

TITLE: COMPLETE GENOME SEQUENCE OF *Pediococcus pentosaceus* ST65ACC ISOLATED FROM ARTISANAL RAW-MILK CHEESE

AUTHORS: OLIVEIRA, F.S.; RODRIGUES, R.S.; CARVALHO, A.F.; NERO, L.A.

INSTITUTION: INSPOA, UNIVERSIDADE FEDERAL DE VIÇOSA, VIÇOSA, MG (AVENIDA PETER HENRY HOLFS, S/N, CEP 36570-900, VIÇOSA - MG, BRAZIL)

ABSTRACT:

Pediococcus pentosaceus ST65ACC was obtained from a Brazilian artisanal cheese and characterized as bacteriocinogenic; this strain also presented beneficial properties, indicating it as a potential probiotic candidate. In this study, we aimed to carry out a deep characterization of this strain based on whole genome sequencing (WGS), including taxonomy, biotechnological properties, bacteriocin clusters and safety related genes. WGS of *P. pentosaceus* ST65ACC was determined using the Illumina MiSeq platform and the genome was annotated with the Prokaryotic Genome Annotation (Prokka). *P. pentosaceus* ST65ACC taxonomy was investigated using an Average Nucleotide Identity (ANI) and Type Strain Genome Server (TYGS), based on complete genomes of *P. pentosaceus* published in the NCBI. Bacteriocin genes clusters were identification by BAGEL4, metabolic pathways were analyzing by Kyoto Encyclopedia of Genes and Genomes (KEGG), using the KEGG Automatic Annotation Server (KAAS) and safety related genes were checked through CARD, ResFinder, VFDB, PHASTER, CRISPRCasFinder and KEGG. *P. pentosaceus* ST65ACC genome presented a circular chromosome of 1.933.194 bp with a GC content of 37.00%, and encoded 1.950 protein coding sequences (CDSs), 6 rRNA, 55 tRNA, 1 tmRNA and no plasmids were detected. The results confirmed the identification of *P. pentosaceus* ST65ACC as it; *P. pentosaceus* SRCM102736 was identified as the closest neighbor of the strain based on the ANI method. The analysis revealed absence of a CRISPR/Cas system in *P. pentosaceus* ST65ACC, but bacteriocin gene clusters for pediocin PA-1/AcH and penocin-A were identified. Genes related to beneficial properties, such as stress adaptation genes (*atpF1ABGDE*, *atpF0AB*, *nhaC*, *clp*, *dnaK*, *hsp20* and *hslO*) and adhesion genes (*ltaS*, *eno*, *groEL*), were identified. Also, *lacZ* and *galKTEM* genes related to milk lactose utilization were identified in the *P. pentosaceus* ST65ACC genome, as well as components of the proteolytic system, such as oligopeptide transport system (*oppABCD*), some amino acid permeases and peptidases (*metQIN*, *pepC*, *pepN*, *pepX*, *pepO*). Furthermore, genes related to biogenic amines and virulence related genes were not detected. The *lsa*, *penP*, *dltABCD*, *abcA/amrA* genes related to antibiotic resistance were identified using KEEG, but not in prophage regions. Based on the obtained results, the beneficial potential of *P. pentosaceus* ST65ACC was confirmed, allowing is characterization as a potential probiotic candidate.

Keywords: bacteriocin, *Pediococcus*, whole genome sequencing

Development Agency: CAPES