

**TITLE:** CHARACTERIZATION GENOMIC OF A NEW TEMPERED PHAGE OF *Staphylococcus aureus* ISOLATED FROM BOVINE MILK

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**ABSTRACT:**

Bacteriophages (phages) are viruses able to infect and destroy bacteria. The phages are researched as alternative therapy of the bacterial infections resistant to conventional antimicrobials. Thus, in this study we characterized genotypically a *Staphylococcus aureus* phage isolated from bovine milk. Whole-genome sequencing was performed in Illumina MiSeq® platform, with v2 500-cycle kit (paired-end). DNAs libraries were prepared with Nextera XT sample preparation kit following the manufacturer's instructions (Illumina™). The quality of generated sequences was evaluated using FastQC tool. Low-quality sequences were trimmed with the aid of FastQ Toolkit V.2.2.0. The paired-end sequence reads were assembled into contigs with SPAdes genome assembler v.3.9.0. The assemblies were confirmed by mapping reads to contigs Geneious Software (version R9). In addition, genome annotation was carried by web server PHASTER (Phage Search Tool Enhanced Release). Subsequently, it was verified that the genome has 41.396 bp, GC-content 33.97% and 61 putative ORFs. Fifty-four ORFs were located on the minus strand and only seven ORFs were presented on the plus strand. The phage contains functional modules, such as phage structure, host lysis, lysogeny, phage DNA packaging, and replication. Four proteins were involved in phage structure, namely putative major tail protein (ORF52), putative phage head tail adapter (ORF55), tail length tape measure protein (ORF48), and capsid protein (ORF58). The host lysis proteins identified were holin (ORF42) and amidase (ORF41). Ten proteins were identified to be involved in lysogenic, DNA packaging, modification, replication, and transcription, including DNA packaging protein (ORF56), single strand DNA binding protein (ORF21), dUTP nucleotidohydrolase (ORF7), transcriptional activator RinB (ORF5), integrase (ORF38), portal protein (ORF60), repressor (ORF34), anti-repressor (ORF29), cro (ORF33), and putative restriction-modification protein (ORF40). The majority of proteins verified (n=29) constitute hypothetical proteins (47.5%). Additionally, the integrase protein was identified and its presence indicates that phage can insert the viral DNA into the host. Thus, beyond lytic cycle, temperate phage also has a lysogenic cycle. Here, we characterized genotypically a new temperate phage, isolated from milk bovine named *Staphylococcus* phage B\_UFSM4 (B\_UFSM4).

**Keywords:** *Staphylococcus aureus*, new phage, bovine milk, bacteriophages.

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