



Draft Genome Sequences of *bla*_{KPC}-Containing *Enterobacter aerogenes*, *Citrobacter freundii*, and *Citrobacter koseri* Strains

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ABSTRACT We report here the draft genome sequences of four *bla*_{KPC}-containing bacteria identified as *Klebsiella aerogenes*, *Citrobacter freundii*, and *Citrobacter koseri*. Additionally, we report the draft genome sequence of a *K. aerogenes* strain that did not contain a *bla*_{KPC} gene but was isolated from the patient who had the *bla*_{KPC-2}-containing *K. aerogenes* strain.

Klebsiella pneumoniae carbapenemase (KPC) was initially described in *K. pneumoniae*; however, the *bla*_{KPC} gene that encodes KPC has since been identified in diverse bacteria, including other *Klebsiella* species and in *Citrobacter* species (1–15). Thus, whole-genome sequencing is an important tool for providing insight into the dissemination of the *bla*_{KPC} genes among diverse species, including those that are not a frequent cause of human illness but may serve as reservoirs for antibiotic resistance genes.

The *Citrobacter freundii* strains (YDC691 and YDC692-2) described in this report were isolated in 2015 from a sputum sample (YDC691) and a bronchoalveolar lavage fluid sample (YDC692-2) from the same patient, collected a week apart. The *Klebsiella aerogenes* strains (YDC581 and YDC581-4) and *Citrobacter koseri* strain YDC582 were isolated in 2012 from either blood (YDC581 and YDC581-4) or Jackson-Pratt drain fluids (YDC582), which were collected on the same day from the same patient. The *Klebsiella* and *Citrobacter* strains were tested for their susceptibilities to 21 antibiotics by determining their MICs using the Sensititre Gram-negative breakpoint plates. All of the strains exhibited resistance to ticarcillin-clavulanic acid, piperacillin-tazobactam, aztreonam, ceftazidime, and cefotaxime. Also, all of the strains except for YDC581-4 exhibited resistance to ertapenem, and only strain YDC692-2 exhibited resistance to imipenem and doripenem.

Genomic DNA was extracted from the *K. aerogenes* and *Citrobacter* strains using the Sigma GenElute genomic DNA kit (Sigma-Aldrich, St. Louis, MO). The genomes were sequenced using paired-end 500-bp-insert libraries on the Illumina HiSeq 4000. The genomes were assembled using SPAdes version 3.7.1 (16) and were filtered to contain only contigs ≥ 500 bp in length and with $\geq 5\times$ coverage. Antibiotic resistance genes were detected in each of the genome assemblies using the Comprehensive Antibiotic Resistance Database (CARD) version 1.1.8 (17).

The draft genome assemblies of the *C. freundii* strains had sizes of 5.17 to 5.74 Mb and a GC content of 51.6%. The *C. koseri* strain YDC582 had an assembly size of 4.65 Mb and a GC content of 53.78%. The *K. aerogenes* genome assemblies had sizes of 5.18 and 5.37 Mb and a GC content of 55%. The genome assemblies of the *C. freundii* strains all contained the *bla*_{KPC-3} gene, as well as the *bla*_{OXA-9}, *bla*_{SHV-7}, and *bla*_{TEM-1} genes. The

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strains isolated from the second patient included *K. aerogenes* strain YDC581, which contained *bla*_{KPC-2}, and *K. aerogenes* strain YDC581-4, which was isolated from the same patient sample but did not contain any detectable *bla*_{KPC} genes. The second patient also had *C. koseri* strain YDC582, which was isolated from a sample different from that of strains YDC581 and YDC581-4, and it contained a *bla*_{KPC-2} gene. All three strains from this patient also contained a *bla*_{TEM-1} gene.

In summary, we report the draft genome sequences of four *bla*_{KPC}-containing *K. aerogenes*, *C. freundii*, and *C. koseri* strains, as well as one *K. aerogenes* strain that did not contain a *bla*_{KPC} gene. These genome sequences are significant because they represent two sets of strains that were coisolated from samples from two different patients and provide insight into the transmission of the *bla*_{KPC} gene between multiple species from the same patient.

Accession number(s). The draft genome assemblies of *C. koseri* strain YDC582, *K. aerogenes* strain YDC581-4, *K. aerogenes* strain YDC581, *C. freundii* strain YDC691, and *C. freundii* strain YDC692-2 have been deposited in GenBank under the accession numbers PGIF00000000, PGIG00000000, PGIH00000000, PGIJ00000000, and PGII00000000, respectively.

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