Reply to Referee 1

We thank the Referee for the comments and the acknowledgement of "*solid science*" as well as of the worth of the data to be published.

However, we suppose that there is a misunderstanding in the summary of our paper given by the referee. The referee states: *"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."* In fact, our data show that, in response to a breakdown of phytoplankton cell numbers, the PA-community was richer in high CO_2-treatments. This was also accompanied by higher BPP (as investigated by Piontek et al., and referenced in our manuscript). This is summarized in the last three sentences of our abstract (page 10727 lines 18 to 26): "In response to the breakdown of a picophytoplankton bloom (phase 3 of the experiment), number of ARISA-band classes in the PA-community were reduced at low and medium CO_2 (~180 - 600 µatm) by about 25%, while it was more or less stable at high CO_2 (~650-800 µatm). We hypothesise that enhanced viral lysis and enhanced availability of organic substrates at high CO_2 resulted in a more diverse PA-bacterial community in the post-bloom phase. Despite lower cell numbers and extracellular enzyme activities in the post-bloom phase, bacterial protein production was enhanced in high CO_2-treatments, suggesting a positive effect of community richness on this function and on carbon cycling by bacteria."

The main criticism by the referee is that our dataset "*needs substantial support from other studies of this mesocosm bulk submission*". However, it was the intention of this experiment to give a large group of researchers the opportunity to interpret their specific results in the context of a diverse array of biotic and abiotic variables investigated by many other researchers. Despite the fact that the data cannot be presented in this manuscript, the results of Brussard et al., Piontek et al., Schulz et al., Riebesell et al., Abele et al., Zhang et al. and Engel et al. (found in the same special issue) are used to interpret our data. Also after discussion with Engel et al., we do not see a benefit for the reader of this special issue in combining the community composition of particle associated and free living bacteria with phytoplankton primary production in one paper.

The referee also expresses some general concerns about the ARISA-fingerprinting method. ARISA has been reported to have a much higher resolution than DGGE (Danovaro et al., 2006; also discussed in the Manuscript), which was used in most similar studies so far. In this way the use of ARISA poses an advancement of fingerprinting technology compared to earlier studies. We are not sure what the term "*more advanced molecular tools*" refers to. ARISA is among the methods allowing for the highest OUT resolution which could probably only be exceeded by certain sequencing methods having other limitations (see answer to referee #2). However, this experiment has to be discussed in the context of earlier (e.g. PEeCE I-III) and later (KOSMOS Bergen, Tvärminne…) mesocosm studies, where also fingerprinting methods were applied to study the bacterial community. The fact that these studies have been carried out in different environments, to discriminate between general and regional responses, highlights the need to get comparable results by well-established methods.

Piont by point response:

Referee: "*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*."

Response: We agree with the referee, the term "…composition and richness…" in our abstract is misleading and will be changed to "…diversity and richness...". The term diversity is separated from richness, as ARISA can not only resolve the richness of band-classes but also give an estimate of their relative abundance inferred from fluorescence intensity of the bands. These data are reflected in our analyses of Bray-Curtis similarity matrices.

Referee: "*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*."

Response: The values given by us in the abstract refer only to the range sampled in this study. 800 ppm pCO_2 represent the mean value of the highest CO_2 treatment in our study, having 1050 ppm initially (Schulz et al., Czerny et al., same issue). We agree that it is irritating that we used both, initial and mean pCO_2-values in the abstract. This will be changed to using only initial values to enhance comparability also with other manuscripts in the SI.
Description of the full set-up was given in the methods section to provide the reader with an overview of the total experimental set-up and to relate to other papers of the SI. In the first sentence of the sampling section in material and methods we state which part of the setup was sampled by us. For further clarification, we will include this information also after describing the total set-up.

Referee: "*The introduction is interesting but it reads like a review and is much too long and could be shortened by 50%*."

Response: We will revise again the introduction.

Referee: "*Minor comment: L describes the reverse and D the forward primer*."

Response: The notation is identical to the original source. We realized that the reference is missing:

Ranjard L., Brothier E. and Nazaret S.: Sequencing bands of ribosomal intergenic spacer analysis fingerprints for characterization and microscale distribution of soil bacterium populations responding to mercury spiking. Appl Environ Microbiol, 66, 5334–5339, 2000.

We will add this reference to the manuscript.