

Estimation of trophic position in marine ecosystems based on nitrogen isotope of amino acids: prey-predator interaction

CHIKARAISHI, Yoshito^{1*}, FUJIKURA, Katsunori¹, TSUCHIYA, Masashi¹, YOSHIDA, Takao¹, FUJIWARA, Yoshihiro¹, KITAMURA, Minoru¹, LINDSAY, Dhugal J.¹, UMEZU, Yuichi², NAGABORI, Atsushi¹, SHINOZAKI, Ayuta², OGAWA, Nanako O.¹, OHKOUCHI, Naohiko¹

¹JAMSTEC, ²Hiroshima University, JAMSTEC

Estimate of the accurate trophic position of organisms in food webs allows better understanding of not only biomass flow and trophic linkages in complex networks of natural ecosystems but also function and niche of individual organisms, species, and communities in the ecosystems. Combination of ultra-sensitive carbon and nitrogen isotope analyses of bulk whole samples (or tissues) and nitrogen isotope analysis of amino acids of the samples is a potential powerful tool to access the above subjects.

In this presentation, we will show a comprehensive data set on the isotope signatures for various organisms collected from marine surface photosynthetic and deep-sea chemosynthetic communities in Sagami bay, and will discuss 1) applicability of this method to chemosynthetic communities, 2) nitrogen flow into the deep-sea food web from photosynthetic (i.e., sinking particle) and chemosynthetic (i.e., seep water) communities, and 3) characteristics of specific nitrogen (or amino acids) transfer system during symbiosis between chemosynthetic bacteria and host organisms.