Biogeosciences Discuss., 11, C4447–C4450, 2014
www.biogeosciences-discuss.net/11/C4447/2014/

Biogeosciences Discussions
Open Access

Interactive comment on "Protist community composition during early phytoplankton blooms in the naturally iron-fertilized Kerguelen area (Southern Ocean)" *by* C. Georges et al.

Anonymous Referee #2

Received and published: 17 August 2014

bg-2014-337

Protist community composition during early phytoplankton blooms in the naturally iron-fertilized Kerguelen area (Southern Ocean)

C.G., Georges, S.M., Monchy, S.G., Genitsaris, and U.C., Christaki

Review

This manuscript consists a very interesting – though quite descriptive - study, which adds up to current knowledge and which is very well written and as concise as it can be. I have minor comments and suggestions for further amelioration of the manuscript,

as well as points that I would like them to be clarified.

Keywords

Line 37: While 18S rRNA and tag pyrosequencing do not need further explanation and facilitate only keyword searches, terms such as “planktonic protists” and “Southern Ocean” are briefly explained in the text, since they provide the highlights and the significance of the study. I would encourage the authors also to explain briefly the “natural iron fertilization” keyword, not only for consistency but mainly because it is the driving force of their study.

Materials and Methods

2.1 Sample collection and DNA extraction

Line 106: The authors state that they pooled all three 47 mm diameter filters in the starting tube of the Power Water kit. Though these tubes are quite larger than e.g. the Power Soil ones, they are still smaller than 15 ml falcon tubes. My personal experience is that it is highly unlike that all three filters were efficiently beaten. Losses might have occurred from this approach to the extraction and contributed to some of the discrepancies that are speculated later in the manuscript. My suggestion for the future would be to extract separately from each filter and elute them altogether.

2.3 Quality filtering and taxonomic affiliations of the sequences

Lines 140-150: In Line 141, the authors state that the dataset provided a representative overview of the diversity based on rarefaction curves that reached a plateau in most of the cases. About 1,000 sequences for R_300m indicate a very undersampled station. However, what concerns me the most is whether these rarefaction curves were generated before or after the removal of the metazoan OTUs, since the adequacy of the rarefaction curves statement precedes the one about the metazoan OTUs removal and the downstream analysis (L145). In any case, the rarefaction curves should reflect the final dataset. Furthermore, I would like to see a Table with the number of the reads

BGD

11, C4447–C4450, 2014

before and after the removal for each library, or the number of reads (sequences) in Table 2.

Results

3.2 Composition and distribution of protistan assemblages

Lines 185-188: The numbers that the authors report on the NbOTUs/Schao1 ratio and the number of OTUs here do not correspond to Table 2, whether they refer to the sum of OTUs in each station (all depths) or to a specific depth in each of them. Please correct if there is any discrepancy.

3.2.1 High level taxonomic groups

Last Line: This is a more general comment. Station F-L seems to stand out for all metrics (e.g. highest temperature and Chla) and patterns (e.g Radiolaria very high relative abundance at 300m, but also broader distribution along different depths). What is the significance of this station from an ecological perspective, to be at the Northern side of the Polar Front compared to all other stations? Same in line 239, a much different station.

Discussion

4.1.1 Phytoplankton

Line 274: Has this survey (Armand et al. 2008) also taken place during blooms? Please clarify to emphasize the relevance.

Line 282: Were the Fragilariopsis-related OTUs also counted other than observed? Could it also be that they did not consist a considerable fraction that would overcome the overall 1% PCR limitation?

Lines 286-294: My question about the retrieval of unaffiliated sequences in Figures 3 and 4 becomes more relevant here. Please see comments on these figures. Also, could the authors please report the average length of their final high quality sequences?

BGD

11, C4447–C4450, 2014

Figures 3,4: Was taxonomy assigned to all sequences and at which confidence level? It is striking to me that unaffiliated sequences were not retrieved at all. Has taxonomy been subsequently assigned “manually” and on what was it based if so.

Figure 6: I do not see the asterisks (a) and the dashed lines (b) either.

Interactive comment on Biogeosciences Discuss., 11, 11179, 2014.