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Note (Genome Announcement)

Complete genome sequence of *Cutibacterium acnes* KCOM 1861 isolated from a human jaw osteomyelitis lesion

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사람 악골 골수염에서 분리된 *Cutibacterium acnes* KCOM 1861의 유전체 염기서열 해독

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Cutibacterium acnes (formerly *Propionibacterium acnes*) is an anaerobic, Gram-positive rod and that is a normal flora of human skin and mucosal surface as well as an opportunistic pathogen related to acnes vulgaris, sarcoidosis, brain abscess, endocarditis, periodontitis, and endodontic infections. *C. acnes* KCOM 1861 (= ChDC B594) was isolated from a human jaw osteomyelitis lesion. Here, we present the complete genome sequence of *C. acnes* KCOM 1861.

Keywords: *Cutibacterium acnes*, human, jaw osteomyelitis

Cutibacterium acnes (formerly *Propionibacterium acnes*) is an anaerobic, Gram-positive rod that forms part of normal microbiota on oral cavity, skin, external ear canal, large intestine, and conjunctiva (McDowell *et al*., 2013; Niazi *et al*., 2016; Scholz and Kilian, 2016; Aubin *et al*., 2017). It has been reported that *C. acnes* was identified as an opportunistic pathogen related to acnes vulgaris (Leyden, 2001), sarcoidosis (Eishi *et al*., 2002), brain abscess (Mathisen *et al*., 1984), endocarditis (Gunthard *et al*., 1994), periodontitis (Handal *et al*., 2004), and endodontic infections (Lee *et al*., 2005; Niazi *et al*., 2016). *C. acnes* KCOM 1861 (= ChDC B594) was isolated from a human jaw osteomyelitis lesion. In this report, we present the complete genome sequence of *C. acnes* KCOM 1861.

The *C. acnes* KCOM 1861 was grown at 37°C on tryptic soy broth (TSB, Difco) 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 DNAs were prepared using a G-spin™ Genomic DNA Extraction kit (iNtRON Co.) according to the manufacturer's instructions. The DNA concentrations were determined by UV-spectrophotometry (Ultrospec 2000, Pharmacia Biotech.) at wavelengths of 260 nm and 280 nm.

The genomic DNA of *C. acnes* KCOM 1861 was sequenced by the Illumina Hiseq 2,000 platform. *De novo* assembly was performed by ALLPATHS-LG (Gnerre *et al*., 2011) which

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produced one circular large scaffold and 4 tiny scaffolds. All 27 gaps among the scaffolds were filled by GapCloser (Luo *et al*., 2012; http://sourceforge.net/projects/soapdenovo2/files/GapCloser). And we confirmed that the 4 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 *C. acnes* KCOM 1861 is 2,522,438 bp in length and has a G+C content of 60% (Table 1). A total of 2,436 protein-coding sequences (CDSs), 18 rRNAs, and 45 tRNAs were annotated (Table 1). The genome sequence contained virulence factors such as beta-lactamase, macrolide export ATP-binding/permease protein MacB, ATP-dependent zinc metalloprotease FtsH, zinc metalloprotease Rip1, vancomycin high temperature exclusion protein, multiple antibiotic resistance protein MarR, cephalosporin-C deacetylase, outer membrane porin F precursor, hemolysin C, antitoxin/MT0933, antitoxin YqcF, diphtheria toxin repressor, and Christie-Atkins-Much-Petersen (CAMP) factor (Cfa). The complete genome included genes responsible for the biosynthesis of biofilm, such as glycosyltransferase Gtf1, glycosyltransferase EpsJ, and biofilm regulatory protein A precursor. The genome contained oxidative stress-response genes such as superoxide dismutase, thiol peroxidase, thioredoxin-2, thoredoxin reductase, and catalase. The genome also contained bacterial type II secretion system protein F domain protein, the nine two-component systems, one unmatched DNA-binding response regulator, and one unmatched sensor histidine kinase. This complete genome is informative for comparative genome analysis of *C. acnes*.

Table 1. Genome features of *Cutibacterium acnes* KCOM 1861

Attribute	Value
Genome size (bp)	2,522,438
GC content (%)	60.0
No. of contigs	1
Total genes	2,502
Protein-coding genes	2,277
tRNA	45
rRNA (5S, 16S, 23S)	18 (6, 6, 6)
ncRNA	3
Pseudogene	159

Nucleotide sequence accession number

This whole genome sequence was deposited in GenBank under accession number NZ_CP012647.

적 요

Cutibacterium acnes (이전 학명 = *Propionibacterium acnes*)은 혐기성, 그람 양성 간균으로 사람 피부 및 점막조직 표면의 정상 세균총에 해당할 뿐만 아니라 여드름, 유육종증, 뇌종양, 심내막염, 전립선암, 치주질환 및 치수감염질환과도 연관성이 있는 것으로 보고되고 있다. *C. acnes* KCOM 1861 (= ChDC B594) 균주가 사람 악골 골수염 병소에서 분리되었으며 그 유전체 염기서열을 해독하여 보고한다.

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