

Genome Reports

Complete Genome Sequence of *Priestia flexa* DMP08 Isolated from Kimchi, Traditional Korean Fermented Vegetables

Junghyun Park¹, Jong Hun Kim², and Do-Won Jeong^{1*}

¹Department of Food and Nutrition, Dongduk Women's University, Seoul 02748, Republic of Korea

²Department of Food Science and Biotechnology, Sungshin University, Seoul 01133, Republic of Korea

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Strain *Priestia flexa* DMP08, isolated from traditional Korean fermented vegetables kimchi, exhibits protease activity and lipase activity. The complete genome of strain DMP08 includes a single circular 3,999,911-bp chromosome without plasmids. The G+C content of the genome is 38.1 mol%. The genome includes 38 protease- and 3 lipase-encoding genes.

Keywords: *Priestia flexa*, genome, kimchi, protease, lipase

Priestia flexa was reclassified from *Bacillus flexus* based on phylogenomic and comparative genomic analyses [1]. *P. flexa* is endospore-forming and it has been isolated from sources including feces, soil, the upper atmosphere, and sea sediment. The major research interest in *P. flexa* has concerned enzyme activity, such as of proteases and lipases [2, 3], as well as arsenic remediation [4]. Because of these enzymatic and remediative activities, *P. flexa* has been suggested to be a useful microorganism for detergents, food technology, pharmaceuticals, and biomedical science [5]. The β -amylase from *P. flexa* AE-BAF has been used as a food-grade enzyme [3]. However, genomic information on *P. flexa* is limited. In our previous study, *P. flexa* strain DMP08 was isolated from kimchi, traditional Korean fermented cabbage [6].

Strain DMP08 exhibited protease activity on tryptic

soy agar (Becton Dickinson and Co., USA) supplemented with 2% skim milk (w/v), and lipolytic activity on tributyrin agar (Sigma-Aldrich, USA) supplemented with 1% glyceryl tributyrate (w/v) (Fig. 1). In food fermentation, protease and lipase activities contribute to sensory enhancement through proteolysis and lipolysis [7, 8]. To shed light on its potential as a starter candidate strain for food fermentation, we determined the complete genome sequence of *P. flexa* DMP08. Whole-genome

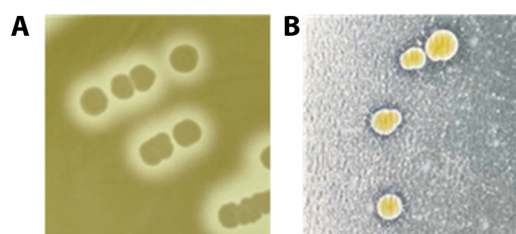


Fig 1. Protease (A) and lipase (B) activities of *Priestia flexa* DMP08. Protease and lipase activity were determined on TSA containing 2% skim milk (w/v) and tributyrin agar containing 1% tributyrin (w/v), respectively. The formation of a clear zone around the colony is determined to be positive enzymatic activity.

***Corresponding author**

Phone: +82-2-940-4463, Fax: +82-2-940-4610

E-mail: jeongdw@dongduk.ac.kr

Table 1. Genome features of *Priestia flexa* DMP08.

Feature	Value
Genome size (bp)	3,999,911
G+C content (mol%)	38.1
Total number of genes	4,156
Protein coding genes (CDS)	4,015
rRNA genes	37
tRNA genes	99
Other RNA genes	5

sequencing was performed using the PacBio Sequel 10K system (PacBio, USA) at CJ Bioscience, Inc. (South Korea). One contig was generated from the obtained sequencing reads (231,996 reads, 352× coverage) by the FLYE assembler (version 2.8.3) in SMRT Link (PacBio) and annotated by using the NCBI Prokaryotic Genome Annotation Pipeline (version 4.6). Annotated gene functions were analyzed using the Clusters of Orthologous Groups (COG) database [9] and Rapid Annotation using

Table 2. Putative protease and lipase genes identified in the genome of *Priestia flexa* DMP08.

Gene locus	E.C. no.	Product	COG	Gene
Lipase				
LZP85_RS00260	3.1.1.3	Triacylglycerol lipase	S	<i>lip</i>
LZP85_RS04510	3.1.1.3	Triacylglycerol lipase	S	<i>lip</i>
LZP85_RS17025	3.1.1.5	Lysophospholipase	I	<i>pldB</i>
Protease				
LZP85_RS00215	3.4.-.-	Peptidoglycan L-alanyl-D-glutamate endopeptidase CwIK	M	<i>cwIK</i>
LZP85_RS02900		Uncharacterized 42.1-kDa protein in intracellular alkaline protease 3'- region	S	
LZP85_RS04965		ATP-dependent Clp protease ATP-binding subunit ClpA-like protein CD4A	O	
LZP85_RS05570		Putative membrane protease YugP	S	
LZP85_RS06485	3.4.24.89	Pro-Pro endopeptidase	S	<i>zmp1</i>
LZP85_RS07875	3.4.-.-	Probable peptidoglycan endopeptidase LytE	S M	<i>lytE</i>
LZP85_RS10595	3.4.-.-	D-gamma-glutamyl-meso-diaminopimelic acid endopeptidase CwIS	S M	<i>lytE</i>
LZP85_RS12145	3.4.21.-	Alkaline protease	O	<i>epr</i>
LZP85_RS12170	3.4.21.107	Peptidase Do	O	<i>degP</i>
LZP85_RS13055		Protease synthase and sporulation protein PAI	K	
LZP85_RS13235	3.4.13.19	Membrane dipeptidase	E	<i>DPEP</i>
LZP85_RS13295	3.4.24.-	Probable inactive metalloprotease YmfF	O	<i>pqqL</i>
LZP85_RS13335	3.4.21.92	Endopeptidase Clp	O	<i>clpP</i>
LZP85_RS13375	3.4.24.-	Uncharacterized zinc protease YmxG	O	<i>pqqL</i>
LZP85_RS13460	3.4.24.-	Probable protease eep	M	<i>rseP</i>
LZP85_RS13665		ATP-dependent protease ATPase subunit HslU	O	
LZP85_RS13670	3.4.25.2	HslU-HslV peptidase	O	<i>hslV</i>
LZP85_RS14050	3.4.23.-	Sporulation sigma-E factor-processing peptidase	S	<i>spolIGA</i>
LZP85_RS14440		Protease PrsW	S	
LZP85_RS14960	3.4.21.116	SpoIVB peptidase	M	<i>spoIVB</i>
LZP85_RS15230	3.4.21.105	Rhomboid protease	S S	<i>gluP</i>
LZP85_RS15595	3.4.24.78	GPR endopeptidase	O	<i>gpr</i>
LZP85_RS15745	3.4.-.-	Uncharacterized protease YrrO	O	
LZP85_RS15750	3.4.-.-	Uncharacterized protease YrrN	O	
LZP85_RS16225	3.4.21.53	Endopeptidase La	O	<i>lon</i>
LZP85_RS16230	3.4.21.53	Endopeptidase La	O	<i>lonB</i>
LZP85_RS16235		ATP-dependent Clp protease ATP-binding subunit ClpX	O	
LZP85_RS16735	3.4.21.-	Putative signal peptide peptidase SppA	OU	<i>sppA</i>
LZP85_RS17695	3.4.-.-	L-Ala-D-Glu endopeptidase	M	<i>lytH</i>

Table 2. Continued.

Gene locus	E.C. no.	Product	COG	Gene
LZP85_RS17965	3.4.21.92	Endopeptidase Clp	O	<i>clpP</i>
LZP85_RS18135	3.4.21.102	C-terminal processing peptidase	M	<i>prc</i>
LZP85_RS18370	3.4.-.-	Probable endopeptidase p60	M M	<i>lytE</i>
LZP85_RS18490	3.4.21.-	Major intracellular serine protease	O	<i>vpr</i>
LZP85_RS18685		Putative zinc metalloprotease YwhC	S	
LZP85_RS19085	3.4.21.107	Peptidase Do	O	<i>degP</i>
LZP85_RS19555		Sporulation-specific protease YabG	S	
LZP85_RS19695	3.4.24.-	ATP-dependent zinc metalloprotease FtsH	O	<i>ftsH</i>
LZP85_RS20345		Rhomboid protease GluP	S	

The Enzyme Commission (EC) number is a numerical classification scheme for enzymes, based on the chemical reactions they catalyze. The EC numbers are based on the genes of strain DMP08 and gene are assigned by BlastKoALA. The Clusters of Orthologous Group (COG) categorization was generated by annotated gene functions.

Subsystem Technology [10].

The complete genome of *P. flexa* strain DMP08 consists of a circular 3,999,911-bp chromosome (Table 1). The G+C content of the genome is 38.1 mol%. The average nucleotide identity of the DMP08 genomic sequence showed 99.2% and 74.4% similarity with *P. flexa* KLBMP 4941 and *P. aryabhatai* KNUC0118, respectively. The genome was predicted to contain 4,156 open reading frames, 99 tRNA genes, and 37 rRNA genes. COG functionally categorized 3,780 genes and major COG categorizations are related to amino acid transport and metabolism (315 genes, 8.33%), transcription (260 genes, 6.88%), and carbohydrate transport and metabolism (244 genes, 6.46%). The SEED subsystem categorized 1,647 genes and the most abundant subsystem category was related to amino acids and derivatives (308 genes, 18.70%), followed by carbohydrates (254 genes, 15.42%). The genome of *P. flexa* strain DMP08 contains 38 protease- and 3 lipase-encoding genes (Table 2), and those genes contribute to the protease and lipase activities of *P. flexa* strain DMP08. *P. flexa* enzymes, which identified effective enzymes among them, alone or as strains that produce enzymes will help fermented foods or food processing processes.

Nucleotide Sequence Accession Number. The complete genome sequence of *P. flexa* DMP08 has been deposited in DDBJ/ENA/GenBank under accession number NZ_CP090431.

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Conflict of Interest

The authors have no financial conflicts of interest to declare.

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