

Genome Announcement

Complete genome sequence of a cold-adapted humic acid degrading bacterium *Pedobacter* sp. PAMC 27299 from the Antarctic seashore

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남극 해안으로부터 저온적응 부식산 분해 *Pedobacter* sp. PAMC 27299의 유전체 서열 해독

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ABSTRACT: *Pedobacter* sp. PAMC 27299 with humic acid cultivated on low temperature was isolated from the moss debris on the coast of the Barton Peninsula of King George Island of the maritime Antarctic region. Here, we present the complete genome sequence of *Pedobacter* sp. PAMC 27299, which contains 6,147,290 bp with a G+C content of 40.54%. PAMC 27299 may possess cold-adapted humic acid degradation enzymes with implication on global warming.

Key words: antarctica, degradation, global warming, humic acid

Antarctica seashore, extremely cold region, is the storage of huge amount of organic sources and mosses nearby seashore are great reservoir of humic substances through long-term accumulation by bacterial degradation in low rate (Park *et al.*, 2015). Global warming lead to increasing of bacterial ability to degrade humic substances even in low temperatures and not only increase emission of carbon dioxide but also leach dissolved organic carbon (DOC) to the Southern Ocean. In order to identify cold-adapted humic acid degrading bacteria and obtain genetic information, *Pedobacter* sp. PAMC 27299, a Gram-negative, an aerobic bacterium, was isolated from moss debris collected on the coast of the Barton Peninsula of King George Island of the maritime Antarctic region (62° 13' S, 58° 47' W) during the austral summer. One gram of collected Antarctic moss debris was homogenized in 10% glycerol and placed at

4°C in 1h. The supernatants (100 µl) were spread on minimal medium (MB Cell) containing humic acid (MB Cell) as sole carbon source at 15°C. The bacterial cells grown on humic acid plates were re-cultured in fresh humic acid medium. Final bacterial cells grown on re-culturing condition were considered humic acid degrading isolates (Park *et al.*, 2015). The genomic DNA of *Pedobacter* sp. PAMC 27299 was isolated with the MGTM Genomic DNA Purification kit (MG MED, Inc.). The extracted DNA was used to construct 20 kb SMRTbellTM template libraries. The whole genome sequencing of *Pedobacter* sp. PAMC 27299 was determined using PacBio RS II platform (Pacific Biosciences). *De novo* assembly was conducted by using Hierarchical Genome Assembly Process (HGAP, Version 2.3) workflow, including consensus polishing with Quiver (Chin *et al.*, 2013). As the estimated genome size was 6 Mbp and average was about 214X for 1,282,028,238 bp filtered subreads. We performed error correction based the longest 30X (180 Mbp) seed bases with rest shorter reads and then assembled

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with error corrected reads. A contig of 6,179,929 bp from HGAP polish process was checked and trimmed for genome closure using MUMmer 3.5 (Kurtz *et al.*, 2004). The complete genome of *Pedobacter* sp. PAMC 27299 is made up of a circular chromosome of 6,147,290 bp with 40.54% G+C contents. Putative gene coding sequences (CDSs) from the assembled contig were identified by Glimmer v3.02 (Delcher *et al.*, 2007) and 5,435 predicted open reading frames (ORFs) were obtained. The ORFs were searched by Blastall alignment against the NCBI Non-redundant protein database for all species. GO annotation was assigned to each of ORFs by Blast2GO software (Conesa *et al.*, 2005) analyzing the best hits

of the BLAST results. Ribosomal RNAs and transfer RNAs were predicted by using RNAmmer 1.2 (Lagesen *et al.*, 2007) and tRNAscan-SE 1.4 (Lowe and Eddy, 1997). Twenty three rRNAs and 75 tRNAs were found in the genome (Table 1 and Fig. 1).

This Antarctic *Pedobacter* strain will contribute to a better understanding of increasing humic acid degradation from current climate change resulting in accelerating carbon dioxide emission and leaching dissolved organic carbon (DOC) to the Southern Ocean.

Nucleotide sequence accession numbers

The *Pedobacter* sp. PAMC 28299 is available at KCTC (accession no. KCTC 42781). The complete genome sequence of *Pedobacter* sp. PAMC 28299 was deposited in GenBank under the accession no. CP012996.

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Table 1. Genome features of *Pedobacter* sp. PAMC 27299

Genome features	Value
Genome size (bp)	6,147,290
Contig	1
G + C content (%)	40.54
rRNA	23
tRNA	75
Protein coding genes	5,458
Protein coding genes with function prediction	5,435

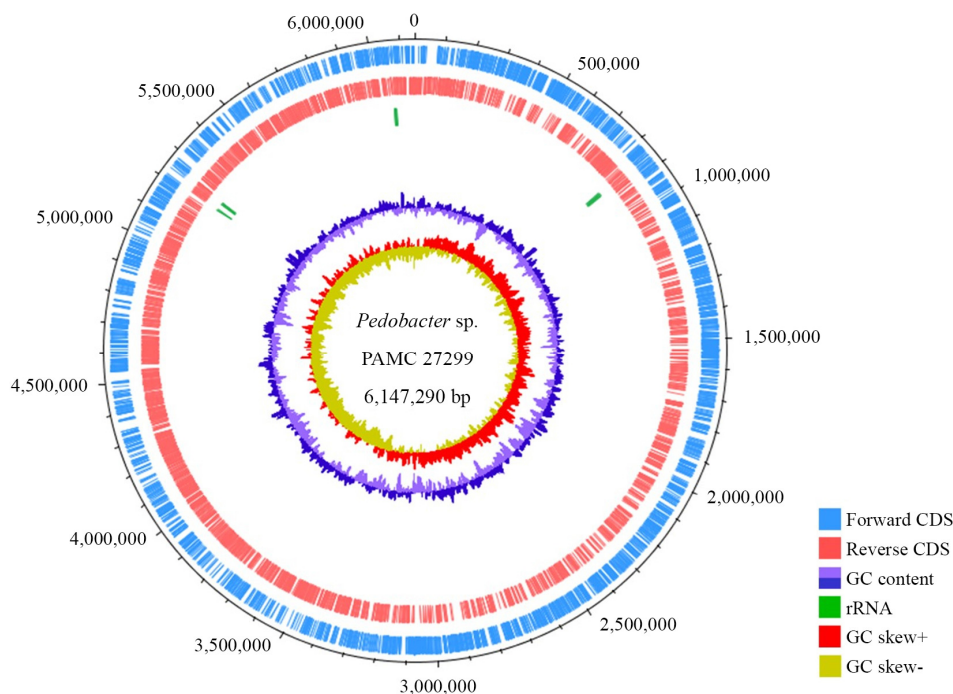


Fig. 1. Forward CDS, reverse CDS, rRNA, plot of GC percent, and GC skew (G-C)/(G+C) of *Pedobacter* sp. PAMC 27299 from outer to inner circles.

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적 요

부식산(humic acid)을 이용하여 저온에서 배양된 *Pedobacter* sp. PAMC 27299는 남극 바톤 반도(Barton Peninsula) King George Island의 해안가 이끼(moss debris)로부터 분리되었다. 본 연구에서는 *Pedobacter* sp. PAMC 27299의 유전체 서열을 해독하였으며 크기 6,147,290 bp, G+C 함량 40.54%의 PAMC 27299는 지구 온난화 관련 저온적응 부식산 분해 효소를 보유하는 것으로 확인되었다.

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