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Microbial life in continental salt pan sediments and their response to climate variability in Northern South Africa

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The environmental history of southwestern African mainland is largely unknown. Since there are no lacustrine systems with constant water coverage in this area, we investigated a continental salt pan as a terrestrial geoarchive with the potential to preserve climate signals. Within the frame of the research project “GeoArchives” (part of the SPACES program, funded by the German Federal Ministry of Education and Research, BMBF) we aimed to reconstruct climate variabilities during the late Pleistocene to Holocene.

The presented study is focused on variations within the microbial community structure and abundance of key organisms in a salt pan with special regards to sediment age and geochemical parameters. A combined approach of a 16S rDNA-based quantification method and lipid biomarker analysis was used to demonstrate the response of the microbial communities with respect to environmental changes. The phospholipid derived fatty acids (PLFAs) in sedimentary deposits are characteristic markers for living *Bacteria*, whereby their side chain represents a fingerprint of the community structure on a broad taxonomic level. Archaeol and isoprenoid glycerol dialkyl glycerol tetraethers (iGDGTs) were used as characteristic makers for *Archaea* whereas branched GDGTs (brGDGTs) are typical biomarkers for *Bacteria*. In contrast to PLFAs, they represent dead microbial biomass and thus the past microbial communities in older sediments, since they are already partly degraded.

Samples from the Witpan, located in the northwest of South Africa and representing a depths profile from the Late Pleistocene to Holocene, were gathered. Despite the extreme environment with rather low TOC values, restricted availability of water and high salt concentration markers for *Bacteria* and *Archaea* were observed. A series of saturated, branched and unsaturated PLFAs were identified. The diversity and concentration of PLFAs were highest in the top layers (up to 30000 ng g_{sed}^{-1}, 0-10 cm) and characteristic markers for cyanobacteria were most abundant. The community composition changed with depths and both the copy numbers of 16S rDNA genes of bacteria (varied from 10^2 to 10^5 cell g_{sed}^{-1}) and the amount of PLFAs (up to 3000 ng g_{sed}^{-1}) reflected a low abundance of microorganisms despite increasing feedstock in deeper sediments. Thus, the actual salt pan microbial community is mainly located in the top layers and decreases with depth. In contrast archaeol and GDGTs increased at the transition from Holocene to deeper Late Pleistocene sediments (from 40 up to 3400 ng g_{sed}^{-1}) indicating a higher past microbial abundance during the Late Pleistocene. The increase of GDGTs, TOC, acetate and formate suggested a higher supply of organic matter and a higher microbial activity in this period. Therefore, we assumed an increased precipitation during the Late Pleistocene compared to the arid Holocene in southwestern Africa. We could show the potential of continental salt pans to preserve climate signals during deposition and we demonstrated their potential as a Late Quaternary geoarchive by means of lipid biomarker studies.

To describe the environmental habitat, a detailed analysis of diversity and abundance of microorganisms using Next Generation Sequencing is planned.