Draft Genome Sequence of *Salimicrobium* sp. Strain MJ3, Isolated from Myulchi-Jeot, Korean Fermented Seafood

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***Salimicrobium* sp. strain MJ3 was isolated from myulchi-jeot, traditional fermented seafood made from anchovy in South Korea. Here we announce the draft genome sequence of *Salimicrobium* sp. MJ3 with 2,717,782 bp, which consists of 45 contigs (>500 bp in size), and provide a description of their annotation.**

Salted and fermented seafood, called jeotgal in Korean, is widely produced and consumed in South Korea. Jeotgal is usually made by the fermentation of highly salted (about 25% [wt/wt]) marine animals such as shrimp, anchovy, oyster, clam, fish roe, and squid. Myulchi-jeot, made by fermentation of salted anchovy (*Engraulis japonica*), is representative and is one of the best-selling fermented seafoods in Korea. Previous taxonomic studies have shown that members of the genus *Salimicrobium* are likely to be key players responsible for jeotgal fermentation (2; J. Y. Jung, S. H. Lee, and C. O. Jeon, submitted for publication). It has been known that members of the genus *Salimicrobium*, placed within the family of *Bacillaceae*, are Gram-positive, endospore-forming, nonmotile cocci and moderately halophilic bacteria (1, 7). A strain of the genus *Salimicrobium*, designated strain MJ3, was isolated from salted fermented anchovy jeotgal. Here we report the draft genome sequence and annotation of *Salimicrobium* sp. strain MJ3.

The genome of strain MJ3 was sequenced using a combination approach of Illumina (Solexa) sequencing with a 150-bp paired-end library and PacBio sequencing with a 5-kb library at Chunlab (South Korea), which generated 1,214.3 Mb (8,041,836 reads, about 446.8-fold genome coverage) and 69.92 Mb (51,913 reads, about 25.7-fold genome coverage), respectively. The resulting sequences were assembled using CLC Genomics Workbench 5.1 (CLC Bio, Aarhus, Denmark) and Celera Assembler 7.0 (5). The assembled draft genome sequences consisted of 45 contigs ranging from 552 to 271,263 bp in size. The draft genome sequence of strain MJ3 was submitted to the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (6). The tRNA and rRNA genes were annotated using the tRNAscan-SE (4) and RNAmmer software programs (3), respectively.

The draft genome size of *Salimicrobium* sp. strain MJ3 was 2,717,782 bp with a G+C content of 46.27%. The genome of strain MJ3 contains 2,732 predicted protein-coding sequences, 5 rRNA loci, and 64 tRNA genes coding for 20 amino acids on the

genome. The coding density of the draft genome is 87.4%, with an average gene length of 869 bp.

Nucleotide sequence accession number. The draft genome information of *Salimicrobium* sp. strain MJ3 is available in NCBI under GenBank accession number [AMPO1000000](https://www.ncbi.nlm.nih.gov/nuclseq/AMPO1000000).

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