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Short Research Communication

Draft Genome Sequence of *Brevibacillus borstelensis* cifa_chp40, a Thermophilic Strain Having Biotechnological Importance

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Abstract

Brevibacillus borstelensis cifa_chp40 is a thermophilic, strictly aerobic gram positive motile bacteria isolated from the alkaline hot water spring located in the Eastern Ghats zone of India. It could grow in a wide range of temperature and degrade low-density polythene at 37°C. The strain cifa_chp40 produces essential enzymes like protease, lipase, esterase and amidase at 50°C. Here, we report the draft genome sequence of *B. borstelensis* cifa_chp40 which will provide further insight into the metabolic capabilities, function and evolution of this important organism.

Key words: *Brevibacillus borstelensis*, Hot water spring, Enzyme production, Draft genome.

Introduction

Brevibacillus borstelensis sp. nov., nom. rev. belonging to family *Paenibacillaceae* has been classified into a distinct group based on the phenotypic characteristics, DNA base composition, re-association analyses and results of cellular fatty acid and isoprenoid quinone composition analyses (1). *B. borstelensis* is closely related with *Bacillus centrosporus* (2) and *Bacillus choshinensis* (3). *B. borstelensis* has been described as strictly aerobic, gram-positive, spore forming, rod-shaped, motile bacteria. *B. borstelensis* isolated from different ecosystems have shown potential application in polythene degradation (4). *B. borstelensis* have been also reported to produce industrially important enzymes like amidase (5), amylase (6) and protease (7).

Brevibacillus borstelensis cifa_chp40 was isolated from Attri hot water spring (20°09'N 85°18'E) of Odisha, India. The bacteria can grow in a wide range of temperature from 20°C to 65°C and is able to degrade low-density polythene at 37°C. The strain produces industrially important enzymes like amidase, lipase, protease and esterase at an optimum growth temperature of 50°C. Production of enzymes by thermophilic *B. borstelensis* at high temperatures has been previously reported (5, 8-10). For in depth genomic study and potential applications of the bacteria, *B. borstelensis* cifa_chp40 was subjected to whole genome sequencing on Illumina MiSeq platform (Illumina Inc., CA) using 2 × 250 bp sequencing kit. Genomic DNA was extracted from the bacterial culture grown in Nutrient broth medium at 50°C. Following DNA fragmentation and adapter ligation, the paired-end sequencing library was prepared using Illumina TruSeq DNA library preparation kit. After quality filtration (mean quality score ≥ 25) and adapter trimming using Trimmomatic software, high quality data was assembled using CLC genomics workbench based on default set of parameters (Mismatch cost = 2,

Insertion cost = 3, Deletion cost = 3, Length fraction = 0.5 and Similarity fraction = 0.8) to obtain the scaffolds. The coding sequences (CDS) were predicted from the scaffolds using 'Prodigal' software, which is a microbial gene-finding program (11). Ribosomal and transfer RNAs were identified by aligning the scaffolds to Rfam database (12). The predicted CDS were annotated by comparison with non-redundant protein database of NCBI using BLASTX (13). Functional annotation of the sequences was performed using Gene Ontology (GO) terms with Blast2GO V2.8.0 software. Transposable elements were identified by Transposon PSI program (http://transposonpsi.sourceforge.net). Simple sequence repeats were determined using 'MISA', that allows the identification and localization of different microsatellites.

A total of 37,456,348 high quality paired-end reads with 347X coverage (mean read length 147 bp) were obtained. The total length of the genome was found to be 5,196,578 bp assembled into 38 scaffolds with 14 scaffolds having >20,000 bp and 6 scaffolds having >30,000 bp length. The G+C content was 51.90%. The draft genome of *B. borstelensis* cifa_chp40 harbored 5103 genes that encoded 4831 protein-coding genes including 113 tRNA and 3 rRNA genes (Table 1). Based on GO annotation, maximum CDS were categorized under molecular functions (615) followed by biological processes (468) and cellular components (159). Greater number of sequences was classified under the GO categories *viz*., catalytic activity, metabolic process, cellular process, binding, cell, cell part, localization and macromolecular complex (Figure 1). Besides, three transposable elements (ISC1316, LINE and ISC1316) and four simple sequence repeats were identified. The genome sequence of *B. borstelensis* cifa_chp40 encoded chaperone proteins and essential enzymes involved in large scale processes and required for production of different biomolecules. These enzymes include metalloprotease, serine peptidase, phospholipase, metallophosphoesterase, penicillin amidase and amidohydrolase and are involved in various biosynthesis and metabolic processes. The draft genome features of *B. borstelensis* cifa_chp40 indicate the biotechnological implication of the thermophilic bacteria in producing enzymes of industrial significance.

Table 1. Genome features of *Brevibacillus borstelensis* cifa_chp40.

Features	Values
Genome size	5,196,578 bp
Total number of scaffolds	38
G+C content	51.90%
Total number of genes	5103
Total number of protein-coding genes	4831
Plasmid	0
tRNA genes	113
rRNA genes	3

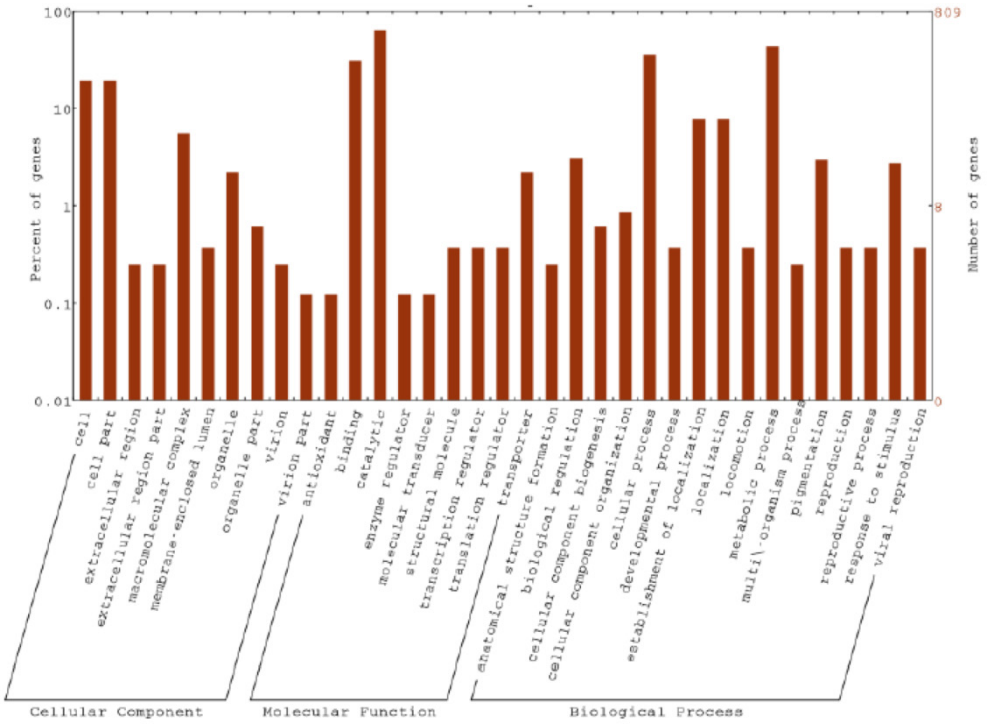

Figure 1. Classification of protein-coding genes based on gene ontology into three main categories: biological processes, molecular functions and cellular components. The y-axis on the right indicates the number of genes in a category. The y-axis on the left indicates percentage of a specific category of genes in the main category.

Nucleotide sequence accession number

The draft genome sequence of *Brevibacillus borstelensis* cifa_chp40 was deposited in the Genbank database under the accession number JPRB00000000.

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Competing Interests

The authors have declared that no competing interest exists.

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