



# Complete genome sequence of drought tolerant plant growth-promoting rhizobacterium *Glutamicibacter halophytocola* DR408

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## 내건성 식물생장 촉진 균주인 *Glutamicibacter halophytocola* DR408의 유전체 분석

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*Glutamicibacter halophytocola* DR408 isolated from the rhizospheric soil of soybean plant at Jecheon showed drought tolerance and plant growth promotion capacity. The complete genome of strain DR408 comprises 3,770,186 bp, 60.2% GC-content, which include 3,352 protein-coding genes, 64 tRNAs, 19 rRNA, and 3 ncRNA. The genome analysis revealed gene clusters encoding osmolyte synthesis and plant growth promotion enzymes, which are known to contribute to improve drought tolerance of the plant.

**Keywords:** *Glutamicibacter halophytocola*, complete genome, drought tolerance, plant growth promotion

The genus *Glutamicibacter* newly reclassified from *Arthrobacter*, grouped in the family Micrococcaceae (Busse, 2016; Feng *et al.*, 2017). *Glutamicibacter* strains isolated from coastal halophyte root and coastal soil have been reported as a plant growth-promoting Actinobacteria showing high tolerance to osmotic and salt stress (Siddikee *et al.*, 2010; Qin *et al.*, 2018). We have isolated the strain DR408 from the rhizo-

spheric soil of the soybean (*Glycine max*) exposed to periodic drought in Jecheon, Republic of Korea. Phylogenetic analysis of its 16S rRNA gene sequence revealed that the strain DR408 closed to genus *Glutamicibacter* and had the highest similarity to *Glutamicibacter halophytocola* KCTC 39692 (99%) (Feng *et al.*, 2017). Unexpectedly, only one complete genome sequence belonging to this species are available in public database (NZ\_CP012750). Here, we describe the complete genome sequence and annotation of *Glutamicibacter halophytocola* DR408. The strain was deposited in the Korean Culture Center of Microorganisms with accession number of KCCM 43330.

The strain DR408 was cultured in tryptic soy broth (BD Bacto™) and shaken at 120 rpm in 28°C for 3 days. The genomic DNA was extracted and purified using the FastDNA SPIN KIT (MP Biomedicals) following the protocol recommended by the manufacturer. The purified genomic DNA was quantitated through fluorescence measurements made with the PicoGreen™ dsDNA quantitation kit and sequenced by the Macrogen facility (Macrogen). Size, purity, and concentration of the sample were determined by Agilent Technologies 2100

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Bioanalyzer to confirm the initial quality of DNA. Genome sequencing was performed using the PacBio RSII (Pacific Biosciences Inc.) and the Illumina HiSeq 2500 (Illumina). The sequence reads were assembled using a *de novo* assembler HGAP3 (The subreads were extracted using the following parameters: min. subread length: 500 bp; min. polymerase read quality: 0.80; min polymerase read length: 100 bp), and the contigs were polished by using Pilon (v1.21). Gene prediction and genome annotation was performed using the NCBI Prokaryotic Genome Annotation Pipeline ([https://www.ncbi.nlm.nih.gov/genome/annotation\\_prok](https://www.ncbi.nlm.nih.gov/genome/annotation_prok)) with best-placed reference protein set GeneMarkS 2 (v4.7). Default parameters were used for all software.

The complete genome of the strain DR408 consists of one circular chromosome that is 3,770,186 bp with 60.2% GC-content. A total of 3,470 predicted genes, 3,352 protein coding genes, 64 tRNA, 19 rRNA, 3 ncRNA, and 32 pseudo genes were annotated (Table 1). The genome of the strain DR408 contains the osmolyte synthesis genes and osmoregulation proteins such as trehalose-6-phosphate synthase (QDY67375.1), trehalose phosphatase (QDY67374.1), glutamate synthase (QDY67977.1), proline dehydrogenase (QDY66062.1), Na<sup>+</sup>/H<sup>+</sup> antiporter (QDY66084.1, QDY66082.1, QDY66081.1), and OsmC family protein (QDY66334.1). It also contains essential functional genes and proteins for the plant-bacteria symbiosis including 1-aminocyclopropane-1-carboxylate deaminase (ri-

bosome maturation factor, RimM QDY65158.1), tryptophan synthase (QDY65559.1, QDY65560.1), siderophore-interacting protein (QDY67200.1), iron-siderophore ABC transporter substrate-binding protein (QDY66743.1), glucose-6-phosphate dehydrogenase (QDY65509.1), phosphate ABC transporter permease (QDY68095.1, QDY67034.1, QDY67033.1), which contribute to plant growth promotion activity (Bruto *et al.*, 2014; Gupta *et al.*, 2014; He *et al.*, 2018; Li *et al.*, 2018). The strain DR408 possesses around 14 genes related to antioxidant biosynthesis genes potentially contributing to reduce the environmental stress. The complete genome sequence of *G. halophytocola* provides a framework for further genetic studies to understand the mechanism of drought tolerance regulated through the plant-bacteria symbiosis.

#### Nucleotide sequence accession numbers

The complete genome sequence of *Glutamicibacter halophytocola* DR408 has been deposited to GenBank under accession number CP042260.

## 적 요

제천에서의 콩 근권 시료로부터 분리한 *Glutamicibacter halophytocola* DR408 균주는 내건성 식물생장촉진력을 보이고 있다. 본 연구에서 DR408 균주의 완전한 유전체 서열을 획득한 결과, 유전체의 크기는 3.77 Mbp였으며, G + C 함량이 60.2%였다. 또한 총 3,352개의 유전자 서열과 65개의 tRNA, 19개의 rRNA, 3개의 ncRNA가 존재하였다. 유전체 분석을 통해 식물의 내건성을 향상시킬 수 있는 삼투질 합성과 식물생장촉진 효소를 코딩하는 유전자를 다수 포함하는 것을 확인하였다.

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**Table 1.** General features of *Glutamicibacter halophytocola* DR408 genome

Features	Chromosome
Number of contigs	1
Genome size (bp)	3,770,186
Average coverage (Depth)	231
GC contents %	60.2
Total genes	3,470
Total CDSs	3,384
Genes (coding)	3,352
CDSs (with protein)	3,352
Genes (RNA)	86
Complete rRNAs	7, 6, 6 (5S, 16S, 23S)
tRNA	64
ncRNA	3
Pseudo Genes	32

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