

Complete genome sequence of *Deinococcus puniceus* DY1^T, a radiation resistant bacterium

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방사선 내성 세균 *Deinococcus puniceus* DY1^T의 완전한 게놈 서열 분석

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Cells of *Deinococcus puniceus* DY1^T are Gram-positive, coccus-shaped, and crimson color-pigmented. Strain DY1^T was isolated from soil irradiated with 5 kGy gamma radiation and showed resistance to UVC and gamma radiation. In this study, we report the complete genome sequence of a bacterium *Deinococcus puniceus* DY1^T is consist of circular chromosome comprised of 2,971,983 bp, with the G + C content of 62.5%. The complete genome sequence was obtained using the PacBio RS II platform, it included 2,617 coding sequences (CDs), 2,762 genes, and 88 pseudogene.

Keywords: *Deinococcus*, complete genome, nucleotide excision repair, PacBio RS II, radiation resistance

The radiation resistant bacteria belonging to the genus *Deinococcus* are known to have extreme DNA repair mechanism and protein system to repair the damaged DNA after the radiation (White *et al.*, 1999; de Groot *et al.*, 2009; Daly, 2012; Yu and Lee, 2017). The bacterial species belonged to the genus

Hymenobacter (Kim *et al.*, 2017a; Srinivasan *et al.*, 2017) and *Spirosoma* (Kim *et al.*, 2017b), have been reported for radiation resistance. Strain DY1^T was isolated from soil irradiated with 5 kGy gamma radiation and showed resistance to gamma irradiation with the D₁₀ value of 10 kGy. Cells of *Deinococcus puniceus* DY1^T are Gram-positive, coccus-shaped, and produced crimson colored pigments (Lee *et al.*, 2015).

To understand the genomic features of radiation resistance, we determined the genome sequence of *Deinococcus puniceus* DY1^T. The genome annotation confirmed the presence of key enzymes involved in the recovery of damaged DNA from ionizing radiation. The nucleotide excision repair (NER) pathway was reported from other highly radiation-resistant bacteria such as *D. radiodurans* (Battista and Cox, 2006; Blasius *et al.*, 2008).

The genome of the strain DY1^T was sequenced by Pacific Biosciences RS II platform, and a library was constructed according to Pacific Biosciences RS II Sequencing method. The 104,937 sequence reads were obtained and assembled using the PacBio SMRT Analysis (version 2.3.0) with default

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options. The protein-coding sequences (CDS) were predicted by Glimmer (version 3.02), 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 rRNAmmer and tRNAscan-SE, respectively.

The complete genome of *Deinococcus puniceus* DY1^T contain a chromosome of 2,971,983 bp with a G + C mol of 62.6%, a total of 2,815 genes (Fig. 1); 2,759 genes with protein-coding and 56 are RNA genes were assigned a putative function, and the remaining was annotated as hypothetical or conserved hypothetical proteins (Table 1).

The complete genome sequence of *Deinococcus puniceus* DY1^T showed the presence of the NER pathway enzymes, the key enzymes including excinuclease UvrABC complex, which recognizes and repair the structural changes caused by ionizing

radiation (Petit and Sancar, 1999). The genome of strain *Deinococcus puniceus* DY1^T also contained the UV damage repair endonuclease (UvdE) coding gene and several genes for homologs recombination; that plays a central role in the nucleic acid metabolism. The genomic information about radiation

Table 1. General features of *Deinococcus puniceus* DY1

Features	Chromosome
Length (bp)	2,971,983
G + C content (%)	62.56
Number of genes	2,815
Protein coding genes	2,759
Pseudogenes	88
CDS	2,617
rRNA gene	9
tRNA genes	47

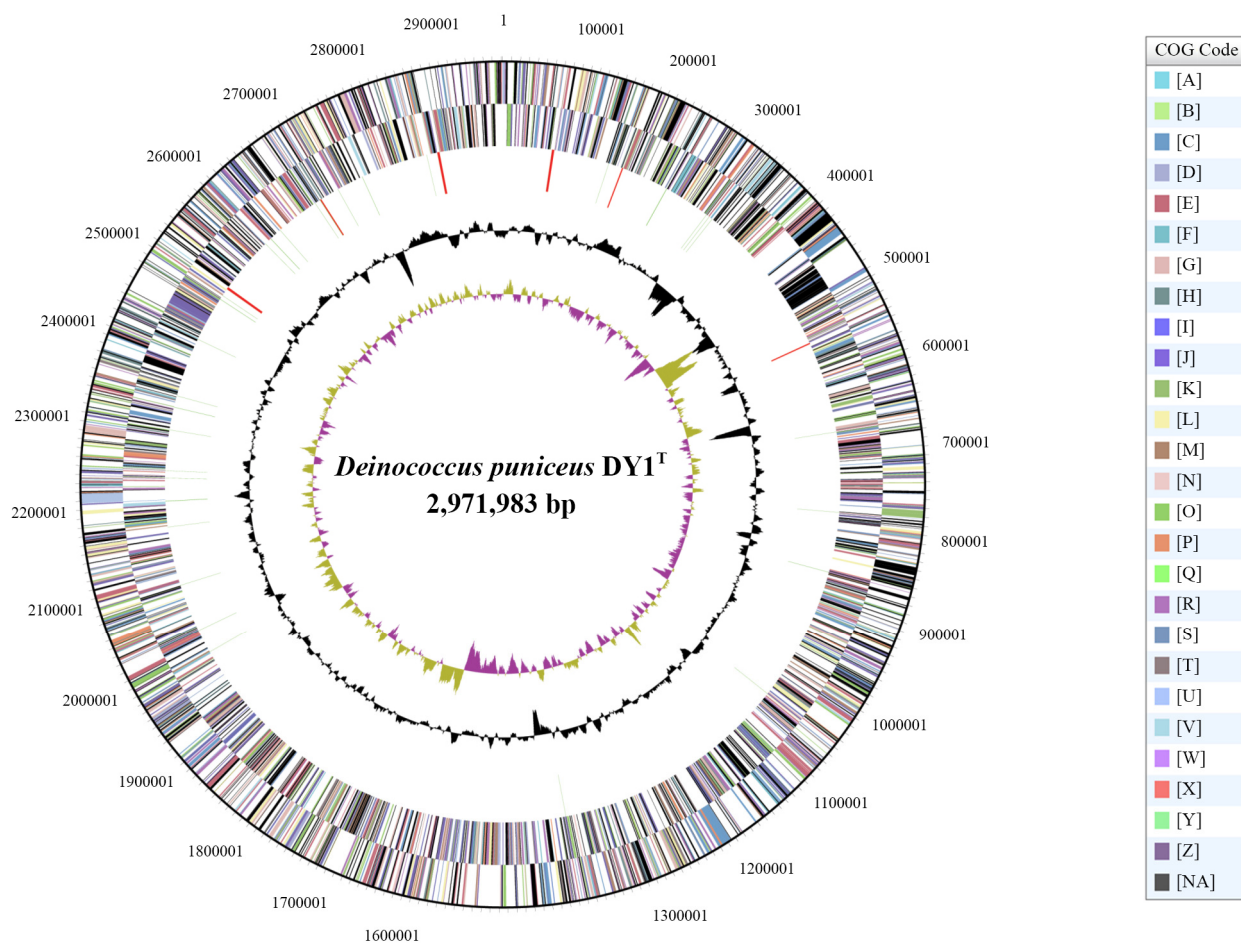


Fig. 1. Graphical circular map of *Deinococcus puniceus* DY1^T. From outside to the center: Genes on forward strand, Genes on reverse strand, RNA genes (tRNAs green, rRNAs red, other RNAs black), GC content, GC skew.

resistance can be very useful to understand the mechanisms and also apply it in the field of radiation biotechnology.

Nucleotide sequence accession number

The genome sequence was deposited in DDBJ/EMBL/GenBank under the accession number CP011387. The strain is deposited at the Korean Collection for Type Cultures, and its ID is KCTC 33027^T.

적 요

이 연구에서는 5 kGy 의 감마선에 조사된 토양으로부터 분리된 *Deinococcus puniceus* DY1^T 의 완전한 게놈서열을 분석하였다. 이 균주는 UVC 와 감마선에 대한 저항성을 보였으며, PacBio RS II platform 을 통해 시퀀싱을 진행하였다. 해당유전체의 분석결과 G+C 함량이 62.5%인 2,971,983 bp 크기의 원형 염색체를 확인하였으며, 해당 염색체는 2,617 개의 코딩 서열과 2,762 개의 유전자 그리고 88 개의 위유전자를 포함하고 있다.

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