

TITLE: DETERMINATION THE BACTERIA AND ARCHAEA COMMUNITIES AND EVALUATION OF HEAVY METALS INFLUENCE ON ANTIMICROBIALS RESISTANCE PROFILES IN GUANABARA BAY WATERS.

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ABSTRACT:

The Guanabara Bay is the largest bay of the Brazil coast located in the Rio de Janeiro. Although its waters are constantly renewed with sea water, it is the final recipient of several effluents generated in its margins and watersheds of 55 rivers and streams. Despite the importance of preserving the Guanabara Bay, the lack of sanitary structure and the irregular disposal of solid and liquid wastes constitute one of the main problems that affect this ecosystem. In addition, other sources of pollution such as industries, maritime terminals, commercial ports, various shipyards and oil refineries also contribute to the eutrophication of this environment. The objective of this study was to determine the bacteria and archaea communities by the metagenomic approach and evaluation of heavy metals influence on antimicrobials resistance profiles in Guanabara Bay waters. High concentrations of copper and arsenic were detected in all samples using inductively coupled plasma optical emission spectrometry. The microbial diversity was analyzed by the new generation sequencing of the V4 region of 16S rRNA gene and the sequences were analyzed by Qiime software and Silva database. A greater abundance of *Proteobacteria* was revealed in 58% (7/12) of the samples, being most of the sequences belonging to the *Gammaproteobacteria* class. Significant differences were also observed regarding the seasonality of the samples collections. In addition, eight Archaea phylum were revealed predominating *Euryarchaeota* and *Thaumarchaeota* in 75% (9/12) and 45% (3/12) of the samples, respectively. One hundred and thirty heavy metals tolerant bacteria were isolated. After 16S rRNA gene sequencing, 30 bacterial genera were revealed. The *Acinetobacter* spp. (n = 6), *Enterobacter* spp. (n = 12), *Pseudomonas* spp. (n = 17), *Klebsiella* spp. (n = 17) and *Escherichia* spp. (n = 18) were selected as representatives of this study. The antimicrobial susceptibility, by the disc-diffusion method, revealed several resistance profiles against different antimicrobials classes. The strains susceptible to all antimicrobials were again evaluated in media containing metals and revealed the co-resistance mechanism to heavy metals and antimicrobials. Our results contribute to a better understanding the influence of pollutants on the microbial community's behavior of and the co-selection of the microbial resistome.

Keywords: Microbial Diversity; Antimicrobial Resistance; Co-resistance; Heavy metal; Guanabara Bay.

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