



Genome announcement

Complete genome sequence of *Staphylococcus equorum* KS1039 isolated from Saeu-jeotgal, Korean high-salt-fermented seafood

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ABSTRACT

Staphylococcus equorum KS1039 was isolated from a form of traditional Korean high-salt-fermented seafood called Saeu-jeotgal, and exhibited growth at a NaCl (w/v) concentration of 25%. Comparative genome analyses with two other strains revealed the presence of two potassium voltage-gated channel genes uniquely in KS1039, which might be involved in salt tolerance. This first complete genome sequence of the species will increase our understanding of the genetic factors allowing it to be safely consumed by humans and to inhabit high-salt environments.

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Saeu-jeotgal is a form of traditional Korean high-salt-fermented seafood made by adding up to 30% sea salt (w/w) to tiny sea shrimp (*Acetes japonicus*). The combination becomes palatable through subsequent fermentation. During the fermentation period over one year, it has been shown that this seafood attains rich flavors, pleasing tastes, and the unique Saeu-jeotgal structure through autolytic and microbial proteolysis. Our previous study involving analysis of the cultivable bacterial community of Saeu-jeotgal revealed that *Staphylococcus equorum* was the most populous species (Guan et al., 2011). The members of this predominant species can be potential starter candidates to produce quality Saeu-jeotgal products and to shorten the manufacturing time. To select a safe and efficient starter for Saeu-jeotgal production, the safety for human consumption and the technological properties of 126 *S. equorum* isolates were assessed (Jeong et al., 2014). The selected strain KS1039 was found to be susceptible to 15 kinds of antibiotic and did not express the activities of hemolysis, biofilm formation, and biogenic amine production. The strain exhibited protease, lipase, and nitrate reductase activities, as well as growth on tryptic soy agar supplemented with 25% NaCl (w/v). To confirm that the genetic background of *S. equorum* KS1039 makes it a safe and efficient starter candidate for Saeu-jeotgal production, its complete genome sequence was determined.

Whole-genome sequencing was performed using a combination of the Illumina Miseq system and the PacBio single-molecule real-time (SMRT) sequencing system at ChunLab, Inc. (Seoul, Republic of Korea). The Illumina reads were assembled using CLC Genomics Workbench ver. 7.5.1 (CLC Bio, Aarhus, Denmark) and CodonCode Aligner (CodonCode Co., Centerville, MA, USA). Gene prediction was performed using Glimmer 3 (Delcher et al., 2007), followed by annotation through a search against the Clusters of Orthologous Groups (COG) (Tatusov et al., 1997) and SEED databases (Disz et al., 2010).

The complete genome of *S. equorum* KS1039 contains a circular chromosome of 2,822,193 bp with G + C content of 33.07% (Table 1). It contains 2681 protein-encoding sequences, 61 tRNA genes, and 22 rRNA genes.

Gene category analysis showed that most of the genes are related to membrane transport, carbohydrate metabolism, amino acid metabolism, and lipid metabolism. The large number of genes involved in nutrient acquisition and utilization suggests that

Table 1Features of the genome of *Staphylococcus equorum* KS1039.

Features	Value
Genome size (bp)	2,822,193
G + C content (%)	33.07
Total number of genes	2681
rRNA genes	22
tRNA genes	61

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S. equorum KS1039 has the ability to survive in a large variety of habitats and can also degrade a wide range of nutrients in fermented foods. Comparative genome analyses with two previously reported genome sequences of the species revealed the existence of two potassium voltage-gated channel genes, SE1039-03700 and SE1039-03710, only in the *S. equorum* KS1039 genome (Irlinger et al., 2012; Calcutt et al., 2013). The potassium channel of rice was reported to confer salt tolerance to yeast and rice cells (Obata et al., 2007). Therefore, the above-mentioned genes might contribute to the growth of the strain at a NaCl concentration of 25%.

Genome analysis revealed that *S. equorum* KS1039 does not encode any of the virulence factors found in the well-known food pathogen *Staphylococcus aureus*. This trait and its high salt tolerance fulfill the requirements of a starter candidate for producing high-salt-fermented foods. The complete genome sequence of *S. equorum* KS1039 will provide a basis for further comparative and functional genomic analyses and help to determine which strains are suitable for use in producing foods for human consumption.

Strain deposition and nucleotide sequence accession number

S. equorum KS1039 has been deposited in the Korean Culture Center of Microorganisms under the number of KCCM 43182 and its complete genome sequence has been deposited in GenBank under accession number CP013114.

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References

- Calcutt, M.J., Foecking, M.F., Hsieh, H.Y., Perry, J., Stewart, G.C., Middleton, J.R., 2013. Genome sequence analysis of *Staphylococcus equorum* bovine mastitis isolate UMC-CNS-924. *Genome Announc.* 17, 1–2.
- Delcher, A.L., Bratke, K.A., Powers, E.C., Salzberg, S.L., 2007. Identifying bacterial genes and endosymbiont DNA with Glimmer. *Bioinformatics* 23, 673–679.
- Disz, T., Akhter, S., Cuevas, D., Olson, R., Overbeek, R., Vonstein, V., Stevens, R., Edwards, R.A., 2010. Accessing the SEED genome databases via Web services API: tools for programmers. *BMC Bioinformatics* 11, 319.
- Guan, L., Cho, K.H., Lee, J.H., 2011. Analysis of the cultivable bacterial community in jeotgal, a Korean salted and fermented seafood, and identification of its dominant bacteria. *Food Microbiol.* 28, 101–113.
- Irlinger, F., Loux, V., Bento, P., Gibrat, J.F., Straub, C., Bonnarme, P., Landaud, S., Monnet, C., 2012. Genome sequence of *Staphylococcus equorum* subsp. *equorum* Mu2, isolated from a French smear-ripened cheese. *J. Bacteriol.* 194, 5141–5142.
- Jeong, D.W., Han, S., Lee, J.H., 2014. Safety and technological characterization of *Staphylococcus equorum* isolates from jeotgal, a Korean high-salt-fermented seafood, for starter development. *Int. J. Food Microbiol.* 188, 108–115.
- Obata, T., Kitamoto, H.K., Nakamura, A., Fukuda, A., Tanaka, Y., 2007. Rice shaker potassium channel OsKAT1 confers tolerance to salinity stress on yeast and rice cells. *Plant Physiol.* 144, 1978–1985.
- Tatusov, R.L., Koonin, E.V., Lipman, D.J., 1997. A genomic perspective on protein families. *Science* 278, 631–637.