Klebsiella pneumoniae, a bacterium belonging to the ESKAPE group (Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter species), is responsible for serious community- and hospital-acquired infections (1–5). The difficulty in treating infections caused by K. pneumoniae is increasing due to its ability to acquire antibiotic resistance genes (6–8), including carbapenemases (9).

Despite the clinical importance of this bacterium, the number of identified and characterized virulence factors has remained relatively low (10–13). Nucleotide and whole-genome mapping comparisons among several strains led to the identification of a high heterogeneity zone (HHZ) (14), which includes the capsular polysaccharide biosynthesis gene cluster (HHZ subregion 4) and a hot spot (HHZ subregion 3), which in strain K. pneumoniae NTUH-K2044 is the point of insertion of a fragment that includes a pathogenicity island related to that found in Yersinia species. This fragment includes the genes coding for the yersiniabactin siderophore system, a region previously identified in a K. pneumoniae hot spot (HHZ subregion 3), which in strain K. pneumoniae is increasing due to its ability to acquire antibiotic resistance genes (6–8), including carbapenemases (9).

Despite the clinical importance of this bacterium, the number of identified and characterized virulence factors has remained relatively low (10–13). Nucleotide and whole-genome mapping comparisons among several strains led to the identification of a high heterogeneity zone (HHZ) (14), which includes the capsular polysaccharide biosynthesis gene cluster (HHZ subregion 4) and a hot spot (HHZ subregion 3), which in strain K. pneumoniae NTUH-K2044 is the point of insertion of a fragment that includes a pathogenicity island related to that found in Yersinia species. This fragment includes the genes coding for the yersiniabactin siderophore system, a region previously identified in a Klebsiella plasmid, and genes coding for conjugation functions (10, 14, 15).

K. pneumoniae strains harboring carbapenem resistance genes, such as blαKPC or blαNDM-1, are becoming more frequent and extremely problematic. K. pneumoniae strains usually harbor several plasmids (4, 6, 16). Analysis of the nucleotide sequences of strains Kb140 and Kb677 showed homology to the IncFII-FIB-like plasmids pKPN- and pKpQIL-type (17, 18), pI,nC-ShV (17), and pKP1780-kpc (accession no. KF874497), pNJST258C1, pNJST258C2 (19), pBK31551, pBK15692 (20), pI (accession no. CP006657), pr55 (21), and the K. pneumoniae subsp. rhinoscleromatis pKRH (22).

Nucleotide sequence accession numbers. The GenBank accession no. for K. pneumoniae Kb140 and Kb677 are AQRD01000001 to AQRD01000008 and AQP01000001 to AQP01000012, respectively.
ACKNOWLEDGMENTS
This work was supported by Public Health Service grants 2R15AI047115 (to M.E.T.), the U.S. Department of Energy Joint Genome Institute through the Office of Science of the U.S. Department of Energy under contract DE-AC02-05CH11231, the Cleveland Department of Veterans Affairs, the Veterans Affairs Merit Review Program award I101BX001974, and the Geriatric Research Education and Clinical Center VISON 10. This work was also supported by funds from the National Institute of Allergy and Infectious Diseases of the National Institutes of Health, under award numbers R01AI063517 and R01AI10056 (to R.A.B.), and through the Antibiotic Resistance Leadership Group under National Institutes of Health award UM1AI104681 (to D.V.D.) and the Clinical and Translational Science Collaborative of Cleveland, UL1TR000439 from the National Center for Advancing Translational Sciences (NCATS) component of the National Institutes of Health (to D.V.D. and F.P.).

The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

REFERENCES