

Prospering microbial communities developing at hydrothermal vent sites are strictly dependent on the hydrothermal fluid flow. They are primary producers living at the expense of energy available in the reduced substrates provided by the geochemical processes of hydrothermal vents. Knowledge on microbial diversity and ecological niches at hydrothermal vent ecosystems is still fragmentary. The proposed work will focus on the diversity of microbial communities associated with hydrothermal vent habitats of the Mid-Atlantic Ridge and function related analysis of these communities. It will include eubacterial and archaeal diversity as well as diversity of functional genes of importance for these ecosystems, which code for CO₂ fixation, aerobic methane oxidation (*pmoA*) and sulfur oxidation (*soxB*). The distribution of major representative groups of microorganisms along temperature and chemical gradients will be determined, important physiological functions will be measured, and the microorganisms involved in these transformations will be identified. The proposed work will include experimental set ups to investigate temperature adaptation of natural microbial communities within artificial temperature gradients, activity measurements with natural samples, isolation and characterisation of the pure cultures.