

## Assessment of the Prokaryotic Diversity Associated with Selected Caribbean Corals

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Coral reefs are among the most productive and speciose ecosystems on the planet, supporting one quarter of all marine species. Unfortunately, these systems are being degraded on a global scale due to infectious disease, anthropogenic disturbance, and climate change. Microorganisms account for most of the biodiversity in coral reefs, yet most remain unidentified. Corals naturally form associations with assemblages of microorganisms, and these assemblages are thought to play vital roles in coral ecology as symbionts or as pathogens; however, the biodiversity within these communities and the potential changes in microbe/coral interactions, particularly with respect to the global degradation of coral ecosystems, are poorly understood. Our current research is a survey of the diversity of microalgae, archaea, and bacteria associated with three species of Caribbean corals: *Montastrea faveolata*, *Acropora palmata*, and *Pseudopterogorgia americana*. This work incorporates culture-based isolation and culture-independent molecular techniques to evaluate and compare the diversity and composition of microbial assemblages associated with the surface mucopolysaccharide layer (SML) and tissues of these corals. Moreover, we are assessing the potential differences in microbial communities between healthy coral colonies and colonies that are compromised by disease or bleaching. The work presented here focuses on determining the community structure and biodiversity of the bacteria present in the SML and tissues of *M. faveolata* using denaturing gradient gel electrophoresis and cloning/sequencing of 16S rDNA genes. Additionally, we are beginning construction of metagenomic libraries that will enable us to simultaneously examine the metabolic capabilities and phylogenetics of coral-associated microbial assemblages. We are particularly interested in comparing the bacterial communities among healthy and diseased colonies of *M. faveolata* to elucidate potential changes in bacterial communities that are related to the declining health of the host organism.

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