



Draft Genome Sequence of *Burkholderia vietnamiensis* Strain RS1, a Nitrogen-Fixing Endophyte Isolated from Sweet Potato

Rina Shinjo,^a Kazuma Uesaka,^b Kunio Ihara,^b Shunsuke Sakazaki,^a Katsuya Yano,^a Motohiko Kondo,^a Aiko Tanaka^a

^aGraduate School of Bioagricultural Sciences, Nagoya University, Chikusa, Nagoya, Japan

^bCenter for Gene Research, Nagoya University, Chikusa, Nagoya, Japan

ABSTRACT *Burkholderia vietnamiensis* strain RS1 is an endophytic bacterium with nitrogen-fixing ability that was isolated from tuberous roots of sweet potato. Here, we present its draft genome of 6,542,727 bases that contains a cluster of genes associated with nitrogen fixation. This genome sequence will provide important insights into the plant growth-promoting potential of endophytic bacteria.

Sweet potato (*Ipomoea batatas*) is a staple root crop in Asia and Africa and can grow well in infertile nitrogen-poor soil (1). Endophytic nitrogen fixation by microorganisms has been suggested to contribute to nitrogen acquisition from the atmosphere in sweet potato (2, 3). However, there is little information about the genetic and physiological characteristics of endophytic bacteria of sweet potato. Understanding these characteristics would elucidate the molecular mechanisms of plant-diazotroph symbiosis and thereby promote effective utilization of nitrogen-fixing bacteria.

Bacterial strains were isolated from tuberous roots of *I. batatas* cv. Beniazuma, grown in a pot placed in an experimental field at Nagoya University, Nagoya, Aichi, Japan. The tuberous roots were cut into pieces (weighing approximately 5 g [fresh weight] each) and washed under running tap water for 30 min. The washed tissues were surface sterilized by soaking in 70% ethanol for 1 min and then in 0.3% NaOCl (in 0.002% Tween 20) for 2 min. After surface sterilization, the tuberous root tissues were rinsed three times with sterile water, ground in a sterilized mortar, and suspended in 5 ml of 0.3 M phosphate buffer containing 0.2 M sucrose. A 50- μ l aliquot of ground material was plated onto a yeast mannitol agar medium (4) and incubated for 5 days at 28°C under aerobic conditions. The sequenced bacterium RS1, which was selected as an *nifH*-containing strain, was identified as *Burkholderia vietnamiensis* based on partial sequencing of 16S rRNA. *B. vietnamiensis* is a diazotrophic bacterium belonging to the *Burkholderia cepacia* complex. Other strains of *B. vietnamiensis* have been isolated from soil or roots of rice, sugarcane, and nipa palm (5–7).

The genomic DNA of *B. vietnamiensis* RS1 was extracted using a genomic DNA purification kit (Promega, USA). Paired-end DNA libraries were prepared for sequencing with the MiSeq platform (Illumina, USA). A total of 641,426 high-quality paired-end reads were generated. *De novo* assembly was performed using the SPAdes genome assembler version 3.9.0 (8) with three options, “-k auto,” “-careful,” and “-cov-cutoff 10.0,” which yielded 70 contigs. The draft genome of *B. vietnamiensis* strain RS1 consists of 6,542,727 bases with a G+C content of 67.6%. Annotation of the contigs was performed using the DFAST version 1.0.0 pipeline (9), which identified 5,797 putative coding sequences.

The genome annotation confirmed the presence of the *nif* gene locus for nitrogen fixation. The *nif* gene cluster, which is 46.4 kb in length, is composed of 61 open reading frames, including *nifXQNEKDHOTSSZBAUVPW* and *nif*-related genes (*modACE*, *fdxBN*, and *fixAB*). In addition, several genes related to plant growth promotion, such as siderophore production and 1-aminocyclopropane-1-carboxylic acid degradation, have

Received 5 June 2018 Accepted 27 July 2018
2018 Published 26 July 2018

Citation Shinjo R, Uesaka K, Ihara K, Sakazaki S, Yano K, Kondo M, Tanaka A. 2018. Draft genome sequence of *Burkholderia vietnamiensis* strain RS1, a nitrogen-fixing endophyte isolated from sweet potato. *Microbiol Resour Announc* 7:e00820-18. <https://doi.org/10.1128/MRA.00820-18>.

Editor David A. Baltus, University of Arizona

Copyright © 2018 Shinjo et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Aiko Tanaka, aikotana@agr.nagoya-u.ac.jp.

been identified. A comparison of the RS1 genome with other *B. vietnamiensis* genomes (10, 11) revealed high similarity to *B. vietnamiensis* strain LMG 10929 (=TVV75), with 98.7% average nucleotide identity (12).

Data availability. The genome sequence of *B. vietnamiensis* strain RS1 was deposited in DDBJ/EMBL/GenBank under the accession no. [BGKC0100001](https://doi.org/10.1093/bioinformatics/btx713) to [BGKC0100077](https://doi.org/10.1093/bioinformatics/btx713).

ACKNOWLEDGMENT

We thank Sanjay Saikia (Biotelliga, New Zealand) for English editing and critical comments on the manuscript.

REFERENCES

- Hartemink AE, Johnston M, O'Sullivan JN, Poloma S. 2000. Nitrogen use efficiency of taro and sweet potato in the humid lowlands of Papua New Guinea. *Agric Ecosyst Environ* 79:271–280. [https://doi.org/10.1016/S0167-8809\(00\)00138-9](https://doi.org/10.1016/S0167-8809(00)00138-9).
- Hill WA, Hortense D, Hahn SK, Mulongoy K, Adeyeye SO. 1990. Sweet potato root and biomass production with and without nitrogen fertilization. *Agron J* 82:1120–1122. <https://doi.org/10.2134/agronj1990.00021962008200060019x>.
- Yoneyama T, Terakado J, Masuda T. 1997. Natural abundance of ¹⁵N in sweet potato, pumpkin, sorghum and castor bean: possible input of N₂-derived nitrogen in sweet potato. *Biol Fertil Soils* 26:152–154. <https://doi.org/10.1007/s003740050359>.
- Keele BB, Hamilton PB, Elkan GH. 1969. Glucose catabolism in *Rhizobium japonicum*. *J Bacteriol* 97:1184–1191.
- Govindarajan M, Balandreau J, Kwon S-W, Weon H-Y, Lakshminarasimhan C. 2008. Effects of the inoculation of *Burkholderia vietnamiensis* and related endophytic diazotrophic bacteria on grain yield of rice. *Microb Ecol* 55:21–37. <https://doi.org/10.1007/s00248-007-9247-9>.
- Govindarajan M, Balandreau J, Muthukumarasamy R, Revathi G, Lakshminarasimhan C. 2006. Improved yield of micropropagated sugarcane following inoculation by endophytic *Burkholderia vietnamiensis*. *Plant Soil* 280:239–252. <https://doi.org/10.1007/s11104-005-3223-2>.
- Tang S-Y, Hara S, Melling L, Goh K-J, Hashidoko Y. 2010. *Burkholderia vietnamiensis* isolated from root tissues of nipa palm (*Nypa fruticans*) in Sarawak, Malaysia, proved to be its major endophytic nitrogen-fixing bacterium. *Biosci Biotechnol Biochem* 74:1972–1975. <https://doi.org/10.1271/bbb.100397>.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>.
- Tanizawa Y, Fujisawa T, Nakamura Y. 2018. DFAST: a flexible prokaryotic genome annotation pipeline for faster genome publication. *Bioinformatics* 34:1037–1039. <https://doi.org/10.1093/bioinformatics/btx713>.
- Gillis M, Van Van T, Bardin R, Goor M, Hebban P, Willems A, Segers P, Kersters K, Heulin T, Fernandez MP. 1995. Polyphasic taxonomy in the genus *Burkholderia* leading to an emended description of the genus and proposition of *Burkholderia vietnamiensis* sp. nov. for N₂-fixing isolates from rice in Vietnam. *Int J Syst Evol Microbiol* 45:274–289. <https://doi.org/10.1099/00207713-45-2-274>.
- Johnson SL, Bishop-Lilly KA, Ladner JT, Daligault HE, Davenport KW, Jaissle J, Frey KG, Koroleva GI, Bruce DC, Coyne SR, Broomall SM, Li P-E, Teshima H, Gibbons HS, Palacios GF, Rosenzweig CN, Redden CL, Xu Y, Minogue TD, Chain PS. 2015. Complete genome sequences for 59 *Burkholderia* isolates, both pathogenic and near neighbor. *Genome Announc* 3(2):e00159-15. <https://doi.org/10.1128/genomeA.00159-15>.
- Goris J, Konstantinidis KT, Klappenbach JA, Coenye T, Vandamme P, Tiedje JM. 2007. DNA-DNA hybridization values and their relationship to whole-genome sequence similarities. *Int J Syst Evol Microbiol* 57:81–91. <https://doi.org/10.1099/ijs.0.64483-0>.