

# Complete genome sequence of *Pediococcus acidilactici* CACC 537 isolated from canine

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## Competing interests

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

## Abstract

*Pediococcus acidilactici* CACC 537 was isolated from canine feces and reported to have probiotic properties. We aimed to characterize the potential probiotic properties of this strain by functional genomic analysis. Complete genome sequencing of *P. acidilactici* CACC 537 was performed using a PacBio RSII and Illumina platform, and contained one circular chromosome (2.0 Mb) with a 42% G + C content. The sequences were annotated and revealed 1,897 protein-coding sequences, 15 rRNAs, and 56 tRNAs. It was determined that *P. acidilactici* CACC 537 genome carries genes known to be involved in the immune system, defense mechanisms, restriction-modification (R-M), and the CRISPR system. CACC 537 was shown to be beneficial in preventing pathogen infection during the fermentation process, help host immunity, and maintain intestinal health. These results provide for a comprehensive understanding of *P. acidilactici* and the development of industrial probiotic feed additives that can help improve host immunity and intestinal health.

**Keywords:** *Pediococcus acidilactici*, Canine, Whole-genome sequencing

Lactic acid bacteria (LAB) are mostly used as probiotics in functional foods and feed additives [1]. Among them, *Pediococcus* sp. is used as a beneficial microorganism in the context of food and livestock microbiology, and it has been reported that *P. acidilactici* CACC 537 (KACC 8198BP) has acid and bile tolerance, intestinal adhesion activity, and antibacterial activity against livestock pathogens [2].

This study attempted to genetically determine the useful effects and functions of CACC537 using whole-genome sequencing. The complete genome of CACC 537 was sequenced using a PacBio RS II (Pacific Biosciences, Menlo Park, CA, USA) and Illumina (San Diego, CA, USA) platform with a SMRTbell™ template at Macrogen (Seoul, Korea), and the reads were assembled using HGAP version 3.0 [3]. The annotation of the sequence used automatic results from the National Center for Biotechnology Information (NCBI) Prokaryotic Genome Annotation Pipeline (PGAP) and analyzing Rapid Annotations using Subsystems Technology (RAST) tools [4]. The complete genome

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Not applicable.

**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, Jang HJ.  
 Formal analysis: Kim JA.  
 Methodology: Kim JA, Son YK.  
 Software: Kim JA.  
 Validation: Kim JA, Kim DH.  
 Investigation: Kim Y.  
 Writing - original draft: Kim Y.  
 Writing - review & editing: Kim JA, Jang HJ, Kim DH, Son YK, Kim Y.

**Ethics approval and consent to participate**

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

of CACC537 consists of one circular chromosome with a total length of 2,035,984 bp and a DNA G + C content of 42.0%. it includes 1,897 protein-coding genes (CDSs) and 71 RNA genes (15 rRNA and 56 tRNA genes) (Table 1 and Fig. 1A). The 1,782 genes were categorized as functional proteins based on designations through the Clusters of Orthologous Groups (COGs) database. Most assigned CDSs were found to be involved in carbohydrate transport and metabolism; transcription; translation, ribosomal structure and biogenesis; replication, recombination and repair; and cell wall/membrane/envelope biogenesis (225, 146, 142, 107, and 104 genes, respectively) (Fig. 1B).

In the genome of strain CACC 537, the presence of *ldhD*, *ldhL*, *pyk*, *eno*, *fbaA*, *pfk*, and *pgi*, which are involved in lactic acid production as key genes of homo-fermentation in the Embden-Meyerhof-Parnas (EMP) pathway, was detected [5]. We also identified genes encoding lysozymes, chitinases, and proteases, commonly predicted as able to exert antibacterial functions against pathogens; and the *fab* gene cluster, in charge of producing fatty acids that can protect the intestinal mucosal from pathogens. Interestingly, the short-chain fatty acids (SCFA) produced as metabolic by-products play an important role in intestinal homeostasis and have been reported to be associated with immune enhancement and liver function improvement [6–8]. In addition, we identified a type II-A CRISPR/CRISPR-related (Cas) gene with two CRISPR (1 and 2) regions, and a CRISPR 9 region; and genes involved in immune and defense mechanisms, including some for restriction-modification (R-M) systems. This strain prevents fermentation failure due to bacterial phage and pathogen infection in the fermentation process, and has an intestinal function to help host immunity and maintain intestinal health [9–10] (Table 2).

This study on the complete genome sequence of *P. acidilactici* CACC 537 showed that it has potential probiotic effects, and thus may be useful for the development of health-promoting products.

**Nucleotide sequence accession number**

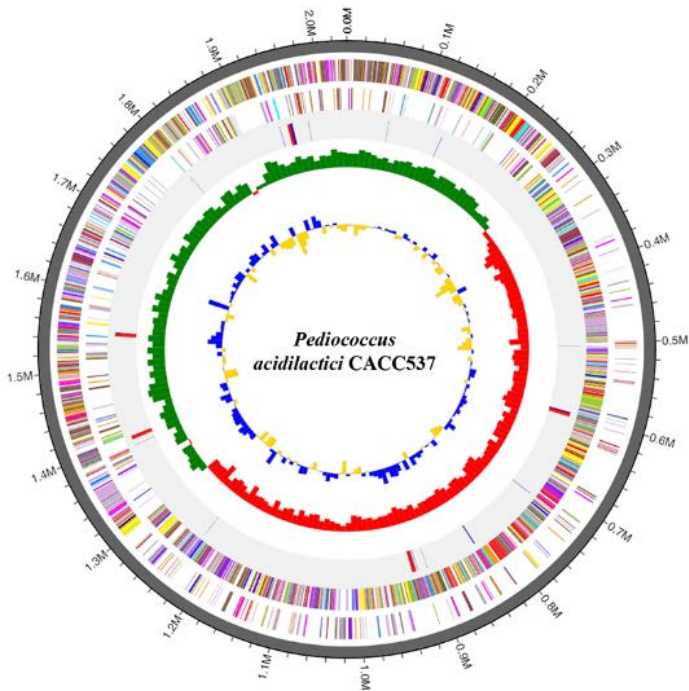
The complete genome of *P. acidilactici* CACC 537 has been deposited in the NCBI GenBank database under the accession number CP048019.

**Table 1. Genome overview of *Pediococcus acidilactici* CACC 537**

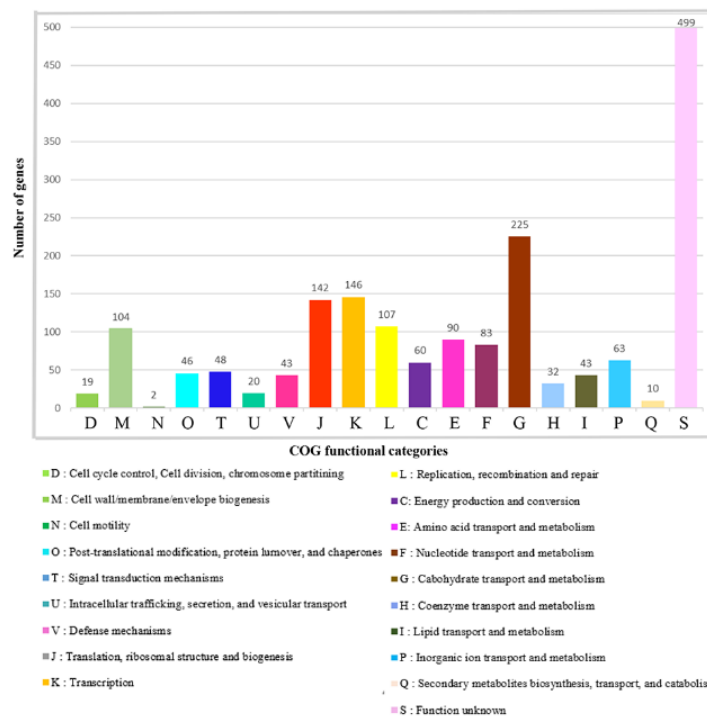
Feature	Values
Genome size (bp)	2,035,984
No. of contigs	1
GC content	42.0 %
Protein-coding genes (CDSs)	1,897
rRNA	15
tRNA	56
Genbank Acession No.	CP048019

bp, base pair.

A



B



**Fig. 1. Genome features of *Pediococcus acidilactici* CACC 537.** (A) Circular genome maps of the *P. acidilactici* CACC537 chromosome. Circles from the outside to the center denote rRNA and tRNA genes, reverse strand CDSs, forward strand CDSs, GC skew, and GC content. (B) COG functional category annotation numbers on CACC 537 genome. CDS, coding sequences; GC, guanine cytosine; COG, clusters of orthologous groups.

Table 2. Predicted genes involved in probiotic potency in *Pediococcus acidilactici* CACC537

Predicted function	<i>Pediococcus acidilactici</i> CACC 537			
	Predicted genes	Products	Gene position	Length (bp)
Homolactic-fermentation related				
	<i>ldhD</i>	D-Lactate dehydrogenase	195437..196432	996
	<i>ldhL</i>	L-Lactate dehydrogenase	940686..941657	972
			c(1521565..1522485)	921
	<i>pyk</i>	Pyruvate kinase	c(408957..410720)	1,764
	<i>eno</i>	Phosphopyruvate hydratase	c(1111207..1112493)	1,287
			1802875..1804197	1,323
	<i>fbaA</i>	Fructose-bisphosphate aldolase	730570..731433	864
	<i>pfk</i>	6-Phosphofruktokinase	c(410797..411765)	969
			c(552661..553572)	912
	<i>pgi</i>	Glucose-6-phosphate isomerase	c(727794..729146)	1,353
Antimicrobial resistance-related				
Bacteriolytic enzyme				
	-	Lysozyme	c(465359..466543)	1,185
	-	Chitinase	1707522..1708034	513
			2026125..2027144	1,020
	<i>glup</i>	Rhomboid protease	125912..126601	690
Fatty acid biosynthesis (Clusters)				
	<i>fabI</i>	Enoyl-(acyl-carrier-protein) reductase	187972..188730	759
	<i>accA,D,C</i>	Acetyl-CoA carboxylase	184990..187955	2,966
	<i>fabZ1</i>	3-Hydroxyacyl-(acyl-carrier-protein) dehydratase	184563..184973	411
	<i>accB</i>	Acetyl-CoA carboxylase	184125..184550	426
	<i>fabF,G,D</i>	$\beta$ -Ketoacyl-ACP synthase II, $\beta$ -ketoacyl-ACP reductase, acyl-carrier protein	181121..184120	3,000
	<i>acpP</i>	Acyl carrier protein	180858..181094	237
	<i>fabH,Z2</i>	$\beta$ -Ketoacyl-ACP synthase III, $\beta$ -hydroxyacyl-ACP dehydratase	179410..180831	1,422
Restriction-modification system				
	<i>hsdR</i>	Type I site-specific deoxyribonuclease	1445338..1448211	2,874
	<i>hsdM</i>	Site-specific DNA-methyltransferase	1448232..1449824	1,593
	<i>hsdS</i>	Type I site-specific deoxyribonuclease	1449821..1453105	3,284
Immune system				
	<i>cas9</i>	CRISPR-associated endonuclease	1747125..1751225	4,101
	<i>cas1</i>	CRISPR-associated endonuclease	1751443..1752348	906
	<i>cas2</i>	CRISPR-associated endonuclease	1752326..1752631	306
	<i>yajC</i>	Immunogenic membrane protein	c(647443..647826)	384
	<i>cfa</i>	Cyclopropane-fatty-acyl-phospholipid synthase	1113749..1114924	1,176
	<i>dacA</i>	Diadenylate cyclase	1814096..1814947	852
	<i>myh6</i>	TNF receptor protein	1730618..1733290	2,673

bp, base pair; c, complement.

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