



Comparative metagenomics of microbial communities inhabiting different hydrothermal chimneys

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Deep-sea hydrothermal vent chimneys harbor a high diversity of largely unknown microorganisms. Comparative genomic analyses of metagenomes from different hydrothermal vent chimneys including sulfide chimneys from Juan de Fuca, Guaymas Basin, and a carbonate chimney from Lost City, were conducted to reveal the common and specific adaptation mechanisms of the chimney microorganisms to the deep-sea vent environments. Genes for mismatch repair and homologous recombination were found enriched in all the samples, suggesting that the microbial communities have evolved extensive DNA repair systems to cope with the extreme conditions that have potential deleterious effects on the genomes. The major metabolic pathways in the chimney samples were also revealed and compared, sulfur metabolizing pathways were found enriched in the sulfide chimneys, consistent with the environmental conditions. Furthermore, a metatranscriptome of the microbial community from a chimney sample from Guaymas Basin was determined and analyzed, this is the first transcription analysis of a chimney microbial community.