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Complete genome sequence of *Pseudoalteromonas donghaensis* HJ51^T isolated from seawater

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해수에서 분리된 *Pseudoalteromonas donghaensis* HJ51^{T}의 유전체 서열분석

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The whole genome sequencing using PacBio RS II platform was performed for a marine bacterium *Pseudoalteromonas donghaensis* HJ51^T isolated from East Sea of Korea. As a result, three assembled contigs consisting of a chromosome (size of 3,646,857 bp, and G + C content of 41.8%) and two plasmids (size of 842,855 bp and 244,204 bp, and G + C content of 41.3% and 40.4%, respectively) were obtained. The genome included 4,083 protein coding genes and 127 RNA genes. This result could be used for gene sources of biopolymers degradation and the development as a new host with secretion system similar to *Escherichia coli*.

Keywords: *Pseudoalteromonas donghaensis* HJ51^T, complete genome sequence, seawater

Marine *Gammaproteobacteria* of the genus *Pseudoalteromonas* were reclassified from the genus *Alteromonas*, based on 16S rRNA gene sequences and phylogenetic analyses (Gauthier *et al*., 1995). The genus *Pseudoalteromonas* was known to play important interactions in marine habitats by producing a variety of bioactive compounds with anti-bacterial and anti-fouling activities, extracellular enzymes and polysaccharides, and toxins (Holmström and Kjelleberg, 1999; Bowman, 2007). Especially, extracellular proteases produced from several *Pseudoalteromonas* spp., have shown high activity under either low temperature or high salts environments and also have been reported to inhibit a marine harmful algae (Lee *et al*., 2000; He *et al*., 2004; Yan *et al*., 2009). *Pseudoalteromonas donghaensis* HJ51^T isolated from seawater samples (depth of 200–500 m) of East Sea of Korea was reported as a novel marine bacterium and produced various extracellular enzymes such as protease, DNase, amylase, chitinase, and agarase (Oh *et al*., 2011). The protease secreted from this strain showed relatively high activity under alkaline pH environment (Oh *et al*., 2015).

For analysis of the genome sequence, the cells were incubated at 25°C in marine broth 2216 (Difco) and the genomic DNA was extracted using genomic DNA extraction kit (Solgent). The genome was sequenced using PacBio RS II system (Pacific Biosciences). The total 994,261,639 bases were obtained with 99,225 sequence reads, and the individual reads were assembled with the Hierarchical Genome Assembly Process (HGAP version 3.0, Pacific Biosciences). As a result of the assembly, 3 contigs consisting of a chromosome and two plasmids were generated (Fig. 1). The complete genome size of *P. donghaensis* HJ51^T was 4,733,916 bp with G + C content of

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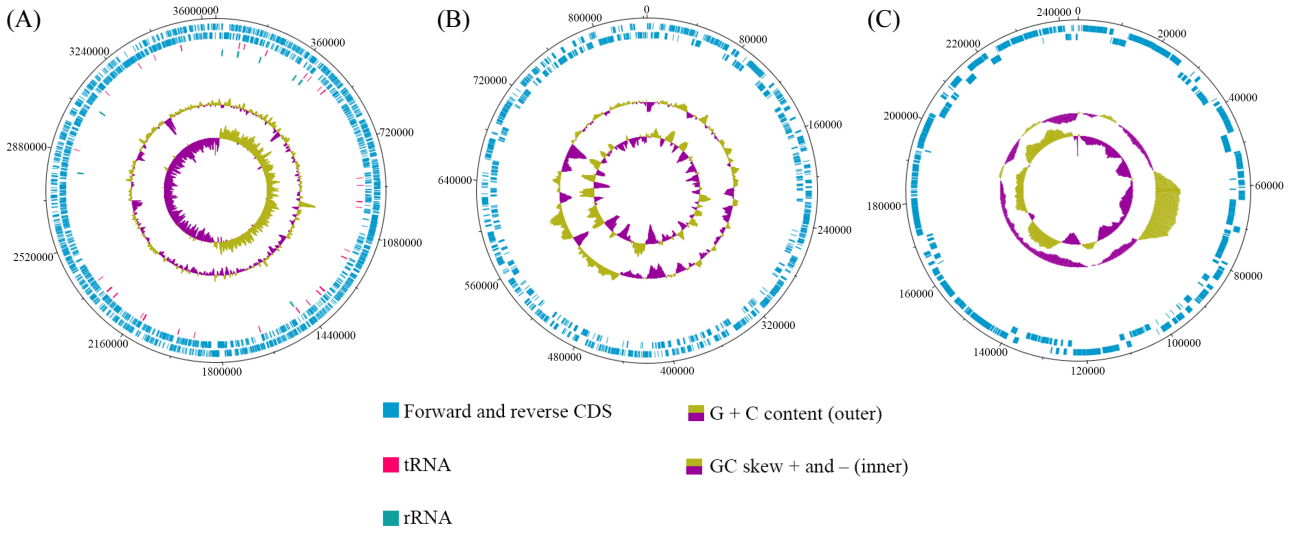

Fig. 1. Circular map of contig 1 (A, chromosome), contig 2 (B, plasmid 1), and contig 3 (C, plasmid 2). Marked characteristics are shown from outside to the center: CDS on forward strand, CDS on reverse strand, tRNA, rRNA, GC content, and GC skew.

Table 1. Genome features of *Pseudoalteromonas donghaensis* HJ51^T

Genome features	Value		
Contig	1 (Chromosome)	2 (Plasmid 1)	3 (Plasmid 2)
Depth (X)	174	171	211
Genome size (bp)	3,646,857	842,855	244,204
G + C content (%)	41.8	41.3	40.4
CDS	3,150	704	229
tRNA	102	0	0
rRNA	25	0	0

41.6% (Table 1). Total 4,210 coding sequences including 102 tRNAs and 25 rRNAs were identify and annotated by Prokka (Seemann, 2014) and BlastKOALA (Kanehisa *et al*., 2016).

A variety of extracellular enzyme genes such as protease, DNase, amylase, chitinase, agarase and lipase were identified in the genome. Interestingly, a cold-adapted halophilic extracellular serine protease with a catalytic domain (Peptidase S8 family) and two PPC (pre-peptidase C-terminal) domains similar to one of *Pseudoalteromonas* sp. SM9913 (Yan *et al*., 2009) was found. The bacterial secretion system of this strain was the same as type II system of *Pseudoalteromonas haloplanktis* and *Pseudoalteromonas atlantica* (de Pascale *et al*., 2010; Uniprot Consortium, 2017). These secretions are similar to *E. coli* BL21 (DE3), which is a widely used host for recombinant protein production (Jeong *et al*., 2015), except that the leader peptidase (GspO) and Sec-SRP secretion monitor (SecM) are defective in extracellular secretion system. If these two defective genes were inserted into the genome, it could be used as a host for the production of secretory proteins.

Nucleotide sequence accession numbers

The type strain *Pseudoalteromonas donghaensis* HJ51^T is available at KCTC 22219 and LMG 24469. The complete genome sequences for a chromosome and two plasmids are accessible in GenBank under the accession number CP032090, CP032091, and CP032092, respectively.

적 요

이 연구에서는 PacBio RS II 플랫폼을 사용하여 동해에서 분리된 해양 미생물 *Pseudoalteromonas donghaensis* HJ51^{T}의 전체 유전체 서열화를 수행하였다. 그 결과, 크기 3,646,857 bp, G + C 함량 41.8%인 염색체와 함께 크기 842,855 bp, G + C 함량 41.3% 및 크기 244,204 bp, G + C 함량 40.4%인 두 개의 플라스미드로 구성된 3개의 유전체 서열을 획득하였다. 이 유전체는 4,083개의 단백질 암호화 유전자와 127개의 RNA 유전자를 포함하고 있다. 다양한 생체 고분자 분해효소의 유전자원과 대장균과 유사한 세포외 단백질 분비 숙주로서의 개발에 이용될 수 있을 것으로 생각된다.

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