Functional genomics of the As-Fe-S biogeochemical cycle in a shallow-sea hydrothermal system, Milos, Greece

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Increasing evidence suggests that the mobilization and redox state of arsenic in environments can be strongly influenced by microbial activity. Archaea and bacteria use multiple genes to carry out aerobic and anaerobic arsenite oxidation and arsenate reduction, both for energy aquisition and detoxification. Hydrothermal vents enriched in arsenic have been shown to host these arsenic-transforming microbes, and 16S data indicate that the vents at Paleochori Bay (Milos Island, South Aegean Sea, Greece) are no exception. The vent fluid expelled at Paleochori is hot (~70ºC) and acidic (pH~4), indicating a highly altered source that diffuses vertically and horizontally through the overlying sediment. The complex geochemical pattern shows that the profile is affected not only by seawater dilution and fluid convection but also by microbial regulation. Many of the 16S sequences are related to known arsenic, iron and sulfur-transforming microbes. 16S data reflect the effects of submarine venting on sediment microbial communities, both vertically and horizontally in the predicted fluid flow path, and they provide the most comprehensive investigation of genetic potential for biogeochemical cycling of As-Fe-S. Metagenomic analysis of sediment-hosted communities at this site suggest insight into microbially mediated biogeochemical cycling, including the presence of genes that encode proteins involved in arsenite oxidation and arsenate reduction, sulfur and iron metabolisms, and autotrophic carbon fixation. The active hydrothermal emissions in Milos support complex microbial communities and functional metabolic capabilities. Combined microbiological and geochemical analyses are fundamental in providing insight into the functioning of the biogeochemical cycle in this dynamic systems.