Did life emerge in a deep-sea metal sulfide chimney? New insights from an archaeal genome and a nanoscale microbe-silicate assemblage

*Hinako Takamiya¹, Hiroki Mukai², Mariko Kouduka¹, Shingo Kato⁴, Motoo Ito³, Yohey Suzuki¹

1. Earth and Planetary Science Graduate School of Science, The University of Tokyo , 2. National Institute of Advanced Industrial Science and Technology, 3. Kochi Institute for Core Sample Research JAMSTEC, 4. RIKEN

Deep-sea hydrothermal activities have continued for 3.8 billion years on Earth. After the formation of metal sulfide chimneys from high-temperature fluid, their low-temperature interactions with ambient seawater potentially provide the cold, stable habitat for microbial life. In such a challenging habitat with metal toxicity, 16S rRNA gene sequences formerly affiliated within Deep-Sea Hydrothermal Vent Euryarchaeota Subtype 6 (DHVE6) and recently reclassified as Pacearchaeota are dominantly detected by 16S rRNA gene sequence analysis. However, the distribution and metabolic activities of Pacearchaeota in metal sulfide chimneys are largely unknown. In this study, a metal sulfide chimney collected from a deep-sea hydrothermal field in South Mariana Trough was subjected to genome-resolved metagenomics analysis. It was revealed that a near-complete Pacearchaeota genome has carbon metabolism genes involved in glycolysis and pentose phosphate pathway linked to nucleotide salvage pathway with light-independent CO₂ incorporating ribulose bisphosphate carboxylase/oxygenase (RubisCO). By comparative analysis of Pacearchaeota genomes from deep-sea metal sulfide deposits and terrestrial subsurface aquifers, the carbon metabolism was commonly found with genes annotated for Cu detoxification. Based on the NanoSIMS ion imaging analysis, we found an evidence of a dense microbial colonization inside the chimney where the surface of chalcopyrite (CuFeS₂) was overlayered with a silica-bearing material enriched in CN, S and P. Our results explain the geographically and physicochemically diverse distributions of Pacearchaeota indicated by 16S rRNA gene sequence analysis as well as the predominance of Pacearchaeota in the metal sulfide chimney where energy sources from photosynthesis and hydrothermal fluid are limited. The carbon metabolism operated by Pacearchaeota in one of candidate environments for the origin of life could be relevant to that operated by primitive life on early Earth.

Keywords: hydrothermal vent, metagenomic analysis, extremophile ecology, origin of life, microbial carbon metabolism, Rock life detection