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Draft genome sequence of *Caballeronia jiangsuensis* EK, a phosphate-solubilizing bacterium isolated from the rhizosphere of reed

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갈대 뿌리로부터 분리한 인산가용화 *Caballeronia jiangsuensis* EK 균주의 유전체 분석

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We report the draft genome sequence of a phosphate-solubilizing bacterium, *Caballeronia jiangsuensis* EK, isolated from the rhizosphere of *Phragmites australis* (reed). The genome of strain EK comprised 8.87 Mbp with a G + C content of 62.6%, 7,922 protein-coding genes, and 55 tRNAs. Several genes related to phosphate solubilization were found including alkaline phosphatase, C-P lyase, and exopolyphosphatase. Further, genes involved in auxin biosynthesis were identified. These indicates that strain EK possesses potential plant growth-promoting activity.

Keywords: *Caballeronia*, phosphate-solubilizing bacteria, plant growth stimulation

The genus *Caballeronia* was first proposed in 2011 (Gyaneshwar *et al.*, 2011) but its name was validated and reclassified from *Burkholderia* only recently (Dobritsa and Samadpour, 2016). Over the past few decades, *Burkholderia* has been considered a pathogenic species. However, most of the potentially beneficial plant-associated *Burkholderia* were moved to the genera *Paraburkholderia* and *Caballeronia* during reclassification (Dobritsa and Samadpour, 2016; Dobritsa *et al.*, 2017). Phosphorous is an essential factor for plant growth. However, the most phosphorous in soil exists ion-complex from (calcium, aluminum, or iron), which is unavailable form for plant use (Rodriguez and Fraga, 1999). Phosphate-solubilizing bacteria play a role for releasing phosphorous from inorganic or organic phosphorous (Rodriguez and Fraga, 1999). To obtain plant growth-stimulating bacteria, we tried to isolate a phosphate-solubilizing bacterium from the rhizosphere of a plant.

Strain EK was isolated from the rhizosphere of *Phragmites australis* (reed) using Pikovskayas agar (Pikovskaya, 1948). The root of the reed was washed with saline solution, and the washed solution was used as the inoculum. After two weeks of incubation, a clear halo was observed on Pikovskayas agar. A cream white colony with a halo was picked and transferred several times to a new medium for isolation. The cells were routinely cultured at 25°C on an R2A plate.

DNA was extracted using the CTAB method (Hurt *et al.*, 2001). Genomic DNA sequencing was performed at Macrogen on an Illumina Hiseq4000 system. A DNA library was prepared using the TruSeq Nano DNA kit. Raw reads were filtered by FastQC and were assembled using SOAPdenovo. Annotation was performed using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAP). To predict more protein functions, KEGG, COG, and Pfam domain searches were analyzed as

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Table 1. Genomic features of strain EK and *Caballeronia jiangsuensis* MP-1

Genomic features	*Caballeronia jiangsuensis* EK	*Caballeronia jiangsuensis* MP-1
Length	8,866,612	8,611,053
Number of scaffolds	77	168
G + C	62.6	62.6
Coverage	137×	100×
Genes	8,233	7,791
Coding genes	7,922	7,631
rRNAs (5S, 16S, 23S)	3(3*),4(1*),3	1,1,1
tRNAs	55	55
Completeness†	100	100
Contamination†	1.34	2.12
Strain heterogeneity†	0.0	0.0
Accession number	JACSUE01	JFHF01

* Complete rRNAs.
† Data from CheckM analysis.

reported previously (Kim *et al.*, 2019). Average nucleotide identity (ANI) and average amino acid identity (AAI) were analyzed using JSpeciesWS and CompareM, respectively. The genome completeness was analyzed by CheckM (Parks *et al.*, 2015). The genome of strain EK contained 77 scaffolds with 137× coverage. The genome length was 8.87 Mbp with a G + C content of 62.6 (Table 1). The genome comprised 7,922 protein-coding genes, 55 tRNAs, and 10 rRNAs. Among the total protein-coding genes, 6,179 genes (78.0%) were assigned to COG. Genes categorized into COG classification were associated with general function prediction only (R, 10.6%), function unknown (S, 9.7%), transcription (K, 9.7%), and amino acid metabolism and transport (E, 9.1%).

Based on the 16S rRNA gene sequence, the closest related strain of strain EK was *Caballeronia jiangsuensis* MP-1, a methyl parathion (MP)-degrading bacterium (99.6% similarity)

Table 2. Genes related to plant growth promotion in the genome of strain EK

Function	Locus tag	Annotation	Gene
Reduction of ACC	IAG25_23140	1-aminocyclopropane-1-carboxylate deaminase	
Production of IAA	IAG25_38455	indole-3-glycerol phosphate synthase TrpC	*trpC*
	IAG25_38460	anthranilate phosphoribosyltransferase	*trpD*
	IAG25_14870	tryptophan synthase subunit beta	*trpB*
	IAG25_14880	tryptophan synthase subunit alpha	*trpA*
	IAG25_38465	aminodeoxychorismate/anthranilate synthase component II	*trpG*
	IAG25_38470	anthranilate synthase component I	*trpE*
Phosphate solubilization	IAG25_13340	alpha-D-ribose 1-methylphosphonate 5-triphosphate diphosphatase	*phnM*
	IAG25_13345	phosphonate C-P lyase system protein PhnL	*phnL*
	IAG25_13350	phosphonate C-P lyase system protein PhnK	*phnK*
	IAG25_13355	alpha-D-ribose 1-methylphosphonate 5-phosphate C-P-lyase PhnJ	*phnJ*
	IAG25_13360	carbon-phosphorus lyase complex subunit PhnI	*phnI*
	IAG25_13365	phosphonate C-P lyase system protein PhnH	*phnH*
	IAG25_13370	phosphonate C-P lyase system protein PhnG	*phnG*
	IAG25_13375	phosphonate metabolism transcriptional regulator PhnF	*phnF*
	IAG25_16020	exopolyphosphatase	*ppx*
	IAG25_16025	polyphosphate kinase 1	*ppk1*
	IAG25_16030	phosphate regulon sensor histidine kinase PhoR	*phoR*
	IAG25_16035	phosphate regulon transcriptional regulator PhoB	*phoB*
	IAG25_16040	phosphate signaling complex protein PhoU	*phoU*
	IAG25_16045	phosphate ABC transporter ATP-binding protein PstB	*pstB*
	IAG25_16050	phosphate ABC transporter permease PstA	*pstA*
	IAG25_16055	phosphate ABC transporter permease PstC	*pstC*
	IAG25_16060	phosphate ABC transporter substrate-binding protein PstS	*pstS*
	IAG25_32010	quinoprotein glucose dehydrogenase	*gcd*
	IAG25_13290	alkaline phosphatase D	*phoD*
	IAG25_14335	alkaline phosphatase D	*phoD*

(Liu *et al.*, 2014). The ANI and AAI of the genome of strain EK was 95.3% and 97.5%, respectively, compared with that of *C. jiangsuensis* MP-1. This indicated that strain EK was *Caballeronia jiangsuensis* EK based on the criteria for species definition (Konstantinidis and Tiedje, 2005; Konstantinidis *et al.*, 2006).

The genome of strain EK contained several genes related to phosphate solubilization (Table 2). It encoded alkaline phosphatase D (PhoD; IAG25_13290 and IAG25_14335) and C-P lyase (IAG25_13340~IAG25_13375) for releasing free orthophosphate from organic phosphorus. It also encoded exopolyphosphatase (Ppx; IAG25_16020) and polyphosphate kinase (Ppk; IAG25_16025), which hydrolyze inorganic polyphosphate. Gluconic acid produced by quinoprotein glucose dehydrogenase (gcd, IAG25_32010) of strain EK might indirectly hydrolyze orthophosphate from inorganic phosphorus. Furthermore, genes related to the production of indole-acetic acid (IAA) and reduction of 1-aminocyclopropane-1-carboxylate (ACC) could also contribute to the plant growth-promoting activity of strain EK. These genomic features indicate that strain EK could be a plant growth-promotiong rhizobacteria (PGPR) candidate.

Nucleotide sequence accession numbers

The strain EK was deposited to the Korean Collection for Type Cultures (KCTC) as 18763P. The genomic DNA information for strain EK is available at NCBI GenBank under accession JACSUE010000000.

적 요

인산 가용화 능력을 가지는 *Caballeronia jiangsuensis* EK 균주의 유전체 분석을 실시하였다. 그 결과 EK 균주의 유전체는 8.87 Mbp, 62.6 G + C값을 가지며, 총 7,922개의 단백질 코딩 유전자를 포함하고 있었다. Alkaline phosphatase, C-P lyase, exopolyphosphatase 같은 인산 가용화 관련 유전자들을 EK 유전체 내에서 확인할 수 있었다. 또한, 옥신 생합성과 관련된 유전자를 포함하고 있었다. 이러한 결과는 *Caballeronia jiangsuensis* EK가 식물 생장 촉진 잠재능을 가진 미생물임을 보여준다.

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Conflict of Interest

We have no conflicts of interest to report.

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