Korean Journal of Microbiology (2019) Vol. 55, No. 2, pp. 149-151
DOI https://doi.org/10.7845/kjm.2019.8111

pISSN 0440-2413
eISSN 2383-9902

Complete genome sequence of *Parvimonas micra* KCOM 1037 isolated from human postoperative maxillary cyst lesion

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사람 수술후상악낭종 병소에서 분리한 *Parvimonas micra* KCOM 1037의 유전체 염기서열 완전 해독

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(Received December 24, 2018; Revised December 30, 2018; Accepted January 16, 2019)

Parvimonas micra is Gram-positive, strict anaerobic, non-motile, and non-spore forming coccus. It is a member of oral flora and is related to oral infectious diseases as well as systemic diseases. *P. micra* KCOM 1037 (= ChDC B276) was isolated from human postoperative maxillary cyst lesion. Here, we present the complete genome sequence of *P. micra* KCOM 1037.

Keywords: *Parvimonas micra*, genome sequence, postoperative maxillary cyst

Parvimonas micra (formerly *Peptostreptococcus micros*) is a Gram-positive, strict anaerobic, non-motile, and non-spore forming coccus (Murdoch and Shah, 1999; Tindall and Euzéby, 2006). It is a member of oral flora and is related to oral infectious diseases (Haffajee and Socransky, 1994; de Sousa *et al*., 2003) as well as systemic diseases (Murdoch *et al.*, 1988; Civen *et al.*, 1995; Bartz *et al.*, 2005; Endo *et al.*, 2015; Gomez *et al.*, 2015). *Parvimonas micra* KCOM 1037 (= ChDC B276) was isolated from human postoperative maxillary cyst lesion. In this report, we presented the complete genome sequence of *P. micra* KCOM 1037.

The *P. micra* KCOM 1037 was grown in a tryptic soy broth (TSB, 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) maintained using a gas mixture of 10% H_2, 5% CO_2, and 85% N_2 (Park and Kook, 2013).

The bacterial genomic DNA was prepared as previously described (Cho *et al*., 2015). Genomic DNA of *P. micra* KCOM 1037 was sequenced using PacBio RSII SMRT sequencing platform using a 20 kb SMRTbell template library and Illumina HiSeq platform with 100 × 2 bp reads using 350 bp insert size library by Macrogen Inc. Approximately 777.3 Mb (457.7 ×) with 153,365 filtered subreads (mean subreads length: 5,068 bp) were generated and assembled into a single contig by HGAP (version: 3.0, default setting) in PacBio's SMRT portal (http://www.pacb.com/products-and-services/analytical-software/smrt-analysis). The initial assembly was polished by Pilon (version: 1.21) with 1,561.6 Mb paired-end reads (939.7

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Table 1. Genome features of *Parvimonas micra* KCOM 1037

Attribute	Value
Genome size (bp)	1,661,863
GC content (%)	28.9
No. of contig	1
Total genes	1,854
Protein-coding genes	1,540
tRNA	41
Complete rRNA (5S, 16S, 23S)	10 (4, 3, 3)
ncRNA	3
Pseudogene	44
CRISPR arrays	1

×, trimmed by trimmomatic 0.36) from Illumina Hiseq 2500 (Walker *et al*., 2014). Genome annotation was conducted by the NCBI Prokaryotic Genome Annotation Pipeline (Tatusova *et al*., 2016).

The complete genome of *P. micra* KCOM 1037 was composed of 1 contig, 1,661,863 bp in length. The average G+C content of the genome was 28.9% (Table 1). A total of 1,540 protein-coding sequences, 10 rRNAs, and 41 tRNAs were annotated (Table 1).

The genome sequence contained several proteinase; putative protease YdcP, putative zinc metalloprotease, putative cysteine protease YraA, carboxy-terminal processing protease CtpA, serine protease Do-like HtrA, and ATP-dependent zinc metalloprotease FtsH. It contained biofilm formation-related gene, glycosyltransferase EpsH. It also contained antibiotic-resistance-related genes; putative multidrug resistance ABC transporter ATP-binding/permease protein YheI, multiple antibiotic resistance protein MarA, multidrug resistance protein NorM/MdtK, tetracycline resistance protein TetM, vancomycin B-type resistance protein VanW, and daunorubicin/doxorubicin resistance ATP-binding protein DrrA. It also contains type II secretion system protein F epsF, ESX secretion system protein EccC, and protein translocase subunit SecA/SecY/SecE. The genome also contained the oxidative stress-response gene, thioredoxin reductase.

P. micra KCOM 1037 strain was deposited into the Korean Collection for Oral Microbiology.

Nucleotide sequence accession number

This whole genome sequence was deposited in GenBank under the accession number CP031971.

적 요

*Parvimonas micra*는 그람 양성, 절대 혐기성, 비운동성 및 아포를 생성하지 않는 구균이다. 이 세균 종은 구강의 정상 세균 총 하나이며, 구강 감염성질환 및 전신질환고도 연관이 있다. *P. micra* KCOM 1037 (= ChDC B276) 균주가 수술후상악낭종 병소에서 분리되었다. 여기에서 *P. micra* KCOM 1037 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).

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