

Metagenomic studies of the diversity and function of chemosynthetic microbial communities at oceanic spreading zones

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Hydrothermal vents at mid-ocean ridges are unique, highly productive environments amidst the predominantly food-limited deep-sea. To obtain a more comprehensive understanding of the genetic capabilities of primary producers in hydrothermal sediments, metagenome analysis is proposed. The focus will be set on the upper layers of typically white-covered sediments, exhibiting up to 100°C in 28 cm depth, in the Logatchev hydrothermal vent area. Based on results of our diversity studies, metagenomic fosmid libraries have been constructed and will be analysed in the remaining two years of the SPP. We will focus on metagenomic clones carrying genes encoding key proteins of methane and sulfide oxidation. Bioinformatic tools will be used to link metagenomic fragments to defined species or phylogenetic groups. The study will be complemented by fosmid insert-end sequencing, to get a broader access to the genetic capabilities of the microbial communities. Messenger RNA expression analysis will serve to evaluate whether specific genes are expressed or not. The results will be compared with results obtained by cultivation and other cultivation-independent methods and correlated to geological and fluid geochemical data. The joint analysis of the data will lead to a more detailed understanding of biogeochemical processes at hydrothermal vents, and of the transfer of energy and material from mantle to ocean.