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Complete Genome Sequence of *Priestia megaterium* S1, Isolated from the Soybean Soil

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This research presents the whole-genome sequence of *Priestia megaterium* S1, which was isolated from the soil of soybean (*Glycine max*). The genome of the strain is composed of a single chromosome with 5,297,673 bp, and the GC content is 38.12%.

Keywords: *Priestia megaterium*, soybean soil, whole genome sequencing

Priestia megaterium, a Gram-positive bacterial species, has attracted considerable scholarly interest owing to its extensive array of prospective applications. Predominantly isolated from terrestrial habitats, this bacterium has been observed to flourish in symbiotic association with *Glycine max*, commonly known as soybean. Although the exact nature of its ecological function within the soybean rhizosphere remains incompletely understood, existing research indicates that *P. megaterium* is frequently located adjacent to the plant's root system, implicating a potential symbiotic interaction [1–3].

In this study, *P. megaterium* strain S1 was isolated from the rhizosphere of soybean samples collected in Daegu, South Korea (35°52'43.1"N 128°47'37.3"E). For bacterial isolation, 1 g of soil was serially diluted; subsequently, dilutions from 10^{-1} to 10^{-6} were spread on tryptic soy agar (TSA). The culture plates underwent incubation at a temperature of 30℃ for a period ranging between 48 and 72 h. Subsequent to this, bacterial colonies were selected based on unique morphological characteristics. A singular colony of the target strain was isolated and subjected to multiple rounds of subculturing to obtain a homogeneous colony. Prior to its taxonomic identification, this isolated colony was cultivated in Tryptic Soy Broth (TSB) for a duration of 24 h.

The genomic DNA of *P. megaterium* strain S1 was extracted employing the Wizard genomic DNA purification system (Promega, USA), following the manufacturer's protocol. Quantification of the DNA was conducted using a Qubit 3.0 fluorometer (Thermo Fisher Scientific, USA). Additionally, the integrity and purity of the DNA were confirmed with a NanoDrop One/OneC microvolume UV-visible spectrophotometer (Thermo Fisher Scientific). The sequencing library was generated in compliance with the manufacturer's protocol using the SQK-LSK109 ligation sequencing kit from Oxford Nanopore Technologies (ONT), in conjunction with the NEBNext companion module (New England Biolabs, USA). Subsequently, genome sequencing was conducted using the ONT MinION platform, utilizing a FLO-MIN111 flow cell (R10.3; ONT) with a run time of 72 h. The creation of FASTQ files was achieved through the execution of base calling via Guppy software version 4.4.1, operating in a

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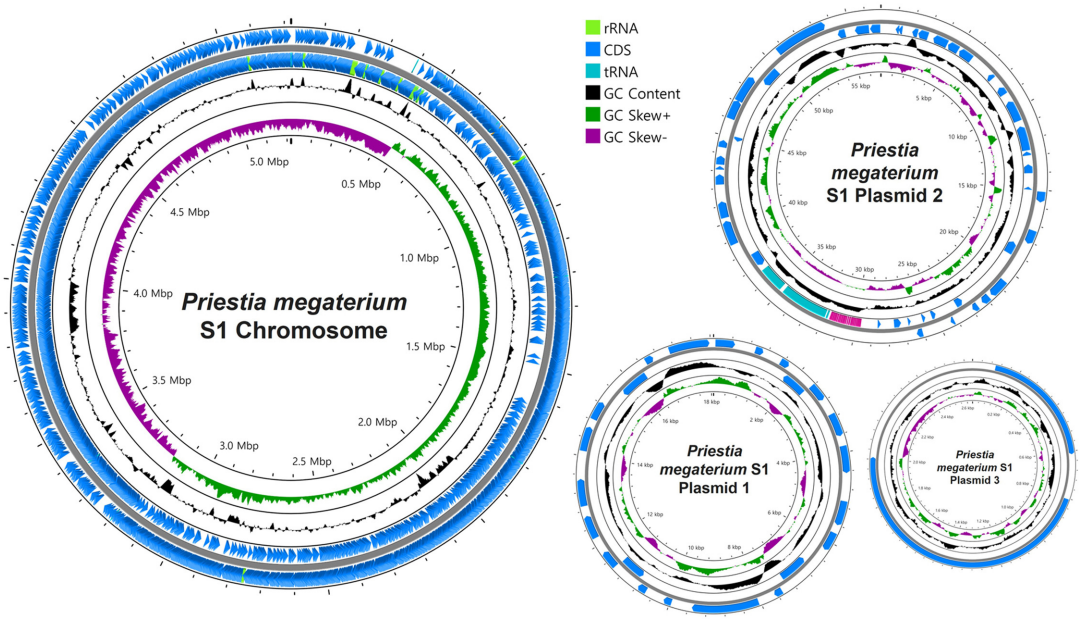

Fig. 1. Genome map of the *P. megaterium* S1 circular chromosome and plasmid sequences, generated using the CGView visualization tool.

high-accuracy modality. A quality trimming process was employed, in which sequence data exhibiting Phred scores below 7 were excluded from the analyses that followed. The de novo assembly procedure was facilitated by the use of Flye software version 2.9.2-b1786. Despite the adherence to default parameters, modifications were made specifically for the genome size option (–nano-raw –genome-size 6m –threads 72) [4].

The genome of *P. megaterium* S1 was sequenced at a size of 5,297,673 bp with four contigs of 5,220,057 bp, 56,911 bp, 18,072 bp, and 2,633 bp, respectively, with an N_{50} value of 5,220,057 bp and a coverage of 163.0×. Verification of the assembled genome was carried out using dotplots generated via Gepard software [5], and CGView [6] was used to visualize the entire genome sequence (Fig. 1). In addition, annotation of the genome was conducted through the use of both NCBI PGAP and RAST servers [7]. As a result, 5,252 protein-coding genes, 45 ribosomal RNAs, 137 transfer RNAs, 6 non-coding RNAs, and 41 pseudogenes were identified (Table 1). Moreover, the information of genomic profile of plasmids were described in Table 2.

Table 1. Genome feature of *P. megaterium* S1.

Genome features	Value
Genome size (bp)	5,297,673
GC contents (%)	38.12
N_{50}	5,220,057
No. of contig	4
Total genes	5,481
CDSs	5,252
rRNA	45
tRNA	137
ncRNA	6
pseudogenes	41

Table 2. Genome feature of plasmids of *P. megaterium* S1.

Genome features	Plasmid1	Plasmid2	Plasmid3
Genome size (bp)	56,911	18,072	2,633
GC contents (%)	35.93	35.11	32.21
Total genes	66	21	2
CDSs	43	21	2
rRNA	3	0	0
tRNA	22	0	0
ncRNA	0	0	0
pseudogenes	41	0	0

Data Availability

The complete genome sequence data for *P. megaterium* S1 have been submitted to the DDBJ/ENA/GenBank database with the accession number CP130476, CP130477, CP130478, and CP130479. The raw sequencing data are available under the SRA accession number SRR25375793.

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Conflict of Interest

The authors have no financial conflicts of interest to declare.

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