AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements

Draft Genome Sequence of a Multidrug-Resistant *Klebsiella quasipneumoniae* subsp. *similipneumoniae* Isolate from a Clinical Source

Egon A. Ozer,[a] Andrew R. Morris,[b] Fiorella Krapp,[a] Christopher S. Henry,[c] Keith E. Tyo,[d] Wyndham W. Lathem,[b] Alan R. Hauser[a,b]

Division of Infectious Diseases, Department of Medicine, Northwestern University, Chicago, Illinois, USA[a]; Department of Microbiology-Immunology, Northwestern University, Chicago, Illinois, USA[b]; Mathematics and Computer Science Division, Argonne National Laboratory, Lemont, Illinois, USA[c]; Department of Chemical and Biological Engineering, Northwestern University, Evanston, Illinois, USA[d]

We report here the draft genome sequence of a multidrug-resistant clinical isolate of *Klebsiella quasipneumoniae* subsp. *similipneumoniae*, KP_Z4175. This strain, isolated as part of a hospital infection-control screening program, is resistant to multiple β-lactam antibiotics, aminoglycosides, and trimethoprim-sulfamethoxazole.

Received 5 April 2016 **Accepted** 8 April 2016 **Published** 26 May 2016

Citation Ozer EA, Morris AR, Krapp F, Henry CS, Tyo KE, Lathem WW, Hauser AR. 2016. Draft genome sequence of a multidrug-resistant *Klebsiella quasipneumoniae* subsp. *similipneumoniae* isolate from a clinical source. Genome Announc 4(3):e00422-16. doi:10.1128/genomeA.00422-16.

Copyright © 2016 Ozer et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Address correspondence to Egon A. Ozer, e-ozer@northwestern.edu.

Klebsiella quasipneumoniae, formerly *Klebsiella pneumoniae* phylogroup KpII, was recently taxonomically reclassified as a new sister species of *K. pneumoniae* with two subspecies, *K. quasipneumoniae* subsp. *quasipneumoniae* and *K. quasipneumoniae* subsp. *similipneumoniae* (1). *K. quasipneumoniae*, like *K. pneumoniae*, can cause human infections but is considered less pathogenic and more often associated with carriage than clinical disease (1, 2). However, severe human infections with *K. quasipneumoniae* have been reported (3, 4). Here, we report the draft genome sequence of a multidrug-resistant *K. quasipneumoniae* subsp. *similipneumoniae* strain, isolated from the gastrointestinal tract of a hospitalized patient.

K. quasipneumoniae subsp. *similipneumoniae* strain KP_Z4175 was isolated from a screening rectal culture obtained for infection control purposes from a 53-year-old patient. The patient had a remote history of simultaneous pancreas-kidney transplant, was currently receiving immunosuppressive treatment, and had recently undergone colectomy for an obstructing cecal lymphoma. He was admitted to a tertiary care hospital with increased ostomy output that resolved with medical management. There were no signs of active infection throughout the hospitalization. The isolate was identified as having extended-spectrum β-lactamase activity by CLSI double-disk diffusion Kirby-Bauer testing (5).

KP_Z4175 DNA was sequenced on the MiSeq platform (Illumina Inc., San Diego, CA, USA) generating 2 × 301-bp paired-end reads. A total of 15,256,306 reads were produced comprising 1,540,886,906 bases after adapter sequence trimming. *De novo* assembly was performed using SPAdes version 3.6.2 (6, 7) to generate 97 contigs at least 200 bp in length for a total sequence of 5,598,139 bp. The assembly N_{50} was 332,350 bp, and the average GC content was 57.6%. Annotation was performed by the NCBI Prokaryotic Genome Annotation Pipeline and contained 5,398 coding sequences. Speciation was confirmed by *fusA*, *gapA*, *gyrA*, *leuS*, and *rpoB* analysis (1) and predicted DNA-DNA hybridization of 93.7% against *K. quasipneumoniae* subsp. *similipneumoniae* strain 07A044 (accession no. CBZR00000000) using the GGDC 2.1 software (8).

To examine the antibiotic resistance profile of *K. quasipneumoniae* subsp. *similipneumoniae* strain KP_Z4175, antibiotic resistance genes were identified using ResFinder version 2.1 (9). In addition to $bla_{\text{OKP-B-1}}$, a β-lactamase characteristic of *K. quasipneumoniae* (10), β-lactamase $bla_{\text{OXA-10}}$ and the extended-spectrum β-lactamase $bla_{\text{SHV-12}}$ were identified. Also identified were three aminoglycoside resistance genes (*aadA1*, *aacA4*, and *aac(6′)-IIc*), two fluoroquinolone resistance genes (*aac(6′)Ib-cr* and *QnrB4*), one macrolide-lincosamide-streptogramin B resistance gene (*ere(A)*), two phenicol resistance genes (*cmlA1* and *floR*), one rifampin resistance gene (*ARR-2*), two sulfonamide resistance genes (*sul1* and *sul2*), one tetracycline resistance gene (*tet(D)*), and one trimethoprim resistance gene (*dfrA14*). All identified resistance genes had nucleotide identities of 98.35 to 100% over 85 to 100% of the reference gene lengths. Broth microdilution testing using CLSI breakpoints for *Enterobacteriaceae* indicated that KP_Z4175 is resistant to gentamicin (MIC >64), tobramycin (=32), cefazolin (>64), ceftriaxone (>64), aztreonam (>64), and trimethoprim-sulfamethoxazole (>64). The isolate had intermediate resistance to ampicillin-sulbactam (=16) and pipericillin/tazobactam (=32), and was sensitive to ertapenem (≤0.03), imipenem (=1), meropenem (≤0.03), amikacin (=0.5), cefepime (=8), and ciprofloxacin (=1).

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number LVCD00000000. The version described in this paper is version LVCD01000000.

ACKNOWLEDGMENTS

This work was supported by the National Institute of Allergy and Infectious Diseases (NIAID) grants K24 AI104831, R01 AI053674, and R01

AI118257 (to A.R.H.) and American Cancer Society grant MRSG-13-220-01 (to E.A.O.).

We thank Chao Qi at the Northwestern Memorial Hospital Clinical Microbiology Laboratory and the Special Infectious Diseases Research Laboratory at the Ann & Robert H. Lurie Children's Hospital of Chicago.

FUNDING INFORMATION

This work, including the efforts of Alan R Hauser, was funded by HHS | NIH | National Institute of Allergy and Infectious Diseases (NIAID) (K24 AI104831, R01 AI053674, and R01 AI118257). This work, including the efforts of Egon Anderson Ozer, was funded by American Cancer Society (ACS) (MRSG-13-220-01).

REFERENCES

1. **Brisse S, Passet V, Grimont PA**. 2014. Description of *Klebsiella quasipneumoniae* sp. nov., isolated from human infections, with two subspecies, *Klebsiella quasipneumoniae* subsp. *quasipneumoniae* subsp. nov. and *Klebsiella quasipneumoniae* subsp. *similipneumoniae* subsp. nov., and demonstration that *Klebsiella singaporensis* is a junior heterotypic synonym of *Klebsiella variicola*. Int J Syst Evol Microbiol **64:**3146–3152. http://dx.doi.org/10.1099/ijs.0.062737-0.
2. **Holt KE, Wertheim H, Zadoks RN, Baker S, Whitehouse CA, Dance D, Jenney A, Connor TR, Hsu LY, Severin J, Brisse S, Cao H, Wilksch J, Gorrie C, Schultz MB, Edwards DJ, Nguyen KV, Nguyen TV, Dao TT, Mensink M, Minh VL, Nhu NT, Schultsz C, Kuntaman K, Newton PN, Moore CE, Strugnell RA, Thomson NR**. 2015. Genomic analysis of diversity, population structure, virulence, and antimicrobial resistance in *Klebsiella pneumoniae*, an urgent threat to public health. Proc Natl Acad Sci U S A **112:**E3574–E3581. http://dx.doi.org/10.1073/pnas.1501049112.
3. **Breurec S, Melot B, Hoen B, Passet V, Schepers K, Bastian S, Brisse S**. 2016. Liver abscess caused by infection with community-acquired *Klebsiella quasipneumoniae* subsp. *quasipneumoniae*. Emerg Infect Dis **22**. http://dx.doi.org/10.3201/eid2203.151466.
4. **Arena F, Henrici De Angelis L, Pieralli F, Di Pilato V, Giani T, Torricelli F, D'Andrea MM, Rossolini GM**. 2015. Draft genome sequence of the first hypermucoviscous *Klebsiella quasipneumoniae* subsp. *quasipneumoniae* isolate from a bloodstream infection. Genome Announc **3**(5): e00952-15. http://dx.doi.org/10.1128/genomeA.00952-15.
5. **Clinical and Laboratory Standards Institute**. 2014. Performance standards for antimicrobial susceptibility testing: 24th informational supplement, M100–S24. Clinical and Laboratory Standards Institute, Wayne, PA.
6. **Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA**. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol **19:**455–477. http://dx.doi.org/10.1089/cmb.2012.0021.
7. **Nurk S, Bankevich A, Antipov D, Gurevich AA, Korobeynikov A, Lapidus A, Prjibelski AD, Pyshkin A, Sirotkin A, Sirotkin Y, Stepanauskas R, Clingenpeel SR, Woyke T, McLean JS, Lasken R, Tesler G, Alekseyev MA, Pevzner PA**. 2013. Assembling single-cell genomes and mini-metagenomes from chimeric MDA products. J Comput Biol **20:** 714–737. http://dx.doi.org/10.1089/cmb.2013.0084.
8. **Meier-Kolthoff JP, Auch AF, Klenk HP, Göker M**. 2013. Genome sequence-based species delimitation with confidence intervals and improved distance functions. BMC Bioinformatics **14:**60. http://dx.doi.org/10.1186/1471-2105-14-60.
9. **Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, Lund O, Aarestrup FM, Larsen MV**. 2012. Identification of acquired antimicrobial resistance genes. J Antimicrob Chemother **67:**2640–2644. http://dx.doi.org/10.1093/jac/dks261.
10. **Haeggman S, Löfdahl S, Paauw A, Verhoef J, Brisse S**. 2004. Diversity and evolution of the class A chromosomal beta-lactamase gene in *Klebsiella pneumoniae*. Antimicrob Agents Chemother **48:**2400–2408. http://dx.doi.org/10.1128/AAC.48.7.2400-2408.2004.