Biogeosciences Discussions

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Comment on bg-2021-220

Anonymous Referee #1

Referee comment on "Contrasting patterns of carbon cycling and DOM processing in two phytoplankton-bacteria communities" by Samu Markku Elovaara et al., Biogeosciences Discuss., https://doi.org/10.5194/bg-2021-220-RC1, 2021

This study compared carbon cycling and microbial communities in two phytoplankton-bacteria cultures and found while primary production and respiration were higher in the dinoflagellate A. malmogiense culture, DOC produced by cryptophyte R. marina was more labile and supported more bacterial production. It also showed that two phytoplankton also supported different bacterial community structures. This work generates a variety dataset in two model systems and has implications on how different phytoplankton species may shape carbon transfer among trophic levels and interactions between microorganisms. But there are certain aspects need to be addressed to convey the study more clearly. First, the description of incubation design is somewhat confusing. The DOM consumption experiment is to see how bacteria respond to dissolved pool excreted by phytoplankton. But the DOM release experiment DOM line mix is also inoculating bacteria to phytoplankton exudate in dissolved phase, what is the difference between this and DOM consumption experiment? Just different incubation time length, or using phytoplankton exudate harvested at different growth stage? Looks like DOM consumption experiment use phytoplankton exudate in later stage when cell density is high, but KPI 2,3 is also at high cell density. Or is the DOM line just used as a control comparison to the production line? The purpose of the experimental design need to be better explained here. Second, in a lot of figures and results, the DOM release experiment and DOM consumption experiment are all mixed up, it is hard to follow when talking these two back and forth. To me, DOM release experiment may be focusing on the production of DOM and the interaction between phytoplankton and bacteria at different phytoplankton growth phase, while DOM consumption experiment is focusing on how bacteria respond to this produced DOM. If these two parts can be more separated in a clear logical way in the results, this can improve the structure to be more explicit.

Specific comments:

L12: What two later phases? Stationary and decay phase?

L113: Is 4C winter Baltic Sea temperature?

L131: As the phytoplankton culture is not axenic, how will the co-cultured original bacteria community affect the result? Any no-TFF inoculum treatment as a control to compare?

L176: How much particle-attached bacteria will retain on 0.8um filter?

L183: You mean at beginning, the inoculated bacteria only account for a small fraction in the original phytoplankton-bacteria culture?

L319: intracellular phosphate storing in phytoplankton? And then will be released?

Fig.2a: KPI for A.malm is at early exponential, late exponential and stationary phase, while KPI for R.marina is at early exponential and two decline phase, will this cause the comparison between two biased?

Fig.2b: Cannot tell which is white, which is grey, left bar is grey but too small to show?

L344: Why do you measure both leucine and thymidine incorporation? One indicate protein synthesis while the other indicate DNA, what does their ratio indicate? Introduce it either in method or in result.

L388: This result is from which table or figure?

L405: Community of KPI 2 and 3 are more similar than KPI 1, because these two sampling time more close to each other? Is this corresponding to the growth curve?

L424: This is confusing, Betaproteobacteriales is in the class of Gammaproteobacteria?

L430: This tight grouping is interesting, consistent with the less labile DOM in A.malm, may add some discussion on this point to connect bacteria community shift with DOM lability

Fig.7: Why don't start with same DOC concentration at the beginning of DOM consumption experiment? This will avoid dose effect when comparing between two phytoplankton-derived DOM.

L464: "comparable **between two phytoplankton** and higher than in the control"

L482: Need clarification here. What does trend similar mean? All showing increasing trend of DOC from KPI 1 to KPI 3, so DOC is produced instead of consumed here?

L503: less labile DOM is revealed from peak C here?

L507: excessive production of protein-like DOM by phytoplankton will explain the increase of peak T, but how to explain increase of peak C? phytoplankton production and bacterial consumption both occur? And optical characteristics is measured before the start of KPI, so this is from original co-existing bacteria in phytoplankton culture? And production is larger than consumption so overall DOC is increasing as mentioned in L482?

L579: Why? What is Bacteroidia related to? They tend to degrade less active DOM?

L607: But final bacterial communities are different between two phytoplankton culture in Fig.5. What do you mean here?