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Draft genome sequence of *Pelagicola* sp. DSW4-44 isolated from seawater

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해수에서 분리된 *Pelagicola* sp. DSW4-44의 초안 유전체 서열분석

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The draft genome sequencing for *Pelagicola* sp. DSW4-44 (= KCTC 62762 = KCCM 43261), isolated from deep seawater of East Sea in Korea, was performed using Illumina HiSeq platform. As a result, the draft genome was comprised of a total length of approximately 4.85 Mbp with G + C content of 54.3%, and included a total of 4,566 protein-coding genes, 3 rRNA genes, 48 tRNA genes, 3 non-coding RNA genes, and 67 pseudo genes. In the draft genome, the strain DSW4-44 contained genes involved in the nitrogen metabolism of dissimilatory nitrate reduction to ammonium (DNRA) and denitrification, which were not found other strains in the genus *Pelagicola*.

Keywords: *Pelagicola* sp. DSW4-44, draft genome sequence, Illumina HiSeq

The family *Rhodobacteraceae*, belong to the order *Rhodobacterales* of the class *Alphaproteobacteria*, currently comprises 161 genera (List of Prokaryotic Names with Standing in Nomenclature; http://www.bacterio.net). Members of the family *Rhodobacteraceae* are known to inhabit in various marine environments and participate in biogeochemical cycling of sulfur and carbon, and symbiosis with micro- and macro-organisms (Pujalte *et al.*, 2014). The genus *Pelagicola*, belong to the family *Rhodobacteraceae*, was first proposed by Kim *et al.* (2008), and includes 2 type species: *P. litoralis* (Kim *et al.*, 2008) and *P. litorisediminis* (Park *et al*., 2013). To date, a total of 3 genomes of the genus *Pelagicola* were sequenced and annotated, and *Pelagicola* sp. LXJ1103 was reported that it contained genes for sulfur metabolism such as sulfate transporter, sulfate permease, sulfate adenylyltransferase, and phosphoadenosine phosphosulfate reductase (Zhao *et al.*, 2018). In this report, we describe the draft genome sequence and annotation of *Pelagicola* sp. DSW4-44 isolated from East Sea of Korea.

The *Pelagicola* sp. DSW4-44 was isolated from deep seawater (depth of 200~500 m, 38° 21’ 25” N 128° 35’ 30” E), using a standard dilution plating method on marine agar 2216 (MA; Difco). Among the type strains of EzBioCloud server (https://www.ezbiocloud.net/), *Pelagicola litoralis* CL-ES2^T had the closest 16S rRNA similarity (96.5%) to strain DSW4-44. For the sequencing of the draft genome, the cells were incubated at 25°C in marine broth 2216 (MB; Difco) for 5 days and the genomic DNA was extracted using MagAttract® HMW DNA kit (Qiagen). The sequencing of the draft genome was performed on the Illumina Hiseq platform by Macrogen Inc. Quality checking of sequencing data was performed by FastQC (version 0.11.5) and the de novo assembly was performed by

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SPAdes (version 3.10.0). The potential contamination of the draft genome was assessed using ContEst16S (Lee *et al.*, 2017). Genome annotation and functional characterization of genome were conducted by the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/) (Tatusova *et al.*, 2016) and Blast-KOALA (Kanehisa *et al.*, 2016).

The draft genome of *Pelagicola* sp. DSW4-44 consisted of 23 contigs with a total length of 4,852,500 bp and N50 size of 413,599 bp. The sequencing depth of coverage was 157.4 X and the genomic DNA G + C content was 54.3 mol%. A total of 4,566 protein coding genes, 3 rRNA genes (each 1 for 5S rRNA, 16S rRNA, and 23S rRNA), 48 tRNA genes, 3 non-coding RNA, and 67 pseudo genes were predicted (Table 1).

The genome sequence contained genes for sulfur metabolism. L-Cysteine S-thiosulfotransferase *soxAX*, S-sulfosulfanyl-L-cysteine sulfohydrolase *soxB*, sulfane dehydrogenase subunit *soxC*, S-disulfanyl-L-cysteine oxidoreductase *soxD* and sulfur-oxidizing protein *soxYZ*, involved in the oxidation of thiosulfate to sulfate by SOX system, were detected. Interestingly, the genome also contained genes for nitrogen metabolism, which were not found other strains in the genus *Pelagicola*. Periplasmic nitrate reductase *napA* and cytochrome c-type protein *napB*, involved in first common step of the dissimilatory nitrate reduction to ammonium (DNRA) and denitrification genes for conversion of nitrate to nitrite, has been identified. For DNRA, nitrite reductase (NADH) large subunit *nirB*, nitrite reductase (NADH) small subunit *nirD*, related to second step (respiratory nitrite reduction to ammonium), were detected. Nitrite reductase (NO-forming) / hydroxylamine reductase *nirS*, nitric oxide reductase subunit B *norB*, nitric oxide reductase subunit C *norC* and nitrous-oxide reductase *nosZ* were detected, which were related to denitrification of nitrate to nitrogen. These genes in the sulfur and nitrogen metabolism in *Pelagicola* sp. DSW4-44 are thought to play an important role in biogeochemical cycling.

Table 1. Genome features of *Pelagicola* sp. DSW4-44

Genome features	Value
No. of contigs	23
Depth (X)	157.4
Genome size (bp)	4,852,500
G + C content (%)	54.3
Protein-coding genes	4,566
tRNA genes	48
rRNA genes (5S, 16S, 23S)	3 (1, 1, 1)
Non-coding RNA genes	3
Pseudo genes	67

Nucleotide sequence accession numbers

The strain *Pelagicola* sp. DSW4-44 is available at KCTC 62762 and KCCM 43261. The draft genome sequence is accessible in GenBank under the accession number VAUA 00000000. The version described in this paper is Version VAUA01000000.

적 요

이 연구에서는 Illumina Hiseq platform을 사용하여 동해 심층 해양수로부터 분리된 *Pelagicola* sp. DSW4-44 (= KCTC 62762 = KCCM 43261)의 초안 유전체 염기서열 해독을 수행하였다. 그 결과, 유전체는 대략 4.85 Mbp의 길이 및 54.3%의 G + C 함량으로 구성되었고, 전체 4,566개의 단백질 암호 유전자, 3개의 rRNA 유전자, 48개의 tRNA 유전자, 3개의 non-coding RNA 유전자 및 67개의 위유전자(pseudo gene)가 확인되었다. 초안 유전체에서 균주 DSW4-44는 *Pelagicola* 속의 다른 균주에서 발견되지 않는 이화적 질산염의 암모늄 환원과 탈질화의 질소대사 유전자를 가지고 있었다.

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