

Microbial diversity of hydrothermal environments in the Yonguni Knoll IV: comparison between *in situ* temperature, geochemistry and microbial diversity in hydrothermal fluids and sediments

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Many uncultivated lineages of microbes have been detected 16S rRNA gene clone analyses in hydrothermal environments as well as deep-sea sediments and their ecological roles have not been revealed with few exceptions. In order to know the physiology and ecology of uncultivated prokaryotes distributed in deep-sea hydrothermal vent environments, we compared microbial diversity, *in situ* temperature and geochemistry of hydrothermal sediments and fluids that were collected from sediment-hosted hydrothermal field at the Yonaguni Knoll IV, Southern Okinawa Trough. Hydrothermal sediments cores were obtained 50cm, 2m and 5m from a vent emission. *In situ* temperature of sediments was determined by multi-sensor temperature probe and temperature of the sediments ranged from 5 to 60°C. Microbial community structures were determined by cultivation analyses of thermophilic methanogen, *Thermococcales* and *Epsilonproteobacteria*, and clone analysis and quantitative PCR of 16S rRNA gene and *mcrA*.

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