



Metagenome and metatranscriptome analysis revealed key metabolic pathways in a simulated anaerobic methane oxidation - sulfate reducing community

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Here we report the metagenome and metatranscriptome analysis of a highly enriched, active AOM-SR (anaerobic oxidation of methane - sulfate reduction) community obtained through a continuous high-pressure bioreactor system. The community has a very high diversity of bacteria, besides SRB within delta-Proteobacteria, gamma-Proteobacteria closely related with Methylophaga, Methylobacter and Marinobacter, was found most abundant. The archaeal components in the system are rather simple with only ANME2 and Marine Benthic Group D detected. A complete hydrogenotrophic methanogenesis pathway including the previously missing mer gene in the ANME1 genome was easily identified in the metagenome. Phylogenetic analysis of the core enzymes in the methanogenesis pathway (Mer, MtrABCDEH, McrA) revealed two evolutionary distinct methane oxidizing archaea / methanogen clades : one embedded in the Methanosarcinales order (ANME2 belong to), the other differentiate greatly from all known methanogens and methanotrophs. Besides the methanogenesis and sulfate reducing pathways, pathways for complete denitrification, nitrogen fixation, and aerobic methane/methyl oxidization were all identified in the metagenome, suggesting diverse syntrophic relationships among the microorganisms within the system. The expressions of these pathways were checked by metatranscriptome analysis and discussed further.