

Nitrogen isotopic compositions of amino acids from microorganisms as a tool for studying microbial processes

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Microorganisms that have driven the biogeochemical cycles have largely occupied the Earth's surface environment. For example, it has been considered that uptake of organic matter by oceanic heterotrophic bacteria and archaea (microbial loop or detritus food chain) is a major carbon-flow pathway and the overall patterns of carbon cycle can be modified from its variability (e.g. Azam and Malfatti, 2007). However, most of microbial processes in biogeochemical cycles still have been treated as a black box and their individual roles and dynamics also are remained uncertain. Recently nitrogen isotopic compositions ($\delta^{15}\text{N}$) of individual amino acids was reported to be a useful tool for studying grazing food chain which is composed of primary producers and following consumers including plants and animals in both aquatic and terrestrial environments (e.g. Chikaraishi et al. 2007). The method is also potentially useful for the investigation of microbial food chain. However, although the rules in plants and animals are well characterized, the variation of $\delta^{15}\text{N}$ of amino acids in microorganisms (including prokaryotes and eukaryotes) has been poorly studied and the rules are not determined.

To clarify the rules of $\delta^{15}\text{N}$ of amino acids in microorganisms, we have been culturing several heterotrophic microorganisms (e.g. *Escherichia coli*, *Vibrio harveyi*, *Saccharomyces cerevisiae*, etc) within various nitrogen sources (e.g. ammonium, amino acids). Amino acid $\delta^{15}\text{N}$ of the cultured microorganisms are analyzed. In this presentation, we will report preliminary data of present culture studies and discuss their controlling factors.

Azam and Malfatti (2007) *Nature Rev. Microbiol.* 5, 782-791.

Chikaraishi et al. (2007) *Mar. Ecol. Prog. Ser.* 342, 85-90.