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Complete genome sequence of *Pseudomonas moraviensis* EFBE32, a biocontrol bacterium against pepper bacterial wilt

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고추 풋마름병을 억제하는 세균 *Pseudomonas moraviensis* EFBE32의 전체 게놈 서열

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Pseudomonas moraviensis strain EFBE32 is a biocontrol bacterium against bacterial wilt which is known as most destructive disease caused by *Ralstonia solanacearum*. Here, we report the whole genome sequence of *P. moraviensis* strain EFBE32. The sequence analysis revealed that *P. moraviensis* strain EFBE32 has a single 6,030,129 bps circular chromosome with a DNA G + C-content of 60.1%. This chromosome contains 5,239 coding sequences and 16 rRNA and 69 tRNA genes. In the result of sequence analysis, it is revealed that strain EFBE32 possessed genes coding the disease suppression related enzymes, acyl-homoserine lactone acylase (QuiP and PvdQ) which is known as quorum quenching enzyme, and hydrogen cyanide synthase (HcnA, B, and C).

Keywords: *Pseudomonas moraviensis*, bacterial wilt, biocontrol, EFBE32, genome

Bacterial wilt (BW) caused by *Ralstonia solanacearum* is known as one of the most destructive diseases of plant, especially affecting serious loss on yield of diverse solanaceous crops including potatoes, tomatoes, pepper and eggplant worldwide (Garcia *et al*., 2019). To date, multifaceted approaches based on physical, chemical, cultural, and biological methods have been applied to manage BW. Among them, biological control of BW has emerged as a promising method for eco-friendly and sustainable agricultural practice and alternatives to use of chemical pesticides that raise problems such as soil environmental pollution, residual toxicity, and occurrence of pesticide-resistance strains (Garcia *et al*., 2019; Lahlali *et al*., 2022).

Pseudomonas moraviensis strain EFBE32 was isolated from the branch of apple in Eumseong, Chungcheongbuk-do, Korea and grown in tryptic soy broth (TSB) at 28°C for 48 h under aerobic condition. *Pseudomonas moraviensis* strain EFBE32 showed the antagonistic activity against *Ralstonia solanacearum* on TSA medium and the control effect against development of BW in pepper seedling. The strain EFBE32 was deposited to the Korean Agricultural Culture Collection (KACC) (accession number KACC 81246BP).

Genomic DNA was extracted from the cultured *P. moraviensis* strain EFBE32 cells using a QIAamp DNA mini kit (Qiagen), according to the manufacturer's protocols. The whole genome of *P. moraviensis* strain EFBE32 was sequenced with a 20-kb SMRTbell™ template library using the Pacific Biosciences (PacBio) RSII Single Molecule Real Time sequencing platform, and Illumina NovaSeq6000 platform at Macrogen. The genome

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was assembled using Microbial Assembly Application by Macrogen, and annotated using NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (Tatusova *et al*., 2016). The complete genome sequence of *P. moraviensis* strain EFBE32 was found to comprise 6,030,129 bp, with an average DNA GC-content of 60.1%. The *P. moraviensis* strain EFBE32 chromosome contains 5,239 protein-coding sequences (CDSs), 16 rRNA and 69 tRNA genes with no plasmids (Table 1). The OrthoANI values, which are calculated using the OrthoANI algorithm version v0.93.1 (Lee *et al*., 2016), showed that the strain EFBE32 shared an average nucleotide identity (ANI) of 98.75–98.78 (99.65% of 16S rRNA gene) with *Pseudomonas moraviensis* strains (Fig. 1). The strain EFBE32 genome showed to possess genes coding the disease suppression related enzymes, such as hydrogen cyanide synthase (HcnA, B, and C) (Pacheco-Moreno *et al*., 2021), and acyl-homoserine lactone acylase (QuiP and PvdQ) which is known as quorum quenching enzyme (Rodríguez *et al*., 2020). Further antiSMASH analysis (Blin *et al*., 2021) revealed that the strain EFBE32 genome contains a secondary metabolite biosynthetic gene cluster of the lipopeptide surfactant, putisolvin, which is found to inhibit biofilm formation and degrading existing biofilms and associate with the antimicrobial activity (Kuiper *et al*., 2004; Ye *et al*., 2014).

Overall, the sequence analysis of the *P. moraviensis* strain EFBE32 genome revealed that it possesses several genes that are potential for use in biocontrol against plant pathogenic microbes. We expect that this strain would be used for constructing the eco-friendly strategy for biocontrol against BW disease.

Table 1. Genome features of *Pseudomonas moraviensis* EFBE32

Genome features	Chromosome
Genome size (bp)	6,030,129
G + C content (%)	60.1
Protein-coding genes (CDSs)	5,239
Number of rRNAs	6, 5, 5 (5S, 16S, 23S)
Number of tRNAs	69
ncRNAs	4
Number of pseudogenes	52
Plasmids	0
Accession number (GenBank)	CP107544

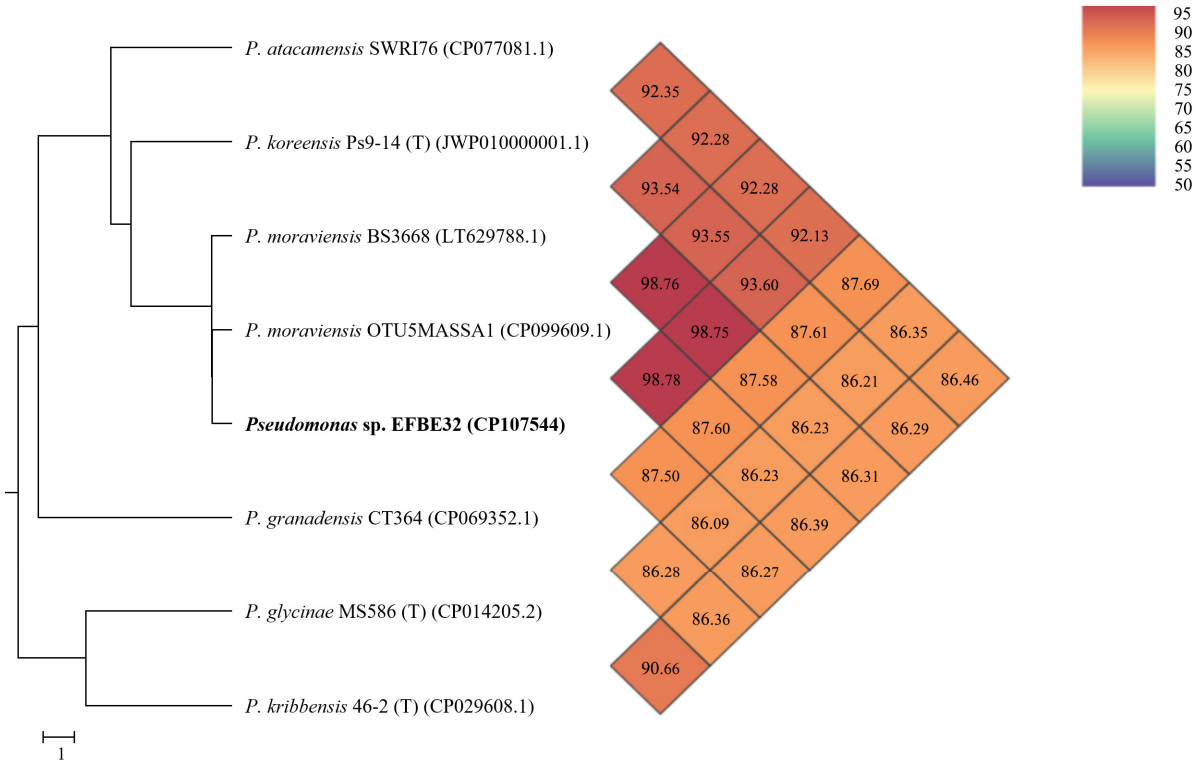

Fig. 1. UPGMA and Heatmap generated with OrthoANI values calculated from the OAT software. The letter (T) means type strain of the species. The scale bar means 1% sequence divergence.

Nucleotide sequence accession number

The whole genome sequence of *P. moraviensis* strain EFBE32 described in this study was deposited to the National Center for Biotechnology Information (NCBI) with the accession number CP107544.

적 요

풋마름병은 *Ralstonia solanacearum*에 의해 발생하는 가장 파괴적인 식물병으로 알려져 있다. 풋마름병을 억제하는 활성을 가진 *Pseudomonas moraviensis* EFBE32 균주의 전장 유전체 염기서열 분석은 EFBE32 균주가 6,030,129 bp를 가진 단일 환형 염색체로서 G + C 함량은 60.1%로 구성되었다는 것을 보여준다. 이 유전체는 5,239개의 단백질을 암호하는 염기서열을 가졌으며 16개의 rRNA와 69개의 tRNA 유전자를 포함한다. 염기서열 분석을 통해 EFBE32 균주가 병 억제와 관련된 정족수 소거 효소, acyl-homoserinelactone acylase (QuiP and PvdQ)와 시안화수소를 합성하는 효소, hydrogen cyanide synthase (HcnA, B, and C)를 암호화하는 유전자를 가졌음을 밝혔다.

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Conflict of Interest

The authors have no conflict of interest to report.

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