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

Anonymous Referee #2

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The manuscript of Domaizon et al. ‘DNA from lake sediments reveals the long-term dynamics and diversity of *Synechococcus* assemblages’ is a nice work presented in a clear manner, which fits in the Biogeosciences journal.

I found it interesting to read certainly because there is not much of those long term studies using multi-approaches. Also, the authors used common tools with a lot of cares for the integrity of their numerous samples, and explained carefully the reasons of such handling. They relied on molecular methods and used diverse softwares in a comprehensive manner to analyse their data. I really appreciated these efforts to explain that it is not trivial.

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Minor comments: There are several citations in the result part, I would suggest removing most of them, or transferring these parts of text in the discussion. ITS is for internally transcribed spacer, please correct all along the text, and in the abstract I would suggest writing ‘the 16S rRNA and the following internally transcribed spacer (ITS)’ as you used the one between 16S and 23S, not the one between the subunits 23S and 5S.

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. Page 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 ($20 \mu\text{mol photon m}^{-2} \text{ s}^{-1}$). Also, 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://>. Page 2529 ‘Total organic Carbon (TOC)’ because you use TOC after that. Here and in the following paragraphs, the Fig 1 is used, but the fig.1 is not readable on the website of the journal, the letters above and inside the schema are too small, even for the years on the sides of the profiles, we guess them rather than we read. This is misleading, for example you wrote page 2530 ‘the highest amounts of Synechococcus being recorded between 1975 and 1999’ according to E this is not true, but to D it is. Indeed you could simplify this figure by keeping what you really describe in the result, and removing the rest (last part of the schema) 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. Page 2531 BF3 from 2000-2001, similar error in the Table 2 and its legend. 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. Moreover, give the accession numbers of the sequences retrieved from databanks, as the names of the strains is not enough, e.g.

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MA0607B in NCBI leads nowhere, but on Swissprot leads to the phycocyanonin protein of the strain MA0607B, and I don't think it was the sequence you used. 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, moreover the work of Ernst et al., 2003 concerns also subalpine lake (Konstanz lake), so revise the sentence. 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. Page 2533 change 16S rRNA, and 'approximately' by 'about' or explain what approximately means in terms of number of sequence. 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 biased and I wonder how much the PCA would change if you remove the 2008-2009 samples. '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. As fig 1 and 3, the table 2 is not readable. Change Blast and BlastN by BLAST and BLASTN Page 2539 all *Synechococcus* are unicellular, so no need to specify it lines 12 and 21. *In situ* and *versus* to write in italic.

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BGD

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