



Diversity of Functional Genes for Sulphate Reduction at Sites with High Activity of Anaerobic Oxidation of Methane

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The anaerobic oxidation of methane (AOM) in marine sediments is a significant sink in the global methane cycle. It has previously been shown that a consortium of archaea (ANME) and sulphate-reducing bacteria is responsible for AOM. The fact that the AOM-mediating microorganisms predominantly occur in structured physical associations led to the speculation that AOM is based on a symbiotic relationship between these organisms. However, it is still unclear if a syntrophic consortium is actually necessary to mediate AOM. Since it is possible that the ANME organisms possess the enzymatic apparatus to mediate both, AOM and sulphate reduction, the phylogenetic diversity of sulphate-reducing prokaryotes (SRP) in AOM-active samples originating from the well-characterized sites in the Black Sea and at Hydrate Ridge was investigated using clone libraries to see, whether sulphate-reducing genes of archaeal origin are present at these sites. These analyses were based on the dissimilatory sulfite reductase (*dsrAB*) and adenosine-5-phosphosulphate reductase (*apsA*) genes. Both genes were successfully amplified from microbial communities of Hydrate Ridge sediment and Black Sea microbial mats. The detailed phylogenetic analyses revealed at least seven major phylogenetic groups. These were related to the aromatics-degrading strain mXyS1, the *Desulfoarculus/Desulfomonile* group, the genera *Desulfosarcina* and *Desulfobacter*, the families *Desulfobulbaceae* and *Syntrophobacteraceae*, and deep branching organisms of unknown bacterial affiliation. In summary, the sequence analyses of *dsrAB* and *apsA* clones revealed a diverse SRP community at both the

Hydrate Ridge sediment and the Black Sea microbial mat AOM sites, but no hint for archaeal sulphate reduction.