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Draft Genome Sequence of *Herbaspirillum huttiense* subsp. *putei* IAM 15032, a Strain Isolated from Well Water

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Here we report the one-scaffold draft genome of *Herbaspirillum huttiense* subsp. *putei* strain 7-2^T (IAM 15032), which was isolated from well water.

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Herbaspirillum huttiense subsp. *putei* strain 7-2^T (IAM 15032) is a betaproteobacterium isolated from well water in Osaka, Japan. It was first described as a new species, *Herbaspirillum putei*, closely related to *H. huttiense* (1). Later, 16S rRNA gene resequencing and DNA-DNA hybridization analysis led to the reclassification of *H. putei* as a subspecies of *H. huttiense*, and it is now named *H. huttiense* subsp. *putei* (2).

The genome sequence of *H. huttiense* subsp. *putei* was determined using mate-paired libraries on a SOLiD4 sequencer (Life Technologies), producing a total of 102,768,904 paired reads of 50 bp. These libraries were used for *de novo* genome assembly using Velvet v.1.2.03 (3). Gap closure was achieved by using in-house scripts.

The *H. huttiense* subsp. *putei* draft genome was assembled in one scaffold containing 32 contigs. The estimated genome size is 5.7 Mb with a 62.2% G+C content. Previously estimated genome size was 3.9 Mb with a 62.1% G+C content (2). Automatic annotation using RAST (4) revealed 5,317 open reading frames (ORFs) covering 86% of the chromosome, 49 tRNA genes, and 2 16S-23S-5S rRNA operons.

Our analysis indicated the absence of *nif* genes, confirming that this species is not a nitrogen fixer. On the other hand, genes involved in nitrate/nitrite metabolism were observed. *H. huttiense* subsp. *putei* is able to grow using nitrate as the sole nitrogen source (data not shown), and analyses indicated genes with high similarity to *H. seropedicae nasA, nirD, nirB, narK*, and *nasFED*, whereas genes *narG, narH, narI, narU*, and *narXL* are not present, reinforcing that this bacterium is capable of reducing nitrate as a nitrogen source (assimilative metabolism) and suggesting that it cannot use nitrate as an electron acceptor in anaerobic respiration (dissimilative metabolism).

The *H. huttiense* subsp. *putei* genome has genes coding for all the enzymes required for the Embden-Meyerhof-Parnas pathway. Genes coding for the Entner-Doudoroff, the pentose phosphate, and the tricarboxylic acid cycle (TCA) pathways were also observed. Although *H. seropedicae* and *H. lusitanum* show two potential pathways for trehalose biosynthesis (5, 6), *H. huttiense* subsp. *putei* seems to have only the pathway involving *otsA* and *otsB*, which may be related to the differences among the environments from which these species were isolated.

Studies on plant interaction of *H. huttiense* subsp. *putei* are not available; however, a gene coding for 1-aminocyclopropane-1-carboxylate (ACC) deaminase was observed, which may suggest contributions to plant development under stress conditions (5). Although secretion systems type I, II, and V were observed, the type III secretion system, which was suggested to be involved in plant-bacterium interaction, was not observed in *H. huttiense* subsp. *putei*. An interesting feature was the presence of a gene cluster for cellulose biosynthesis (*wss*) and degradation that was reported only in *H. rubrisubalbicans* M1 and seems to be involved in enhanced colonization of maize (7).

Nucleotide sequence accession number. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ANJR00000000. The version described in this paper is the first version, ANJR01000000.

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