



Draft Genome Sequence of Hyperthermophilic, Halotolerant *Parageobacillus toebii* PW12, Isolated from the Tattapani Hot Spring, Northwest Himalayas

Parul Sharma,^a Sonika Gupta,^a Anuradha Sourirajan,^a David J. Baumler,^{b,c,d} Kamal Dev^{a,b}

^aFaculty of Applied Sciences and Biotechnology, Shoolini University, Solan, Himachal Pradesh, India

^bDepartment of Food Science and Nutrition, University of Minnesota—Twin Cities, St. Paul, Minnesota, USA

^cMicrobial and Plant Genomic Institute, University of Minnesota—Twin Cities, St. Paul, Minnesota, USA

^dBiotechnology Institute, University of Minnesota—Twin Cities, St. Paul, Minnesota, USA

ABSTRACT Here, we report the genome sequence of hyperthermophilic and halophilic *Parageobacillus toebii* PW12, isolated from the Tattapani hot spring in the northwest Himalayas. The genome size of *Parageobacillus toebii* PW12 is 3,210,377 bp. The G+C content is 42.05%, and 3,382 coding sequences (CDS), 80 tRNAs, 5 noncoding RNAs (ncRNAs), and 4 CRISPR arrays were predicted.

Thermophilic microorganisms belonging to the *Archaea* and *Bacteria* inhabit hot springs, thermal pools, and fumaroles that are found throughout the world (1). Since the discovery of thermophilic microorganisms and novel enzymes, such as *Taq* polymerase from *Thermus aquaticus*, a large number of thermophiles have found industrial applications, including their importance as sources of thermostable enzymes (proteases, amylase, lipase, xylanase, cellulase, and DNA restriction enzymes) and other products of industrial utility (2–4). *Geobacillus* spp. were first classified by Nazina et al. (5) and constitute the most abundant thermophiles isolated from a wide range of environments (6), and they have huge biotechnological potential (7). Recently, poly-genomic studies showed that the genus *Geobacillus* consists of two distinct genera, viz., major *Geobacillus* and minor *Parageobacillus* (8). The objective of this study was to explore thermophilic bacteria from the Tattapani hot spring in the Himalayas that can be used for decomposition of cellulosic biomass in different polluted environments.

We isolated *Parageobacillus toebii* strain PW12 from a Tattapani hot spring water sample by spreading the water sample on nutrient agar medium and incubating it at 70°C (9). Isolated colonies were purified by the streaking method. The bacterial strain was identified by amplification and sequencing of 16S rRNA genes. The nucleotide sequence was subjected to a BLASTN (<http://blast.ncbi.nlm.nih.gov>) search of the NCBI database for taxonomic identity and submitted to NCBI under GenBank accession number [KJ509869](https://doi.org/10.1128/MRA.01163-18). The bacterial strain showed optimum cellulase enzyme activity at 80 to 90°C and pH 6 to 8.0, and cellulase activity was tolerant to metal ions (Mn²⁺, Co²⁺, Fe²⁺, Cd²⁺, and Hg²⁺), detergents (SDS, Triton X-100), solvents (toluene, cyclohexane, H₂O₂, *n*-butanol, ethanol), and EDTA (9). For genome sequencing, genomic DNA was extracted by a standard method for bacterial DNA isolation (10) and separated on 1% agarose gel by using TAE buffer (40 mM Tris base, 1 mM EDTA, and 20 mM glacial acetic acid) (10) and visualized by using a gel documentation unit (Alpha Innotech). A Qubit 2.0 fluorometer was used for determining DNA concentration. The paired-end (PE) sequencing library was prepared using an Illumina TruSeq Nano DNA high-throughput (HT) library preparation kit, and the PCR-amplified library was analyzed with a Bioanalyzer 2100 (Agilent Technologies) instrument using a high-sensitivity (HS) DNA chip, per the manufacturer's instructions, and loaded onto an Illumina HiSeq 2500 platform for

Citation Sharma P, Gupta S, Sourirajan A, Baumler DJ, Dev K. 2019. Draft genome sequence of hyperthermophilic, halotolerant *Parageobacillus toebii* PW12, isolated from the Tattapani hot spring, northwest Himalayas. *Microbiol Resour Announc* 8:e01163-18. <https://doi.org/10.1128/MRA.01163-18>.

Editor Frank J. Stewart, Georgia Institute of Technology

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Address correspondence to David J. Baumler, dbaumler@umn.edu, or Kamal Dev, kamaldevbhardwaj1969@gmail.com.

Received 20 August 2018

Accepted 20 December 2018

Published 24 January 2019

TABLE 1 Global statistics of the genome sequence of *Parageobacillus toebii* PW12

Parameter	Statistic
Total sequence length (bp)	3,238,931
No. of genes (total)	3,462
No. of CDS (total)	3,382
No. of genes (coding)	3,006
No. of CDS (coding)	3,006
No. of RNA genes	80
Total no. (type) of rRNAs	2 (5S), 5 (16S), 5 (23S)
No. (type) of complete rRNAs	2 (5S)
No. (type) of partial rRNAs	5 (16S), 5 (23S)
No. of tRNAs	63
No. of ncRNAs	5
No. of CRISPR arrays	4
No. of scaffolds	232
Scaffold N_{50} (bp)	26,951
Scaffold L_{50}	35
No. of contigs	570
Contig N_{50} (bp)	16,823
Contig L_{50}	53

cluster generation and sequencing. A total number of 1,707,006 paired-end reads with 512,101,800 bp was obtained using 2×150 -bp chemistry on the Illumina platform. The *de novo* genome assembly of high-quality PE reads and scaffolding was accomplished using SOAPdenovo v.2 (11), with a genome coverage of $150.0\times$. In the Illumina sequencing, each base in a read with a Phred score of 30 was assigned a quality score by a Phred-like algorithm (12). The assembled genome sequence of *Parageobacillus toebii* PW12 consists of 3,238,931 bp, arranged into 232 scaffolds. The G+C content was 42.05%. Totals of 3,382 coding sequences (CDS), 80 RNAs, 5 noncoding RNAs (ncRNAs), and 4 CRISPR arrays were predicted using the National Center for Biological Information (NCBI) Prokaryotic Genome Annotation Pipeline and the best-placed reference protein set of GeneMarkS+ (Annotation Software v.4.6), as described (13, 14). Three trinucleotide [(CGC)₅, (ATA)₅, and (CTT)₅] and two dinucleotide [(TA)₆ and (CT)₆] simple sequence repeats (SSRs) were identified using the MicroSatellite identification tool (MISA), as described (15). Genome statistics are summarized in Table 1.

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [QREZ00000000](https://www.ncbi.nlm.nih.gov/nuccore/QREZ00000000). The version described in this paper is version QREZ01000000. Raw sequence reads are available at NCBI under BioProject accession number [PRJNA484024](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA484024), BioSample accession number [SAMN09756839](https://www.ncbi.nlm.nih.gov/biosample/SAMN09756839) (Tattapani hot spring [Himachal Pradesh] isolate), and SRA accession numbers [SRX5163167](https://www.ncbi.nlm.nih.gov/sra/SRX5163167) (*Parageobacillus toebii* PW12 experiment) and [SRR8352206](https://www.ncbi.nlm.nih.gov/sra/SRR8352206) (*Parageobacillus toebii*_PW12_R1.fq.gz run).

ACKNOWLEDGMENTS

We acknowledge Prem Kumar Khosla, Vice Chancellor, and the members of the Yeast Biology Laboratory (YBL), Shoolini University, for supporting this project.

This work was funded by Shoolini University (to K.D.) to promote research under the Center for Omics and Biodiversity Research.

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