Complete genome sequence of *Peribacillus butanolivorans* KJ40, a soil bacterium alleviating drought stress in plants

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 식물의 가뭄 스트레스를 저감하는 토양 세균, *Peribacillus butanolivorans* KJ40의 전체 게놈 서열

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*Peribacillus butanolivorans* strain KJ40, a soil bacterium isolated from the rhizosphere soil of pepper, ameliorates drought stress in the host plant. Here, we report the whole genome sequence of strain KJ40. The sequence analysis revealed that strain KJ40 possesses a single 5,451,105 bp circular chromosome with an DNA G + C-content of 38.13%. This chromosome contains 4,945 protein-coding sequences and 39 rRNA and 84 tRNA genes. Thereafter using the sequencing data, the major genes related to stress tolerance and plant growth processes, such as proline and spermidine synthesis, and butanediol production, were identified.

**Keywords:** *Peribacillus butanolivorans*, drought stress, genome, KJ40, plant tolerance

Plants are constantly exposed to various biotic and abiotic stresses, such as plant pathogens, pests, temperature, salinity, and water, which affect plant growth and crop productivity (Pandey *et al.*, 2017). Drought stress is considered as one of major abiotic stresses that negatively affect plant growth and crop productivity (Jaleel *et al.*, 2009). Many chemical fertilizers and biofertilizers are used to ameliorate biotic and abiotic stresses. Moreover, beneficial microorganisms are used as biostimulants to improve the growth and yield of crops. *Bacillus* strains are known as the most useful bacteria for plant and have been investigated and used for the promotion of plant growth, control of plant pathogens, and alleviation of stress tolerance (Kim *et al.*, 2017; Yoo *et al.*, 2019; Saxena *et al.*, 2020). Previously, we reported that the *Peribacillus butanolivorans* (reclassified from the genus *Bacillus*, Patel and Gupta, 2020) strain KJ40 could be used as a potential biostimulant for the alleviation of drought stress tolerance in chili pepper and that the plants inoculated with this bacterial strain had increased shoot fresh weight, chlorophyll, and stomatal conductance and decreased malondialdehyde levels under natural drought conditions (Kim *et al.*, 2019). To better understand the molecular mechanisms of abiotic stress tolerance induced by this strain in plants, we analyzed the whole genome sequence of strain KJ40.

Strain KJ40 was isolated from the pepper rhizosphere soil and grown in tryptic soy broth at 28°C for 40 h under aerobic condition. Genomic DNA was extracted from the cultured strain KJ40 cells using a QIAamp DNA mini kit (Qiagen),...
according to the manufacturer’s protocols. The whole genome of strain KJ40 was sequenced with a 20-kb SMRTbell™ template library using the Pacific Biosciences (PacBio) RSII Single Molecule Real Time (SMRT) sequencing platform at Chunlab. The genome was assembled and annotated using previously described analytical procedures (van Heel et al., 2013; Weber et al., 2015; Kim et al., 2017). The complete genome sequence of strain KJ40 was found to comprise 5,541,105 bp, with an average DNA GC-content of 38.13%; no plasmids were detected (Fig. 1). Strain KJ40 chromosome contains 4,945 protein-coding sequences (CDSs), and 39 rRNA and 84 tRNA genes (Table 1). The sequencing analysis revealed that strain KJ40 possesses a large number of genes associated with plant abiotic stress tolerance and growth promotion. It also contains genes related to proline and spermidine biosynthesis (proA, B, and C, speA, B, D, and E), which encode organic osmolytes, thereby inducing plant stress tolerance, and a gene (fabG) involved in the biosynthesis of abscisic acid. The genome of strain KJ40 also contains other genes related to osmotic stress.

Table 1. Genome features of *Peribacillus butanolivorans* KJ40

<table>
<thead>
<tr>
<th>Genomic features</th>
<th>Chromosome</th>
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<tbody>
<tr>
<td>Genome size (bp)</td>
<td>5,451,105</td>
</tr>
<tr>
<td>Number of contigs</td>
<td>1</td>
</tr>
<tr>
<td>G + C content (%)</td>
<td>38.13</td>
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<tr>
<td>Protein-coding genes (CDSs)</td>
<td>4,945</td>
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<tr>
<td>rRNA genes</td>
<td>39</td>
</tr>
<tr>
<td>tRNA genes</td>
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<td>ncRNA genes</td>
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<tr>
<td>Pseudogenes</td>
<td>180</td>
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<td>Plasmids</td>
<td>0</td>
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<tr>
<td>Accession number (GenBank)</td>
<td>CP050509</td>
</tr>
</tbody>
</table>

Fig. 1. Circular genome maps of the *Peribacillus butanolivorans* KJ40 complete genome. The circular map consists of five circles. From the outermost circle to the inner, each circle contains information about (1) rRNA/ tRNA, (2) Reverse CDS, (3) Forward CDS, (4) GC Ratio, and (5) GC Skew.
and heat shock tolerance and genes for acetoin utilization (acuA, B, and C) and acetylactate synthase (ilvB and ilvH), which are involved in butanediol biosynthesis and are known to promote plant growth. Strain KJ40 genome has genes associated with the synthesis of siderophores (iucA, B, C, and D), which are known to stimulate plant health. It also possesses genes related to exopolysaccharide production (csgB and D, epsC and exoO).

Overall, the genome analysis of strain KJ40 genome revealed that it possesses several genes that are essential for alleviating drought stress in plants and thus is a promising biostimulant for improving crop productivity.

Nucleotide sequence accession number

The whole genome sequence of strain KJ40 described in this study was deposited to the National Center for Biotechnology Information (NCBI) with the accession number CP050509. Additionally, the strain was deposited to the Korean Agricultural Culture Collection (KACC) under the accession number KACC 92262P.

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References


