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Draft genome sequence of *Zhongshania marina* DSW25-10^T isolated from seawater

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해수에서 분리된 *Zhongshania marina* DSW25-10^{T}의 유전체 서열분석

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The draft genome sequencing for *Zhongshania marina* DSW25-10^T, 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 4.08 Mbp with G + C content of 49.0%, and included a total of 3,702 protein-coding genes, 3 rRNA genes, 39 tRNA genes, 4 non-coding RNA genes, and 36 pseudogenes. In addition, the metabolic pathways of aliphatic and aromatic compounds were identified. In light of these metabolic pathways, *Zhongshania marina* DSW25-10^T is expected to be a useful bioremediation resource.

Keywords: *Zhongshania marina* DSW25-10^T, draft genome sequence, Illumina HiSeq

The genus *Zhongshania* in the class *Gammaproteobacteria* was first described by Li *et al*. (2011), and currently comprises 4 type species and an invalid published species: *Z. antarctica* (Li *et al*., 2011), *Z. goukunii* (Li *et al*., 2011), *Z. aliphaticivorans* (Lo *et al*., 2014), *Z. borealis* (Jang *et al*., 2011; Lo *et al*., 2014), and '*Z. ponticola*' (Park *et al*., 2018). These species were isolated from marine environments, such as coastal attached ice, seawater and marine sediment, and characterized as Gram-negative, catalase-, and oxidase-positive, aerobic, and rod-shaped motile by single polar flagellum. Especially, *Z. aliphaticivorans*, isolated from crude oil contaminated sea-tidal flats, could be able to degrade aliphatic hydrocarbons, and identified the alkane 1-monooxygenase coding genes, catalyzing *n*-alkanes to fatty alcohols, by full genome sequencing (Jia *et al*., 2016). In addition, the genome sequence of the strain *Zhongshania* sp. ZX-21 has been determined (PQGG00000000, unpublished).

The *Zhongshania marina* DSW25-10^T was isolated from 200~500 m deep seawater, using a standard dilution plating method on marine agar 2216 (MA; Difco). For analysis of the genome sequence, 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 genome was sequenced using Illumina HiSeq platform by Macrogen Inc. The *de novo* assembly was performed by SPAdes (version 3.10.0) (Bankevich *et al*., 2012). The potential contamination of the draft genomes was assessed using ContEst16S (Lee *et al*., 2017). The total of 46 contigs were obtained with N50 length of 170,247 bp and 150.6 × sequencing depth of coverage. The draft genome size was 4,084,538 bp with G + C content of 49.0%. Genome annotation was conducted by the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/) and BlastKOALA

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(Kanehisa *et al*., 2016). A total of 3,702 protein-coding genes, 3 rRNA genes (5S, 16S, and 23S), 39 tRNA genes, 4 non-coding RNA genes, and 36 pseudogenes were predicted (Table 1).

The other strains of genus *Zhongshiania* have three to four alkane 1-monooxygenases whereas the strain DSW25-10^T has one alkane 1-monooxygenases and 44% amino acid sequence identity with that (WP_062384540) of *Z. aliphaticivorans*. The draft genome also contained degradation metabolisms of aromatic compounds. Phenol hydroxylase gene cluster *dmpKLMNOP* for benzene degradation pathway and catechol *meta* cleavage pathway gene clusters *xylEFGHIJKQ* and *mhpDEF* were found. Associated with toluene degradation pathway, toluene monooxygenase gene cluster *tmoABCDEF* and aryl-alcohol dehydrogenase were found, but benzaldehyde dehydrogenase (NAD) was not found. Benzene degradation pathway was known that had two primary pathways in first oxidation step, conversion of benzene to phenol by benzene monooxygenase or toluene monooxygenase and benzene to *cis*-dihydrobenzenediol by benzene 1,2-dioxygenase (Zamanian and Mason, 1987; Tao *et al*., 2004; Choi *et al*., 2013). The draft genome of *Zhongshania marina* DSW25-10^T did not include benzene monooxygenase and benzene 1,2-dioxygeanse, but toluene monooxygenase gene cluster was shown comparatively high amino acid sequence similarity with *Pseudomonas mendocina* KR1 and *Ralstonia picketti* PKO1, known as oxidize benzene to phenol by toluene monooxygenase. Based on this, it is assumed that *Zhongshania marina* DSW25-10^T might oxidize benzene to phenol by toluene monooxygenase, and then phenol is converted to catechol through phenol hydroxylases.

The *Zhongshania marina* DSW25-10^T, containing degradation metabolisms of saturated and aromatic hydrocarbons, is expected to be a useful biological resource for bioremediation of oil-polluted marine environments.

Table 1. Genome features of *Zhongshania marina* DSW25-10^T

Genome features	Value
No. of contigs	46
Depth (×)	150.6
Genome size (bp)	4,084,538
G + C content (%)	49.0
Protein-coding genes	3,702
tRNA genes	39
rRNA genes (5S, 16S, 23S)	3 (1, 1, 1)
Non-coding RNA genes	4
Pseudogenes	36

Nucleotide sequence accession numbers

The strain *Zhongshania marina* DSW25-10^T is available at KCCM 43273 and JCM 17372. The draft genome sequence is accessible in GenBank under the accession number RHGB 00000000. The version described in this paper is version RHGB01000000.

적 요

이 연구에서는 Illumina Hiseq platform을 사용하여 동해 심층 해양수로부터 분리된 *Zhongshania marina* DSW25-10^{T}의 유전체 염기서열 해독을 수행하였다. 그 결과, 유전체는 대략 4.08 Mbp의 길이 및 49.0%의 G + C 함량으로 구성되었고, 전체 3,702개의 단백질 암호 유전자, 3개의 rRNA 유전자, 39개의 tRNA 유전자, 4개의 non-coding RNA 유전자 및 36개의 위유전자(pseudogenes)가 확인되었다. 또한, 지방족 및 방향족 화합물의 대사 경로가 확인되었다. 이러한 대사 경로들로 비추어 *Zhongshania marina* DSW25-10^{T}는 유용한 생물 정화 자원으로 사용될 수 있을 것으로 기대된다.

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