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Partitioning of Bacterial Communities in Hot Spring Travertine Depositional Facies

Bacterial communities are strongly partitioned among the travertine depositional facies that comprise the surface drainage system of Spring AT-1 at Angel Terrace, Mammoth Hot Springs, Yellowstone National Park. Polymerase chain reaction (PCR) amplification and sequencing of bacterial 16S rRNA genes (rDNA) using universal bacterial primers was completed on travertine, microbial mat, and spring water samples collected from each facies. 657 gene sequences were identified that are affiliated with 221 unique rDNA types and 21 bacterial divisions. 88% of the gene sequences and 77% of the affiliated rDNA types occurred in only one of the five travertine depositional facies. This indicates that little down stream transport of bacterial cells takes place despite the rapid flow of spring water across the Spring AT-1 system. These results suggest that: (1) bacterial communities are sensitive biological indicators of environmental physical and chemical conditions; and (2) travertine morphology and chemistry, when evaluated within a rigorous depositional facies context, may provide a sensitive indicator of the composition and diversity of bacterial communities present during precipitation.