

Complete genome sequence of *Flavisolibacter tropicus* LCS9^T, a radiation resistant bacterium

Myung Kyum Kim¹, Eun-Hwa Sohn², Hee-Young Jung^{3,4*}, and Sathiyaraj Srinivasan^{1*}

¹Department of Bio & Environmental Technology, College of Natural Science, Seoul Women's University, Seoul 01797, Republic of Korea

²Department of Herbal Medicine Resources, Kangwon National University, Samcheok 25949, Republic of Korea

³School of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea

⁴Institute of Plant Medicine, Kyungpook National University, Daegu 41566, Republic of Korea

방사선 내성 세균 *Flavisolibacter tropicus* LCS9^T의 완전한 게놈 서열

김명겸¹ · 손은화² · 정희영^{3,4*} · 스리니바산 사티아라지^{1*}

¹서울여자대학교 자연과학대학 생명환경공학과, ²강원대학교 생약자원개발학과, ³경북대학교 농업생명과학대학 응용생명과학부 응용생물학전공, ⁴경북대학교 식물의학연구소

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Flavisolibacter tropicus LCS9^T was isolated from a soil sample collected from tropical zone within the Ecorium of the National Institute of Ecology in Seochon, central-western Korea. In this study, we report the complete genome sequence of the bacterium *Flavisolibacter tropicus* LCS9^T, which possesses a circular chromosome comprised of 5,940,863 bp with the G + C mol content of 41.5%. The genome sequence annotation showed that the complete genome includes 5,075 genes, 337 pseudogenes, and 59 rRNA genes. The radiation resistance genes such as excinuclease UvrABC complex and UvdE were present in the genome.

Keywords: *Flavisolibacter tropicus* LCS9^T, complete genome, nucleotide excision repair, PacBio RS II, radiation resistance

The family *Chitinophagaceae* belongs to the phylum *Bacteroidetes* and was created by Kämpfer *et al.* (2011) with *Chitinophaga* as the type genus. The family *Chitinophagaceae*

includes 27 genera (www.bacterio.net/chitinophagaceae.html) along with the genus *Flavisolibacter* and the members are Gram-stain-negative, aerobic or facultative anaerobic bacteria. Species of *Chitinophagaceae* were observed in gamma irradiated sediments along with others members of the phylum *Bacteroidetes* (Brown *et al.*, 2015). The radiation resistant bacteria known to have advanced DNA repair and protein system to survive the ionizing irradiation (White *et al.*, 1999; de Groot *et al.*, 2009; Daly, 2012; Yu and Lee, 2017).

In this study, we report a complete genome sequence of *Flavisolibacter tropicus* LCS9^T belonging to the family *Chitinophagaceae* isolated from tropical soil within the Ecorium of the National Institute of Ecology in Seochon (Lee *et al.*, 2016). *Flavisolibacter tropicus* LCS9^T is characterized as Gram-stain-negative, non-motile, deep yellow, rod-shaped bacterium. Strain LCS9^T showed lower level of gamma irradiation resistance (Lee *et al.*, 2016). To understand the genomic features of radiation resistance, we determined the genome sequence of *Flavisolibacter tropicus* LCS9^T. The genomic features of strain LCS9^T confirmed the presence of the main enzymes involved in the

*For correspondence. (S. Srinivasan) E-mail: drsini@swu.ac.kr;
Tel.: +82-2-970-5667; Fax: +82-2-970-5974 / (H.Y. Jung) E-mail:
heeyoung@knu.ac.kr; Tel.: +82-53-950-5760; Fax: +82-53-950-6758

recovery of damaged DNA from ionizing radiation.

The genomic DNA was extracted using a genomic DNA purification kit (Promega). A library was constructed according to Pacific Biosciences RS II sequencing method. The 44,196 sequence reads were obtained and assembled using the PacBio SMRT Analysis (version 2.3.0) with default 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 tRNAscanSE, respectively.

Flavisolibacter tropicus LCS9^T contains a chromosome of 5,940,863 bp with a G + C mol of 41.5%, a total of 5,075 genes; 5,016 genes with protein-coding and 59 are RNA genes were assigned a putative function, and the remaining was annotated as hypothetical or conserved hypothetical proteins. The complete

genome of the strain LCS9^T revealed the key enzymes involved in the DNA recovery after the gamma and UV irradiation rehabilitation. The genome annotation showed the presence of UvrABC pathway and RecA and MutS mediated pathways that repair the damaged DNA (Truglio *et al.*, 2006).

Table 1. General features of *Flavisolibacter tropicus* LCS9

Features	Chromosome
Length (bp)	5,940,863
G + C content (%)	41.5
Genes	5,075
Pseudo Genes	337
Protein coding genes	5,016
rRNA gene	9
tRNA genes	49
Protein coding genes with function	3,576
Protein coding genes with enzymes	901
Protein coding genes with COGs	2,489

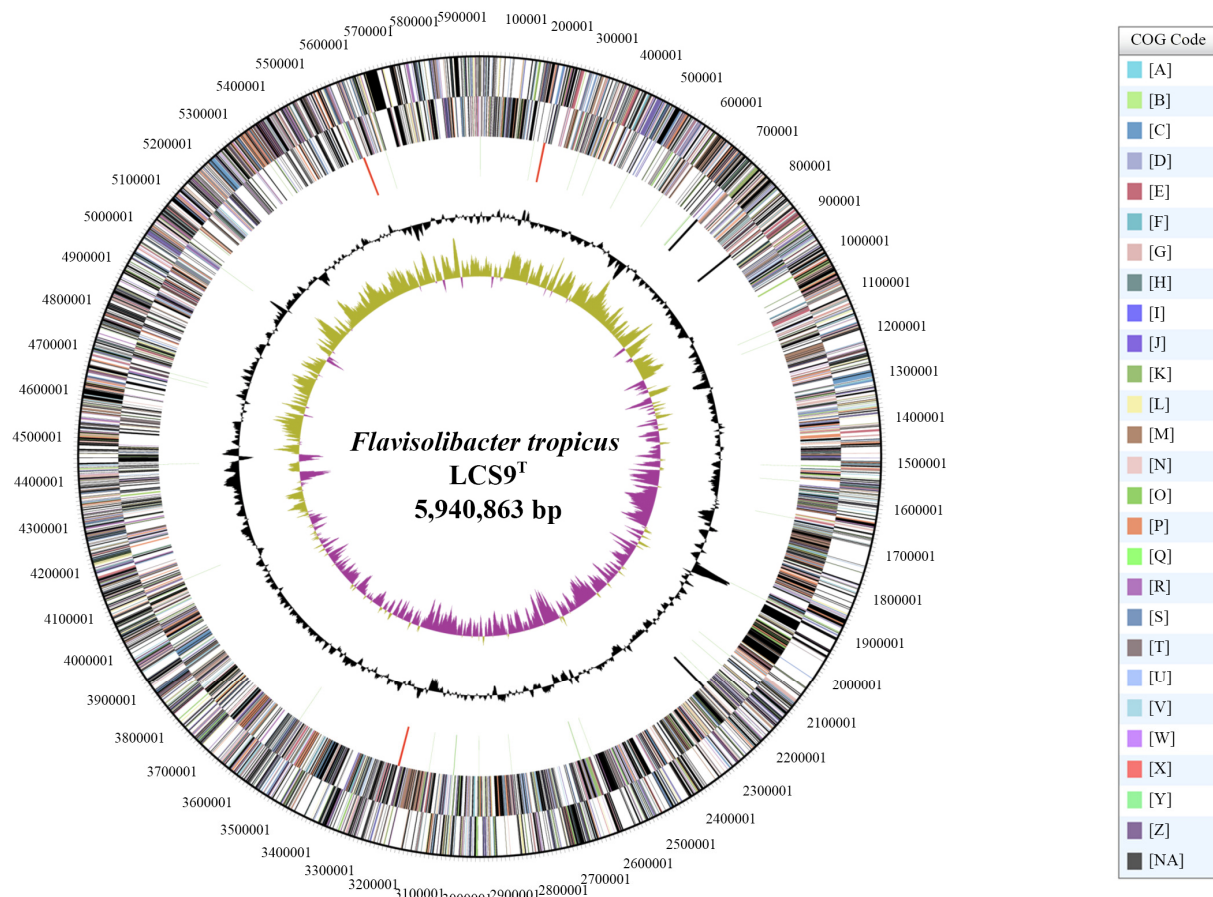


Fig. 1. Graphical circular map of *Flavisolibacter tropicus* LCS9^T. From outside to the center: Genes on forward strand, Genes on reverse strand, RNA genes (tRNAs green, rRNAs red, other RNAs black), GC content, GC skew.

The excinuclease UvrABC complex recognizes and repair the structural changes caused by ionizing radiation by creating dual incisions 5' and 3' to the damaged site (Petit and Sancar, 1999). The cluster of genes involving in the nucleotide excision repair (NER) are also present in the genome, which include copies of excinuclease ABC subunit A, an excinuclease ABC subunit B and excinuclease ABC subunit C (Battista and Cox, 2006; Blasius *et al.*, 2008). The radiation resistant mechanisms of *Flavisolibacter tropicus* LCS9^T can be potentially used for environmental bioengineering and radiation biotechnology.

Nucleotide sequence accession number

The genome sequence was deposited in DDBJ/EMBL/GenBank under the accession number CP011390. The strain is deposited at the Korean Collection for Type Cultures, and its ID is KCTC 42070^T.

적 요

Flavisolibacter tropicus LCS9^T 은 한국 중서부에 위치한 서천 국립생태원 에코리움 내 열대관 토양에서 분리되었다. 이 연구에서 G + C 함량이 41.5%인 5,940,863 bp 의 원형 염색체로 구성된 *Flavisolibacter tropicus* LCS9^T 의 완전한 게놈서열을 분석하였다. 이 완전한 게놈서열은 5,075 개의 유전자, 337 개의 위유전자 그리고 59 개의 rRNA 유전자를 포함하고 있다. 유전체 특징은 감마선 및 UVC 에 대응하는 주요 효소를 포함하였다.

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