

# Composition and structure of microbial communities from stromatolites of Hamelin Pool in Shark Bay, Western Australia

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Stromatolites - organosedimentary structures formed by microbial activity - are found throughout the geological record and are important markers of biological history. More conspicuous in the past, stromatolites occur today in a few shallow marine environments, including Hamelin Pool in Shark Bay, Western Australia. The Hamelin Pool stromatolites have often been considered contemporary analogs to ancient stromatolites, yet little is known about the microbial communities that build them. We used DNA-based molecular phylogenetic methods that do not require cultivation to study the microbial diversity of an irregular stromatolite and of the surface and interior of a domal stromatolite. To identify the constituents of the stromatolite communities, small subunit ribosomal RNA genes were amplified by PCR from community genomic DNA with universal primers, cloned, sequenced and compared to known rRNA genes. The communities were highly diverse and novel. Average sequence identity of Hamelin Pool sequences compared to the >200,000 known rRNA sequences was only ~92%. Clone libraries were ~90% bacterial, ~10% archaeal and eucaryotic rRNA genes were not detected in the libraries. The most abundant sequences were representative of novel proteobacteria (~28%), planctomycetes (~17%) and actinobacteria (~14%). Sequences representative of cyanobacteria, long considered to dominate these communities, comprised <5% of clones. Approximately 10% of the sequences were most closely related to those of  $\alpha$ -proteobacterial anoxygenic phototrophs. These results provide a framework for understanding the kinds of organisms that build contemporary stromatolites, their ecology and their relevance to stromatolites preserved in the geological record.