

**RECONSTRUCTION OF CHANGES IN ENVIRONMENT AND ANCIENT BIODIVERSITY IN ACE LAKE AND ELLIS FJORD USING DNA AND LIPID BIOMARKER STRATIGRAPHY**

JK Volkman<sup>1</sup>, MJL Coolen<sup>2</sup>, WIC Rijpstra<sup>3</sup>, B Abbas<sup>3</sup>, S Schouten<sup>3</sup>, JS Sinninghe Damste<sup>3</sup>, G Muyzer<sup>4</sup>

<sup>1</sup>*CSIRO Marine and Atmospheric Research, Hobart, Tasmania, Australia*, <sup>2</sup>*Woods Hole Oceanographic Institution, Woods Hole, Massachusetts, United States*, <sup>3</sup>*Royal Netherlands Institute for Sea Research, Texel, Netherlands*, <sup>4</sup>*Kluyver Laboratory for Biotechnology, Delft University of Technology, Delft, Netherlands*

The distribution of organic compounds preserved in sediments provides a record of ancient aquatic microbial communities and, hence, can be used to reconstruct variations in climate and their impacts on biodiversity. However, the interpretation of these data can be complicated by the limited source specificity of some traditional biomarkers and constraints caused by the effects of differential preservation. The ultimate biomarkers are ribosomal RNA genes (rDNA), the sequences of which provide information at the species level through phylogenetic comparisons. It is generally believed, however, that labile biomacromolecules such as DNA become rapidly degraded within sediments. Here we show that DNA of planktonic phototrophic algae and bacteria survived degradation in the Holocene anoxic sediments of Ace Lake located in the Vestfold Hills of Antarctica, allowing the fossil community members to be identified by comparative sequence analysis. The similar concentration profiles of rRNA genes of haptophytes and their traditional biomarkers (alkenones) revealed that fossil rDNA can be used as a quantitative biomarker in this environment. In contrast, DNA was not as well preserved in putatively similar anoxic sediments of the Ellis Fjord. Here an unusual highly branched isoprenoid alkene indicative of a diatom origin was well preserved in the sediments by sulfurisation, but the DNA of the presumed source organisms was not. Nonetheless, sequence analysis revealed a diversity of organic contributions to the sediment. This novel approach of rDNA stratigraphy combined with lipid biomarker analysis can reveal an unprecedented detailed view on the impact of environmental changes on ancient aquatic microbial diversity.