

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

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Deep-sea hydrothermal vents and seeps are among the most productive environments on earth. Primary production at these sites is based on chemoautotrophic processes such as the oxidation of hydrogen, methane, ferrous iron, and sulfide. To get deeper insights into the biochemical potential of microorganisms that are both abundant and involved in a coupling of biological and geochemical processes at hydrothermal vents, the application of metagenome analyses is proposed. Large genomic DNA fragments will be extracted from the sample and cloned into Fosmid vectors. The resulting libraries will be characterised with respect to the microbial diversity covered within them. Subsequently they will be screened for genes encoding proteins supposedly relevant for biogeochemical processes at that particular site, including, e.g., genes coding for proteins involved in the transformation of the two most common substrates of marine microbial chemosynthesis, methane and sulfide. The results on the genetic capabilities of the predominant members of the microbial community 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.