Revealing the blackbox since 1999: ^{13}C-depleted amino acids and lipids in deep-sea methane biogeochemistry

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Microorganisms play a central role in the global methane cycle for both production and consumption. The anaerobic oxidation of methane (AOM) in marine sediments is an important microbial process in the global carbon cycle and greenhouse gas emission constraints. Since the pioneering reports of ^{13}C-depleted lipids mediated by modern anaerobic methanotrophic archaea (ANME)[1], the carbon isotopic composition has been recognized as an indicator of ongoing microbial methanotrophy [2]. Cold seep ecosystems are a biological hot spot for ANME communities. Therefore, the Black Sea is an ideal natural laboratory for the study of methane biogeochemistry and microbial anaerobic methanotrophy driven by modern ANME communities [3]. For the reason that laboratory-based pure culture and isolation of ANME archaea are currently difficult, the fate of sub-seafloor ^{13}C-depleted methane emission is still unclear on their biosynthetic pathways during anaerobic oxidation process. To address this important issue, we conducted compound-specific carbon and nitrogen isotopic analyses for protein type amino acids by using ANME communities from a methane seep site in the Black Sea [4]. We observed a significant stepwise ^{13}C-depletion trend in association with increasing carbon numbers of protein amino acids down to -114‰ relative to the PDB standard. Here, we discuss the metabolic pathway of bioavailable sub-seafloor methane and the central role of pyruvate family amino acids as the *de novo* biosynthetic precursors, resulting the extreme ^{13}C-depleted lipid signatures during the AOM process in the deep-sea microbial oasis.

REFERENCES

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