

## Unique microbiome in the hydrothermal plumes in Okinawa Trough sediment hosted back arc hydrothermal systems

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Deep-sea hydrothermal plume harbors chemolithoautotrophic microbes depending on high concentration of sulfur, methane and hydrogen supplied from hydrothermal fluid. The most major constituent of the plume microbe is SUP05, which utilize sulfur as energy source. It occupy more than 80% of the elevated microbial population in Izu-Mariana hydrothermal plume. In the Okinawa trough hydrothermal plume, their contribution to the elevated plume microbes is lower than those of Izu-Mariana plume and methane utilizing *Methylococcus* play more important roles. However these two groups are responsible for 50-70% of the elevated microbial population in the Okinawa plume. In this work, I examine the microbial community structure analysis based on 16S rRNA gene using NGS with higher resolutions. The microbial community structures are varied among 7 hydrothermal and 1 methane seep sites. Potential chemolithoautotrophs (*Thaumarchaeota*, *Thermogemmatispora*, *Surfurimonas*) and heterotrophs (*Marinobacter*, *Caulobacter*, *Sphingomonas*) are detected. These data will be useful for baseline microbial community structures in hydrothermal plume against the deep sea mining in the future.

Keywords: hydrothermal plume, MiSeq, microbial community structure, Okinawa Trough