



# Draft Genome Sequence of *Bacillus urumqiensis* BZ-SZ-XJ18<sup>T</sup>, a Moderately Haloalkaliphilic Bacterium Isolated from a Saline-Alkaline Lake

Ziya Liao,<sup>a</sup> Chao Ren,<sup>a</sup> Xiaomeng Guo,<sup>a</sup> Yanchun Yan,<sup>a</sup> Jun Li,<sup>b</sup> Baisuo Zhao<sup>a</sup>

<sup>a</sup>Graduate School, Chinese Academy of Agricultural Sciences, Beijing, People's Republic of China

<sup>b</sup>Institute of Agricultural Resources and Regional Planning, Chinese Academy of Agricultural Sciences, Beijing, People's Republic of China

**ABSTRACT** The moderately haloalkaliphilic bacterium *Bacillus urumqiensis* BZ-SZ-XJ18<sup>T</sup> was isolated from a saline-alkaline lake located in the Xinjiang Uyghur Autonomous Region of China. Optimum growth occurred at the total Na<sup>+</sup> concentration of 1.08 M, with a broad optimum pH of 8.5 to 9.5. The draft genome consists of approximately 3.28 Mb and contains 3,228 predicted genes. A number of genes associated with adaptation strategies for osmotic balance and alkaline pH homeostasis were identified, providing pertinent insight into specific adaptations to the double-extreme environment.

The moderately haloalkaliphilic bacterium *Bacillus urumqiensis* BZ-SZ-XJ18<sup>T</sup> was isolated from a saline-alkaline lake in the Xinjiang Uyghur Autonomous Region of China (1). Its growth occurs at a total Na<sup>+</sup> concentration of 0.22 to 4.32 M (optimum concentration, 1.08 M Na<sup>+</sup>) and at pH 6.5 to 10.0 (optimum pH, 8.5 to 9.5). To understand the adaptive strategies for survival under saline-alkaline conditions, draft genome sequencing of strain BZ-SZ-XJ18<sup>T</sup> was performed using the Illumina Miseq sequencing platform.

Genomic DNA was extracted using an iTop microbial DNA isolation kit (Beijing, China) following the manufacturer's instructions. A library for genome sequencing was constructed using the whole-genome shotgun (WGS) approach on the Illumina platform (2). Sequencing was performed with a paired-end read length of 2 × 300 bp at approximately 382× coverage. Genomic contigs were *de novo* assembled through the A5-miseq v 20150522 pipeline (3). Quake and Burrows-Wheeler Aligner (BWA) were used to detect and correct errors in preassembly and postassembly sequences (4, 5). The total length of the draft genome sequence was 3,280,710 bp, and there were 26 contigs, with a GC content of 51.7% and an *N*<sub>50</sub> value of 219,019 bp. Automated gene annotation was obtained using the NCBI Prokaryotic Genome Annotation Pipeline ([www.ncbi.nlm.nih.gov/genome/annotation\\_prok](http://www.ncbi.nlm.nih.gov/genome/annotation_prok)). Subsequently, the genome files in GenBank format (gb file) were uploaded to the Integrated Microbial Genomes Expert Review (IMG ER) tool (<https://img.jgi.doe.gov/cgi-bin/submit/main.cgi>) for functional annotation after an Analysis Project identification number (ID) was registered in the GOLD Database (<https://gold.jgi.doe.gov/index>). Among the identified 3,228 genes, there are 3,157 putative protein-coding sequences (CDSs). A total of 71 RNA genes (4 5S rRNAs, 1 16S rRNAs, 3 23S rRNAs, 59 tRNAs, and 4 other RNA genes) were predicted.

The genome sequence revealed the presence of a number of genes encoding putative proteins potentially related to the strategies for surviving in double-extreme conditions of elevated salinity and alkaline pH. Two *ectA* genes, 2 *ectB* genes, and 1 *ectC* gene for ectoine synthesis, 1 *glnA* gene for L-glutamine synthesis, and 1 *speE* gene for spermine synthesis were identified. Two genes for glycine betaine synthesis from

Received 19 April 2018 Accepted 24 April 2018 Published 31 May 2018

**Citation** Liao Z, Ren C, Guo X, Yan Y, Li J, Zhao B. 2018. Draft genome sequence of *Bacillus urumqiensis* BZ-SZ-XJ18<sup>T</sup>, a moderately haloalkaliphilic bacterium isolated from a saline-alkaline lake. Genome Announc 6:e00460-18. <https://doi.org/10.1128/genomeA.00460-18>.

**Copyright** © 2018 Liao 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 Jun Li, [jlj@caas.ac.cn](mailto:jlj@caas.ac.cn), or Baisuo Zhao, [bszhao@live.com](mailto:bszhao@live.com).

choline, 6 genes for the glycine betaine-carnitine-choline transporter (BCCT) family, and 1 gene encoding the sodium/proline symporter of the solute-sodium symporter (SSS) family were found. These demonstrate a mechanism, a means of coping with hyperosmotic conditions (higher external salinity), by amassing large quantities of compatible solutes, including ectoine, glutamine, spermine, and glycine betaine (6–9). The presence of 3 *trkA* genes and 2 *trkH* genes, which participate in the Trk system for potassium uptake protein synthesis, indicated that strain BZ-SZ-XJ18<sup>T</sup> also maintains osmotic balance by inducing a massive uptake of K<sup>+</sup> in high-salinity environments (10). As a haloalkaliphile, *B. urumqiensis* must have an adaptive strategy for both salinity homeostasis and pH homeostasis. The genome harbors 2 genes for calcium/proton antiporters of the Ca<sup>2+</sup> calcium antiporter (CaCA) family, 1 gene encoding potassium/proton antiporters of the CPA1 family, 1 gene for the sodium/proton antiporter of the CPA1 family, 7 multisubunit sodium/proton antiporters, 10 genes for F<sub>1</sub>F<sub>o</sub>-ATP synthase, and 1 gene encoding a sodium/proton antiporter of the NhaC family deployed for alkaline pH homeostasis (11). As described in this report, various predicted genes on the genome of *B. urumqiensis* offer valuable insights to reveal the adaptive mechanisms of this haloalkaliphile.

**Accession number(s).** The draft genome sequence of *B. urumqiensis* BZ-SZ-XJ18<sup>T</sup> has been deposited at DDBJ/ENA/GenBank under the accession number [PVNS00000000](https://doi.org/10.1093/nar/gkz000).

## ACKNOWLEDGMENTS

This work was supported by grants 31570110 and 31370158 from the National Science Foundation of China (NSFC) and grant 1610042017001 from the Foundation of Graduate School of the Chinese Academy of Agricultural Sciences (CAAS).

## REFERENCES

- Zhang S, Li Z, Yan Y, Zhang C, Li J, Zhao B. 2016. *Bacillus urumqiensis* sp. nov., a moderately haloalkaliphilic bacterium isolated from a salt lake. *Int J Syst Evol Microbiol* 66:2305–2312. <https://doi.org/10.1099/ijsem.0.001028>.
- Aparicio S, Chapman J, Stupka E, Putnam N, Chia JM, Dehal P, Gelpke MDS. 2002. Whole-genome shotgun assembly and analysis of the genome of *Fugu rubripes*. *Science* 297:1301–1310. <https://doi.org/10.1126/science.1072104>.
- Kelley DR, Schatz MC, Salzberg SL. 2010. Quake: quality-aware detection and correction of sequencing errors. *Genome Biol* 11:R116. <https://doi.org/10.1186/gb-2010-11-11-r116>.
- Li H. 2013. Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM. *arXiv 1303.3997* [q-bio.GN]. <https://arxiv.org/abs/1303.3997>.
- Cardozo FA, Vargas NCA, Zimpel CK, Pessoa A, Rivera ING. 2016. Draft genome sequence of *Aeromonas caviae* CH129, a marine-derived bacterium isolated from the coast of São Paulo State, Brazil. *Genome Announc* 4:e01336-16. <https://doi.org/10.1128/genomeA.01336-16>.
- Kuhlmann AU, Bremer E. 2002. Osmotically regulated synthesis of the compatible solute ectoine in *Bacillus pasteurii* and related *Bacillus* spp. *Appl Environ Microbiol* 68:772–783. <https://doi.org/10.1128/AEM.68.2.772-783.2002>.
- Roberts MF. 2005. Organic compatible solutes of halotolerant and halophilic microorganisms. *Saline Systems* 1:5. <https://doi.org/10.1186/1746-1448-1-5>.
- Saum SH, Sydow JF, Palm P, Pfeiffer F, Oesterheld D, Muller V. 2006. Biochemical and molecular characterization of the biosynthesis of glutamine and glutamate, two major compatible solutes in the moderately halophilic bacterium *Halobacillus halophilus*. *J Bacteriol* 188:6808–6815. <https://doi.org/10.1128/JB.00781-06>.
- Kasukabe Y, He L, Nada K, Misawa S, Ihara I, Tachibana S. 2004. Overexpression of spermidine synthase enhances tolerance to multiple environmental stresses and up-regulates the expression of various stress-regulated genes in transgenic *Arabidopsis thaliana*. *Plant Cell Physiol* 45:712–722. <https://doi.org/10.1093/pcp/pch083>.
- Jones MK, Warner E, Oliver JD. 2008. Survival of and in situ gene expression by *Vibrio vulnificus* at varying salinities in estuarine environments. *Appl Environ Microbiol* 74:182–187. <https://doi.org/10.1128/AEM.02436-07>.
- Padan E, Bibi E, Ito M, Krulwich TA. 2005. Alkaline pH homeostasis in bacteria: new insights. *Biochim Biophys Acta Biomembranes* 1717:67–88. <https://doi.org/10.1016/j.bbamem.2005.09.010>.