

## Influence of microorganisms on metal cycling of seafloor massive sulfides

Shingo Kato<sup>1\*</sup>, Katsuhiko Suzuki<sup>2</sup>, Akihiko Yamagishi<sup>1</sup>

<sup>1</sup>Tokyo Univ. Pharm. Life Sci., <sup>2</sup>IFREE, JAMSTEC

Microorganisms play potential roles in biogeochemical cycle between the ocean and crust through the surface of ocean floor (Edwards et al., 2005). Diverse microorganisms are abundant on/within the oceanic crusts (e.g., Santelli et al., 2008). These microorganisms would influence dissolution and absorption of elements of the crusts, leading to large impact on element fluxes from and into the ocean. Seafloor massive sulfides (SMS) occur on mid-ocean ridges, volcanic arcs and back-arc spreading basins, and are attracting attention as resources of metals, e.g., Cu, Fe and Zn (Hoagland et al., in press). Even if the SMS are hydrothermally inactive, microorganisms are rich and phylogenetically highly diverse (Suzuki et al, 2005; Kato et al, unpublished). However, it is unclear whether and how these microorganisms affect dissolution and absorption of elements of the SMS. The goals of this study are (i) to determine the microorganisms inhabiting on the SMS, and (ii) to assess influence of the microorganisms on the dissolution and absorption of elements. A hydrothermal sulfide deposit was collected in the Southern Marina Trough during YK05-09 cruise. Chips (10 mm x 10 mm x 1 mm) of the deposit were sterilized and washed with ethanol and acetone. The chips and slurry of the deposit were incubated in artificial seawater media (pH 7.3) containing low concentration of organic compounds at 40C, in the dark under non-shaking conditions for 71 days. The pH, element concentrations and cell density of the media sampled with time were determined. After 71 days, 16S rRNA gene analysis and microscopic observation of the chips and media were performed. Control experiments (without chips or slurry inoculations) were also done.

The pH of all media shifted from 8.1 at a starting point to 7.3. The cell densities increased slightly (doubling time, 95 to 108 hrs). Microbial colonization on the chips was observed by fluorescence microscopy. Dissolution of Cu and Zn from the chips and absorption of Mn and Si to the chips were detected by chemical analysis using ICP-AES. Rates of the dissolution and absorption were faster with cells than those without cells (17 to 131%). Note that Ba concentration decreased only in the incubates with cells and chips. The 16S rRNA gene analysis indicated the presence of highly diverse microorganisms in the original sulfide deposit sample. However, a phylotype related to *Halomonas* was dominant after 71 days in the libraries constructed from the chips and media of the incubates. Unique phylotype related to *Marinobacter* or *Pseudomonas* was detected only in either of the chips or media, respectively. Our results suggest the influence of microorganisms attached to SMS on the metal cycling in the ocean.

Keywords: geochemical cycle, seafloor massive sulfide, microbial community