

Pyrosequencing of planktonic and benthic biota above the sediment-water interface in methane hydrate-bearing areas in the eastern margin of the Japan Sea

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In this study, we have conducted pyrosequencing analysis of eukaryotic community structures from the water columns and the sediment-water interfaces at sites associated with and without methane seeping and bacterial mats in the area associated with the shallow methane hydrate deposits in the Joetsu Basin, Japan Sea. Dominant 18S rRNA gene sequences from shallow water columns at water depths of ~50 m and ~200 m were related to marine dinoflagellates of the genera *Gyrodinium*, copepods of the genera *Centropages*, radiolarians of the subclass Acantharia. From bottom seawater at water depths of ~1000m, the community structures were distinct at the sites associated with methane seeping and bacterial mats from that at the reference site. The former structures were abundantly composed of the genera *Nanomia* and *Pantachogon* of Cnidaria phylum. Although marine dragon nematodes of the family Chromadorea were dominantly detected from shallow sediments at the site associated with methane seeping and bacterial mats, the overall community structures from shallow sediments were similar at all investigated sites.

This study was conducted as a part of the shallow methane hydrate exploration project of METI.

Keywords: methane hydrate, 18S rRNA, Pyrosequencing, Eukaryotic communities, DNA