

Complete genome sequence of *Antarcticibacterium flavum* JB01H24^T from an Antarctic marine sediment

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ABSTRACT

Antarcticibacterium flavum JB01H24^T was isolated from a marine sediment of the Ross Sea, Antarctica. Whole-genome sequencing of the strain *Antarcticibacterium flavum* JB01H24^T was achieved using PacBio RS II platform. The resulting complete genome comprised of one closed, complete chromosome of 4,319,074 base pairs with a 40.87% G + C content, where genomic analyses demonstrated that it is constituted mostly by putative ORFs with unknown functions, representing a novel genetic feature. It is the first complete genome sequence of the *Antarcticibacterium* strain.

1. Introduction

The genus *Antarcticibacterium* of the family *Flavobacteriaceae* within the phylum *Bacteroidetes* is newly established with one species, *Antarcticibacterium flavum* JB01H24^T which was isolated from surface sediment collected from the Ross Sea, Antarctica (Li et al., 2018). *A. flavum* JB01H24^T with the highest 16S rRNA gene sequence similarity with *Gillisia mitskevichiae* KCTC 12261^T (95.3%) formed an independent lineage with members of the genus *Gillisia* within the family *Flavobacteriaceae* (Li et al., 2018). The predominance of the phylum *Bacteroidetes* is known in the previous studies of bacterial communities from marine sediments of Antarctica (Bowman and McCuaig, 2003; Baldi et al., 2010; Lee et al., 2014). In particular, strains of the family *Flavobacteriaceae* are known for their specialized roles in the uptake and degradation of the high-molecular-mass fraction of dissolved organic matter and in remineralization processes, both in freshwater and in marine ecosystems (Kirchman, 2002; Lee et al., 2014). However, *A. flavum* JB01H24^T was not able to hydrolyze those macromolecules and only hydrolyze Tween 20 and 80 contrasting to the strains in the genus *Gillisia* that hydrolyze macromolecules such as starch, casein, urea, and/or gelatin (Trappen et al., 2004; Bowman and Nichols, 2005; Nedashkovskaya et al. 2005; Lee et al., 2006; Roh et al., 2013; Li et al., 2018). The physiological characteristics of *A. flavum* JB01H24^T were reported by Li et al. (2018) reporting this strain as the type strain of the genus *Antarcticibacterium*. However, the complete genomic information of *A. flavum* JB01H24^T

which helps to understand the biosynthetic potential and provides further insight into environmental adaptation is not yet available. Thus, we performed genome sequencing and present the complete genome sequence of *A. flavum* JB01H24^T.

2. Data description

A. flavum JB01H24^T was obtained from the Korean Collection for Type Cultures (KCTC) and cultured on marine agar (Difco, USA) plate at 25 °C. Genomic DNAs were extracted using a MagAttract DNA Kit (Qiagen, USA) according to the manufacturer's instructions. Sequencing was performed using the PacBio RS II (Pacific Biosciences, USA) by constructing a 20-kb insert library at Lab Genomics (Korea) and 1,124,344,045 bp were generated from 98,827 subreads. For sequence assemblies, Hierarchical Genome Assembly Process (HGAP.3) (Chen-Shan et al., 2014) was performed. Genome annotation was performed using the Rapid Annotation using Subsystems Technology (RAST) server (Aziz et al., 2008). Clusters of orthologous groups of proteins (COGs) were predicted by COGNITOR (Tatusov et al., 1997) and metabolic pathways were predicted by using KEGG Automatic Annotation Server (KAAS) (Moriya et al., 2007).

The resulting complete genome comprised of 4,319,074 nucleotides with 40.87% GC content (Table 1). No plasmid was found. The predicted protein-coding sequences on the chromosome were 4169. The genome contains 46 tRNA genes and 3 rRNA operons (Table 1). Among the 4169 genes, we assigned 902 genes (21.63%) to a

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Table 1
General features of *Antarcticibacterium flavum* JB01H24^T and MIGS mandatory information.

Items	Description
General feature	
Current classification	Domain <i>Bacteria</i> Phylum <i>Bacteroidetes</i> Class <i>Flavobacteriia</i> Order <i>Flavobacteriales</i> Family <i>Flavobacteriaceae</i> Genus <i>Antarcticibacterium</i> Species <i>flavum</i> Strain JB01H24 ^T
Gram-staining	Negative
Cell shape	Oval to rod
Motility	Non-motile
Temperature	4–40 °C (optimum, 25–30 °C)
Salinity	0–8‰ (optimum, 3‰)
pH range	7.0–9.0 (optimum, 7.5–8.0)
MIGS data	
Submitted to insdc	CP040812
Investigation type	Bacteria
Geographic location	Antarctica: Ross Sea
Latitude and longitude	77°35′ 17.88″ S, 165°34′ 9.84″ E
Collection date	2015-02
Environment (biome)	Marine biome [ENVO:00000447]
Environment (feature)	Cold environment [ENVO: 01000309]
Environment (material)	Marine sediment [ENVO: 03000033]
Relationship to oxygen	Strict aerobic
Sequencing platform	PacBio RS II with P6-C4 chemistry
Fold coverage	260.32 ×
Assembler	HGAP.3
Genome features	
Genome size (bps)	4,319,074
GC content (%)	40.87
CDSs	4169
CDSs assigned to subsystem in RAST	902
CDSs assigned to COGs	1491
CDSs assigned to KEGG	2490
Hypothetical protein	1775
rRNA operons	3
tRNA genes	46

subsystem using the SEED method (Overbeek et al., 2013), and 1491 genes to KEGG pathway. The function of 2490 genes was categorized by comparison with the COGs (Tatusov et al., 2000). The function of 1775 genes (42.57%) was not assigned in RAST server, representing a novel genetic feature. The graphic circular map of the genome was generated using DNAPlotter (Ver. 10.2) (Carver et al., 2008) (Fig. 1).

Genomic analysis revealed the presence of the complete gene set for glycolysis, pentose phosphate pathway, citrate cycles, and the genes related to starch synthesis. F-type ATPase were encoded for ATP synthesis. Genes encoding ABC transporters related to Iron (III) (AfuA, AfuB, and AfuC), lipopolysaccharide (RfbA and RfbB), and lipoprotein (LolC, LolE, and LolD) were identified while ABC transporters genes related to oligosaccharide, polysaccharide and amino acid were not identified. Three cold shock proteins were identified which may support the growth of *A. flavum* JB01H24^T at low temperature (4 °C). No putative genes involved in the fermentation were found while genes of cytochrome *c* oxidase were found consistently with strictly aerobic growth from the culture-based experiment (Li et al., 2018). However, it was still difficult to predict the physiological roles of *Antarcticibacterium flavum* JB01H24^T from genomic data because protein functions of 1775 genes (42.57%) out of 4169 CDSs were largely unknown. Further study on these proteins with unknown function will provide the clue of the role and adaptation mechanism of the *A. flavum* JB01H24^T in the sediment and will help to broaden the function of the unknown proteins.

Nucleotide sequence accession numbers

The complete genome sequence of *A. flavum* JB01H24^T has been deposited at GenBank under the accession number CP040812. This strain is available from Korean Collection for Type Cultures (KCTC) and Guangdong Microbial Culture Collection Center (GDMCC) with the accession number KCTC 52984 and GDMCC 1.1229, respectively.

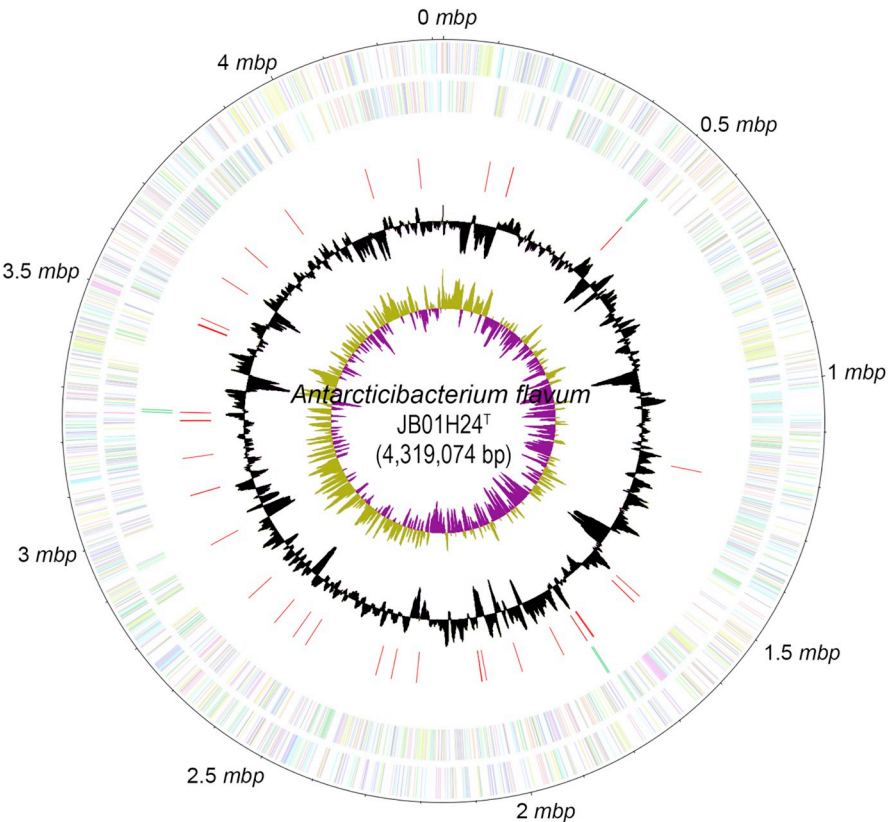


Fig. 1. Circular map of the *Antarcticibacterium flavum* JB01H24^T genome. Labeling from outside to the center: genes on forward strand, genes on reverse strand, RNA genes (rRNAs green, tRNAs red), GC content (black), and GC skew (olive/purple). Individual genes are colored by COG categories: J (translation, ribosomal structure, and biogenesis), A (RNA processing and modification), K (transcription), L (replication, recombination, and repair), B (chromatin structure and dynamics), D (cell cycle control, cell division, and chromosome partitioning), Y (nuclear structure), V (defense mechanisms), T (signal transduction mechanisms), M (cell wall/membrane/envelop biogenesis), N (cell motility), Z (cytoskeleton), W (extracellular structures), U (intracellular trafficking, secretion, and vesicular transport), O (posttranslational modification, protein turnover, and chaperones), X (mobilome: prophages and transposons), C (energy production and conversion), G (carbohydrate transport and metabolism), E (amino acid transport and metabolism), F (nucleotide transport and metabolism), H (coenzyme transport and metabolism), I (lipid transport and metabolism), P (inorganic ion transport and metabolism), Q (secondary metabolites biosynthesis, transport, and catabolism), R (general functional prediction only), and S (function unknown).

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Declaration of Competing Interest

There are no conflicts of interest to declare.

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