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Discussions

Interactive comment on "Insignificant effects of elevated CO_2 on bacterioplankton community in a eutrophic coastal mesocosm experiment" *by* Xin Lin et al.

Anonymous Referee #2

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The goal of this study was to assess the effect of ocean acidification (OA) on the bacterial community during an "induced phytoplankton bloom" in a coastal area. The coastal water was filtered onto 0.1 μm (but some bacteria were present at the start of the experiment) then three xenic phytoplankton cultures were added to the mesocosms. Despite the massive sequencing work, there are important points that have not been addressed by the authors in the experimental design as well as in the sampling and analysis steps thus weakening the paper.

The authors do not show the community structure of the "contaminated water" at the beginning of the experiment (prior phytoplankton amendment) and this is a critical point in order to be able to state whether there is an effect or not of OA on bacterial commu-

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nity structure. It would be important to discuss how different the contaminated water community was in comparison to the bacterial community associated with the phytoplankton strains. I would encourage the authors to present also the bacterial abundance data (the authors say that bacteria were present in the "contaminated water and I assume that they have counted them) that will be very useful to understand the bacterial dynamic and response to OA. Furthermore, the DOC and POC data should be included here since the authors state that data those have been packaged in another paper.

The section Environmental parameters and experimental timeline is confusing. The authors could consider to include a table that summarizes the nutrient trends and if possible other important data (bacteria count, viral count, phytoplankton count, DOC and POC)

Some graphs in the main text and in the SI are not very informative such as phylum distribution and genus distribution graphs and confuse the message of the paper.

The SI material needs more explanation and for instance the PCA graphs do not show very clearly the findings.

It would be useful that the authors would comment the use of their primers in the light of the Environ Microbiol. 2016 May;18(5):1403-14. doi: 10.1111/1462-2920.13023. Epub 2015 Oct 14: Every base matters: assessing small subunit rRNA primers for marine microbiomes with mock communities, time series and global field samples by Parada et al.

The English and the structure of the paper should be revised.

Interactive comment on Biogeosciences Discuss., doi:10.5194/bg-2017-10, 2017.

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