

Comparative analysis of microbiota associated with healthy and diseased acroporid corals

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Acropora spp. corals have suffered region-wide declines throughout the Caribbean during the past two decades, prompting their recent designation as ‘threatened’ under the U.S. Endangered Species Act. A diverse microbiota is associated with the surface mucus layer of these corals and is thought to participate in health and disease processes. Previous examinations of these microbial communities have yielded conflicting results. This study used multiple approaches to ascertain whether a predictable microbial assemblage is associated with healthy and/or diseased corals. Replicate samples were collected from healthy and diseased acroporid colonies at six sites in the Florida Keys and Dry Tortugas during a mortality event in 2003. Three different sample processing methods were used in parallel during sample collection. Individual 16S rRNA gene libraries were generated from each sample (~20,000 usable clone sequences from 69 libraries). In addition, over 600 bacterial isolates were identified from these samples and each sample was directly screened by PCR for known coral pathogens. Our results indicate that sampling methodology introduces significant variability into the microbial community composition detected, perhaps explaining the conflicting results in earlier studies. Analysis of healthy coral mucus revealed consistent microbial composition between samples, with only nominal differences introduced by geographic locale and species. Members of the families Pseudomonadaceae and Xanthomonadaceae were consistently present in healthy corals. Diseased samples from the northern Florida Keys had unique microbial profiles, including increased prevalence of Vibrionaceae and Flavobacteriaceae, when compared to healthy corals. Diseased corals from the southern sampling sites were not significantly different from reference corals. This concurs with the histopathology that indicated disease signs were distinct from those of corals at the northern sites, thus suggesting two different disease pathologies occurred during this outbreak event.

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