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Note (Genome Announcement)

Draft genome sequence of *Porphyromonas gingivalis* KCOM 2797 isolated from a human periodontitis lesion

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사람 치주질환 병소에서 분리된 *Porphyromonas gingivalis* KCOM 2797의 유전체 염기서열 해독

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Porphyromonas gingivalis is a Gram-negative, obligately anaerobic, and nonmotile rod. *P. gingivalis* is a pathogen of periodontitis and endodontic infection as well as is associated with systemic diseases including atherosclerosis, preterm, and Alzheimer's diseases. *P. gingivalis* KCOM 2797 (= JS2) was isolated from a human periodontitis lesion. Here, we present the draft genome sequence of *P. gingivalis* KCOM 2797.

Keywords: *Porphyromonas gingivalis*, human, periodontitis

Porphyromonas gingivalis is a Gram-negative, obligately anaerobic, and nonmotile rod (Shah and Collins, 1988). *P. gingivalis* is a pathogen of periodontitis and endodontic infection as well as is associated with systemic diseases including atherosclerosis, preterm, and Alzheimer's diseases, (Hasegawa-Nakamura *et al*., 2011; Hajishengallis *et al*., 2012; Olsen *et al*., 2016; Rajaram *et al*., 2016). *P. gingivalis* KCOM 2797 (= JS2) was isolated from a human periodontitis lesion. In this report, we present the draft genome sequence of *P. gingivalis* KCOM 2797.

The *P. gingivalis* KCOM 2797 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 *P. gingivalis* KCOM 2797 was sequenced using the Illumina Hiseq 2000 platform by Macrogen Inc.. The library of 5 kb mate-pair was sequenced which reached coverage of 1,021 ×. 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 GapCloser (Luo *et al*., 2012; http://sourceforge.net/projects/soapdenovo2/files/GapCloser). And

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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. gingivalis* KCOM 2797 is 2,394,377 bp in length and has a G + C content of 48.0% (Table 1). A total of 1,988 protein-coding sequences (CDSs), 3 rRNAs, and 47 tRNAs were annotated (Table 1). The genome sequence contained virulence factors such as alpha-hemolysin translocation ATP-binding protein HylB, hemolysin C, sialidase, Lys-gingipain, gingipain R1/R2, ATP-dependent zinc metalloprotease FtsH, putative protease SohB/YhbU, Calpain family cysteine protease, CtpA-like serine protease, multidrug resistance protein MdtA/MdtB/MdtE/NorM, multidrug export protein EmrA/MepA, antibiotic transporter, penicillinase, and β-lactamase hydrolase-like protein. The genome contained bacteriophage Mu Gam like protein, phage virion morphogenesis family protein, phage Mu protein F like protein, bactoprenol glucosyl transferase homolog from prophage CPS-53, and oxidative stress-response genes such as superoxide dismutase, NAD(P)H nitroreductase, and thioredoxin reductase. The draft genome encodes for involving the biofilm formation such as glycosyltransferase EpsJ and pheromone autoinducer 2 transporters. It also contained type IV secretion system protein virB4, type IV secretion-system coupling protein DNA-binding domain protein, preprotein translocase subunit SecA/SecD/SecE/SecG/SecY/YajC, one unmatched sensor histidine kinase (TmoS), and six unmatched transcription regulatory proteins (QseB, ZraR, LiaR, SrrA, and ZraR). The *P. gingivalis* KCOM 2797 strain was deposited in the Korean Collection for Oral Microbiology.

Table 1. Genome features of *Porphyromonas gingivalis* KCOM 2797

Attribute	Value
Genome size (bp)	2,394,377
GC content (%)	48.0
No. of contigs	44
Total genes	2,153
Protein-coding genes	1,988
tRNA	47
rRNA (5S, 16S, 23S)	3 (1, 1, 1)
ncRNA	2
Pseudogene	113

Nucleotide sequence accession number

This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession NHRU00000000. The version described in this paper is version NHRU01000000.

적 요

*Porphyromonas gingivalis*는 그람 음성이면서, 절대 혐기성 및 비운동성 간균이다. *P. gingivalis*는 치주염 및 치근관 감염의 원인균일 뿐만 아니라, 동맥경화증, 조산 및 알츠하이머 질환과 같은 전신질환과도 연관성이 있다. *P. gingivalis* KCOM 2797 (= JS2) 균주가 사람 치주염 병소에서 분리되었다. *P. gingivalis* KCOM 2797 균주의 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.

Hajishengallis, G., Darveau, R.P., and Curtis, M.A. 2012. The keystone pathogen hypothesis. *Nat. Rev. Microbiol.* **10**, 717–725.

Hasegawa-Nakamura, K., Tateishi, F., Nakamura, T., Nakajima, Y., Kawamata, K., Douchi, T., Hatae, M., and Noguchi, K. 2011. The possible mechanism of preterm birth associated with periodontopathic *Porphyromonas gingivalis*. *J. Periodontal.*

Res. **46**, 497–504.

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.

Olsen, I., Taubman, M.A., and Singhrao, S.K. 2016. *Porphyromonas gingivalis* suppresses adaptive immunity in periodontitis, atherosclerosis, and Alzheimer's disease. *J. Oral Microbiol*. **8**, 33029.

Otto, T.D., Sanders, M., Berriman, M., and Newbold, C. 2010. Iterative Correction of Reference Nucleotides (iCORN) using second generation sequencing technology. *Bioinformatics* **26**, 1704–1707.

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.

Rajaram, A., Kotrashetti, V.S., Somannavar, P.D., Ingalagi, P., and Bhat, K. 2016. Culture-based identification of pigmented *Porphyromonas* and *Prevotella* species in primary endodontic infections. *J. Dent. Res. Dent. Clin. Dent. Prospects* **10**, 136–141.

Shah, H.N. and Collins, M.D. 1988. Proposal for reclassification of *Bacteroides asaccharolyticus*, *Bacteroides gingivalis*, and *Bacteroides endodontalis* in a new genus, *Porphyromonas*. *Int. J. Syst. Bacteriol.* **38**, 128–131.