

Note (Genome Announcement)

Complete genome sequence of *Bacillus velezensis* T20E-257, a plant growth-promoting bacterium, isolated from tomato (*Solanum lycopersicum* L.) root

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토마토 뿌리에서 분리한 식물생육촉진 세균 *Bacillus velezensis* T20E-257균주의 유전체 염기서열

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Bacillus velezensis T20E-257 was isolated from the root tissue of a tomato plant and exhibited plant growth-promoting activity. Here we present the complete genome of strain T20E-257. The genome contains 3,900,066 base pairs with a G + C content of 46.7% in 2 contigs. The genome includes 3,708 coding sequences, 27 rRNAs, and 86 tRNAs. We found gene clusters encoding secondary metabolites with an antimicrobial activity and genes related to the production of indole-3-acetic acid and 2,3-butanediol, which play a role in plant growth and health.

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

Bacillus velezensis is a species with a strong biocontrol activity (Kim *et al.*, 2017). *B. velezensis* produces a diverse spectrum of secondary metabolites involved in antimicrobial activities (Chowdhury *et al.*, 2015). Furthermore, some strains of *B. velezensis* have been reported to release chemical compounds such as plant hormones and volatile compounds which are related to plant growth promotion (Meng *et al.*,

2016). These beneficial functions for plants suggest that *B. velezensis* is a potential candidate to be used as a biocontrol and biofertilizer agent to improve the crop productivity in sustainable agricultural systems.

We isolated strain T20E-257 from the root endosphere of tomato plants grown in a greenhouse in Yecheon, Republic of Korea (36.7175690 N 128.4988780 E). Strain T20E-257 was assigned to *B. velezensis* based on the sequences of 16S rRNA and *gyrB* genes. The strain exhibited plant growth promotion activity (unpublished data).

The *B. velezensis* T20E-257 genome was sequenced using a 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 (PGAAP) (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/) and the RAST server (Aziz *et al.*, 2008). The genes involved in the secondary metabolite production were analyzed using antiSMASH

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Table 1. Genome features of *Bacillus velezensis* T20E-257

Genome features	Contig 1	Contig 2	Total
Genome size (bp)	3,893,083	6,983	3,900,066
G + C content (%)	46.7	39.4	46.7
Protein-coding genes	3,701	7	3,708
Number of tRNA	86		86
Number of rRNA (5S, 16S, 23S)	27 (9, 9, 9)		27 (9, 9, 9)
Number of Pseudogene	82	1	83
Accession number	CP021976	CP021977	

version 4.0.0 (Blin *et al.*, 2017).

The complete genome of *B. velezensis* T20E-257 consists of 3,900,066 bp with a G + C content of 46.7% in two contigs (Table 1). One circularized contig with 3,893,083 bp is the chromosome, and the other small contig with 6,983 bp may be a plasmid. The genome contains 3,708 coding sequences, 27 rRNAs, 86 tRNAs, 5 ncRNAs, and 83 pseudogenes. Strain T20E-257 includes gene clusters devoted to peptides (fengycin, surfactin, bacilysin, and bacillibactin) and polyketides (bacillaene, difficidin, and macrolactin) made by non-ribosomal synthesis, and peptides (amyolysin and amylocyclicin) made by ribosomal synthesis. These secondary metabolites have antimicrobial activities and are similar to those found in the genomes of *B. velezensis* strains LS69 and FZB42 (Kim *et al.*, 2017; Liu *et al.*, 2017). We also detected genes related to the biosynthesis of indole-3-acetic acid (IAA), a phytohormone auxin that regulates plant growth and development (Spaepen and Vanderleyden, 2011). Moreover, the genome includes several genes involved in the production of 2,3-butanediol, a volatile compound that enhances plant growth and induced systemic resistance (ISR) (Yi *et al.*, 2016). The complete genome sequence will allow further functional and comparative genome analyses for better understanding of the genomic traits involved in plant growth and health.

Nucleotide sequence accession numbers

The complete genome sequence of *B. velezensis* T20E-257 has been deposited at NCBI under the GenBank accession no. CP021976 and CP021977.

적 요

토마토 뿌리에서 분리한 *Bacillus velezensis* T20E-257 균주

는 식물촉진효과가 있었고, 본 연구에서 T20E-257 균주의 유전체 서열을 해독하였다. 유전체 초안에서 포함된 2개 contig는 총 염기서열이 3,900,066 bp고, G + C content가 46.7%이었다. 유전체에서 단백질 유전자 3,708개, rRNA 유전자 27개, tRNA 유전자 86개를 확인하였다. 항균활성을 가지는 2차 대사산물 생합성 관련 유전자군과 식물생육촉진에 관여하는 IAA와 2,3-butanediol 생합성 관련 유전자를 T20E-257 균주 유전체에서 확인하였다.

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References

- Aziz, R.K., Bartels, D., Best, A.A., De Jongh, M., Disz, T., Edwards, R.A., Formsma, K., Gerdes, S., Glass, E.M., Kubal, M., *et al.* 2008. The RAST server: Rapid annotations using subsystems technology. *BMC Genomics* 9, 75.
- Blin, K., Wolf, T., Chevrette, M.G., Lu, X., Schwalen, C.J., Kautsar, S.A., Suarez Duran, H.G., de Los Santos, E.L.C., Kim, H.U., Nave, M., *et al.* 2017. Antismash 4.0-improvements in chemistry prediction and gene cluster boundary identification. *Nucleic Acids Res.* 45, W36–W41.
- Chowdhury, S.P., Hartmann, A., Gao, X., and Borriss, R. 2015. Biocontrol mechanism by root-associated *Bacillus amyloliquefaciens* FZB42 - a review. *Front. Microbiol.* 6, 780.
- Kim, S.Y., Lee, S.Y., Weon, H.Y., Sang, M.K., and Song, J. 2017. Complete genome sequence of *Bacillus velezensis* M75, a biocontrol agent against fungal plant pathogens, isolated from cotton waste. *J. Biotechnol.* 241, 112–115.
- Liu, G., Kong, Y., Fan, Y., Geng, C., Peng, D., and Sun, M. 2017. Whole-genome sequencing of *Bacillus velezensis* LS69, a strain with a broad inhibitory spectrum against pathogenic bacteria. *J. Biotechnol.* 249, 20–24.
- Meng, Q., Jiang, H., and Hao, J.J. 2016. Effects of *Bacillus velezensis* strain BAC03 in promoting plant growth. *Biol. Control* 98, 18–26.
- Spaepen, S. and Vanderleyden, J. 2011. Auxin and plant-microbe interactions. *Cold Spring Harb. Perspect. Biol.* 3, a001438.
- Yi, H.S., Ahn, Y.R., Song, G.C., Ghim, S.Y., Lee, S., Lee, G., and Ryu, C.M. 2016. Impact of a bacterial volatile 2,3-butanediol on *Bacillus subtilis* rhizosphere robustness. *Front. Microbiol.* 7, 993.