

MOLECULAR SURVEY AND BIOPROSPECTING OF THE MICROBIAL COMMUNITIES IN HOMESTAKE DUSEL

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ABSTRACT

In accordance with the current activities of developing the former Homestake mine as a Deep Underground Science and Engineering Laboratory (DUSEL), we focused on identification of microbial community structures and metabolic diversity using culture-independent and culture-dependent methods. Molecular characterization of microbial communities in DUSEL water and weathered soil-like samples was carried out by 16S rDNA sequence analysis. Geochemical analyses indicated that both samples were high in sulfur, rich in nitrogen and salt, but with significantly different metal concentrations, high in the soil and low in the water. 16S rDNA sequence analysis showed that phylogenetic diversity of archaeal communities was low and novel, whereas that of bacterial communities was high. In particular, bacteria operational taxonomic units (OTUs) containing the highest percentage of sequences classified to the same order as sulfur oxidizing soil bacteria such as *Thiobacillus plumbophilus* and *Thiohalomonas nitratreducens*. Community members of bacteria from individual Homestake ecosystems were heterogeneous and distinctive to each community with several unique phylotypes identified from the water sample. As part of bioprospecting for novel extremophiles, we identified thermophilic *Geobacillus* strains isolated from weathered soil-like samples to produce high levels of cellulases and hemicellulases. These findings offer critical information on the microbial community compositions of the drifts and water from upper layers of the mine, the deeper part of which is currently submerged. Archiving this information is critical as the current dewatering program proceeds and the ecological conditions in the mine continue to change, thus affecting subsequent changes in the microbial diversity.