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# Complete Genome Sequence of *Priestia megaterium* Hyangyak-01 Isolated from Rhizosphere Soil of *Centella asiatica*

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**In this study, we report the complete genome sequence of *Priestia megaterium* strain HyangYak-01, which was isolated from the rhizosphere soil of *Centella asiatica*. The genome consists of 5,086,279 bp of sequences with 38.2 percent GC content and 5,111 coding genes. The genome contains several important genes related to plant growth-promoting activities, which were also confirmed with in vitro media assays.**

**Keywords: *Priestia megaterium*, plant growth-promoting rhizobacteria, *Centella asiatica*, sustainable agriculture**

*Centella asiatica*, commonly known as Indian pennywort, is an important medicinal plant using as traditional medicine in Southeast Asia [1]. Active compounds extracted from *C. asiatica* leaves have been widely used for medical and cosmetic purposes, especially triterpenoids such as madecassoside and asiaticoside [2]. Maximizing the yield of its active compounds can directly lead to increased profits. Among the numerous ways to increase yields, we focused on plant growth-promoting rhizobacteria (PGPR) in this study. Under the worldwide carbon neutrality challenge, PGPR is attracting attention as a potential alternative fertilizer for sustainable agriculture. *Priestia megaterium*, formerly known as *Bacillus megaterium*, is a well-known PGPR [3]. In this study, we isolated and genetically analyzed a potential PGPR agent to increase the advantage in *C. asiatica*.

*P. megaterium* HyangYak-01 was isolated from the rhizosphere soil of *C. asiatica*. Planted field was Cosmax HyangYak herb garden, located at 11–37, Yugugyebong-gil, Yugu-eup, Gongju-si, Chungcheongnam-do, Korea. Isolates were identified based on the 16S rRNA gene. The identified strain was subsequently used for genomic DNA extraction for whole-genome sequencing. Bacterial genome was extracted using the Promega Wizard Genomic DNA Purification Kit (Promega, USA) following the provided protocol. Extracted DNA was checked to confirm quantity and quality using Qubit fluorometer 2.0 (Waltham, USA) and NanoDrop Onec (Thermo Fisher Scientific, USA). Sequencing was performed with two different platforms to obtain both short and long sequencing reads for hybrid assembly. Long read sequences were

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sequenced using the Oxford Nanopore MinION Mk1C platform using flow cell (R10.4.1) and barcoding kit 24 V14 (Oxford Nanopore Technologies, UK). Short-read sequencing was performed with the DNBSEQ-G400RS platform (MGI Tech, China) using the PE50 kit. Both sequencing was performed at NGS Core Facility (Kyungpook National University, Daegu, South Korea). Sequencing raw reads were assembled with the Maryland Super Read Cabog Assembler (MaSuRCA, version 4.1.0). The assembled contigs were scaffolded with the Contig Scaffolding tool using Algebraic rearrangements (CSAR) and polished with Polypolish. Polished genome was subsequently confirmed to be complete with the NCBI Prokaryotic Genome Annotation Pipeline (PGAP). The completed genome was finally annotated with functional genes to confirm the existence of PGP-related genes and visualized with Proksee web.

The completed genome has a total length of 5,086,279 bp with 38.2% G + C content. The total gene count is 5,289, including 5,111 protein-coding sequences (CDS), 48 pseudogenes, 44 ribosomal RNAs, 126 transfer RNAs, and 8 other RNAs (Table 1). Several plant growth-promoting activities-related genes were found from result of functional gene annotation (Fig. 1). Regarding auxin-producing activity, genes related to tryptophan-dependent pathways of bacterial indole-3-acetic acid were found such as *aldH* and *trp* genes [4]. For urease activity, *ure* genes were found, which involved in the urease operon [5, 6]. Lastly, regarding phosphate solubilization activity, genes related to the bacterial phosphorus cycle were found such as *phnW* and *pho* genes [7, 8].

**Table 1 Genetic features of *P. megaterium* HyangYak-01.**

| Features | Values |
|---|---|
| Genomic Size | 5,086,279 bp |
| GC contents | 38.2% |
| Total genes | 5289 |
| CDSs | 5111 |
| Pseudo-genes | 48 |
| Ribosomal RNAs | 44 |
| Transfer RNAs | 126 |
| Other RNAs | 8 |

## Nucleotide Sequence Accession Nnumber(s)

The genome sequence of *P. megaterium* Hyangyak-01 have been deposited in NCBI under the accession number PRJNA956741.

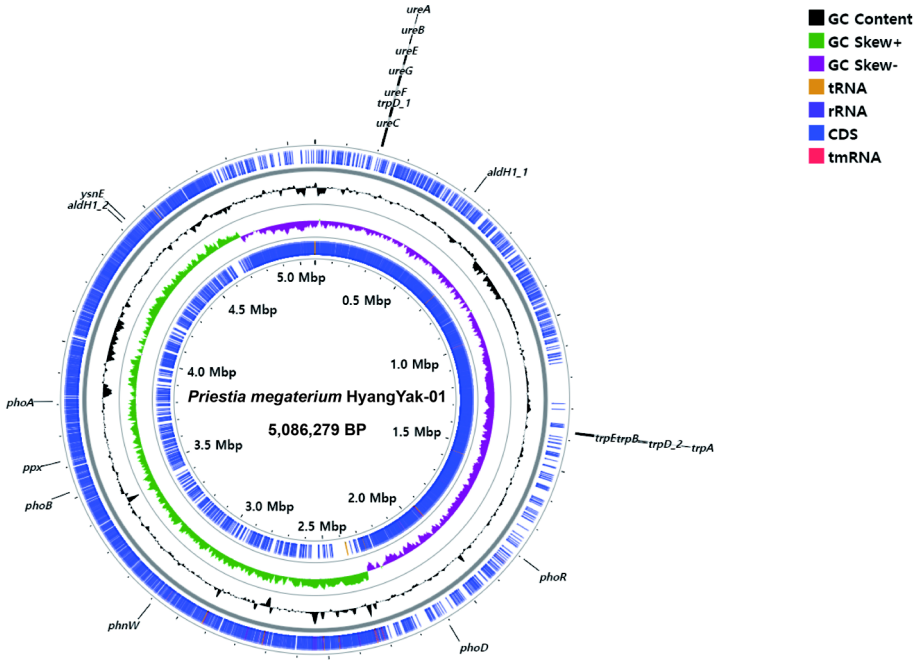


**Fig. 1. Circular representation of *P. megaterium* HyangYak-01 using Proksee.** Plant growth-promoting activity related genes were highlighted on the figure.

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## Conflict of Interest

The authors have no financial conflicts of interest to declare.

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