



Genome Announcement

Complete genome sequence of *Hymenobacter swuensis*, an ionizing-radiation resistant bacterium isolated from mountain soil



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ABSTRACT

Hymenobacter swuensis is a gamma-radiation resistant bacterium isolated from mountain soil in South Korea (N 35°51'38", E 127°44'47"; altitude 1500 m). The complete genome of *H. swuensis* consists of one chromosome (4,904,241 bp) with three plasmids. The genomic sequence indicated that *H. swuensis* includes a series of genes involved in 2'-hydroxy-carotenoid biosynthesis. This is the first report describing the *Hymenobacter* genome and key enzymes in the 2'-hydroxy-carotenoid biosynthesis pathway. These data may provide opportunities for genetic engineering and antioxidant 2'-hydroxy-carotenoid production.

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Carotenoids are natural isoprenoid pigments, and the best-known scavengers of reactive oxygen species. Because carotenoids have beneficial effects on health, such as preventing cancer and reducing the risk of cardiovascular disease, they are popularly used in the food, cosmetic and pharmaceutical industries as color-reagents and nutraceutical supplements (Anunciato and da Rocha Filho, 2012; Shegokar and Mitri, 2012). Among carotenoid producing bacteria, radiation-resistant bacteria, such as *Deinococcus*, produce a unique carotenoid, deinoxanthin, which has higher antioxidant activity than lycopene, and β -carotene and protects cells from damage caused by harsh environment (Tian et al., 2007). *Hymenobacter* are also radiation-resistant bacteria classified in the class *Cytophagia* and the phylum *Bacteroidetes*. These species are known to survive in harsh conditions such as desiccation or irradiation (Buczolits et al., 2006); indeed, some species were isolated from the desert and uranium mines (Chung et al., 2010; Zhang et al., 2009). Currently, 23 species are classified as *Hymenobacter* based on microbiological and chemotaxonomic properties. Most *Hymenobacter* produce unique 2'-hydroxy-carotenoids (2'-hydroxyflexixanthin) and their hexosyl, pentosyl, and methyl derivatives (Klassen and Foght, 2008). However, no report has examined the genome features associated with 2'-hydroxy-carotenoid biosynthesis. Here, we present the

complete genome sequence of a red-pink pigmented and radiation-resistant bacterium *Hymenobacter swuensis* (Lee et al., 2014) and describe its genetic features related to 2'-hydroxy carotenoid production.

The genome of *H. swuensis* was sequenced using a hybrid strategy with a Roche 454 GS FLX Titanium (8 kb paired-end) and Illumina HiSeq 2000 (150 bp paired-end). The 454 pyrosequencing yielded 8.3-fold coverage, whereas the HiSeq 2000 read 814-fold genome coverage. The draft sequence was assembled using gsAssembler 2.6–4 scaffolds with 19 contiguous sequences (contigs). The gaps between contigs were closed via PCR and Sanger sequencing. The ORF was predicted by Glimmer 3.02 (Delcher et al., 2007) and its function was verified using BLASTP and InterProScan (Altschul et al., 1990; Zdobnov and Apweiler, 2001).

The complete genome of *H. swuensis* consists of a circular chromosome and three plasmids (Table 1). The chromosome contains 4357 ORFs (2636 of which are predicted to be hypothetical proteins) and has a GC content of 59.7%, 43 tRNAs and nine rRNAs organized into three operons. Interpretation of the *H. swuensis* genome based on Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis shows that carotenoid biosynthesis genes are localized as a cluster, which contains β -carotene hydroxylase (Hsw_1151), 4,4'-diapophytoene desaturase (Hsw_1153), phytoene desaturase (Hsw_1154), phytoene synthase (Hsw_1155), 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (Hsw_1158) and β -carotene ketolase (Hsw_1159). Additionally, lycopene cyclase (Hsw_0139), and diapophytoene

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Table 1
Genome statistics.

Features	Chromosome	Plasmid pHsw1	Plasmid pHsw2	Plasmid pHsw3
Length (bp)	4,904,241	299,298	41,562	6969
DNA-coding region (bp)	4,272,654	237,006	31,523	3336
GC content (%)	59.67	59.77	53.27	56.75
ORFs	4305	262	43	6
rRNA genes	9	–	–	–
tRNA genes	43	–	–	–

dehydrogenase (Hsw_1881) were identified in the genome, along with two additional phytoene desaturase homologs (Hsw_0009, 4190). These data provide considerable information regarding the 2'-hydroxy carotenoid synthesis pathway that can be exploited to improve production.

1. Nucleotide sequence accession number

The complete genome sequence of *H. swuensis* is now available in GenBank database under accession number CP007145 (chromosome), CP007144 (plasmid pHsw1), CP007143 (plasmid pHsw2), and CP007146 (plasmid pHsw3). The strain is available from Prof. Myung-Kyum Kim (Department of Bio & Environmental Technology, College of Natural Science, Seoul Women's University, Republic of Korea) or Dr. Sangyong Lim (Research Division for Biotechnology, Korea Atomic Energy Research Institute).

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