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Development, Structure, and Diversity of Microbial Lotic Calcareous Mat Communities

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ABSTRACT

The phylogenetic diversity of microbial communities in calcareous mats from Spearfish Creek, a freshwater stream located in the Black Hills of South Dakota, was examined using PCR-based 16S rDNA sequence analysis. In this study, two types of calcareous mats were compared: mature mats formed on the natural substrate of rock surfaces and developing mats on an artificial substrate of glass slides. Among 63 unique isolates from a clone library of 16S rRNA genes from mature mat samples, there were 8 phyla of *Bacteria* represented. The predominant phylum was *Proteobacteria* (48%), with the β subclass being the largest group. Denaturing gradient gel electrophoresis (DGGE) analysis of 16S rRNA genes from slide samples collected at intervals for four months showed considerable diversity of the microbial community from the earliest stages of community development. Amplicons isolated from DGGE gels and sequenced indicated that community succession has occurred without increasing microbial diversity. However, light microscopic analysis revealed a significant increase in microbial cell density throughout the community development. Scanning electron microscopy of mat samples provides evidence that diatoms are also important members of calcareous mat communities.