

Meta-omics mining of active microbial communities in hydrogen and iron-rich deep-sea hydrothermal plumes

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Hydrothermal activity plays an important role in ocean biogeochemistry. [1,2] The Kairei Hydrothermal Field (KHF), located along the Central Indian Ocean Ridge (CIR), is globally among the most hydrogen-rich vent fields. [3] Additionally, previous studies have reported high iron concentrations in its end-member fluids. [4] Despite extensive research and broad interest in the site's unique geochemistry, the microbial community composition and activity within the KHF hydrothermal plume remains largely unexplored. In this study, we systematically investigate the microbial community within KHF plume along multiple transects. First, we sequenced the V3-V4 hypervariable region by 16S rRNA metabarcoding. Comparative 16S rRNA analysis of environmental samples indicated a decrease in the relative abundance of the genus *Sulfurimonas* along the spatial gradient toward the aged plume. Meanwhile, the SUP05 clade exhibited a stable relative abundance over the same distance. Guided by geochemical data to refine sample selection, a meta-omics approach is conducted to explore the active members of the microbial community. Metagenomics and -transcriptomics already revealed actively transcribed functional traits of plume-associated microbes. A further aim is to elucidate how both taxa thrive in different sections of the plume and what metabolic adaptations they exhibit. Additionally, on board enrichment experiments were conducted to assess the influence of sulfur, hydrogen and iron on microbial communities of this unique hydrothermal system. Cell staining and catalyzed reporter deposition fluorescence *in situ* hybridization (CARD-FISH) confirmed a change of the microbial community composition. We will integrate molecular, geochemical and physical oceanographic data to understand the far-field effect along a transect extending up to a few kilometers from vent emission. This multidisciplinary approach will contribute to a deeper understanding of the interactions between hydrothermal plume-enriched waters and their microbial communities, shedding light on their role in biogeochemical cycling, microbial dispersal, and ecosystem connectivity in the deep sea.

References

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