

**ANCIENT DNA AS A NEW BIOMARKER TO IDENTIFY PAST MICROBIAL COMMUNITIES: A STUDY ON PRESERVATION OF DNA IN ELLIS FJORD, ANTARCTICA**

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The analysis of ancient DNA preserved in sediments provides a very specific and sensitive tool to study past microbial communities and hence obtain information about climate change in the past (Coolen et al., 2006). However, to date, little is known about differential preservation of DNA among taxa or celltypes while this information is essential for understanding to what extent this novel field provides an accurate mirror of past species composition.

The Small Meromictic Basin (SMB) in Ellis Fjord, Antarctica offers an excellent opportunity to study preservation in more detail because ancient DNA is found to be well preserved under relatively constant anoxic, sulfidic conditions during the deposition of the up to 2700-year-old sediments analyzed. Our results show that during this period algal species from the oxygenated photic zone as well as obligate anoxygenic photolithoautotrophic green sulfur bacteria (GSB) from the sulfidic chemocline were preserved in the sediments.

To study the preservation of DNA we conducted the following analyses: (1) a comparison of the qualitative (phylogenetic) information derived from rDNA sequence analysis of past diatoms, dinoflagellates and GSB vs. their specific lipid biomarkers (i.e. highly branched isoprenoids, dinosterol and the carotenoids isorenieratene and chlorobactene, respectively); (2) the ratio between DNA copy numbers and the associated lipid biomarker provided information about the preservation of group-specific DNA relative to the preservation of the lipids; and (3) the extent of fragmentation of ancient DNA from those species was studied by quantifying DNA copy numbers in various size classes of DNA.

Highly branched isoprenoids (HBIs) were dominant lipids in the polar fraction and our molecular tools revealed that of all known HBI-producing diatoms (Sinninghe Damsté et al., 2004), only species related to *Navicula* and *Haslea* were present in the sediments. The diatom assemblage was however dominated by cyst-forming *Chaetoceros sp.*, of which the DNA fragmentation was minimal as compared to the non-cyst-forming HBI-producers, suggesting

that the ancient DNA inside cysts is much better preserved than that of non-cyst-forming species.

The present and ancient chemocline of SMB has constantly been dominated by a green sulfur bacterium closely related to *Chlorobium phaeovibrioides*. No correlation between the number of its 16S rDNA copies and the concentration of fossil carotenoids was found. Interestingly, despite the fact that GSB are Gram-negative bacteria, suggesting that their DNA would be more fragmented than DNA of cyst-forming organisms, DNA fragmentation was comparable to that of *Chaetoceros* cyst DNA.

Dinosterol was found throughout the core but its concentration increased suddenly below 60 cm, suggesting that dinoflagellate production was higher in the past than it is today. However, phylogenetic analysis of dinoflagellate DNA revealed that the cyst-forming *Polarella glacialis*, which is not a known source of dinosterol, dominated in the upper 60 cm. The sediments below 60 cm. also contained species related to dinosterol-biosynthesizing *Gymnodinium* species. This clearly shows that the sole analysis of dinosterol does not provide an accurate qualitative view of its biological source and is perhaps not even a reliable quantitative marker for palaeoproductivity. Despite the phylogenetic relation to cyst-forming dinoflagellates, the number of 18S rDNA copies of dinoflagellates decreased rapidly. The fragmentation of dinoflagellate DNA thus seems higher than the fragmentation of diatoms and even green sulphur bacteria.

Our results show that a combination of genetic and traditional biomarkers provides essential information which is not available from biomarker analysis alone. For successful application of the technique however, it is essential to gain a better insight in group-specific fragmentation of DNA. Our results show for instance that DNA of cyst-forming species like dinoflagellates is not by definition better protected against degradation than DNA of species that do not produce resting stages.

## REFERENCES

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