

Note (Genome Announcement)

Complete genome sequence of *Chryseobacterium* sp. T16E-39, a plant growth-promoting and biocontrol bacterium, isolated from tomato (*Solanum lycopersicum* L.) root

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토마토 뿌리에서 분리한 식물생육촉진과 생물방제 세균 *Chryseobacterium* sp. T16E-39 균주의 유전체 서열

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Chryseobacterium sp. strain T16E-39, isolated from roots of a tomato plant, promotes plant growth and suppresses phytophthora blight and bacterial wilt diseases. The complete genome of strain T16E-39 consists of a circular chromosome with 4,872,888 base pairs with a G + C content of 35.22%. The genome includes 4,289 coding sequences, 15 rRNAs, and 71 tRNAs. We detected genes involved in phosphate solubilization, phytohormone regulation, antioxidant activity, chitin degradation, and the type IX secretion system (T9SS) that may be related to growth promotion and disease suppression in plants.

Keywords: *Chryseobacterium*, biocontrol, genome sequence, plant growth-promoting bacteria

The genus *Chryseobacterium*, a member of the family *Flavobacteriaceae*, is commonly known for nonmotile, non-spore-forming, oxidase-positive, and Gram-negative bacteria (Vandamme *et al.*, 1994). *Chryseobacterium* species are widely distributed in various environments such as soil, fresh water,

plant rhizosphere, fish, meat, and milk (Kook *et al.*, 2014). Some *Chryseobacterium* strains isolated from the plant rhizosphere and endosphere have been shown to have plant growth promotion and biocontrol activity (Sang *et al.*, 2008; Dardanelli *et al.*, 2009).

Strain T16E-39 was isolated from the root endosphere of tomato plants grown in a greenhouse in Buyeo, Republic of Korea (36.2934270 N 126.9317180 E). It was assigned to the genus *Chryseobacterium* based on the 16S rRNA gene sequence; the most closely related species was *Chryseobacterium xinjiangense* with 97.7% sequence similarity. We observed that strain T16E-39 promoted tomato plant growth and suppressed phytophthora blight and bacterial wilt diseases (unpublished data). In an *in vitro* assay, the strain displayed indole-3-acetic acid (IAA) production and 1-aminocyclopropane-1-carboxylate (ACC) deaminase activity (unpublished data), which are both related to plant growth and development (Spaepen and Vanderleyden, 2011). To identify genes related to tomato growth and health, we conducted whole genome sequencing.

The *Chryseobacterium* sp. T16E-39 genome was sequenced

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using the Pacific Biosciences (PacBio) RSII single-molecule real-time (SMRT) sequencing platform with a 20 kb SMRTbell™ template at ChunLab Inc. All generated reads were assembled *de novo* using SMRT Analysis version 2.3.0. Gene prediction and functional annotation were carried out using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (Angiuoli et al., 2008) and the RAST server (Aziz et al., 2008).

The complete genome of the *Chryseobacterium* sp. strain T16E-39 consists of a 4,872,888 bp circular chromosome with 35.22% G + C content (Table 1). A total of 4,289 coding sequences, 15 rRNAs, 71 tRNAs, 3 ncRNAs, and 54 pseudogenes were detected. The genome contained genes involved in phosphate solubilization (phytase and quinoprotein glucose dehydrogenase) and phytohormone regulation (ACC deaminase), which are related to plant growth promotion (Spaepen and Vanderleyden, 2011; Sharma et al., 2013). The genes encoding several antioxidant enzymes, such as peroxidase, catalase, and superoxide dismutase, were detected in the genome; these are known to play roles in abiotic or biotic stress responses (Gross et al., 2013). The gene encoding the chitinase, which is hydrolytic enzyme responsible for degrading fungal cell walls composed of chitin, was also present and may be related to biocontrol activity (Zhang et al., 2001). Furthermore, strain T16E-39 possesses genes (*gldK*, *gldL*, *gldM*, and *gldN*) involved in the type IX secretion system (T9SS), which is associated with gliding motility (Abby et al., 2016). The secretion complex has been reported to be responsible for root colonization and plant defense (Kolton et al., 2014). The whole genome sequence provides genetic information for improving understanding of beneficial bacteria in plants and facilitates its future applications.

Table 1. Genome features of *Chryseobacterium* sp. T16E-39

Genome features	Value
Genome size (bp)	4,872,888
Number of contigs	1
G + C content (%)	35.22
Protein-coding genes	4,289
Number of tRNA	71
Number of rRNA (5S, 16S, 23S)	15 (5, 5, 5)
Number of pseudogene	54

Nucleotide sequence accession numbers

The complete genome sequence of *Chryseobacterium* sp. T16E-39 has been deposited at NCBI under the GenBank accession no. CP022282. The strain has been deposited in the Korean Agricultural Culture Collection (KACC) under the accession number KACC 81042BP.

적 요

토마토 뿌리에서 분리한 *Chryseobacterium* sp. T16E-39 균주는 식물생육촉진과 역병, 시들음병에 대한 억제효과가 있었다. 이 균주의 유전체 염기서열은 4,873,888 염기쌍이었으며 G + C 함량은 35.22%이었다. 이 유전체는 4,289개 단백질 유전자, 15개 rRNA 유전자, 71개 tRNA 유전자를 포함하였다. T16E-39 균주의 유전체에서 인산가용화, 식물호르몬 조절, 항산화 활성, 키틴 분해, 제9형 분비시스템에 관여하는 유전자를 확인하였으며, 이들 유전자는 식물의 생육을 촉진하고 병 발생을 억제하는 기작과 관련되어 있을 것으로 판단된다.

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