

Genome Announcement

Complete genome sequence of *Spirosoma montaniterrae* DY10^T isolated from gamma-ray irradiated soil

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감마선 조사된 토양에서 분리된 박테리아 *Spirosoma montaniterrae* DY10^T의 완전한 게놈 서열

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(Received February 21, 2017; Revised February 27, 2017; Accepted February 27, 2017)

A Gram-negative, yellow-pigmented, long-rod shaped bacterium *Spirosoma montaniterrae* DY10^T was isolated from a soil sample collected at Mt. Deogyusan, Jeonbuk Province, Republic of Korea. Cells showed extreme gamma radiation resistance with the D₁₀ value of 12 KGy. The complete genome sequence of strain DY10^T is consist of a circular chromosome (5,797,678 bp) encoding 5,116 genes, 9 rRNA genes and 39 tRNA genes. The genomic features contain the key enzymes for gamma and UVC radiation.

Keywords: *Spirosoma*, nucleotide excision repair, radiation resistance

Ironing radiation such as gamma rays produce reactive oxygen species and damages the intracellular proteins and lipids, which leads to cell death (Daly, 2012). However, the radiation resistant bacteria such as *Deinococcus*, *Hymenobacter*, *Spirosoma*, *Pontibacter* (Kim *et al.*, 2015; Srinivasan *et al.*, 2015), known to have extreme DNA repair mechanisms and protein production system to repair the damaged DNA (White

et al., 1999). Strain DY10^T was isolated from the isolated from a soil sample collected at Mt. Deogyusan, Jeonbuk Province, South Korea (Lee *et al.*, 2015).

Spirosoma montaniterrae DY10^T is Gram-negative, yellow pigmented, long rod-shaped bacterium and exhibited exceptional resistance to UVC and gamma irradiation with the D₁₀ value of 12 KGy. The complete 16S rRNA gene sequence of *Spirosoma montaniterrae* DY10^T showed similarity with *Spirosoma arcticum* R2-35^T (91.0%) and *Spirosoma lingual* DSM 74^T (90.8%). To understand the genomic features of radiation resistance, we determined the genome sequence of *Spirosoma montaniterrae* DY10^T. The genome annotation confirmed the presence of the main 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* (Blasius *et al.*, 2008).

The complete genome was sequenced using Pacific Biosciences RS II platform, and a library was constructed according to Pacific Biosciences RS II Sequencing method manual. The 32,660 sequence reads were obtained and assembled using the PacBio SMRT Analysis (version 2.3.0) with default options.

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The protein-coding sequences (CDS) were predicted using Glimmer [Version 3.02 (Delcher *et al.*, 2007)], 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 (Lagesen *et al.*, 2007) and tRNAscan-SE

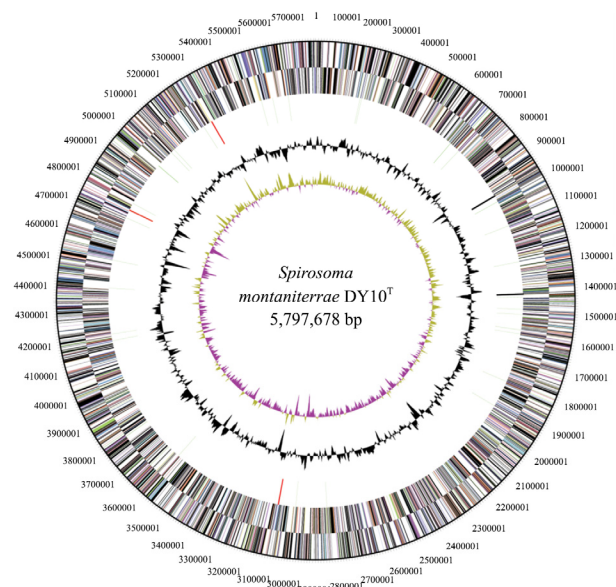


Fig. 1. Graphical circular map of *Spirosoma montaniterrae* DY10^T.

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

Table 1. General features of *Spirosoma montaniterrae* DY10^T

Features	Chromosome
Length (bp)	5,797,678
Genome coverage	72.4
G + C content (%)	52.7
No. of contigs	1
Genes	5,116
Protein-coding genes	5,066
rRNA gene	9
tRNA genes	39
Genes with function prediction	3,615
Genes assigned to COGs	2,660
Genes assigned Pfam domains	3,824
Genes with signal peptides	786
Genes with transmembrane helices	1,159

Abbreviation: bp, base pair, DNA, deoxyribonucleic acid, RNA, ribonucleic acid

(Lowe and Eddy, 1997), respectively.

Spirosoma montaniterrae DY10^T contain a chromosome of 5,797,678 bp with a G + C mol of 52.7%, a total of 5,116 genes; 5,066 genes with protein coding genes; 39 are tRNA genes and the remaining was annotated as hypothetical or conserved hypothetical proteins. A total of 2,660 genes is categories into Cluster of Orthologues Groups (COGs) (Tatusov *et al.*, 2003) were predicted (Table 1 and Fig. 1). *Spirosoma montaniterrae* DY10^T contains the NER pathway enzymes, which includes the excinuclease UvrABC complex, that recognizes and repair the structural changes caused by gamma radiation by creating dual incisions 5' and 3' to the damaged site (Petit and Sancar, 1999). The genome of strains *Spirosoma montaniterrae* DY10^T also contained the UV damage repair endonuclease (UvdE) coding gene.

The genome of strain *Spirosoma montaniterrae* DY10^T also encodes several genes for homologs recombination; that plays a central role in the nucleic acid metabolism. The DNA repair pathway was reported in the *D. radiodurans* genome (Earl *et al.*, 2002; Battista and Cox, 2006). The radiation resistant in strain *Spirosoma montaniterrae* DY10^T is achieved by a combination of various DNA recovery pathways. The genomic information of radiation resistant can be very useful to understand the mechanisms and apply it on radiation biotechnology.

Nucleotide sequence accession number

The genome sequence was deposited in DDBJ/EMBL/GenBank under the under accession number CP014263. This strain is available from the Korean Collection fortype Cultures, South Korea with the accession number KCTC 23999^T.

적 요

그람 음성이며 황색인 긴 막대 모양의 세균 *Spirosoma montaniterrae* DY10^T는 전라북도 덕유산에서 분리가 되었다. 이 세균의 세포는 감마선에 대해 12 KGy의 D₁₀ 값을 보이며 극 단적인 감마선 저항성을 보였다. DY10^T 균주의 완전한 게놈 서열은 5,116개의 유전자, 39개의 tRNA 유전자를 포함하는 원형 염색체(5,797,678 bp)로 구성되었다. 유전체 특징은 감 마선 및 UVC에 대응하는 주요 효소를 포함하였다.

Acknowledgements

This work was supported by a research grant from Seoul Women's University (2017) and by a grant from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea (NIBR201501113).

References

- Battista, J. and Cox, M.** 2006. Genome reconstitution in the extremely radiation resistant bacterium *Deinococcus radiodurans*. In Cigna, A. and Durante, M. (eds.), Radiation Risk Estimates in Normal and Emergency Situations. Springer, Netherlands.
- Blasius, M., Sommer, S., and Hubscher, U.** 2008. *Deinococcus radiodurans*: what belongs to the survival kit? *Crit. Rev. Biochem. Mol.* **43**, 221–238.
- Delcher, A.L., Bratke, K.A., Powers, E.C., and Salzberg, S.L.** 2007. Identifying bacterial genes and endosymbiont DNA with glimmer. *Bioinformatics* **23**, 673–679.
- Earl, A.M., Rankin, S.K., Kim, K.P., Lamendola, O.N., and Battista, J.R.** 2002. Genetic evidence that the *uvrE* gene product of *Deinococcus radiodurans* R1 is a UV damage endonuclease. *J. Bacteriol.* **184**, 1003–1009.
- Kim, M.K., Srinivasan, S., Back, C.G., Joo, E.S., Lee, S.Y., and Jung, H.Y.** 2015. Complete genome sequence of *Deinococcus swuensis*, a bacterium resistant to radiation toxicity. *Mol. Cell Toxicol.* **11**, 315–321.
- Lagesen, K., Hallin, P., Rodland, E.A., Staerfeldt, H.H., Rognes, T., and Ussery, D.W.** 2007. Rnammer: consistent and rapid annotation of ribosomal rna genes. *Nucleic Acids Res.* **35**, 3100–3108.
- Lee, J.J., Kang, M.S., Joo, E.S., Kim, M.K., Im, W.T., Jung, H.Y., and Srinivasan, S.** 2015. *Spirosoma montaniterrae* sp. nov., an ultraviolet and gamma radiation-resistant bacterium isolated from mountain soil. *J. Microbiol.* **53**, 429–434.
- Lowe, T.M. and Eddy, S.R.** 1997. Trnscan-se: A program for improved detection of transfer rna genes in genomic sequence. *Nucleic Acids Res.* **25**, 955–964.
- Petit, C. and Sancar, A.** 1999. Nucleotide excision repair: from *E. coli* to man. *Biochimie* **81**, 15–25.
- Srinivasan, S., Kim, M.K., Joo, E.S., Lee, S.Y., Lee, D.S., and Jung, H.Y.** 2015. Complete genome sequence of *Rufibacter* sp. DG31D, a bacterium resistant to gamma and uv radiation toxicity. *Mol. Cell Toxicol.* **11**, 415–421.
- Tatusov, R.L., Fedorova, N.D., Jackson, J.D., Jacobs, A.R., Kiryutin, B., Koonin, E.V., Krylov, D.M., Mazumder, R., Mekhedov, S.L., Nikolskaya, A.N., et al.** 2003. The COG database: an updated version includes eukaryotes. *BMC Bioinformatics* **4**, 41.
- White, O., Eisen, J.A., Heidelberg, J.F., Hickey, E.K., Peterson, J.D., Dodson, R.J., Haft, D.H., Gwinn, M.L., Nelson, W.C., Richardson, D.L., et al.** 1999. Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1. *Science* **286**, 1571–1577.