

Comparative metagenomics reveals contrasting microbial communities inhabiting deep-sea chimneys at different stages of activity

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Deep-sea hydrothermal vents (DSHV) are inhabited by diverse microbial communities which are strongly influenced by the complex interplay between physical and chemical features of hydrothermal fluids over the lifetime of the vent. However, due to difficulties in sampling and methodological limitations, mechanisms and factors driving the change in the structure and functioning of microbial communities during the lifecycle of black-smoker chimneys largely remain elusive. Here, we performed comparative metagenomic analysis to decipher the differences in microbial composition and metabolic potential of microbial communities inhabiting two black-smoker chimneys located on the East Pacific Rise at 9°N at distinct states of activity: a still active chimney at L vent and a chimney at M vent that stopped emanating high temperature fluids following a volcanic eruption in 2006. Taxonomic profiles reflected that presumptive chemoautotrophic Epsilonproteobacteria and Aquificae were the abundant community members in the L vent chimney, while the microbial community of the M vent chimney was dominated by a more diverse assemblage of Gamma-, Alpha- and Deltaproteobacteria, Nitrospirae and Bacteroidetes. Furthermore, communities in the two chimneys further exhibited distinct metabolic pathways and differed in their potential for carbon, nitrogen and sulfur metabolism. Our data clearly demonstrate a pronounced shift in the structure and metabolic functioning of microbial communities occurring at different stages in the lifespan of hydrothermal chimneys, helping to further understand the succession of DSHV microbial communities and their roles in biogeochemical cycling.