



Genome announcement

Complete genome sequence of carotenoid-producing *Microbacterium* sp. strain PAMC28756 isolated from an Antarctic lichen



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ABSTRACT

Microbacterium sp. strain PAMC28756, of the family *Microbacteriaceae*, was isolated from *Stereocaulon* sp., an Antarctic lichen. Complete genome sequencing of *Microbacterium* sp. PAMC28756 revealed, for the first time in the genus *Microbacterium*, a series of key genes involved in C₅₀ carotenoid biosynthesis. An analysis of the *Microbacterium* sp. PAMC28756 genome will lead to a better understanding of the carotenoid biosynthesis pathway. Furthermore, the sequence data will provide novel insight into UV radiation resistance in extremely cold environments.

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Carotenoids, natural pigments synthesized by bacteria, archaea, algae, fungi, and plants, have diverse functions such as light protection and membrane stabilization (Lazrak et al., 1987; Shahmohammadi et al., 1998; Britton et al., 2004). Some species of carotenoid-producing bacteria in the genera *Corynebacterium*, *Haloarcula*, and *Halobacterium* exhibit the biosynthesis and accumulation of C₅₀ carotenoids (Dummer et al., 2011; Heider et al., 2012; Yang et al., 2015). Members of the genus *Microbacterium* (phylum, *Actinobacteria*; family, *Microbacteriaceae*) are Gram-positive, aerobic, heterotrophic bacteria that are widespread in nature (Richert et al., 2007). Although many species of *Microbacterium* were recently identified based on microbiological and chemotaxonomic properties, no studies have examined the genomic features associated with C₅₀ carotenoid biosynthesis. Here, we report the full genome sequence of *Microbacterium* sp. PAMC28756. This information will provide the basis for understanding C₅₀ carotenoid biosynthesis.

Carotenoid-producing *Microbacterium* sp. PAMC28756 (deposited as PAMC in the Polar and Alpine Microbial Collection, Korea Polar Research Institute, Incheon, Korea) was isolated from *Stereocaulon* sp., an Antarctic lichen species collected on Barton Peninsula, King George Island, Antarctica (62°13'S, 58°47'W). Genomic DNA was extracted from *Microbacterium* sp. PAMC28756

using a QIAamp DNA Mini Kit (Qiagen, Valencia, CA), and the quantity and purity were determined using an Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA). Genome sequencing was performed using PacBio RS II single-molecule real-time (SMRT) sequencing technology (Pacific Biosciences, Menlo Park, CA). Ten-kilobase SMRTbell library inserts were sequenced using SMRT cells. Raw sequence data were generated from 91,864 reads and 1,339,504,176 bp that were *de novo* assembled using the hierarchical genome-assembly process (HGAP) protocol (Chin et al., 2013) and RS HGAP Assembly 2 in SMRT analysis version 2.3 software (Pacific Biosciences; <https://github.com/PacificBiosciences/SMRT-Analysis>).

The complete circular chromosome was 3,539,061 bp with a G+C content of 70.4%. Coding DNA sequences (CDSs) were predicted and annotated using NCBI Prokaryotic Genome Annotation Pipeline (PGAP) and the Rapid Annotation using Subsystem Technology (RAST) server (Aziz et al., 2008). Predicted gene sequences were translated and searched against the National Center for Biotechnology Information (NCBI) non-redundant database, Clusters of Orthologous Groups (COG), and Kyoto Encyclopedia of Genes and Genomes (KEGG). A total of 3,328 CDSs were predicted; the coding region accounted for 89.02% of the *Microbacterium* sp. PAMC28756 genome. In addition, 47 tRNA and 6 rRNA were predicted in the complete genome (Table 1). Sequence analyses revealed that carotenoid biosynthesis genes were localized as a cluster that included genes encoding geranylgeranyl diphosphate synthases (AXH82_01415 and AXH82_16850), phytoene synthase (AXH82_01420),

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Table 1
Genome features of *Microbacterium* sp. PAMC28756.

| Feature | Value |
|----------------------|-----------|
| Genome size (bp) | 3,539,061 |
| Contig numbers | 1 |
| G+C content (%) | 70.4 |
| Protein coding genes | 3328 |
| rRNA genes | 6 |
| tRNA genes | 47 |

phytoene dehydrogenases (AXH82.01425 and AXH82.10930), C₅₀ carotenoid epsilon cyclases (AXH82.01430 and AXH82.01435), and lycopene elongase (AXH82.01440). Additionally, geranylgeranyl pyrophosphate synthetase (AXH82.03090) and 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (AXH82.11875) genes were identified in the genome. An analysis of the whole genome sequence of *Microbacterium* sp. PAMC28756 will lead to a better understanding of C₅₀ carotenoid biosynthesis in extremely cold environments. Furthermore, whole genome data may lead to biotechnological applications involving the use of UV-resistant *Microbacterium* sp. PAMC28756 for C₅₀ carotenoid biosynthesis.

Nucleotide sequence accession numbers

The complete genome information of *Microbacterium* sp. PAMC28756 was deposited in GenBank under the accession number CP014313.

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