

U020-14

Room:304

Time:May 23 14:40-14:55

A new approach for clarifying the population genetic structure of chemoautotrophic bacteria in deep-sea hydrothermal fields

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Deep-sea hydrothermal fields are areas on the seafloor of high biological productivity fueled primarily by microbial chemosynthesis. Chemoautotrophic Epsilonproteobacteria utilizing inorganic substrates such as H₂S and H₂ are dominant in deep-sea hydrothermal vents around the world. Beside deep-sea chemoautotrophs, the class Epsilonproteobacteria contains important human pathogens, i.e. *Helicobacter pylori* and *Campylobacter jejuni*. Previous population genetic studies about these pathogenic Epsilonproteobacteria have revealed that they have extremely high rates of genetic mutation and recombination. However, little is known about the population genetic structure of deep-sea Epsilonproteobacteria. In this study, we performed multilocus sequence analysis (MLSA) on deep-sea Epsilonproteobacteria to clarify their population genetic structure.

Epsilonproteobacterial strains used in this study were isolated from geographically separated hydrothermal fields by using dilution-to-extinction method. We focused on strains sharing similar 16S rRNA gene sequences. Based on some housekeeping gene sequences, various population genetic analyses including the construction of phylogenetic trees were performed.

The phylogenetic trees inferred from all concatenated loci led to the identification of geographic barriers isolating Epsilonproteobacterial populations, although 'everything is everywhere; the environment selects' is widely accepted in microbiology.

In our presentation, the biogeography and evolution of deep-sea Epsilonproteobacteria will be discussed.