Neutrophilic, Fe(II)-oxidizing organism isolated from 1.4 km-depth in Cu/Zn Mine, Canada

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The existence of a diverse biosphere in the deep terrestrial subsurface has long been established. Recent investigations have expanded our understanding of the microbial ecology, the feedbacks between geochemistry and microbial metabolism, and energtics/diversity/adaptation of microbial metabolisms [1, 2]. Environments that were considered void of life (extreme physical conditions, lack of photosynthetically derived substrates) have been shown to contain diverse communties with unique and sustainable metabolisms [3].

Here we investigated a unique biofilm community located at 1.4 km depth, in the Triple 7 Cu/Zn mine (Flin Flon, Canada). We studied this community (including borehole fluids and the associated Fe-precipitate and biofilm) using molecular and cultivation techniques. The groundwater geochemistry is oxic, circumneutral, saline (4.7%) and metal rich. 16S gene sequencing identified two organisms, similar to *Flexibacter tractuosus* and *Marinobacter* spp. (typically marine organisms) present in the borehole fluids; while only *Marinobacter* spp. was detected in the biofilm. Isolates of the neutrophilic, halophilic *Marinobacter* spp. were obtained, and it was demonstrated to be capable of organotrophic growth (anaerobically and aerobically) and lithotrophic growth on Fe (II) with O_2 in gradient tubes [4].

To examine the biogeochemical Fe- and trace metal-cycling in this deep subsurface setting, incubation experiments were carried out with the Fe (II)-oxidizing *Marinobacter* isolate and pyritic (non-metal) and mineralized (metal-containing ore) material in batch and column flow-through settings. The activity of the *Marinobacter* isolate resulted in an increase in the mobilization of Fe, S and trace metals (Cu, Zn) from all materials. These results indicate that microbial activity in the subsurface affects the mobilization of Fe and trace elements, and that Fe (II)-oxidation may be an important biogeochemical process in the deep subsurface.

[1] MacLean *et al*. (2007) *Geomicrobiol J* **24**, 491–504. [2] Sahl *et al*. (2008) *Appl. Environ. Microbiol*. **74**, 143–152. [3] Lin *et al*. (2006) *Science* **314**, 479–482. [4] Emerson & Moyer (1997) *Appl. Environ. Microbiol*. **63**, 4784–4792.

Metatranscriptomic insights into the geomicrobiology of deep-sea hydrothermal plumes

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Geomicrobiological processes within deep-sea hydrothermal plumes mediate the fate of hydrothermal inputs in the oceans, but little is known about the microorganisms underpinning these reactions. Recent results from Guaymas Basin (GB) show enhanced microbially-mediated Mn (II) oxidation rates in plumes [1], but microbial diversity that is indistinguishable from surrounding ambient seawater [2]. Enhanced microbial activity in the plumes is also reflected by RNA concentrations that are ~four times higher than background.

Here we report metagenomic and metatranscriptomic analyses of microbial communities in GB plumes versus background deep-sea waters. Of ~3 million 454 Titanium pyrosequencing metatranscriptomics reads, 85% were rRNAs, providing deep views into the relative activity of specific taxa. Analysis of 16S rRNA gene transcripts at coarse phylogenetic levels revealed no major differences between plume and background. In constrast, large differences in protein-coding genes were observed, including overexpression in the plume of genes for sulfur oxidation, electron transport proteins, and a multicopper oxidase potentially involved in Mn (II) oxidation. Transcripts of genes for ammonium uptake and ammonia oxidation were prevalent in both plume and background.

Assembly of ~2 million metagenomic sequence reads produced near-complete genomes of dominant populations including SUP05-like Gammaproteobacteria, Crenarchaeota, and SAR324 Deltaproteobacteria. Comparative genomic analyses are underway to assess the metabolic potential of these plume poppulations relative to genomes retrieved from other marine environments.

Overall, our results suggest that microorganisms active in GB hydrothermal plumes are indigenous to the ambient deep sea. Shifts in their physiological state, manifested by shifts in gene expression, appear to underpin enhanced geomicrobiological activity observed in deep-sea hydrothermal plumes.

[1] Dick *et al*. (2009) *GCA* **73**, 6517–6530. [2] Dick *et al*. (in press) *Environ. Microbiol*.