



## Genome announcement

# Complete genome sequence of the xylan-degrading *Mucilaginibacter* sp. strain PAMC26640 isolated from an Arctic lichen



Tae-Jin Oh<sup>a</sup>, So-Ra Han<sup>a</sup>, Seunghyun Kang<sup>b</sup>, Hyun Park<sup>b,c,\*</sup>, Augustine Yonghwi Kim<sup>d,\*\*</sup>

<sup>a</sup> Department of BT-convergent Pharmaceutical Engineering, SunMoon University, #100, Kalsan-ri, Tangjeong-myeon, Asansi, Chungnam 31460, Republic of Korea

<sup>b</sup> Korea Polar Research Institute (KOPRI), 213-3, Songdo-dong, Yeonsu-gu, Incheon 21990, Republic of Korea

<sup>c</sup> Polar Sciences, University of Science & Technology, Yuseong-gu, Daejeon 34113, Republic of Korea

<sup>d</sup> Department of Food Science and Technology, Sejong University, 98 Kunja-dong, Kwangjin-gu, Seoul 05006, Republic of Korea

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## ABSTRACT

*Mucilaginibacter* sp. PAMC26640 is a xylan-degrading bacterium isolated from the Arctic lichen *Stereocaulon* sp. Here, we present the first complete genome sequence of *Mucilaginibacter* sp. strain PAMC26640, which contains several genes involved in xylan utilization. This genome information provides new insights into the genetic basis of its physiology and further analysis of key metabolic genes related to the xylan degradation pathway.

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The genus *Mucilaginibacter*, belonging to the family *Sphingobacteriaceae*, phylum *Bacteroidetes*, was first proposed by Pankratov et al. (2007) for two novel Gram-negative species, *Mucilaginibacter paludis* and *Mucilaginibacter gracilis*, made up of non-motile rods. Members of *Mucilaginibacter* are known to hydrolyze organic matter such as xylan, pectin and laminarin, and produce large amounts of extracellular polymeric substances (Han et al., 2012; Madhaiyan et al., 2010; Pankratov et al., 2007). Recently, a xylan-degrading strain designated YC7004<sup>T</sup> was isolated from a piece of rotten wood and represented a novel species with the proposed name of *Mucilaginibacter jinjuensis* sp. nov. (Khan et al., 2013). Although xylan is one of the most abundant natural polysaccharides in the terrestrial environment, little is known about this xylan-degrading bacterium other than its taxonomic data. In addition, the full genome for the genus *Mucilaginibacter* has not been reported. Here, we report for the first time the complete genome sequence of *Mucilaginibacter* sp. PAMC26640.

*Mucilaginibacter* sp. PAMC26640, a xylan-degrading strain, was isolated from the lichen *Stereocaulon* sp., collected in Ny-Ålesund, Svalbard, Arctic (78°55'N, 11°56'E), and deposited in the Polar and Alpine Microbial Collection (Incheon, Korea). Genomic DNA was

extracted from *Mucilaginibacter* sp. PAMC26640 using a QIAamp DNA Mini Kit (Qiagen Inc., Valencia, CA, USA), and the quantity and purity were determined using an Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA, USA). Genome sequencing was performed using PacBio RS II single-molecule real-time (SMRT) sequencing technology (Pacific Biosciences, Menlo Park, CA, USA). SMRTbell library inserts (20 kb) were sequenced using SMRT cells. Raw sequence data were generated from 54,186 reads and 684,778,036 bp that were assembled *de novo* using the hierarchical genome-assembly process (HGAP) protocol (Chin et al., 2013) and RS HGAP Assembly 2 in SMRT analysis software (ver. 2.3; Pacific Biosciences [<https://github.com/PacificBiosciences/SMRT-Analysis>]).

Strain PAMC26640 has one circular chromosome of 5,611,374 bp, with a G+C content of 43.32%, and a plasmid (6,647 bp with 55.03% G+C). The coding DNA sequences (CDSs) were predicted and annotation was performed with the Rapid Annotation using Subsystem Technology (RAST) server (Aziz et al., 2008). The predicted gene sequences were translated and searched against the National Center for Biotechnology Information (NCBI) nonredundant database, the Clusters of Orthologous Groups (COG) and Kyoto Encyclopedia of Genes and Genomes (KEGG) databases. A total of 4831 CDSs were predicted and the coding region accounted for 86.8% of the *Mucilaginibacter* sp. PAMC26640 genome; 46 tRNA and 3 rRNA operons were predicted in the complete genome (Table 1). A total of 3808 genes were assigned a putative function. The genes were classified into 21

\* Corresponding author at: Korea Polar Research Institute (KOPRI), 213-3, Songdo-dong, Yeonsu-gu, Incheon 21990, Republic of Korea.

\*\* Corresponding author.

E-mail addresses: [hpark@kopri.re.kr](mailto:hpark@kopri.re.kr) (H. Park), [kimyh@sejong.ac.kr](mailto:kimyh@sejong.ac.kr) (A.Y. Kim).

**Table 1**  
Genome features of *Mucilaginibacter* sp. PAMC26640.

Features	Chromosome	Plasmid
Genome size (bp)	5,611,374	6,647
Contigs	1	1
G + C content (%)	43.32	55.03
Protein coding genes	4831	6
rRNA genes	9	–
tRNA genes	46	–

COG functional categories. As a result, we identified 22 genes encoding enzymes involved in xylan utilization: five endo-1,4- $\beta$ -xylanase A genes (A0256.04465, A0256.09080, A0256.13165, A0256.17000 and A0256.20190), an endo-1,4- $\beta$ -xylanase B gene (A0256.08285), two  $\beta$ -xylosidase genes (A0256.07395 and A0256.22715), five  $\alpha$ -L-arabinofuranosidase genes (A0256.02640, A0256.07430, A0256.07605, A0256.13170 and A0256.16465), three acetyl xylan esterase genes (A0256.02705, A0256.04925 and A0256.09600), three polysaccharide ABC transporter genes (A0256.02125, A0256.10590 and A0256.22880), a xylose isomerase gene (A0256.16550), and two xylulose kinase genes (A0256.04825 and A0256.16545). Because enzymatic hydrolysis of the polysaccharide is one of the most important potential applications, this complete genome information of *Mucilaginibacter* sp. PAMC26640 may provide a better understanding of its evolution under the Arctic lichen-associated environment and inform potential industrial applications using xylan-degrading enzymes.

#### Nucleotide sequence accession numbers

The complete genome sequence has been deposited at GenBank/EMBL/DDBJ under the accession number CP014772 and CP014773.

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