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

Vanely de Souza, a Vitor C. Piro, a Helisson Faoro, b Michelle Z. Tadra-Sfeir, b Vanessa K. Chicora, b Dieval Guizelini, a Vinicius Weiss, b Ricardo A. Ville, a Rose A. Monteiro, b Maria Berenice R. Steffens, b Jeroniza N. Marchaukoski, a Fabio O. Pedrosa, b Leonardo M. Cruz, b Leda S. Chubatsu, b Roberto T. Raittz a

Laboratory of Bioinformatics, Professional and Technological Education Sector, Federal University of Paraná, Curitiba, PR, Brazil; b Department of Biochemistry and Molecular Biology, Federal University of Paraná, Curitiba, PR, Brazil

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

Received 28 December 2012 Accepted 7 January 2013 Published 21 February 2013


Copyright © 2013 de Souza et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license.

Address correspondence to Roberto T. Raittz, raittz@gmail.com.

H. huttiense subsp. putei strain 7-2T (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-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. luminatum 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.

ACKNOWLEDGMENTS

This genome-sequencing project was supported by the Brazilian Program of National Institutes of Science and Technology-INCT/Brazilian Research Council-CNPq/MCT, a grant to the INCT of Biological Nitrogen Fixation. We are also grateful to CNPq and CAPES for fellowships.

We thank V. Baura, R. Prado, and M. Lamour for technical assistance and E. M. Souza for criticism in reading the manuscript.

REFERENCES

1. Ding L, Yokota Y. 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, [Pseudomo-
nas] lanceolata, [Aquaspirillum] delticatul and, [Aquaspirillum] autotrophicum as Herbaspirillum huttiense comb. nov., Curvibacter lanceo-

2. Dobrsla AP, Reddy MCS, Samadpour M. 2010. Reclassification of Herbaspirillum putei as a later heterotypic synonym of Herbaspirillum hut-


