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GENOME ANNOUNCEMENT

Genome Sequence of Extracellular-Protease-Producing *Alishewanella jeotgali* Isolated from Traditional Korean Fermented Seafood

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***Alishewanella jeotgali* MS1^T (= KCTC 22429^T = JCM 15561^T) was isolated from a traditional Korean fermented seafood, gajami sikhae (jeotgal), and has been reported as a novel species. *A. jeotgali* was proven to have extracellular proteolytic activity, which may play an important role in the fermentation environment of food containing fish flesh. Here, we present the genome sequence of *Alishewanella jeotgali* MS1^T as the first sequenced strain in the genus *Alishewanella* and its taxonomic relatives.**

Salty fermented seafood (jeotgal) is an essential part of the Korean diet. Because of the lack of starting inocula, the fermentation process relies on naturally occurring microorganisms that are already present in ingredients. Despite the important role of microorganisms in food fermentation, the diversity, abundance, and roles of microorganisms in such foods have not yet been elucidated. *Alishewanella jeotgali* MS1^T (= KCTC 22429^T = JCM 15561^T) was isolated from a traditional Korean fermented seafood, gajami sikhae (jeotgal), and reported as a novel species (2). Stain MS1^T can hydrolyze casein, form a biofilm, and produce pellicles (unpublished data).

The *A. jeotgali* MS1^T genome was sequenced using a combination of an Illumina GA IIx genome analyzer (San Diego, CA) with a 100-bp paired-end library (25,425,184 reads) and the 454 GS FLX Titanium system (Roche Diagnostics, Branford, CT) with an 8-kb paired-end library (195,025 reads). The Illumina and 454 GS FLX reads were assembled using CLC Genomics Workbench 4.7.2 (CLCbio, Denmark) and GS assembler 2.5.1 (Roche Diagnostics, Branford, CT). The assembled sequences obtained from the 2 approaches resulted in 1 scaffold that consisted of 65 large contigs at 678.7-fold coverage. Genome annotation was achieved using Rapid Annotation in the Subsystem Technology (RAST) server (1) and the National Center for Biotechnology Information (NCBI) Prokaryotic Genome Automatic Annotation Pipeline (4, 5).

The *A. jeotgali* MS1^T genome contains 3,844,563 bp with a G+C content of 50.66%, 3,669 coding sequences (CDS), 64 tRNA genes, and 6 rRNA genes. It does not have a plasmid. The RAST analysis showed that the *Pseudoalteromonas* species genome was closest to the *A. jeotgali* MS1^T genome, followed by the *Alteromonas* and *Shewanella* genomes. A total of 2,202 CDS were classified using the Cluster of Orthologous Groups (COG) database (7). The most abundant groups of proteins were those that are involved in replication, recombination, and repair (COG category L [5.7%]) and in nucleotide transport and metabolism (COG category F [5.7%]). As the ability of the MS1^T strain to hydrolyze gelatin and casein implies, the strain contains 2 extracellular proteases, which are homologues of the proteases of *Shewanella denitrificans* OS217 and *Idiomarina loihiensis* L2TR (reference 2 and unpublished data).

Currently, the genus *Alishewanella* contains 4 type species, which have been isolated from different habitats such as human fetus (8), tidal flat sediment (6), landfill soil (3), and fermented food (2). The fact that organisms in this genus have been isolated from various sources implies that *Alishewanella* species may have great adaptability to diverse environments and unique genetic requirements for each habitat. *A. jeotgali* MS1^T is the first strain whose genome has been sequenced from among all the known *Alishewanella* strains and taxonomic relatives such as *Rheinheimera* and *Alkalimonas*. To investigate the role of *A. jeotgali* MS1^T in food fermentation and the ecology- and habitat-specific evolution of the genus *Alishewanella*, additional genome sequencing, comparative genomics, and analysis of food environments are being performed.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. AHTH00000000. The version described in this paper is the first version, AHTH01000000.

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