Draft Genome Sequence of *Staphylococcus saprophyticus* subsp. *saprophyticus* M1-1, Isolated from the Gills of a Korean Rockfish, *Sebastes schlegeli* Hilgendorf, after High Hydrostatic Pressure Processing

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A bacterium designated M1-1 was isolated from the gills of a Korean rockfish, *Sebastes schlegeli* Hilgendorf, after high hydrostatic pressure processing. Studies of 16S rRNA phylogeny and comparative genomics demonstrated that the isolate belongs to *Staphylococcus saprophyticus* subsp. *saprophyticus*. Here, we report the draft genome sequence of *S. saprophyticus* subsp. *saprophyticus* M1-1 (KACC 16562).

High hydrostatic pressure (HHP) processing is a method of food treatment with minimal heat exposure that generates better flavor, texture, and nutrition retention than thermal processing (13). Sterilization based on HHP is widely used in the food industry since most microorganisms do not tolerate high-pressure conditions (e.g., >60 MPa, similar to 600 atm) at a temperature of 30°C for 48 h (14). Bacteria that survive such conditions could be a threat to food safety. An HHP-resistant strain designated M1-1 was isolated from the gills of a Korean rockfish after being pressurized at 350 MPa for 25 min using plate count agar (PCA) medium incubated at 20°C. We analyzed the genome sequence and genomic characteristics of this strain for further physiological characterization related to potential food-borne pathogenicity using HHP processing.

The genome sequence was determined by using a combination of Illumina HiSeq 2000 (100-bp paired-end sequencing yielding 7,118,979 reads; >292-fold coverage) and Roche 454 (8-kb insert paired-end sequencing yielding 84,073 reads; >13-fold) sequencing systems. A hybrid assembly was conducted using CLC genomic workbench (CLC Bio, Denmark), GS Assembler 2.3 (Roche Diagnostics, Branford, CT), and CodonCode Aligner (CodonCode Co.). The final draft genome consisted of 58 contigs representing 2,619,936 bases with a G+C content of 33.1%, and 2,490 open reading frames (ORFs), 65 tRNA genes, and 5 rRNA genes were predicted (1, 12). The predicted ORFs were annotated by a homology search against the COG and SEED databases (2, 9). Among the COG categories, R (general function prediction only; 274 CDS) and S (function unknown; 233 CDS) were abundant, followed by category E (amino acid transport and metabolism; 222 CDS).

The 16S rRNA gene of strain M1-1 was extracted using rRNA selector (7), and taxonomic identification was performed using the EzTaxon-e database (6). Strain M1-1 showed the highest 16S rRNA gene sequence similarity to *Staphylococcus saprophyticus* subsp. *saprophyticus* ATCC 15305^T (99.93%). To compare and determine the similarity between whole-genome sequences from strain M1-1 and ATCC 15305^T, the average nucleotide identity (ANI) value was calculated (4). The ANI values between strains M1-1 and ATCC 15305^T were 98.96% (M1-1 as a query sequence)

and 99.46% (ATCC 15305^T as a query sequence). Based on a 16S rRNA gene similarity and the ANI value, strain M1-1 can be confidently identified as a strain of *Staphylococcus saprophyticus* subsp. *saprophyticus*.

Staphylococcus saprophyticus subsp. *saprophyticus* is a coagulase-negative staphylococcus and known as the causative agent of an uncomplicated urinary tract infection in young female outpatients (5, 8, 10, 11). We found that strain M1-1 contained genes encoding a urease and a cell wall-anchored protein that have been reported as potential uropathogenic factors (3). Although strains M1-1 and ATCC 15305^T share highly similar gene contents, strain M1-1 contains slightly more genes in K (transcription), E (amino acid transport and metabolism), and R (general function prediction only) categories. Strain M1-1 was deposited in the Korean Agricultural Culture Collection (Suwon, Republic of Korea) under the accession number KACC 16562. Further comparative analyses and experimental works will be carried out to determine the potential pathogenicity of this isolate in light of microbiological food safety.

Nucleotide sequence accession numbers. The draft genome sequence of *S. saprophyticus* subsp. *saprophyticus* M1-1 (KACC 16562) has been deposited in GenBank under the accession number [AHKB000000000](https://www.ncbi.nlm.nih.gov/nuclseq/AHKB000000000). The version described in this paper is the first version, AHKB01000000.

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