



Draft Genome Sequences of Endophytic Isolates of *Klebsiella variicola* and *Klebsiella pneumoniae* Obtained from the Same Sugarcane Plant

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ABSTRACT Endophytic *Klebsiella variicola* KvMx2 and *Klebsiella pneumoniae* KpMx1 isolates obtained from the same sugarcane stem were used for whole-genome sequencing. The genomes revealed clear differences in essential genes for plant growth, development, and detoxification, as well as nitrogen fixation, catalases, cellulases, and shared virulence factors described in the *K. pneumoniae* pathogen.

Klebsiella variicola has been described as an endophyte and has been identified in different plants (1). However, *Klebsiella pneumoniae* is considered a pathogen in humans and equally as an endophytic bacterium; nevertheless, few data and scarce genomes have been described for isolates obtained from plants. In the case of *K. pneumoniae* 342, obtained from maize (2), the isolate actually corresponds to *K. variicola* (3). A clear difference between these species is the capacity of *K. variicola* to fix atmospheric nitrogen and promote plant growth (1, 3–6). For this study, *Klebsiella* species colonies were obtained from the root of a sugarcane plant (ATMEX 96-40) grown in Cuautla, Morelos, Mexico. A multiplex PCR (M-PCR-1) (7) was used for the proper identification and differentiation of *K. variicola* and *K. pneumoniae* isolates. Colonies of both the *K. variicola* KvMx2 and *K. pneumoniae* KpMx1 isolates were identified and then used for whole-genome sequencing.

Total genomic DNA was extracted and purified using the DNeasy kit (Qiagen, Germany). Whole-genome sequences were generated using an Illumina (MiSeq) platform, and a total of 4,706,652 paired-end reads in *K. variicola* KvMx2 and 2,562,748 paired-end reads in *K. pneumoniae* KpMx1 with a length of 150 bp were obtained. Quality-based trimming was performed with the SolexaQA software, and *de novo* assembly was done with SPAdes version 3.1.1. The contigs were subjected to a scaffolding process with SSPACE version 2.0. For *K. variicola* KvMx2 and *K. pneumoniae* KpMx1, respectively, a total of 37 contigs (N_{50} , 397,617 bp) and 50 contigs (N_{50} , 377,295 bp) and estimated genome sizes of 5,528,301 bp (128× coverage) and 5,371,602 bp (72× coverage) were determined. Gene prediction and annotation were carried out using the bioinformatic MicroScope platform (8). In the *K. variicola* KvMx2 genome, a total of 5,431 coding DNA sequences (CDSs), 75 tRNA genes, and 6 rRNAs were found. In the *K. pneumoniae* KpMx1 genome, a total of 5,324 CDSs, 82 tRNA genes, and 9 rRNAs were found. The average G+C contents were similar in the two genomes, at 57.39% for

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K. variicola KvMx2 and 57.46% for *K. pneumoniae* KpMx1. An average nucleotide identity (ANI) >95% (9) confirmed the bacterial species.

A genomic comparison between *K. variicola* KvMx2 and *K. pneumoniae* KpMx1 showed a pangenome of 6,306 families of proteins, with a core genome of 4,306 families and a variable genome of 1,078 families of proteins for *K. variicola* KvMx2 and 922 families of proteins for *K. pneumoniae* KpMx1. The *K. variicola* KvMx2 genome revealed genes essential for the biosynthesis of indole-3-acetic acid (IAA), acetoin and 2,3-butanediol, and rhodanase, which are involved in plant growth, development, and detoxification of cyanide compounds (10), respectively. Likewise, the *K. variicola* genome contains the *nifJ-NifQ* nitrogen fixation gene cluster and is a clear difference between the two bacterial species. Otherwise, the catalase genes *bglX* and *katGE* are contained in both bacterial species; however, the cellulase *bglH* gene is contained only in *K. variicola* KvMx2.

With respect to virulence factors, the *entB*, *mrkABCFHJL*, *ureA*, *uge*, and *wabG* genes are contained in both the *K. variicola* KvMx2 and *K. pneumoniae* KpMx1 genomes. Only in the *K. variicola* KvMx2 genome was the *kfuABC* operon identified. Finally, *K. pneumoniae* KpMx1 contained the copper resistance *pcoABCDER* operon.

Accession number(s). The annotated genome sequences are available at the European Nucleotide Archive under accession numbers FLLH01000001 to FLLH01000037 (*K. variicola* KvMx2) and FLLB01000001 to FLLB01000050 (*K. pneumoniae* KpMx1).

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