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Draft genome sequence of the psychrophilic bacterium *Lacinutrix jangbogonensis* PAMC 27137^T

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ABSTRACT

Lacinutrix jangbogonensis PAMC 27137^T is a psychrophilic bacterial strain isolated from the marine sediment of the Ross Sea, Antarctica. Here we present an annotated draft genome sequence of the strain PAMC 27137^T which showed the narrower range in the growth temperature than other type strains of the genus *Lacinutrix*. The draft genome of 4,017,559 bp with a G + C content of 30.6% comprised 14 scaffolds of 46 contigs containing 3589 protein-coding genes and 46 RNA genes. The function of 2185 (60.1%) proteins was predicted and 1943 (53.4%) proteins were assigned to COG functional categories. Comparative analysis of the draft genome across other type strains may provide clues into the mechanism of growth in narrow temperature range.

1. Introduction

The genus *Lacinutrix* which belongs to the phylum *Bacteroidetes* currently consists of five type species and members of the genus *Lacinutrix* have been known to produce extracellular protease in marine sediments of Antarctica (Bowman and Nichols, 2005; Nedashkovskaya et al., 2008; Srinivas et al., 2013; Zhou et al., 2013; Lee et al., 2014). Type strains of the genus *Lacinutrix* were all isolated from copepod, algae, or sediments of polar areas (Bowman and Nichols, 2005; Nedashkovskaya et al., 2008; Srinivas et al., 2013; Lee et al., 2014). All type strains of the genus *Lacinutrix* have been reported to grow at low temperature and exhibit wider growth temperature ranges (from −2–4 °C to 20–25 °C). However, strain PAMC 27137^T showed a relatively narrower range of growth temperatures (4 °C to 10 °C) compared to other type strains of the genus *Lacinutrix*. To better understand the molecular basis of low-temperature constraints on the growth, we performed a genomic analysis of *Lacinutrix jangbogonensis* PAMC 27137^T.

Genomic DNAs were extracted using a DNeasy Tissue and Blood Kit (Qiagen) according to the manufacturer's instructions. The genome of *L. jangbogonensis* PAMC 27137^T was sequenced using 454 technology. Both single-end library and an 8-kb paired-end library were constructed and sequenced using 454 GS FLX Titanium system (Roche Diagnostics, Branford, CT), which generated 100,494 reads totaling 101,402,380 bps and 88,196 reads totaling 39,549,198 bps, respectively. Celera Assembler (Ver. 7.0) was used for assemblies (Myers et al., 2000). 454 reads were converted to the FRG file format using sffToCA for assembling. Assembly was performed with the parameters overlapper = ovl, unitigger = bogart, merSize = 22, and doOverlapBasedTrimming = 1. The initial Celera assembly had a total size of 4,017,559 bps, containing 46 contigs (N50 contig size, 181,213 bps) that can be assembled into 14 scaffolds (N50 scaffold size, 907,640 bps). Genome annotation was performed using the automated Bacterial Annotation System (BASys) (Van Domselaar et al., 2005). BASys predicted the coding sequence using Glimmer (Delcher et al., 2007) and provided COG function, signal peptides, transmembrane regions and Pfam information for CDS through the BASys annotation engines. tRNA genes and ribosomal RNA genes were predicted using the rapid annotations using subsystems technology (RAST) (Aziz et al., 2008).

The draft genome of *L. jangbogonensis* PAMC 27137^T was comprised of 4,017,559 nucleotides and the G + C content was 30.6% (Table 1). There are 3589 predicted protein-coding regions. A total of 2185 genes (60.1%) have been assigned to a predicted function while the remainders have been designated as hypothetical proteins (Table 1). Genes for the complete pathways for glycolysis, the Krebs cycles and the pentose phosphate pathway were found, but some essential genes in the pathway of Urea cycle, arginine biosynthesis and starch synthesis could not be identified. As a distinctive feature of *L. jangbogonensis* PAMC 27137 ^{T}, *L. jangbogonensis* PAMC 27137^T has an additional *dnaK* gene which may serve a different function such as the *dnaK* multigene family in the *Cyanobacteria* (Nimura et al., 2001). More detailed analysis of this genome and a comparative analysis with other strains of *Lacinutrix* may provide further insights into the growth of PAMC

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Table 1
General features of *L. jangbogonensis* PAMC 27137^T draft genome.

Attribute	Value	% of total
Genome size (bp)	4,017,559	100
DNA coding region (bp)	3,498,419	87.1
DNA G + C content (bp)	1,229,775	30.6
Number of scaffolds	14	
Number of contigs	46	
Total gene	3637	100
tRNA genes	38	1.0
rRNA operons[a]	2	
Protein-coding genes	3589	98.7
Genes with function prediction	2185	60.1
Genes assigned to COGs	1943	53.4
Genes assigned Pfam domains	1505	41.4
Genes with signal peptides	1183	32.5
Genes with transmembrane helices	857	23.6

[a] 3 copies of 5S, 2 copies of 16S and 3 copies of 23S.

27137^T in narrow temperature range compared to other type strains of *Lacinutrix*.

2. Nucleotide sequence accession number

The whole genome shotgun project has been deposited in DDBJ/EMBL/GenBank under accession number JSWF00000000 and was deposited in the Genomes On Line Database under Gp0109128.

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