

## Note (Genome Announcement)

# The draft genome sequence of *Pectobacterium carotovorum* subsp. *actinidiae* KKH3 that infects kiwi plant and potential bioconversion applications

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## 키위 나무에서 분리한 *Pectobacterium carotovorum* subsp. *actinidiae* KKH3 균주의 유전체 분석 및 이를 통한 생물전환 소재로서의 가능성 연구

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*Pectobacterium carotovorum* subsp. *actinidiae* KKH3 is an Enterobacteriaceae bacterial pathogen that infects kiwi plants, causing canker-like symptoms that pose a threat to the kiwifruit industry. Because the strain was originally isolated from woody plants and possesses numerous plant cell wall-degrading enzymes, this draft genome report provides insight into possible bioconversion applications, as well as a better understanding of this important plant pathogen.

**Keywords:** *Pectobacterium carotovorum* subsp. *actinidiae*, bioconversion, plant pathogen

*Pectobacterium carotovorum* is a plant pathogenic bacterium that causes soft rot disease (Mansfield *et al.*, 2012). Most

*Pectobacterium* species produce plant cell wall-degrading enzymes to break down the plant structure; hence they are also considered potentially useful for the bioconversion applications (Lagaert *et al.*, 2009). Recently, a new strain (KKH3) was isolated from kiwifruit *Actinidia chinensis* cv. Hort16A displaying bacterial canker-like symptoms, and a subsequent polyphasic analysis designated the strain as the novel subspecies *P. carotovorum* subsp. *actinidiae* (Koh *et al.*, 2012). Since this may be the first *P. carotovorum* subspecies known to infect woody plants, the genome sequence of this strain may help to better understand its distinct characteristics.

A genomic library of *P. carotovorum* subsp. *actinidiae* KKH3 was sequenced using a mixed sequencing strategy with 454 SE and PE, Illumina HiSeq, and PacBio platform. The sequencing data provided approximately 2,747-fold coverage with an N<sub>50</sub> of 4,068,673 bp. Generated paired-end sequencing

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**Table 1.** Genome features of *P. carotovorum* subsp. *actinidiae* KKH3

Genome Information	Total
Genome size (bp)	4,922,167
DNA G + C content (%)	51.54
Total genes	4,476
tRNA genes	74
rRNA genes	20

reads were assembled using gsAssembler 2.6 (Roche), CLC genomics workbench 6.5.1 (CLC Bio), and SMRT Portal 2.0, and manually adjusted using CodonCode Aligner 3.7.1 (CodonCode Corp.). The final obtained genomic sequence of contigs was corrected by remapping with raw reads to check errors and dubious regions. Open reading frames (ORFs) were predicted by Glimmer 3.02 (Delcher *et al.*, 2007), and ORFs were compared with catalytic families (catFam) and the NCBI COG database by rpsBLAST, and with NCBI reference sequences (RefSeq) and SEED databases by BLASTP for functional annotation (Tatusov *et al.*, 2000; Overbeek *et al.*, 2005; Yu *et al.*, 2009; Pruitt *et al.*, 2012). tRNA-Scan-SE was used for tRNA identification (Lowe and Eddy, 1997), and rRNA searches were performed using HMMER with EzTaxon-e rRNA profiles (Kim *et al.*, 2012).

The draft genome sequence of *P. carotovorum* subsp. *actinidiae* KKH3 consists of three contigs. The draft genome size is 4,922,167 bp, and the G + C content is 51.54% (Table 1). A total of 4,476 ORFs were predicted, of which 3,189 ORFs were functionally assigned. Additionally, 74 tRNA genes and 20 rRNA genes were identified. KKH3 also contains numerous genes encoding plant cell wall-degrading enzymes such as glycosyl hydrolase, cellulase,  $\beta$ -glucosidase, pectin lyase, pectate lyase, and polygalacturonase. However, genes related to the lysis of woody materials were not found. Rather, xanthine dehydrogenase-related genes involved in the oxidative metabolism of purines and type IV conjugative transfer system-related genes were plentiful, despite not being in other *P. carotovorum* species. Genomic differences among *P. carotovorum* species may influence the host range, but further intensive study is needed before meaningful conclusions can be drawn. The discovery of additional factors from genome sequences will likely facilitate not only a more comprehensive understanding and ability to control this plant pathogen, but may also facilitate

its application in the field of biotechnology.

#### Nucleotide sequence accession number

The Whole Genome Shotgun data for *P. carotovorum* subsp. *actinidiae* KKH3 has been deposited at GenBank under the accession number JRMH01000000. The strain was deposited in the Korean Collection for Type Culture (KCTC 23131) and the BCCM/LMG Bacterial Collection (LMG 26003).

## 적 요

*Pectobacterium carotovorum* subsp. *actinidiae* KKH3는 Enterobacteriaceae에 속하는 세균으로서, 키위 나무에 동고병과 같은 병을 일으키는 병원성 균주이다. 이 균주는 목본에서 분리되었으며 다양한 식물 세포벽 분해 효소를 가지고 있다. 따라서, 본 연구에서 제공하는 유전체 정보는 KKH3 균주의 병원성 기작을 이해하는 것뿐만 아니라 bioconversion 연구를 위한 토대로 활용될 수 있다.

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