

**TITLE:** SPATIAL VARIATION OF BACTERIOPLANKTON ALONG THE INVERSE GRADIENT OF SALINITY IN A SEMIARID ESTUARY, NORTHEASTERN BRAZIL

**AUTHORS:** TAVARES, T.C.L.<sup>1</sup>; BARROSO, H.S.<sup>1</sup>; BEZERRA, W.M.<sup>2</sup>; OLIVEIRA, S. A.<sup>2</sup>; SOARES, M.O.<sup>1</sup>; MELO, V.M.M.<sup>2</sup>

**INSTITUTION:** <sup>1</sup>INSTITUTO DE CIÊNCIAS DO MAR – UFC (LABOMAR-UFC) (AVENIDA ABOLIÇÃO, 3207, CEP 60170-151, FORTALEZA - CE, BRAZIL); <sup>2</sup>LABORATÓRIO DE ECOLOGIA MICROBIANA E BIOTECNOLOGIA (LEMBIOTECH-UFC) (CAMPUS DO PICI, CENTRO DE CIÊNCIAS, AVENIDA HUMBERTO MONTE, 2775, CEP 60440-554, FORTALEZA – CE, BRAZIL)

**ABSTRACT:**

In semiarid estuaries, the salinity gradient observed in classical estuaries is often inverted due to a negative water budget and hypersalinity can be observed, *i.e.* upstream zones can exhibit more elevated salinities than those found near or on the coast. In this study, the spatial distribution of bacterioplankton was evaluated at December 2015, a year of severe drought, in six stations distributed along Piranji river estuary (CE, northeastern Brazil). For analyzing its composition, water samples were subjected to DNA extraction using Power Water kit sequenced on Illumina MiSeq System, and the sequences were analyzed *in silico* using Qiime v. 1.8. Proteobacteria was the most abundant phylum, with abundances of Alphaproteobacteria varying from 20% in the upstream to 30% downstream, and Gammaproteobacteria fluctuating from 10% upstream to 20% near the mouth of the estuary. Dominant Alphaproteobacteria belonged to the family Rhodobacteraceae while dominant Gammaproteobacteria were from the halophilic family Halomonadaceae. Bacteroidetes, represented mainly by Flavobacteriaceae, also showed increase towards the sea, reaching 15% downstream. For its turn, Actinobacteria, present in similar amounts to Bacteroidetes, was more stable along the estuary, being dominated by Actinomycetales and Acidimicrobiales C111 and OCS155. For this latter phylum, there was a strong reduction of 15% in all stations to only 2% in the more coastal station. It is worth highlighting the class Synechococcophycidae, from Cyanobacteria, whose abundances were very low throughout the estuary (5% in the upstream station), but reached 20% near the estuary mouth. This group was composed mainly of the marine genus *Synechococcus*. Therefore, it is possible to note a trend of reduced bacterioplankton in the upper part of the estuary, where salinity reached 60 (P1 and P2). The same zone presented the highest values of chlorophyll-a as well as was rich in sequences belonging to photoautotrophic eukaryotes. As advanced towards the sea, salinities reduced, by 50 in the intermediate zone (P3 and P4), and reached 40 in the mouth (P5 and P6), as well as chlorophyll-a. The dataset analysis suggested that in the upstream estuary, under hypersalinity conditions, primary productivity is not maintained by bacterioplankton, but by eukaryotic species. In the estuary mouth, dominated by marine characteristics, there is a shift to prokaryotic marine picoplankton, which possibly sustains primary productivity.

**Keywords:** drought, hypersalinity, phytoplankton, rRNA 16S

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