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Biogeosciences Discussions

Interactive comment on "Effect of elevated CO_2 on the dynamics of particle attached and free living bacterioplankton communities in an Arctic fjord" *by* M. Sperling et al.

Anonymous Referee #1

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"Effect of elevated CO2 on the dynamics of particle attached and free living bacterioplankton communities in an Arctic fjord"

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Due to lower water temperatures the Arctic Ocean could be one of areas highly affected by atmospheric CO2 increase and ocean acidification. As part of the Arctic campaign EPOCA, Sperling et al. investigated the impact of different CO2 concentrations and an induced phytoplankton bloom on the bacterial richness for a mesocosm experiment covering 185 to 1050 initial μatm pCO2. Bacterial richness was estimated by ARISA and resulting number of bands interpreted by several statistical analyses. This was

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done for free-living (FL) as well as particle-attached (PA) bacteria. The principle outcome was that both, FL and PA, exhibited a temporal development mostly driven by temperature and phytoplankton. Only for the post-bloom phase a reduction of the PA community was detected for mesocosms of lower and medium CO2. In consequence, the authors concluded that the PA community could significantly be reduced at the end of this century, where these pCO2-values should be of importance. Taken together, the results presented here are not groundbreaking but principally solid science and worth to be published somewhere. I am not really convinced by the ARISA approach because it does not, as the authors postulate in the abstract, the bacterial composition but only the richness. Moreover, the taxonomic or even functional background remains obscure, making real insights into causes for bacterial succession difficult to evaluate. For sure, it is allowed to use ARISA to analyze dynamics. But I am wondering why these really expensive and time-consuming mesocosm experiments have not been gone along with more advanced molecular tools. In consequence, the results should be discussed really carefully and pure speculation avoided. It is irritating that within the abstract a range of 185 to 1050, in material & methods even up to 1420 initial μatm pCO2, as basis for this study is described which, in fact, has not fully been analyzed and practically ends at 800 pCO2. What is the reason for this and why are the higher values even mentioned? This should be explained. The introduction is interesting but it reads like a review and is much too long and could be shortened by 50%. Concerning EPOCA several manuscripts have been submitted to BG in parallel. And it seems to me that the outcomes out of this mesocosm studies were divided into, as many as possible, different manuscripts. (Probably) Doing this, the dataset presented by Sperling et al. is limited and needs substantial support from other studies of this mesocosm bulk submission. And this even within the abstract, e.g., protein production. After revision the results of Sperling et al should be published but integrated within another manuscript of EPOCA, for instance Engel et al. (14C primary production. Minor comment: L describes the reverse and D the forward primer.

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9, C4200–C4202, 2012

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