

Draft genome sequence of a bacterial plant pathogen *Erwinia pyrifoliae* strain EpK1/15 isolated from an apple twig showing black shoot blight

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가지검은마름병 병징을 보이는 사과나무 가지에서 분리한 식물병원세균인 *Erwinia pyrifoliae* EpK1/15 균주의 유전체 해독

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Erwinia pyrifoliae is a Gram-negative bacterium causing black shoot blight in apple and Asian pear trees. *E. pyrifoliae* strain EpK1/15 was isolated in 2014 from an apple twig from the Pocheon, Gyeonggi-do, South Korea. In this study, we report the draft genome sequence of *E. pyrifoliae* EpK1/15 using PacBio RS II platform. The draft genome is comprised of a circular chromosome with 4,027,225 bp and 53.4% G + C content and a plasmid with 48,456 bp and 50.3% G + C content. The draft genome includes 3,798 protein-coding genes, 22 rRNA genes, 77 tRNA genes, 13 non-coding RNA genes, and 231 pseudo genes.

Keywords: *Erwinia pyrifoliae*, apple, black shoot blight, draft genome sequence, PacBio RS II

Erwinia pyrifoliae is primarily a bacterial pathogen of Asian or Nashi pear (*Pyrus pyrifolia*), causing black shoot blight and has been reported only in Korea and Japan since 1990's (Rhim *et al.*, 1999; Kim *et al.*, 1999; McGhee *et al.*, 2002; Geider *et al.*, 2009). Disease symptoms caused by this pathogen are very similar to fire blight caused by *E. amylovora*, which is widely

distributed worldwide (van der Zwet *et al.*, 2012). *E. pyrifoliae* belongs to the Enterobacteriaceae, which is a large family of Gram-negative, facultative anaerobe (Octavia *et al.*, 2014). To date, the complete genome sequences of *E. pyrifoliae* strains Ep1/96 and DSM12163 isolated in 1996 in South Korea have been reported (Kube *et al.*, 2010; Smits *et al.*, 2010). In this study, the new strain EpK1/15 (KACC 19528) was isolated from an apple twig showing black shoot blight in Pocheon, Gyeonggi-do, South Korea in 2014. To further understand the differences between *E. pyrifoliae* strains that were isolated with a few decades' interval, we present here the draft genome sequence of *E. pyrifoliae* EpK1/15.

Total genomic DNA of *E. pyrifoliae* EpK1/15 was extracted with the DNeasy Blood & Tissue Kit (Qiagen), and the extracted DNA was used to generate 20 kb SMRTbell™ template libraries. Genome sequencing was performed at ChunLab, Inc. using the Pacific Biosciences RSII sequencing method. The sequencing depth was 272.82 × coverage of the genome, and the sequence was assembled *de novo* into 2 contigs with the PacBio SMRT Analysis pipeline version 2.3.0. Genes in the resulting draft genome sequence were annotated with the National Center for Biotechnology Information (NCBI) Prokaryotic Genome

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Table 1. Genome features of *Erwinia pyrifoliae* EpK1/15

Genomic features	Chromosome	Plasmid
Genome size (bp)	4,027,225	48,456
G + C content (%)	53.4	50.3
Total genes	3,856	54
Protein-coding genes	3,744	54
rRNA genes (5S, 23S, 16S)	22 (8, 7, 7)	0
tRNA genes	77	0
Non-coding RNA genes	13	0
Pseudo genes	221	10

Annotation Pipeline (PGAP) (http://www.ncbi.nlm.nih.gov/genome/annotation_prok). The draft genome of EpK1/15 consists of one chromosome with 4,027,225 bp (53.4% G + C content) and one circular plasmid with 48,456 bp (50.3% G + C content). A total of 3,798 protein-coding genes, 22 rRNA genes (5S, 23S, and 16S), 77 tRNA genes, 13 non-coding RNA, and 231 pseudo genes were predicted. It carries one intact *hrp* gene cluster to form a Hrp type III secretion system and to encode important effector genes, *dspA/E* and *eopB*, and two harpin genes, *hrpN* and *hrpW*, in its chromosome for virulence in host plants. Interestingly, the plasmid in EpK1/15 strain is larger than the largest plasmids in both Ep1/96 and DSM12163 and also three small plasmids reported in Ep1/96 and DSM12163 strains were missing in this draft genome sequence of EpK1/16 strain. Because *E. pyrifoliae* strain EpK1/15 was isolated 20 years later than the first sequenced strain Ep1/96, further in-depth comparative analysis of the EpK1/15 genome would provide insights on the evolution of *E. pyrifoliae* species in field conditions.

Nucleotide sequence accession numbers

The draft genome sequences of a chromosome and a plasmid of *E. pyrifoliae* strain EpK1/15 have been deposited in the GenBank database under accession numbers CP023567 (chromosome) and CP023568 (plasmid), respectively.

적 요

*Erwinia pyrifoliae*는 그람 음성 세균으로 사과와 배에 가지검은마름병을 일으킨다. *E. pyrifoliae* EpK1/15 균주가 병징을 보이

는 경기도 포천지역의 사과나무 가지에서 2014년도에 분리되었다. 본 논문에서는 PacBio RS II 플랫폼을 이용하여 *E. pyrifoliae* EpK1/15 균주의 전체 유전체를 분석하여 보고한다. 본 균주는 G + C 비율이 53.4%이며, 4,027,225 bp로 구성된 염색체와 G + C 비율이 50.3%이며, 48,456 bp로 구성된 plasmid를 지니고 있다. 이들 염색체와 plasmid DNA에서 3,798개의 단백질 코딩 유전자, 22개의 rRNA, 77개의 tRNA, 13개의 non-coding RNA 및 231개의 위유전자(pseudo gene)가 확인되었다.

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