

Title: Depcting the diversity and the functions of *Planctomyces* in mangrove soils

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Among terrestrial ecosystems, mangroves stand out due to the particular combination of environmental conditions, which result in the evolution of species able to colonize these sites. Such unique conditions include high salinity and the frequent lack of oxygen in these soils. Much of the microbial diversity in mangroves soils is already known, but some important fractions remain unexplored, requiring further studies, such as the *Planctomyces* group. They occur ubiquitously in mangroves areas, showing a higher frequency in this environment than those observed in other soils. Therefore, the aim of this study, through a combination of dependent and independent cultivation methods, is to describe the diversity and possible functional features of bacterial members of this phylum detected in mangrove soils. We worked with three mangrove areas in different states of preservation located in Bertioga / SP [BrMgv01 (mangrove with point 1 oil spill), BrMgv02 (mangrove with oil spill in points 2 and 3), BrMgv03 (mangrove with anthropogenic contamination)]. Initially, analysis of 16S rDNA partial gene sequences, carried out by pyrosequencing, indicated the presence of specific clusters, suggesting a variety of specific *Planctomyces* in this environment. This observation was confirmed by sequence analysis of the same gene of 40 isolates (also compared by Box-PCR methodology) obtained by cultivation in M13 culture medium plus vitamins solution, salts and metals. Genomic analysis of the isolates obtained will complement this data. In addition, sequence analysis of the metagenomic and metatranscriptomic dataset, determined by Illumina HiSeq methodology associated with the annotation on MG-RAST platform, revealed a higher abundance of sequences affiliated to *Planctomyces* in the metatranscriptomic analysis when compared with the metagenomic data. The functions assigned to this group should indicate its importance in the functioning of mangrove soils that so far has been attributed to functions related to sulfur mineralization, performed by sulphatase enzymes. These results indicate that mangroves can host specific groups of *Planctomyces*, and give the first basis for inferences about the role of these organisms in the tropical and coastal environment.

Keywords: *Planctomycetes*, Mangrove, Metagenomic, Metatranscriptomic, Isolation.

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