

TITLE: PHYLOGENETIC ANALYSIS AND THE BIOTECHNOLOGICAL POTENTIAL OF MEMBERS OF THE *EXIGUOBACTERIUM* GENUS

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ABSTRACT:

The *Exiguobacterium* genus includes species described from a wide range of polar, temperate and tropical habitats that grow with temperatures varying from -12 to 55°C, in a broad variation of pH and salinity, such as permafrosts, hot springs and saline lakes. Thus, because these microorganisms withstand extreme conditions, are classified as extremophiles. Due the great adaptability these organisms a biotechnological interest have aroused, however there are few studies about comparative genomic analysis, focusing on genomic mining for genes potentially involved with secondary metabolites (SM) synthesis. This study aimed to investigate the phylogenetic relationships between 11 *Exiguobacterium* genus strains with sequenced genome and their biotechnological potential. The multilocus sequence analysis (MLSA) was applied using the 16S rRNA, and two others genes (*groEL* and *rpoB*), in fasta format, which were obtained from the GenBank database and subsequently concatenated. BioEdit was used to align and manually trim the sequences and for phylogenetic analyses. Phylogenetic trees were constructed in MEGA version 6 using the neighbor-joining method, with a 1000 replicate bootstrap resampling. The concatenated sequences of all three genes were joined in the following order: 16S rRNA, *groEL* and *rpoB*. Putative secondary metabolites gene clusters were identified with antiSMASH version 4.0 using default settings. The topology of the generated tree demonstrated the formation of two clades, separating psychrophilic from thermophilic bacteria. These groups delineations had high bootstrap values, approximately 100% of support, demonstrating a clear diversification within the genus from the temperature conditions along the evolution of the group. About 24 and 20 SM gene clusters were detected in bacteria from cold and hot climate, respectively, indicating a variety of biosynthetic pathways and SM with antifungal and antibacterial activities. Gene clusters encoding the biosynthesis of lugdunin, thiopeptide, bacillomycin D, lantipeptide, bacteriocins, microcines and pimaricins, as well as terpenoids were identified. Genome mining has revealed the diversity and abundance of secondary metabolite potential of the *Exiguobacterium* genus, but poorly characterized. Bioinformatic analysis of this genus identified biosynthetic enzymes suggesting that these extremophile organisms potentially produce promising new compounds.

Keywords: Biomining, *in silico*, MLSA.

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