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Title: A Comparative Analysis Of Bacterial Communities Associated With Apparently Healthy And Diseased Corals Inhabiting The Wider Caribbean Region

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ABSTRACT

Although diseases of hermatypic corals, some of proven or suspected bacterial origin, pose a serious global threat to coral reefs, the composition of bacterial communities on healthy corals and those exhibiting signs of disease remains poorly understood. This investigation compared bacterial communities associated with multiple pairs of apparently healthy and diseased *Montastraea annularis* (species complex) colonies from offshore reefs in The Bahamas, U.S. Virgin Islands, Cayman Islands, Bermuda, the Florida Keys National Marine Sanctuary, and the Flower Garden Banks National Marine Sanctuary. Bacterial communities from apparently healthy colonies and nearby colonies exhibiting signs consistent with white plague type II (WP2) were evaluated using both molecular and culture-dependent methods. Length heterogeneity PCR (LH-PCR) molecular fingerprints and multitag pyrosequencing (MTPS) were used to characterize the diversity and relative abundance of both whole and culturable communities.

A comparison of the whole-bacterial community molecular fingerprint, regardless of tissue type, with amplicons derived from the cultured community suggests that more than 1% of coral tissue-associated bacterial taxa can be cultured and that these also represent the most abundant bacteria. Bacterial communities associated with diseased corals, regardless of geographical location, were more similar to each other than to communities associated with apparently healthy tissues. No significant difference was detected in the composition of bacterial communities associated with samples of apparently healthy tissue and healthy tissue from colonies exhibiting signs of disease. MTPS corroborated the patterns discerned by LH-PCR. Numerous bacterial families were common to all tissue types and represented the most abundant taxa. Shifts in the relative abundances of bacterial taxa account for the significant differences in community composition between WP2-diseased and apparently healthy coral

tissues. The dominant bacterial family associated with diseased tissue was the *Rhodobacteraceae*, with *Roseovarius*, *Silicibacter*, and *Thallosobius* being the most abundant genera. Examination of the microscopic anatomy in diseased tissues revealed a complete loss of normal architecture and large proportions of associated rod-shaped bacterial cells. The 16S rRNA gene sequence of *Aurantimonas coralicida* was not found in any samples.