Japan Geoscience Union Meeting 2012
(May 20-25 2012 at Makuhari, Chiba, Japan)

BPT26-P07 Room:Convention Hall Time:May 23 17:15-18:30

Estimation of trophic position in marine ecosystems based on nitrogen isotope of amino acids: host-symbiont relationship

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This study aims to clarify the trophic position (TP) of marine organisms to understand food web structures in marine ecosystems based on the stable isotope analysis of amino acid that we mainly focused on 1) the food web structures of marine ecosystems, and 2) the host-symbiont interactions. Combined analyses using stable isotopes along with ecologic, biochemical, and genetic analyses will clarify the relationships among prey-predator interactions in marine organisms and illustrate the dynamics and evolution of marine ecosystems.

We clarified the host-symbiont interactions between *Calyptogena* clam, and endosymbiotic bacteria. TP of *Calyptogena* muscle and symbiotic bacteria shows 2.0 and 3.1, respectively. TP increases 1.1 from symbiotic bacteria to muscle. We assumed that host *Calyptogena* muscle obtained almost 100 % of nutritional source from symbiotic bacteria as amino acid. On the other hand, *Bathymodiolus* species have same TP value (=1.2) among the host *Bathymodiolus* (muscle, mantle and foot), symbiont-bearing gill, and symbiotic bacteria. It means that *Bathymodiolus* may have different mechanisms of nutrient requirement than *Calyptogena*.

Keywords: nitrogen isotope of amino acids, trophic position, host-symbiont relationships, chemosynthetic ecosystem, Calyptogena species, Bathymodiolus species