

## Note (Genome Announcement)

# Complete genome sequence of *Spirosoma rigui* KCTC 12531<sup>T</sup>, a bacterium isolated from fresh water from the Woopo wetland for taxonomic study

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## 계통분류학적 연구를 위한 우포늪에서 분리된 박테리아 *Spirosoma rigui* KCTC 12531<sup>T</sup>의 완전한 게놈 서열

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*Spirosoma rigui* KCTC 12531<sup>T</sup> was isolated from fresh water from the Woopo wetland, Korea. In this study, we report the complete genome sequence of a bacterium *Spirosoma rigui* KCTC 12531<sup>T</sup>, its complete genome sequence was obtained using the PacBio RS II platform. The genome comprised of 5,828,404 bp with the G + C content of 54.4%, the genome included 4,774 genes were predicted, among them, 4,647 genes are protein-coding genes.

**Keywords:** *Spirosoma*, fresh water, PacBio RS II, wetland, Woopo

The family *Flexibacteraceae* is one of the major phylogenetic lineages within the phylum *Bacteroidetes* (Garrity and Holt, 2001). The family *Flexibacteraceae* constitutes a phylogenetically diverse group within the phylum *Bacteroidetes*. One of the lineages in this group comprises the genera *Spirosoma*, *Runella*, *Larkinella* and *Dyadobacter* currently classified in the family *Flexibacteraceae* (Baik *et al.*, 2007). In

case of *Spirosoma*, Larkin and Borrall (1984) was first proposed the genus *Spirosoma* is a member of the family *Flexibacteraceae*.

Woopo wetland, located in the east of the Nakdong river, is the largest undisturbed wetland in the Republic of Korea (Baik *et al.*, 2008). As the Ramsar wetland, it was declared a nature conservation area in 1997 (<http://ramsar.wetlands.org/>). Due to its special features of biodiversity, this wetland have drawn a great public attention. However, whole genomic information of isolates from this site is still lacking. Therefore, we sequenced and analyzed the genome of *Spirosoma rigui* KCTC 12531<sup>T</sup> for the increase of understanding of ecological niche of wetland.

In this study, we report a complete genome sequence of *Spirosoma rigui* KCTC 12531<sup>T</sup> was isolated from fresh water from the Woopo wetland, Korea using the standard dilution plating technique (Baik *et al.*, 2007). Strain KCTC 12531<sup>T</sup> is characterized as a Gram-reaction-negative, yellow-pigmented and gliding motility bacterium. The genomic DNA was extracted using a genomic DNA purification kit (Promega). A library was

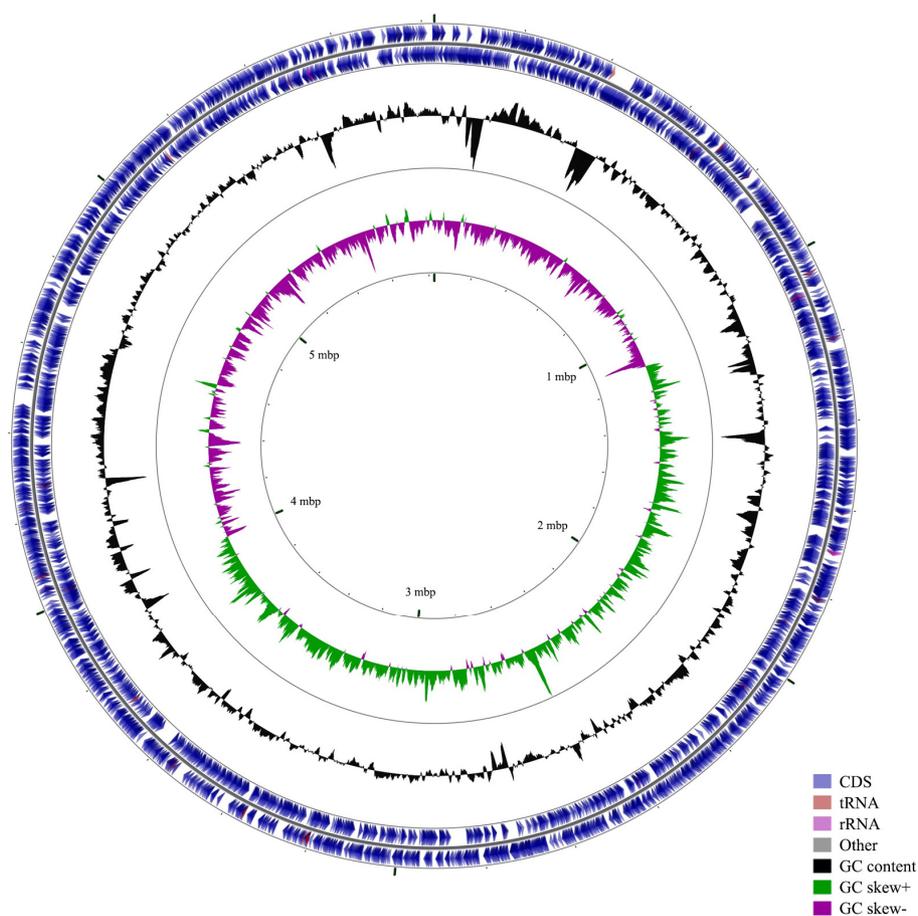
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constructed according to Pacific Biosciences RS II sequencing method manual. The 161,346 sequencing reads were obtained and were assembled using the PacBio SMRT Analysis (version, 2.3.0) with default options. Genome sequencing and annotation were carried out using Pacific Biosciences RS II platform. CGview software was used to construct the genome map (Grant and Stothard, 2008). The final assembly resulted in 1 contig generating corresponding genome size of 5,828,404 bp. The protein-coding sequences (CDS), rRNA, tRNA and the genome annotation was performed by NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAP, <http://www.ncbi.nlm.nih.gov/books/NBK174280/>) (Tatusova *et al.*, 2013). The genome of strain KCTC 12531<sup>T</sup> consists of a circular chromosome of the size 5,828,404 bp with the GC content of 54.4%. A total of 4,774 genes were predicted, among them, 4,647 genes are protein-coding genes, 9 rRNA genes, 43 tRNA genes and 73 pseudogene were assigned (Fig. 1 and Table 1). The genome of

strain *Spirosoma rigui* KCTC 12531<sup>T</sup> encodes several genes for defense against protein damage like DNA damage and ionizing radiation. Clp protease system including proteolytic subunit, ATPase subunits (ClpA, ClpB and ClpX) is one of the well-known cluster of genes responsible for restoration. Among these genes, ClpX is important for the radiation resistance and the regulation of cell division (Kim *et al.*, 2017).

**Table 1.** Genome features of *Spirosoma rigui* KCTC 12531<sup>T</sup>

Attribute	Value
Genome size (bp)	5,828,404
DNA G + C content (bp)	54.4%
No. of contigs	1
Total genes	4,774
Protein-coding genes	4,647
rRNA	9
tRNA	43
Pseudogene	73



**Fig. 1.** Graphical circular map of *Spirosoma rigui* KCTC 12531<sup>T</sup>. From outside to the center: Genes on forward strand, Genes on reverse strand, RNA genes (tRNAs peach, rRNAs pink, other RNAs grey), GC content, GC skew.

The *Spirosoma rigui* KCTC 12531<sup>T</sup> is available at KCTC 12531<sup>T</sup> and NBRC 101117<sup>T</sup>.

#### Nucleotide sequence accession number

The genome sequence was deposited in DDBJ/EMBL/GenBank under the under the accession number CP020105.

## 적 요

이 연구에서는 우포늪의 깨끗한 물에서 분리된 *Spirosoma rigui* KCTC 12531<sup>T</sup>의 완전한 게놈 서열을 분석하였다. 이 게놈은 G + C 함량이 54.4%인 5,828,404 bp으로 구성되어 있고 4,774개의 유전자와 4,647개의 단백질 코딩 유전자, 9개의 rRNA 유전자 그리고 43개의 tRNA 유전자 및 73개의 위유전자(pseudogene)를 포함하고 있다.

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