



Genome announcement

Complete genome sequence of *Pedobacter cryoconitis* PAMC 27485, a CRISPR-Cas system-containing psychrophile isolated from Antarctica



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ABSTRACT

Pedobacter cryoconitis PAMC 27485, an aerobic, Gram-negative, facultatively psychrophilic bacterium, was isolated from Antarctic soil. Here we report the complete genome of *P. cryoconitis* PAMC 27485, which contains a type II CRISPR-Cas system and genes encoding useful enzymes (e.g. proteases). The genome sequence of *P. cryoconitis* PAMC 27485 could provide insights into its adaptive immune system against foreign genetic elements and biotechnological potential.

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Members of the genus *Pedobacter* have been frequently isolated from various terrestrial and aquatic environments, including soil, freshwater, drinking water, compost, wood falls, and cold environments (Margesin et al., 2003; Wong et al., 2011; Da et al., 2015). Especially, psychrophiles belonging to the genus *Pedobacter* are of extraordinary interest because of their potential for biotechnological applications in the field of detergent production, textile industry, food industry, and bioremediation (Gerday et al., 2000). *Pedobacter cryoconitis*, first isolated from alpine glacier cryoconite (i.e., strain A37^T), is a Gram-negative, facultatively psychrophilic, and aerobic bacterium, which is placed within the family Sphingobacteriaceae (Margesin et al., 2003). *P. cryoconitis* A37^T is able to degrade diesel oil and showed high-yield production of proteases at low temperatures (Margesin et al., 2003). Another strain isolated from Antarctic soil samples, *P. cryoconitis* BG5, can produce extracellular antimicrobial compounds that inhibit the growth of food pathogens (Wong et al., 2011). A subsequent sequencing effort revealed that the pMWK1 plasmid in the strain BG5 possessed a putative toxin-antitoxin system, but the chromosomal DNA or other plasmids were suggested as possible locations of other valuable genes (Wong et al., 2013). Considering that some *Pedobacter* spp. possess a CRISPR-Cas system (Poehlein et al., 2015), which is an adaptive immune system against foreign genetic elements

derived from bacteriophages or exogenous plasmids, the genome sequencing of *P. cryoconitis* may provide a better understanding of its adaptive immune system and biotechnological potential.

P. cryoconitis PAMC 27485 was isolated from a soil sample collected in King George Island, Antarctica (62°14'11" S, 58°43'04" W). Genomic DNA from *P. cryoconitis* PAMC 27485 was extracted using the i-genomic BYF Mini Kit (iNtRON Biotechnology, Republic of Korea) and used to construct a 20 kb insert library. Genome sequencing was performed using Pacific Biosciences (PacBio) RS II single-molecule real-time (SMRT) sequencing technology (Pacific Biosciences, CA) (Eid et al., 2009). *De novo* assembly was conducted for 65,139 reads with 11,248 nucleotide bases on the average (732,709,199 bp in total) using the hierarchical genome assembly process (HGAP) pipeline in the SMRT analysis software version 2.3.0 (Chin et al., 2013), which resulted in one circular chromosome sequences with 110-fold coverage. The protein coding sequences (CDSs) were predicted by Prokaryotic Dynamic Programming Genefinding Algorithm (Prodigal) version 2.6.1 (Hyatt et al., 2010). The functional annotation was performed using UniProt (Wu et al., 2006), Pfam (Finn et al., 2014), and COG (Tatusov et al., 2003). The CRISPRs were identified by CRISPR recognition tool (Bland et al., 2007). The genome of *P. cryoconitis* PAMC 27485 consists of a single circular chromosome of 5,950,539 bp in size and has an average G + C content of 38.8%. The genome contains 4922 predicted protein coding genes, 19 rRNA, and 67 tRNA genes. General features for the complete genome of *P. cryoconitis* PAMC 27485 are shown in Table 1.

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Table 1
Pedobacter cryoconitis PAMC 27485 genome features.

Feature	Chromosome
Size [bp]	5,950,539
GC content (%)	38.8
Total number of genes	5044
Protein coding genes (CDSs)	4922
Genes with a predicted function	3098
rRNAs (5S, 16S, 23S)	19
tRNAs	67

Among 4922 predicted genes, 3,098 CDSs were assigned with predicted functions. According to the annotation results, the genome of the strain PAMC 27485 has a type II CRISPR–Cas system. The CRISPR locus is composed of 65 repeats with a direct repeat length of 45 nucleotides and the genome encodes a cas cluster, comprising cas1 (AY601.1217), cas2 (AY601.1218), and cas9 (AY601.1216). Although the complete prophage region was not present, phage-related proteins, such as integrases (e.g. AY601.0464), tail protein (e.g. AY601.2694), and head protein (AY601.4085), were identified. Genes encoding industrially useful enzymes, such as proteases (i.e., 96 putative proteases; 52 metallo- and 38 serine-), carotenoid synthases, glycosyl hydrolases, non-ribosomal peptide synthases and polyketide synthases, were also identified. Additionally, responsible genes for resistance to cold stress and to heavy metals (i.e., copper, mercury, cobalt, zinc, and cadmium) were found in the genome.

Nucleotide sequence accession number

The genome sequence of *P. cryoconitis* PAMC 27485 has been deposited at GenBank under the accession number CP014504 (chromosome). The strain PAMC 27485 is available from the Polar and Alpine Microbial Collection (Korea Polar Research Institute, Incheon, Republic of Korea).

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