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Complete genome sequence of *Fusobacterium vincentii* KCOM 2931 isolated from a human periodontitis lesion

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사람 치주염 병소에서 분리된 *Fusobacterium vincentii* KCOM 2931의 유전체 염기서열 해독

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Recently, *Fusobacterium nucleatum* subsp. *vincentii* was reclassified as *Fusobacterium vincentii* based on the average nucleotide identity and genome-to-genome distance analyses. *F. vincentii* is a Gram-negative, anaerobic, and filament-shaped bacterium. *F. vincentii* is a member of normal flora of human oral cavity and plays a role in periodontal diseases. *F. vincentii* KCOM 2931 was isolated from a periodontitis lesion. Here, we present the complete genome sequence of *F. vincentii* KCOM 2931.

Keywords: *Fusobacterium vincentii*, human, periodontitis

Fusobacterium nucleatum subsp. *vincentii* was classified as one of four or five subspecies of *F. nucleatum* by DNA-DNA hybridization (DDH) and polyacrylamide gel electrophoresis (PAGE) protein pattern of whole-cell proteins (Dzink *et al*., 1990). *F. nucleatum* subsp. *vincentii* and *F. nucleatum* subsp. *fusiforme* were combined as the same subspecies named *F. nucleatum* subsp. *vincentii* by multilocus sequence analysis (MLSA) using a single sequence (24,715 bp) of 22 concatenated housekeeping genes (Kook *et al*., 2013). Recently, *F. nucleatum* subsp. *vincentii* was reclassified as *Fusobacterium vincentii* based on the average nucleotide identity and genome-to-genome distance analyses (Kook *et al*., 2017). *F. vincentii* is a Gram-negative, anaerobic, and filament-shaped bacterium (Strauss *et al*., 2008). *F. vincentii* is a member of normal flora of human oral cavity and plays a role in periodontal diseases (Haffajee and Socransky, 1994; Han, 2015). *F. vincentii* might scavenge oxygen and oxidative free radicals from dental plaque (Diaz *et al*., 2002). *F. vincentii* produces butyric acid that irritates the fibroblast of the gingiva (Han *et al*., 2000). *F. vincentii* KCOM 2931 was isolated from a human subgingival plaque of gingivitis lesion. In this report, we present the complete genome sequence of *F. vincentii* KCOM 2931.

The *F. vincentii* KCOM 2931 was grown in brain heart infusion (BHI, Difco Laboratories) 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 an

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anaerobic chamber (Model Bactron I) was maintained using a gas mixture of 10% H_2, 5% CO_2, and 85% N_2 (Park *et al*., 2013). The bacterial genomic DNA was prepared as described previously (Cho *et al*., 2015).

The genomic DNA of *F. vincentii* KCOM 2931 was sequenced using PacBio RSII SMRT sequencing platform using a 20 kb SMRTbell template library and Illumina HiSeq platform with 100 × 2 bp reads using 350 bp insert size library by Macrogen Inc. Approximately 975 Mb (467 ×) with 131,626 reads and 7,406 bp of mean subreads length and 967 Mb (463 ×) with 9,573,156 reads were generated from the PacBio and Illumina HiSeq sequencing, respectively. The *de novo* assembly was performed by RS HGAP (version: 3.0) in PacBio's SMRT portal with the subreads from PacBio (http://www.pacb.com/products-and-services/analytical-software/smrt-analysis). After assembly, the resulting contigs were polished by Pilon (version: 1.21) with the Paired-end reads from Illumina HiSeq 2500 (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/).

The complete genome of *F. vincentii* KCOM 2931 is 2,087,706 bp in length and has a G + C content of 27.2% (Table 1). A total of 1,885 protein-coding sequences (CDSs), 15 rRNAs, and 47 tRNAs were annotated (Table 1). The genome sequence contained virulence factors such as ATP-dependent zinc metalloprotease FtsH, putative cysteine protease YraA, putative protease YdcP, extracellular serine protease, protease HtpX, hemolysin A, hemolysin transporter protein ShlB, sialic acid TRAP transporter permease protein SiaT, sialic acid-binding periplasmic protein SiaP, outer membrane porin F, putative antitoxin YwqK/HigA/YefM, toxin YoeB/RelG, toxin-antitoxin biofilm protein TabA, putative multidrug export ATP-binding/permease protein, multidrug export ATP-binding/permease protein, multidrug export protein MepA, beta-lactamase, macrolide export protein MacA, macrolide export ATP-binding/permease protein MacC, and AI-2 transport protein TqsA. The genome contained SPBc2 prophage-derived glycosyltransferase SunS and phage-like element PBSX protein XkdM. It also contained type II secretion system protein D/E/F and protein translocase subunit SecA/SecE/SecY.

The genome also contained the oxidative stress-response genes such as anaerobic nitric oxide reductase, peptide methionine sulfoxide reductase MsrA, thioredoxin reductase, and thiol-disulfide oxidoreductase ResA. The genome contained the four two-component systems (YpdA/YpdB and YehU/putative response regulatory protein).

Table 1. Genome features of *Fusobacterium vincentii* KCOM 2931

Attribute	Value
Genome size (bp)	2,087,706
GC content (%)	27.2
No. of contigs	1
Total genes	2,027
Protein-coding genes	1,885
tRNA	47
Complete rRNA (5S, 16S, 23S)	15 (5, 5, 5)
ncRNA	3
Pseudogene	77

The *F. vincentii* KCOM 2931 strain was deposited in 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 NZ_CP024749. The version described in this paper is version NZ_CP024749.1

적 요

최근 *Fusobacterium nucleatum* subsp. *vincentii*는 average nucleotide identity 및 genome-to-genome distance 분석법에 의해 *Fusobacterium vincentii*로 재분류 되었다. *F. vincentii*는 그람 음성이면서, 혐기성 및 가는 섬유 모양의 세균이다. *F. vincentii*는 사람의 구강 내 정상세균총의 하나이고, 치주질환에 중요한 역할을 한다. *F. vincentii* KCOM 2931 균주가 사람 치주염 병소에서 분리되었다. *F. vincentii* KCOM 2931 균주 유전체 염기서열을 해독하여 보고한다.

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