S. gordonii, a member of the Mitis group streptococci, is a normal commensal in the human oral cavity (1, 2). S. gordonii is known to form biofilms on tooth surfaces together with other bacteria (2–5). Even though S. gordonii is a commensal, it can escape its niche and cause diseases, such as infective endocarditis and septic arthritis (6, 7). S. gordonii is known to possess genes contributing to adhesion, fibrinogen binding, and platelet binding, all of which are important factors for the pathogenesis of infective endocarditis (8–10). S. gordonii ATCC 10558T was isolated from a patient with subacute endocarditis, and in 1989, S. gordonii ATCC 10558 was announced as a type strain (11). Here, we report the draft genome sequence of S. gordonii ATCC 10558T, together with the description of its genomic sequencing and annotation.

Bacterial cells of S. gordonii ATCC 10558T were inoculated into Todd-Hewitt broth (Statens Serum Institut [SSI], Denmark) and incubated under standard conditions. Template DNA was extracted using the MasterPure Gram-positive DNA purification kit (Epicentre, USA), to which 5,000 U/ml mutanolysin from Strepomyces globisporus ATCC 21553 (Sigma-Aldrich, USA) was added.

Paired-end DNA libraries were constructed, with an insert size of 500 bp, and sequenced by BGI, Hong Kong, using Illumina HiSeq 2000. A total of 2,657,236 reads, with a read length of 2 bp, were assembled with SOAPdenovo version 2.04, using a k-mer setting of 15 (12).

We obtained a draft genome of S. gordonii ATCC 10558T, composed of 66 contigs, with an N50 of 121,161 bp and an N50 of 34,144 bp. The longest contig was 323,737 bp. The estimated size of the whole genome is 2,154,510 bp (mean coverage depth, 60.53X), with a G+C content of 40.48%.

The sequence was annotated by the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/) and by the Rapid Annotations using Subsystems Technology (RAST) server (13, 14). PGAP predicted 2,100 genes, including 1,982 coding sequences (CDSs), 31 tRNAs, 84 pseudogenes, and one 5S-16S-23S rRNA operon. In addition, PGAP predicted one clustered regularly interspaced short palindromic repeat (CRISPR). RAST allocated 52% of the genome into 338 different subsystems, of which 45 of the genes were allocated into the subsystem virulence, defense, and disease. RAST annotated CDSs for fibrinogen-binding protein, laminin-binding surface protein, and collagen adhesion protein, which all seem to be factors of importance for the pathogenesis in infective endocarditis (15–17). In addition, RAST annotated a CDS for IgA1 protease, which may cleave the human immunoglobulin A1 (18).

The GenBank entry of S. gordonii ATCC 10558T will contribute to research on the pathogenesis of endocarditis and to the identification of Mitis group streptococci.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession no. LOBS0000000. The version described in this paper is the first version, LOBS0100000.

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