Genome Announcement

Complete genome sequence of human pathogen Kosakonia cowanii type strain 888-76T

Xue-Jing Yang, Sai Wang, Jun-Min Cao, Jia-Hui Hou

The First Affiliated Hospital of Zhejiang Chinese Medical University, Department of Clinical Laboratory, Hangzhou, PR China
Zhejiang Sci-Tech University, College of Life Science, Zhejiang Province Key Laboratory of Plant Secondary Metabolism and Regulation, Hangzhou, PR China
The First Affiliated Hospital of Zhejiang Chinese Medical University, Department of Hospital Infection Control, Hangzhou, PR China

Article history:
Received 3 February 2017
Accepted 3 March 2017
Available online 19 July 2017
Associate Editor: John McCulloch

Keywords:
Kosakonia cowanii
Genome sequence
Antibiotic resistance

ABSTRACT

Kosakonia cowanii type strain 888-76T is a human pathogen which was originally isolated from blood as NIH group 42. In this study, we report the complete genome sequence of K. cowanii 888-76T. 888-76T has 1 chromosome and 2 plasmids with a total genome size of 4,857,567 bp and C+G 56.15%. This genome sequence will not only help us to understand the virulence features of K. cowanii 888-76T but also provide us the useful information for the study of evolution of Kosakonia genus.

© 2017 Sociedade Brasileira de Microbiologia. Published by Elsevier Editora Ltda. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

Kosakonia cowanii (formally Enterobacter cowanii) is a Gram-negative, motile, rod-shaped pathogen, which was originally isolated from blood as NIH group 42. Although the type strain was first isolated from patient, this species were also frequently isolated from plant, soil and infant formula. These results suggest the diversity of this species. Although K. cowanii becomes more and more important, the complete genome sequence of this species has still not been reported. In this case, the type strain of this species, K. cowanii 888-76T was completely sequenced in this study. This genome sequence will not only help us to understand the virulence features of this species but also provide useful information for understanding the evolution of Kosakonia genus.

The culture of strain 888-76T used to prepare genomic DNA for sequencing was a laboratory stock and grown on LB (Lysogeny Broth, BD, USA) at 37 °C with vigorous shaking. 2.5 mL of culture broth was used to isolate the genomic DNA by using Wizard Genomic DNA Purification Kit (Promega,
The quality of purified genomic DNA was tested by using NanoDrop 2000 UV–vis spectrophotometer (Thermo Scientific, MA, USA). Sequencing was performed on the PacBio RS II sequencer. After read filtering and adapter trimming, the genome was first de novo assembled using HGAP assembly protocol. After this first round, PBJelly V14.1.14 was used to fill and reduce as many captured gaps as possible to produce upgraded draft genomes. 

Protein coding genes, tRNA and rRNA annotations were done by NCBI Prokaryotic Genome Annotation Pipeline. In addition, GO and COG programs were used to further functional analysis of all annotated ORFs. Specifically, the virulence genes and MDR genes were searched based on VFDB and ARGannot.

The genome of K. couanii 888-76T consists of one circular chromosome (4,647,241 bp, 56.2% G+C), and two circular plasmid, named as p888-76-1 (113,443 bp, 53.5% G+C) and p888-76-2 (96,883 bp, 56.2% G+C) respectively. A total of 4448 CDSs were predicted. Of these, 3347 could be assigned to a COG number. In addition, 107 RNAs including tRNA and rRNA were identified. Strikingly, after searching at ARGannot database, we found 23 genes were responsible for antibiotic resistance. Of these, 6 genes encode β-lactamase, which is a typical features in Enterobacteriaceae strains. 262 genes were predicted to be virulence genes, suggesting the pathogenesis of this strain. In these, 9 genes are encoded for type III secretion system, 5 genes are related to type IV pilus biogenesis and 41 genes are flagellar associated genes. The genomic information of K. couanii 888-76T will be important to clarify the virulence and MDR mechanisms as well as for understanding the evolution history of Kosakonia genus.

The assembled contigs were deposited in DDBJ/ENA/GenBank and published in the accession number CP019445 (chromosome), CP019446 and CP019447 (Plasmid). The version described in this paper is the first version.

Conflicts of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Acknowledgments

The authors would like to thank Bo-Zhu and Wei-Jie Song for his critical discussion and editing of the manuscript. This work was funded by Science and Technology Program of Zhejiang Province (No. 2013C33181) and Zhejiang Provincial Medical and Health Science and Technology project (No. 2016KYB216).

References

1. Inoue K, Sugiyama K, Kosako Y, Sakazaki R, Yamai S. Enterobacter couanii sp. nov., a new species of the family Enterobacteriaceae. Curr Microbiol. 2000;41:417–420.
2. Brady C, Cleenwerck I, Venter S, Coutinho T, De Vos P. Taxonomic evaluation of the genus Enterobacter based on multilocus sequence analysis (MLSA): proposal to reclassify E. nihmipressuralis and E. ammigenus into Lelliottieta gen. nov. as Lelliottieta nihmipressuralis comb. nov. and Lelliottieta ammigena comb. nov., respectively. E. gergoviae and E. pyrus into Pluralibacter gen. nov. as Pluralibacter gergoviae comb. nov. and Pluralibacter pyrus comb. nov., respectively, E. couanii, E. radicincitans, E. oryzae and E. arachidis into Kosakonia gen. nov. as Kosakonia couanii comb. nov., Kosakonia radicincitans comb. nov., Kosakonia oryzae comb. nov. and Kosakonia arachidis comb. nov., respectively, and E. turicensis, E. helveticus and E. pulvis into Cronobacter as Cronobacter zurichensis nom. nov., Cronobacter helveticus comb. nov. and Cronobacter pulvis comb. nov., respectively, and emended description of the genera Enterobacter and Cronobacter. Syst Appl Microbiol. 2013;36:309–319.
3. Yang JE, Park YJ, Chang HC. Cloning of four genes involved in limonene hydroxylation from Enterobacter couanii 6L. J Microbiol Biotechnol. 2007;17:1169–1176.
4. Brady CL, Venter SN, Cleenwerck I, et al. Isolation of Enterobacter couanii from Eucalyptus showing symptoms of bacterial blight and dieback in Uruguay. Lett Appl Microbiol. 2009;49:461–465.
5. English AC, Richards S, Han Y, et al. Mind the gap: upgrading genomes with Pacific Biosciences RS long-read sequencing technology. PLoS ONE. 2012;7:e47768.
6. Pruitt KD, Tatusova T, Brown GR, Maglott DR. NCBI Reference Sequences (RefSeq): current status, new features and genome annotation policy. Nucleic Acids Res. 2012;40:D130–D135.
7. Ashburner M, Ball CA, Blake JA, et al. Gene ontology: tool for the unification of biology. Nat Genet. 2000;25:25–29.
8. Tatusov RL, Galperin MY, Natale DA, Koonin EV. The COG database: a tool for genome-scale analysis of protein functions and evolution. Nucleic Acids Res. 2000;28:33–36.
9. Chen L, Zheng D, Liu B, Yang J, Jin Q. VFDB 2016: hierarchical and refined dataset for big data analysis—10 years on. Nucleic Acids Res. 2016;44:D694–D697.
10. Gupta SK, Padmanabhan BR, Diene SM, et al. ARG-ANNOT, a new bioinformatic tool to discover antibiotic resistance genes in bacterial genomes. Antimicrob Agents Chemother. 2014;58:212–220.
11. Bush K. Alarming beta-lactamase-mediated resistance in multidrug-resistant Enterobacteriaceae. Curr Opin Microbiol. 2010;13:558–564.