



Sedimentary microbial lipids at active methane seeps in the Congo-Angola margin (SE Atlantic).

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A giant pockmark area (REGAB area) along the passive Congo-Angola margin (South East Atlantic) was first discovered and then surveyed during the ZAIANGO and BIOZAIRE projects (IFREMER-TOTAL). The area is colonised by dense cold-seep assemblages and microbial mats (Ondreas et al., 2005; Olu-Le Roy et al., in press) while large methane levels and also hydrate outcrops were observed (Charlou et al., 2004). Within the REGAB area and in the framework of the BIOZAIRE project (2001-2003) we investigated two short cores sampled with the *ROV-Victor 6000* submersible (BIOZAIRE 2 cruise) in the vicinity of active gas venting sites using molecular biogeochemical tools. We focused on specific and diagnostic lipids and their carbon isotope composition aiming to gain insight into microbial assemblages and processes in this methane-rich setting and assess their variability possibly related to environmental conditions. Although lipid compositions in the two cores show significant inputs from the water column, related to surface marine productivity and terrestrial supply, major microbial compounds occur. These are archaeal biomarkers (isoprenoidal dialkyl glycerol diethers, PMI, crocetane) and bacterial ones (mainly non-isoprenoidal glycerol mono- et di-ethers, various hopanoids, branched fatty acids). Archaeal lipids are deeply ^{13}C -depleted (down to *ca.* -140 ‰) and their composition indicates the presence of both ANME-1 and ANME-2 methanotrophic archaeal groups. Strong down core gradients in amounts, carbon isotopic composition and relative abundance of archaeal lipids reveal changes in archaeal biomass (and possibly archaeal assemblages) as well down core zonation of the anaerobic oxidation of methane (AOM). Bacterial lipids are diverse and show ^{13}C -depletions as well (down to -90‰). Their down

core variability possibly reflects changes in the bacterial assemblages. Variations of ^{13}C -depleted lipids diagnostic of sulphate reducing bacteria (SRB) appear not coupled with those of ANME- lipids. Abundant ^{13}C -depleted bacterial hopanoids and sterols assigned to methanotrophic bacteria and their dowcore profile indicates transitions from the AOM zone at depth to an aerobic methane oxidation zone in the upper centimetres. Differences observed between the two cores are assigned to differences in methane fluxes (Charlou et al., 2004). Distributions of ^{13}C -depleted lipids assigned to methane-related microbial assemblages are also compared to available data from phylogenetic studies (Nadalig et al., 2002).