

Influence of Coral Health on Composition and Structure of Bacterial Communities Associated with the Surface Mucopolysaccharide Layer and Tissues of *Montastrea Faveolata*.

Wesley Johnson^{1,2}, Reney A. Henderson³, Garriet W. Smith⁴, Ernesto Weil⁵, Karen E. Nelson⁶, and Pamela J. Morris^{1,2,6,7}

¹*Marine Biomedicine and Environmental Sciences Center, Medical University of South Carolina, Charleston, SC*

²*Hollings Marine Laboratory, Charleston, SC*

³*Department of Biology, Howard University, Washington, D.C.*

⁴*The J. Craig Venter Institute, Rockville, MD*

⁵*University of South Carolina Aiken, Aiken, SC*

⁶*Department of Cell Biology and Anatomy, Medical University of South Carolina, Charleston, SC*

⁷*Center for Coastal Environmental Health and Biomolecular Research, NOAA National Ocean Service, Charleston, SC*

Corals naturally form associations with complex assemblages of microorganisms that are thought to play vital roles in coral ecology. However, the composition of these communities and potential structural changes related to disease are poorly understood. Our objectives in this work were to 1) assess the composition of the bacterial communities associated with the coral, *Montastrea faveolata*, 2) Compare the communities of healthy and diseased colonies of *M. faveolata*, and 3) Compare the assemblages from the surface mucopolysaccharide layer (SML) to those of the coral tissues. Samples were collected from La Parguera, Puerto Rico in March 2006. SML from three healthy and three diseased colonies was collected by aspirating with a syringe. Tissues from the same colonies were collected by chiseling a small fragment from each colony. Community DNA was isolated and clone libraries of the 16S rDNA genes were constructed and sequenced. Comparisons of community structure were also performed using denaturing gradient gel electrophoresis (DGGE). Results from clone libraries showed tissues to be dominated by sphingobacteria, while SML communities were composed mostly of α -proteobacteria. Diseased tissues had fewer *Clostridium* sequences than did healthy tissues. SML samples also showed differences between healthy and diseased colonies, with healthy colonies containing numerous sequences of *Lactococcus lactis*, which is completely absent from diseased samples. DGGE showed differences between SML communities of healthy and diseased colonies that were not observed between healthy and diseased tissues. These data indicate shifts in the structure of *M. faveolata* bacterial assemblages related to host health. Furthermore, these results indicate that SML communities may be less stable than those associated with tissues, and that the occurrence of disease is linked to a shift from a stable, low-diversity community to a species-rich assemblage of opportunists.

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