure this comes out clearly in the discussion.

(2) The current manuscript, in particular the method section, is hard to follow. One of the reasons is likely that some information is only available in figure caption (e.g., Fig. A1). It is recommended that the authors move all information about the methods described in the figure captions to the methods section of the text. The other reason is probably that the manuscript contains many experimental lines having diverse chemical and biological analyses. I guess it's better to combine Fig. 1 and Table A1 to overcome this issue.

Authors: The method section will be made more comprehensive by including text presented so far only in the figure captions. We will try to make the methods section easier to follow. We will consider moving everything from Appendix A into the methods section.

(3) I could not understand the reason why the authors set the DOM line mix.

Authors: The DOM line served mainly as a control for the production line. We wanted to investigate if any changes would happen in bacterial abundance and optical DOM properties already within the 12 h key point incubation. This is explained in lines 153-154 but will be explained in more detail. As there were no changes in the DOM line variables, we pooled all the time points of DOM line. The role of the DOM line was bigger in the design of the experiment than it turned out to be. We still wanted to describe the experiment how it really happened, even though some of it might seem redundant now. The measurement of nutrient concentrations before and after the exclusion of phytoplankton also allowed us to measure nutrient concentrations in phytoplankton cells.

In addition, the authors seemed to determine the cell specific BP by tracer experiments of production line mix and bacterial abundance of DOM line mix. Are these two results directly comparable to determine cell specific BP?

Authors: You are correct, tracer incorporation in production line mix was divided by bacterial abundance from DOM line mix. This was a practical necessity and indeed not the most optimal solution. However, the results are only used to compare the two phytoplankton treatments. As the same procedure was followed for both species, this approach should be enough for this purpose.

(4) It is recommended that a subsection regarding with carbon cycling (e.g., points described in graphical abstract) is added to the beginning of discussion section. Some descriptions in the result section and the 4.3 subsection may be able to move this new subsection.

Authors: Good suggestion. A short summary of the main results will be added at the beginning of the discussion.

Specific minor comments

L 131-133: Please add this information in Fig. 1.

Authors: Will be added.

L 679-383: I could not understand how the authors determined the incorporation of ¹⁴C-labeled DOC and bacterial production by ³H-thymidine and ¹⁴C-leucine and. Please explain it with more details. Again, please move these descriptions in the method section of the

text. In addition, it is recommended that the meaning of ratio of leucine to thymidine incorporation is explained here.

Authors: ^{14}C activity in DOM and in bacterial biomass was determined using ^{14}C - NaHCO_3 , which was given to phytoplankton, who then converted it to DOM. Incorporation rates of ^3H -thymidine and ^{14}C -leucine were only measured as indicators of bacterial production. We will write this more clearly in the methods. The meaning of leucine:thymidine incorporation ratio will also be explained in the methods.

Figure 2 and other similar figures: In Figure 2 and other similar figures, the results of A. maim. located left side in the time series (Fig. 2a) but that located right side in the box and whisker plot (Fig. 2b). I was sometimes confused by this difference. I think it is better to place the A. main. data on the right (or left) side of every panel in all figures.

Authors: The positions of the growth curves in Fig. 2a will be swapped.

Figure 5: I assume that the bacterial community composition of DOM release experiment and that of Day1 in DOM consumption experiment should be similar, because the major fraction of bacteria in these experiments was derived from the same non-axenic phytoplankton culture. However, bacterial community compositions seem to be largely different between two treatments in Fig. 5. Why?

Authors: In the DOM release experiment all the bacteria were present but in the DOM consumption experiment we tried to remove most of the bacteria by filtering. Filtering likely removed larger cells more efficiently, which caused the differences in the initial conditions of the DOM consumption experiment.

L443-445: It is recommended that the DOC data is added in Fig. B1.

Authors: Will be added.

L482-484: I don't agree with this conclusion. The qualitative parameters of DOM, namely S₂₇₅₋₂₉₅, HIX, BIX etc, changed significantly with incubation time and differed among KPI3 1-3 (Fig. 7B).

Authors: This statement was poorly formulated, we apologize. We meant to say, that the trend was similar between the two phytoplankton species. I.e. if a variable was rising in one phytoplankton treatment from KPI 1 to 3 it did so also in the other treatment. We did not mean to say that the KPIs were similar. Will be corrected.

L495-496: "are be able to". Please rephrase it.

Authors: Will be corrected.

Please let us know, if you would prefer some issue to be solved in a different way or if you think that any of your questions were not answered properly. We are happy to discuss further.