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Biogeosciences Discussions



# *Interactive comment on* "Crustal uplifting rate associated with late-Holocene glacial-isostatic rebound at Skallen and Skarvsnes, Lützow-Holm Bay, East Antarctica: evidence of a synchrony in sedimentary and biological facies on geological setting" *by* Y. Takano et al.

**Anonymous Referee #2**

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The manuscript tried to reconstruct the isostatic rebound history of the studied area, and is well organized in terms of its geological and geochemical descriptions.

However, I greatly doubt about the applicability of 16S rRNA-based DGGE profiling to increase the accuracy of the reconstructed geo-history.

First, the DNA signatures in the sediments are of modern-living organisms that may not necessarily reflect the changes in the past.

In the case of ancient DNA studies, genetic materials are extracted from geologically "fixed" samples such as ice cores, permafrost, amber, salt rock halite, etc. Shallow sediments are not regarded as such.

Second, if diatoms were to be targeted, 18S-rRNA based, not 16S based, characterization should be done.

Should the extracted bulk DNA samples be still available, then it looks very easy to do the work. There are diatom-targeted PCR primers published.

Third, the DGGE is not a best way to characterize microbial communities of the past or modern.

It is well known that DGGE profiles are variable due to the DNA extraction methods, quality of extracted DNA, and PCR conditions including primers.

Moreover, even the DGGE bands at the same position may result in different sequences. For this reason, some laboratories including my lab perform "all bands sequencing" for every DGGE occasion, though we are not usually inclined to DGGE.

For the reasons stated above, I would conclude that DGGE decreases or damage greatly the accuracy of the proposed geo-history.

In other words, the ms without DGGE will be more informative.

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Interactive comment on Biogeosciences Discuss., 7, 4341, 2010.