

Interactive comment on "Sedimentary ancient DNA and pollen reveal the composition of plant organic matter in Late Quaternary permafrost sediments of the Buor Khaya Peninsula (north-astern Siberia)" by Heike Hildegard Zimmermann et al.

Anonymous Referee #3

Received and published: 21 October 2016

I read with interest this manuscript that offers interesting results in good agreement with similar recent studies conducted by other researchers on similar settings from lakes and peat. The manuscript presents the results of ancient pollen and sedimentary DNA study extracted from permafrost from the Buor Khaya Peninsula. It shows several important methodological results of interest for readers working with plant ancient DNA from bulk sediments. It shows first that combination of classical palynological analyses is often not sufficient to resolve flora composition and that DNA is an important com-

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plementary tool to investigations of this kind. It confirms (and this should perhaps be strengthened even more by the authors) that DNA signal is local in origin and this fact helps when combined with pollen proxies that we know may have limitations linked to the fact that pollen is transported over long distances. Among papers that should be cited for this result are: Pedersen et al 2016, Sjögren et al 2016 and Parducci et al 2013.

I am less familiar with the type of statistical analyse the authors used and I cannot comment on that in details. I can perhaps comment generally that they seem to me to overanalyse and over interprete their data. For example I di not I didn't understand why to calculate terrestrial-aquatic and Poaceae-Cyperaceae ratios as well as the PCA analysis if these calculations are not later even used and discussed.

I have some more specific comments.

I reply here also to one of the other referee to state that pollen contains all three plant DNA genomes (mitochondrial, nuclear and chloroplast) regardless of the type of inheritance of the organelle DNA of the mother plant (paternal or maternal). There is however an increase or a decrease of the mitochondrial or chloroplast organelles in pollen after mitosis 1, depending on inheritance. So Pollen contains cpDNA as well as mtDNA in addition to the nuclear of course. This has been demonstrated in a number of different experimental studies in the lab conducted on fresh pollen (e.g. Nagata et al 1999) as well as in sito in ancient sediments: cpDNA has been amplified from pollen of plants with maternal inherithance and viceversa for mtDNA in conifers for ex. It is now know, but it still require some studies, that plant and in sediments comes mainly from plant tissues like macros and that likely it mainly present in its extracellular forms in sediments (linked and protected by solid particles). However this is a field that requires lots of studies in the future: taphonomy of plant ancient DNA in sediments.

it is not clear in the results how many samples are analysed for DNA. The authors write of extraction batches of 11 samples. But how many in total? In that paragraph this

should be stated more clearly. Were all 32 samples analysed for pollen also analysed for DNA?

The authors write that they run up to 4 PCR per samples. This is not very good if it means that some samples perhaps have been amplified only one for example. State in a table how many PCR per sample or state the minimum number amplified. Why not amplify the same number for all samples?

Did the authors sequenced the positive blanks?

Paragraph 6-14 on page 8 should be moved earlier in the paragraph.

I did not understand the sentence on page 18 line 18: The sedDNA record does not contain conifer-derived DNA (with reference from Birks and van der Knaap). Why are these two reference are used here? To confirm what, that DNA of conifer is not detectable by sedDNA. this is not the case. Not clear.

Page 19, line 17-18. the authors should ca consider to use MapDamage 2.0 to test for patterns and rates of DNA damage and assure for authenticity of their reads.

The manuscript and especially discussion is long and can be shortened in my opinion.

Interactive comment on Biogeosciences Discuss., doi:10.5194/bg-2016-386, 2016.