

海洋堆積物中アミノ酸の動態における微生物の寄与 Microbial processes in the biogeochemical dynamics of amino acids in marine sediments

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Sedimentary organic matter (OM) is the major reservoir of carbon and nitrogen in the global biogeochemical cycle. For example, burial of organic matter in sediments plays a role in controlling atmospheric CO₂ and O₂ levels on long time scales. There remains, however, much debate about the controlling factors of OM preservation and the processes of OM degradation in marine sediments. Amino acids are major nitrogenous components in OM and also the important intermediate during the OM degradation by microbes. Composition, D/L ratio, and compound-specific isotopic composition have been used as the indicators of amino-acids biogeochemistry in marine sediments.

In this presentation, we report our results of composition, D/L ratio, and nitrogen isotopic composition (d15N) of amino acids in the surface sediments collected at off-Akita, Japan Sea (KT10-06) and the deep-subsurface sediments collected at off-Boso, Northwestern Pacific (CK09-03). We observed difference of d15N and/or D/L ratio between total hydrolysable amino acids (THAA) and dissolved/extractable amino acids. Based on the results of culture experiments of microbes for amino-acids d15N and simple mass-balance calculation, we estimated the contribution to the dissolved/extractable amino acids from the microbial biomass in the sediments and that from the THAA. For example, in the surface sediments in Japan Sea, we observed 3-5 permill enrichment in the d15N of free glutamic acids (Glu) from the THAA-Glu d15N. Based on the 15N-enrichment factor (8 permill) of Glu in the cultured microbes, we estimated that the release from microbial biomass would contribute to 30-40% in the free Glu. These results suggests that recycle of amino acids by microbes would be significant during the degradation of amino acids.

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