

Draft Genome Sequence of *Defluviimonas indica* Strain 20V17^T, Isolated from a Deep-Sea Hydrothermal Vent Environment in the Southwest Indian Ocean

Lijing Jiang (姜丽晶),^{a,b,c,d} Minnan Long (龙敏南),^d Zongze Shao (邵宗泽)^{a,b,c}

State Key Laboratory Breeding Base of Marine Genetic Resources, Xiamen, China^a; Key Laboratory of Marine Genetic Resources, Third Institute of Oceanography, SOA, Xiamen, China^b; Key Laboratory of Marine Genetic Resources of Fujian Province, Xiamen, China^c; School of Energy Research, Xiamen University, Xiamen, China^d

Here, we present the draft genome sequence of *Defluviimonas indica* 20V17^T, which was isolated from a deep-sea hydrothermal vent chimney sample in the southwest Indian Ocean. The draft genome sequence contains 4,268,338 bp, with a G+C content of 66.33%.

Received 30 April 2014 Accepted 14 May 2014 Published 5 June 2014

Citation Jiang L, Long M, Shao Z. 2014. Draft genome sequence of *Defluviimonas indica* strain 20V17^T, isolated from a deep-sea hydrothermal vent environment in the southwest Indian Ocean. *Genome Announc.* 2(3):e00479-14. doi:10.1128/genomeA.00479-14.

Copyright © 2014 Jiang et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Zongze Shao, shaozz@163.com.

Defluviimonas indica 20V17^T (CGMCC 1.10859 = JCM 17871 = MCCC 1A01802) was isolated from a hydrothermal sulfide chimney sample in the Southwest Indian Ridge (1). The genus *Defluviimonas* was first proposed by Foesel et al. (2), which classified it within the family *Rhodobacteraceae*. Currently, the genus contains only three species, while strain 20V17^T is the first isolate from the deep-sea hydrothermal environment in the genus *Defluviimonas*.

The draft genome of 20V17^T was sequenced by Illumina paired-end sequencing technology at Beijing Genomics Institute (BGI) (Shenzhen, China). The reads were assembled using SOAPdenovo (version 1.05), and 236 contigs were generated, with a maximum contig size of 155,100 bp and an *N*₅₀ contig length of 39,530 bp. The assembled genome comprises 4,268,338 nucleotides with a G+C content of 66.33%. Gene annotation was carried out by the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP). A total of 4,190 genes were predicted, including 4,119 protein-coding genes, 42 tRNAs, and 4 rRNAs.

D. indica 20V17^T was able to oxidize reduced sulfur compounds as energy sources. RAST annotation also revealed that the draft genome contains sulfur oxidation genes (*soxRSVWXYZABCD*). Moreover, 11 genes encoding an [NiFe] hydrogenase were found in the draft sequence, indicating that strain 20V17^T might also be able to use H₂ as an electron donor. The metabolic plasticity of *D. indica* 20V17^T, which uses both molecular hydrogen and reduced sulfur compounds

as energy sources, might represent a very useful strategy for living in deep-sea hydrothermal vent systems. The draft genome sequence of 20V17^T will enable further studies on the physiology and metabolic potential of this species, especially its roles involved in sulfur and H₂ oxidation, which are major energy metabolisms in deep-sea hydrothermal vent environments.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession no. [AYXI000000000](https://www.ncbi.nlm.nih.gov/nuclseq/AYXI000000000/). The version described in this paper is the first version, AYXI01000000.

ACKNOWLEDGMENTS

This work was financially supported by the National Natural Science Foundation of China (41106150), National Program on Key Basic Research Project (973 Program) (2012CB417300), COMRA program (DY125-15-R-01), and the Natural Science Foundation of Fujian Province, China (2011J01219).

REFERENCES

- Jiang LJ, Xu HX, Shao ZZ, Long MN. 2014. *Defluviimonas indica* sp. nov., a marine bacterium isolated from a deep-sea hydrothermal vent environment. *Int. J. Syst. Evol. Microbiol.* <http://dx.doi.org/10.1099/ijs.0.061614-0>.
- Foesel BU, Drake HL, Schramm A. 2011. *Defluviimonas denitrificans* gen. nov., sp. nov., and *Pararhodobacter aggregans* gen. nov., sp. nov., non-phototrophic *Rhodobacteraceae* from the biofilter of a marine aquaculture. *Syst. Appl. Microbiol.* 34:498–502. <http://dx.doi.org/10.1016/j.syapm.2011.08.006>.