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Note (Genome Announcement)

Complete genome sequence of *Bacillus velezensis* YC7010, an endophytic bacterium with plant growth promoting, antimicrobial and systemic resistance inducing activities in rice

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식물생육촉진, 항균 및 저항성 유도 효과를 나타내는 내생세균 *Bacillus velezensis* YC7010의 유전체 염기서열

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Bacillus velezensis YC7010 is an endophytic bacterium isolated from the rice rhizosphere in Jinju, Republic of Korea, with properties conductive to growth promotion, antibiosis and induced systemic resistance to significant, soil-borne rice fungal and bacterial pathogens. The genome of *B. velezensis* YC7010 comprises a 3,975,683 bp circular chromosome which consists of 3,790 protein-coding genes (86tRNA and 27rRNA genes). Based on genomic analysis, we identified genes involved in colonization and establishment inside the plant, biosynthesis of antibiotic compounds such as surfactin, plipapastatin, bacillibactin, and bacillaene, as well as the production of the phytohormones and volatile compounds which serve to promote the plants growth and development.

Keywords: *Bacillus velezensis* YC7010, antibiotic compounds, endophytic bacterium, phytohormones, volatile compounds

The species of *Bacillus velezensis*, strain CR-502^{T} and CR-14b were initially isolated from the river Ve’lez at Torredel Mar in Ma’laga, southern Spain, and was found to be capable of synthesizing new lipopeptides with surfactant and/or antimicrobial activity (Ruiz-Garcia *et al.*, 2005). An endophytic strain, YC7010 (isolated from rice root), has been classified as *Bacillus oryzicola* YC7010 (Chung *et al.*, 2015). However, it’s taxonomy has been a source of controversy, and it has been suggested that it be renamed *B. velezensis* (Dunlap *et al.*, 2016). Many species of *Bacillus* are frequently found in the soil which comprises the rhizosphere and inside tissues of plants in the form of endophytes (Hallmann and Berg, 2006). The endophytic *Bacillus* strains have been used for promotion of plant growth and biological control of plant diseases caused by soil-borne pathogens (Shahzad *et al.*, 2017).

The endophytic strain *B. velezensis* YC7010 was deposited in the Korean Agricultural Culture Collection (KACC, National Academy of Agricultural Science, Jeonju, Republic of Korea) with the designated accession number of KACC18228. We have recently reported that the strain of *B. oryzicola* has plant growth promoting properties and seems to actively inhibit the growth of the significant and destructive fungal and bacterial

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diseases afflicting rice plants caused by *Fusarium fujikuroi* and *Burkholderia glumae* via antibiotic production and induced systemic resistance (ISR) (Chung *et al.*, 2015; Hossain *et al.*, 2016).

The complete genome of *B. velezensis* YC7010 was sequenced and characterized by Macrogen using the PacBio single molecule real-time (SMRT) technology (Eid *et al.*, 2009). The PacBio DNA Sequencing Kit 4.0 and eight SMRT cells were used for sequencing. The reads were assembled, *de novo*, with Hierarchical Genome Assembly Process 3 (HGAP3) within the SMRT Analysis version 2.3.0 software (Chin *et al.*, 2013). The best assembly was selected, and Minimus 2 was used for trimming the circular contig (Sommer *et al.*, 2007). The Prokaryotic Genome Annotation System (Prokka) pipeline was used for annotation of the genome (Seemann, 2014).

The complete genome sequence of *B. velezensis* YC7010 was characterized by a single circular chromosome of 3,975,683 bp with an average 46.5% G + C content. A total of 3,790 protein coding genes were anticipated, along with 86 tRNAs and 27 rRNA genes (Table 1). We identified genes (or gene clusters) involved in the oxidative stress or uptake of nutrients (proteins and sugars) released by plant roots, which may directly impact, or at least be in some way connected to, biofilm formation and colonization inside the plant. These key genes are potentially related to plant growth promotion by biosynthesis of phytohormones, indole acetic acid and volatile compounds, acetoin and 2, 3-butanediol. Additionally, genes (or gene clusters) associated the biosynthesis of some antimicrobial secondary metabolites like surfactin, plipapastatin, bacillibactin and bacillaene were also identified.

The genome sequencing and analysis of *B. velezensis* YC7010 in this study may provide valuable insights and information to further explore and reveal the molecular mechanism of plant growth promotion, antimicrobial action and ISR for the utilization of this endophytic bacterium as biological control agent in the future.

Table 1. Genome sequence information of *Bacillus velezensis* YC7010

Features	Chromosome
Genome size (bp)	3,975,683
G + C content (%)	46.5
Number of CDSs	3,790
tRNA	86
rRNA	27

Nucleotide sequence accession number

The complete genome sequence of *B. velezensis* YC7010 has been deposited in NABIC (http://nabic.rda.go.kr/) under the accession number NG-0523-000001.

적 요

식물 내생 세균인 *Bacillus velezensis* YC7010은 벼의 병원성 세균과 곰팡이에 대해 전신유도저항성을 일으키며, 식물생육촉진 및 항생작용의 특징을 가지고 있다. 대한민국 진주지역 벼의 근권에서 분리된 *B. velezensis* YC7010의 유전체는 3,790개의 단백질-암호화 유전자(86 tRNAs와 27 rRNA 유전자)로 구성되어 있으며, 3,975,683 염기쌍의 환상 염색체이다. 유전체 분석을 통해 식물의 발달과 생육을 촉진하는 휘발성 화합물, 식물호르몬 생산, surfactin, plipapastatin, bacillibactin, bacillaene 같은 활성 화합물의 생합성, 식물 내부정착 및 군집화와 관련된 유전자들이 유전체에 존재하는 것을 확인하였다.

References

Chin, C.S., Alexander, D.H., Marks, P., Klammer, A.A., Drake, J., Heiner, C., Clum, A., Copeland, A., Huddleston, J., Eichler, E.E., *et al.* 2013. Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. *Nat. Methods* **10**, 563–569.

Chung, E.J., Hossain, M.T., Khan, A., Kim, K.H., Jeon, C.O., and Chung, Y.R. 2015. *Bacillus oryzicola* sp. nov., an endophytic bacterium isolated from the roots of rice with antimicrobial, plant growth promoting, and systemic resistance inducing activities in rice. *Plant Pathol. J.* **31**, 152–164.

Dunlap, C.A., Kim, S., Kwon, S., and Rooney, A.P. 2016. *Bacillus velezensis* is not a later heterotypic synonym of *Bacillus amyloliquefaciens* ; *Bacillus methylotrophicus*, *Bacillus amyloliquefaciens* subsp. *plantarum* and "*Bacillus oryzicola*" are later heterotypic synonyms of *Bacillus velezensis,* based on phylogenomics. *Int. J. Syst. Evol. Microbiol.* **66**, 1212–1217.

Eid, J., Fehr, A., Gray, J., Luong, K., Lyle, J., Otto, G., Peluso, P., Rank, D., Baybayan, P., Bettman, B., *et al.* 2009. Real-time DNA sequencing from single polymerase molecules. *Science* **323**, 133–138.

Hallmann, J. and Berg, G. 2006. Spectrum and population dynamics of bacterial root endophytes, pp. 15–31. *In* microbial root endophytes. Springer, Berlin, Heidelberg.

Hossain, M.T., Khan, A., Chung, E.J., Rashid, M.H., and Chung, Y.R. 2016. Biological control of rice bakanae by an endophytic *Bacillus oryzicola* YC7007. *Plant Pathol. J.* **32**, 228–241.

Ruiz-Garcia, C., Bejar, V., Martinez-Checa, F., Llamas, I., and Quesada, E. 2005. *Bacillus velezensis* sp. nov., a surfactant-producing bacterium isolated from the river Vélez in Málaga, southern Spain. *Int. J. Syst. Evol. Microbiol.* **55**, 191–195.

Seemann, T. 2014. Prokka: Rapid prokaryotic genome annotation. *Bioinformatics* **30**, 2068–2069.

Shahzad, R., Khan, A.L., Bilal, S., Asaf, S., and Lee, I.J. 2017. Plant growth-promoting endophytic bacteria versus pathogenic infections: An example of *Bacillus amyloliquefaciens* RWL-1 and *Fusarium oxysporum* f. sp. *lycopersici* in tomato. *PeerJ.* **5**, e3107.

Sommer, D.D., Delcher, A.L., Salzberg, S.L., and Pop, M. 2007. Minimus: a fast, lightweight genome assembler. *BMC Bioinformatics* **8**, 64–75.