Biogeosciences Discuss.,
doi:10.5194/bg-2015-606-RC2, 2016

Biogeosciences Discussions

Interactive comment on "Shifts in the microbial community in the Baltic Sea with increasing CO_2" *by* K. J. Crawfurd et al.

Anonymous Referee #2

Received and published: 19 May 2016

The authors present mesocomos experiment in which they test the effect of ocean acidification on microbial community, by increasing CO2 levels. Since the ongoing climate change this research is of high importance and data presented in this msc are very valuable. The authors focused on the phytoplankton size fraction ËĆ20 μm, as well as to heterotrophic procaryotes and viruses. The experiment set u is well explained and the msc is in general well written. I do recommend the msc to be published after major revision Key points that I would recommend to be answered: 1. All dough, the target organisms are of key importance for ecosystem functioning, I do not agree that the results are relevant if not being in correlation to the whole phytoplankton community, at least presented as Chl a concentration. If those data exist I highly recommend including them in the msc. 2. In Material and Methods it is stated that the samples of surrounding water were taken, but there are not presented in results or at least dis-

cussed. It is essential to discuss those data. I would recommend including those data into the graphs reporting about the microbial community changes. Also, I am not sure if I have understood it correctly – but it seems that CO2 was added to all mesocosms? In that way you do not have control and any change in microbial community could have been because of some other factor? What about the temperature? What is the usual phytoplankton development dynamics in the Baltic Sea? Also, I do not see any shifts in microbial community, but changes in specific group abundances during the experiment. 3. Since every experiment need to be repetitive and results comparable with other study site and experiment set up it would be necessary to know the community structure of microbial community. I am aware of the difficulty of taxonomical recognition of size fraction below 20μm, but it is essential. Flow cytometry in an excellent tool, but in an experiment set up of this range I do not believe it is enough. I did like the way how the investigated groups were divided, but the next step in research should be the taxonomical identification. Not all organisms in the same size fraction have same physiological response to environment drivers. Also, the authors in the discussion, do not discuss their data, but cite different authors and their research. If you did not go to the species level – those data cannot be discussed. 4. The analyzed groups were good explained except the cyanobacteria. The authors distinguish Synechococcus, but no Prochlorococcus. Since the oligotrophy Prochlorococcus could develop in the environment and it can be separated by flow cytometry. Then stated that the prokaryotes include bacteria, archea and unicellular cyanobacteria (together marked as HP) – what cyanobacteria could it be? 5. The tittle also does not represent the results – there is not shift in microbial community presented. It is not easy to follow the results and discussion with given abbreviations (M1, M5...) for mesocosm experiments. It is not clear enough. Maybe a table would be a good way to explain the abbreviations. The discussion needs to be rewritten. The results would need to be discussed in more detail. The cited literature and results are maybe not the best choice for the results presented.