

Draft genome sequence of *Streptococcus constellatus* KCOM 1039 isolated from human postoperative maxillary cyst lesion




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사람 수술후 상악낭종 병소에서 분리된 *Streptococcus constellatus* KCOM 1039의 유전체 염기서열 완전 해독

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Streptococcus constellatus is Gram-stain-positive, facultative anaerobic, and non-spore forming coccus. It is a member of normal flora of human oral cavity. *S. constellatus* KCOM 1039 was isolated from human postoperative maxillary cyst lesion. In this report, we present the draft genome sequence of *S. constellatus* KCOM 1039.

Keywords: *Streptococcus constellatus*, human, postoperative maxillary cyst

Streptococcus constellatus is Gram-stain-positive, facultative anaerobic, and non-spore forming coccus which are round to slightly oval and occur in pairs and short chain (Whiley *et al.*, 1999). It showed beta-hemolytic activity and produced a streptolysin S-like protein (Tabata *et al.*, 2014). The bacterium is primarily inhabits the human oral cavity and is considered to be an opportunistic human pathogen (Tabata *et al.*, 2014). *S. constellatus* KCOM 1039 (= ChDC B280) was isolated from

human periodontitis lesion. In this report, we presented the draft genome sequence of *S. constellatus* KCOM 1039.

S. constellatus KCOM 1039 was grown in brain heart infusion (BHI, Difco Laboratories) medium in an anaerobic chamber (Model Bactron I) maintained using a gas mixture of 10% H₂, 5% CO₂, and 85% N₂. Genomic DNA of *S. constellatus* KCOM 1039 was prepared as previously described (Cho *et al.*, 2015).

Genomic DNA of *S. constellatus* KCOM 1039 was sequenced using the Illumina Hiseq 2000 platform by Macrogen Inc. Three libraries of 350 bp paired-end, 5 kb mate-pair, and 8 kb mate-pair were sequenced which reached coverage of 657.0 ×, 646.2 ×, and 955.7 ×, respectively. The *de novo* assembly was performed by SPAdes (<http://bioinf.spbau.ru/spades>) (Bankevich *et al.*, 2012). All gaps among the scaffolds were filled by GapCloser (<http://soap.genomics.org.cn/soapdenovo.html>) (Luo *et al.*, 2012). Error correction was performed by Pilon (<https://github.com/broadinstitute/pilon/wiki>) (Walker *et al.*, 2014). Genome annotation was conducted by the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (https://www.ncbi.nlm.nih.gov/genome/annotation_prok/) (Tatusova *et al.*, 2016).

The draft genome of *S. constellatus* KCOM 1039 was

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Table 1. Genome features of *Streptococcus constellatus* KCOM 1039

Attribute	Value
Genome size (bp)	1,885,802
GC content (%)	38.0
No. of contigs	2
Total genes	1,898
Protein-coding genes	1,730
tRNA	58
Complete rRNA (5S, 16S, 23S)	9 (3,3,3)
ncRNA	3
Pseudogene	97

composed of 2 contigs; 1,883,587 bp and 2,215 bp in length. The average G+C content of the genome was 38.0%. A total of 1,730 protein-coding sequences, 9 complete rRNA operons (3 5S rRNAs, 3 16S rRNAs, and 3 23 rRNAs), 58 tRNAs, and 3 ncRNAs were identified (Table 1).

In the genome, genes involved in proteinase were identified; putative protease YdcP/YdeA, protease HtpX, ATP-dependent zinc metalloprotease FtsH, putative zinc metalloprotease, Lon protease, rhomboid protease GluP, serine protease Do-like HtrA, and putative zinc protease AlbF. It also contained antibiotic-resistance-related genes; multiple antibiotic resistance protein MarA/MarR, daunorubicin/doxorubicin resistance ATP-binding protein DrrA, putative multidrug resistance ABC transporter ATP-binding/permease protein YheI/YheH, multidrug resistance protein NorM, and tetracycline resistance protein TetM from transposon TnFO1. It also contained biofilm formation-related genes; toxin-antitoxin biofilm protein TabA, putative glycosyl-transferase EpsH/EpsJ/CsbB, biofilm regulatory protein A, and D-inositol-3-phosphate glycosyltransferase. It also contained type II secretion system protein F, protein translocase subunit SecA/SecY, and ESAT-6 secretion accessory factor EsaA. The genome also contained the oxidative stress-response genes; glutathione reductase and thioredoxin reductase. Hemolysin A and diphtheria toxin repressor were also found in the genome sequence.

The *S. constellatus* KCOM 1039 strain was deposited into the Korean Collection for Oral Microbiology.

Nucleotide sequence accession number

This whole genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession QWKV00000000. The version described in this paper is version QWKV00000000.

적 요

*Streptococcus constellatus*는 그람 염색에 양성을 띄며, 조건 혐기성이면서 아포를 생성하지 않는 구균이다. *S. constellatus*는 사람 구강의 정상 세균 총에 속한다. 수술후 상악낭종 병소에서 *S. constellatus* KCOM 1039 균주가 분리되었다. 여기에서 *S. constellatus* KCOM 1039 균주의 유전체 염기서열을 결정하여 보고한다.

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