

## Draft genome sequence of *Dialister pneumosintes* KCOM 1685 isolated from a human postoperative maxillary cyst lesion

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## 사람 수술후상악낭종 병소에서 분리된 *Dialister pneumosintes* KCOM 1685의 유전체 염기서열 해독

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*Dialister pneumosintes* is a Gram-staining-negative, anaerobic, non-fermenting, and rod-shaped bacterium. *D. pneumosintes* is considered to be a periodontal pathogen. *D. pneumosintes* KCOM 1685 (= ChDC B414) was isolated from a human postoperative maxillary cyst lesion. In this report, we present the draft genome sequence of *D. pneumosintes* KCOM 1685.

**Keywords:** *Dialister pneumosintes*, human, postoperative maxillary cyst

*Dialister pneumosintes* is a Gram-stain-negative, anaerobic, non-fermenting, nonsporulating, non-motile, and rod-shaped bacterium. It forms transparent, entire, circular, smooth, clear, shiny, and convex colonies on blood agar (Doan *et al.*, 2000). The bacterium is considered to be a periodontal pathogen (Ghayoumi *et al.*, 2002). *D. pneumosintes* KCOM 1685 (= ChDC B414) was isolated from a human periodontitis lesion. In this report, we present the draft genome sequence of *D.*

*pneumosintes* KCOM 1685.

*D. pneumosintes* KCOM 1685 was grown in brain heart infusion (BHI, Difco Laboratories) medium supplemented with 0.5% yeast extract, 0.05% cysteine HCl-H<sub>2</sub>O, 0.5 mg/ml of hemin, 2 µg/ml of vitamin K<sub>1</sub>, and 5% sheep blood in an anaerobic chamber (Model Bactron I) maintained using a gas mixture of 10% H<sub>2</sub>, 5% CO<sub>2</sub>, and 85% N<sub>2</sub> (Park *et al.*, 2013). Genomic DNA of *D. pneumosintes* KCOM 1685 was prepared as previously described (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 *D. pneumosintes* KCOM 1685 was sequenced using the Illumina HiSeq 2000 platform by Macrogen Inc. Tree libraries of 350 bp paired-end, 5 kb mate-pair, and 8 kb mate-pair were sequenced which reached coverage of 1,466.7 ×, 1,752.7 ×, and 1,407.3 ×, 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

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(<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/](https://www.ncbi.nlm.nih.gov/genome/annotation_prok/)) (Tatusova *et al.*, 2016).

The draft genome of *D. pneumosintes* KCOM 1685 was composed of 3 contigs; 1,244,600 bp, 1,438 bp, and 1,369 bp in length. The average G+C content of the draft genome was 35.2%. A total of 1,154 protein-coding sequences (CDSs), 13 rRNAs, and 50 tRNAs were annotated (Table 1).

The genome sequence contained antibiotic-resistance-related genes; multidrug export ATP-binding/permease protein, multidrug resistance protein MdtC/MdtN/NorM, multidrug export protein MepA, macrolide export ATP-binding/permease protein MacB, and macrolide export protein MacA. It contained several proteinase genes; protease HtpX/YdcP/CtpB, lon protease 1/2, modulator of FtsH protease HflK, putative protease YdcP, ATP-dependent zinc metalloprotease FtsH, and metalloprotease MmpA. Biofilm formation-related genes toxin PezT, toxin-antitoxin biofilm protein TabA, putative glycosyltransferase EpsJ, putative peptidoglycan glycosyltransferase FtsW, and peptidoglycan glycosyltransferase MrdB were also found in the genome sequence. It contained type II secretion system protein G, putative type II secretion system protein E/F, and protein translocase subunit SecA/SecY/SecE. The genome also contained the oxidative stress-response gene, thioredoxin reductase. The genome contained the one two-component system, pdtaS/pdtaR.

The *D. pneumosintes* KCOM 1685 strain was deposited into the Korean Collection for Oral Microbiology.

**Table 1.** Genome features of *Dialister pneumosintes* KCOM 1685

Attribute	Value
Genome size (bp)	1,247,407
GC content (%)	35.2
No. of contig	3
Total genes	1,230
Protein-coding genes	1,154
tRNA	50
Complete rRNA (5S, 16S, 23S)	13 (5,4,4)
ncRNA	3
Pseudogene	9
CRISPR arrays	1

## Nucleotide sequence accession number

This whole genome sequence has been deposited at DDBJ/ENA/GenBank under the accession QWKU00000000. The version described in this paper is version QWKU01000000.

## 적 요

*Dialister pneumosintes*는 그람 음성이며, 혐기성, 비발효성 및 막대 모양의 세균이다. *D. pneumosintes*는 치주질환병원성세균으로 알려져 있다. *D. pneumosintes* KCOM 1685 (= ChDC B414) 균주가 수술후상악동낭종 병소에서 분리되었다. *D. pneumosintes* KCOM 1685 균주 유전체 염기서열을 해독하여 보고한다.

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