

In Silico Characterization of Integrative and Conjugative Elements (ICEs) in *Klebsiella variicola*

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

The Gram-negative bacillus *Klebsiella variicola*, which is found in various reservoirs such as food, plants, water, and the environment, has a global distribution and is emerging as an opportunistic pathogen in humans and animals. This microorganism, belonging to the Enterobacteriaceae family and the *Klebsiella pneumoniae* species complex (KpSC), possesses significant virulence factors (VFs). Virulence factors in *K. variicola* are attributed to the production of siderophores (enterobactin), type I and III fimbriae, and lipopolysaccharides (LPS). Mobile genetic elements (MGEs) such as Integrative and Conjugative Elements (ICEs) play a crucial role in carrying virulence genes, including the siderophore Yersiniabactin, which is well-established in *K. pneumoniae* but remains uncharacterized in *K. variicola*. Emphasizing this significance, the objective of this study was to search for integrative and conjugative elements in the genomes of *K. variicola*. Thus, complete genomes were obtained from the National Center for Biotechnology Information (NCBI). The search for typical conjugative modules of ICEs was conducted using the databases oriTfinder and CONJscan. Delimitation and inspection of the ICE were performed manually. Functional annotation was carried out using the EggNOG-mapper database. The ICE's dissemination was assessed through MegaBLAST alignment (>98% coverage/identity). We obtained 91 complete genomes. Among these genomes, we detected only one potential ICE, which we named ICEKv1 (unknown reservoir). ICEKv1 has a size of 79.2 Kb, a GC content of 52%, a Tyr recombinase-type integrase, a tRNA-Asn integration site, and a MOB_C family relaxase. Functional annotation of ICEKv1 genes is associated with categories involving cellular processes (28.3%), virulence (28.3%), ICE core (32%), and unknown function (11.4%). Among the virulence-associated genes, we highlight those encoding the yersiniabactin siderophore. ICEKv1 shares 99.6% identity and 45% coverage with ICEKp14 and 99.9% identity and 96% coverage with ICEKp1, both described in *K. pneumoniae*. ICEKv1 is not widespread in *K. variicola* and other species. In conclusion, this work characterizes a potential new ICE, named ICEKv1, in *K. variicola* for the first time. ICEKv1 carries genes encoding the siderophore Yersiniabactin, a determinant virulence factor that categorizes *K. variicola* as an emerging pathogen.

Key words: Yersiniabactin, virulence, emerging pathogen, *Klebsiella*.

Caracterização *In Silico* de Elementos Integrativos e Conjugativos – ICEs em *Klebsiella variicola*

Neste estudo, tivemos como objetivo buscar por elementos integrativos e conjugativos em genomas de *K. variicola*. Identificamos um EIC putativo ICEKv1, tamanho de 79,2Kb e com o uso do preditor, verificamos a presença de um gene de virulência associado ao sideróforo Yersiniabactina. Anotação funcional mostrou associação com as categorias processos celulares (28.3%), virulência (28.3%), ICE core (32%) e função desconhecida (11.4%). Concluindo, este trabalho caracteriza pela primeira vez em *K. variicola* um possível novo ICE denominado ICEKv1. O ICEKv1 transporta genes que codificam para o sideróforo yersiniabactina, um fator de virulência determinante para elencar *K. variicola* como patógeno emergente.

Palavras-chave: Yersiniabactina, Virulência, Patógeno emergente, *Klebsiella*

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