

Combined molecular and mineralogical analyses on the microbial community structure in rock samples from Higashi-Aogashima Knoll Caldera hydrothermal field

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In 2015, the Higashi-Aogashima Knoll Caldera hydrothermal field was newly discovered at Izu-Ogasawara Arc. The water depth of the caldera floor is about 600–800 m. Sulfide mineral-rich mounds with high Au and Ag concentrations as well as containing large native gold grains were discovered from Central Cone Site of the Higashi-Aogashima Knoll Caldera hydrothermal field. Seafloor massive sulfide (SMS) deposits formed by hydrothermal activity is recognized as potentially important mineral resources for future deep-seabed mining. Bioleaching is one of the metal recovery methods from constituent sulfide minerals by microorganisms such as sulfur-oxidizing and iron-oxidizing bacteria which convert insoluble metal sulfides into soluble metal sulfates. However, an available microbial strain for the bioleaching method aiming to treat sulfide minerals in the SMS deposit is still limited because of its high salinity, acidic and metal rich conditions.

In this study, we conducted both molecular and mineralogical analyses on rock and ambient seawater samples collected from the Higashi-Aogashima Knoll Caldera hydrothermal field to seek microbes available for bioleaching and understand the microbial-mineral interactions. 68 rock and 7 ambient seawater samples were collected from four hydrothermal sites of Central Cone, Southeast, East and South of East Sites. Rock samples were collected from mound, active and dead chimney, hydrothermal crust and altered volcanoclastic rock. Microbial community composition was characterized using 16S rRNA gene tag sequencing. Element concentrations of the rock samples were determined by inductively coupled plasma-mass spectrometry (ICP-MS) with the mixed acid digestion method.

The microbial community composition of the rock samples was different from that of the ambient seawater samples. Our results also showed that composition and diversity of microbial communities in the rock samples varied with the sampling site and its element concentrations (constituent minerals). Especially, the highest relative abundance of sulfur-oxidizing bacteria *Acidithiobacillaceae* was observed in the mound samples from Central Cone Site which has the high Au concentration. Our results provide insight into the patterns in the distribution of microorganisms along with types of rock and metal element