***IN SILICO* PHYLOGENETIC ANALYSIS OF BACTERIOCINS PRODUCED BY *Streptococcus thermophilus***

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Microbiological contamination of foods by spoilage and pathogenic bacteria can lead to economic and public health problems. Several works have demonstrated the potential of lactic acid bacteria (LAB) and its bacteriocins as an alternative for dairy preservation. *Streptococcus* spp. is widespread among dairy products, being *S*. *thermophilus* one of the most ubiquitous species. In this context, the use of software capable of prospecting bacteriocins from genomic sequences is a viable and fast alternative in the screening of new bacteriocins produced by LAB. This work aimed analyze *in silico* the bacteriocins produced by *S*. *thermophilus* through a comparison of the peptide sequence variability with the 16S phylogenetic similarity of the strains. 16S rRNA sequences were retrieved from 25 *S*. *thermophilus* strains and a multiple alignment of the 16S rRNA nucleotides was generated using MUSCLE. The 16S phylogenetic tree was constructed using the neighbor-joining method with a bootstrap value of 1,000. BAGEL3 was used to analyze 25 chromosomes and two plasmids retrieved from the NCBI database. The genome mining of the strains revealed the presence of 29 putative bacteriocin clusters in the population: seven gene clusters related with class I (24.1%) and 23 associated with class II (75.9%) synthesis. Four putative clusters of lanthipeptides, one of circular bacteriocins and two of sactipeptides comprised representative class I bacteriocins. Despite 16S phylogenetic similarity (overall mean distance of 0.0009), putative bacteriocin sequences diverged for lanthipeptides (overall mean distance of 1.74), sactipeptides (overall mean distance of 1.36) and putative class II bacteriocins (overall mean distance of 0.74). These results demonstrated that bacteriocin sequences are less conserved in the population despite highly conserved 16S rRNA sequence and consequent genetic similarity. In conclusion, novel antimicrobial peptides were described for *S*. *thermophilus* and class II appears to be a widespread among the strains. Further studies focused on the structural and biochemical characterization of these peptides could be useful to understand their antimicrobial activity and mechanisms of action in order to develop new strategies for dairy preservation.

Keywords: BAGEL, phylogeny, food safety.

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