

Exploring Resistance and Virulence Factors in *Klebsiella variicola* Genomes: An *In Silico* Investigation

Letícia Cabral Soares ¹, Jéssica Nogueira Rosa ¹, Mariana Dias de Melo ¹, Matheus Machado Guidini ¹; Bruna Araújo Euzébio Alves Jacob Lopes ¹; Denise Mara Soares Bazzolli ^{1*}

¹ Laboratory of Molecular Genetics of Bacteria, Federal University of Viçosa (UFV) – Microbiology Department, Biotechnology applied to agriculture Institute (BIOAGRO) - Vila Matoso, 205 - Santo Antonio, Viçosa - MG, 36570-000, Brazil.

* Corresponding author. E-mail: dbazzolli@ufv.br

Klebsiella variicola is a Gram-negative bacillus widespread worldwide, having emerged as an opportunistic pathogen in humans and animals. However, it can also be found in food, soil, and water environments. It belongs to the Enterobacteriaceae family and is a *Klebsiella pneumoniae* Species Complex (KpSC) member, known for its significant multidrug resistance phenotype. Bacteria within this complex, as well as several other members of the Enterobacteriaceae family, are recognized for their resistance to β -lactams, production of Extended-Spectrum Beta-Lactamase (ESBL), and even resistance to carbapenems. This species's genetic repertoire of virulence and resistance and its ecological niche across different reservoirs is little known. Consequently, this study aimed to discern antibiotic resistance genes (ARs) and virulence factors (VFs) in complete genomes of *K. variicola* from diverse reservoirs. Complete genomes were accessed from the NCBI database, and subsequently, from the curated database, these genomes were analyzed for the presence of ARs using the CARD program (90% identity and 60% coverage) and for VFs using the oriTfinder program tool based on BLASTp (>80% identity and coverage). Consequently, 91 complete genomes of *K. variicola* originating from various sources were selected: human (51.6%), environmental (11%), animal (9.9%), plant (9.9%), food (6.6%), and unknown (11%) reservoirs. Remarkably, 98.9% of the investigated genomes harbored at least one genetic marker linked to antimicrobial resistance, spanning 11 antimicrobial classes, including beta-lactams (33.3%), fluoroquinolones (9.1%), aminoglycosides (7.2%), tetracyclines (6.8%), macrolides (5.6%), and others (38%). The most common resistance mechanism identified was antibiotic efflux (62.3%), followed by antibiotic target alteration (20.5%). The VFs present in the genomes were categorized into 13 classes, with iron transport (32.05%), type I fimbriae (15.41%), type III fimbriae (13.72%), and LPS biosynthesis (8.4%) being the most prevalent. Interestingly, siderophores such as aerobactin (43.39%) and salmochelin (8.47%) were abundant in the analyzed genomes. In conclusion, this study reveals that *K. variicola* is a potential emerging pathogen in diverse ecological niches and possesses an extensive array of virulence and resistance genes, posing a new challenge in public health.

Key words: Multidrug Resistance; Virulence; Enterobacteriaceae; OneHealth

Explorando Fatores de Resistência e Virulência em Genomas de *Klebsiella variicola*: Uma Investigação *In Silico*

Este estudo teve como objetivo uma investigação abrangente dos genomas de *Klebsiella variicola* e explorou a presença de genes de resistência a antibióticos (ARs) e fatores de virulência (FVs). A análise de 91 genomas revelou que 98,9% carregavam ARs em 11 classes antimicrobianas, com destaque para os beta-lactâmicos (33,3%) e fluoroquinolonas (9,1%). FVs, como o transporte de ferro e fímbrias, foram prevalentes. Isso ressalta o potencial de *K. variicola* como patógeno emergente em diversos ecossistemas, desafiando a saúde pública.

Palavras-chave: Multidrogas-resistente; Virulência; Enterobacteriaceae; OneHealth.

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