



Comparative metagenomics of microbial communities inhabiting different hydrothermal chimneys

Xiang Xiao (1), Jinqun Chen (1), Wei Xie (2), Anna-Louise Reysenbach (3), Stefan M Sievert (4), AnLong Xu (2), and Fengping Wang (1)

(1) School of Life Sciences and Biotechnology, State Key Laboratory of Ocean Engineering, Shanghai Jiaotong University, Shanghai, PR China (xoxiang@sjtu.edu.cn), (2) College of Life Sciences, Sun Yat-Sen (Zhongshan) University, Guangzhou, P.R.China, (3) Department of Biology, Portland State University, Portland, Oregon 97201, USA, (4) Biology Department, Woods Hole Oceanographic Institution, Woods Hole, Massachusetts, MA 02543, USA

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 Fuan 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.