

Complete genome sequence of *Eikenella corrodens* KCOM 3110 isolated from human subgingival dental plaque of periodontitis lesion




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사람 치주염 병소의 치은연하치면세균막에서 분리된 *Eikenella corrodens* KCOM 3110의 유전체 염기서열 완전 해독

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Eikenella corrodens is Gram-negative, facultatively anaerobic, and rod-shaped bacterium. It is a part of the normal human mucosal flora that can cause several systemic diseases such as endocarditis, liver abscess, and intracranial bacterial infection. *E. corrodens* KCOM 3110 (= JS217) was isolated from human subgingival dental plaque of periodontitis lesion. Here, we present the complete genome sequence of *E. corrodens* KCOM 3110.

Keywords: *Eikenella corrodens*, genome sequence, periodontitis

Eikenella corrodens is Gram-negative, facultatively anaerobic, and rod-shaped bacterium (Jackson and Goodman, 1972). It is a part of the normal human mucosal flora, predominantly of the oropharynx (Perez Trallero *et al.*, 1988) and is related to endocarditis, liver abscess, and intracranial bacterial infection (Das *et al.*, 1997; Moazzam *et al.*, 2015; Nordholm *et al.*, 2018).

E. corrodens KCOM 3110 (= JS217) was isolated from the human subgingival dental plaque of periodontitis lesion. Herein, we presented the complete genome sequence of *E. corrodens* KCOM 3110.

E. corrodens KCOM 3110 was grown in a tryptic soy broth (TSB, 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) maintained using a gas mixture of 10% H₂, 5% CO₂, and 85% N₂ (Park *et al.*, 2013).

The bacterial genomic DNA was prepared as previously described (Cho *et al.*, 2015). Genomic DNA of *E. corrodens* KCOM 3110 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 587.5 Mb (239.0 × of coverage) with 65,227 filtered subreads (9,007 bp of mean subreads length and 14,371 bp of N50) were generated and assembled into a single contig by HGAP (version: 3.0, default setting) in PacBio's SMRT portal (<http://www.pacb.com/>)

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products-and-services/analytical-software/smrt-analysis). The initial assembly was polished by Pilon (version: 1.21) with 1,386.2 Mb paired-end reads ($563.9 \times$ of coverage, 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 genome of *E. corrodens* KCOM 3110 was composed of one contig, 2,458,478 bp in length. The G+C content of the genome was 56.0%. A total of 2,306 protein-coding sequences, 12 ribosomal RNAs (rRNAs) and 51 transfer RNAs (tRNAs) were annotated (Table 1).

The genome of *E. corrodens* KCOM 3110 contained antibiotic-resistance-related genes; multidrug resistance protein Stp/NorM, bifunctional polymyxin resistance protein ArnA, bicyclomycin resistance protein Bcr, multidrug efflux pump subunit AcrA/AcrB, peptide antibiotic transporter SbmA, and beta-lactamase hydrolase-like protein Blh. The *E. corrodens* KCOM 3110 genome also contained stress-related genes; TRAP-T-associated universal stress protein TeaD, acid stress protein IbaG, general stress protein 14 YwrO, ATP-dependent Clp protease ClpX/ClpP, persistence and stress-resistance toxin PasT, and persistence, and stress-resistance antitoxin PasI. It also contained ferri-enterobactin receptor FepA, ferri-bacillibactin esterase BesA, ferric enterobactin PfeA, hemolysin secretion protein D plasmid HlyD, hemolysin A HlyA, hemolysin transporter protein ShlB, leukotoxin-activating lysine-acyltransferase LtxC, autotransporter adhesion NhhA, adhesin MafA, lipopolysaccharide (LPS)-assembly lipoprotein LptD/LptE, ADP-heptose-LPS heptosyltransferase 2 RfaF, tellurite-resistance protein TehA, putative glycosyltransferase EpsJ, toxin FitB, and antitoxin

Table 1. Genome features of *Eikenella corrodens* KCOM 3110

Attribute	Value
Genome size (bp)	2,458,478
GC content (%)	56.0
No. of contig	1
Total genes	2,477
Protein-coding genes	2,306
tRNA	51
rRNA (5S, 16S, 23S)	12 (4, 4, 4)
ncRNA	4
Pseudogene	104

FitA/vapB1.

E. corrodens KCOM 3110 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 CP034670.

적 요

*Eikenella corrodens*는 그람 음성, 통성 혐기성이며 막대 모양의 세균이다. 이 세균 종은 사람의 심내막염, 간농양 및 두개 내 세균감염 등과 같은 전신질환과 연관이 있을 뿐만 아니라 점막의 정상 세균총에 속한다. *E. corrodens* KCOM 3110 (= JS217) 균주가 사람 치주질환 병소의 치은연하치면세균막에서 분리되었다. 여기에서 *E. corrodens* KCOM 3110 균주의 유전체 염기서열을 완전 해독하여 보고한다.

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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.
- Das M, Badley AD, Cockerill FR, Steckelberg JM, and Wilson WR. 1997. Infective endocarditis caused by HACEK microorganisms. *Annu. Rev. Med.* **48**, 25–33.
- Jackson FL and Goodman YE. 1972. Transfer of the facultatively anaerobic organism *Bacteroides corrodens* Eiken to a new genus *Eikenella*. *Int. J. Syst. Bacteriol.* **22**, 73–77.
- Moazzam AA, Rajagopal SM, Sedghizadeh PP, Zada G, and Habibian M. 2015. Intracranial bacterial infections of oral origin. *J. Clin. Neurosci.* **22**, 800–806.
- Nordholm AC, Vøgg ROB, Permin H, and Katzenstein T. 2018. *Eikenella corrodens* endocarditis and liver abscess in a previously healthy male, a case report. *BMC Infect. Dis.* **18**, 35.

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.

Perez Trallero E, Garcia Arenzana JM, Cilla Eguiluz G, and de Toro Rios P. 1988. Extraoral origin of *Eikenella corrodens* infection. *Lancet* **1**, 298–299.

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.