

Molecular phylogenetic analysis of a bacterial community in Sulphur River, Parker Cave, Kentucky

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ABSTRACT

Sulphur River in Parker Cave, Kentucky receives sulfurous water (11–21 mg sulfide/L) from the Phantom Waterfall and contains a microbial mat composed of white filaments. We extend a previous morphological survey with a molecular phylogenetic analysis of the bacteria of the microbial mat. This approach employs DNA sequence comparisons of small subunit ribosomal RNA (SSU rRNA) genes obtained from the mat with those from an extensive database of rRNA sequences. Many of SSU rRNA gene clones obtained from the mat are most similar to rRNA sequences from sulfur-oxidizing bacteria (*Thiothrix* spp., *Thiomicrospira denitrificans*, and “*Candidatus Thiobacillus baregensis*”). The Sulphur River SSU rRNA gene clones also show specific affiliations with clones from environmental surveys of bacteria from deep-sea hydrothermal vent communities and subsurface microcosms. Affiliations with sequences from bacteria that are known to have the ability to obtain energy for CO₂ fixation from the oxidation of inorganic compounds (chemoautotrophs), in combination with the environmental conditions surrounding the microbial mat, indicate that chemoautotrophic metabolism of bacteria in this mat may contribute to the biomass of Sulphur River. Cave communities, such as the one identified in Sulphur River, provide sites to study such relatively autonomous chemoautotrophic communities that are much more accessible than similar communities associated with deep-sea hydrothermal vents. Subsurface microbiology and the contribution of microbial activity on cave development are also discussed.