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Draft Genome Sequence of Type Strain *Streptococcus gordonii* ATCC 10558

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***Streptococcus gordonii* ATCC 10558^T was isolated from a patient with infective endocarditis in 1946 and announced as a type strain in 1989. Here, we report the 2,154,510-bp draft genome sequence of *S. gordonii* ATCC 10558^T. This sequence will contribute to knowledge about the pathogenesis of infective endocarditis.**

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Streptococcus 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 10558^T 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 10558^T, together with the description of its genomic sequencing and annotation.

Bacterial cells of *S. gordonii* ATCC 10558^T 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 *Streptomyces 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 × 100 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 10558^T, composed of 66 contigs, with an N_{50} of 121,161 bp and an N_{90} 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, 60.53×), 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 10558^T 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. [LOBS000000000](https://www.ncbi.nlm.nih.gov/nuclink/LOBS000000000). The version described in this paper is the first version, [LOBS010000000](https://www.ncbi.nlm.nih.gov/nuclink/LOBS010000000).

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