

Draft Genome Sequence of *Dietzia alimentaria* 72^T, Belonging to the Family *Dietziaceae*, Isolated from a Traditional Korean Food

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Actinobacterial strain 72^T, named *Dietzia alimentaria*, which belongs to the family *Dietziaceae*, was isolated from a traditional Korean food made from clams. The draft genome sequence of *D. alimentaria* 72^T contains 3,352,817 bp, with a G+C content of 67.34%.

Salted and fermented seafood products (“jeotgal” in Korean) are widely produced in Asia (6). Strain 72^T was isolated from a traditional fermented food called clam jeotgal. The genus *Dietzia* currently includes 12 species isolated from various environments, including human clinical specimens (3, 13), the air in a duck barn (4), plant tissues (7), soils (9), a soda lake (2), and drain pool water (15). Strain 72^T was described as Gram-positive, aerobic, nonmotile, opaque, and coral red pigmented. Based on the 16S rRNA gene sequences of validly published *Dietzia* species, strain 72^T shared the highest similarity with *D. maris* ATCC 35013^T (98.6%) (5). The only member of the genus *Dietzia* where the complete genome sequence has been reported is *D. cinnamea* P4. This announcement reports the genome sequence of *D. alimentaria* 72^T, which was isolated from a traditional salt-fermented seafood.

The genome of strain 72^T was sequenced using a combined approach with the 454 GS FLX Titanium system (Roche Diagnostics, Branford, CT) with an 8-kb paired-end library (167,204 reads) and the Illumina GA IIx (San Diego, CA) with a 100-bp paired-end library (10,951,513 reads). The 454 and Illumina reads were assembled using GS Assembler 2.5.1 (Roche Diagnostics, Branford, CT) and CLC Genomics Workbench 4.7.2 (CLCbio, Denmark). The 454 GS FLX sequencing achieved about 15-fold coverage, while 266-fold read coverage was achieved by Illumina paired-end sequencing. The draft genome (about 3.4 Mbp) contains 39 contigs, which can be assembled into 17 scaffolds (N50 contig size of approximately 216 kb). The genome of strain 72^T has a G+C content of 67.34%. Gene prediction (1, 8) and annotation were conducted using an in-house annotation system with several open databases (10–12, 14). The genome of strain 72^T contains 3 rRNA genes and 50 tRNA genes. Of the 3,341 predicted protein-coding sequences (CDSs) in the genome, 1,092 (32.7%) open reading frames (ORFs) matched hypothetical coding sequences with unknown function in public databases. The CDSs were annotated using the COG database and classified into 18 categories (J, K, L, D, O, M, N, P, T, C, G, E, F, H, I, Q, R, and S). The genome contains 188 predicted genes for amino acid transport and metabolism (8.36%). A more detailed analysis of

this genome and a comparative analysis with other *Dietzia* sp. genomes could identify further genes after the finalization of the genome.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession number AGFF00000000. The version described in this paper is the first version, AGFF01000000.

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