

Draft Genome Sequence of *Staphylococcus vitulinus* F1028, a Strain Isolated from a Block of Fermented Soybean

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***Staphylococcus vitulinus* is a coagulase-negative staphylococcus in the family *Staphylococcaceae*. This report describes the draft genome sequence of *S. vitulinus* F1028, which was isolated from a traditional Korean soybean food (meju). This 2.56-Mbp genome sequence is the first *S. vitulinus* genome of a strain isolated from a fermented soybean product.**

Staphylococcus is a group of Gram-positive bacteria that form grape-like clusters. It currently contains 47 species (<http://www.bacterio.cict.fr/>), which normally inhabit the skin and mucosal surfaces of humans and other animals (4). Most *Staphylococcus* strains are known to be harmless, but some strains of *S. aureus*, *S. pseudintermedius*, and *S. epidermidis* can cause severe infections (2). Therefore, most of the 573 available *Staphylococcus* genomes are focused on the pathogenic potential of these microorganisms (<http://www.ncbi.nlm.nih.gov/genome/>). *Staphylococcus* spp. are known to be major components of Korean soybean paste (8) and Japanese miso (5), while they are readily isolated from fermented sausages (3). Thus, there is a need for genomic data to understand the roles of nonpathogenic *Staphylococcus* spp. in fermentation processes. *Staphylococcus vitulinus* and *S. pulvereri* were first described as novel *Staphylococcus* spp. in 1994 (11) and 1995 (12), respectively, although *S. pulvereri* was identified as a junior synonym of *S. vitulinus* in 2004 (10). In this study, a new strain, *S. vitulinus* F1028, which shares 99.5% 16S rRNA gene sequence similarity with *S. vitulinus* ATCC 51145^T, was isolated from a traditional Korean fermented soybean food product, meju. This report announces the first sequenced genome of a *Staphylococcus* strain that participates in soybean fermentation.

The genomic DNA of *S. vitulinus* F1028 was extracted using a G-spin bacterial genomic extraction kit (iNtRON Biotechnology, Republic of Korea). The draft genome sequence of *S. vitulinus* F1028 was determined using an Ion Torrent personal genome machine (PGM) with 316 100-Mb sequencing chips (150-bp library), according to the manufacturer's instructions (9). Approximately 2,723,000 reads were produced, with an average read length of 91 bases (total, 237 Mb). The reads were assembled into 223 contigs (>1 kb in size) with an approximately 93-fold coverage using the CLC Genomics Workbench 5.0.1 program (CLC Bio, Denmark) and the Newbler assembler (454 Life Sciences, Branford, CT). The draft genome of *S. vitulinus* F1028 measured 2,561,113 bp in length, with a G+C content of 32.4%. Gene prediction and annotation of the assembled contigs were performed by combining the outputs of the following analytical tools: RNAMmer 1.2 for rRNAs (6), tRNA scan-SE 1.23 for tRNAs (7), and RAST 4.0 (Rapid Annotation using Subsystem Technology) for proteins (1). The draft genome sequence contained a single copy of the 16S rRNA gene, a single copy of the 23S rRNA gene, and 26 copies of tRNA genes. Of the 2,539 predicted protein-coding genes, 97 genes were assigned putative functions, and 537

genes were assigned as hypothetical proteins based on the subsystem categorization. Using the functional annotation by the COG (Clusters of Orthologous Groups) database, 2,110 genes were classified into 21 COG classes and 1,453 COG families. No toxin-related genes that may be harmful to humans, such as enterotoxin proteins, were present in the genome. Further in-depth analysis will be necessary to elucidate fully the genomic differences between pathogenic and nonpathogenic *Staphylococcus* strains and to understand the roles of *Staphylococcus* in fermentation processes.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited in DDBJ/EMBL/GenBank under accession no. AJTR00000000. The version described here is the first version, AJTR00000000.

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