

## Note (Genome Announcement)

# Complete genome sequence of *Herbaspirillum* sp. meg3 isolated from soil

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## 토양에서 분리된 *Herbaspirillum* sp. meg3의 유전체 염기서열 분석

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*Herbaspirillum* sp. meg3 belonging to *Betaproteobacteria* was isolated from soil in Jeju island. Here, we report the complete genome sequence of strain meg3 with a size of approximately 5.47 Mb and a mean G + C content of 57.1%. The genome included 4,816 coding sequences, and 9 ribosomal RNA and 51 transfer RNA genes. In the genome, two incomplete prophage regions have been identified. Also, we propose that strain meg3 has a potential capability for aromatic-compounds degradation based on the result of genome analysis.

**Keywords:** *Herbaspirillum*, genome, soil

The genus *Herbaspirillum* was first reported by Baldani *et al.* (1986) which was classified into a member of the *Betaproteobacteria*. To date, there are validated 16 species isolated mostly from terrestrial environments including plants; *H. aquaticum* (Dobritsa *et al.*, 2010), *H. aurantiacum* (Carro *et al.*, 2012), *H. autotrophicum* (Ding and Yokota, 2004), *H. canariense* (Carro *et al.*, 2012), *H. chlorophenicum* (Im *et al.*, 2004), *H. frisingense* (Kirchhof *et al.*, 2001), *H. hiltneri* (Rothballer *et al.*, 2006), *H. huttiense* (Ding and Yokota, 2004), *H. lusitanum* (Valverde *et al.*, 2003), *H. massiliense* (Lagier *et al.*, 2012), *H. psychrotolerans* (Bajerski *et al.*, 2013), *H. putei*

(Ding and Yokota, 2004), *H. rhizosphaerae* (Jung *et al.*, 2007), *H. rubrisubalbicans* (Baldani *et al.*, 1996), *H. seropedicae* (Baldani *et al.*, 1986), and *H. soli* (Carro *et al.*, 2012). Some strains have been reported to promote growth of plants, and be present in human fecal flora (Lagier *et al.*, 2012). Here, we describe the complete genome sequence and annotation of *Herbaspirillum* sp. meg3 isolated from soil in Jeju, Republic of Korea.

A genomic DNA library was constructed following the protocol provided by Pacific Biosciences. Briefly, genomic DNA was sheared to an average fragment length of 20 kb by using the SAGE ELF (Sage Science), end repaired, and then blunt-end ligated with single-molecule real-time (SMRT) bell oligonucleotide adaptors to construct a DNA fragment library for sequencing on the Pacific Biosciences RSII instrument. A single SMRT cell produced a total of 1.27 Gb (184 × in depth) in 165,285 polymerase reads that passed filtering. Finally, single contig closed was obtained using RS HGAP assembly (ver. 3.0). The complete genome size of the strain meg3 is *ca.* 5.46 Mb with 57.1% G + C content. Putative genes in the genome were predicted using Prokka (ver. 1.12b) (Seemann, 2014).

The genome includes 4,816 coding sequences (CDSs), and 9 ribosomal RNA and 51 transfer RNA genes (Table 1). A number of genes related to central metabolisms such as carbohydrate were identified. Among them, 2,692 CDSs were matched in KEGG database, in which most of them were affiliated into

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**Table 1.** *Herbaspirillum* sp. meg3 genome assembly and its general features

Item	Description
Genome Assembly Data	
Assembly Method	RS HGAP Assembly (v3.0)
Genome Coverage	184 ×
Sequencing Technology	PacBio
Genome features	
Size (bp)	5,465,798
GC content (%)	57.1
Coding sequences	4,816
rRNA (23S, 16S, 5S)	9 (3, 3, 3)
tRNA	51

environmental processing category. Genes involved in nitrate assimilation (*nrtABCD*) were identified in the genome. On the other hand, the strain meg3 appeared to harbor genes responsible for aromatic-compounds degradation such as catechol.

Clustered regularly interspaced short palindromic repeat (CRISPR) finder (Grissa *et al.*, 2007) did not find any CRISPR sequence in the genome. Annotation results also showed no CRISPR-associated proteins and no transposable elements. Two incomplete prophage regions were identified by PHAST (Zhou *et al.*, 2011), in which 15 and 6 CDSs were observed within the length of 12.1 kb and 8.5 kb, respectively.

#### Accession number

The genome sequence of *Herbaspirillum* sp. meg3 has been deposited in NCBI GenBank under accession number CP022736.

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## 적 요

*Betaproteobacteria*에 속하는 *Herbaspirillum* sp. meg3을 제주도 토양으로부터 분리하였다. 본 연구에서는 대략 5.47 Mb의 크기와 57.1%의 평균 G + C 함량을 가진 meg3 균주의 완전한 유전체를 보고한다. 유전체는 4,816개의 코딩 서열, 9개의 리보솜 RNA 및 51개의 전사 RNA 유전자가 존재하며,

두 개의 불완전한 프로파지 영역이 발견되었다. 또한 유전체 분석 결과는 meg3 균주가 방향족 화합물에 대한 분해능을 가지고 있음을 제시하고 있다.

## References

- Bajerski, F., Ganzert, L., Mangelsdorf, K., Lipski, A., Busse, H.J., Padur, L., and Wagner, D. 2013. *Herbaspirillum psychrotolerans* sp. nov., a member of the family Oxalobacteraceae from a glacier forefield. *Int. J. Syst. Evol. Microbiol.* **63**, 3197–3203.
- Baldani, J.I., Baldani, V.L.D., Seldin, L., and Döbereiner, J. 1986. Characterization of *Herbaspirillum seropedicae* gen. nov., sp. nov., a root-associated nitrogen-fixing bacterium. *Int. J. Syst. Bacteriol.* **36**, 86–93.
- Baldani, J.I., Pot, B., Kirchoff, G., Falsen, E., Baldani, V.L., Olivares, F.L., Hoste, B., Kersters, K., Hartmann, A., Gillis, M., *et al.* 1996. Emended description of *Herbaspirillum*; inclusion of [*Pseudomonas*] *rubrisubalbicans*, a milk plant pathogen, as *Herbaspirillum rubrisubalbicans* comb. nov.; and classification of a group of clinical isolates (EF group 1) as *Herbaspirillum* species 3. *Int. J. Syst. Bacteriol.* **46**, 802–810.
- Carro, L., Rivas, R., Leon-Barrios, M., Gonzalez-Tirante, M., Velazquez, E., and Valverde, A. 2012. *Herbaspirillum canariense* sp. nov., *Herbaspirillum aurantiacum* sp. nov. and *Herbaspirillum soli* sp. nov., isolated from volcanic mountain soil, and emended description of the genus *Herbaspirillum*. *Int. J. Syst. Evol. Microbiol.* **62**, 1300–1306.
- Ding, L. and Yokota, A. 2004. Proposals of *Curvibacter gracilis* gen. nov., sp. nov. and *Herbaspirillum putei* sp. nov. for bacterial strains isolated from well water and reclassification of [*Pseudomonas*] *huttiensis*, [*Pseudomonas*] *lanceolata*, [*Aquaspirillum*] *delicatum* and [*Aquaspirillum*] *autotrophicum* as *Herbaspirillum huttiense* comb. nov., *Curvibacter lanceolatus* comb. nov., *Curvibacter delicatus* comb. nov. and *Herbaspirillum autotrophicum* comb. nov. *Int. J. Syst. Evol. Microbiol.* **54**, 2223–2230.
- Dobritsa, A.P., Reddy, M.C., and Samadpour, M. 2010. Reclassification of *Herbaspirillum putei* as a later heterotypic synonym of *Herbaspirillum huttiense*, with the description of *H. huttiense* subsp. *huttiense* subsp. nov. and *H. huttiense* subsp. *putei* subsp. nov., comb. nov., and description of *Herbaspirillum aquaticum* sp. nov. *Int. J. Syst. Evol. Microbiol.* **60**, 1418–1426.
- Grissa, I., Vergnaud, G., and Pourcel, C. 2007. CRISPRfinder: a web tool to identify clustered regularly interspaced short palindromic repeats. *Nucleic Acids Res.* **35**, W52–W57.
- Im, W.T., Bae, H.S., Yokota, A., and Lee, S.T. 2004. *Herbaspirillum chlorophenolicum* sp. nov., a 4-chlorophenol-degrading bacterium. *Int. J. Syst. Evol. Microbiol.* **54**, 851–855.
- Jung, S.Y., Lee, M.H., Oh, T.K., and Yoon, J.H. 2007. *Herbaspirillum rhizosphaerae* sp. nov., isolated from rhizosphere soil of *Allium*

- victoralis* var. *platyphyllum*. *Int. J. Syst. Evol. Microbiol.* **57**, 2284–2288.
- Kirchhof, G., Eckert, B., Stoffels, M., Baldani, J.I., Reis, V.M., and Hartmann, A.** 2001. *Herbaspirillum frisingense* sp. nov., a new nitrogen-fixing bacterial species that occurs in C4-fibre plants. *Int. J. Syst. Evol. Microbiol.* **51**, 157–168.
- Lagier, J.C., Gimenez, G., Robert, C., Raoult, D., and Fournier, P.E.** 2012. Non-contiguous finished genome sequence and description of *Herbaspirillum massiliense* sp. nov. *Stand Genomic Sci.* **7**, 200–209.
- Rothballer, M., Schmid, M., Klein, I., Gattinger, A., Grundmann, S., and Hartmann, A.** 2006. *Herbaspirillum hiltneri* sp. nov., isolated from surface-sterilized wheat roots. *Int. J. Syst. Evol. Microbiol.* **56**, 1341–1348.
- Seemann, T.** 2014. Prokka: rapid prokaryotic genome annotation. *Bioinformatics* **30**, 2068–2069.
- Valverde, A., Velazquez, E., Gutierrez, C., Cervantes, E., Ventosa, A., and Igual, J.M.** 2003. *Herbaspirillum lusitanum* sp. nov., a novel nitrogen-fixing bacterium associated with root nodules of *Phaseolus vulgaris*. *Int. J. Syst. Evol. Microbiol.* **53**, 1979–1983.
- Zhou, Y., Liang, Y., Lynch, K.H., Dennis, J.J., and Wishart, D.S.** 2011. PHAST: a fast phage search tool. *Nucleic Acids Res.* **39**, W347–W352.