

EUKARYOTIC MICROBIAL DIVERSITY WITHIN BIOFILM AND SEEP-WATER SAMPLES ISOLATED FROM THE FORMER HOMESTAKE GOLD MINE, LEAD, SOUTH DAKOTA

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ABSTRACT

A metagenomic approach was used to obtain an early assessment of the eukaryotic diversity in biofilm and water samples taken from the former Homestake mine during initial re-entry activities in preparation for its conversion to a Deep Underground Science and Engineering Laboratory (DUSEL). The samples consisted of a biofilm scraping taken from a depth of 610-meters at the Ross Shaft, and DNA extracted from water taken from a seep running from ~200 to 914 meters along the mineshaft. The ITS1-5.8S-ITS2 region of the rDNA locus was amplified, cloned and sequenced. The resulting sequence data were screened for chimeras, and aligned to existing sequences in GenBank in order to identify the taxa within the samples. We identified unique sequences, classifying to either Protista or Fungi, with a low percent identity to previously sequenced taxa, with some exhibiting low similarity even at the taxonomic level of Division. Not surprisingly, a number of the sequences classify to Fungi or Protista commonly found in terrestrial ecosystems and waters. This is likely the result of introduction of microbes to the subsurface during mining operations. Further analysis of deeper, pristine regions of the DUSEL will provide new knowledge of the diversity of the eukaryotic microorganisms capable of surviving in the deep subsurface. Likewise, further metagenomic research into the eukaryotic diversity of the DUSEL will lead to an understanding of how introduced surface-dwelling microbes evolve to adapt to life in the subsurface, and how their introduction affects endemic subsurface microbial populations.