An antibiotic-susceptible and hypermucoviscous clinical isolate of _Klebsiella variicola_ (K. variicola 8917) was obtained from the sputum of an adult patient. This work reports the complete draft genome sequence of _K. variicola_ 8917 with 103 contigs and an annotation that revealed a 5,686,491-bp circular chromosome containing a total of 5,621 coding DNA sequences, 65 tRNA genes, and an average G+C content of 56.98%.

In the last decade, a new hypervirulent (hypermucoviscous) variant of _Klebsiella pneumoniae_ has been described (1). Most isolates of hypervirulent _K. pneumoniae_ are very susceptible to antimicrobials (except ampicillin). However, a multidrug-resistant and hypervirulent variant of _K. pneumoniae_ has also been described as the next “superbug” (2). On the other hand, _Klebsiella variicola_ is a Gram-negative rod of the _Enterobacteriaceae_ family; it was described as a new bacterial species in 2004 (3). Currently, _K. variicola_ is known to be an endophyte of plants (3, 4), a symbiont in insects (5), and a pathogen in humans (3). A susceptible and multiresistant phenotype of _K. variicola_ has been identified, corresponding to an extended spectrum β-lactamase (ESBL)—producing _K. variicola_, encoding the SHV-type and CTX-M-15 genes (6, 7).

It is difficult to distinguish _K. variicola_ from _K. pneumoniae_ biochemically as bacterial species. Therefore, it is necessary to use molecular tools such as the _rpoB_ analysis. Accordingly, our team developed a multiplex PCR assay for the proper differentiation of these sister bacteria (7). Using this molecular tool, a screening for antibiotic-susceptible and multiresistant _K. pneumoniae_ clinical isolates was carried out in several Mexican hospitals (7). As a result, the susceptible _K. variicola_ clinical isolate 8917 was identified. This isolate was obtained from the sputum of a 76-year-old man at the Hospital Regional Centenário de la Revolución Mexicana in Morelos, Mexico, in 2011. This isolate was initially identified as a susceptible (except to ampicillin) _K. pneumoniae_ isolate using a MicroScan Walkaway system (Dade Behring, West Sacramento, CA, USA). Subsequently, it was identified as _K. variicola_ using the M-PCR-1; this was confirmed by the phylogeny analysis of the _rpoB_ gene (7). The hypermucoviscous phenotype of _Klebsiella variicola_ isolate 8917 was determined using the semiquantitative string test (8) and then was considered for whole-genome sequencing.

A total genomic sample of _K. variicola_ isolate 8917 was extracted and purified using the DNeasy kit (Qiagen, Germany). The whole-genome sequence was generated using pyrosequencing on the 454 Roche FLX Titanium platform. The sequence data totaled 250,217 reads, with a range in length of 30 to 953 bp. Reads longer than 500 bp were used for _de novo_ assembly with the CLC Genomics Workbench version 4.0 (CLC bio). In total, 103 contigs with an _N_50 of 257,189 bp were obtained. The estimated genome size was 5,686,491 bp with a 20X coverage, and 99.93% of the bp were above Q40. Gene prediction and annotation were carried out using the bioinformatic MicroScope platform (9). A total of 5,621 coding DNA sequences and 65 tRNA genes were determined. The BLAST searching analysis of the _magA_, _rmpA_, and _rmpA2_ genes described in hypervirulent _K. pneumoniae_ turned out to be negative on the hypermucoviscous _K. variicola_ 8917 genome. However, the following virulence-associated determinants were positive with different amino acid identities: _uge_ (99.10%), _ureA_ (100%), _wabG_ (99.47%), _iroA_ (64.9%), _iutA_ (72.9%), _kiuABC_ (>98.6%), _mceG_ (53.1%), _mrkABCDFHIIJ_ (>86.8%), and _entB_ (99.6) and a nucleotide identity of 100% with _wzc-932_ (serotype). Further analyses are required to identify the genes involved in the hypermucoviscous phenotype on _K. variicola_ clinical isolate 8917.

**Nucleotide sequence accession number.** The annotated genome sequence is available at the European Nucleotide Archive under the accession number CEGG01000001.

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