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# Complete Genome Sequence of *Cytobacillus firmus* T8, Isolated from the Rhizosphere of Pepper (*Capsicum annuum* L.)

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**This study presents the complete genome sequence of *Cytobacillus firmus* strain T8, which was obtained from the rhizosphere soil of pepper (*Capsicum annuum* L.). The genome of the strain consists of a single chromosome with a total size of 4,383,751 bp and the GC content of 42%.**

**Keywords:** ***Cytobacillus firmus*, complete genome, pepper, rhizosphere**

*Cytobacillus firmus* (synonym *Bacillus firmus*), which was first reported in 1933, is an aerobic Gram-positive bacterium, capable of producing endospores [1]. It is known for several useful biological properties, such as its ability to tolerate extreme environmental conditions, its ability to degrade pollutants, and its nematocidal activity [2–4]. Also, *C. firmus* has gained attention in sustainable agriculture due to its potential as a plant growth-promoting rhizobacteria (PGPR) [5, 6].

In this study, *C. firmus* T8 was isolated from the rhizosphere soil of pepper (*Capsicum annuum* L.), which was sampled from the greenhouse of Kyungpook National University (Republic of Korea). Shortly, 1 g of rhizosphere soil was serially diluted, plated on tryptic soy agar (TSA), and incubated at 30℃ for 5 days. One colony of the strain was isolated and repeatedly subcultured to obtain a single pure colony. Isolate was identified as *C. firmus* based on the 16S rRNA gene, and the sequence deposited in GenBank under accession number OR857502.

The genomic DNA of identified strain was extracted using DNA purification kit (Promega, USA) according to the manufacturer's instructions. The quality and quantity of the extracted DNA was assessed using a Qubit Flex fluorometer (Thermo Fisher Scientific, USA) and a NanoDrop One microvolume UV-Vis spectrophotometer (Thermo Fisher Scientific). The library was prepared following the manufacturer's guidelines using the SQK-LSK109 ligation sequencing kit (Oxford Nanopore Technologies [ONT], UK) with the NEBNext companion module (New England Biolabs, USA). Sequencing was performed on the MinION platform (ONT) with a FLO-MIN111 R10.3 flow cell for 48 hours at the KNU NGS Core Facility (Republic of Korea).

To generate FASTQ files, base calling was carried out using Guppy v4.4.1 software in high accuracy mode (HAC). For quality trimming, sequences with Phred scores of < 7 were excluded from subsequent analyses. *De novo* assembly was performed using Flye v2.8.3-b1695 with default parameters.

The genome of *C. firmus* T8 was assembled with a size of 4,383,751 bp consisting of 1 contig, with a coverage of

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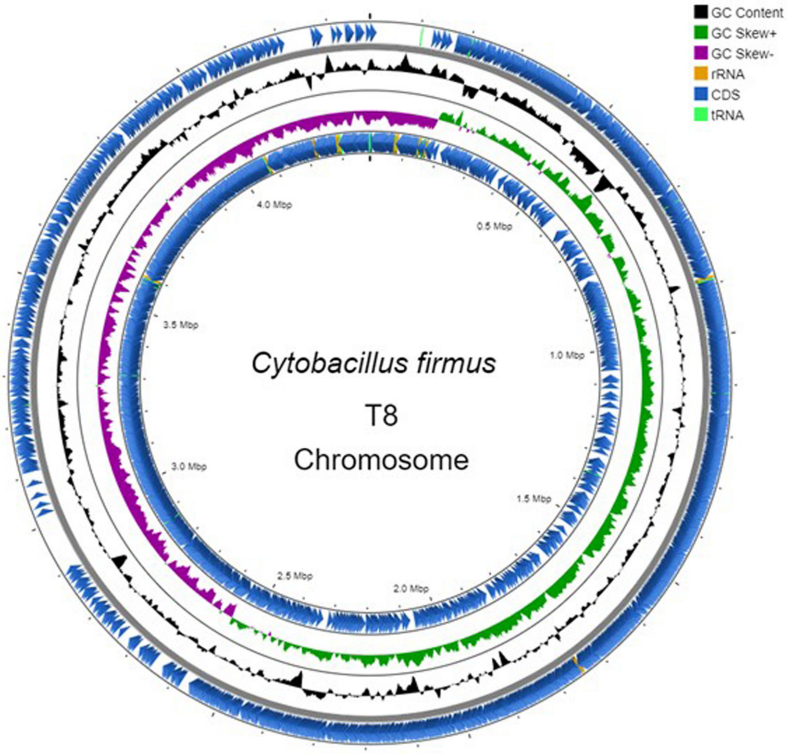


**Fig. 1. Genome map of the circular chromosome sequence of *C. firmus* T8, generated through the visualization tool (CGView).**

300.0x and 42% of GC content. To confirm the circular form of the assembled genome, a detailed analysis was performed using a dot plot generated with Gepard v2.1. This analysis revealed a continuous overlap between the start and end of the genome sequence, indicative of a circular conformation. The overlapping regions showed high sequence similarity, further supporting the circular structure of the genome. Visualization of the whole genome sequence was performed using the CGview website (Fig. 1). This visualization provided a comprehensive view of the genome, highlighting its circular structure with specific markers and annotations. The circular genome map generated by CGview clearly displayed the genomic features and their positions, confirming the circular nature of the assembly. Furthermore, the genome was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP). The annotation process identified genes, regulatory elements, and other genomic features consistent with a genome. The summarized results of this annotation are presented in Table 1, which includes detailed information on the number and types of genes, coding sequences, and other relevant genomic elements.

**Table 1. Genetic feature of *C. firmus* T8.**

| Feature | Value |
|---|---|
| Genome size (bp) | 4,383,751 |
| Number of contigs | 1 |
| G + C ratio (%) | 42 |
| Total number of genes | 4,472 |
| Number of protein-coding genes | 4,099 |
| rRNA genes (5S, 16S, 23S) | 11, 12, 12 |
| tRNA genes | 106 |
| ncRNA genes | 6 |
| Pseudo genes | 226 |

## Data Availability

The complete genome sequence of strain T8 has been deposited in NCBI GenBank database under accession number CP086235.1 (https://www.ncbi.nlm.nih.gov/nuccore/CP086235.1/).

## Acknowledgments

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## Conflict of Interest

The authors have no financial conflicts of interest to declare.

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