**Klebsiella variicola** Reference Strain F2R9 (ATCC BAA-830)

**Genome Sequence**

Ulises Garza-Ramos,a Nadia Rodriguez-Medina,a Luis Lozano-Aguirre,b Jesús Silva-Sancheza, Margarita Sanchez-Arias,a Jeannet Rodriguez-Olguina, and Esperanza Martínez-Romeroa

aInstituto Nacional de Salud Pública (INSP), Centro de Investigación Sobre Enfermedades Infecciosas (CISEI), Cuernavaca, Morelos, Mexico

bCentro de Ciencias Genómicas, Laboratorio de Genómica Evolutiva, Universidad Nacional Autónoma de México, Cuernavaca, Morelos, Mexico

**ABSTRACT** Klebsiella variicola F2R9 was isolated from banana root, and its sequence has been deposited as ATCC BAA-830. It corresponds to sequence type 11 (ST11) and contains no identifiable plasmids. The genome showed few antimicrobial resistance and virulence genes and several plant association genes. The strain showed susceptibility to most antimicrobials and avirulent behavior.

**K** lebsiella variicola was described as a new bacterial species in 2004 and is considered to belong to the Klebsiella pneumoniae complex (1). Studies on the molecular epidemiology of K. variicola (2) and comparative genomics of multidrug-resistant isolates (3) as well as species-differentiating approaches within the K. pneumoniae complex have been reported. K. variicola may cause different infections, in some cases with a high mortality, and is currently considered an emerging pathogen of humans (4).

KL16 according to the Kaptive database (9). F2R9 only showed ampicillin resistance in culture medium, with avirulent behavior in mice (10). We recommend using the *Klebsiella variicola* F2R9 (ATCC BAA-830) genome as the reference genome mainly for *K. variicola* comparative genomics studies and for *in vitro* and *in vivo* assays.

**Data availability.** This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession no. CP072130. The raw sequence reads are available under the SRA accession no. SRR1414549 and SRR14530140.

**ACKNOWLEDGMENTS**

We thank Marco Marco A. Rogel for excellent technical assistance. This work was funded by the Consejo Nacional de Ciencia y Tecnología (CONACyT) with SEP-CONACYT grant no. 215146 and IN200021 from PAPIIT UNAM.

**REFERENCES**