

Inferred Bioenergetics of an Uncultured Bacterium Common in Fracture Fluids of South African Deep Mines

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A deep-branching clade of nearly identical *Desulfotomaculum*-like 16S rDNA sequences (>99% homology) has been identified in 6 boreholes in 4 mining complexes separated by as much as several hundred km, including artesian boreholes sampled quickly after intersection with mining and containing water ages on the order of millions of years. The *Desulfotomaculum*-like organism (DLO) was the dominant bacterium (>90-100% of clones) present in libraries from very high quality sample sets in two different mines, and their dominance was retained throughout a several month time series in one case, and a 648-meter vertical depth profile in the other case. Sulfate reduction is inferred to be the dominant terminal electron accepting process in these sample sets based on geochemical

and isotopic data and thermodynamic calculations. The closest cultured relative is *Desulfotomaculum kuznetsovii* (90% similarity) and the closest sequence in Genbank is an environmental clone recently recovered from oceanic crustal fluid (95% similarity).

DNA from samples apparently dominated by the DLO has been hybridized to comprehensive 16S microarrays in an effort to confirm its dominance and to further infer, via phylogeny-physiology relationships, how the DLO may interact with other organisms in the community. To gain a better understanding of the degree of genetic novelty of the DLO and to determine the degree of heterogeneity in the population, we have filtered large quantities of fissure water from a sample dominated by the DLO in order to provide adequate biomass for community DNA sequencing. We hope to be able to assemble a large fraction of the 'archetypical' genome from this organism, analyze genome content and structure relative to other sequenced microbes to evaluate the novelty of the genome, and deduce the energy-generating pathways and lifestyles the bacterium is capable of and relate this to the biogeochemistry of the South African mine environments. Owing to the geologic and hydrologic isolation of these particular deep environments, the genome sequence may also provide insights into the evolutionary history of genome structure.