

On the role of amino acid metabolism and a biogeochemical linkage

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Deep-sea sediments harbor a novel and vast biosphere with yet unconstrained importance in the global biogeochemical cycle. To explore these habitats is interdisciplinary challenges for the biogeochemical and geomicrobiological scientific community. The limits of deep biosphere are on-going subject, which were not yet known in terms of environmental properties, including depth, temperature, energy availability, and geologic age; however, it is known that seafloor microbes play a significant role in chemical reactions that were previously thought to have been abiotic.

Since the novel classification by Woese and Fox (1977), Archaea, one of three domains of life, had been originally believed to exist in extreme environments including high temperature, high salinity, low oxygen concentration. However, recent advances in molecular and phylogenetic approaches revealed their widespread distribution in marine and terrestrial environment including deep subsurface biosphere. The planktonic and benthic archaeal assemblages include two major phyla Euryarchaeota and Crenarchaeota. The novel phylum have been also proposed recently as Thaumarchaeota, Korarchaeota, and Nanoarchaeota.

In the present study, we reviewed the recent knowledge of prokaryotic ecology and biogeochemistry from molecular-specific isotopic signatures. Among these, we focused on the role of amino acid metabolism and a biogeochemical linkage mediated by deep-sea benthic archaea.

[References]

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