

Draft genome sequence of *Miniimonas arenae* KCTC 19750^T isolated from sea sand

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해양모래로부터 분리된 *Miniimonas arenae* KCTC 19750^T의 유전체 분석

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Miniimonas arenae KCTC 19750^T belonging to family *Beutenbergiaceae* of the phylum *Actinobacteria* was isolated from sea sand. I report here the draft genome sequence of strain KCTC 19750^T. The draft genome comprises a size of 3,402,690 bp, a mean G + C content of 73.6%, 2,957 coding sequences, 2 ribosomal RNA genes, and 44 transfer RNA genes. Also, we found that genes involved in osmotic stress response were identified in its genome. The availability of the genome sequences will provide a more understanding of strain KCTC 19750^T as a unique member of the genus *Miniimonas*.

Keywords: *Miniimonas*, genome, type strain

The genus *Miniimonas* belonging to family *Beutenbergiaceae* of the phylum *Actinobacteria* was first reported by Ue *et al.* (2011). To date, the genus comprises only one validated species isolated from sea sand, *Miniimonas arenae* NBRC 106267^T. Cells of strain NBRC 106267^T are Gram-stain-positive, non-motile, coccoid- to rod-shaped, non-spore-forming, and form a vermilion-colored colony. The predominant menaquinone is MK-8(H₄) (Ue *et al.*, 2011). Although there is only one recognized member, the character of the genus has been identified as Gram-stain-positive, non-motile, and chemoheterotrophs.

Here, we describe the draft genome sequence and annotation of *Miniimonas arenae* as a type strain of the genus *Miniimonas*.

Miniimonas arenae NBRC 106267^T was obtained from Korean Collection for Type Cultures (KCTC, KCTC 19750^T), and was revived and grown on an LB medium at 30°C in the incubator under dark condition. Total genomic DNA (gDNA) was extracted and purified by a Monarch® Genomic DNA Purification Kit (NEB), according to the manufacturer's instructions. The quality and quantity of the extract gDNA were estimated by a DS-11+ spectrophotometer (DeNovix Inc.). For genome sequencing, a standard DNA library was prepared using the TruSeq DNA PCR-Free kit (Illumina). Sequentially, whole-genome sequencing was conducted on a MiSeq sequencer (Illumina) with paired-end read lengths of 151 bp. The qualified reads passed filtering a total of 7.52 Gb (ca. 710X in depth) in sequenced raw reads (about 11.9 Gb) using FastQC (<http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>) and Trimmomatic (Bolger *et al.*, 2014) used into scaffold assembly. *De novo* assembly of the qualified and cleaned reads was performed by SOAPdenovo2 (v.2.04). Finally, 148 contigs were obtained in this study. To estimate genome completeness and quality, we used checkM (Parks *et al.*, 2015). The resulting assembled sequences were annotated by NCBI Prokaryotic Genome Annotation Pipeline with GeneMarkS + version 4.5, using the best-placed reference protein method (Angiuoli *et al.*, 2008).

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Table 1. *Minimonas arenae* KCTC 19750^T genome assembly and its general features

Item	Description
Genome assembly data	
Assembly method	SOAPdenovo2 (v.2.04)
Genome coverage	710X
Sequencing technology	Illumina MiSeq
Genome features	
Size (Mbp)	3.40
GC content (%)	73.6
Number of contigs	148
Average contig length (bp)	22,991
No. of total predicted genes	3,006
No. of total coding sequences	2,957
No. of coding sequences	2,846
No. of rRNA	1, 1 (16S, 23S)
No. of tRNA	44

The draft genome size of the strain KCTC 19750^T is ca. 3.40 Mb with 73.6% G + C content. The result from CheckM estimation observed genome completeness at 97.0% with 0.58% contamination and no strain heterogeneity.

Total 3,006 genes have been predicted in the draft genome, in which 2,957 coding sequences (total CDSs), and 2 ribosomal RNA and 44 transfer RNA genes (Table 1). Only 1,037 CDSs were matched in KEGG database (about 35.1% of total CDSs). Also, most of the predicted CDSs were classified into COG categories: translation, ribosomal structure and biogenesis, transcription, carbohydrate transporter and metabolism, amino acid transport and metabolism, amino acid transport and metabolism, and general function prediction as a dominant category (above 5% of total CDSs genes). Interestingly, we found ABC (ATP-binding cassette) transporter for osmoprotectant (OpuBCBA) related to a salt stress (Sevin *et al.*, 2016). Moreover, genes (*glgCABPXYZ*) involved in trehalose biosynthesis and two-component regulatory system (*mtrBA*) for osmotic stress response were identified in the draft genome. Taken together, it might deduce that this strain can survive under high salt condition.

Unexpectedly, the genome has 22 questionable (length ranges 64–2,985 bp) CRISPRs (clustered regularly interspaced short palindromic repeats) by CRISPR finder (Grissa *et al.*, 2007).

Accession number

The whole genome shotgun project of the strain KCTC

19750^T has been deposited at DDBJ/ENA/GenBank under the accession VEP00000000. The version described in this paper is version VEP01000000.

적 요

Actinobacteria 문 *Beutenbergiaceae* 과에 속하는 *Minimonas arenae* KCTC 19750^T는 해양모래에서 분리되었다. 본 연구에서는 KCTC 19750^T의 비완전 유전체를 보고한다. 본 유전체는 3,402,690 bp의 크기와 73.6%의 평균 G + C 함량을 지니고 있으며, 2,947개의 단백질 코딩 유전자, 2개의 ribosomal RNA 및 44개의 transfer RNA로 구성되어 있다. 또한, 삼투압과 관련된 유전자를 포함하고 있다. 본 유전체 서열의 가용성은 *Minimonas* 속의 유일한 구성원으로 KCTC 19750^T에 대한 더 많은 이해를 제공할 것이다.

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