

LIPID CHARACTERIZATION OF METHANE SEEP SEDIMENTS ALONG THE NORTHERN US ATLANTIC MARGIN

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More than 550 gas plumes were recently identified along the northern US Atlantic margin (USAM) using multibeam water-column backscatter data (Skarke et al., 2014). In order to understand the gas sources of these seeps and the fundamental biogeochemical processes that regulate the flux and transformation of carbon along this margin, a multidisciplinary study was piloted aboard the R/V Sharp in September 2015. A large scale sediment and water column program was conducted, which included imaging of seafloor sediments and water column methane plumes, seafloor heat flow measurements, piston coring, multi coring, and sampling of methane plumes in the water column.

Geochemical analysis of pore water gases indicates a microbial origin for methane, with stable carbon isotope values ranging from -70 per mil to -90 per mil. Methane concentrations in sediments and the water column exhibit an inverse distribution between the southern and northern sector of northern USAM. Northern sector sites are characterized by a high flux of methane in the sediments with sulfate-methane transition zones (SMTZs) at 100 to 400 cmbsf and low concentrations of methane (2-20 nM) in the water column, while southern sector sites have a comparably higher flux in sedimentary methane with shallow SMTZs at 15 cmbsf, but up to 30 times elevated methane concentrations in the water column. In order to further understand microbial controls on methane flux and cycling within the sediment and the sediment-water interface, we are currently investigating the microbial community composition using a combined microbiological, lipid biomarker and isotopic approach. 16S rRNA gene sequencing results show strong community differentiation by location. Archaeal communities of the high-methane southern sector sites are dominated by anaerobic methane oxidizing archaea (ANME)-1 while the northern sector sites show a more diverse archaeal community structure including Thermoplasmatales, Marine Benthic Group-B and Deep Sea Hydrothermal Vent Group (DSHVG). Bacterial communities of the southern sites are dominated in equal amounts of Proteobacteria and Atribacteria (JS-1), while northern site exhibits a more diverse bacterial community with notable contributions of Chloroflexi, Planctomycetes, Actinobacteria, Aminicenantes, and an increasing dominance of Atribacteria with depth.

This presentation will report on the distribution of intact polar lipids (IPL) of archaea and bacteria that inhabit these contrasting sedimentary environments. The IPL investigations will be accompanied by head-group specific stable carbon isotope analyses in order to gain insights into the major groups of organisms involved in methane cycling. In light of this, we will discuss the potential to use specific IPLs as diagnostic biomarkers for the detected microbial groups by 16S rRNA gene sequencing. For instance, we will evaluate the use of the newly identified butantriol dibiphytanyl glycerol tetraether (BDGT) as a characteristic biomarker for the methanogens related to the Thermoplasmatales (Becker et al., 2016) and if

intact archaeols and hydroxyarchaeols can be used as exclusive markers for archaea involved in methane cycling. We expect that compound-specific stable carbon isotope analysis in a methane-rich environment may also yield important insights into source organisms of orphan biomarkers, such as branched glycerol dibiphytanyl glycerol tetraethers (GDGTs), overly branched GDGTs and isoprenoid-branched GDGTs that were abundantly detected in the USAM sediments. Respiratory quinones will be profiled as complementary chemotaxonomic and activity markers for both archaea and bacteria (e.g., Elling et al. 2016).

References

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