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Note (Genome Announcement)

# Complete genome sequence of *Streptococcus intermedius* ChDC B718 isolated from a human pulpitis lesion

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# 사람 치수염 병소에서 분리된 *Streptococcus intermedius* ChDC B718의 유전체 염기서열 해독

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*Streptococcus intermedius* is a Gram-positive, obligately anaerobic, nonsporeforming, and nonmotile cocci. *S. intermedius* is a member of oral flora and is endodontic infection, respiratory infections, infective endocarditis, brain abscess, and liver abscess. *Streptococcus intermedius* ChDC B718 (= KCOM 1545) was isolated from a human pulpitis lesion. Here, we present the complete genome sequence of *S. intermedius* ChDC B718.

**Keywords:** *Streptococcus intermedius*, human, pulpitis

*Streptococcus intermedius* is a Gram-positive, obligately anaerobic, nonsporeforming, and nonmotile cocci (Whiley and Beighton, 1991). *S. intermedius* is a member of oral flora and is associated with endodontic infection (Heimdahl *et al.*, 1985; Ledezma-Rasillo *et al.*, 2010; Matsui *et al.*, 2014), cervical facet joint infection and associated epidural abscess (Gomez *et al.*, 2015; Kaye and Protopsaltis, 2016), liver abscess (Ioannou *et al.*, 2016), brain abscess (Basyuni *et al.*, 2015; Yakut *et al.*, 2015), respiratory infections (Noguchi *et al.*, 2014, 2015), infective endocarditis (Tran *et al.*, 2008). *S. intermedius* ChDC B718 (= KCOM 1545) was isolated from a human pulpitis lesion. In this report, we present the complete genome sequence of *S. intermedius* ChDC B718.

The *S. intermedius* KCOM 1545 was grown on brain heart infusion (BHI, Difco Lab.) medium supplemented with 0.5% yeast extract, 0.05% cysteine HCl-$H_2O$, 0.5 mg/ml of hemin, 2 μg/ml of vitamin $K_1$, and 5% sheep blood in anaerobic atmosphere (10% $H_2$, 5% $CO_2$, and 85% $N_2$). 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. intermedius* KCOM 1545 was sequenced by the Illumina Hiseq 2000 platform. The library of 5 kb mate-pair was sequenced which reached coverage of 2,276X. The *de novo* assembly was performed by ALLPATHS-LG (Gnerre *et al.*, 2011) which produced one circular large

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scaffold and 3 tiny scaffolds. All 23 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 NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (https://www.ncbi.nlm.nih.gov/genome/annotation_prok/).

The complete genome of *S. intermedius* KCOM 1545 is 1,908,201 bp in length and has a G+C content of 37.6% (Table 1). A total of 1,746 protein-coding sequences (CDSs), 6 rRNAs, and 67 tRNAs were annotated (Table 1). The genome sequence contained virulence factors such as sialidase, multidrug resistance ABC transporter ATP-binding/permease protein YheH/ YheI, multidrug resistance-like ATP-binding protein MdlB, multiple antibiotic resistance protein MarA/EmrY/Bmr3/NorM/MdlT, tetracycline resistance protein TetM from transposon TnFO1, lantibiotic streptin immunity protein, ATP-dependent zinc metalloprotease FtsH, serine protease Do-like HtrA, zinc protease AlbF, capsular polysaccharide type 8 biosynthesis protein cap8A, and hemolysin A. The genome contained bacteriocin, bacteriocin class II with double-glycine leader peptide, antilisterial bacteriocin subtilosin biosynthesis protein AlbE, class IIc cyclic gassericin A-like protein, and oxidative stress-response genes such as superoxide dismutase, Glutathione reductase, Ferredoxin--NADP reductase 2, and glutathione peroxidase homolog BsaA, NADPH-dependent FMN reductase, oxidoreductase YcjS, NAD(P)H nitroreductase, thioredoxin reductase, and glutaredoxin-like protein NrdH. The complete genome encodes for involving the biofilm formation, glycosyltransferase CsbB, glycosyltransferase EpsE/EpsD/EpsH, fibronectin-binding protein A, biofilm regulatory protein A (BrpA), AI-2 transport protein TqsA, toxin A, and toxin-antitoxin biofilm protein TabA. It also contained type II secretion system protein E/F, Protein translocase subunit SecY/SecE/SecG/SecA, ESX-1 secretion system protein EccCa1, the eight two-component systems (AgrC/AgrA, ComD/ComE, CiaH/CiaR, Ihk/Irr, LiaS/LiaR, SaeS/SaeR, VicK/VicR, and YesM/YesN), and one unmatched sensor histidine kinase (DskK).

**Table 1. Genome features of *Streptococcus intermedius* ChDC B718 (= KCOM 1545)**

| Attribute | Value |
|---|---|
| Genome size (bp) | 1,908,201 |
| GC content (%) | 37.6 |
| No. of contigs | 1 |
| Total genes | 1,851 |
| Protein-coding genes | 1,746 |
| tRNA | 67 |
| rRNA (5S, 16S, 23S) | 6 (2, 2, 2) |
| ncRNA | 1 |
| Pseudogene | 67 |

## Nucleotide sequence accession number

This whole genome sequence was deposited in GenBank under accession number CP012718.

## 적 요

*Streptococcus intermedius*는 그람 양성이면서, 통성 혐기성, 비스포아형성 및 운동성 구균이다. *S. intermedius*는 사람의 구강 내 정상세균총의 하나이고, 치근관 감염, 호흡기 감염, 감염성 심내막염, 뇌 낭종 및 간 낭종이 있다. *S. intermedius* ChDC B718 (= KCOM 1545) 균주가 사람 치수염 병소에서 분리되었다. *S. intermedius* KCOM 1545 균주 유전체 염기서열을 해독하여 보고한다.

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