Comparative analysis of syntrophic bacteria genomes within methane consuming consortium to understand the mechanisms of anaerobic methane oxidization (AOM) in marine sediment

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Methane is a highly effective greenhouse gas with greenhouse effect about 20 times higher than CO₂. Marine sediments are the largest methane reservoir but very little methane is emitted from the ocean mainly because of anaerobic methane oxidation within the anoxic sediments. Anaerobic methane oxidization is conducted by anaerobic methane oxidizing archaea(ANME) which usually appears in syntrophic consortium with bacteria partner in marine sediment. These metabolically interdependent consortia facilitate AOM and share the obtained energy. The AOM consortia mainly consist of ANME and sulphate reducing bacteria(SRB) that belong to the Deltaproteobacteria, performing AOM in couple with sulphate reduction. Meanwhile, accumulating evidences suggested that AOM consortia may contain divergent bacterial partners, for example, apart from the Desulfosarcina/Desulfococcus group (DSS) of Deltaproteobacteria, Betaproteobacteria were also found forming consortium with ANME-2. Since neither ANME nor the bacteria partner in the consortium have been obtained in pure culture, it remains challenging to fully understand the mechanisms of how they live in syntrophy as well as the versatile mechanisms of AOM in the ocean. Here we obtained 4 bacterial genomes from the AOM consortia formed with ANME-2, 2 of them are nearly complete (completeness > 96%). They belong to Desulfobacteraceae of Deltaproteobacteria and Limnobacter of Betaproteobacteria (Chen et,al, 2016) respectively. Comparative genomic analysis shows that they share certain set of genes which may provide information of AOM consortia syntrophic mechanisms and help us understand the way they contribute to methane sink in marine sediment.