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Data in Brief

Draft genome sequence of *Bacillus okhensis* Kh10-101T, a halo-alkali tolerant bacterium from Indian saltpanPilla Sankara Krishna^a, Ara Sreenivas^b, Deepak Kumar Singh^a, Sisinthy Shivaji^b, Jogadhenu S.S. Prakash^{a,*}^a Department of Biotechnology & Bioinformatics, School of Life Sciences, University of Hyderabad, Hyderabad 500046, India^b Centre for Cellular and Molecular Biology, Uppal Road, Hyderabad 500007, India

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ABSTRACT

We report the 4.86-Mb draft genome sequence of *Bacillus okhensis* strain Kh10-101T, a halo-alkali tolerant rod shaped bacterium isolated from a salt pan near port of Okha, India. This bacterium is a potential model to study the molecular response of bacteria to salt as well as alkaline stress, as it thrives under both high salt and high pH conditions. The draft genome consist of 4,865,284 bp with 38.2% G + C, 4952 predicted CDS, 157 tRNAs and 8 rRNAs. Sequence was deposited at DDBJ/EMBL/GenBank under the project accession JRJU00000000.

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Specifications	
Organism	<i>Bacillus okhensis</i>
Strain	Kh10-101T
Sequence or array type	Roche 454 GS (FLX titanium)
Data format	Processed
Experimental factors	Microbial strain
Experimental features	Whole genome sequence of <i>Bacillus okhensis</i> Kh10-101T, assembly and annotation
consent	N/A
Sample source location	Salt pan near port of Okha, Gujarat, India

1. Direct link to the deposited data

<http://www.ncbi.nlm.nih.gov/bioproject/261559>

2. Experimental design, materials and methods

The organism in this study is *Bacillus okhensis* strain Kh10-101T (here after *B. okhensis*), a Gram-positive, strictly aerobic, rod like bacterium. The *B. okhensis* was first isolated from a salt pan in India, near port of Okha by Nowlan et al., 2006 [1]. *B. okhensis* is tolerant to both high salt and high pH, can grow from neutral to high pH (pH 7–11) and from low to high salt (0.5–12% NaCl) concentrations. The genomic DNA was extracted from an active log phase culture (grown in CMB medium [1],

pH 10 and 5% NaCl) as per Sambrook et al. 1989 [2]. The genome of Kh10-101T was sequenced using Roche 454 GS (FLX titanium) pyrosequencing platform. Functional annotation was carried out using RAST tool [3], identification of tRNA genes by tRNAscan-SE [4] and rRNA genes by RNAmerr [5].

3. Summary

Genome sequencing resulted in a total of 3,18,628 high quality reads with approximately 28× coverage of the entire genome. All reads were assembled using Newbler assembler (Roche Life sciences). Assembly resulted in an average contig size of 49,645 bp. N50 contig size is 115,121 bp and the largest contig size is 349,697 bp. Total 98 high quality contigs, with size greater than 500 bp were assembled. Final assembled draft genome size is 4,865,284 bp (4.86 Mb) with 38.2% GC content. The genome size of *B. okhensis* is relatively larger than its closest and sequenced relatives, *Bacillus halodurans* (4.2 Mb) and *B. pseudofirmus* (3.85 Mb) showing its evolutionary significance. Annotation with RAST has shown a total of 4952 coding sequences, (45% annotated and 55% hypothetical) (Fig. 1). 165 RNA coding genes and 8 rRNA (6 numbers of 5S rRNA, one 23S rRNA and one 16S rRNA) genes were present (Table 1). Of the total protein coding genes, genes involved in carbohydrate metabolism, amino acid metabolism, cofactors, vitamins, prosthetic groups, protein metabolism, nucleic acid metabolism, respiration were dominant (Fig. 1). In addition, RAST annotation server predicted 136 genes to be involved in various stress responses. However, none of these stress responsive genes coded for acid stress responsive

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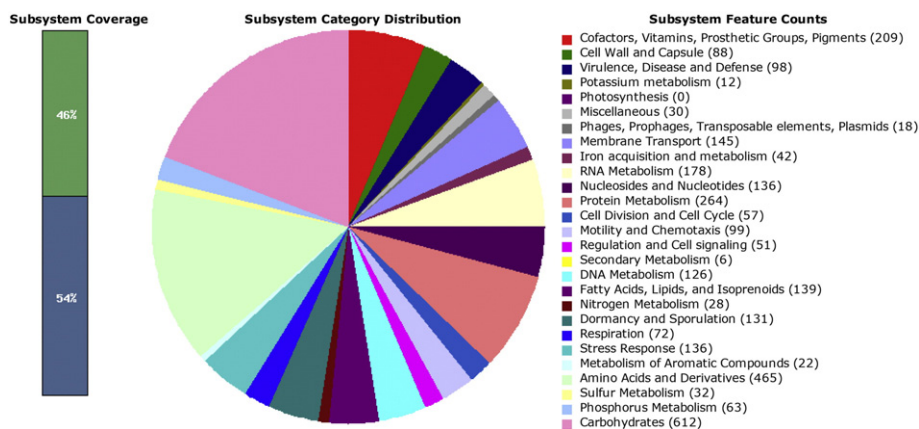


Fig. 1. Subsystem category distribution statistics for *B. okhensis* strain Kh10-101T. The complete genome sequence of *B. okhensis* was annotated using the Rapid Annotation System Technology (RAST) server. The pie chart showed the count of each subsystem feature and the subsystem coverage. The green bar of the subsystem coverage corresponds to the percentage of the proteins included in the subsystems while the blue bar corresponds to the percentage of the proteins that are not included in the subsystems.

Table 1

Genome features of *Bacillus okhensis* Kh10-101T.

Feature	<i>Bacillus okhensis</i> Kh10-101T
Genome size	4,865,284 bp
G + C content	38.2%
Total contigs	98
Protein coding genes	4952
tRNA genes	157
rRNA genes	8

proteins. Further, despite the fact that *B. okhensis* is aerobic, genes involved in fermentation and acid production were identified. In addition, 145 genes code for the proteins that are involved in transport across the membrane, such as ABC transporters and cation transport proteins. Interestingly, it was observed that though spore formation does not occur in high salt and high pH conditions in *B. okhensis*, its genome has 131 genes encoding proteins related to spore formation and dormancy. The *B. okhensis* strain Kh10-101T whole genome shot gun (WGS) project has been deposited at DDBJ/EMBL/GenBank under the project accession JRJU00000000. The project (01) has the accession number JRJU01000000 and consists of sequences JRJU01000001:JRJU01000098. The version described in this paper is the first version. Comparative genome analysis and genome wide transcriptomic analysis of this halo-alkali tolerant strain will be helpful in better understanding of the mechanisms involved in salt and high pH tolerance.

Conflict of interest

The authors declare that there is no conflict of interest on any work published in this paper.

Acknowledgments

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