

Microbial community succession and hydrogen utilization in hydrogen-gas rich hydrothermal plume of Kairei field, CIR

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Deep sea hydrothermal plume is important interface between solid earth and ocean. In the hydrothermal plume, various and large energy is yielded for chemolithoautotrophic microorganisms through the oxidation-reduction reaction between the reduced chemicals in the hydrothermal fluids and oxygen in the seawater. The microbial community structures varied among different hydrothermal systems (Sunamura and Yanagawa 2015) and epsilon proteobacteria has been specifically detected in the hydrogen-rich hydrothermal plume of Kairei hydrothermal field (KHF). Here, I report the microbial community structure in the hydrothermal plume and statistical analysis based on physical, chemical, and biological parameters in the hydrothermal plume of KHF.

As results, we found 16 microbial families, e.g. *Cenarchaeaceae* (Archaea), *Helicobacterceae* (epsilon proteobacteria), SUP05 (gamma proteobacteria), SAR324 (delta proteobacteria), and 3 methylotrophs, in 251 microbial families are determined to be the active and important microbial groups in the hydrothermal plume. Based on the ratio (20/1) of hydrogen and methane gas in the end member fluids of KHF, we estimate the consumed hydrogen gas from the hydrogen and methane gas concentration in each hydrothermal plume samples. The estimated consumed hydrogen gas is strongly correlated with *Helicobacterceae* population ($R=0.65$, $n=28$). Relatives of *Helicobacterceae* are known to utilize hydrogen gas/reduced sulfur compounds as electron donor. Our result suggest the *Helicobacterceae* in the hydrothermal plume of KHF obtain energy from hydrogen gas and the variation of H₂/CH₄ ratio in the plume would due to their activity.

Keywords: deep sea hydrothermal plume, microbes, hydrogen gas