AMERICAN SOCIETY FOR MICROBIOLOGY
Microbiology Resource Announcements

GENOME SEQUENCES

Genome Sequence of *Bacillus vallismortis* TD3, a Salt-Tolerant Strain Isolated from the Sediments of a Solar Saltern in Tamil Nadu, India

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ABSTRACT Various *Bacillus* spp. capable of producing enzymes with industrially desirable properties have been isolated from adverse environments. Here, we announce the 3.91-Mbp draft genome sequence of a moderately salt-resistant *Bacillus vallismortis* strain, TD3, capable of producing several industrially relevant enzymes.

Bacteria colonizing under adverse environmental conditions are potential sources for bioprospecting industrially important enzymes with specific characteristics (1). *Bacillus* is one of the most popular bacterial genera that is frequently detected in various environments, including hostile habitats. For example, extremophilic *Bacillus* spp. that have adapted to live in environments such as hydrothermal vents (2), the permafrost (3), heavy-metal-contaminated areas (4), oil-contaminated waters (5), and high-salinity environments (6) have been reported earlier. From an industrial perspective, halophilic bacteria are attractive candidates for exploitation, as their enzymes have also adapted to function under adverse reaction conditions (7). Our lab has also identified and characterized industrially important enzymes from halotolerant bacteria (8, 9).

Isolate TD3 was originally recovered from the sediments of a solar saltern at Tuticorin, Tamil Nadu, India, which is a port town located in the Coromandel Coast of the Bay of Bengal. TD3 was a Gram-positive motile rod, which was moderately halophilic, with the ability to grow easily in the presence of 10% (wt/vol) NaCl. Isolate TD3 was identified as *Bacillus vallismortis* by partial sequencing and analysis of its 16S rRNA gene. Total genomic DNA from *B. vallismortis* TD3 was isolated using the HiPurA bacterial genomic DNA purification kit (HiMedia, Mumbai, India), and the genome sequence of *B. vallismortis* TD3 was generated at Genotypic Technology, Bangalore, India, by Illumina sequencing. Illumina paired-end libraries were constructed per manufacturer-recommended protocols, targeting a read length of 100 bp, and were sequenced on a HiSeq system. The resulting reads were subjected to quality control using SeqQC version 2.2 (Genotypic Technology, Bangalore, India) for adapter trimming, B trimming, and low-quality end trimming. The remaining high-quality reads were assembled *de novo* using SPAdes version 3.1.0 (10), generating 152 contigs yielding a total length of 3,914,588 bp and an N_{50} value of 228,120 bp. These 152 contigs were then subjected to scaffolding using SSPACE version 2.0 (11), yielding a final sequence length of 3,912,114 bp in a set of 29 scaffolds, with a final N_{50} value of 258,393 bp.

Coding sequences in the *B. vallismortis* TD3 genome, which had a GC content of 43.9%, were predicted using the Rapid Annotations using Subsystems Technology (RAST) server (12). A total of 4,206 genes were predicted, including those coding for 113 RNAs (rRNA and tRNA). *B. vallismortis* TD3 encoded osmotolerance determinants mostly restricted to the accumulation of compatible solutes, as opposed to the accumulation

Received 5 June 2018 **Accepted** 14 June 2018 **Published** 12 July 2018

Citation Suganthi C, Mageswari A, Shankar M, Gothandam KM, Karthikeyan S. 2018. Genome sequence of *Bacillus vallismortis* TD3, a salt-tolerant strain isolated from the sediments of a solar saltern in Tamil Nadu, India. Microbiol Resour Announc 7:e00817-18. https://doi.org/10.1128/MRA.00817-18.

Editor John J. Dennehy, Queens College

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of salts in the cytoplasm, as is typical of *Halobacterium* species. We detected genes encoding mechanisms for the uptake of K^+ ions, glycine-betaine, carnitine, and proline, all of which are known to be involved in the response to osmotic stress (13). We also identified genes coding for α-amylase, pectin lyase, endoglucanase, several proteases, and a β-glucosidase. We are currently exploring the characteristics of these enzymes and their potential applications in relevant industries. Additionally, we are also pursuing the genes and proteins that contribute to the various molecular mechanisms of halotolerance in *B. vallismortis* TD3.

Data availability. This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession no. NXEM00000000. The version described in this paper is the first version, NXEM01000000.

ACKNOWLEDGMENTS

We gratefully acknowledge research infrastructure and support from Vellore Institute of Technology, Vellore, India. We also thank Genotypic Technology, Bangalore, India, for facilitating genome sequencing and providing required bioinformatics support.

REFERENCES

1. Coker JA. 2016. Extremophiles and biotechnology: current uses and prospects. F1000Res 5:1–7. https://doi.org/10.12688/f1000research.7432.1.
2. Filippidou S, Wunderlin T, Junier T, Jeanneret N, Johnson S, McMurry K, Gleasner CD, Lo C-C, Li P-E, Vuyisich M, Chain PS, Junier P. 2015. Genome sequence of *Bacillus alveayuensis* strain 24KAM51, a halotolerant thermophile isolated from a hydrothermal vent. Genome Announc 3:e00982-15. https://doi.org/10.1128/genomeA.00982-15.
3. Brenner EV, Brouchkov AV, Kurilshikov AM, Griva GI, Kashuba E, Kashuba VI, Melefors O, Repin VE, Melnikov VP, Vlassov VV. 2013. Draft genome sequence of *Bacillus cereus* strain F, isolated from ancient permafrost. Genome Announc 1:e00561-13. https://doi.org/10.1128/genomeA.00561-13.
4. Jung J, Jeong H, Kim HJ, Lee D-W, Lee SJ. 2016. Complete genome sequence of *Bacillus oceanisediminis* 2691, a reservoir of heavy-metal resistance genes. Mar Genomics 30:73–76. https://doi.org/10.1016/j.margen.2016.07.002.
5. Hao K, Li H, Li F, Guo P. 2016. Complete genome sequence of *Bacillus pumilus* PDSLzg-1, a hydrocarbon-degrading bacterium isolated from oil-contaminated soil in China. Genome Announc 4:e01079-16. https://doi.org/10.1128/genomeA.01079-16.
6. Kumar RM, Kaur G, Kumar A, Bala M, Singh NK, Kaur N, Kumar N, Mayilraj S. 2015. Taxonomic description and genome sequence of *Bacillus campisalis* sp. nov., a member of the genus *Bacillus* isolated from a solar saltern. Int J Syst Evol Microbiol 65:3235–3240. https://doi.org/10.1099/ijsem.0.000400.
7. Oren A. 2010. Industrial and environmental applications of halophilic microorganisms. Environ Technol 31:825–834. https://doi.org/10.1080/09593330903370026.
8. Suganthi C, Mageswari A, Karthikeyan S, Anbalagan M, Sivakumar A, Gothandam KM. 2013. Screening and optimization of protease production from a halotolerant *Bacillus licheniformis* isolated from saltern sediments. J Genet Eng Biotechnol 11:47–52. https://doi.org/10.1016/j.jgeb.2013.02.002.
9. Mageswari A, Subramanian P, Chandrasekaran S, Sivashanmugam K, Babu S, Gothandam KM. 2012. Optimization and immobilization of amylase obtained from halotolerant bacteria isolated from solar salterns. J Genet Eng Biotechnol 10:201–208. https://doi.org/10.1016/j.jgeb.2012.09.001.
10. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski 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.
11. Boetzer M, Henkel CV, Jansen HJ, Butler D, Pirovano W. 2011. Scaffolding pre-assembled contigs using SSPACE. Bioinformatics 27:578–579. https://doi.org/10.1093/bioinformatics/btq683.
12. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. BMC Genomics 9:75. https://doi.org/10.1186/1471-2164-9-75.
13. Sleator RD, Hill C. 2002. Bacterial osmoadaptation: the role of osmolytes in bacterial stress and virulence. FEMS Microbiol Rev 26:49–71. https://doi.org/10.1111/j.1574-6976.2002.tb00598.x.