



Genome announcement

Complete genome sequence of *Hymenobacter* sp. strain PAMC26554, an ionizing radiation-resistant bacterium isolated from an Antarctic lichen



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ABSTRACT

A Gram-negative, rod-shaped, red-pink in color, and UV radiation-resistant bacterium *Hymenobacter* sp. strain PAMC26554 was isolated from *Usnea* sp., an Antarctic lichen, and belongs to the class of *Cytophagia* and the phylum of *Bacteroidetes*. The complete genome of *Hymenobacter* sp. PAMC26554 consists of one chromosome (5,244,843 bp) with two plasmids (199,990 bp and 6421 bp). The genomic sequence indicates that *Hymenobacter* sp. strain PAMC26554 possesses several genes involved in the nucleotide excision repair pathway that protects damaged DNA. This complete genome information will help us to understand its adaptation and novel survival strategy in the Antarctic extreme cold environment.

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Radiation causes various forms of direct DNA damage, including double-strand breaks that lead to the loss of genetic material (Slade and Radman, 2011), as well as severe indirect damage to proteins through reactive oxygen species (Daly, 2012). Several bacteria in the genus *Deinococcus*, *Hymenobacter* and *Pontibacter* have been reported as radiation-resistant and they possess a highly specialized DNA repair system (Makarova et al., 2007; Srinivasan et al., 2015; Yu et al., 2015). Recently, some genome sequences of *Hymenobacter* were analyzed for genes involved in recovery from ionizing radiation (Jung et al., 2014; Kim et al., 2016; Koo et al., 2014). In addition, we have reported the complete genome sequence of *Hymenobacter* sp. strain PAMC26628 isolated from Arctic lichen *Stereocaulon* sp. and identified several genes involved in nucleotide excision repair, a DNA damage removal pathway (Ahn et al., 2016). To gain insight into the genes related to extreme cold environments that have high levels of solar UV radiation, we describe herein the full genome sequence of *Hymenobacter* sp. PAMC26554, isolated from Antarctica lichen, to elucidate the key

genes involved in the recovery of DNA damage from these special ionizing radiation conditions.

The ionizing radiation-resistant bacterium *Hymenobacter* sp. PAMC26554 (deposited as PAMC26554 in the Polar and Alpine Microbial Collection, Korea Polar Research Institute, Incheon, Korea) was isolated from the lichen *Usnea* sp., collected from Barton Peninsula, King George Island, Antarctica (62°13'S, 58°47'W). Genomic DNA was extracted from *Hymenobacter* sp. PAMC26554 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 96,815 reads and 1,509,251,115 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>]). The complete genome of *Hymenobacter* sp. PAMC26554 contains a circular chromosome of 5,244,843 bp with 60.9% G+C content and two circular plasmids of 199,990 bp and 6421 bp in length. The coding DNA sequences (CDSs) were predicted and annotation was performed with the Rapid Annotation using Subsystem

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Table 1
Genome features of *Hymenobacter* sp. PAMC26554.

Features	Chromosome	Plasmid 1	Plasmid 2
Genome size (bp)	5,244,843	199,990	6421
Contig numbers	1	1	1
G + C content (%)	60.93	60.84	62.03
Protein coding genes	4405	195	9
rRNA genes	9	–	–
tRNA genes	45	–	–

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 the Kyoto Encyclopedia of Genes and Genomes (KEGG) databases. A total of 4405 CDSs were predicted and the coding region accounted for 83.9% of the *Hymenobacter* sp. PAMC26554 genome; 45 tRNA and 3 rRNA operons were predicted in the complete genome (Table 1). A total of 3534 genes were assigned a putative function. The genes were classified into 23 COG functional categories.

The genome sequence of *Hymenobacter* sp. PAMC26554 contains genes involved in recovery from ionizing radiation, including the nucleotide excision repair (NER) pathway. Based on the complete genome annotation, the key enzymes were identified: three copies of excinuclease UvrABC subunits A (A0257_03325, A0257_13580 and A0257_19160), subunit B (A0257_15865) and two subunit C (A0257_12015 and A0257_18170). The UvrABC excinuclease complex can recognize DNA structural changes and repair them by creating dual incisions 5' and 3' to the site damaged by UV irradiation (Petit and Sancar, 1999). Additionally, the genome also contains the UV DNA damage endonuclease (UvdE) (A0257_08375), which retains full UV resistance (Earl et al., 2002). In a previous study, similar genes involved in the NER pathway that play a substantial role in DNA repair were reported in the same genus *Hymenobacter*, and it seems that ionizing radiation resistance is achieved by a combination of various proteins (Ahn et al., 2016; Jung et al., 2014; Kim et al., 2016). These findings allow us to develop an integrated understanding of the molecular basis of resistance to UV radiation, particularly in the extreme cold environment of the Antarctic.

Nucleotide sequence accession numbers

The complete genome sequence has been deposited at GenBank/EMBL/DBJ under the accession number CP014769-CP014771.

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