

Proteogenomics of a marine sediment community dominated by ANME-1

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Sulfate-reducing methanotrophy by anaerobic methanotrophic archaea (ANME) and sulfate-reducing bacteria (SRB) is a major biological sink of the green house gas methane in anoxic methane-enriched marine sediments. The physiology of a microbial community in the G11 pockmark at Nyegga dominated by free-living ANME-1 was investigated by a proteogenomic approach. Total DNA was subjected to 454-pyrosequencing (829, 527 reads) and 16.6 Mbp sequence information was assembled into contigs. Taxonomic analysis supported a high abundance of Euryarchaea (70%) with 66% of the assembled metagenome belonging to ANME-1. Extracted proteins were separated on 1D-SDS-PAGE, and gel slices were in-gel tryptic digested and subjected to liquid chromatography and mass spectrometry (LTQ-Orbitrap XL). Of 356 identified proteins, 245 were expressed by ANME-1. Expression of cold-adaptations and gas vesicle proteins reflects adaptation of the ANME-1 community to a permanently cold environment and possibly to positioning in specific sediment depths, respectively. Furthermore, except N_5N_{10} -methylene-tetrahydro-methanopterin reductase all enzymes in the reverse methanogenesis pathway as well as red-ox protein components homologous to SRB, were expressed by ANME-1. Sulfite reductase and adenosine-5'-phosphosulfate (APS) -reductase in the dissimilatory sulfate reduction pathway were expressed by sulfate reducing δ -proteobacteria. In addition, an APS-reductase affiliated with cluster IV comprising Gram-positive SRB and related sequences [1], was present in the proteome.

[1] Meyer and Kuever (2007), *Microbiology* **153**, 2026-2044

Deep-sea coral records of surface water properties in Gulf of Mexico and the South Eastern United States over the last millennium

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In this study we report on the use of radiocarbon measurements to investigate growth rates and age distributions of deep-water black corals (*Leiopathes* sp.) in the Gulf of Mexico and the southeastern United States. Results from five specimens show that these animals have been growing continuously for at least the last two millennia, with growth rates ranging from 8 to 22 $\mu\text{m yr}^{-1}$. These results are compared to SEM work to image growth rings and measure relative trace elements concentrations. The counting growth rings counts by two different methods on the SEM images and peaks in iodine concentration are in good agreement (typically within the ^{14}C uncertainty and a 10% counting uncertainty) with the radiocarbon results allowing for the development of independent age models.

In this study we also use a multi-proxy approach in order to better understand the combination of biological and physical factors controlling the isotopic and trace element content of deep-sea corals. Both $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$ signatures along with trace element paleoindicators of eutrophication and oxygen levels (V, Mo, U, Re, Cu and I) can be used to infer changes in surface water conditions related to nutrient loading, eutrophication, and hypoxia in the Gulf of Mexico over the last millennium. Important changes are noted over the last 900 years and over the last century.