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PROKARYOTES

Draft Genome Sequence of *Pectobacterium atrosepticum* PB72 and Complete Genome Sequence of the Specific Bacteriophage PP90

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ABSTRACT We present the draft genome sequence of *Pectobacterium atrosepticum* strain PB72 infecting potatoes in Russia. PB72 is similar to the previously reported strain 21A. Considering potential biocontrol of this pathogen, an infectious bacteriophage was isolated and characterized. Phage vB_PatP_PP90 is a lytic podovirus of narrow host range belonging to the *KP34virus* genus.

Pectobacterium atrosepticum is a plant pathogen (1) associated with blackleg disease of potatoes (2, 3), with sequenced strain SCRI1043 (4) used as a model (5). *P. atrosepticum* is rated among the most destructive plant pathogens in Russia, and bacteriophage application is used as a biocontrol method (6, 7).

Both *P. atrosepticum* strain PB72 and phage PP90 were isolated from diseased potatoes in the Moscow Region of Russia in 2014. Bacteria were grown in LB medium at 27°C, and the phage was propagated using strain PB72 as a host. Bacterial and phage genomic DNA was extracted using a standard phenol-chloroform protocol and subjected to ultrasound fragmentation by a Bioruptor (Diagenode) to obtain a mean fragment size of 500 bp. Fragment libraries were constructed using a NEBNext Ultra kit (New England Biolabs). Sequencing was performed on an Illumina MiSeq platform using paired-end 150-bp reads. After sequencing, all reads were subjected to stringent quality filtering and trimming with CLC Genomics Workbench 10.0 (Qiagen). Sequencing adapters were trimmed with the SeqPrep tool (https://github.com/jstjohn/SeqPrep). Reads of both PB72 and PP90 were assembled with SPAdes 3.10.0 (8).

A total of 1,133,659 read pairs were used for *de novo* assembly of strain PB72. The obtained draft genomic assembly consisted of 50 scaffolds of 4,986,032 nucleotides (nt) in total and an N_{50} value of 238,550 nt, with average read coverage of 67×. Genome annotation was performed using Prokka (9). Coding sequences were predicted using Prodigal (10), tRNA genes and transfer-messenger RNA were predicted by ARAGORN (11), rRNA genes by Barrnap (http://www.vicbioinformatics.com/software.barrnap.shtml), and noncoding RNAs by Infernal (12). CRISPRs were detected by MinCED (https://github.com/ctSkennerton/minced). The PB72 genome with a GC content of 51.1% contains 4,421 protein coding sequences, 10 rRNA genes, 70 tRNAs, and 2 CRISPR loci. Organization of the PB72 chromosome and gene content and order are very similar to those of *P. atrosepticum* 21A (13), except for mostly phage-related horizontally transferred sequences, accounting for 35 unique genes in PB72. No plasmids were identified among the reads, in contrast to strain 21A.

Received 30 April 2018 **Accepted** 4 June 2018 **Published** 5 July 2018

Citation Shneider MM, Kabanova AP, Korzhenkov AA, Miroshnikov KK, Vo Thi NH, Toshchakov SV, Miroshnikov KA, Ignatov AN. 2018. Draft genome sequence of *Pectobacterium atrosepticum* PB72 and complete genome sequence of the specific bacteriophage PP90. Genome Announc 6: e00473-18. https://doi.org/10.1128/genomeA.00473-18.

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Bacteriophage PP90 has a very narrow host range, not infecting *P. atrosepticum* 21A and SCRI1043 or 60 other tested *Pectobacterium* and *Dickeya* strains. It forms 1- to 2-mm plaques with a pronounced halo. Negative staining electron microscopy shows podoviral phage morphology, and thus the phage can be referred to as vB_PatP_PP90 (14).

The genome of PP90 consists of 44,570 bp with a GC content of 56%. Average genome coverage was 64×. Genome annotation using GeneMarkS (15), Glimmer (16), RAST (17), and BLASTP (18) reveals 56 ORFs and no tRNAs. The closest (95.61% average nucleotide identity [ANI]) published phage isolate is *P. atrosepticum* phage Peat1 (NC_029081) (19), but PP90 has a unique orf11, orf14, and orf16. The general genome layout and the composition of the lysis module make PP90 a member of the genus *KP34virus*. To date, all characterized *P. atrosepticum* bacteriophages were isolated using strain SCRI1043 or uncharacterized strains (20, 21). Hence, this work is a first report of the phage infecting a 21A-group strain that is genetically diverse from SCRI1043 (13, 22).

Accession number(s). The NCBI nucleotide sequence accession numbers for this project are PDDK00000000 for the *P. atrosepticum* PB72 genome assembly and KX278419 for bacteriophage PP90.

ACKNOWLEDGMENT

This work was supported by Russian Scientific Foundation grant 16-16-00073.

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