INTRODUCTION. Phages infecting spoilage microorganisms have been considered as alternative biocontrol agents, and the study of their genomes is essential to their safe use in foods. UFV-P2 is a Pseudomonas fluorescens-specific phage that has been tested for its ability to inhibit milk proteolysis. In this study, we show its genome analysis. MATERIAL AND METHODS: Phage UFV-P2 was isolated from wastewater of a dairy industry, and its genome was extracted and sequenced using an Illumina Genome Analyzer II. The genome was assembled and analyzed using CLC Genomics Workbench (CLC bio). Approximately 92 open reading frames were predicted and functionally annotated using BlastX searches against GenBank and UniProt databases. Only 41 ORFs (44.57%) presented significant similarities to known proteins. Additionally, the presence of tRNA genes was predicted using tRNAscan-SE version 1.21. RESULTS AND DISCUSSION: The phage UFV-P2 has a 45,517-bp DNA genome with no tRNA genes, a GC content of 51.5%, and 41 ORFs, representing a gene density of 0.9008/kb. The ORFs were annotated to five different protein groups, consisting of 14 hypothetical proteins with unknown function, one chaperone, four constitutive and seven structural protein genes (including a major head, a portal, and a hypothetical tail collar domain), and 15 enzymes, including one lysozyme, the terminase subunits, an exonuclease, an endonuclease, a primase/helicase and two parts of the DNA polymerase. The analyses showed 53.61% identity to the genome of the temperate Pseudomonas phage PaP3 and a genome organization similar to the MR299-2, PaP3 and LUZ24 phage genomes, recently grouped as LUZ24-like viruses. CONCLUSIONS: According to the genomic analysis, the φUFV-P2 belongs to the LUZ24-like genus. Knowledge of this group is still limited, and further analyses are needed to confirm the safety of UFV-P2 and its potential as an agent for biocontrol of milk contaminants.

Keywords: Bacteriophages, Genome analysis, Milk proteolysis, Pseudomonas fluorescens
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