TITLE: BACTERIOCINS AND CYANOBACTINS FROM *Microcystis aeruginosa* CACIAM 03: AN *IN SILICO* GENOME MINING APPROACH

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ABSTRACT:
Cyanobacteria is a group of gram-negative photoautotrophic prokaryotes which produce a spectrum of secondary metabolites, with applications in areas ranging from pharmaceuticals to biofuels. Among the strains of cyanobacteria with high potential to produce diversity of bioactive substances is the genus *Microcystis*. Many studies have already reported the ability of this genus to produce toxins and enzyme inhibitors with pharmacological potential, either by of way ribosomal or non-ribosomal. Thus, the aim of this study was to perform the *in silico* mining of the *Microcystis aeruginosa* CACIAM 03 genome, with special interest in the metabolic pathways of bacteriocins and cyanobactins. The genome was obtained from GenBank (accession number MCIH00000000.1). Putative secondary metabolites gene clusters were identified with antiSMASH version 4.0 using the following default settings: *(i) KnownClusterBlast; (ii) smCoG analysis; (iii) Align Trans-AT PKS domains; (iv) ClusterBlast; (v) ActiveSiteFinder; (vi) Whole-genome PFAM analysis; (vii) SubClusterBlast; (viii) Detect TTA codons*. A total of 42 putative gene clusters of biosynthetic pathways were found. Among them, three possibly involved with bacteriocin and cyanobactin biosynthesis. Two of the gene clusters were classified as bacteriocins-cyanobactins, presenting 88% of similarity with microcyclamide gene cluster. Microcyclamide gene clusters showed 100% of similarity compared to same clusters in *M. aeruginosa* strains (PCC 7806, NIES-298, SPC777, 9809 WGS). This compound exhibits cytotoxic activity and may have biological activity against serine protease, suggesting a possible antibiotic function. Regarding the third cluster, 28% of genes showed similarity with *M. aeruginosa* Yersiniabactin gene cluster, which is related with the biosynthetic pathway of siderophore produced by NRPS/PKS hybrid mechanism that exhibits functionality as a virulence factor. These results reveal the potential of *M. aeruginosa* CACIAM03 in producing bacteriocin and cyanobactin and its application in future biotechnological studies.

KEYWORDS: antimicrobial, genome mining, bacteriocins, cyanobactins

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