

The Microbial Functional Structure associated with Healthy and Yellow Band Diseased *Montastraea faveolata*, a Caribbean Reef-building Coral

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Microbial communities are ubiquitous across ecosystems and often live symbiotically within eukaryotic organisms. For example, the human gut houses an abundant and diverse population of microorganisms essential for digestion and metabolism. Moreover, variations in the human gut microbiome are thought to play a role in human health by influencing disease etiology. Likewise, coral-associated microbial communities are increasingly recognized as important components of the coral holobiont that influence coral health; however, few studies directly address the functional role of these communities. We hypothesize that variation between the phylogenetic structure of coral-associated microbial communities found in healthy and diseased corals result in a shift of functional potential associated with the microbiome. In our study, we examined the functional potential of the coral-associated microbial community found in the surface mucopolysaccharide layer (SML) and tissue of a Caribbean coral, *Montastraea faveolata*. The samples were collected from healthy and yellow band diseased (YBD) colonies off the coast of La Parguera, Puerto Rico. The GeoChip 2.0, a functional gene array, was used to investigate the presence of over 10,000 biogeochemical cycling genes. We detected 6728 genes present in the microbial communities associated with *M. faveolata*. The relative percentages of genes found in each biogeochemical process surveyed are as follows: carbon cycling (19%), sulfur cycling (7.5%), nitrogen cycling (21.5%), metal homeostasis (19%), and xenobiotic degradation (33%). Our analysis revealed a significant difference in functional structure of healthy and YBD *M. faveolata* colonies. Furthermore, those differences were specific to the physical niche examined. This study is the first broad screening of functional genes in coral-associated microbial communities and provides insights regarding their biogeochemical cycling capacity in healthy and diseased states.

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