

TITLE: *SALMONELLA* PHAGE UPF_BP2: NEW LYTIC BACTERIOPHAGE FOR *SALMONELLA* ENTERIC BIOCONTROL

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ABSTRACT:

Salmonella spp. is one of the major pathogens involved in outbreaks of foodborne diseases. They may be resistant to antimicrobials, bringing risks to human and animal health. Our study aimed to find alternatives to fight these pathogens using biological control with bacteriophages, instead of the already known chemical control. Also called phage, they are obligate, host-specific, intracellular bacterial viruses that infect only prokaryotes. The genome of a new lytic bacteriophage, with potential for biological control against *Salmonella* enterica serovars was isolated, characterized and sequenced. Once the absence of profago was confirmed, we used *Salmonella* Bredeney as host bacterium for the phage. As source of isolation, residual water from poultry slaughtering was used. The sample was incubated with the host bacterium and culture medium for enrichment (36 ± 1 ° C, 24 h.). After centrifugation and filtration, the sample was pipetted in TSA with semi-solid overlay with the host, incubated (36 ± 1 ° C, 24 h.) and verified the presence of halo lysis and phenotypic characteristics. It was evaluated the lytic action against 12 serovars of *Salmonella* enterica (Brandenburg, Anatum, Tennessee, Agona, Bredeney, Schwarzengrund, Infantis, Rissen, Lexington, Panama, Enteritidis and Typhimurium). The phage lysed 7 of the 12 serovars tested (Brandenburg, Bredeney, Infantis, Rissen, Panama, Enteritidis and Typhimurium), despite having virulence genes, antimicrobial resistance and/or biofilm formation capacity. For sequencing purified DNA, of this phage was used to construct genomic libraries and sequencing was done using pair end sequencing (2x150bp) on the MiSeq (Illumina®) equipment. The genome assembly, was conducted using the softwares Newbler and Velvet, as well the subsequent analyzes in the softwares BLAST, PHAST, Virfam and Geneious. The sequencing outcome identified a new bacteriophage, double-stranded DNA genome, 54,894 bp and 446 identified ORFs (> 100 bp), with only 41 of these ORFs, yielding results in BLASTP, belonging to the order Caudovirales and to the Myoviridae family Type 1 Group 7, until then not described. It was named *Salmonella Phage* UPF_BP2, registered in GenBank under the number KX826077. This new lytic phage may be an alternative to the use of antimicrobials, establishing an innovation for the biocontrol of *Salmonella* enterica in food, animals, and environment as well.

Keywords: bacteriophages; biocontrol; *Salmonella* enterica