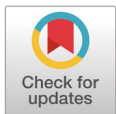


Complete genome sequence of the acidic cellulase producer *Bacillus amyloliquefaciens* ATC6

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Competing interests

No potential conflict of interest relevant
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Abstract

Here we report the complete genome sequence of *Bacillus amyloliquefaciens* ATC6, which produces acidic cellulase, isolated from pig feces. The genome is 4,062,817 bp in length and has a guanine-cytosine (GC) content of 46.27%. Among the predicted 3,913 protein-coding genes, two glucanase genes, which are involved in lichenan and cellulose degradation, were found. This genome analysis helps clarify the mechanism involved in cellulose biodegradation and support its application for efficient use of livestock feeds.

Keywords: Acidic cellulase, *Bacillus amyloliquefaciens*, Feed additive

INTRODUCTION

A number of *Bacillus* strains reported to degrade non-digestible carbohydrates, including cellulose and hemicellulose, have been used as feed additives to increase feed efficiency [1,2]. *Bacillus amyloliquefaciens* ATC6 was originally isolated from pig feces, and produces acidic cellulase [3]. Here we sequenced the complete genome of *B. amyloliquefaciens* ATC6. *B. amyloliquefaciens* ATC6 was grown in Nutrient Broth (Difco, Franklin Lakes, NJ, USA) at 37°C for 12 h. The genomic DNA was prepared as described previously [4], and the genome quality was checked using a spectrophotometer (UV-1601PC, Shimadzu, Kyoto, Japan). The genomic DNA of *B. amyloliquefaciens* ATC6 was sequenced using the PacBio RSII platform (ver. 2.0; Pacific Biosciences, CA, USA) at Macrogen. (Korea). All generated reads were *de novo* assembled using RS HGAP Assembly (ver. 3.0) [5]. Functional annotation was performed using the InterProScan (ver. 5.30–69.0) (<http://www.ebi.ac.uk/interpro/>), GO (<http://geneontology.org/page/go-database>), BLAST (ver. 2.6.0+) (<http://blast.ncbi.nlm.nih.gov/>) with UniProt (ver. 2018_06) (<http://www.uniprot.org/>), and EggNOG (ver. 4.5) (<http://eggnogdb.embl.de/#/app/home>) databases, and the genome was submitted to GenBank (<https://www.ncbi.nlm.nih.gov/>) (No. PRJNA639017).

The complete genome of strain ATC6 was 4,062,817 bp in length with a guanine-cytosine (GC) content of 46.27% (Table 1). No plasmid was detected (Fig. 1). The chromosome contained a total of 3,913 protein-coding sequences, 27 ribosomal RNAs, and 86 transfer RNAs that were annotated (Table 1). Analysis of the genomic sequences revealed that ATC6 possessed genes involved in cellulose degradation, as shown in our previous report [3]. This genome also contained genes associated with the degradation of other non-digestible carbohydrates, such as xylan and mannan. The genomic information of *B. amyloliquefaciens* ATC6 will help clarify the biodegradation mechanism of non-digestible carbohy-

Availability of data and material

Upon reasonable request, the datasets of this study can be available from the corresponding author.

Authors' contributions

Conceptualization: Kang DK.
 Data curation: Kim SH, Oh JK, Kim YH.
 Formal analysis: Kim SH, Oh JK.
 Methodology: Kim SH, Oh JK, Kim YH.
 Validation: Kang DK.
 Investigation: Kim SH, Oh JK, Kim YH.
 Writing - original draft: Kim SH, Kang DK.
 Writing - review & editing: Kang DK.

Ethics approval and consent to participate

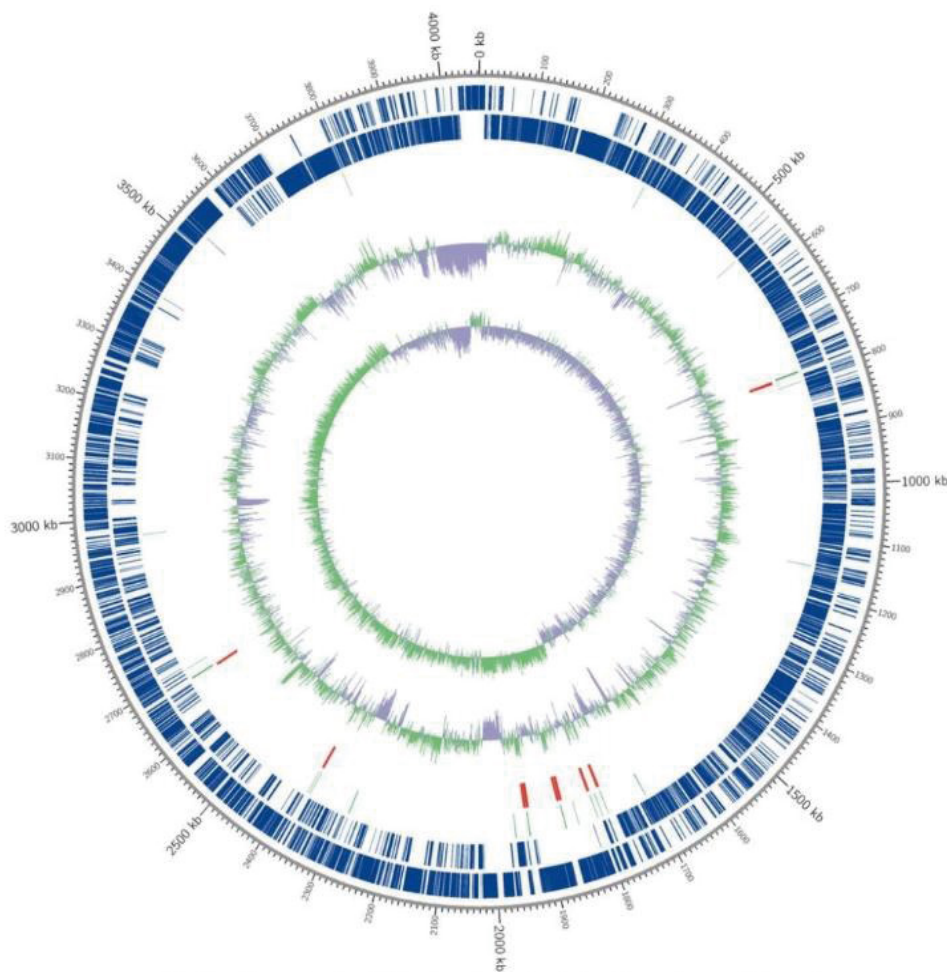
This article does not require IRB/IACUC approval because there are no human and animal participants.

drates, which could increase animal feed efficiency.

Table 1. Genome features of *Bacillus amyloliquefaciens* ATC6

Attribute	Value
Genome size (base pair)	4,062,817
GC content (%)	46.27
No. of contigs	1
Total genes	4,026
Protein-coding genes	3,913
tRNAs	86
rRNAs	27

GC, guanine-cytosine.



Circles illustrate the following characteristics from the outside to the center:
 (1) coding sequences in forward strand, (2) coding sequences on reverse strand,
 (3) Transfer RNAs (tRNAs), (4) ribosomal RNAs (rRNAs), (5) GC content, and (6) GC skew.

Fig. 1. Chromosome map of *Bacillus amyloliquefaciens* ATC6. GC, guanine-cytosine.

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