

Mobilome and antimicrobial resistance: impact of the animal production chain using *Escherichia coli* as a model.

Jordano Alexandre de Carvalho¹, Nayla Kellen de Oliveira Ventura¹, Rodrigo Sebastião Machado de Freitas¹, Gabriel Alves Silva de Oliveira¹, Luís Augusto Nero¹, Ricardo Seiti Yamatogi¹

¹ Universidade Federal de Viçosa, Departamento de Veterinária, Viçosa/ MG, Brasil

Multidrug-resistant (MDR) organisms pose a significant challenge in the worldwide context. Resistance genes are prone to mutation and are transmitted through horizontal mechanisms. This work outlined a genotypic antibiotic resistance profile in *Escherichia coli* isolates sourced from animal production chains. A total of 273 isolates (n = 273) were obtained from five production systems: cattle (n = 73), fish (n = 19), dairy (n = 40), swine (n = 63), and poultry (n = 78). The isolates were subjected to massive sequencing and analyzed with bioinformatics tools for quality pre-assembly (Trimmomatic v0.39), assembly (SPAdes v3.15.5), and annotation (Prokka v1.14.5). Transposons (MGEFinder v1.1.2), plasmids (MOB Suite v3.1.8), and prophages (Virsorter2 v2.2.4) of each isolate were identified, and the resistance genes present in these mobile genetic elements were characterized (ABRicate v1.0.1, CARD database). Among the prophages, *cpxA* (aminoglycoside/aminocoumarin) was the most frequent gene, and aminocoumarins, tetracyclines, and disinfectant agents were the classes with the highest number of resistance genes. Plasmid investigation exhibited 575 different plasmids, with 167 different types with *rep_cluster_2350*, *Col(MG828)*, *rep_cluster_125*, *IncFIB*, and *IncI-gamma/K1* as the most frequent. Aminoglycosides and sulfonamides were the main classes inside these structures, and *qacEdelta1* and *sul1* were the most frequently reported genes. Regarding transposons, genes within proximity of up to 5 kbp from the transposon or insertion sequence were considered co-located with the mobile element. The frequent classes reported in the analysis were the aminoglycosides, tetracyclines, and fluoroquinolones, and *sul2*, *blaTEM-1*, and *floR* were the frequent genes reported. Important Extended Spectrum Beta-Lactamase (ESBL) genes such as *blaCMY*, *blaSHV*, *blaCTX-M*, and colistin genes as *mcr* families were reported following the transposon. This work demonstrated a large presence of resistance genes in animal production chains inside mobile genetic elements highlighting the surveillance and monitoring of antimicrobial resistance.

Agradecimentos: DTI-UFV, Fapemig, Capes, CNPq, UFV

