

Molecular characterization of a novel phage GW1 lysing *Cronobacter*

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Took *Cronobacter* strains as the host for phage isolation, we isolated some phages from Pearl River of Guangzhou, China. More importantly, we obtained a newly identified lytic *Cronobacter* phage GW1, which had a linear double-stranded DNA genome of 39,695 nucleotides with an average GC content of 53.18 %. Among the identified 49 open reading frames (ORFs), genes for rRNA, tRNA, antibiotic resistance, and virulence factors were not found in the phage genome. In BLASTn, the data revealed that the genome of phage GW1 had the highest identity of 94% to *Citrobacter* phage SH4, followed by 93% identity to *Cronobacter* phage Dev2. The morphology, genomic features, and phylogenetic analyses

revealed that GW1 represented a new species of the T7virus genus. This novel lytic *Cronobacter* phage GW1 may provide an alternative phage therapy and biocontrol against *Cronobacter*.

Speaker Biography

Haiyan Zheng did her Ph.D in Wuhan Institute of Virology , Chinese Academy of Sciences, Biochemistry and Molecular Biology, Bachelor of Medicine, Department of Medical Laboratory, Xiangya School of Medicine, Central South University. Pollution prevention and control and pathogenic mechanism of food-borne *Cronobacter*. Awards, honors and representation of academic groups at home and abroad: She received the National Scholarship, the First East Lake Academic Forum Excellent Exhibition Board Award, and the third prize of Hubei Excellent Academic Paper.

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