

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

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The submitted manuscript discusses data obtained for a 2-m-long gravity core, which was retrieved in a fjord of West Spitsbergen. The authors compare the foraminiferal ancient DNA extracted from the sediment with the foraminiferal fossil record. This principal segment of the data was published previously (Pawłowska et al. 2014). Now the dataset is appended with grain size and stable oxygen isotope measurements, and the new story focuses on the climate change during the last millennium and on the ancient DNA signal from the numerous and abundant soft-shelled foraminifera, the shells of which are not preserved in the fossil record.

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I believe this ancient DNA approach needs to be publicized in the micropaleo community, and the journal of *Climate of the Past* is an appropriate platform. The earlier publication (Pawłowska et al. 2014) was a kind of a pilot description of the ancient DNA data array. I encourage the authors to publish this new paper as a more informative story, which will demonstrate the applicability of the aDNA approach to foram research.

I comprehend that meeting all my comments, and some of them are rather critical, may postpone publishing for months. This is not my intention. The authors, I believe, will choose comments that help.

The general comments are separated into groups: Age constrain and Ancient DNA.

Age constrain

1. The chronology of the core was based on 11 AMS-radiocarbon dated mollusk shells. The data were shown in the previous publication (Pawłowska et al. 2014). The core depth vs. age relationship was completely chaotic, which is generally considered to designate redeposition of the sediment. The authors had to discard 7 out of 11 dates to compile a sequence without obvious age inversions. Then the retained specimens were assumed to be in situ, and the sediment sections containing the discarded specimens were interpreted to be redeposited. This is a weakly supported age model, but at least it was published. In the new paper, the chronology is made even less convincing. The age model is implicitly replaced (p 3672 line 7-8). There is no explanation why the published age model is discarded and which way the new model is more reliable. Moreover, the scatter of the radiocarbon dates is disregarded, redeposition vanishes magically, and the authors do not hesitate interpreting an uninterrupted sequence of climatic events.

2. There are additional indications of sediment redeposition. Of the four retained dated specimens (Table 1), at least one is probably allochthonous. *Hiatella arctica* is shallow water species preferring active currents. This bivalve is unlikely to occur in muds at ca. 200mwd. The taxonomic composition of the dated bivalves is strange. I would expect

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the assemblage from fjord-basin muds to consist mainly of nuculanids and *Thyasira*.

3. The foraminiferal assemblage is strange too. If the bottom currents are sluggish and the sediments are muds, the assemblage contains way too high proportion of the sessile *Cibicides lobatulus*, and thus suggests redeposition. The extremely high number of foraminifera per gram in certain intervals (p.3674 line 5) may mean winnowing.

4. Thus the radiocarbon dates and other evidence indicate that the core was retrieved from a redeposited package. Lobes of dislodged sediments are common under the flanks of the fjords of Svalbard. If the authors will insist their core is from a normal-accumulation area, then instead of the single sentence “Four out of 11 samples were in chronological order and were used to establish an approximated age model for the sediment core” (p. 3672) I recommend they provide more solid information on age control:

- Based on which data (bathymetry, seismics, else) the coring location was selected.
- What are the modern sediments at the location (based on box cores).
- On which basis the shells were selected for dating.
- Why some “shells identified to the highest possible taxonomic level” were identified to “*Bivalvia* n.d.” and “*Gastropod* n.d.”? The mollusk fauna of Svalbard is comprehensively studied (consult with Włodarska-Kowalczyk). What was wrong with these shells?
- Where the bivalve shells paired and did they have in-situ position?

5. I believe environmental DNA degrades rapidly with age. If the suggested age model is valid, then please demonstrate and discuss the deterioration of ancient DNA from the modern surface to the layers ~1000 yr old at the bottom of the core.

6. There is 10-fold variation in the calculated sedimentation rate (Fig.3A). Such large variation is not very plausible for the Late Holocene and is probably produced by the imperfectness of the age model. In such a situation, derived variables, e.g. flux, calcu-

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lated via sedimentation rate become meaningless. Please replace the derived fluxes (IRD, foram shells) with direct data (e.g. per g sediment).

Ancient DNA

7. Does this paper target the micropaleo community? I think it does. To be appreciated by the micropaleo auditorium, the paper, I believe, should have introduced a concise overview that specifically answers the reader's most obvious question: Whether the metagenomic technique provides a picture congruent to my fossil assemblages. To follow the discussion the reader needs to feel how robust the metagenomic approach is, what the scale of the mismatch between the fossil assemblage and aDNA in taxonomic and numerical sensitivity is. The only relevant sentence in the Introduction provides insufficient information "The study showed that aDNA record contained almost all of the species reported for Hornsund from previous micropalaeontological investigations" (p.3668) and refers to the previous paper (Pawłowska et al. 2014). Ok, I go to that paper. But I cannot find comprehensive information. There is a rather confusing diagram; the description is too general, non-specific, like the cited sentence above. And there is no control against the fossilizable part of the assemblage that would show how accurate the technique is. So I have to do this control myself, and I go to the data table (Supplement 2). The first surprise is that operational taxonomic units (OTUs) assigned to one species (e.g. *Elphidium excavatum*) are scattered through the list. This may indicate that nobody has really analyzed this table, because otherwise he would have certainly grouped OTUs of the same taxon together. I choose the rotaliids, because they are least susceptible to postmortem decay, then lump all intervals, because the sediment package is dislodged, then select the most abundant fossil species in the census table (Supplement 1), and finally calculate their relative frequencies. In order of abundance the principal rotaliids of the fossil assemblage are:

Elphidium excavatum 46 percent [the editorial software has a bug with the percent sign; see the attached XL file]

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Cassidulina reniforme 24

Nonion labradoricum 11

Cibicides lobatulus 9

Islandiella norcrossi/helenae 5

Buccella spp. 4

subtotal 100

The aDNA table shows numerous reads only for *E.excavatum* and *C.lobatulus*. *Nonion labradoricum* is represented by a few reads, which is obviously an artifact. The other major species are not detected. The control reveals that the aDNA technique fails to recognize 4 of the 6 major species. Thus the technique fails to reveal the structure of the assemblage on the species level. I suppose this conclusion applies equally to the monothalamids. I am not an expert and have no idea what is behind this poor performance: the incompleteness of the modern foram DNA database; taxonomic or sequence mistakes in the modern database; the used SSU gene fragment is too long and degrades rapidly beyond recognition. Anyway, this is an important result that should have been pronounced and discussed.

The undetected rotaliid taxa are extremely numerous in the fjords. Their DNA is certainly out there, and it cannot just disappear into thin air. A plausible assumption is their sequences are in the table but misidentified. I look into the massive reads of the exotic rotaliids.

- *Globocassidulina biora* is absent from the northern hemisphere. These numerous reads may represent *Islandiella norcrossi/helenae*.
- *Pullenia carinata* is absent or nearly so in the fjords. Its numerous reads most likely are misidentified *N.labradoricum*.
- *Cassidulina laevigata* is nearly absent here. These numerous reads are probably

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misidentified *C. reniforme*.

- *Cibicides wuellerstorfi* does not dwell in the fjords. The numerous sequences are probably misidentified, and then they may append to the *C. lobatulus* reads.

- *Epistominella exigua* and *E. vitrea* occur in the fjords, but these numerous reads may be *Buccella* spp.

With these guesses the DNA frequencies of the principal rotaliids are:

Elphidium excavatum 10 percent [the editorial software has a bug with the percent sign; see the attached XL file]

Cassidulina reniforme 35

Nonion labradoricum 11

Cibicides lobatulus 25

Islandiella norcrossi/helenae 3

Buccella spp. 15

subtotal 100

The correspondence to the fossil frequencies above is not perfect, but at least now it is not a hopeless mismatch. The match perhaps could have been better if the sediments were in situ.

8. The aDNA shows that *Stainforthia* sp. is a major player in the assemblage (Supplement 2). Its frequency in the fossil assemblage is severely underestimated probably because of the small size (e.g. *Stainforthia feylingi*). A mesh size smaller than 100µm (which is commonly used in Svalbard) would have retained the important small taxa. This may be a message that will reach the micropaleo community.

Other comments

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9. Avoid discussing outliers (e.g. p.3679 line 13 and many others). It will be a good habit to consider only those peaks that are supported by three or more data points.

10. The figures are of good quality. The figures will probably change after revision, so I will not speak now whether they all are necessary. The 'Years AD' scale is used in several figures. Its irregular increment is extremely confusing. I suggest the use of a core depth scale. The estimated ages can be shown on an additional age-model graph within each figure.

11. The language is quite good but will need some amendment.

Minor matters

- The water depth at the coring location and its coordinates are never mentioned. There is a large distance discrepancy between the coring location shown in this paper (Fig.1) and in the previous one (Pawłowska et al. 2014). The M&M section reports that the core was taken in the central part of the fjord (not clear whether it means along the axis or between the flanks), in another place it is written that the core was taken under the southern flank. Please, find out where the core was located.

- The Study Area section lacks information on the modern setting at the coring location.

- Fig. 1: There must be at least two latitude marks.

- Please provide captions for the supplements.

p.3666 line 10: "the distant position of the glaciers" is not very clear

p.3668 line 17: do not capitalize Eukaryotes.

line22: almost all species

lines 25-29: not specific, vague meaning

p.3669, line 10: a wide no-sill outlet

line 10: "facilitates its penetration by oceanic waters" is awkward. Rephrase.

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line 11: awkward “coastline is variable”

line 11: “basins, separated by sills” is geometrically unclear

p.3683 lines 3-9: not specific, vague meaning.

Please also note the supplement to this comment:

<http://www.clim-past-discuss.net/11/C2035/2015/cpd-11-C2035-2015-supplement.zip>

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