

Draft Genome Sequence of Thermophilic *Exiguobacterium* sp. Strain JLM-2, Isolated from Deep-Sea Ferromanganese Nodules

De-Chao Zhang,^a Yan-Xia Liu,^a Ying-Yi Huo,^b Xue-Wei Xu,^b Xin-Zheng Li^a

Institute of Oceanology, Chinese Academy of Sciences, Qingdao, China^a; Laboratory of Marine Ecosystem and Biogeochemistry, Second Institute of Oceanography, State Oceanic Administration, Hangzhou, China^b

***Exiguobacterium* sp. strain JLM-2 is a thermophilic bacterium isolated from deep-sea ferromanganese (FeMn) nodules. The estimated genome of this strain is 2.9 Mb, with a G+C content of 48.32%. It has a novel circular 15,570-bp plasmid. The draft genome sequence may provide useful information about Mn-microbe interactions and the genetic basis for tolerance to environment stresses.**

Received 9 June 2015 Accepted 16 June 2015 Published 23 July 2015

Citation Zhang D-C, Liu Y-X, Huo Y-Y, Xu X-W, Li X-Z. 2015. Draft genome sequence of thermophilic *Exiguobacterium* sp. strain JLM-2, isolated from deep-sea ferromanganese nodules. *Genome Announc* 3(4):e00794-15. doi:10.1128/genomeA.00794-15.

Copyright © 2015 Zhang 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 Xin-Zheng Li, lixzh@qdio.ac.cn.

The genus *Exiguobacterium* was first described in 1983 by Collins et al. (1), and the species formerly described as *Brevibacterium acetylicum incertae sedis* was included in the genus *Exiguobacterium* as *E. acetylicum* in 1994 (2). *Exiguobacterium* spp. have been isolated from, or molecularly detected in, many extreme environments, such as Antarctic ice (3), Himalayan glaciers (4), Siberian permafrost (5), deep-sea hydrothermal vents (6), and hot/hyperalkaline springs (7, 8).

The isolate *Exiguobacterium* sp. strain JLM-2 was isolated from deep-sea FeMn nodule samples, which were collected at a water depth of 3,573 m using Jiaolong's operated submersible loaded on the Xiangyanghong 09 scientific exploration ship from Jiaolong Seamount's dormant hydrothermal vent, South China Sea, during the first experimental application cruise on 3 July 2013. The concentrations of MnO and Fe₂O₃ in the FeMn nodules were 40% and 10%, respectively, by inductively coupled plasma-mass spectrometry (ICP-MS).

Exiguobacterium sp. JLM-2 is a Gram-positive extracellular amylase-producing bacterium that can grow at 4 to 53°C and has resistance to Mn²⁺ (220 mM). Based on 16S rRNA gene phylogeny, the isolate is closely related to group II within the *Bacillales* family XII *incertae sedis*, *Firmicutes* (7).

Genomic DNA was extracted and sequenced using the Illumina HiSeq 2500 platform and assembled using Velvet version 1.0 (9). This assembly generated 23 contigs, with an *N*₅₀ length of 343,188 bp and an average length of 126,112 bp, which were assembled into 12 scaffolds, with an *N*₅₀ length of 2,092,945 bp and an average length of 241,796 bp. The draft genome of *Exiguobacterium* sp. JLM-2 consists of a total 2,998 open reading frames (ORFs). Its genome has a novel circular 15,570-bp plasmid with 19 ORFs. The draft genome is 2.9 Mb, with a G+C content of 48.32%.

Nucleotide sequence accession number. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [LDNY00000000](https://www.ncbi.nlm.nih.gov/submit/ldny00000000/).

ACKNOWLEDGMENTS

This work was supported by the Strategic Priority Research Program of the Chinese Academy of Sciences (grant XDA11030201) and the "135" fund of Institute of Oceanology, Chinese Academy of Sciences (no. 2012IO060105).

REFERENCES

- Collins MD, Lund BM, Farrow JAE, Schleifer KH. 1983. Chemotaxonomic study of an alkaliphilic bacterium, *Exiguobacterium aurantiacum* gen. nov., sp. nov. *J Gen Microbiol* 129:2037–2042.
- Farrow JA, Wallbanks S, Collins MD. 1994. Phylogenetic interrelationships of round-spore-forming bacilli containing cell walls based on lysine and the non-spore-forming genera *Caryophanon*, *Exiguobacterium*, *Kurtzia*, and *Planococcus*. *Int J Syst Bacteriol* 44:74–82. <http://dx.doi.org/10.1099/00207713-44-1-74>.
- Frühling A, Schumann P, Hippe H, Sträubler B, Stackebrandt E. 2002. *Exiguobacterium undae* sp. nov. and *Exiguobacterium antarcticum* sp. nov. *Int J Syst Evol Microbiol* 52:1171–1176.
- Chaturvedi P, Shivaji S. 2006. *Exiguobacterium indicum* sp. nov., a psychrophilic bacterium from the Hamta glacier of the Himalayan mountain ranges of India. *Int J Syst Evol Microbiol* 56:2765–2770. <http://dx.doi.org/10.1099/ijs.0.64508-0>.
- Rodrigues DF, Goris J, Vishnivetskaya T, Gilichinsky D, Thomashow MF, Tiedje JM. 2006. Characterization of *Exiguobacterium* isolates from the Siberian permafrost. Description of *Exiguobacterium sibiricum* sp. nov. *Extremophiles* 10:285–294. <http://dx.doi.org/10.1007/s00792-005-0497-5>.
- Crapart S, Fardeau ML, Cayol JL, Thomas P, Sery C, Ollivier B, Combet-Blanc Y. 2007. *Exiguobacterium profundum* sp. nov., a moderately thermophilic, lactic acid-producing bacterium isolated from a deep-sea hydrothermal vent. *Int J Syst Evol Microbiol* 57:287–292. <http://dx.doi.org/10.1099/ijs.0.64639-0>.
- Vishnivetskaya TA, Kathariou S, Tiedje JM. 2009. The *Exiguobacterium* genus: biodiversity and biogeography. *Extremophiles* 13:541–555. <http://dx.doi.org/10.1007/s00792-009-0243-5>.
- Cabriaa GLB, Argayosa VB, Lazaroa JEH, Argayosa AM, Arcillad CA. 2014. Draft genome sequence of haloalkaliphilic *Exiguobacterium* sp. strain AB2 from Manleluag Ophiolite spring, Philippines. *Genome Announc* 2(4):e00840-14. <http://dx.doi.org/10.1128/genomeA.00840-14>.
- Zerbino DR, Birney E. 2008. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. *Genome Res* 18:821–829. <http://dx.doi.org/10.1101/gr.074492.107>.