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Biogeosciences
Discussions

Interactive comment on "DNA from lake sediments reveals the long-term dynamics and diversity of *Synechococcus* assemblages" *by* I. Domaizon et al.

I. Domaizon et al.

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We thank the reviewer for the valuable comments that will improve the manuscript.

Minor comments

1.Remove or transfer in the discussion part most of the citations 'listed' in the result part.

Reply:As suggested by the reviewer we removed a large part of the citations (precisely: 8 bibliographic references) from the results' section.

2.Correct Internally transcribed spacer all along the text

Reply:It is corrected in the revised version

3.In the abstract write the 16S rRNA and the following internally transcribed spacer (ITS).

Reply:It is corrected in the revised version

4. Page 2523. The average size of a cyanobacterial genome 4.2Mb (Vaitomaa et al.,2003). Since that time, numerous cyanobacterial genomes were released, size reaching today up to 12.5Mb (Dagan et al., 2013). Thus, I doubt that the average size is still that low, and you might underestimate the total counts of cyanobacteria.

Reply: The reviewer is right, as reported by Dagan et al 2013, some cyanobacterial groups exhibit genome size larger than 4.2Mb (for instance Dagan et al reported the size distribution of 5 stigonematales strains being of 5.9 +/- 2 Mb). Here we used an average genome size that was estimated based on a list of cyanobacterial taxa that were known to be present in this lake (from results of sequencing performed on sedimentary DNA, or from counts preformed on plankton); It seems to us that it was a rather relevant approximation, or at least the less imperfect approximation for this study. We can include a sentence (in the revised version of the MS) in order to mention that we cannot exclude a possible underestimate of total counts of cyanobacteria. The reference to Dagan et al. (2013) publication will thus be added. However, we have to keep in mind that, the quantitative importance of Synechococcus in the whole cyanobacterial assemblage is rather high, and consequently Synechococcus (genome size about 3 Mb) probably contribute to limit the global average genome size of the cyanobacterial assemblage (even though some taxa have genome size larger than 4.2Mb).

5. Minor corrections - 2525, add '(' before Huber et al., 2004, - correct BALSTN by BLASTN. - Page 2526, correct Maximum Likelihood method and GenBank. - Page 2527, the strains were obtained from 'the Thonon Culture Collection (TCC)' and the light intensity is measured in (20_mol photon môĂĂĂ2 sôĂĂĂ1). - Please clarify, Berthon et al., has not date, while in the appendix it is Berthon et al., 2013, and it

is not even cited in the References. -Page 2528, add '(' before http:/.

Reply: All these changes were made in the revised version. The paper by Berthon et al is now 'in press' in Journal of Limnology, and it was added in the bibliographic list. Berthon V, Marchetto A., Rimet F., Dormia E., Jenny J.P., Pignol C., Perga M.E. Trophic history of French sub-alpine lakes over the last ∼150 years: phosphorus reconstruction and assessment of taphonomic biases. J. Limnol., in press

6.Suggestion regarding Figure 1 : the fig.1 is not readable on the website of the journal, ...you could simplify this figure by keeping what you really describe in the result, and removing the rest or you could also place this large figure in supplement in a much larger format and having the essential message in the fig 1 of the main text.

Reply :In order to get the figure easily readable, we divided the initial figure in 2 new figures.

7. Minor corrections : - Page 2531 BF3 from 2000-2001, similar error in the Table 2 and its legend. It has been corrected in the revised version. 8. Suggestion regarding Figure 3 : Fig 3 is again problematic to read on the website of the journal. I would suggest to split is in two just under the group 8, this would magnify the upper and lower part of the tree.

Reply:We corrected accordingly (2 figures are proposed in the revised version)

9. page 2532,you wrote 'including 8 Synechococcus isolates from 3 deep subalpine lakes (Thonon culture collection) and 39 reference sequences from other lakes (e.g. Crosbie et al.,2003; Ernst et al., 2003; Jasser et al., 2011).' I don't think the 'Thonon culture collection'is necessary here, morevover the work of Ernst et al., 2003 concerns also subalpine lake (Konstanz lake), so revise the sentence.

Reply: We corrected accordingly for the revised version

10. Tighe et al., unpublished, and latter Rajaniemi-Wacklin, unpublished can be removed, you used available sequences deposited on databases, thus the accession

number is more pertinent for anyone that would like to redo your work, could be also friendly to render your alignment available.

Reply : The bibliographic references were removed, and only the accession number appear now.

11. Minor corrections: Page 2533 change 16S rRNA, and 'approximately' by 'about' or explain what approximately means in terms of number of sequence.

Reply : we included these changes in the revised version of the manuscript

12. Page 2034. In the PCA you oppose 2008-2009 to 1972-1973, but indeed 2008-2009 does not contains same kind of samples, as you noticed at the beginning of the results 'This upper layer corresponds to the most recent deposit (2008–2009) and may contain fresh material that had not yet undergone diagenesis.'. so this comparison is biaised and I wonder how much the PCA would change if you remove the 2008-2009 samples.

Reply : Since the most recent deposit may contain fresh material, the quantification of Cyanobacteria could be biased (higher levels of DNA) but the phylogenetic composition is not necessarily biased. To answer the question of the reviewer, we performed the UNIFRAC analysis without the layer BF1. Finally with this new analysis, the associations between layers are not different as you can see (see attached the Figure 1-PCA without BF1).

13.'Therefore, the highest diversity within the Synechococcus community was detected through the analyses of the ITS region.' This last sequence is not pertinent. Hopefully the ITS was more variable and discriminative than the 16S otherwise you would study clones of the organism.

Reply: Indeed, we removed the sentence, we agree

14. Minor corrections : -Change Blast and BlastN by BLAST and BLASTN -Page 2539 all Synechoccocus are unicellular, so no need to specifiy it lines 12 and 21. -In situ and

versus to write in italic.

Reply : we made the changes accordingly

Interactive comment on Biogeosciences Discuss., 10, 2515, 2013.

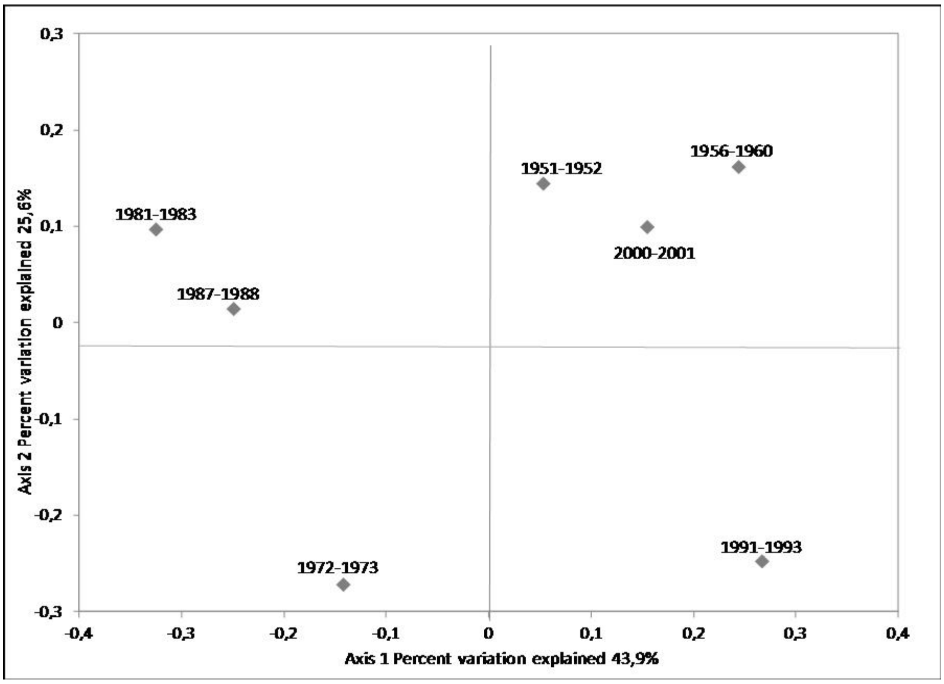

Fig. 1.