Clim. Past Discuss., 11, C2563–C2566, 2015
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Climate of the Past Discussions

Interactive comment on "Palaeoceanographic changes in Hornsund Fjord (Spitsbergen, Svalbard) over the last millennium: new insights from ancient DNA" *by* J. Pawłowska et al.

Anonymous Referee #2

Received and published: 5 December 2015

Abstract Page 3666 line 12: The early LIA. . ..This is a strong claim since only one sample in this climate interval was analyzed for aDNA. Here, as well as throughout the manuscript there is a need to describe the growth or environmental requirements of described species in more detail.

Page 3666 line 17: Also here, only an expert would know what an increase in the relative abundance of these two species implies. In general: Are environmental sequences really that informative that you can say which exact species were present? I think that you can only describe environmental sequences at species-level if the corresponding microfossil is present. If not, it is a safer bet to stay at genus or family level.

Introduction Page 3667 Line 13: However, to fully understand. . ..This paragraph seems to be out of place. Namely, this study does not result in the full understanding of the consequences of climate changes in the Arctic. Please stick to claims and aims that you have studied and discussed. The first few paragraphs should only discuss what is known about past climate in the region. Then: what the big unknowns are, how forams can help, limitations of the analysis of fossils, how aDNA can help, followed by what you did here and a few lines about the major findings.

Line 26: Therefore, it is crucial. . .This is a very big claim since a complete model of past environmental changes in the Arctic fjords is not provided with this study. Hence, the need for better structuring the introduction.

Page 3668 Line 19: Metagenetics (the analysis of many genes) is a cool but also vague term. Please be more specific about what "metagenomics" was performed (i.e., the identification of past foraminifera including non-fossilized taxa through PCR amplification and sequencing analysis of preserved sedimentary taxonomic marker genes.

Page 3668 Line 25 and following: The ignorant reader might wonder why you can detect the DNA but not the microfossils. Please say a few words about why the DNA might still be present.

Page 3669 Line 3: The Pawlowska et al., 2014 seems to be very important to cross read to fully explore this study. I was unable to get an electronic version despite being able to use the online libraries of two major universities. I strongly suggest to describe major findings and relevant methods from this paper in more detail also in this paper.

Page 3671 Line 14: Please describe in a bit more details what this statistical approach exactly does.

Page 3671 Line 19: For reasons mentioned two comments ago: Please provide a brief summary of these methods here. I don't think that the reader needs to be able to cross read the 2014 paper to find out what methods have been used.

Results Page 3673 Line 18: Spell out VPDB the first time.

Page 3674 Line 21 and following: It would have been nice to have seen a similar type of analysis to identify indicator taxa and their importance to explain environmental stages for the molecular data. However, to do so you would need a much higher sampling resolution such as was the case for the microfossil work. I am not sure why the sampling resolution for the aDNA data is not the same. Extracting DNA and subsequent sequencing has become very cheap. It would have been a month or so extra work to get all the DNA extracts, do the PCRs and to prepare the libraries for sequencing. I have more comments about this later on.

Page 3675 Line 10 and following: Please provide more detail in the methods so that it becomes clear how the # of OTUs was determined. The reader should not have to get a copy of the 2014 paper to understand this study.

Same page line 24: Are these the only possible most similar sequences (i.e., top hit returns from BLAST)? Often several species or genera have the same sequence similarity. Please make sure to be precise about the true taxonomic level that can be revealed from the sequences. See also earlier comment about this.

Page 3676 Line 8 and following: As mentioned earlier: This claim is based on only one sample from that climate interval.

Discussion: Page 3677 Line 9: I think that the sampling resolution is too low to make such claims. Please inform a bit more about what is known about the growth or environmental requirements of Toxisarcon.

Same page line 17: Is the d18O at 1600 AD really that different to link this to an increase of melt water delivery etc?

Page 3678 Line 8 and following: I don't see why this is obvious when looking at Fig. 3. When looking at the scale, Islandiella spp. seem to have never exceeded more than 3.5% of the total foram distribution.

Page 3682 Line 25: This is true but with a substantially higher sampling resolution throughout the core, it would have been possible to perform an indicator species analysis to identify which taxa show a statistically significant response to the various environmental stages. This way even unnamed environmental sequences could potentially become proxies for certain conditions in comparable settings.

Page 3682 final paragraph: This paragraph about the problems with aDNA work is highly speculative. You don't actually have empirical proof that your DNA is degraded and if this differs between intervals. The sediments analyzed here are relatively young. A much higher sampling resolution (e.g. every other cm or so) combined with statistical approaches will most likely reveal highly significant changes in the species distribution as a result of major climate shifts. There will probably be less need to write a negative and speculative paragraph about the things that can go wrong with the aDNA approach. Right now this paragraph is totally out of place.

Table S2: Please make sure to identify the highest taxonomic level for each OTU based on Blast results (e.g., if an OTU shows the same highest similarity with multiple species use genus or even family level).

Interactive comment on Clim. Past Discuss., 11, 3665, 2015.