

Title: PHYLOGENY OF *Nostoc*-like CYANOBACTERIAL STRAINS ISOLATED FROM CAATINGA

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Abstract:

Nostoc is a cyanobacterial genus that contains both free-living and symbiotic species distributed on every continent in a wide range of terrestrial and aquatic ecosystems, comprising strains able to fix atmospheric nitrogen. Caatinga is an exclusively Brazilian biome distributed throughout the semi-arid northeast and cover about 10% of the Brazilian territory. This biome has undergone intense process of degradation due to human activities and studies on microbial diversity that inhabits this environment are scarce. The aim of this study was to characterize eight cyanobacterial strains isolated from Caatinga. These strains were previously isolated from freshwater and soil samples collected in the Ceará, Bahia and Paraíba States in 2010 and are being maintained in the Cyanobacteria Culture Collection at the Laboratory of Cell and Molecular Biology of CENA, USP. The morphological characterization was based on observations under an optical microscope and support of specialized literature. For the genetic characterization, genomic DNA was extracted from each strain and the 16S rDNA was amplified (~ 1500 nt), cloned and sequenced. The generated sequences were processed in order to remove all bases with low quality (quality score <20) and compared with other sequences available at GenBank (NCBI). Morphologically, the eight studied strains presented uniseriate, isopolar and non-branched filaments, with presence of intercalary and terminal heterocytes and akinetes, congruent to *Nostoc* morphological description. The 16S rDNA sequence Blast analysis revealed an identity of 97-99% with sequences of *Nostoc*-like morphotypes available in database. However, the phylogenetic reconstruction revealed that the sequences obtained herein were distantly related with the typical clade of *Nostoc* genus. The 16S rDNA sequences grouped in four clades, one formed exclusively by the CENA216, CENA255, CENA261 and CENA296 Brazilian strains. These results show that the genetic variability of *Nostoc*-like morphotypes overlaps the morphological variability and indicate that Caatinga may hold new phylogenetic groups not yet described.

Keywords: 16S rRNA; PCR; systematic; taxonomy.

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