





Complete genome sequence of *Cohnella* sp. HS21 isolated from Korean fir (*Abies koreana*) rhizospheric soil

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구상나무 근권 토양으로부터 분리된 *Cohnella* sp. HS21의 전체 게놈 서열

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The genus *Cohnella*, which belongs to the family *Paenibacillaceae*, inhabits a wide range of environmental niches. Here, we report the complete genome sequence of *Cohnella* sp. HS21, which was isolated from the rhizospheric soil of Korean fir (*Abies koreana*) on the top of Halla Mountain in the Republic of Korea. Strain HS21 features a 7,059,027 bp circular chromosome with 44.8% GC-content. Its genome contains 5,939 protein-coding genes, 78 transfer RNA (tRNA) genes, 27 ribosomal RNA (rRNA) genes, 4 noncoding RNA genes (ncRNA), and 90 pseudogenes. The bacterium contains antibiotic-related gene clusters and genes encoding plant cell wall-degrading enzymes.

Keywords: complete genome sequence, Korean fir, rhizospheric bacteria

The genus *Cohnella* was proposed by Kämpfer *et al.* (2006) to contain Gram-positive, spore-forming, aerobic, rod-shaped bacteria belonging to the family *Paenibacillaceae*. Species belonging to this group were found in a wide range of

environmental niches, including mammals (Khiangam *et al.*, 2012), the starch production industry (Kämpfer *et al.*, 2006), fresh water (Shiratori *et al.*, 2010), plant root nodules (Flores-Félix *et al.*, 2014), and soils (Huang *et al.*, 2014; Lee *et al.*, 2015). We have recently isolated the bacterium strain HS21 from the rhizospheric soil of Korean fir (*Abies koreana*) on Halla Mountain in the Republic of Korea. Phylogenetic analysis of its 16S rRNA gene sequence revealed that strain HS21 belonged to genus *Cohnella* and had the highest similarity to *Cohnella luojiensis* HY-22R^T (97.9%). HS21 was thus regarded as a novel species of *Cohnella* based on the novel species recognition threshold of 98.6% (Kim *et al.*, 2014). To facilitate future research on this bacterium, and to improve the availability of *Cohnella* sp. genomes for comparative analysis, we determined the complete genome sequence of *Cohnella* sp. HS21.

The strain HS21 was cultured in tryptic soy broth (TSB, Difco laboratories) and shaken at 150 rpm at 25°C for 5 days. Genomic DNA was extracted and purified using the HiGeneTM Genomic DNA Prep Kit (BioFact) following the protocol recommended by the manufacturer. The purified genomic DNA was sequenced by the Macrogen facility (Macrogen)

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using the PacBio RSII (Pacific Biosciences Inc.) and the Illumina HiSeq 2500. The sequence reads were assembled using the FALCON-integrate (v1.8.8) assembler, and the contigs were polished using Pilon (v1.21). Genome annotation was performed using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) with best-placed reference protein set GeneMarkS 2 (v4.7).

The complete genome of HS21 consists of one circular chromosome that is 7,059,027 bp with 44.8% GC-content. A total of 5,938 protein-coding genes, 78 tRNA, 27 rRNA, 4 ncRNA, and 90 pseudogenes were annotated (Table 1). The housekeeping genes *gyrA* and *gyrB* in *Cohnella* sp. HS21 exhibit great similarity to those in *Cohnella* sp. 18JY8-7 (*gyrA*, 74.7%) and *Paenibacillus* sp. BIHB4019 (*gyrB*, 75%), respectively. The HS21 genome contains antibiotic resistance genes against antibiotics such as vancomycin B-type (*vanW*), daunorubicin/doxorubicin (*drrA* and *drrB*), tetracycline (*tetA*), and penicillin (*pbpX* and *pbp4*). It also contains genes associated with plant cell wall-degrading enzymes such as endo- β -xylanase A and endo-1,4- β -xylanase Z. The proteins in HS21 were classified using EggNOG (Huerta-Cepas et al., 2016) into the following major categories: “function unknown” (S, 30.2%),

carbohydrate transport and metabolism (G, 10.8%), transcription (K, 8.8%), general function prediction only (R, 7.1%), and signal transduction mechanisms (T, 6.7%).

Nucleotide sequence accession numbers

The complete genome sequence of *Cohnella* sp. HS21 has been deposited to GenBank under accession number AP019400. The 16S rRNA gene sequence was registered at the National Center for Biotechnology Information under accession number MK418757. The strain is available at the Korean Collection for Type Culture (accession number KCTC 43028) and at the China Center for Type Culture Collection (accession number CCTCC AB 2019010).

적 요

*Paenibacillaceae*계의 *Cohnella* 속은 다양한 환경 속에서 서식한다. 여기에 우리는 한국 한라산 꼭대기의 구상나무 (*Abies koreana*) 근권 토양으로부터 분리된 *Cohnella* sp. HS21의 전체 게놈 서열을 보고한다. 균주 HS21은 원형 염색체 7,059,027 bp와 44.8%의 GC 함량을 가지고 있다. 5,939개의 단백질 코딩 유전자와 78개의 트랜스퍼 (tRNA) 유전자, 27개의 리보솜 RNA (rRNA) 유전자, 4개의 비 코딩 RNA 유전자 (ncRNA), 90개의 위 유전자가 존재했다. 박테리아는 항생제 관련 유전자 클러스터와 식물 세포벽 분해 효소를 코딩하는 유전자를 포함하고 있다.

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Table 1. General features and properties of the genome sequence of *Cohnella* sp. HS21

| Features | <i>Cohnella</i> sp. HS21 |
|-------------------------------|-----------------------------|
| GenBank sequence accession ID | AP019400 |
| Genome assembly | |
| Assembly method | FALCON-integrate (v1.8.8) |
| Sequencing technology | PacBio RSII; Illumina HiSeq |
| Error correction | Pilon (v1.21) |
| Annotation | NCBI PGAP |
| Genome coverage | 284× |
| Genome features | |
| Genome length (bp) | 7,059,027 |
| GC-content (%) | 44.8 |
| Number of contigs | 1 |
| Total no. of genes | 6138 |
| Protein-coding genes | 5939 |
| RNA | |
| rRNAs (5S, 16S, 23S) | 27 (9, 9, 9) |
| tRNAs | 78 |
| ncRNAs | 4 |
| Pseudogenes | 90 |

producing bacterium isolated from soil. *Int. J. Syst. Evol. Microbiol.* **64**, 3320–3324.

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