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Population genetic structure of deep-sea vent chemolithoautotrophs

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Deep-sea hydrothermal fields are areas on the seafloor of high biological productivity fueled primarily by microbial chemosynthesis. Chemolithoautotrophic *Epsilonproteobacteria* with an ability to utilize inorganic substrates such as H_2S and H_2 are dominant in deep-sea hydrothermal vents around the world. Beside the non-pathogenic deep-sea chemolithoautotrophs, the class *Epsilonproteobacteria* contains important human pathogens, i.e. *Helicobacter pylori* and *Campylobacter jejuni*. These pathogenic *Epsilonproteobacteria* have extremely high frequencies of genetic mutation and horizontal gene transfer. Little is known, however, about deep-sea epsilonproteobacterial population genetic structure. In our previous study, we clarified that *Epsilonproteobacteria* Group B population were geographically separated, and that they had high mutation rates. However, there are still many questions to resolve, e.g. whether these trends are common to all epsilonproteobacterial subgroups and non-epsilonproteobacterial chemolithoautotrophs. In this study, we performed multi-locus sequence analysis (MLSA) on deep-sea vent chemolithoautotrophs of *Epsilonproteobacteria* Group A, B, F and the genus *Persephonella* to clarify their population genetic structures.

Chemolithoautotrophic strains used in this study were isolated from chimney structures, vent fluids, and hydrothermal sediments. The hydrothermal samples were collected from geographically separated hydrothermal areas of the South Mariana Trough, Okinawa Trough and Central Indian ridge. We carried out various population genetic analyses including the construction of phylogenetic trees, estimation of mutation and recombination rates based on sequences of various housekeeping genes.

The MLSA revealed that the deep-sea chemolithoautotrophs commonly had extensive genetic diversity and their population genetic structure were influenced by geographic location. In addition, we found that their genetic diversity were controlled by mutation rather than recombination.

In our presentation, we will discuss the biogeography and evolution of deep-sea chemolithoautotrophs.