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Genome Announcement

Complete genome sequence of *Paenibacillus swuensis* DY6^T, a bacterium isolated from gamma-ray irradiated soil

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감마선 조사된 토양에서 분리된 박테리아 *Paenibacillus swuensis* DY6^{T}의 완전한 게놈 서열

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ABSTRACT: Several bacterial species have been reported to be surviving after the ionizing radiation treatment due to the presence of sophisticated enzymes systems and some endospores producing bacterial strains can also resist, due to the presence of thick spore coat. In this study, we report the complete genome sequence of a bacterium *Paenibacillus swuensis* DY6^T, isolated from an irradiated soil sample. The genome comprised of 5,012,599 bp with the G+C content of 49.93%, the genome included 4,463 protein coding genes and 133 RNA genes.

Key words: *Paenibacillus*, endospore, irradiated soil

The members of the *Paenibacillus* are aerobic or facultative aerobic, Gram-positive, have L-ornithine in the cell wall without teichoic acids and produce endospores. The spores without nutrients become metabolically dormant, contain little or no high-energy compounds such as ATP and NADH, exhibit no detectable metabolism (Setlow, 1994). The short period of dormant state during irradiation, will not affect the spore outgrowth, due to DNA repair during spore germination and it ensures the spore survival (Setlow, 2006). In this study, we report a complete genome sequence of *Paenibacillus swuensis* DY6^T isolated from a gamma ray-irradiated soil sample collected from the mountain Deogyusan (GPS; N 35° 51' 38" E 127° 44' 47"; altitude 1,500 m), Jeonbuk Province, South Korea (Lee *et al*., 2014). Strain DY6 is characterized as a Gram-positive, endospore-forming, motile and rod-shaped bacterium, belongs to the family *Paenibacillaceae* in the class *Bacilli*.

The genomic DNA was extracted using a genomic DNA purification kit (Promega). A library was constructed according to Pacific Biosciences RS II sequencing method manual. The 82,221 sequencing reads were obtained and were assembled using the PacBio SMRT Analysis (version, 2.3.0) with default options. Genome sequencing and annotation were carried out using Pacific Biosciences RS II platform. The final assembly resulted in 1 contig generating corresponding genome size of 5,012,599 bp. The protein-coding sequences (CDS) were predicted by Glimmer 3.02 (Delcher *et al*., 1999), and the genome annotation was performed by NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAP, http://www.ncbi.nlm.nih.gov/books/NBK174280/). The rRNA and tRNA were predicted by using RNAmmer ENREF-39 (Lagesen, *et al*., 2007) and

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Table 1. Genome statistics

Attribute	Value	% of Total[a]
Genome size (bp)	5,012,599	100.00%
DNA coding region (bp)	4,507,183	89.92%
DNA G+C content (bp)	2,452,658	48.93%
No. of contigs	1	100%
Total genes	4,596	100.00%
RNA genes	133	2.89%
rRNA operons	30	0.65%
Protein-coding genes	4,463	97.10%
Genes with function prediction	3,597	78.26%
Genes assigned to COGs	2,949	64.16%
Genes assigned Pfam domains	3,765	81.92%
Genes with signal peptides	296	6.44%
Genes with transmembrane helices	1,334	29.03%

[a] The total is based on either the size of the genome in base pairs or the total number of protein-coding genes in the annotated genome.
Abbreviation; bp, base pair; DNA, deoxyribonucleic acid; RNA, ribonucleic acid

Infernal (Nawrocki *et al*., 2009) respectively.

The genome of strain DY6^T consists of a circular chromosome of the size 5,012,599 bp with the GC content of 48.93%. A total of 4,596 genes were predicted, among them, 4,463 genes are protein-coding genes, 133 RNA genes, and 3,597 genes were assigned to have putative functions and remaining genes are annotated as hypothetical or converted hypothetical proteins. A total of 2,949 genes is categories into Cluster of Orthologues Groups (COGs) (Tatusov *et al*., 2003) were predicted (Table 1 and Fig. 1). The genomic features revealed the key enzymes involved in the DNA recovery after the ionizing radiation recovery. The damaged DNA is repaired using UvrABC pathway (Excinuclease ABC subunt A, B, and C), RecFOR (DNA recombination proteins), and UvrD (ATP-dependent DNA helicase) mediated pathways. The cluster of genes involving in the nucleotide excision repair (NER) (Cai *et al*., 2014; Kim *et*

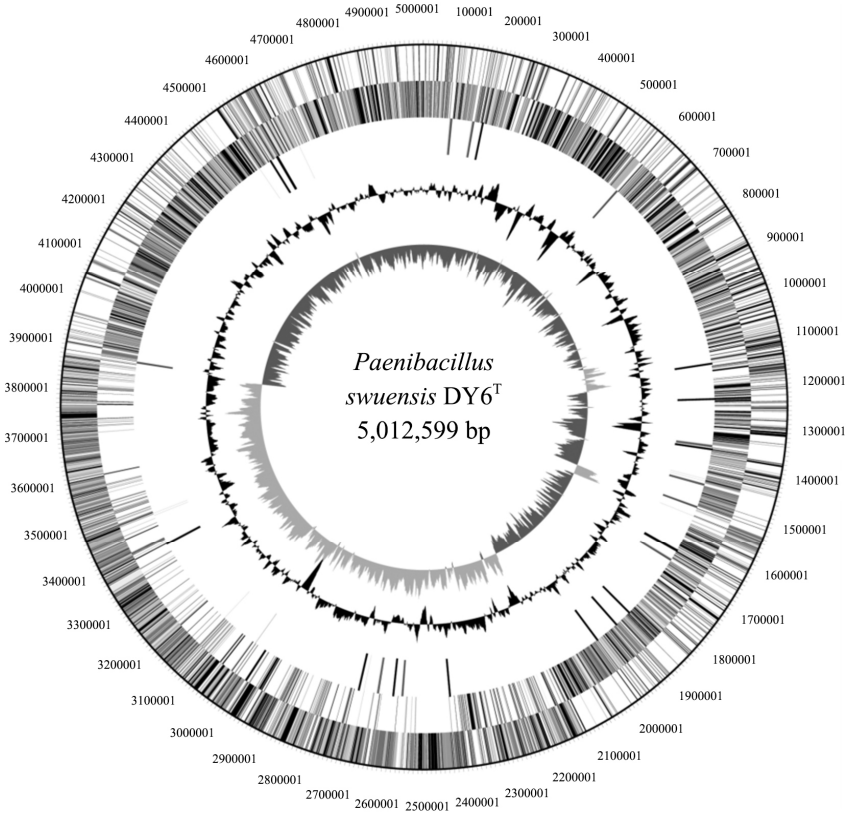

Fig. 1. Graphical circular map of *Paenibacillus swuensis* DY6^T.
From outside to the center:
Genes on forward strand
Genes on reverse strand
RNA genes (tRNAs green, rRNAs red, other RNAs black)
GC content
GC skew

al., 2015; Srinivasan *et al*., 2015) are also present in the genome. The high spore resistance is may be by low core water content that reduced the production of reactive oxygen species (ROS) which damage protein, lipids and nucleic acids of the spore, which leads to cell death. The cells of *Paenibacillus swuensis* DY6^T did not show gamma and UVC radiation, but the endospores in the soil resist the 5 KGy radiation that is used to irradiate the soil sample before the bacterial isolation.

Nucleotide sequence accession number

The genome sequence was deposited in DDBJ/EMBL/GenBank under the under the accession number CP011388. The strain is deposited at the Korean Collection for Type Cultures, and its ID is KCTC 33026^T.

적 요

박테리아 종들은 정교한 효소 시스템의 존재로 인해 이온화 방사선 처리 후에 생존할 수 있는 것으로 보고되어 왔고 몇몇 내생 포자를 생산하는 박테리아 또한 두꺼운 포자껍질의 존재 때문에 방사선에 저항할 수 있다. 이 연구에서는 방사선이 조사된 토양의 시료에서 추출된 *Paenibacillus swuensis* DY6^{T}의 완전한 게놈 서열을 분석하였다. 이 게놈은 G+C 함량이 49.93%인 5,012,599 bp으로 구성되어 있고 단백질 정보를 암호화한 유전자 4,463개와 133개 RNA 유전자를 포함하고 있다.

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