Microbial communities in pumiceous sediments in the Iheya North hydrothermal field.

# Satoshi Nakagawa[1]; Takuro Nunoura[2]; Toshiro Yamanaka[3]; Tomomi Mitsunari[4]; Junichiro Ishibashi[5]; Urumu Tsungai[6]; Ken Takai[1]; Masataka Kinoshita[7]; Juichiro Ashi[8]


The newly developed coring method, NSS (Navigatable Sampling System), has facilitated the recovery of hydrothermal sediments underlying invertebrate colonies. Microbial communities in hydrothermally active sediments of the Iheya North field (Mid-Okinawa Trough) were studied by using culture-dependent and -independent approaches. Our previous studies indicated that phase-separation and -segregation (boiling/distillation of hydrothermal fluids) represent the primary mechanisms causing intra-field variations in vent fluids chemistry and microbiology of Iheya North (Nakagawa et al., 2005). Here we show the microbial communities in pumiceous sediments underlying tubeworm colony and Calyptogena colony, and clayey non-hydrothermal sediments. Earlier geochemical study suggested that vapor-rich hydrothermal fluids supported microbial sulfate reduction coupled with methane oxidation at the Calyptogena colony.

The Calyptogena sediments harbored a diversity of culturable bacteria, such as novel members of epsilon-Proteobacteria (hydrogen/sulfur-oxidizing chemolithoautotrophs) and Fusobacteria (fermentative bacteria). Close relatives of these bacteria have been detected in hydrocarbon-rich environments. However, the MPNs (Most Probable Number) were low. Based on ongoing 16S rRNA study, the sediments harbored mostly uncultured, phylogenetically diverse bacterial/archaeal communities, which differed significantly among the three sites. Consistent with earlier geochemical characterization, only the Calyptogena sediments harbored members of ANME-1 and -2 which previously assigned to the methanotrophic archaea. This study stresses that subseafloor phase-separation and porous pumiceous sediments play an important role in transporting energy and carbon sources to subseafloor microbial communities.

Reference