

Note (Genome Announcement)

Complete genome sequence of *Streptococcus mitis* KCOM 1350 isolated from a human mandibular osteomyelitis lesion

Soon-Nang Park^{1†}, Yun Kyong Lim^{1†}, Ja Young Shin², Hanseong Roh², and Joong-Ki Kook^{1,3*}

¹Korean Collection for Oral Microbiology and Department of Oral Biochemistry, School of Dentistry, Chosun University, Gwangju 61452, Republic of Korea

²Macrogen Inc., Seoul 08511, Republic of Korea

³Oral Biology Research Institute, Chosun University, Gwangju 61452, Republic of Korea

사람 하악 골수염 병소에서 분리된 *Streptococcus mitis* KCOM 1350의 유전체 염기서열 해독

박순남^{1†} · 임윤경^{1†} · 신자영² · 노한성² · 국중기^{1,3*}

¹조선대학교 치과대학 구강생화학교실 및 한국구강미생물자원은행, ²마크로젠, ³조선대학교 구강생물학연구소

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Streptococcus mitis is a Gram-positive, facultative anaerobic, alpha-hemolytic, and nonmotile cocci. *S. mitis* is a viridans streptococci and a normal commensal of throat, nasopharynx, and mouse and is associated with infective endocarditis, septicemia, and meningitis. *S. mitis* KCOM 1350 (= ChDC B183) was isolated from a human mandibular osteomyelitis lesion. Here, we present the complete genome sequence of *S. mitis* KCOM 1350.

Keywords: *Streptococcus mitis*, osteomyelitis

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we present the complete genome sequence of *S. mitis* KCOM 1350.

The *S. mitis* KCOM 1350 was grown in brain heart infusion (BHI, Difco Laboratories) medium supplemented with 0.5% yeast extract, 0.05% cysteine HCl-H₂O, 0.5 mg/ml of hemin, 2 µg/ml of vitamin K₁, and 5% sheep blood in an anaerobic chamber (Model Bactron I) was maintained using a gas mixture of 10% H₂, 5% CO₂, and 85% N₂ (Park *et al.*, 2013). The bacterial genomic DNA was prepared as described previously and 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. mitis* KCOM 1350 was sequenced by the Illumina HiSeq 2000 platform by Macrogen Inc. (Korea). Two libraries of 350 bp paired-end and 5 kb mate-pair was sequenced which reached coverage of 2,894X and 257X, respectively. The de novo assembly was performed by ALLPATHS-LG (Gnerre *et al.*, 2011) which produced one circular large scaffold and 7 tiny scaffolds. All 45 gaps among the scaffolds were filled by GapCloser (Luo *et al.*, 2012; <http://sourceforge.net/>)

[†]These authors contributed equally to this work.

*For correspondence. E-mail: jkook@chosun.ac.kr;
Tel.: +82-62-230-6877; Fax: +82-62-224-3706

Table 1. Genome features of *Streptococcus mitis* KCOM 1350

Attribute	Value
Genome size (bp)	1,906,344
GC content (%)	40.2
No. of contigs	1
Total genes	1,934
Protein-coding genes	1,792
tRNA	46
rRNA (5S, 16S, 23S)	9 (3, 3, 3)
ncRNA	3
Pseudogene	84

projects/soapdenovo2/files/GapCloser). And we confirmed the 7 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 NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (https://www.ncbi.nlm.nih.gov/genome/annotation_prok/).

The complete genome of *S. mitis* KCOM 1350 is 1,906,344 bp in length and has a G + C content of 40.2% (Table 1). A total of 1,792 protein-coding sequences (CDSs), 9 rRNAs, and 46 tRNAs were annotated (Table 1). The genome contained virulence factors such as multidrug export protein MepA, multidrug resistance protein NorM, multidrug resistance ABC transport ATP-binding/permease protein YheI, macrolide export ATP-binding/permease protein MacB, toxin A, toxin B, toxin RelK, toxin-antitoxin biofilm protein TabA, autolysin, IgA protease, zinc metalloprotease, capsule biosynthesis protein CapA, capsule synthesis positive regulator AcpA, and hemolysin A. The genome contained oxidative stress-response genes such as superoxide dismutase, glutathione peroxidase, thiol peroxidase, thioredoxin, thioredoxin reductase, and glutaredoxin. The genome also contained bacteriocin (Lactococcin_972), type II secretion system protein E/F, type II secretory pathway pseudopilin, lactococcin A secretion protein LcnD, and the eleven two-component systems. The *Streptococcus mitis* KCOM 1350 strain was deposited in the Korean Collection for Oral Microbiology.

Nucleotide sequence accession number

This whole genome sequence was deposited in GenBank under accession number NZ_CP012646.

적 요

*Streptococcus mitis*는 그람 양성이며, 통성 혐기성, 알파-용혈성 및 비운동성 구균이다. *S. mitis*는 인후, 비인두 및 구강 내 정상 세균총의 하나이고, 감염성 심내막염, 폐혈증 및 뇌수막염과 연관이 있다. KCOM 1350 (= ChDC B183) 균주가 사 람 하악골 골수염 병소에서 분리되었다. *S. mitis* KCOM 1350 균주 유전체 염기서열을 해독하여 보고한다.

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