COMPLETE GENOME SEQUENCE OF *ERWINIA AMYLOVORA* LYTIC PHAGE KEY

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The genus *Erwinia* includes plant-associated epiphytes as well as pathogens that affect a wide variety of plant species and are, therefore, of great economic importance. *Erwinia amylovora*, the causative agent of fire blight, is a typical representative of this taxon and the object of quarantine activity because of the extremely destructive character and the rapid spread of disease around the world. To our knowledge, a small number of siphoviruses are known to infect the members of the genus *Erwinia* (phages PhiEaH1 and PhiEaH2). According to the literature, this is rather unusual because the *Siphoviridae* phages comprise the most abundant viral family within the order *Caudovirales*. This work presents the genome sequences of the *E. amylovora* siphophage KEY. The aim was to conduct a preliminary bioinformatic analysis of the phage KEY genome.

Phage KEY was originally isolated from quince with symptoms of fire blight. KEY virion DNA was obtained by the phenol-chloroform extraction method. Sequencing was performed using the Illumina HiSeq 2500 platform at The Centre for Applied Genomics in the Hospital for Sick Children, Toronto, Canada. Contigs were assembled using DNASTAR's SeqMan NGen12 software. The genome of phage Key was scanned for potential open reading frames (ORFs) using Glimmer and GeneMark.hmm. All ORFs and their protein products were analyzed using BLASTn and BLASTp against the databases available at NCBI website as well as ExPASy bioinformatics resource portal. Genome annotations were completed by DFAST with subsequent manual curation. tRNA encoding genes were identified using tRNAscan-SE and ARAGORN.

The previous TEM study revealed that the lytic phage KEY belongs to the *Siphoviridae* family with isometric heads of B1 morphotype and long noncontractile tail. The genome of KEY was 119.089 kbp with a G+C content of 38.9%, containing 184 open reading frames (ORFs) and 26 tRNA genes. The 91 ORFs encoded hypothetical proteins and 18 novel ORFs without homologs in the NCBI nonredundant database. The remaining 75 ORFs encoded proteins involved in virion morphogenesis, DNA metabolism, adsorption, and host lysis.

Blast analysis indicated that the bacteriophage KEY showed 71% identity to *Escherichia virus* AKFV33 (QC 41%) and 70% identity to *Escherichia phage* vB_EcoS_FFH1 (QC 41%). According to the genome structure of phage KEY it was classified as a T5-like phage.

The obtained data expand the knowledge of *Erwinia* phages and may be helpful for the epidemiological and phytosanitary control.