

Diversity and adaptations of microbial communities at shallow hydrothermal vent ecosystems: An integrative DNA and lipid-based approach

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Shallow hydrothermal vent ecosystems represent natural laboratories for the study of geosphere and biosphere interactions, as well as the origin and evolution of life on Earth. They are extreme marine environments which form where fluids with high temperatures, low pH, and laden with heavy metals and compounds toxic to higher organisms, discharge from the seafloor. Given the striking absence of abundant higher fauna, unlike at deep-sea vents, microorganisms contribute the main biomass at shallow hydrothermal vent ecosystems. Moreover, microorganisms at shallow vents build the basis of the food chain by autotrophic carbon fixation, both via chemosynthesis and photosynthesis, occurring simultaneously. Despite their importance, little is known how the microbial communities adapt to extreme environments as well as how these conditions and the geochemical habitat heterogeneity influences their diversity and structure.

Using a multidisciplinary approach, comprising DNA and lipid-based techniques, porewater analysis and multivariate statistics, here we investigated cell membrane adaptations and taxonomical diversity patterns across a temperature gradient ranging from 20 – 100° C. Additionally, this study presents results on the comparison of next generation sequencing and lipid-based techniques, to decipher the ecology of microbial communities.

Vent microbial communities differed considerably compared to background sediments, in terms of both their diversity richness and community structure as well as cell membrane lipid composition. These differences could mainly be attributed to the influence of hydrothermal fluids on the sediment geochemistry. Interestingly, cell membrane lipid adaptations in Archaea could be linked to variations in temperature. In contrast shifts in bacterial diversity were mainly driven by changes in pH and not temperature. Our study highlights the usefulness of integration of molecular and lipid-based techniques for gaining a holistic understanding of the ecology of microbial communities at shallow hydrothermal vent ecosystems.