

TITLE: DIVERSITY OF BACTERIA ASSOCIATED TO A SOFT CORAL COLLECTED AT TWO DIFFERENT SITES OF ALAGOAS - BRAZIL

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ABSTRACT:

The genetic and metabolic microbial diversity still unexplored is found in coral reefs, where hosts provide a source of food and specific niches for various microorganisms. The species *Palythoa caribaeorum* is a zooxantellated zoanthid considered as a key species in the Brazilian Northeast reefs, generally dominant where it occurs mainly due to several physiological characteristics. Our work aimed at describing the taxonomic inventory of bacteria associated with *P. caribaeorum* coral through the partial pyrosequencing of the 16S rDNA gene. The collections were carried out in March of 2015, in two places: coral reef of Ponta Verde beach and sandstone reef of Sereia beach, both in Maceió - AL. Fragments from six different healthy colonies of *P. caribaeorum* had their total genomic DNA extracted and sequenced using a platform 454. The sequences obtained were analyzed according to the protocol proposed by the Brazilian Microbiome Project. Were obtained 26,166 sequences, reduced to 8,988 after the quality control, generating 459 OTU's with 97% of identity. Both points presented a large number of microorganisms classified as "non-cultivated", reflecting a vast biotechnological potential that is to be exploited in this environment. In total, were found 21 phyla, of which 10 occurred exclusively in the reef of the Sereia and only one in Ponta Verde. Unifrac results shows a greater similarity among the samples collected at the Sereia reef. Curiously, individuals collected in Ponta Verde had about 25% of the sequences classified as genera associated with human pathogens, such as *Streptococcus*, *Staphylococcus* and *Propionibacterium*. When compared to the Sereia reef, these individuals also presented a markedly lower percentage of groups related to important ecological functions, such as photosynthesis (Chlorobi, Chloroflex and Cyanobacteria) and nitrogen fixation (Nitrospira, Rhizobiales and Rhodobium, for example), besides a high representativeness of members of Firmicutes (12.4%), common at human gut and related to the degradation of organic matter. These changes usually occur in response to environmental disturbances and in response the microbiota changes from benign and/or benign to stress-resistant, potentially pathogenic and opportunistic. We conclude that the species *P. caribaeorum* hosts a rich and diverse associated microbial community, variable between the two collection sites, and that can constitute an alternative for biotechnological prospecting.

Keywords: Pyrosequencing; zoanthid; coral holobiont.

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