

APPLICATION OF BACTERIOHOPANEPOLYOLS AS NOVEL PROXIES FOR METHANE OXIDATION IN THE LATE QUATERNARY MARINE RECORD

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Methane is a strong greenhouse gas known to have perturbed global climate in the past, in particular when released in massive quantities and over short time periods for example from marine gas hydrates. Different trigger mechanisms have been identified, forcing rapid and massive release of stored methane to the ocean floor and/or the atmosphere, instantaneously perturbing climate and impacting on biogeochemical cycles. One prominent methane reservoir is gas hydrates, particularly from continental margins. With global warming, unstable subsurface methane reservoirs such as gas hydrates, pose a potentially large threat to marine slope stability, climate, and society. Recognizing periods of increased methane emission in the past and understanding their source and ocean-atmosphere and biogeochemical feedbacks has therefore become a focal point of (paleo)climate research.

Because of its relevance for global carbon turnover research on methane has mainly focused on anaerobic microbial processes, particularly for anoxic settings. However, an alternative fate of emitted methane is microbial oxidation in the water column, with associated oxygen consumption (Dickens, 2001). This process, its underlying mechanisms, and the exact site of the process within the water column and/or the uppermost few mm of the sediments has received relatively little attention to date but possibly plays a more important role in carbon cycling and oxygen availability in the past ocean than commonly considered.

Here we will present data from our recent analysis of the sedimentary BHP composition of an approximately 1 Ma year sedimentary record from the Congo Fan (ODP Leg 175, Site 1075) revealing remarkable preservation of a group of hopanoid biomarkers including the highly specific marker for aerobic methane oxidising bacteria 35-aminobacteriohopane-30,31,32,33,34-pentol (aminopentol [m/z 830]; Fig. 1; Cvejic et al., 2000). Aminopentol is only known to be produced by aerobic organisms therefore representing either a water column (oxic or sub-oxic; e.g. Blumenberg et al., 2006) and/or an oxic surface sediment signature. This is the first time that aminopentol and related BHPs have been observed in a continuous sedimentary sequence to an age of > 1 Ma years (down to about 100 mbsf; Fig. 1), although preservation of a limited number of less source-specific

BHPs has previously been observed in sediments from the Benguela Upwelling to an age of *ca.* 4.5 Ma (Talbot et al., unpublished data).

This new record pushes direct evidence for aerobic microbial oxidation of methane far back into the geological past, as earlier studies suggesting a similar mechanism were limited to the last 45 ka (e.g. Hinrichs et al., 2003).

We now plan to carry out compound specific stable isotope analysis on side chain cleaved BHPs (cf. Crossman et al., 2001) isolated from selected intervals to further support their origin from aerobic methane oxidising bacteria and to gain insight into the possible origin of the methane (biogenic vs. thermogenic).

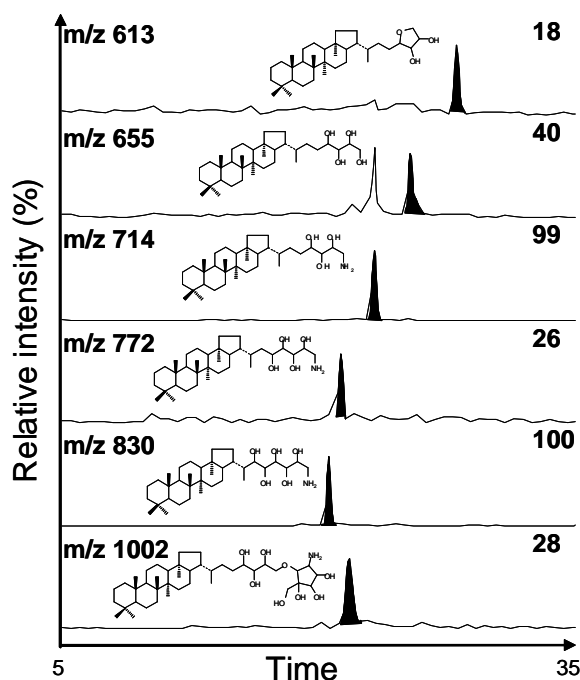


Figure 1. APCI base peak mass chromatograms and parent structures of selected BHPs observed in oldest sediment sample (1051 ka years) analysed from Congo fan (ODP Leg 175, site 1075) including aminopentol (m/z 830). (Note: compounds analysed as acetate derivatives; e.g. Talbot et al., 2003.)

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