Microbial dynamics in deep-sea hydrothermal plumes of the ultra-slow spreading Gakkel Ridge

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Hydrothermal plumes provide a diverse range of energy and nutrient sources for deep-sea microorganisms, depending on the fluid source and geological setting. Here we studied the dynamics of microbial communities associated with the deep plumes (2900-3300 m and 2500-2900 m) of the *Aurora* and *Langseth* vents (Gakkel Ridge, Central Arctic Ocean). Communities of both plumes showed 80-fold higher carbon fixation rates compared to the deep-water background, and 3-fold higher cell numbers. Both plumes contained substantial amounts of methane and hydrogen (1:1 ratio), but 10 times higher at Langseth than at Aurora. Incubation experiments showed that only hydrogen was consumed by the plume communities, but not methane. Amplicon sequencing of the 16S rRNA genes of plume communities showed high abundances of Epsilon- (i.e. *Sulfurimonas*) and Gammaproteobacteria (i.e. SUP05). Metagenome and -transcriptome sequencing support the dominance of hydrogenotrophic life style (i.e. high expression of [NiFe]-hydrogenases) and sulfur oxidation activity (via *sox* pathway) at Auroea vent. Genes for methanotrophy were not differentially expressed in the plumes. Our data indicate that the Gakkel Ridge vent communities are mostly driven by hydrogen emissions, and that methane is not consumed at the surrounding deep water temperatures of −0.9°C.