

# Complete genome sequence of *Bacillus coagulans* CACC834 isolated from canine

Jung-Ae Kim<sup>1,2</sup>, Dae-Hyuk Kim<sup>1,3</sup> and Yangseon Kim<sup>1\*</sup>

<sup>1</sup>Department of Research and Development, Center for Industrialization of Agricultural and Livestock Microorganisms, Jeongeup 56212, Korea

<sup>2</sup>Department of Bioactive Material Science, Jeonbuk National University, Jeonju 54896, Korea

<sup>3</sup>Department of Molecular Biology, Department of Bioactive Material Science, Institute for Molecular Biology and Genetics, Jeonbuk National University, Jeonju 54896, Korea



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## \*Corresponding author

Yangseon Kim

Department of Research and Development, Center for Industrialization of Agricultural and Livestock Microorganisms, Jeongeup 56212, Korea.

Tel: +82-63-536-6712

E-mail: yangseon@cialm.or.kr

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## ORCID

Jung-Ae Kim

<https://orcid.org/0000-0002-0694-477X>

Dae-Hyuk Kim

<https://orcid.org/0000-0002-9948-5313>

Yangseon Kim

<https://orcid.org/0000-0002-8285-3407>

## Competing interests

No potential conflict of interest relevant to this article was reported.

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## Abstract

*Bacillus coagulans* CACC 834 was isolated from canine feces, and its potential probiotic properties were characterized by functional genome analysis. Whole-genome sequencing of *B. coagulans* CACC 834 was performed using the PacBio RSII platforms. The complete genome assembly consisted of one circular chromosome (3.1 Mb) with guanine (G) + cytosine (C) content of 47.1%. Annotation revealed 3,181 protein-coding sequences (CDSs), 30 rRNAs, and 83 tRNAs. Gene associated 11% of the genes were involved in replication, recombination, and repair. We also annotated various stress-related, acid resistance, bile salt resistance and adhesion-related domains in this strain, which likely provide support in exerting probiotic action by survival under gastrointestinal tract. These results add to our comprehensive understanding of *B. coagulans* and suggest potential mammal-related industrial applications.

**Keywords:** *Bacillus coagulans*, Canine, Whole-genome sequencing

*Bacillus coagulans* strains are gram-positive, spore-forming, and produce lactic acid, which possesses the capacity to balance intestinal gut microbiota, ultimately promoting the growth of animals and improving immunity [1,2]. In addition, *B. coagulans* is resistant to high temperatures because of its probiotic activity, modulates and strengthens the immune system to protect against infections, and minimizes inflammation-related tissue damage [3].

We isolated *B. coagulans* CACC 834 (KACC 22145) from the feces of a female 3-year-old Boston terrier in Korea. The samples were incubated under anaerobic conditions at 37 °C [4].

Whole-genome sequencing was performed using the Pacific Biosciences (PacBio) RS II Single Molecule Real Time (SMRT) platform with a 20 kb SMRTbell™ template library at ChunLab. The reads were assembled using the PacBio SMAR Analysis 2.3.0. [5].

The sequences were annotated using the combined results of the automatic National Center for Biotechnology Information (NCBI) Prokaryotic Genome Annotation Pipeline (PGAP) and Rapid Annotations using Subsystems Technology (RAST) [6].

The complete genome of *B. coagulans* CACC 834 was composed of a 3,077,319 bp circular chromosome with 47.1% guanine (G) + cytosine (C) content. The genome contained 3,181 protein-

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**Availability of data and material**

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

**Authors' contributions**

Conceptualization: Kim Y.  
Data curation: Kim JA.  
Formal analysis: Kim JA.  
Methodology: Kim JA.  
Software: Kim JA.  
Validation: Kim JA, Kim DH.  
Investigation: Kim Y.  
Writing - original draft: Kim Y.  
Writing - review & editing: Kim JA, Kim DH, Kim Y.

**Ethics approval and consent to participate**

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

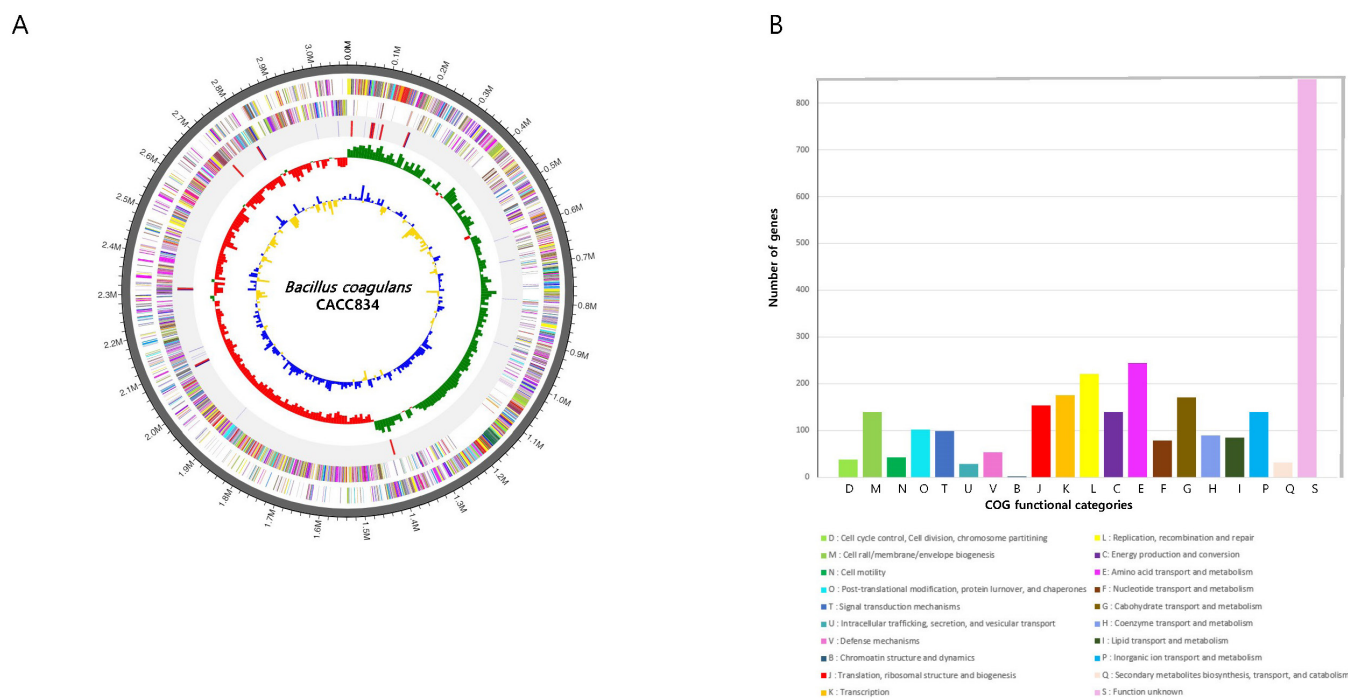
coding sequences (CDS), 30 rRNAs, and 83 tRNAs (Table 1). The genome features of *B. coagulans* CACC 834 are summarized in Fig. 1. Among these CDS, 2,909 genes were classified into 20 clusters of orthologous groups (COG) functional categories (Fig. 1B). More than 41% of genes were involved in transport and metabolism, including amino acid, carbohydrate, inorganic ion, nucleotide, coenzyme, and lipid. Interestingly, 11% of the genes were involved in replication, recombination, and repair (Fig. 1B).

The genome of *B. coagulans* CACC 834 possessed *hsp20*, *hsp60*, *dnaK*, *dnaJ* and *grpE* operons, encoding enzymes and proteins for heat shock. Also, *B. coagulans* CACC 834 has heat shock induced genes, such as *clpB*, *clpP*, *mcsB*, and repair-related genes, such as *recA* and *wvrABC*. The expression of these genes is expected to help promote cell recovery from heat shock by limiting damage caused by stress [7–9]. Furthermore, *B. coagulans* CACC 834 carried genes known to be involved in lactate synthesis, adhesion, acid resistance, and bile resistance (Table 2).

This study on complete genome sequence of *B. coagulans* CACC 834 may increase our

**Table 1. Genome overview of *Bacillus coagulans* CACC834**

Feature	Values
Genome size (bp)	3,077,319
No. of contigs	1
GC content	47.1%
Protein-coding genes (CDSs)	684
rRNA	30
tRNA	83
plasmid	0
Genbank Accession No.	CP076597



**Fig. 1. Genome features of *Bacillus coagulans* CACC834.** (A) Circular genome maps of *B. coagulans* CACC834 chromosome. Circles from the outside to the center denote rRNA and tRNA gene, reverse strand CDS, forward strand CDS, GC skew, and GC content. (B) Genome number of COG category. CDS, protein-coding genes; COG, clusters of orthologous group; G, guanine; C, cytosine.

**Table 2.** Predicted genes involved in probiotic potency in *B. coagulans* CACC834

Predicted function	<i>B. coagulans</i> CACC834			
	Predicted genes	Start position	End position	Length (bp)
Lactate synthesis	<i>ldh</i>	1,433,259	1,434,242	984
Adhesion protein	<i>EpsD</i>	393,741	394,838	1,098
	<i>FliD</i>	724,445	726,531	2,088
Acid resistance-related				
Protection or repair of macromolecules	<i>dnaK</i>	1,737,678	1,737,546	1,827
	<i>dnaJ</i>	1,736,410	1,737,546	1,137
	<i>grpE</i>	1,739,540	1,740,202	663
	<i>recA</i>	125,046	1,226,113	1,068
	<i>uvrABC</i>	765,135	767,135	2,001
	<i>clpB</i>	108,312	110,762	2,451
	<i>clpP</i>	793,689	794,279	591
	<i>mcsB</i>	108,312	110,762	2,451
Fatty acid synthesis	<i>fabF</i>	870,816	871,754	1,242
	<i>fabH</i>	871,824	873,065	939
	<i>fadD</i>	260,088	261,242	1,155
	<i>fabI</i>	903,131	903,910	780
Acid shock response	<i>aspS</i>	1,804,625	180,696	1,773
Metabolic rearrangements	<i>alsD</i>	2,318,874	2,319,623	750
Glycine betain ABC transport system	<i>opuCC</i>	467,919	468,833	915
Bile salt resistance	<i>bass</i>	1,090,675	1,091,145	471

understanding of the probiotic effects in host healthcare and extend its potential application as an industrial strain.

The complete genome of *B. coagulans* strain CACC 834 determined in this study has been deposited in the NCBI GenBank database under accession number CP076597.

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