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Microbial community variation of black band disease on scleractinian corals in different regions of Taiwan

Black band disease (BBD) is a widespread coral disease affecting mainly massive reef-building corals. Another type of coral disease known as red band disease (RBD) closely resembles BBD but is reddish brown in colour. Filamentous cyanobacteria are associated with both diseases. Both diseases are characterized by a darkly pigmented microbial mat that migrates across live coral tissue causing tissue necrosis. Confusion arises as some researchers considered RBD as a separate disease category while others classified it as a variant of BBD. Characterization of microbial communities using culture-independent techniques can provide rapid assessment on the differences in microbes associated with these diseases. In Taiwan waters, 3 different types of BBD (including RBD) were recorded based on morphological observation. Here we characterize the microbial communities associated with these coral diseases using universal bacterial 16S rRNA primer as well as cyanobacterium-specific 16S rRNA gene primer. Sequence analysis of these 16S rRNA genes revealed distinct microbial variation among the different morphologies BBD. Cyanobacteria sequences derived from BBD and RBD bacterial mats were closely affiliated with those from the Great Barrier Reef and Red Sea, respectively. The composition of bacterial 16S rRNA gene clone libraries derived from BBD formed clusters with sequence of alpha-proteobacteria isolated from BBD corals in the Caribbean. However, those from RBD were related to sequences previously retrieved from corals infected with white-plague disease in the Caribbean. Our findings revealed that these different morphological BBD are more complex than previously thought and they should be considered as separate polymicrobial diseases.