

The complete genome sequence of *Rhodobacteraceae* bacterium strain SH-1 isolated from a gut content of whiteleg shrimp *Litopenaeus vannamei*

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흰다리새우 *Litopenaeus vannamei*의 장 내용물로부터 분리된 *Rhodobacteraceae* sp. SH-1의 유전체

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Strain SH-1, a novel bacterium belonging to the family *Rhodobacteraceae* was isolated from a gut content of a whiteleg shrimp *Litopenaeus vannamei* collected from Tongyeong, South Korea. The complete genome sequence which is 3,892,138 bp with 66.1% G + C content was obtained using PacBio RS II platform. The genome annotation showed that the complete genome contains total 3,772 genes including 3,649 CDSs, 47 RNAs and 76 pseudogenes. Subsystems related to biosynthetic gene clusters for vitamins, amino acids and colicin V production protein were also predicted. The results may provide insights for understanding the symbiotic relationship between the strain and its host shrimp.

Keywords: *Litopenaeus vannamei*, *Rhodobacteraceae*, complete genome sequence, whiteleg shrimp

One of the major aquatic bacterial groups in *Alphaproteobacteria*, the family *Rhodobacteraceae* is mainly found in various aquatic environments including fresh water and sea water. Currently, the family comprises more than 100 genera and 300 species and over 60% of them originated from marine

environments (Simon *et al.*, 2017). In marine environments, the family *Rhodobacteraceae* plays important roles in recycling of biochemical resources and symbiotic relationships with various marine eukaryote hosts (Elifantz *et al.*, 2013; Simon *et al.*, 2017). One of the marine invertebrates, a shrimp also has symbiotic relationship with its symbiotic microbiota including the family *Rhodobacteraceae* and studies about the bacterial diversity and interactions between a shrimp and its symbiotic microbiota showed that the microbiota produces various extracellular enzymes and metabolites which are beneficial for their hosts (Corbari *et al.*, 2008; Tzuc *et al.*, 2014; Cowart *et al.*, 2017).

Strain SH-1 was isolated from the gut content of a whiteleg shrimp *Litopenaeus vannamei* collected from a shrimp farm (34° 51' 35.7" N 128° 26' 53" E, Tongyeong, South Korea) using serial dilution method after incubation on Marine Agar (MA, Difco) at 28°C for three days. The 16S rRNA sequence of the strain showed low sequence similarity compared to the close species *Thalassococcus halodurans* DSM 26915^T [96.1%; Lee *et al.* (2007)], *Phaeobacter gallaeciensis* DSM 26640^T [96.09%; Martens *et al.* (2006)], and *Pontibaca methylaminivorans*

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DSM 21219^T [96.03%; Kim *et al.* (2010)] which all belong to the family *Rhodobacteraceae*. Here, we present the genome features of the complete genome of a novel strain SH-1, which may provide insights into the symbiotic relationship in shrimps.

For whole genome sequencing, Genomic DNA Prep Kit (BIOFACT) was used to extract and purify the genomic DNA. PacBio RS II platform (Pacific Biosciences) yielded total 133,108 sequence reads, including 1,178,79,850 bases (N_{50} , 12,787 bp; mean length, 8,855 bp) and *de novo* assembly of sequence reads was performed with Hierarchical Genome Assembly Process [HGAP, Version 3.0; Chin *et al.* (2013)]. The assembly generated a total of six contigs including one chromosome (3,892,138 bp with 66.1 mol% G + C content) and five plasmids (167,434 bp, 61.4 mol%; 78,245 bp, 60.8 mol%; 67,363 bp, 58.5 mol%; 41,166 bp, 61.8 mol%; 16,620 bp, 59 mol%). Rapid Annotations using Subsystems Technology [RAST; (<http://rast.nmpdr.org/rast.cgi>) Aziz *et al.* (2008)] and NCBI Prokaryotic Genome Annotation Pipeline [PGAP; Tatusova *et*

al. (2016)] were used for the functional annotation and gene prediction, respectively. Total 3,772 genes including 3,649 CDSs, 47 RNAs and 76 pseudogenes were annotated by NCBI PGAP. Biosynthetic gene clusters related to vitamins and amino acids biosynthesis were also identified through RAST annotation.

CGView Comparison Tool (Grant *et al.*, 2012) was used to assign genes to Clusters of Orthologous Groups (COGs) category and generate the circular genome map containing genome features (Fig. 1). One CRISPR locus was detected by CRISPRFinder [<http://crispr.i2bc.paris-saclay.fr>; Grissa *et al.* (2007)] and PHAge Search Tool Enhanced Release [PHASTER, <http://phaster.ca/>; Arndt *et al.* (2016)] detected three intact and one incomplete prophage sequences coding tail, head, terminase and phage related proteins of virus from chromosome sequence.

The genome of strain SH-1, as a symbiotic bacterium of whiteleg shrimp, contained various biosynthetic gene clusters for vitamins, amino acids which might be beneficial for host and colicin V which inhibits other bacterial groups to be

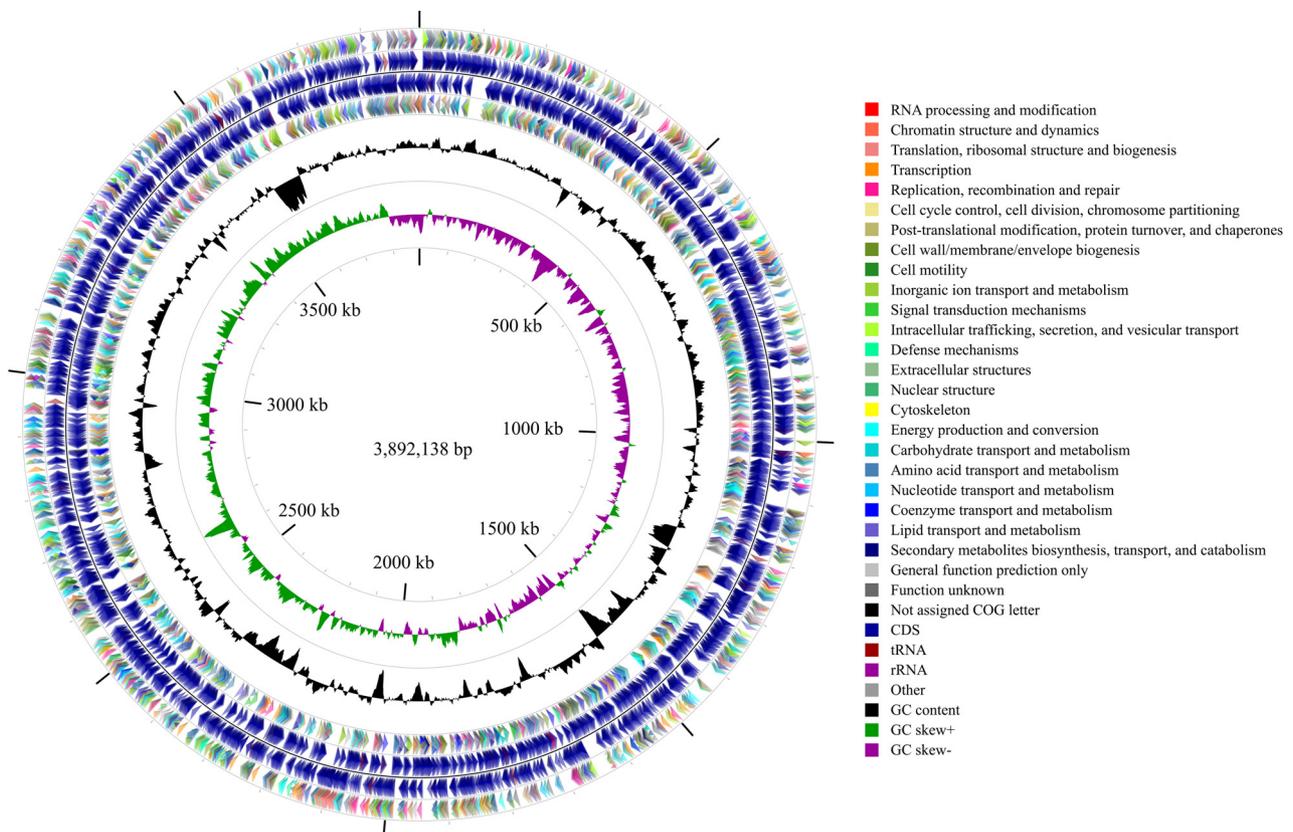


Fig. 1. Complete genome map of *Rhodobacteraceae* sp. SH-1. From the center to the outside: genome size label, GC skew (green and purple), G + C content (black), CDSs colored by COG categories on the reverse strand, CDSs including RNAs on the reverse strand, CDSs including RNAs on the forward strand, CDSs colored by COG categories on the forward strand.

Table 1. General features of *Rhodobacteraceae* sp. SH-1

Feature	Value
Genome size (bp)	3,892,138
G + C content (%)	66.1
Total genes	3,772
Total CDS	3,649
Genes assigned to COGs	2,483
rRNAs (5S, 16S, 23S)	1, 1, 1
tRNAs	41
ncRNAs	3
Pseudogenes	76

dominant in the gut environment. The result may provide a basis for understanding the symbiotic relationship in the host. Further experiments are in progress for identifying characteristics and comprehension of strain SH-1.

Nucleotide sequence accession number

The genome and plasmid sequences of *Rhodobacteraceae* bacterium strain SH-1 have been deposited at GenBank under the accession numbers of CP027665 and CP043619-CP043623, respectively. The strain has been deposited in the Korean Collection for Type Cultures (KCTC) with the preservation number KCTC 62276.

적 요

SH-1 균주는 *Rhodobacteraceae* 과에 속하는 신균으로서 대한민국의 통영에서 채취된 흰다리새우 *Litopenaeus vannamei* 의 장내용물에서 분리되었다. PacBio RS II 분석법을 이용하여 얻어진 전장유전체의 길이는 3,892,138 bp이며 66.1%의 G + C 함유량을 가지고 있다. 이 유전체는 3,649개의 CDS와 47개의 RNA, 76개의 유사유전자를 포함하여 총 3,772개의 유전자를 가지고 있는 것으로 분석되었다. 콜리신 생산 단백질과 비타민 생합성 유전자 클러스터와 관련된 하위체계(subsystem)가 존재하는 것이 확인되었다. 본 결과는 이 균주와 숙주인 새우의 공생관계를 이해하는데 도움을 줄 것이다.

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