

Sub-seafloor methane biogeochemistry and unseen archaeal methanotrophic processes

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Microorganisms play a central role in the global methane cycle for both production and consumption. Methanogenic archaea (methanogens) are a phylogenetically diverse group of strictly anaerobic Euryarchaeota, which grow with the enzymatic formation of methane from H₂ plus CO₂, acetate, and C₁ compounds (e.g. methanol, methylamine) present in anaerobic environments. Kaneko et al. (2014) reported the analytical development for coenzyme factor 430, critical cofactor for biological methanogenesis and reverse-methanogenesis (occasionally), by using high performance liquid chromatography / electrospray ionization mass spectrometry (HPLC/ESI-MS/MS) on the optimized multiple reaction monitoring method during the order of 0.1-1.0 femto mol.

On the other hand, the anaerobic oxidation of methane (AOM) in marine sediments is an important microbial process in the carbon cycle and also greenhouse gas emission constraints. Since the first report of ¹³C-depleted lipids mediated by modern anaerobic methanotrophic archaea (ANME) consortium, the molecular carbon isotopic signatures have been recognized as an indicator of ongoing microbial methanotrophy [e.g., Hinrichs et al., 1999; Elvert et al., 1999]. Cold seep ecosystems, a biological hot spot for ANME communities, is an ideal natural laboratory for the study of methane biogeochemistry and microbial anaerobic methanotrophy driven by modern ANME communities [e.g., Knittel and Boetius, 2009 and literatures therein]. Since laboratory-based culture and isolation of ANME are currently difficult, the fate of sub-seafloor ¹³C-depleted methane emission is still unclear on their biosynthetic pathways during anaerobic oxidation process.

[References]

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Keywords: Sub-seafloor methane biogeochemistry, global methane cycle, Archaea, ANME (ANaerobic MEthanotroph)