Complete genome sequencing of *Pseudomonas parafulva* PpaJBCS1880, a biocontrol and plant growth promoting agent

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식물 병 방제 및 생육촉진 효과를 나타내는 *Pseudomonas parafulva* PpaJBCS1880균주의 유전체 염기서열

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Pseudomonas parafulva PpaJBCS1880 (PpaJBCS1880) isolated from rice seeds showed strong antagonistic activity against bacterial plant pathogens by producing lipopeptide. Furthermore, the strain controlled the incidence of bacterial pustule in soybean plants and promoted the growth of rice plants. Here we present complete genome sequence of PpaJBCS1880. The genome comprises of 5,208,480 bp with GC content of 63.4%, which includes 4,487 predicted protein-coding genes, 19 rRNAs, and 74 tRNAs. Genome analysis revealed genes encoding antimicrobial secondary metabolites such as lipopeptide, pyoverdine, phenazine, and hydrogen cyanide, which are known to play essential roles in biocontrol of plant diseases.

Keywords: antagonism, biocontrol, lipopeptide, PGPR

Pseudomonas parafulva (formerly known as *Pseudomonas fulva*) is a Gram-negative bacterium that is frequently isolated from environment such as rice field (Uchino *et al.*, 2001). In previous reports, *P. parafulva* CRS01-1 showed antagonism against bacterial and fungal plant pathogens probably by pro-

ducing pyrimidine and benzoate (Liu *et al*., 2015). *P. parafulva* PRS09-11288 inhibited *Rhizoctonia solani* via production of phenazine-1-carboxylic acid (Zhang *et al*., 2018). In this study, the *P. parafulva* strain PpaJBCS1880, which was isolated from rice seeds showed strong antibacterial activity against *Xanthomonas axonopodis* pv. *glycines* (causal pathogen of bacterial pustule of soybean), *Burkholderia glumae* (bacterial grain rot of rice), and *Xanthomonas oryzae* pv. *oryzae* (bacterial leaf blight of rice) by producing viscosin-like lipopeptide VLIS2 and suppressed incidence of bacterial pustule in soybean plants (Kakembo and Lee, 2019).

Taken together, the results indicate that the *P. parafulva* strains inhibit bacterial or fungal pathogens by producing various secondary metabolites. Therefore, the genomic information of the potential biocontrol agents ultimately increases our understanding of the functions of the strains, which is vital for practical application of biocontrol in the fields. The strain PpaJBCS1880 was deposited in the Korean Agricultural Culture Collection (KACC) with accession number of KACC 92259P.

Total genomic DNA of PpaJBCS1880 was extracted using the commercial kit (GeneAll® ExgeneTM Cell SV Mini Kit)

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Table 1. The features of *Pseudomonas parafulva* PpaJBCS1880 genome

Features	Genome (Chromosome)
Genome size (bp)	5,208,480
GC ratio %	63.4
CDS (total)	4,544
CDS (coding)	4,487
Coding %	98.75
No. of rRNA genes (5S, 16S, 23S)	19 (7, 6, 6)
No. of tRNA genes	74
No. of pseudogenes	57

and whole-genome sequencing was performed by Macrogen Inc. using PacBio single molecule real-time (SMRT) technology. The sequencing reads were assembled using the RS Hierarchical Genome Assembly Process 3.0 (HGAP) within the SMRT Portal 2.3 (Chin *et al.*, 2013). Annotation of the genome was performed using the National Center for Biotechnology Information (NCBI)'s Prokaryotic Genome Annotation Pipeline 2.0 (PGAP) (Tatusova *et al.*, 2016). Whole genome sequencing by the PacBio platform produced a total of 93,159 reads with an average length of 11,167 bp and genome coverage depth about 157. The complete genome sequence was 5,208,480 bp with the GC content of 63.4%. The chromosome contains 4,487 coding sequences (CDSs), 74 tRNAs and 19 rRNAs (Table 1).

The genome and biosynthetic gene cluster analysis revealed for the first time that PpaJBCS1880 produces novel viscosin-like lipopeptide VLIS2, which predicted to have D-Ser at the second position (Kakembo and Lee, 2019). It also contains genes for the production of pyoverdines, phenazine, and hydrogen cyanide, which contribute to biocontrol activity of the strain (Couillerot *et al.*, 2009). Furthermore, in our hands, PpaJBCS1880 also promoted growth of rice plant. The production of siderophore such as pyoverdine and enzyme such as alkaline phosphatase might contribute to the growth promotion, which requires further exploration (Thakur *et al.*, 2014; Rosier *et al.*, 2018). Overall, the genome analysis indicated that PpaJBCS1880 promises to be a potential candidate for biocontrol as well as plant growth promotion. The complete genome will provide new insight to increase our understanding of the functions of the genes that remain under-explored for biocontrol performance of bacterial biocontrol agents.

Nucleotide sequence accession number

The genome of *P. parafulva* PpaJBCS1880 was made publicly available at NCBI GenBank (Acc. No. CP031641.1).

적 요

벼 종자에서 분리한 *Pseudomonas parafulva* PpaJBCS1880 (PpaJBCS1880) 균주는 lipopeptide를 분비하여 식물의 세균 병원균에 대해 강력한 항균력을 나타냈다. 또한, PpaJBCS1880 는 콩불마름병의 발생을 억제하였을 뿐만 아니라, 벼의 생육 을 촉진하였다. 이에 따라, 본 연구에서는 PpaJBCS1880 균주 의 전체염기서열을 해독하고 분석하였는데, 총 염기서열은 5,208,480 bp였고, GC 함량은 63.4%였다. 염색체는 4,487개 의 단백질을 암호화하였고, 19개의 rRNA와 74개의 tRNA로 구성되어 있었다. 유전체의 분석을 통해 2차 대사산물인 lipo-peptide, pyoverdine, phenazine 및 hydrogen cyanide 등을 생 산하는 것을 확인하였는데, 이들 대사산물에 의해 항균력, 생 물방제 및 생육촉진 효과를 나타내는 것으로 판단된다.

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