



Lithosphere-biosphere interaction at a shallow-sea hydrothermal vent site; Hot Lake, Panarea, Italy

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Deep-Sea hydrothermal systems are unique habitats for microbial life with primary production based on chemosynthesis and are considered to be windows to the subsurface biosphere. It is often overlooked, however, that their far more accessible shallow-sea counterparts are also valuable targets to study the effects of hydrothermal activity on geology, seawater chemistry and finally, on microbial life. Such an area of shallow marine hydrothermal venting is observed approximately 2.5 km east of Panarea Island (Sicily, Italy). This system is characterized by fluid temperatures of up to 135°C, gas emissions dominated by CO₂ and precipitation of elemental sulfur on the seafloor. In an interdisciplinary project to investigate the influence of geofuels on marine microbiota, sediment cores and pore fluids were sampled for geological and geochemical analyses. An attempt was made to link these geochemical data with a characterization of the microbial community.

One of the investigated sites (*Lago Caldo*, Hot Lake) is an oval-shaped (~10 by 6 meters) shallow (~2.5 m deep) depression covered by elemental sulfur. The sediments in this depression are strongly affected by hydrothermal activity: the pH of pore fluids is in a range between 5 and 6; the salinity is approximately two times higher than seawater. *In situ* temperatures of 36°C and 74°C (10 cm sediment depth) at two different locations within Hot Lake indicate variability in hydrothermal flux. The sediment surface layer is anoxic, and with increasing depth from the sediment-water interface, sulfate concentrations decrease from ~30 mM to less than 10 mM, whereas sulfide concentrations increase from less than 50 μM to ~1000 μM at 25 cm sediment depth, thus suggesting a higher potential for energy gain based on sulfur disequilibrium. As indicated by the variability in the sediment temperatures at 10 cm, fluid fluxes and mixing with seawater is not found to be uniform at Hot Lake. This is reflected in variability of the pore fluids geochemistry (anions, cations and stable isotope composition of water and sulfate) of depth profiles.

DNA-fingerprinting techniques (DGGE, ARISA) revealed distinctly different bacterial 16S rRNA gene patterns for three separate sediment cores taken at Hot Lake. Intact polar lipid (IPL) biomarker analysis revealed a dominance of bacterial over archaeal biomass. The bacterial IPLs were mainly comprised of diether and diester phospholipids and ornithine lipids, indicative of viable thermophilic sulfate-reducing and acidophilic sulfide-oxidizing bacteria. Bacterial IPL abundance was highest in the sediment surface layer. Fluorescence *in situ* hybridization showed that with increasing depth and temperature, the abundance of archaea increased relative to that of bacteria. Comparative 16S rRNA gene analysis revealed a moderate diversity of bacteria, and a dominance of epsilonproteobacterial sequences. Cultured representatives of the detected epsilonproteobacterial classes are known to catalyze elemental sulfur reduction and oxidation reactions and to mediate the formation of iron-sulfides, including framboidal pyrite, which was found in sediment samples.

We conclude that mixing between hydrothermal fluids and seawater leads to distinctly different temperature gradients and ecological niches in Hot Lake sediments. From the geochemical profiles and a preliminary characterization of the microbiological community, we found strong evidence of sulfur-related metabolism. Further investigation of certain clusters of bacteria and archaea as well as gene expression analysis will give us a deeper understanding of the interaction between geosphere and biosphere at this site in the future.