




Complete genome sequence of *Prevotella denticola* KCOM 1525 isolated from human periapical abscess




Yun Kyong Lim^{1†} , Soon-Nang Park^{1†} , Se Ho Park², Ja Young Shin³, Hanseong Roh³, and Joong-Ki Kook^{1*} 

¹Korean Collection for Oral Microbiology and Department of Oral Biochemistry, College of Dentistry, Chosun University, Gwangju 61452, Republic of Korea

²School of Dentistry, Chosun University, Gwangju 61452, Republic of Korea

³Macrogen Inc., Seoul 08511, Republic of Korea

사람 치근단 농양에서 분리된 *Prevotella denticola* KCOM 1525의 유전체 염기서열 완전 해독

임윤경^{1†} , 박순남^{1†} , 박세호², 신자영³, 노한성³, 국중기^{1*} 

¹조선대학교 치과대학 구강생화학교실 및 한국구강미생물자원은행, ²조선대학교 치의학전문대학원, ³마크로젠

(Received December 21, 2018; Revised January 18, 2019; Accepted January 18, 2019)

Prevotella denticola is Gram-negative, obligately anaerobic, non-motile, non-spore forming, and rod-shaped bacterium. *P. denticola* is associated with periodontal disease and is a risk indicator of periodontal disease. *P. denticola* KCOM 1525 (= ChDC B698) was isolated from human periapical abscess. Herein, we present the complete genome sequence of *P. denticola* KCOM 1525.

Keywords: *Prevotella denticola*, genome sequence, periapical abscess

Prevotella denticola is Gram-negative, obligately anaerobic, non-motile, non-spore forming, and rod-shaped bacterium (Shah and Collins, 1990). *P. denticola* is associated with periodontal disease and is a risk indicator of periodontal disease (Lourenco *et al.*, 2014). *P. denticola* KCOM 1525 (= ChDC B698) was isolated from human periapical abscess. In this report, we presented the complete genome sequence of *P. denticola*

KCOM 1525.

P. denticola KCOM 1525 was cultured on tryptic soy agar (TSA; BD Difco Laboratories) plate 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) maintained using a gas mixture of 10% H₂, 5% CO₂, and 85% N₂ (Park *et al.*, 2013). Genomic DNA of *P. denticola* KCOM 1525 was prepared as previously described (Cho *et al.*, 2015).

The genomic DNA of *P. denticola* KCOM 1525 was sequenced using PacBio RSII SMRT sequencing platform using a 20 kb SMRTbell template library and Illumina HiSeq 2500 by Macrogen Inc. Approximately 1,473.1 Mb (509.1 × of coverage) with 157,270 filtered subreads (9,366 bp of mean subreads length and 14,006 bp of N50) were generated and assembled by HGAP (version: 3.0, default setting) in PacBio's SMRT portal (<http://www.pacb.com/products-and-services/analytical-software/smart-analysis>). The initial assembly was polished by Pilon (version: 1.21) with 13,629,778 paired-end reads (475.7 × of coverage, trimmed by trimmomatic 0.36) from Illumina HiSeq 2500 (<https://github.com/broadinstitute/pilon/wiki>) (Walker *et*

[†]These authors contributed equally to this work.

*For correspondence. E-mail: jkook@chosun.ac.kr;
Tel.: +82-62-230-6877; Fax: +82-62-236-2734

Table 1. Genome features of *Prevotella denticola* KCOM 1525

Attribute	Value
Genome size (bp)	2,893,847
GC content (%)	50.13
No. of chromosome	2
Total genes	2,383
Protein-coding genes	2,238
tRNA	49
rRNA (5S, 16S, 23S)	12 (4, 4, 4)
ncRNA	3
Pseudogene	81

al., 2014). The pilon fixed 33 INDELS and most of errors were A/T insertions or G/C deletions. Genome annotation was conducted using the NCBI Prokaryotic Genome Annotation Pipeline (Tatusova *et al.*, 2016).

The complete genome of *P. denticola* KCOM 1525 was composed of two chromosomes; 1,846,186 bp and 1,047,661 bp in length. The average G+C content of the genome was 50.13% (Table 1). A total of 2,238 protein-coding sequences, 12 rRNAs, and 49 tRNAs were annotated (Table 1).

The genome sequence contained antibiotic-resistance-related genes; multidrug resistance protein MdtN/NorM/LmrA and multidrug export protein MepA. It contained toxin-related genes; actin cross-linking toxin VgrG1, toxin Doc, and toxin RTX-I translocation ApxIB. It also contained stress-related genes; general stress protein Ctc, ATP-dependent Clp protease ClpC/ClpP, peptide methionine sulfoxide reductase MsrA/MsrB and thioredoxin reductase TrxA/TrxB. Hemolysin TlyC, conserved virulence factor CvfB, ferric aerobactin IutA, putative glycosyltransferase EpsJ, toxin-antitoxin biofilm protein TabA, and type IV secretion system VirB4 were also found in the genome sequence.

The *P. denticola* KCOM 1525 strain was deposited into 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 CP032056/CP032057. The version described in this paper is version CP032056.1/CP032057.1.

적 요

*Prevotella denticola*는 그람 음성, 절대 혐기성, 비운동성이면서 아포를 형성하지 않는 막대 모양의 세균이다. *P. denticola*는 치주질환과 관련이 있으며, 치주질환의 위험 인자 중 하나이다. *P. denticola* KCOM 1525 (= ChDC B698) 균주가 사람 치근단 농양에서 분리되었다. *P. denticola* KCOM 1525 균주의 유전체 염기서열을 완전 해독하여 보고한다.

Acknowledgements

This research was supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (MSIT) (No. 2018R1A2B5002239).

References

- Cho E, Park SN, Lim YK, Shin Y, Paek J, Hwang CH, Chang YH, and Kook JK. 2015. *Fusobacterium hwasookii* sp. nov., isolated from a human periodontitis lesion. *Curr. Microbiol.* **70**, 169–175.
- Lourenco TG, Heller D, Silva-Boghossian CM, Cotton SL, Paster BJ, and Colombo AP. 2014. Microbial signature profiles of periodontally healthy and diseased patients. *J. Clin. Periodontol.* **41**, 1027–1036.
- Park SN, Lim YK, and Kook JK. 2013. Development of quantitative real-time PCR primers for detecting 42 oral bacterial species. *Arch. Microbiol.* **195**, 473–482.
- Shah HN and Collins DM. 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.
- Tatusova T, DiCuccio M, Badretdin A, Chetvermin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, and Ostell J. 2016. NCBI prokaryotic genome annotation pipeline. *Nucleic Acids Res.* **44**, 6614–6624.
- Walker BJ, Abeel T, Shea T, Priest M, Abouelliel A, Sakthikumar S, Cuomo CA, Zeng Q, Wortman J, Young SK, *et al.* 2014. Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement. *PLoS One* **9**, e112963.