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Complete Genome Sequence of *Herbaspirillum hiltneri* N3 (DSM 17495), Isolated from Surface-Sterilized Wheat Roots

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We report the complete genome sequence of *Herbaspirillum hiltneri* N3 (DSM 17495), a member of the genus *Herbaspirillum* of the *Betaproteobacteria*. The genome is contained in a single chromosome, and analysis revealed that N3 lacks the whole nitrogen fixation (*nif*) gene cluster, confirming its inability to fix nitrogen.

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Herbaspirillum hiltneri N3 (DSM 17495) is a betaproteobacterium isolated from surface-sterilized wheat roots, first described by Rothballer et al. (1).

Although the genus *Herbaspirillum* contains diazotrophic species such as *H. seropedicae, H. rubrisubalbicans*, and *H. frisingensis*, with the potential for endophytic and systemic colonization of a variety of plants, *H. hiltneri* strain N3 lacks all genes of the *nif* cluster, confirming that this organism is unable to fix nitrogen, as previously described (Rothballer et al. 2006 [1]). However, the genes involved in the overall regulation of nitrogen metabolism (*glnA*, *glnB*, *glnE*, *glnK*, *ntrB*, *ntrC*, *ntrY*, and *ntrX*) are present.

The genome was sequenced using the SOLiD sequencing platform. Short reads in color space formatted from whole-genome shotgun sequencing (WGS) in fragments (8.4 million) and mate paired (107 million) were partially assembled using the *de novo* pipeline accessory tools 2.0. The best assemblies from each data set were integrated within a hybrid assembly by the assembler Phrap, resulting in 5,970 contigs and 283 scaffolds. To finish the genome sequence, a Nextera paired-end library 250 bp in length was sequenced on an Illumina MiSeq, producing 5,088,454 sequences. All reads were assembled with Velvet 1.2.07 (2), CLC Genomics Workbench 6.5.1, ALLPATHS-LG (3, 4), and Edena V3 (5). The resulting contigs were aligned to the reference genomes of *H. seropedicae* strain SmR1 (6) and *H. lusitanum* P6-12 (7) and, finally, the gaps were closed with FGAP (8).

The complete genome sequence of *Herbaspirillum hiltneri* N3 is 4,965,474 bp long with a G+C content of 61.84%. This genome is 548,413 bp smaller than that of *H. seropedicae* (6). Genome annotation using RAST (9) and our in-house SILA platform predicted 4,581 coding sequences (CDS), tRNAScan predicted 49 tRNAs, and NCBI Blast identified 4 16S-23S-5S rRNA operons.

As in *H. seropedicae* and *H. huttiense* subsp. *putei* IAM, the *H. hiltneri* genome contains the genes for nitrate transport and assimilation, namely, *nasA*, *nirD*, *nark*, and *nasFED*, while lacking all genes involved in the nitrate dissimilatory pathway *narG*, *narH*, *narI*, *narU*, and *narXL*. The gene coding 1-aminocyclopropane-1-carboxylate (ACC) deaminase, an enzyme purportedly involved in relieving ethylene-induced plant stresses, is also present, as in the previously described *Herbaspirillum* spp. genomes. The genome contains genes of the protein secretion systems type I, II, III, V, and VI. Type III has been suggested to be involved in plant–bacterium interactions.

The *H. hiltneri* genome contains all genes of the pentose phosphate pathway and the Entner-Doudoroff and Embden-Meyerhoff-Parnas (EMP) glycolytic/gluconeogenic pathways (except 6-phosphofructokinase [PFK], EC 2.7.1.11). As in *H. seropedicae*, *H. hiltneri* probably enrolls the Entner-Doudoroff and the pentose phosphate pathways to bypass the lack of PFK during glycolysis. The presence of isocitrate lyase supports gluconeogenesis from 2-carbon substrates such as acetyl coenzyme A (acetyl-CoA).

Nucleotide sequence accession number. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number CP011409. The version described in this paper is the first version.

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