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Biogeosciences Discussions

Interactive comment on "Recording of climate and diagenesis through fossil pigments and sedimentary DNA at Laguna Potrok Aike, Argentina" *by* A. Vuillemin et al.

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All modifications in the manuscript are highlighted in red font. The supplementary material has been incremented with new data and bound into one single pdf (see supplement.pdf). This document covers answers to the four referees.

Referee no.3

General comments:

- Given the low number of analyzed clones in general, the relative estimates of abundance might be biased (supplementary material).

- In general, a more recent 16S rDNA community composition analysis from sediments would be useful to compare and to better characterize the community from the water column.

- In spite of the interesting and high descriptive value of the manuscript, much of the conclusions is hypothetical.

Answer: We admit that running statistics on a few hundred of clones cannot provide robust index results. To answer the issue about recent communities in surficial sediments and confirm quantitatively our assemblages, we have decided to add 3 samples from our more recent MiSeq results (i.e. shallow sediment, horizons A and B). Concerning the conclusions, other referees also pointed at the lack of supporting data for post-depositional alteration of sedimentary DNA and its interpretation in terms of diagenesis. We have incremented and clarified the discussion on extant and ancient assemblages in terms of DNA quality, preservation and fragment sizes. Most of the conclusions have been rephrased.

Specific comments:

- P18352, L2: Have the pigment measurements been replicated?

Answer: Because of the expense of core collection and the high number of proxies analyses, only limited amount of sediment was available (see Ohlendorf et al., 2011). Rather than replicate the 2500 samples (at a normal cost of $350,000 USD), emphasis was placed on maximizing the temporal resolution of phototroph analysis. Fortunately, reproducibility of true analytical replicates is typically better than 20% standard deviation of the mean (Leavitt and Hodgson 2001), particularly when there are few changes in preservation environment, as recorded herein. Finally, strong agreement between multiple proxies shows that the results of pigment concentration are robust.

- P18358: Given the abundance of cyanobacteria and diatom pigments during the more recent YD, cyanobacterial and chloroplast sequences should be amplified with

the universal primers 27F and 1492R. Why are they not detected in the clone library?

Answer: As a general answer, specific primers for cyanobacteria often target very short fragments from 300 down to 150 bp (e.g. Pal et al., 2015, Journal of Paleolimnology). Nested PCR can be applied with limited bias after universal primers. In our present study, the length of the targeted DNA fragment probably led to hide fragmented phototroph sequences by heterotroph sequences. Phototrophic sequences may still be present among DGGE bands. Thus, we searched for preserved phototrophic sequences in the recent MiSeq results (iTag primers 515F-806R), which revealed only very limited numbers of Cyanobacteria and Chlorobi sequences (290 bp). We have listed them in a new table available as supplementary material. Our interpretation is that particulate organic matter containing the DNA from planktonic phototrophs is colonized and degraded quickly by heterotrophs during sinking. In contrast, Planctomycetes are better preserved due to more resistant cell membranes. Also the potential habitat (see below) may be an important factor since biomats developing on the steep flanks of the maar can be rapidly sedimented and buried during gravity events. These two aspects (i.e. planktonic vs benthonic bacteria / decantation vs gravity) are now part of the discussion.

- P18263, L1: It is unclear whether direct measurements of methane have been performed. Currently conclusions are drawn from the abundance of genotypes in clone library and ATP measurements.

Answer: Methane measurements were performed and published with d13C compositions of methane gas and fatty acids (Vuillemin et al., 2013 and 2014, Journal of Paleolimnology, Geomicrobiology Journal, respectively).

- P18363, L8: One should read 29 ka old LGM.

Answer: This has been corrected accordingly.

- P18366, L3: The mismatch between isorenieratene pigment composition and DNA

genotype analysis is discussed for green sulfur bacteria. Perhaps it would be helpful to speculate on the potential habitat of green sulfur bacteria in this ecosystem. In contrast to cyanobacteria (and diatoms) living in the epilimnetic water, sulfur bacteria might be able to live on the sediment surface.

Answer: Thank you for this interesting point that we have added to the discussion. Biomats can probably grow on the flanks of the maar and be quickly sedimented during gravity events, whereas planktonic production has to sink through the whole water column. In addition, strong mixing due to the influence of Westerly Winds prevents quick sinking of particles as it leads to OM resuspension in the water column. Thus, the residence time of such particulate OM in the water column is rather high at present in the maar lake.

Specific question:

- What is the situation at present? Is there evidence of (intermittent) lake stratification? In general the preservation of the DNA depends on the degree of deoxygenation of the water column. With a meromictic hypolimnion, cyanobacterial DNA can be recovered from relatively recent sediments (Savichtcheva, et al. 2011. Appl. Environ. Microbiol. 77(24), 8744-8753).

Answer: This point was already mentioned in the study site section. However, we have decided to repeat it in the discussion to complement to the two comments above.

Please also note the supplement to this comment:
http://www.biogeosciences-discuss.net/12/C9766/2016/bgd-12-C9766-2016-supplement.pdf

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Interactive comment on Biogeosciences Discuss., 12, 18345, 2015.