

MIS023-09

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微生物のアミノ酸窒素同位体組成：培養実験および海底堆積物への応用 Nitrogen isotopic signatures of amino acids in microbes: culture experiments and applications to marine sediments

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The microbial roles in biogeochemical cycles remain largely unknown, mainly because of the lack of tools to explore in situ metabolic activities of microbes. The compound-specific nitrogen isotopic composition ($\delta^{15}\text{N}$) of amino acids, especially for glutamic acid (Glu) and phenylalanine (Phe), had been demonstrated as a promising tool for estimating the food sources of organisms in the grazing food web.

Applicability of this amino-acids method to microbes or detritus food web, however, remains uncertain, because the method has been constructed based on the analytical results of aquatic photoautotrophs (cyanobacteria and algae), terrestrial higher plants, and animals, but not chemotrophic microbes. In this study, the nitrogen isotopic compositions of amino acids were investigated in 5 cultured microbes namely a fungus (*Saccaromyces cerevisiae*), a bacterium (*Escherichia coli*) and archaea (*Sulfolobus tokodaii*, *Halobacterium salinarum* and *Methanothermobacter thermautotrophicus*) with controlling their nitrogen sources.

When the microbes synthesized amino acids *de novo*, the relative $\delta^{15}\text{N}$ values of their amino acids were similar to aquatic photoautotrophs, whereas the case the microbes assimilated amino acids from diets, they showed ^{15}N -enrichment on the amino acids close to that of animals. The results suggest that the nitrogen-isotope fractionation process of amino acids are likely common among various organisms covering 3 domains (Eukarya, Bacteria, and Archaea) and among various environmental conditions such as growth temperature, pH, or salinity.

Therefore, nitrogen isotopic composition of amino acids would potentially be a powerful tool to clarify in situ microbial metabolism (amino-acids synthesis or decomposition) and their biogeochemical roles (especially in nitrogen cycle and in organic-matter diagenesis). The small variations in values of Glu and Phe suggest the use of the Glu-Phe pair is the most promising combination as in the case of analysis of grazing food webs. In the presentation, we also show its applications to marine sediments in various settings.

キーワード: 分子レベル同位体組成, アミノ酸, 微生物, 海底堆積物, 有機物変質, 窒素循環

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