

Distribution and Diversity of Microorganisms of Deep, Subpermafrost Brine in the Canadian Arctic

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Saline fracture water (0.3 to 3.7 % TDS) trapped beneath 500 meters of frozen Archean metasediment was collected from boreholes at 880 and 1130 meters depth at Lupin Au mine. Temperatures range from 4 to 10°C, pH from 8 to 9, Eh from -150 to -190 mV. H₂ and CH₄ gas concentration range from 20 to 600 nM and 6 to 55 mM, respectively. The cell density ranged from 400 to 10⁵ cells ml⁻¹ by direct count. Significant hydrogenase activity was detected only in the borehole containing the highest cell density and lowest salinity. This activity was associated with relatively low H₂ and high CO concentrations. The microbial diversity of fracture water yielding the lowest concentration of CH₄ and the greatest ³⁴S fractionation between sulfate and sulfide (10⁰/‰) was characterized using the 16S rDNA gene. The cDNA revealed a predominance of a species that was 95-97% similar to *Thiohalobaccili* and the presence of a species that was 96% similar to *Desulfosporosinus*. No archaeal PCR product was detected. The molecular, geochemical and isotopic data suggest cycling of S is occurring under suboxic conditions beneath the permafrost. The concentrations suggest that this environment has been isolated from the surface for a geologically significant time interval. The persistence of suboxic conditions in this sequestered ecosystem is either caused by a lack of electron donors relative to electron acceptors or mixing with surficial lake water through nearby taliks.