

TITLE: PHOTOSYNTHETIC MICROBIOME OF WATER BODIES SEDIMENTS IN THE CHAPADA DAS MESAS NATIONAL PARK (PNCM), MARANHÃO, BRAZIL

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ABSTRACT:

The Chapada das Mesas National Park (PNCM) is a Conservation Unit that covers a significant area of the Cerrado of Maranhão, a biome considered a biodiversity hotspot. The PNCM has already lost 80% of its natural cover and is threatened by the process of desertification, advance of farming, and tourist activity. Considering that microbial communities are responsible for most of the metabolic activity in river ecosystems, and that the PNCM houses more than 400 springs and many waterfalls of socio-environmental and tourist importance in the region, this study aimed to explore the photosynthesizing microbiological community in water bodies surface sediment samples in 5 waterfalls in the areas of Farinha River and Pedra Caída Touristic complex. This is the first work to describe the diversity of microorganisms in Maranhão using new sequencing technologies. The collected samples were cultivated in selective medium for photosynthesizers. After stabilization of the consortia, total DNA was extracted. The community was investigated by sequencing the hypervariable region V4 of the 16S rRNA gene, using the Ion Torrent platform. The reads were analyzed using the softwares Usearch, Qiime, and Picrust, to assess the functional potential of microorganisms identified. The results highlight the identification of 23 phyla of bacteria, with Proteobacteria, Cyanobacteria and Bacteroidetes being the most abundant in the consortia. The enrichment allowed detection and identification of many genera of cyanobacteria and microalgae in the PNCM, which was not possible by traditional cultivation methods or total microbiome without the enrichment process. A total of 27 genera of the cyanobacteria phylum were classified in the samples from the consortia. We highlight *Geminocystis*, *Pantanalinema* and *Alkalinema*, which are three new genera in tropical saline-alkaline lakes in Maranhão. A total of 14 genera of microalgae were identified. We highlight the genus *Ettlia*, which was the most abundant in all samples. Genes related to carbon fixation, nitrogen metabolism, photosynthesis, energy and methane metabolisms were found, corroborating the literature and the recent description of the methanogenic capacity of some cyanobacteria. This survey provides a basis for detailed studies on the structure of microbial communities in river sediments, their ecological relationships and their responses to changes in physicochemical conditions resulting from natural processes and human activities.

Keywords: bioinformatics, Cerrado biome, cyanobacteria, microalgae, microbial diversity.

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