BGD "Recording of climate and diagenesis…"

General comments

This paper contains a great deal of interesting information on paleological conditions during the Holocene and prior based on analyses of a Patagonian lake core. The lake in question has been the subject of several previous such investigations (e.g. Gebhardt et al., Mayr et al., Kliem et al., Hahn et al.) which have contributed more specifically to climate reconstructions of the region. On the positive side, the present paper has the merit of analyzing sediment DNA focusing on a comparison of the Holocene period with the Last Glacial Maximum. This represents a fairly novel approach in paleo studies – and this in conjunction with microbial pigment analyses provides an assessment of concomitant changes in microbial communities. On the more negative side, this paper is not an easy read, is much too long for the take home message and is somewhat confusing in its discussion of findings. It claims more than it delivers as outlined below, so some recasting and explanation of limitations is in order. While the work is essentially descriptive (and there is nothing problematic with such an approach), it purports to test a hypothesis (p. 18349 lines 15-19) that is not falsifiable and makes no clear predictions. The hypothesis as stated is instead a rather obvious statement: that several factors combine to shape microbial communities… Diagenesis is part of the title yet I could not find much evidence for these processes affecting specifically the DNA results. The question of how microbial community structure changes within sediments post deposition is a really important area of research but it was not clear to me how this question was resolved in this study. There are multiple complications to interpreting 16SrRNA gene data over a sedimentary archive, the most important being how sediment diagenesis affects the community, in essence, erasing any pre-diagenesis or surface sediment lake signals. There may be some overlap here with previous publications Vuillemin et al. (2014)?

Specific comments

Abstract. page 18347: the first paragraph provides information more suitable for the introduction and could be summarized in one sentence. Similarly the last paragraph could be one sentence. The abstract should describe more clearly the specific DNA findings and how these relate to what is known of the lake conditions during those time periods (as nicely illustrated in Fig. 2).

Introduction. page 18348: Lines 9-14. While this is very true, this leads the reader to expect that this problem will be resolved in the current paper which is not entirely correct. I suggest positioning the paper differently – in fact the intro could start with the first sentence then move on to DNA and the challenges of interpreting sediment DNA as articulated in the second paragraph. Revise the hypothesis section (see previous comments above).

Page 18349 lines 25-26. Does this meant cell densities were estimated in a previous study? Such as in Vuillemin et al 2013b? Or is this statement referring to the findings of the present investigation? (Personally I do not like seeing the results in an intro…)

Methods. Section 2.3 can be shortened as these are well established methods but explain what ratios are used and that cyanobacteria for example are then represented as the sum of 3 pigments (which as far as I understand is how they are presented in Fig.3? (there is no breakdown of Nostocales specific pigments in results as implied by the methods section and this is fine but then methods need not explain all these pigments)

Sections on DNA extraction and sequence processing are adequate. A clone library approach was chosen which unfortunately greatly limit the descriptive effort of this study; why was high

throughput 16S rDNA amplicon sequencing not performed? It would have provided more data for the same cost. The clone library approach is detrimental to the exploratory and descriptive aspect of this work as one cannot assess and compare microbial community structures with only a few hundred clones for all samples combined. The number of sequences and OTUs (Fig. 6) on which comparisons are made is very low and these comparisons should be viewed as largely preliminary. What metrics were used to compare community structures? The method section mentions MOTHUR but were the authors able to run some UNIFRAC tests?
I am surprised that pore water chemistry can be retrieved going so far back when sediments must be highly compacted – not sure how useful some of this information is for the purpose of this paper. With exception of course of the chloride shifts but the salinity changes through time has been well established for the lake? So this information is already available?

Results. page 18354. Much of what is presented in section 3.1.1 is a summary of previous findings in other publications this should be moved either to intro or study site section. Move Figure 2 to the study site section as this pulls together information in previous studies on the lake.
Combine some of these sections and focus on the new and novel analyses (pigments and DNA).
Section 3.1.3 page 18356. Lines 3-5. I do not understand how this ratio per se indicates past production "robust" to changes in lake morphometry and diagenesis? Some of this is discussion and best left for that section?
Section 3.2.1 page 18357. Lines 5- 8 this should appear under methods in order to explain why ATP was estimated here. I'm not sure this is terribly meaningful as a measure of microbial activity.
Section 3.2.4. page 18359. Lines 9-11. I don't think you mean gradual "evolution" here…Change perhaps brought on by environmental selection since the environment is changing…? This wording is repeated in the discussion line 9 page 18361

Discussion. page 18360. Section 4.1 revisits much of the information on the known history of the lake. This could be summarized much more succinctly as a comparison between the 2 time periods of most interest here (Fig. 2).
Page. 18364. Line 15 onward. This is important and perhaps should appear much earlier in the discussion so that this point is dealt with (the information here is sufficiently convincing). The quality of the DNA is an important point for interpretation of the results.
Section 4.3 page 18365. is not really necessary as a separate section (and some of the information is repetitive). This maybe fine for the results section but in the discussion what is interesting is the integration of the lines of evidence both DNA and pigments…
Page 18366. I fail to see how the topic sentence of first paragraph (line 3) is supported in anyway by the following sentences. Many of the sentences seem somewhat circular.