

Physiology and ecology of anaerobic chemosynthetic, nitrate-reducing bacteria in the deep-sea hydrothermal vents

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Anaerobic chemosynthetic bacteria do not depend on free oxygen, which is predominantly of photosynthetic origin, and therefore they are, in a strict sense, the primary producers in deep-sea hydrothermal vent ecosystems (Jannasch, 1995). The fundamental goal of this study is to establish the ecological relevance of chemosynthetic nitrate-reducing microorganisms at deep-sea vents, by investigating their physiology and molecular ecology. We initiated shipboard enrichments by inoculating anaerobic culture medium with samples collected during two expeditions onboard of the R/V *Atlantis/Alvin* (during the Summer 2006 and in January 2007) on the East Pacific Rise (EPR), at 9°50'N, 104°17'W. Currently, we have isolated three new species of thermophilic, chemolithoautotrophic, hydrogen oxidizing and nitrate-reducing bacteria. MB-1 and TB6 grow at 55°C and 60°C respectively. These two organisms have been preliminarily identified by 16S rRNA gene sequencing as *Epsilonproteobacteria* related to the genus *Caminibacter* (about 95% sequence similarity). TB-9 grows at 60°C and is in the process of being characterized. These pure cultures were isolated either by the dilution to extinction technique or by isolation of single colonies on Petri dishes that were incubated in anaerobic jars.

An eruption that occurred in 2006 on the EPR at 9°N provided us with the opportunity to investigate early microbial colonization at newly formed vents. In order to investigate the energy metabolism of nitrate-reducing chemolithotrophs, we are studying the functional diversity of the genes encoding for the periplasmic respiratory nitrate-reductase, NapA, which was previously detected in vent *Epsilonproteobacteria* (Voordeckers et al., submitted). We are currently targeting these genes both in pure cultures and environmental samples obtained from experimental microcolonizers that were deployed one year after the 2006 eruption. Preliminary results obtained from both cDNA and DNA libraries indicate that members of the *Epsilonproteobacteria* dominate the community of early colonizers.

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