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GENOME ANNOUNCEMENT

Genome Sequence of the Halotolerant *Staphylococcus* sp. Strain OJ82, Isolated from Korean Traditional Salt-Fermented Seafood

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***Staphylococcus* sp. strain OJ82 was isolated from a Korean traditional fermented squid seafood, ojingeo-jeotgal. *Staphylococcus* sp. OJ82 could grow and show extracellular protease and β-galactosidase activities in the presence of extremely high saline (20%). Here, we report the genome sequence of *Staphylococcus* sp. OJ82.**

Fermented seafoods are an important constituent of the human diet in many countries. Seafood fermentation can be driven by indigenous microorganisms in the raw materials (4). Despite the important role of microorganisms in seafood fermentation, the diversity, abundance, and roles of microorganisms in fermented seafoods have been poorly explored (2). *Staphylococcus* sp. strain OJ82 was isolated from a Korean traditional fermented squid seafood, ojingeo-jeotgal. Salty fermented squid seafood can be prepared with small squid and many different ingredients (salt, fish sauce, hot pepper flakes, green chili pepper, etc.). Among many culturable strains isolated from salty fermented squid seafood, *Staphylococcus* species were dominant bacteria (data not shown). *Staphylococcus* sp. OJ82 maintains its growth in the presence of high salt stress and produces the enzymes β-galactosidase and protease (unpublished data). We sequenced the genome of *Staphylococcus* sp. OJ82 to provide more insight into its genetics and physiology under high-salt conditions.

The *Staphylococcus* sp. OJ82 genome was sequenced using a combination of the 454 GS FLX Titanium system (Roche Diagnostics, Branford, CT) with an 8-kb paired-end library (288,808 reads) and an Illumina GA IIx genome analyzer (San Diego, CA) with a 100-bp paired-end library (44,078,567 reads). The 454 GS FLX and Illumina reads were assembled using GS Assembler 2.6 (Roche Diagnostics, Branford, CT) and CLC Genomics Workbench 5.0 (CLC bio, Denmark). The assembled sequences resulted in 11 scaffolds that consisted of 28 contigs with 1,550.57-fold coverage. Genome annotation was achieved using the National Center for Biotechnology Information (NCBI) Prokaryotic Genome Automatic Annotation Pipeline (5).

The *Staphylococcus* sp. OJ82 genome contains 2,899,115 bp with a G+C content of 32.86%, 2,841 coding sequences (CDS), 58 tRNA genes, and 10 rRNA genes. No plasmids are present in the sequenced strain. A total of 2,305 CDS were classified using the Cluster of Orthologous Groups (COG) database (6). The most abundant group is involved in amino acid metabolism and transport (COG category E [7.39%]), with the next-most-abundant group involved in carbohydrate transport and metabolism (COG category G [6.80%]). Several genes known to be important for survival under saline stress were found. The strain contains 10 Na^+ cotransporter genes, which are homologues of the Na^+ symporter genes of *Staphylococcus saprophyticus* subsp. *saprophyticus* ATCC 15305, *Lentibacillus* sp. strain Grbi, *Staphylococcus pseudintermedius* HKU10-03, and *Macrococcus caseolyticus* JCSC5402, and 6 Na^+/H^+ antiporter genes, which are homologues of the Na^+/H^+ antiporter genes of *Staphylococcus carnosus* subsp. *carnosus* TM300 and *Staphylococcus saprophyticus* subsp. *saprophyticus* ATCC 15305.

Staphylococcus species have been isolated from various environments, such as human skin (7), crude oil-contaminated soil (1), and fermented food (3), which indicates that each *Staphylococcus* species has a unique metabolic capability in its ecological niche. *Staphylococcus* species have been isolated from many fermented seafoods, which suggested that they might play important roles in seafood fermentation. The availability of the genome sequence of *Staphylococcus* sp. OJ82 will provide more insight into the mechanism of halotolerance under high-salt conditions such as seafood fermentation.

Nucleotide sequence accession numbers. The nucleotide sequence of the 16S rRNA from *Staphylococcus* sp. OJ82 has been deposited in GenBank under accession number JX270830. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ALPU00000000. The version described in this paper is the first version, ALPU01000000.

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