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Biogeosciences Discussions

Interactive comment on "Response of bacterioplankton community structure to an artificial gradient of pCO_2in the Arctic Ocean" *by* R. Zhang et al.

Anonymous Referee #1

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General comments: The authors examined the response of bacterioplankton to 9 different concentrations of pCO2 during a mesocosm experiment in the Arctic. The bacterial assemblages were studied in the mesocosms over a 30 days period using TRFLP and clone libraries. The results showed no overall differences with the degree of ocean acidification; however, the authors found that the maximum diversity and richness was lower with higher level of pCO2 implying that ocean acidification have potential impact on bacterial communities. The experiment and the findings are in my opinion unique. The story is well-written, clear and to the point. However, it lacks some information for the reader to understand the experimental setup. Moreover, the authors need to present some background data in order for the reader to be able to follow the succes-

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sion in the experiment. It is not enough to refer to accompanying papers. This is a stand-alone paper. Specific comments: Details on the experimental set-up are lacking, and while the authors refer to another paper they should anyway briefly explain the experimental set-up: motivations for the different treatments, the sizes of the mesocosms, where were they located; at which depth the samples for bacterial community were taken and when exactly the 19 samplings were performed. The author should also explain the motivation for the lack of replication of the mesocosm treatments and the issues related to this. A significant part of the discussion is based on the 3 phases defined from chl. a concentrations in an accompanying paper. A figure or table reporting chl a data is essential for understanding this discussion. The figure could show the 3 phases and be adapted from Schulz, et al. 2012. Likewise, the figure could include bacterial abundance, which appears as another essential background parameter. The choice of the samples for the Smax/Hmax analyses is very unclear and should be explained in more detail (specifically on p10652). Are these data from the same time point for the different treatments? Or at different time points? In that case which and during which phase? Or do they simply represent the time points at which diversity/richness was highest? Please, clarify in the text. Why were only the 30-day samples used for clone libraries and not the samples used for the Smax/Hmax study? Please, explain the choice of samples and the reasoning behind it. From the Trflp and clone library results the pCO2 concentrations had only minor effects on the dominant bacterial taxa over 30 days. The authors discuss that the lack of strong responses could be due to the coupling to phytoplankton only in the very last sentence. The issue of the phytoplankton bloom and its eventual effects should be discussed earlier. In particular, the authors could note the lack of a BIOENV correlation between bacterial community composition and phytoplankton biomass indicates that the response in bacterial community composition is not directly linked to phytoplankton biomass. Was phytoplankton biomass included in the BIOENV analysis? Please, clarify. What about the interactions of other trophic levels? The results of the sister stories from Sperling, et al and Piontek, et al in the same issue of BG showed no effect of the different treatments on free

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living bacteria or a top down control of bacteria, respectively. These results seem to be highly relevant for the present story and should therefore be described in more detail in the present paper. Technical corrections: - In the introduction (l. 23) the reference for the microbial loop should be Azam et al. 1983. - In the material and methods the calculation for richness index and ANOSIM should be explained briefly (paragraph 2.3) - The different groups of mesocosms (high, medium, low pCO2) should be explained earlier in the material and methods (not in the results), so the reader can understand the different colors in the figures. Maybe the different groups could also be reminded in the figures. - P10656, l22-25. Unclear. Please, rephrase - P10657, l28 – P10658, l7. This section on cyanobacteria is highly speculative since no conclusions can be drawn upon the very few cyanobacterial sequences obtain. Please, delete this section. - Fig. 3. Define richness and diversity indices in the legend. - A and B needs to be added to Fig. 4 and to the Fig. 4 figure text. - Fig. 5. Is this the abundance relative to the sum of all peaks?

Interactive comment on Biogeosciences Discuss., 9, 10645, 2012.