

## Note (Genome Announcement)

# Complete genome sequence of *Parvimonas micra* KCOM 1535 isolated from a human periapical abscess lesion

Soon-Nang Park<sup>1†</sup>, Hanseong Roh<sup>2†</sup>, Yun Kyong Lim<sup>1</sup>, and Joong-Ki Kook<sup>1,3\*</sup>

<sup>1</sup>Korean Collection for Oral Microbiology and Department of Oral Biochemistry, School of Dentistry, Chosun University, Gwangju 61452, Republic of Korea

<sup>2</sup>Macrogen Inc., Seoul 08511, Republic of Korea

<sup>3</sup>Oral Biology Research Institute, Chosun University, Gwangju 61452, Republic of Korea

## 사람 치근단 농양에서 분리된 *Parvimonas micra* KCOM 1535의 유전체 염기서열 해독

박순낭<sup>1†</sup> · 노한성<sup>2†</sup> · 임윤경<sup>1</sup> · 국중기<sup>1,3\*</sup>

<sup>1</sup>조선대학교 치과대학 구강생화학교실 및 한국구강미생물자원은행, <sup>2</sup>마크로젠, <sup>3</sup>조선대학교 구강생물학연구소

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*Parvimonas micra* is a Gram-positive, obligately anaerobic, non-spore forming, and non-motile cocci. *P. micra* is a member of oral flora and is associated with oral, respiratory, and gastrointestinal tract infections. *Parvimonas micra* KCOM 1535 (=ChDC B708) was isolated from a human periapical abscess lesion. Here, we present the complete genome sequence of *P. micra* KCOM 1535.

**Keywords:** *Parvimonas micra*, human, periapical abscess

*Parvimonas micra* (formerly *Micromonas micros* or *Peptostreptococcus micros*) is a Gram-positive, obligately anaerobic, non-spore-forming, and non-motile cocci (Murdoch and Shah, 1999; Tindall and Euzéby, 2006). *P. micra* is a member of oral flora and is associated with periodontal disease (Haffajee and Socransky, 1994; Murphy and Frick, 2013), endodontic infection (Heimdahl *et al.*, 1985; De Sousa *et al.*, 2003), infectious endocarditis (Murdoch *et al.*, 1988; Gomez *et al.*, 2015),

spondylodiscitis with epidural abscess (Endo *et al.*, 2015), prosthetic joint infection associated with dental procedures (Bartz *et al.*, 2005), anaerobic empyema (Civen *et al.*, 1995), *Parvimonas micra* KCOM 1535 (=ChDC B708) was isolated from a human periapical abscess lesion. In this report, we present the complete genome sequence of *P. micra* KCOM 1535.

The genomic DNA of *P. micra* KCOM 1535 was sequenced by the Illumina HiSeq 2,000 platform. Two libraries of 350 bp paired-end and 10 kb mate-pair was sequenced which reached coverage of 1,331× and 1,232× each. The de novo assembly was performed by ALLPATHS-LG (Gnerre *et al.*, 2011) which produced one circular large scaffold and 4 tiny scaffolds. All 27 gaps among the scaffolds were filled by GapCloser (Luo *et al.*, 2012; <http://sourceforge.net/projects/soapdenovo2/files/GapCloser>). And we confirmed the 4 tiny 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\\_](https://www.ncbi.nlm.nih.gov/genome/annotation_)

<sup>†</sup>These authors contributed equally to this work.

\*For correspondence. E-mail: jkkook@chosun.ac.kr  
Tel.: +82-62-230-6877; Fax: +82-62-224-3706

**Table 1.** Genome features of *Parvimonas micra* KCOM 1535

Attribute	Value
Genome size (bp)	1,627,009
GC content (%)	28.6
No. of contigs	1
Total genes	1,531
Protein-coding genes	1,419
tRNA	41
rRNA (5S, 16S, 23S)	15
ncRNA	1
Pseudogene	55

prok/).

The complete genome of *P. micra* KCOM 1535 is 1,627,009 bp in length and has a G+C content of 28.6% (Table 1). A total of 1,419 protein-coding sequences (CDSs), 15 rRNAs, and 41 tRNAs were annotated (Table 1). The genome contained several key pathways for carbohydrate, amino acid, and lipids. The genome sequence harbored virulence factors such as metalloproteases, toxin HicA, antibiotic ABC transporter permease, and macrolide ABC transporter ATP-binding protein. The genome contained oxidative stress-response genes such as superoxide dismutase, glutathione peroxidase, thioredoxin, thoredoxin reductase, and glutaredoxin. The genome also contained type IV secretion system protein VirD4, the five two-component systems, two unmatched DNA-binding response regulators, and one unmatched sensor histidine kinase.

#### Nucleotide sequence accession number

This whole genome sequence was deposited in GenBank under accession number CP009761.

## 적 요

*Parvimonas micra*는 그람 양성이며, 절대 혐기성, 비포자형성 및 비운동성 구균이다. *P. micra*는 사람의 구강 내 정상 세균총의 하나이고, 구강, 호흡기 및 위장관계 감염과 연관이 있다. *P. micra* KCOM 1535 (=ChDC B708) 균주가 사람 치근단 농양 병소에서 분리되었으며 그 유전체 염기서열을 해독하여 보고한다.

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## References

- Bartz, H., Nonnenmacher, C., Bollmann, C., Kuh, I.M., Zimmermann, S., Heeg, K., and Mutters, R. 2005. *Micromonas (Peptostreptococcus) micros*: unusual case of prosthetic joint infection associated with dental procedures. *Int. J. Med. Microbiol.* **294**, 465–470.
- Civen, R., Jousimies-Somer, H., Marina, M., Borenstein, L., Shah, H., and Finegold, S.M. 1995. A retrospective review of cases of anaerobic empyema and update of bacteriology. *Clin. Infect. Dis.* **20**, S224–S229.
- De Sousa, E.L., Ferraz, C.C., Gomes, B.P., Pinheiro, E.T., Teixeira, F.B., and De Souza-Filho, F.J. 2003. Bacteriological study of root canals associated with periapical abscesses. *Oral Surg. Oral Med. Oral Pathol. Oral Radiol. Endod.* **96**, 332–339.
- Endo, S., Nemoto, T., Yano, H., Kakuta, R., Kanamori, H., Inomata, S., Ishibashi, N., Aoyagi, T., Hata, M., Gu, Y., *et al.* 2015. First confirmed case of spondylodiscitis with epidural abscess caused by *Parvimonas micra*. *J. Infect. Chemother.* **21**, 828–830.
- Gnerre, S., Maccallum, I., Przybylski, D., Ribeiro, F.J., Burton, J.N., Walker, B.J., Sharpe, T., Hall, G., Shea, T.P., Sykes, S., *et al.* 2011. High-quality draft assemblies of mammalian genomes from massively parallel sequence data. *Proc. Natl. Acad. Sci. USA* **108**, 1513–1518.
- Gomez, C.A., Gerber, D.A., Zambrano, E., Banaei, N., Deresinski, S., and Blackburn, B.G. 2015. First case of infectious endocarditis caused by *Parvimonas micra*. *Anaerobe* **36**, 53–55.
- Haffajee, A.D. and Socransky, S.S. 1994. Microbial etiological agents of destructive periodontal diseases. *Periodontol.* **2000** **5**, 78–111.
- Heimdahl, A., Von Konow, L., Satoh, T., and Nord, C.E. 1985. Clinical appearance of orofacial infections of odontogenic origin in relation to microbiological findings. *J. Clin. Microbiol.* **22**, 299–302.
- 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.
- Murdoch, D.A., Mitchelmore, L.J., and Tabaqchali, S. 1988. *Pepto-*

- streptococcus micros* in polymicrobial abscesses. *Lancet* **1**, 594.
- Murdoch, D.A. and Shah, H.N.** 1999. Reclassification of *Peptostreptococcus magnus* (Prevot 1933) Holdeman and Moore 1972 as *Finegoldia magna* comb. nov. and *Peptostreptococcus micros* (Prevot 1933) Smith 1957 as *Micromonas micros* comb. nov. *Anaerobe* **5**, 555–559.
- Murphy, E.C. and Frick, I.M.** 2013. Gram-positive anaerobic cocci-commensals and opportunistic pathogens. *FEMS Microbiol. Rev.* **37**, 520–553.
- 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.
- Tindall, B. and Euzéby, J.** 2006. Proposal of *Parvimonas* gen. nov. and *Quatronicoccus* gen. nov. as replacements for the illegitimate, prokaryotic, generic names *Micromonas* Murdoch and Shah 2000 and *Quadricoccus* Maszenan et al. 2002, respectively. *Int. J. Syst. Evol. Microbiol.* **56**, 2711–2713.