The Genome of Cronobacter sakazakii Bacteriophage vB_CsaP_GAP227 Suggests a New Genus within the Autographivirinae

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The complete genome sequence of phage vB_CsaP_GAP227 is available in GenBank under the accession no. KJ57834. The complete genome sequence of phage vB_CsaP_GAP227 is available in GenBank under the accession no. KJ57834.

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Cronobacter sakazakii is a life-threatening opportunistic pathogen that causes infections in immunocompromised individuals of all ages (1). Cases of sepsis, necrotizing enterocolitis, and meningitis caused by Cronobacter in neonates and infants have been associated with contaminated milk-based powdered infant formulas (2, 3). As alternative agents, bacteriophages (phages) have been used to control pathogens due to their high specificity and effectiveness (4, 5). Because Cronobacter is antibiotic-resistant (3), phages might be useful for controlling this pathogen. However, before application, it is necessary to obtain sufficient information about the use of a particular phage as a controlling agent to guarantee its safety. Presently, only nine Cronobacter phages have been reported, including five myoviruses (GAP31, GAP161, ES1-2, ES2, and CR3) (6–10), three siphoviruses (ESP2949-1, phiES15, and ENT39118) (11–13), and the unclassified phage phiAS7.

The 41,796-bp double-stranded DNA (dsDNA) genome of phage GAP227 possesses a G+C content of 55.7% and contains 49 open reading frames (ORFs). Discontiguous megablast analysis (16) revealed a significant sequence similarity to Yersinia phages φR8-01 and φ80-18 and Aeromonas phage phiAS7 (17). CoreGenes (18) comparative proteomic analyses confirmed these results, showing that GAP227 shared 71.4% of proteins with φR8-01 and φ80-18 and 63.3% with phiAS7. Since these values are considerably higher than those for shared proteins with the type virus φKMV (36.7%) (19), we propose that these four phages should be grouped in a new genus within the subfamily Autographivirinae.

The proteome of phage GAP227 was screened using BTXpred server to detect potential bacterial toxins (20). Since none were detected, phage GAP227 can be used as a potential controlling agent against Cronobacter sakazakii.

Nucleotide sequence accession number. The complete genome sequence of phage vB_CsaP_GAP227 is available in GenBank under the accession no. KJ57834.

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