Journal of Biotechnology 223 (2016) 50–51

Contents lists available at ScienceDirect

Journal of Biotechnology

journal homepage: www.elsevier.com/locate/jbiotec

Genome announcement

Complete genome sequence of ionizing radiation-resistant *Hymenobacter* sp. strain PAMC26628 isolated from an Arctic lichen

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ARTICLE INFO

Article history:
Received 21 February 2016
Accepted 24 February 2016
Available online 26 February 2016

Keywords:
Hymenobacter sp. PAMC26628
Complete genome sequence
Radiation-resistance
Nucleotide excision repair

ABSTRACT

Ionizing radiation-resistant *Hymenobacter* sp. strain PAMC26628 was isolated from *Stereocaulon* sp., an Arctic lichen. Complete genome sequencing of *Hymenobacter* sp. PAMC26628 revealed one chromosome (5,277,381 bp), one plasmid (89,596 bp), and several genes involved in nucleotide excision repair, a DNA damage removal pathway. An analysis of the *Hymenobacter* sp. PAMC26628 genome will help us understand its evolution and provide novel insight into the adaptations that allow this organism to survive in the extreme cold of the Arctic.

Radiation-resistant bacteria have been isolated from a variety of habitats; the majority belong to the genera *Deinococcus*, *Hymenobacter*, and *Pontibacter*, which have highly effective and specialized DNA repair systems (Makarova et al., 2007; Srinivasan et al., 2015; Yu et al., 2015). Bacteria of the genus *Hymenobacter*, class *Cytophagia*, phylum *Bacteroidetes*, are usually Gram-negative, rod-shaped, red-pink in color, and UV radiation-resistant. The genome sequences of bacteria belonging to the genus *Hymenobacter* were previously analyzed for genes involved in ionizing radiation recovery (Jung et al., 2014; Kim et al., 2016). In addition, a draft genome sequence of *Hymenobacter* sp. strain IS2118, isolated from an ice-covered freshwater lake (L43) in Antarctica, revealed diverse genes for adaptation to cold ecosystems (Koo et al., 2014). However, there have been no reports on the complete genome sequence of *Hymenobacter* from extremely cold environments with high levels of solar UV radiation. We describe here the full genome sequence of *Hymenobacter* sp. PAMC26628. This information will help identify key genes involved in the repair of ionizing radiation-induced DNA damage.

Ionizing radiation-resistant *Hymenobacter* sp. strain PAMC26628 (deposited as PAMC26628 in the Polar and Alpine Microbial Collection, Korea Polar Research Institute, Incheon, Korea) was isolated from *Stereocaulon* sp., an Arctic lichen collected in Ny-Ålesund, Svalbard, Arctic (78°55′N, 11°56′E). Genomic DNA was extracted from *Hymenobacter* sp. PAMC26628 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 88,002 reads and 1,268,894,565 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 5,277,381 bp with a G+C content of 63.1%. Coding DNA sequences (CDSs) were predicted and annotated using 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 4448 CDSs were predicted; the coding region accounted for 85.12% of the *Hymenobacter* sp. PAMC26628 genome. In addition, 41 tRNA and 9 rRNA were predicted in the complete genome (Table 1). A total of 3345 genes were assigned a putative function. The genes were classified into 23 COG functional categories.

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http://dx.doi.org/10.1016/j.jbiotec.2016.02.031
0168-1656/

Table 1
Genome features of *Hymenobacter* sp. PAMC26628.

Features	Chromosome	Plasmid
Genome size (bp)	5,277,381	89,596
Contigs	1	1
G + C content (%)	63.1	59.2
Protein coding genes	4448	77
rRNA genes	9	–
tRNA genes	41	–
Excinuclese UvrABC genes	5	–
Endonuclease UvdE genes	1	–

In addition, the sequence data revealed the presence of nucleotide excision repair (NER) genes encoding subunits that comprise the excinuclease UvrABC protein complex. Specifically, genes encoding three copies of subunit A (AXW84_02695, AXW84_07265 and AXW84_21170), one copy of subunit B (AXW84_18215), and one copy of subunit C (AXW84_19430) were identified. UvrABC excinucleases recognize and repair DNA damage by creating dual incisions 5′ and 3′ of the damaged site (Petit and Sancar, 1999). In addition, the genome contained a UV damage repair endonuclease (UvdE) gene (AXW84_03535), which provides protection against UV irradiation (Earl et al., 2002). An analysis of the whole genome sequence of *Hymenobacter* sp. PAMC26628 will lead to a better understanding of the role of NER in radiation resistance, particularly in the extremely cold environment of the Arctic. Furthermore, our whole genome data may provide considerable information that can be applied to biotechnology.

Nucleotide sequence accession numbers

The complete genome sequence has been deposited at GenBank/EMBL/DDBJ under the accession number CP014303 and CP014304.

Acknowledgements

This work was supported by the Antarctic organisms: Cold-Adaptation Mechanisms and its application grant (PE16070) funded by the Korea Polar Research Institute.

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