TITLE: BIOINFORMATICS OF DNA BAR CODES GENES – IDENTIFYING MICROORGANISMS FROM MINING ENVIRONMENTS

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ABSTRACT:
Typically microorganisms have great biotechnological potential, and may play an important role in bioremediation processes, due to biodegradation or biosorption or even producing products to decrease and/or treat wastes from environments with mining activity. In Brazil, the biodiversity of its environments has not been widely studied and there are possibilities that species with interesting characteristics can occur and/or are being naturally selected in these areas. Therefore, the study aimed to use Bioinformatics bar code genes for identification of microorganisms of mining environments. In this regard, photosynthetic microorganisms were isolated from two sampling sites: A pristine natural lake, located in a region with iron mining activity, and an artificial lake, located in a copper mine, both areas with high concentration of these respective metals, and located on the southern border of Carajás belt, State of Pará, Brazil. The DNA of these microorganisms was sequenced by classical methodologies (Sanger). The DNA sequences of the bar code genes used for the identification were 16S rRNA, 18S rRNA and RuBisCO. Such nucleotide sequences were assembled in contiguous sequences with Genious software and SPAdes software, considering only those with Phred quality greater than 20. Then, were compared with sequences deposited in GenBank of the National Center for Biotechnology Information (NCBI) using the Basic Local Alignment Search Tool (BLAST). The sequences from this study and their hits are then aligned and used to build a phylogenetic tree using MEGA 6 software. The BLAST results showed that isolated presented identity from 92% to 99% for microalgae species, members of the phylum Chlorophyta, in the three genes bar codes used. From the phylogenetic trees analysis, a two clades formation was identified, evidencing an evolutionary approach of the isolated MCITV01 with a genus *Chlamydomonas* and isolated MCITV09 with the genus *Heveochlorella*. Based on the Bootstrap of phylogenetic trees, the most interesting DNA-Barcoding for identification of these microorganisms was 16S rRNA and 18S rRNA, demonstrating that this method represents an important data supplier for species identification and knowledge of biodiversity.

Keywords: Microorganisms, bioinformatics, bioremediation, biotechnological, biodiversity