

Lechuguilla Cave, an ancient, deep, oligotrophic subterranean environment, contains an abundance of iron and manganese oxides, called "corrosion residues" that may be formed in part by microbial processes. To assess this possibility and to investigate the structure of the microbial community in these materials, we carried out a culture-independent, small subunit ribosomal RNA (SSU rRNA) sequence-based study. DNA was extracted from samples from two sites approximately 300 m and 228 m below the surface; rRNA genes were amplified by PCR, cloned, and sequenced. To expand our knowledge of possible manganese- and iron-oxidizing bacteria, additional rRNA gene studies were carried out on manganese and iron enrichment cultures inoculated with corrosion residues. An analysis of the resultant clones revealed that the dominant clone-types in one site originated from mesophilic Archaea in both the Crenarchaeota and Euryarchaeota. In many cases, similarity values to database sequences were extremely low indicating a lack of known close relatives. The second site was dominated almost entirely by lactobacilli. Other clone sequences were most closely related to those of nitrite-oxidizing bacteria, nitrogen-fixing bacteria, actinomycetes,  $\gamma$ -Proteobacteria, and iron- and manganese-oxidizing bacteria. Sequence analysis of enrichment culture clones showed the presence of putative iron- and manganese-oxidizing bacteria, further supporting the presence of these microbes in corrosion residues. Evidence from enrichment cultures and community DNA provides support for our hypothesis that microorganisms may contribute to the dissolution of limestone walls and the formation of manganese and iron oxide-rich materials, and a rich and diverse microbial community in these unusual secondary mineral formations was revealed.