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Does natural fragmentation of fossil DNA differ among cell types? Implications for DNA as a novel paleoecological tool.

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Recently, a number of studies have shown that under anoxic conditions significant amounts of fossil DNA from Holocene water column-dwelling micro organisms can be preserved in the fossil record of lacustrine and marine settings. Various Holocene phototrophic bacterial and algal species were identified at an unprecedented species-level based on their fossil ribosomal DNA sequences (rDNA) [1,2]. Hence, DNA could be the ultimate paleoecological tool to reconstruct past microbial communities and climate-induced environmental change which resulted in variations in community structures. However, the level of preservation of fossil DNA is likely to differ between the various cell types or species and DNA-based paleoecological reconstructions would then be biased towards the identification and quantification of the best preserved DNA. For example, DNA within spore-forming micro organisms is likely to be protected substantially longer compared to DNA in cells that do not form resting stages [3,4]. In addition, DNA might be better protected inside Gram-positive bacteria compared to thinner walled Gram-negative bacteria.

In our study we studied the natural fragmentation of DNA as an important degradation process although various other routes of DNA degradation are also possible [5]. We analyzed the fragmentation of fossil DNA from a larger set of Holocene photic zone-dwelling species within the Holocene sulfidic record of the Small Meromictic Basin (SMB) in Ellis Fjord, Antarctica, where environmental conditions and the past species composition did not alter substantially for the last 2700 years. Using sensitive

and specific molecular biological identification and quantification tools, we studied the natural fragmentation of ancient DNA of cyst-forming dinoflagellates and diatoms vs. non-cyst forming diatom species as well as Gram-negative sulfide-oxidizing obligate photolithotrophic green sulfur bacteria (GSB) which do not form resting stages. We found that even after ∼2700 years of deposition, at least 30% of the DNA of the GSB from the ancient chemocline of SMB was still longer than 23 kilobasepair long and that this low level of fragmentation did not yet affect the efficiency of PCR amplification of their partial 16S rDNA. Although a comparison of the fragmentation of fossil DNA from the various additional ancient photic zone community members is on its way, these initial results imply that the fragmentation of DNA and the variation of the PCR efficiency among the different cell types is perhaps of less importance than initially expected which supports the suitability of fossil DNA as a species-specific paleoecological tool.

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