

TITLE: VARIATION IN THE MICROBIAL COMMUNITY ALONG THE COURSE OF TWO RIVERS LOCATED IN THE APA COSTA DOS CORAIS – ALAGOAS

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ABSTRACT:

Locally, the presence of rivers that deplete coral reefs is also a major source of stress of coral reefs since it naturally leads to an introduction of sediment, nutrients and freshwater, and in addition carry a series of microorganisms with diverse distinct origins. In this study, we wanted to verify how the microbial community vary along the course of rivers Manguaba (MB) and Santo Antônio (SA), at the APA Costa dos Corais (Coastal Preserve Environmental Protection Area - APACC). Samples of surface water (200mL) were collected during low tide at six points along the course towards the seawater, located at rivers Santo Antonio and Manguaba: 3 samples along each river and 3 more, separated each other by 500m, in the marine region immediately after the river mouth. After filtration, the genomic DNA was extracted, the gene 16S rDNA was amplified, purified and the obtained product was applied to Phylochip® microarray. We used the software R® and the package Phyloseq® to analyze the data. In total, were detected 17.898 OTU's, classified in 39 phyla, 66 classes, 112 orders, 196 families and 265 genus. The highest number of OTU's belonged to the Proteobacteria (46%), followed by Firmicutes (18%) and Actinobacteria (11%). Besides lower at SA, the OTU richness remained similar along the rivers, but after reach the seawater it started to decrease at MB and increase at SA. The nMDS using presence/absence and relative abundance data showed similar results, with marked differences among bacterial communities related to seawater samples at both sites, while samples from rivers seems to be more similar among them when analyzing the same site. ANOSIM values were higher at SA ($R^2=0,74$) than MB ($R^2=0,18$) when using presence/absence data, while using intensity data this values were more similar ($R^2=0,55$ and $R^2=0,33$, respectively), suggesting that dissimilarities in SA are slightly more influenced by community composition than it's abundance. Core analysis shows a high degree of OTUs overlapping between samples from rivers and seawater collected at same site, composed of 33,6% (n=2467) of OTU's in SA and 37,8% (n=2579) of OTU's in MB. Results indicates that besides each environment host unique groups possibly more adapted to its unique conditions, they are still sharing a high quantity of OTU's, and that community composition was less variable along MB, and reasons of higher dissimilarity at SA should be more carefully studied.

Keywords: Phylochip, bacteria, river, seawater

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