

Note (Genome Announcement)

Draft genome sequence of *Prevotella intermedia* KCOM 1107 isolated from a human subgingival dental plaque of gingivitis lesion

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사람 치은염 병소의 치은연하치면세균막에서 분리된 *Prevotella intermedia* KCOM 1107의 유전체 염기서열 해독

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Prevotella intermedia is a Gram-negative, obligately anaerobic, nonsporeforming, and nonmotile rod. *P. intermedia* is associated with periodontitis, pregnancy gingivitis, acute necrotic ulcerative gingivitis, endodontic infection, and rheumatoid arthritis. *P. intermedia* KCOM 1107 (= ChDC KB29) was isolated from a human subgingival dental plaque of gingivitis lesion. Here, we present the draft genome sequence of *P. intermedia* KCOM 1107.

Keywords: *Prevotella intermedia*, gingivitis

Prevotella intermedia is a Gram-negative, obligately anaerobic, nonsporeforming, and nonmotile rod (Shah and Collins, 1990). *P. intermedia* is a member of oral flora and is associated with periodontitis, pregnancy gingivitis, acute necrotic ulcerative gingivitis, endodontic infection, and rheumatoid arthritis (Haffajee and Socransky, 1994; Milsom *et al.*, 1996; Okamoto *et al.*, 1999; Papapanou *et al.*, 2000; Moen *et al.*, 2006). *P. intermedia*

KCOM 1107 (= ChDC KB29) was isolated from a human subgingival dental plaque of gingivitis lesion. In this report, we present the draft genome sequence of *P. intermedia* KCOM 1107.

The *P. intermedia* KCOM 1107 was grown in brain heart infusion (BHI, Difco Laboratories) medium supplemented with 0.5% yeast extract, 0.05% cysteine HCl-H₂O, 0.5 mg/ml of hemin, 2 µg/ml of vitamin K₁, and 5% sheep blood in an anaerobic chamber (Model Bactron I) was maintained using a gas mixture of 10% H₂, 5% CO₂, and 85% N₂ (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 *P. intermedia* KCOM 1107 was sequenced using the Illumina HiSeq 2000 platform by Macrogen Inc.. Two libraries of 350 bp paired-end and 5 kb mate-pair was sequenced which reached coverage of 566X and 765X, respectively. The *de novo* assembly was performed by SPAdes (version: 3.8.2) (Bankevich *et al.*, 2012) and AlignGraph (Bao

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et al., 2014). All gaps among the scaffolds were filled by 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 draft genome of *P. intermedia* KCOM 1107 is 2,781,500 bp in length and has a G + C content of 43.2% (Table 1). A total of 2,314 protein-coding sequences (CDSs), 13 rRNAs, and 47 tRNAs were annotated (Table 1). The genome sequence contained virulence factors such as hemolysin secretion protein D, hemolysin C, serine protease, zinc metalloprotease, hemagglutinin A, multidrug resistance protein NorM/MexA/MdtN, multidrug export protein MepA/EmrA, multidrug resistance protein, metallo-beta-lactamase superfamily protein, beta-lactamase HcpC, and extended-spectrum beta-lactamase PER-1. The genome contained bacteriophage Mu Gam like protein, phage-related baseplate assembly protein, phage virion morphogenesis family protein, phage Mu protein F like protein, and oxidative stress-response genes such NAD(P)H nitroreductase and thioredoxin reductase. The draft genome encodes for involving the pheromone autoinducer 2 transporter and glycosyltransferase EpsD/EpsH/EpsJ. It also contained type IV secretion system protein virB4, type IV secretion-system coupling protein DNA-binding domain protein, preprotein translocase subunit SecA/SecE/SecG/SecY, the two two-component systems (YpdA/YehT and YpdA/YehT), three unmatched sensor histidine kinase (TodS, TmoS, and YehU), and three unmatched transcriptional regulatory proteins (AsnC, OmpR, and a putative gene). The

Table 1. Genome features of *Prevotella intermedia* KCOM 1107

Attribute	Value
Genome size (bp)	2,781,500
GC content (%)	43.2
No. of contigs	13
Total genes	2,465
Protein-coding genes	2,314
tRNA	47
rRNA (5S, 16S, 23S)	13 (5, 4, 4)
ncRNA	3
Pseudogene	151

Prevotella intermedia KCOM 1107 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 NHRV00000000. The version described in this paper is version NHRV01000000.

적 요

*Prevotella intermedia*는 그람 음성이면서, 절대 혐기성, 비스포아형성 및 운동성 간균이다. *P. intermedia*는 사람의 구강 내 정상세균총의 하나이며, 치주질환, 임신성 치은염, 급성괴사성괴사성 치은염, 치근관 감염, 및 류마티성 관절염과 관련이 있다. *P. intermedia* KCOM 1107 (= ChDC KB29) 균주가 사람 치은염 병소 치은연하 치면세균막에서 분리되었다. *P. intermedia* KCOM 1107 균주 유전체 염기서열을 해독하여 보고한다.

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References

- Bankevich, A., Nurk, S., Antipov, D., Gurevich, A.A., Dvorkin, M., Kulikov, A.S., Lesin, V.M., Nikolenko, S.I., Pham, S., Prjibelski, A.D., *et al.* 2012. SPAdes: A new genome assembly algorithm and its applications to single-cell sequencing. *J. Comput. Biol.* **19**, 455-477.
- Bao, E., Jiang, T., and Girke, T. 2014. AlignGraph: Algorithm for secondary *de novo* genome assembly guided by closely related references. *Bioinformatics* **30**, i319-i328.
- Cho, E., Park, S.N., Lim, Y.K., Shin, Y., Paek, J., Hwang, C.H., Chang, Y.H., and Kook, J.K. 2015. *Fusobacterium hwasookii* sp. nov., isolated from a human periodontitis lesion. *Curr. Microbiol.* **70**, 169-175.
- Haffajee, A.D. and Socransky, S.S. 1994. Microbial etiological agents of destructive periodontal diseases. *Periodontology 2000* **5**, 78-

- 111.
- Luo, R., Liu, B., Xie, Y., Li, Z., Huang, W., Yuan, J., He, G., Chen, Y., Pan, Q., Liu, Y., et al.** 2012. SOAPdenovo2: An empirically improved memory-efficient short-read *de novo* assembler. *Gigascience* **1**, 18. Erratum in: *Gigascience* 2015. **4**, 30.
- Milson, S.E., Sprague, S.V., Dymock, D., Weightman, A.J., and Wade, W.G.** 1996. Rapid differentiation of *Prevotella intermedia* and *P. nigrescens* by 16S rDNA PCR-RFLP. *J. Med. Microbiol.* **44**, 41–43.
- Moen, K., Brun, J.G., Valen, M., Skartveit, L., Eribe, E.K., Olsen, I., and Jonsson, R.** 2006. Synovial inflammation in active rheumatoid arthritis and psoriatic arthritis facilitates trapping of a variety of oral bacterial DNAs. *Clin. Exp. Rheumatol.* **24**, 656–663.
- Okamoto, M., Maeda, N., Kondo, K., and Leung, K.P.** 1999. Hemolytic and hemagglutinating activities of *Prevotella intermedia* and *Prevotella nigrescens*. *FEMS Microbiol. Lett.* **178**, 299–304.
- Otto, T.D., Sanders, M., Beriman, M., and Newbold, C.** 2010. Iterative correction of reference nucleotides (iCORN) using second generation sequencing technology. *Bioinformatics* **26**, 1704–1707.
- Papapanou, P.N., Neiderud, A.M., Papadimitriou, A., Sandros, J., and Dahlen, G.** 2000. “Checkerboard” assessments of periodontal microbiota and serum antibody responses: a case-control study. *J. Periodontol.* **71**, 885–897.
- Park, S.N., Lim, Y.K., and Kook, J.K.** 2013. Development of quantitative real-time PCR primers for detecting 42 oral bacterial species. *Arch. Microbiol.* **195**, 473–482.
- Shah, H.N. and Collins, D.M.** 1990. *Prevotella*, a new genus to include *Bacteroides elaninogenicus* and related species formerly classified in the genus *Bacteroides*. *Int. J. Syst. Bacteriol.* **40**, 205–208.