

A BROAD-HOST-RANGE LYTIC ERWINIA PHAGE KEY WITH EXOPOLYSACCHARIDE DEGRADING PROPERTIES

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Fire blight, a plant disease caused by *Erwinia amylovora*, leads to significant economic losses in the cultivation of fruit and ornamental trees. Currently, a promising approach for *E. amylovora* biocontrol is usage of phages and phage-based products, such as phage exopolysaccharide depolymerases (EPSDs). Phage EPSDs can target amylovoran and levan, specific capsular polysaccharides of the pathogen, making cells accessible to bactericidal treatment. The aims of this work were comparative genome analysis of *Erwinia* phage Key, identification and characteristics of its genes associated with EPSD activity.

Phage DNA was isolated by the phenol-chloroform extraction method and sequenced using the Illumina HiSeq 2500 platform. The contig was assembled with DNASTAR's SeqMan NGen12 software. The Key genome was scanned for potential genes using Glimmer and GeneMark.hmm. Functional annotation was conducted by the BLASTp, ExPASy and HHpred tools based on homology search. Phylogenetic analysis was performed using the maximum likelihood method after alignment with Clustal W implemented in MEGA XI with 500 bootstraps.

Bacteriophage Key is a lytic siphovirus that was originally isolated from quince with symptoms of fire blight. The host range analysis identified that Key is able to infect the *E. amylovora*, *P. agglomerans* and *E. horticola* strains. On the lawns of the sensitive bacteria Key forms 1-2 mm turbid plaques. But when plated with the *P. agglomerans* g157 or *E. horticola* 60-3m cultures, the large halo zones around plaques increasing over time of incubation are observed. This indicates an EPSD activity of KEY associated with phage virions.

The dsDNA genome of Key is 115,651 bp long with a GC ratio of 39.03%. It contains 182 putative genes and 27 tRNA genes. In total, 57 functionally annotated genes involve in DNA replication, recombination, repair, and packaging, virion morphogenesis, nucleotide metabolism, lysis, phage-host interaction and others. Gp 141 was identified as a potential EPSD that has homologues in many phages *Erwinia*-specific phages and can be responsible for the halo formation observed around the phage Key plaques. Due to the revealed genome synteny as well as protein similarity to T5-like phages, phage Key together with its closest relative, *Pantoea* phage AAS21, are suggested to represent a novel genus within the *Demerecviridae* family.

Broad host-range together with EPSD activity makes phage Key as an attractive candidate for biological control of fire blight. Further experimental studies are needed to test this assumption.