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GENOME SEQUENCES

Complete Genome Sequence of *Streptococcus oralis* SF100, Isolated from Blood Cultures from a Patient with Infective Endocarditis

Ji Hee Lee,[a] Hyun Jung Ji,[a,c] Ho Seong Seo,[a,b] Paul M. Sullam[d]

[a]Research Division for Radiation Science, Korea Atomic Energy Research Institute, Jeongeup, Republic of Korea
[b]Department of Radiation Science, University of Science and Technology, Daejeon, Republic of Korea
[c]Department of Oral Microbiology and Immunology, Dental Research Institute, School of Dentistry, Seoul National University, Seoul, Republic of Korea
[d]Department of Medicine, Veterans Affairs Medical Center and University of California, San Francisco, San Francisco, California, USA

ABSTRACT *Streptococcus oralis* is a commensal viridans group streptococcus of the human oral cavity and a frequent cause of endovascular infection. Here, we report the complete whole-genome sequence of *S. oralis* strain SF100, which was originally isolated from the blood of a patient with infective endocarditis. This strain contains the lysogenic bacteriophage SM1, which enhances the virulence of SF100 in animal models of endocardial infection.

Streptococcus oralis is one of the most frequent causes of infective endocarditis (1, 2). Strain SF100 was originally isolated in 1980 from the blood of a patient with this disease, using standard clinical methods. It was originally identified as *Streptococcus mitis*, based on biochemical testing and 16S RNA gene sequencing (3). However, we now report that strain SF100 more closely resembles members of the species *S. oralis*, based on whole-genome sequencing.

SF100 contains the lysogenic bacteriophage SM1, which encodes several important virulence factors, including PblA, PblB, and $lysin_{SM1}$ (4–6). Disruption of these genes results in a significant reduction in the binding of SF100 to human platelets and reduced virulence in animal models of endocarditis (5, 7). Of note, these adhesins appear to be widely prevalent among *S. oralis* strains of the human oral microbiome (8–10).

For whole-genome sequencing, strain SF100 was grown in Todd-Hewitt broth at 37°C to an optical density (600 nm) of 0.8 to 1.0. Genomic DNA was isolated using the G-spin genomic DNA extraction kit (Intron, Seoul, South Korea). Approximately 100 ng of isolated genomic DNA was sequenced using the RS II platform (Pacific Biosciences [PacBio], Menlo Park, CA, USA) at Macrogen Co., Ltd. (Seoul, South Korea). The DNA library was prepared using a single-molecule real-time (SMRT) Cell 8Pac v3 and the P6 DNA polymerase binding kit (PacBio). Reads were filtered and assembled using Canu v1.7 (correctedErrorRate = 0.015) (11). The sequencing yielded 140,974 subreads (1.11 Gbp). The mean subread length and N_{50} value were 7,905 bp and 12,037 bp, respectively. After assembly, strain SF100 contained one contig of 1,969,104 bp, with a G+C content of 41.5 mol%. To assess the completeness of genome assembly, Benchmarking Universal Single-Copy Orthologs (BUSCO) v3.0 analysis of the bacteria_odb9 data set (148 orthologs) was performed (12). This showed 96.6% complete orthologs and 3.4% missing orthologs. The assembled genome contained 1,909 genes annotated by the Prokaryotic Genome Annotation Pipeline (PGAP) v5.1 of the National Center for Biotechnology Information (13, 14). Protein sequences of each single-copy ortholog group were aligned using MAFFT v7.435 with the auto option (15). A phylogenetic tree of 1,010 single-copy ortholog genes was built by the maximum likelihood method using RAxML v8.2.12 with the -m PROTGAMMAAUTO -p 1000 options (16). In the phylogenetic tree (Fig. 1), strain SF100 clustered with the *S. oralis* group. The results of the

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Address correspondence to Paul M. Sullam, paul.sullam@ucsf.edu.

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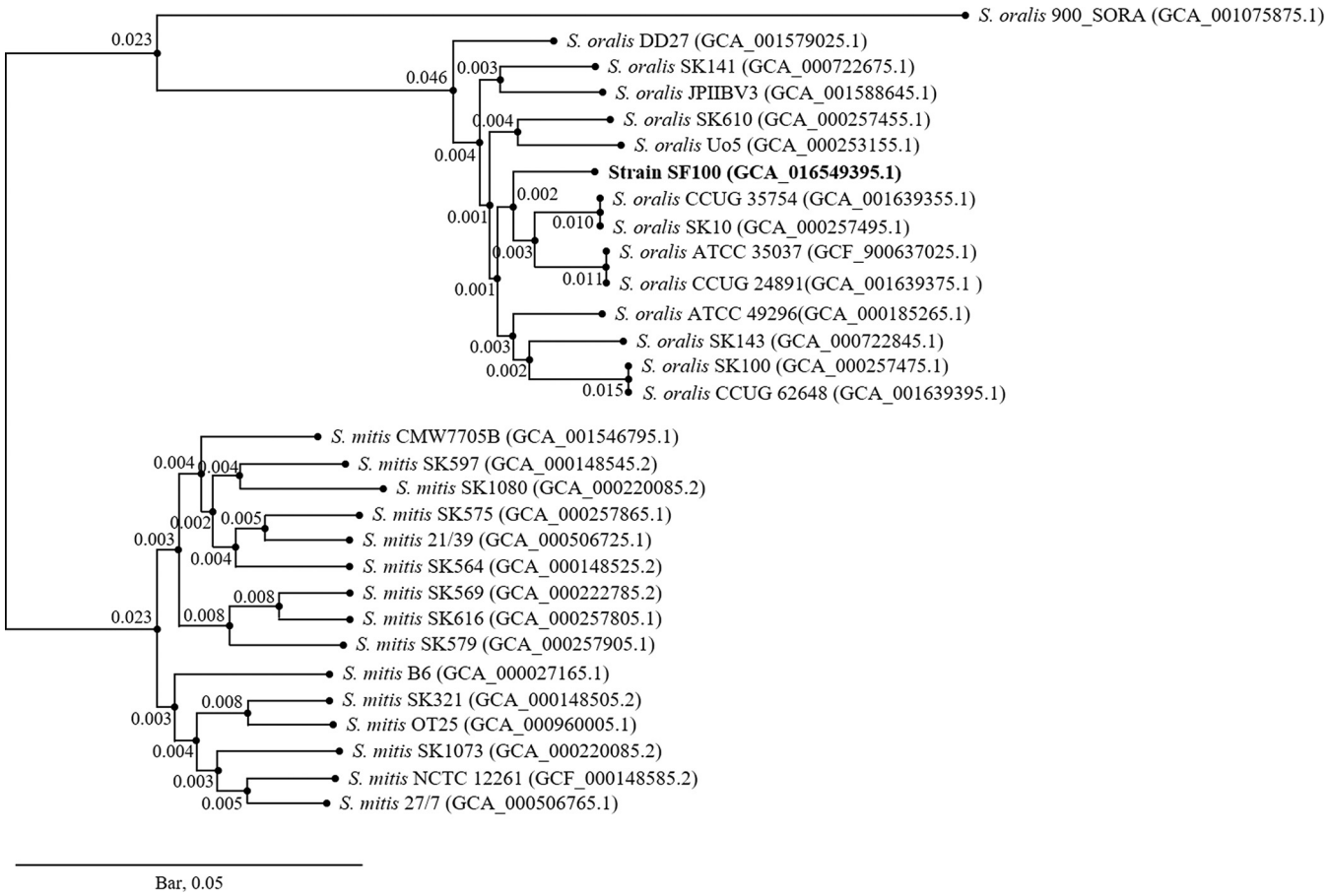

FIG 1 Maximum likelihood phylogenetic tree of single-copy ortholog genes in strains of *S. oralis*, *S. mitis*, and SF100. The GenBank assembly accession number for each strain is shown in parentheses. The numbers indicate the length. The phylogenetic tree showed that the *S. oralis* group and the *S. mitis* group were clearly distinguished, and strain SF100 was closely related to the *S. oralis* group. The scale bar indicates 0.05 substitution per nucleotide position.

phylogenetic tree indicate that SF100 is a member of *S. oralis*. Default parameters were used for all software unless otherwise specified.

Data availability. The whole-genome sequence of *S. oralis* SF100 has been deposited in DDBJ/EMBL/GenBank under the accession number CP066172. The BioProject, BioSample, and SRA accession numbers are PRJNA685325, SAMN17082796, and SRR13854333, respectively.

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