

THE FUNCTIONAL POTENTIAL OF CORAL-ASSOCIATED MICROBIAL COMMUNITIES IN *MONTASTREA FAVEOLATA* FROM LA PARGUERA, PUERTO RICO

Nikole E. Kimes^{1,2}, Joy D. Van Nostrand³, Jizhong Z. Zhou³, Ernesto Weil⁴ and Pamela J. Morris^{1,2,5,6}

¹Marine Biomedicine and Environmental Sciences Center, Hollings Marine Laboratory, Charleston, SC

²Medical University of South Carolina, College of Graduate Studies, Charleston, SC

³Department of Botany and Microbiology, University of Oklahoma, Norman, OK

⁴Department of Marine Sciences, University of Puerto Rico, Mayaguez, PR

⁵Center for Coastal Environmental Health and Biomolecular Research, NOAA National Ocean Service, Charleston, SC

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

Coral-associated microbial communities are increasingly recognized as important components of the coral holobiont that influence coral health and disease. Energy and nutrient cycling is one of the more common mechanisms suggested for their contributions. Few studies, however, directly address the functional role of these communities. In the present study, we examine the functional potential of the coral-associated microbial community found in the surface mucopolysaccharide layer (SML) and tissue of a common Caribbean coral, *Monastrea faveolata*. The samples were collected from both visually healthy and yellow band infected colonies in March of 2007 off the coast of La Parguera, Puerto Rico. DNA was extracted and amplified for use in a functional gene array, the GeoChip II, which targets 10,000 functional genes involved in biogeochemical processes. We identified over 6500 functional genes present in the microbial communities associated with *M. faveolata*. Our preliminary analysis reveals a consistency across all of the samples in the relative percentage of genes found in each biogeochemical process surveyed. These processes include carbon degradation/fixation (16.5%, +/- 1.04), dissimilatory sulfite reduction (7.2%, +/- 0.73), metal homeostasis (21.15%, +/- 1.33), methane generation and oxidation (3.45%, +/- 0.37), nitrogen processing (17.57%, +/- 0.97), and organic chemical degradation (31.75%, +/- 1.16). Interestingly, however, comparisons of the specific genes identified within a given functional category display less than 50% overlap between healthy and diseased samples. Our data suggests that the microbial communities associated with healthy and diseased *M. faveolata* use different mechanisms to fulfill similar functional niches.

This research is supported by a National Science Foundation Graduate Research Fellowship to NEK and a NSF Biodiversity Surveys and Inventories grant (DEB0516347) to PJM.