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Note (Genome Announcement)

Complete genome sequence of *Fusobacterium nucleatum* KCOM 1323 isolated from a human subgingival plaque of periodontitis lesion

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사람 치주질환병소의 치은연하지면세균막에서 분리된 *Fusobacterium nucleatum* KCOM 1323의 유전체 염기서열 해독

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Fusobacterium nucleatum is a Gram-negative, obligately anaerobic and rod- or filament-shaped bacterium. *F. nucleatum* is part of oral microflora and is a causative agent of periodontitis as well as is associated with a wide spectrum of systemic diseases of human. *F. nucleatum* KCOM 1323 (= ChDC F317) was isolated from a human subgingival plaque of periodontitis lesion. Here, we present the complete genome sequence of *F. nucleatum* KCOM 1323.

Keywords: *Fusobacterium nucleatum*, periodontitis

Fusobacterium nucleatum Gram-negative, obligately anaerobic and rod- or filament-shaped bacterium (Strauss *et al*., 2008). *F. nucleatum* is part of oral microflora and is a causative agent of periodontitis as well as is associated with preterm birth, colorectal cancer, inflammatory bowel disease, respiratory tract infections, cardiovascular disease, rheumatoid arthritis, and Alzheimer's disease (Haffajee and Socransky, 1994; Han, 2015). *F. nucleatum* KCOM 1323 (= ChDC F317) was isolated from a human subgingival plaque of periodontitis lesion. In this report, we present the complete genome sequence of *F. nucleatum* KCOM 1323.

The *F. nucleatum* KCOM 1323 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 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 and 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 *F. nucleatum* KCOM 1323 was sequenced using the Illumina Hiseq 2000 platform by Macrogen Inc.. The library of 5 kb mate-pair was sequenced which reached coverage of 1,769X. The *de novo* assembly was performed by SPAdes (version: 3.8.2) (Bankevich *et al*., 2012) and AlignGraph (Bao *et al*., 2014). All gaps among the scaffolds were filled by

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GapCloser (Luo *et al*., 2012; http://sourceforge.net/projects/soapdenovo2/files/GapCloser). And we confirmed the 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 *F. nucleatum* KCOM 1323 is 2,233,010 bp in length and has a G + C content of 27.1% (Table 1). A total of 2,017 protein-coding sequences (CDSs), 12 rRNAs, and 45 tRNAs were annotated (Table 1). The genome sequence contained virulence factors such as hemolysin A, hemolysin transporter protein ShlB, butyrate fermentation-related genes, papain family cysteine protease, serine protease, metalloprotease LoiP, zinc metalloprotease, Carbapenem-hydrolyzing beta-lactamase Sme-1, sialic acid-binding periplasmic protein SiaP, sialic acid TRAP transporter permease protein SiaT, multidrug resistance protein MexA/MdtK/MdtC/NorM, Multidrug export protein MepA, putative multidrug export ATP-binding/permease protein, macrolide export ATP-binding/permease protein MacB, outer membrane porin F, and transport protein TonB. The genome contained phage portal protein, phage tail sheath protein, phage-like element PBSX protein XkdM, phage-related minor tail protein, SPBc2 prophage-derived glycosyltransferase SunS, and oxidative stress-response genes such as, glutathione peroxidase homolog BsaA, nitric oxide reductase NADPH-dependent FMN reductase, light-independent protochlorophyllide reductase subunit B, thioredoxin reductase, nitroreductase A, peptide methionine sulfoxide reductase MsrA/MsrB, glutaredoxin, and putative oxidoreductase. The complete genome encodes for involving the biofilm formation, toxin-antitoxin biofilm protein TabA, fibronectin-binding protein A, and autoinducer-2 (AI-2) modifying protein LsrG. It also contained type II secretion system protein D/E/F/G, protein translocase subunit SecA/SecD/SecE/SecY, preprotein translocase subunit YajC, the three two-component systems (PdtaS/PdtaR, YpdA/YpdB, and YehR/putative response regulatory protein), and seven unmatched response regulatory proteins (MgsR, PmpR, TenI, GabR, ZraR, PhlP, and RecX).

The genome also contained the oxidative stress-response genes such as glutathione peroxidase, glutaredoxin, NADH oxidase, and rubrerythrin (confers superoxide dismutase-like activity). The genome contained the four two-component systems and one unmatched sensor histidine kinase. The *Fusobacterium nucleatum* KCOM 1323 strain was deposited in the Korean Collection for Oral Microbiology.

Table 1. Genome features of *Fusobacterium nucleatum* KCOM 1323

Attribute	Value
Genome size (bp)	2,233,010
GC content (%)	27.1
No. of contigs	1
Total genes	2,173
Protein-coding genes	2,017
tRNA	45
rRNA (5S, 16S, 23S)	12 (8, 2, 2)
ncRNA	3
Pseudogene	96

Nucleotide sequence accession number

This whole genome sequence was deposited in GenBank under accession number CP022122.

적 요

*Fusobacterium nucleatum*는 그람 음성이면서, 절대 혐기성 및 막대 또는 가는 섬유 모양의 세균이다. *F. nucleatum*는 사람의 구강 내 정상세균총의 하나이고, 치주질환의 원인인자이면서 다양한 전신질환과도 연관성이 있다. *F. nucleatum* KCOM 1323 (= ChDC F317) 균주가 사람 치주질환 병소의 치은연하 치면세균막에서 분리되었다. *F. nucleatum* KCOM 1323 균주 유전체 염기서열을 해독하여 보고한다.

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