

Understanding the interaction of biotic and abiotic factors at hydrothermal locations such as the Logatchev vent area is of fundamental importance for understanding of microbial communities at the mid-oceanic spreading axes and the transfer of energy and material from the mantle to the ocean. Therefore a recently developed molecular biological approach, metagenomics, is proposed. The metagenome is defined as the sum of genomes found in a defined site, e.g., in the fluid released from a particular vent or seep. In collaboration with geologists, fluid geochemists, and microbiologists, characteristic sampling sites will be chosen. Biomass will be collected and high molecular weight environmental DNA will be extracted. Large fosmid libraries containing inserts of approximately 40 kb will be produced and screened for the phylogenetic marker 16S rRNA and for functional genes involved in a) CO₂ and N₂ fixation, and b) the transformation of the two most common substrates of marine microbial chemosynthesis, methane and sulfide. The studies will offer first insights into the genomic equipment of the main microbial community members at the sampling sites, their metabolic and biochemical potential, and their evolution. These results will be compared to data obtained by cultivation and PCR-based sequence retrieval, and correlated to fluid chemistry and physics. Detailed information on the microbial catalysis of relevant biogeochemical reactions will be retrieved.