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

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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.

*K. 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. pneumoniae* 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 *Klebsiella 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 N₅₀ 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*, *gptA*, *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*<sub>OKP-B-1</sub>, a β-lactamase characteristic of *K. quasipneumoniae* (10), β-lactamase *bla<sub>OKP-10</sub>* and the extended-spectrum β-lactamase *bla<sub>SHV-12</sub>* were identified. Also identified were three aminoglycoside resistance genes (*aadA1*, *aacA4*, and *aac(6’)/I-IC*), two fluoroquinolone resistance genes (*aac(6’)/Ib-cr* and *QnrB4*), one macrolide-lincosamide-streptogramin B resistance gene (*erm(A)*), two plasmidic resistance genes (*cmh1A* 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), ceftazidime (≥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

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All 118257 (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).

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