

THE CYANOBACTERIAL PROFILE OF DISEASED CORAL, *MILLEPORA ALCICORNIS*, FROM SOUTH ATLANTIC OCEAN

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Abstract

Coral reefs are at risk due to events associated with human activities, which have resulted in the increasing occurrence of coral diseases. Corals live in symbiotic relationships with different microorganisms, such as Cyanobacteria, a very important, but still a poorly studied group. Members of the Cyanobacteria phylum are found in great abundance in the marine environment and may play an essential role in keeping corals healthy as well as in pathogenic activity. Furthermore, some studies are showing a rise in cyanobacteria abundance in coral reefs as a result of climate change. The current study aimed to foster our understanding of the relationship among cyanobacteria and coral's health. For this purpose, three samples (1 cm in size) were collected from a sick colony of *Millepora alcicornis*. The following coral regions were sampled: a healthy region, a sick region and a post-sickness skeleton. The samples were collected approximately 3.7 km offshore and 2 - 3 m water depth in Recife de Fora, Bahia, Brazil. The pieces of coral were stored at -80 °C until analysis and DNA extraction was performed using the ZR Soil Microbe DNA Kit (Zymo Research, USA). The PCR for the cyanobacterial, bacterial and micro-eukaryotic communities were performed using specific primers for each population and the DGGE gels were prepared. The gel fragments containing the bands were removed and the DNA was purified. The DGGE bands intensity was measured using BioNumerics software (Applied Maths, Ghent, Belgium) and the sample clustering was performed. DNA sequences from the excised bands were trimmed and selected for high quality sequences at the Ribosomal Data Project Pipeline. A quality of >20 using the Phred/Phrap software was selected to constitute the final data sets. Sequences were realigned and manually edited using the ClustalW aligner from the MEGA 4.0 program (Tamura et al. 2007). Phylogenetic trees were constructed and the sequences generated by DGGE band excision were deposited in the GenBank. Our results revealed that the cyanobacterial genus GPI (Anabaena) is a possible opportunistic pathogen of the coral species *M. alcicornis* from the South Atlantic Ocean. Furthermore, the bacterial and micro-eukaryotic profile of healthy, sick and in post-sickness regions of diseased coral, indicated that different microorganisms could be involved in this pathogenicity or taking advantage of the diseased state.

Palavras-chaves: Cyanobacteria, coral reef, *Millepora alcicornis*, coral pathogens, Anabaena, DGGE

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