

Genome Reports

# Complete Genome Sequence of *Spirosoma* sp. SC4-14 Isolated from the Rhizosphere of pepper (*Capsicum annuum* L.)

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***Spirosoma* sp. SC4-14 was isolated from the rhizosphere soil of pepper (*Capsicum annuum* L.). The genome of the strain SC4-14 consists of a single chromosome with one plasmid, total size of 8,104,799 bp and the DNA G+C-content is 48.2%. This chromosome contains 6,479 protein-coding sequences and 41 tRNA and 6 rRNA genes.**

**Keywords:** *Spirosoma* sp. SC4-14, genome

*Spirosoma* species are commonly found in various environments, including soil [1–3], water, and extreme habitats such as dust, salt meadow, and herbicide-contaminated soil [4–6]. Some *Spirosoma* sp. have exhibited UV-radiation resistance [6, 7], indicating their potential for environmental applications as long-lasting microbes. In this study, we isolated *Spirosoma* sp. SC4-14 from the rhizosphere of pepper (*Capsicum annuum* L.) infested with above-ground aphids. Comparative analysis revealed its similarity to *S. terrae* 15J9-4 (95.74%) [1], *S. gilvum* 15J10-9T5 (93.38%) [2], *S. aerolatum* KACC 17939 (92.93%) [8], *S. aureum* BT328 (92.93%) [3] and *S. endbachense* I-24 (92.79%) [9], based on 16S rRNA sequence comparison using EzBoCloud server [10]. We proposed *Spirosoma* sp. SC4-14 as a new strain belong to the genus *Spirosoma* and conducted whole genome sequencing.

Genomic DNA extraction was performed using Maxell® RSC Tissue DNA kit (Promega, USA), following the manufacturer's instruction. The quality and quantity of DNA were assessed by using PicoGreen (Thermo Fisher Scientific, USA). High-quality and high-molecular-weight DNA samples were used to prepare size-selected SMRTbell templates with an optimal size range of approximately 7–12 kb. The library preparation involved sequencing 4 µg of input genomic DNA for PacBio Sequel IIe. The actual size distribution was determined using the Femto Pulse System (Agilent) for all size QC assessments. Genomic DNA was sheared using the Megaruptor® 3 (Diagenode) and purified with AMPure PB magnetic beads (Pacific Biosciences) for size selection. A 10 µl library was prepared using the PacBio SMRTbell prep kit 3.0, and SMRTbell templates were annealed using the Sequel II Bind Kit 3.2 and Int Ctrl 3.2. Sequencing was conducted using the Sequel II Sequencing Kit 2.0 and SMRT cell 8M Tray. SMRT cells (Pacific Biosciences) with a 15-hour movie time were captured for each SMRT cell using the PacBio Sequel IIe (Pacific Biosciences)

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sequencing platform by Macrogen (Republic of Korea). The subsequent steps followed the PacBio Sample Net-Shared Protocol, available at <https://www.pacb.com>. HiFi reads generated from the PacBio Sequel IIe system were assembled using the Genome Assembly application of SMRTlink 11.1.0.166339. Default options were used in the analysis, except for the expected genome size and downsampled coverage, set at 63M and 30X, respectively. To enhance assembly quality, the assembly result underwent three rounds of correction using high-quality adapter-trimmed Illumina reads by Pilon v1.21. Assembly quality was assessed using BUSCO (v 5.1.3) analysis with the eukaryota orthologs database v10. Predicted protein sets were annotated using InterProScan v5.30-69.0 and psiblast v2.4.0 with EggNOG DB v4.5.

The genome of *Spirosoma* sp. SC4-14 was assembled with a total size of 8,104,799 bp, consisting of 2 contigs: a single chromosome of 7,756,329 bp and one plasmid with 348,470 bp (Table 1). The GC content is 48.2%, with 6 rRNAs and 41 tRNAs identified (Table 1). The genome of *Spirosoma* sp. SC4-14 contains 6,797 genes and 6,749 protein-coding sequences (CDS) (Table 1). The genome

**Table 1. Genetic features of *Spirosoma* sp. SC4-14.**

Features	<i>Spirosoma</i> sp. SC4-14
Chromosome size (bp)	7,756,329
Plasmid size (bp)	348,470
G + C content (%)	48.2
Total number of genes	6,797
Protein-coding genes	6,749
Number of rRNAs	6
Number of tRNAs	41
Accession number (Genbank)	CP147518 and CP147519

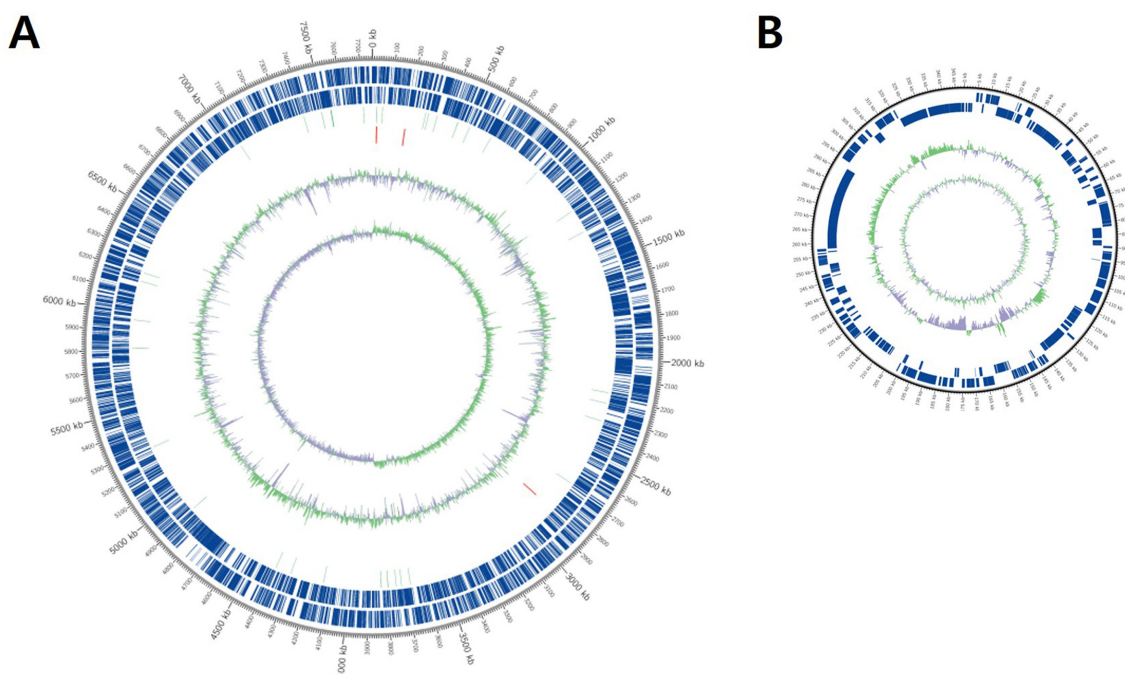
map of *Spirosoma* sp. SC4-14 was depicted in Fig. 1.

### Nucleotide Sequence Accession Number

The whole genome sequence of strain SC4-14 described in this study has been deposited in the NCBI database under accession number CP147518 (Chromosome) and CP147519 (Plasmid 1).

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**Fig. 1. Genome Map of *Spirosoma* sp. SC4-14.** Chromosome (A) and plasmid (B) map of *Spirosoma* sp. SC4-14. Characteristics are depicted from outside to center: CDS on the forward and reverse strands, tRNA (light green), rRNA (red), GC content (exterior light green peak for higher GC percentage, interior lavender peak for higher C content), and GC skew (positive value indicates G dominance, negative value indicates C dominance).

## Conflict of Interest

The authors have no financial conflicts of interest to declare.

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