

Two Genome Sequences of *Klebsiella pneumoniae* Strains with Sequence Type 23 and Capsular Serotype K1

Hsi-Hsu Lin,^{a,b} Yao-Shen Chen,^c Hao-Wen Hsiao,^d Pei-Tan Hsueh,^e Wei-Fen Ni,^d Ya-Lei Chen^d

Section of Infectious Disease, Department of Medicine, E-Da Hospital, Kaohsiung, Taiwan^a; Department of Internal Medicine, E-Da University, Kaohsiung, Taiwan^b; Division of Infectious Diseases, Kaohsiung Veterans General Hospital, Kaohsiung, Taiwan^c; Department of Biotechnology, National Kaohsiung Normal University, Kaohsiung, Taiwan^d; Department of Biological Sciences, National Sun Yat-sen University, Kaohsiung, Taiwan^e

H.-H.L. and Y.-S.C. contributed equally to this work.

Here, we report the whole-genome sequences of *Klebsiella pneumoniae* ED2 and ED23, isolated, respectively, from bacteremic patients with liver abscesses (ED2) and patients with primary liver abscess and metastatic meningitis (ED23). Both strains were of multilocus sequence type 23 with capsule serotype K1.

Received 16 August 2016 **Accepted** 26 August 2016 **Published** 20 October 2016

Citation Lin H-H, Chen Y-S, Hsiao H-W, Hsueh P-T, Ni W-F, Chen Y-L. 2016. Two genome sequences of *Klebsiella pneumoniae* strains with sequence type 23 and capsular serotype K1. *Genome Announc* 4(5):e01097-16. doi:10.1128/genomeA.01097-16.

Copyright © 2016 Lin et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Ya-Lei Chen, dan1001@ms31.hinet.net.

Klebsiella pneumoniae is a Gram-negative, rod-shaped bacterium that causes community- and hospital-acquired infections (1, 2). Worldwide, community-acquired primary liver abscess caused by invasive *K. pneumoniae* with serotype K1 has emerged. In Taiwan, approximately 12% of patients with *K. pneumoniae* liver abscess appeared with a metastatic brain abscess or pyogenic meningitis (3). This unique epidemic of *K. pneumoniae*-caused meningitis has become a public health concern in Taiwan (4).

K. pneumoniae ED2 or ED23 strains were isolated, respectively, from bacteremic patients with liver abscesses and patients with liver abscesses and meningitis. Both strains were of multilocus sequence type 23 with a K1 capsular serotype.

Total DNA was extracted from both strains by a mini-QIAamp DNA isolation kit (Qiagen, Germany). The entire genomic sequence was determined using PacBio technologies (Pacific Biosciences, USA). Continuous long reads with a 20-kb average insert size were generated, and read processing and *de-novo* assembly were performed using the HGAP program version 3 (bioinformatics analysis served by Yourgene Biotech, Inc., New Taipei, Taiwan). A comparison of the ED2 and ED23 whole-genome sequences was performed using the MUMmer program version 3.22 (5).

The assembled genome sizes were 5,412,960 bp with a G+C composition of 57.4% for strain ED2 and 5,374,626 bp with a G+C composition of 57.6% for strain ED23. Strain ED23 harbored a plasmid of 212,770 bp with a G+C composition of 50.1%. The similarity in the chromosomal DNA sequences of both strains

was 99.93%. In total, there were 21 sites with gaps appearing between mutually consistent alignments, 11 sites appearing in sequence rearrangement, and 7 sites with inserted duplication.

Accession number(s). The whole-genome sequences of *K. pneumoniae* ED2 and ED23 have been deposited in GenBank under the accession numbers [CP016813](https://ncbi.nlm.nih.gov/nucl/CP016813) (ED2, chromosome), [CP016814](https://ncbi.nlm.nih.gov/nucl/CP016814) (ED23, chromosome), and [CP016815](https://ncbi.nlm.nih.gov/nucl/CP016815) (ED23, plasmid).

FUNDING INFORMATION

This work, including the efforts of Yao-Shen Chen, was funded by Kaohsiung Veterans General Hospital (VGHKS102-016, VGHKS103-055, and VGHKS104-061). This work, including the efforts of Ya-Lei Chen, was funded by Ministry of Science and Technology, Taiwan (MOST) (MOST104-2320-B-017-001).

REFERENCES

- Podschun R, Ullmann U. 1998. *Klebsiella* spp. as nosocomial pathogens: epidemiology, taxonomy, typing methods, and pathogenicity factors. *Clin Microbiol Rev* 11:589–603.
- Siu LK, Yeh KM, Lin JC, Fung CP, Chang FY. 2012. *Klebsiella pneumoniae* liver abscess: a new invasive syndrome. *Lancet Infect Dis* 12:881–887. [http://dx.doi.org/10.1016/S1473-3099\(12\)70205-0](http://dx.doi.org/10.1016/S1473-3099(12)70205-0).
- Fang CT, Chuang YP, Shun CT, Chang SC, Wang JT. 2004. A novel virulence gene in *Klebsiella pneumoniae* strains causing primary liver abscess and septic metastatic complications. *J Exp Med* 199:697–705. <http://dx.doi.org/10.1084/jem.20030857>.
- Chang WN, Huang CR, Lu CH, Chien CC. 2012. Adult *Klebsiella pneumoniae* meningitis in Taiwan: an overview. *Acta Neurol Taiwan* 21:87–96.
- Hsueh PT, Chen YS, Lin HH, Liu PJ, Ni WF, Liu MC, Chen YL. 2015. Comparison of whole-genome sequences from two colony morphovars of *Burkholderia pseudomallei*. *Genome Announc* 3(5):e01194-15. <http://dx.doi.org/10.1128/genomeA.01194-15>.