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Biogeosciences Discussions

# *Interactive comment on* "Succession within the prokaryotic communities during the VAHINE mesocosms experiment in the New Caledonia lagoon" *by* U. Pfreundt et al.

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In this study, Pfreundt et al. are presenting the bacterial community composition analysis results from the VAHINE mesocosm experiment. The VAHINE experiment deals with constructing mesocosms in the oligotrophic South Pacific, and fertilizing them with phosphorus. The manuscript details the changes in bacterial community in the mesocosm and the ambient waters (the lagoon samples) during the duration of this experiment. The results are presented from the perspective of phosphorus starvation, and whether this has an effect on the bacterial community.

The paper is overall well written, although the language could use a bit of polishing



here and there. Shortening some sentences for clarity may help readers understand the study better. My biggest complaint about this paper is its constant referencing to the sister paper from the same authors "Global analysis of gene expression dynamics within the marine microbial community during the VAHINE meso- cosm experiment in the South West Pacific". I understand that the authors may want to publish the results separately. However, since this paper heavily relies on the transcript data for the discussion part, I'm asking myself why not make one big paper, and save the reader from going back and forth between two papers.

My specific comments to different sections are listed below.

==Abstract and Introduction==

Concise and to the point

==Materials and Methods==

- I understand that in total, three mesocosms were deployed, but only one (M1) one was studied for bacterial community composition. Of course I understand the issue of cost, but it seems like a chance missed to have some replicated.

- Were there any other negative controls, other than the lagoon sampling? A mesocosm without DIP addition?

- Did the authors account for different 16S copies while calculating the pseudo-absolute cell numbers?

- How were the pearson correlations calculated, and why was pearson correlation selected specifically? Is the data normally distributed? Has the significance of these correlations been tested?

- The authors make plenty use of the correlation values in the results and discussion. Another interesting analysis that the authors might consider adding here would be tests of significant associations between the taxa and groups of sites (lagoon vs. mesocosm,

or periods in the mesocosm). These tests are implemented in R package indicspecies.

==Results and Discussion==

- Figures are really hard to read, I think this is also partly because of the pdf format from BGD, but it would greatly help if the authors could increase symbol sizes in figures.

- If I understand correctly, PP, APA, Chla and BP were measured for all mesocosms. If so, it would be good to see the data from M2 and M3 as well.

- The comparison and usage of both pseudo-abundance and relative abundance is confusing, especially since the figures display rather different trends.

- I suspect that the Deferribacteres is just mostly SAR406 clade, please indicate this in the text and figure captions

- In figures 4 and 6, it would be good to mark DIP addition as well

- UCYN-C and A should also marked in the figure captions, the manuscript text and figure captions do not match

- I fail to see this suggested correlation between SAR11 and SAR86 in the data presented by the authors. I also fail to understand why they should be correlated - they occupy a similar niche, but they have different nutrient preferences, but I don't really see how that would lead to a correlation between the two groups.

- There is a big increase in relative abundance of SAR11 clade in the lagoon sample on day16, do the authors have a suggestion as to why that might be?

- Figure 6 is an incredibly busy figure, and it is really hard to find anything in it. The authors should consider splitting the CCA biplot into two complementary figures showing sites and species separately.

- Defluviicoccus issue is interesting, although it's not surprising a bacterium associated with biological phosphorus removal systems would respond to DIP input. The authors



are right that the "genus" is rather broadly defined. Looking at the sequences of this genus, I noticed that there is "marine" and "wastewater" of Defluviicoccus group. It would be interesting if the authors could show that their 16S amplicons associated with Defluviicoccus are indeed falling into this marine branch.

- I searched the Bioproject database with the given accession number, which returned no results. I persisted and searched for the manuscript title, authors and other things, but still got no results. Please make sure your sequences are available to public.

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Interactive comment on Biogeosciences Discuss., 12, 20179, 2015.