

Note (Genome Announcement)

Complete genome sequence of *Streptococcus gordonii* KCOM 1506 isolated from a human acute pulpitis lesion

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사람 급성치수염에서 분리된 *Streptococcus gordonii* KCOM 1506의 유전체 염기서열 해독

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Streptococcus gordonii is a Gram-positive, facultative anaerobic and non-motile cocci. *S. gordonii* is a member of oral flora and a pioneer species that initiate the dental biofilm formation. *S. gordonii* has also been implicated in the pulpitis of primary teeth as well as systemic diseases such as infective endocarditis and septic arthritis. *S. gordonii* is associated with oral, respiratory, and gastrointestinal tract infections. *S. gordonii* KCOM 1506 (= ChDC B679) was isolated from a human acute pulpitis lesion. Here, we present the complete genome sequence of *S. gordonii* KCOM 1506.

Keywords: *Streptococcus gordonii*, acute pulpitis, human

Streptococcus gordonii is one of the pioneer species that initiate the dental biofilm formation on tooth surfaces (Loo *et al.*, 2000). *S. gordonii* has also been implicated in the pulpitis of primary teeth (Ruvière *et al.*, 2007) as well as systemic diseases such as infective endocarditis (Douglas *et al.*, 1993) and septic arthritis (Yombi *et al.*, 2012). *S. gordonii* KCOM 1506 (=

ChDC B679) was isolated from a human acute pulpitis lesion. In this report, we present the complete genome sequence of *S. gordonii* KCOM 1506.

The *S. gordonii* KCOM 1506 was grown on brain heart infusion (BHI, Difco Laboratories) medium in 37°C incubator for 24 h. The bacterial genomic DNA was prepared as described previously (Cho *et al.*, 2015). DNA concentration was determined by the Epoch™ Microplate Spectrophotometer (BioTek Instruments Inc.) at wavelengths of 260 and 280 nm (Cho *et al.*, 2015).

The genomic DNA of *S. gordonii* KCOM 1506 was sequenced using the Illumina HiSeq 2000 platform by Macrogen Inc. The library of 5 kb mate-pair was sequenced which reached coverage of 1,336 folds. The *de novo* assembly was performed by ALLPATHS-LG (Gnerre *et al.*, 2011) which produced one circular large scaffold and 3 tiny scaffolds. All 15 gaps among the scaffolds were filled by GapCloser (Luo *et al.*, 2012; <http://sourceforge.net/projects/soapdenovo2/files/GapCloser>). And we confirmed the 3 tiny scaffolds were placed at gaps on the largest scaffold by dot plot analysis. Finally, the assembly was polished by iCORN2 (Otto *et al.*, 2010). Genome annotation was conducted by the

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Table 1. Genome features of *Streptococcus gordonii* KCOM 1506

Attribute	Value
Genome size (bp)	2,283,306
GC content (%)	40.6
No. of contigs	1
Total genes	2,270
Protein-coding genes	2,129
tRNA	82
rRNA (5S, 16S, 23S)	15 (5, 5, 5)
ncRNA	3
Pseudogene	41

NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (https://www.ncbi.nlm.nih.gov/genome/annotation_prok/).

The complete genome of *S. gordonii* KCOM 1506 is 2,283,306 bp in length and has a G+C content of 40.6% (Table 1). A total of 2,129 protein-coding sequences (CDSs), 15 rRNAs, and 82 tRNAs were annotated (Table 1). The genome sequence contained virulence factors such as hemolysin, toxin A, antitoxin HipB, antiseptic resistance protein, T surface-antigen of pili, staphylococcal secretory antigen SsaA precursor, antirestriction protein (ArdA), zinc metalloproteases, penicillinase repressor, and macrolide export ATP-binding/permease protein MacB. The genome contained oxidative stress-response genes, superoxide dismutase and glutaredoxin-like protein NrdH, bacteriocin class IIc cyclic gassericin A-like protein, and antilisterial bacteriocin subtilisin biosynthesis protein AlbE. The complete genome included genes responsible for biofilm formation, glycosyltransferase EpsE, glycosyltransferase-stabilizing protein Gtf2, glycosyltransferase Gtf1, and AI-2 transport protein TqsA. The genome also contained Type II secretion system protein E/F, the nine two-component systems (VicK/VicR, SaeS/SaeR, CiaH/CiaR, LiaS/LiaR, Ihk/Irr, NisK/NisR, AgrC/AgrA, ComD/ComE, and YesM/YesN), one unmatched sensor histidine kinase (DskK). ESX-1 secretion system protein EccCa1.

Nucleotide sequence accession number

This whole genome sequence was deposited in GenBank under accession number NZ_CP012648.

적 요

*Streptococcus gordonii*는 그람 양성이며, 통성 혐기성.

및 비운동성 구균이다. *S. gordonii*는 사람의 구강 내 정상세균총의 하나이고, 치면 생체막 형성의 선구적 세균 종이다. *S. gordonii*는 감염성 심내막염과 패혈성관절염 뿐만 아니라 유치의 치수염에 연관이 있다. *S. gordonii* KCOM 1506 (= ChDC B679) 균주가 사람 급성치수염 병소에서 분리되었으며 그 유전체 염기서열을 해독하여 보고한다.

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