TITLE: ANTIFUNGAL PONTENCIAL EVALUATION OF *Microcystis aeruginosa* CACIAM 03 THROUGH AN *IN SILICO* APPROACH

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ABSTRACT:

Cyanobacteria are known as a promising source of well diversified secondary metabolites, thus arousing a great deal of industry interest from several areas. This metabolic variety is, in part, due to the presence of non-ribosomal biosynthetic pathways like NRPS and PKS type. The aim of this study is to analyze the genome of the cyanobacteria *Microcystis aeruginosa* CACIAM 03, focusing on the identification and characterization of gene clusters with a possible antifungal activity. The genome of CACIAM 03 was obtained through the NCBI database (MCIH00000000.1). For the gene clusters prediction, the genome, in FASTA format, was submitted to the antiSMASH 4.0 server, with the options enabled: (i) *KnownClusterBlast*; (ii) *smCoGanalysis;* (iii) *Align Trans-AT PKS domains*; (iv) *ClusterBlast*; (v) *ActiveSiteFinder;* (vi) *Whole-genome PFAM analysis*; (vii) *SubClusterBlast;* (viii) *Detect TTA codons.* 42 clusters were identified, of which 3 genic clusters are possibly involved in the synthesis of terpenes, 3 of PKS, 3 of NRPS and 1 PKS-NRPS hybrid system. Terpene clusters presented 77% similarity with a cluster of *Microcystis aeruginosa* PCC7806, 57% similarity with a cluster of *M. aeruginosa* TAIHU9841 and 43% similarity with a cluster of *M. aeruginosa* SPC777, respectively. PKS clusters presented 35% similarity with a cluster of *M. aeruginosa* NIES-2549, 36% of similarity with a cluster of *M. aeruginosa* SPC777 and 66% of similarity with a cluster of *M. aeruginosa* SPC777, respectively. Among the clusters of NRPS, one presented 100% similarity with a cluster of *M. aeruginosa* SPC777, and 85% of its genes are similar to those of the Aeruginosin synthesis pathway. The other NRPS clusters presented 75% and 25% similarity with a cluster of *M. aeruginosa* TAIHU98, the first one presenting 62% similarity with the Pawainaphycins synthesis pathway. The results found in this study, although preliminary, point to the potential of *in silico* mining in the finding of new biotechnological products. Additional analyzes with complementary bioinformatic tools will be performed to confirm the antifugal potential of the clusters found.

KEYWORDS: Secondary metabolites, biomining, antimicrobial potential.

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