

Detection of ESBL-producing *Klebsiella pneumoniae* in samples from meat rabbits

Vanessa Silva^{1,4}, Adriana Silva^{2,4}, Manuela Caniça^{5,6,7}, Rani Rivière⁶, Patricia Poeta^{1,4,5,8}, Gilberto Igrejas^{1,3}

¹LAQV-REQUIMTE, Department of Chemistry, NOVA School of Science and Technology, Universidade Nova de Lisboa, Caparica, Portugal

²Department of Genetics and Biotechnology, University of Trás-os-Montes and Alto Douro (UTAD), Vila Real, Portugal.

³Functional Genomics and Proteomics Unit, University of Trás-os-Montes and Alto Douro (UTAD), Vila Real, Portugal

⁴Microbiology and Antibiotic Resistance Team (MicroART), Department of Veterinary Sciences, University of Trás-os-Montes and Alto Douro (UTAD), Vila Real, Portugal.

⁵Associate Laboratory for Animal and Veterinary Sciences (AL4Animals), Portugal

⁶National Reference Laboratory of Antibiotic Resistances and Healthcare Associated Infections, Department of Infectious Diseases, National Institute of Health Dr. Ricardo Jorge, Lisbon, Portugal

⁷Centre for the Studies of Animal Science, Institute of Agrarian and Agri-Food Sciences and Technologies, University of Porto, Porto, Portugal

⁸CECAV - Veterinary and Animal Research Centre, University of Trás-os-Montes and Alto Douro, Vila Real, Portugal

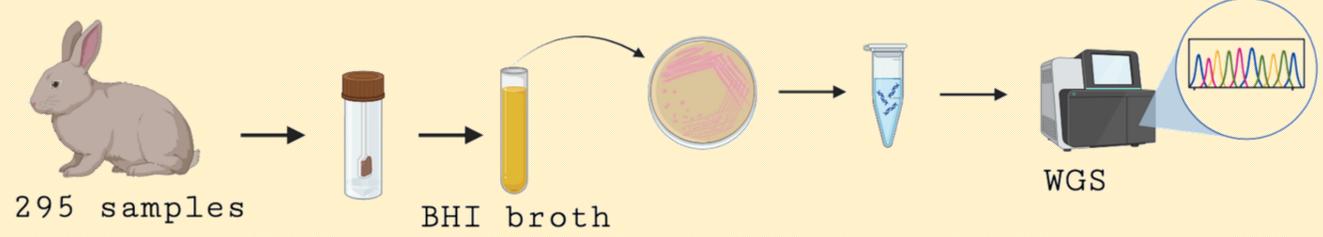
*vanessasilva@utad.pt



Introduction

Klebsiella pneumoniae is an opportunistic pathogen that can acquire multiple antimicrobial resistance mechanisms. The presence of multidrug-resistant *K. pneumoniae* in food-producing animals raises concerns about its potential role in the dissemination of resistance genes. This study aimed to investigate the occurrence of *K. pneumoniae* in healthy meat rabbits and characterize its antimicrobial resistance and virulence profiles.

Materials and Methods



Results

Out of 295 samples, only 6 (2%) were ESBL-producing *K. pneumoniae*. All isolates were multidrug-resistant, carrying genes for resistance to antibiotics such as *bla*_{TEM-1}, *bla*_{CTX-M-15}, *bla*_{SHV} variants, and *bla*_{OXA-1}. Resistance genes for aminoglycosides, tetracyclines, sulfonamides, fluoroquinolones, and fosfomycin were also detected (Figure 1). Heavy metal resistance genes (*sil* and *pco*) were present in all isolates, as well as efflux pump regulators (*ramA*, *marA*, and *baeR*). The isolates belonged to sequence types ST307, ST45, ST193, and ST2026 (Figure 2).

	Aminoglycosides	Cephalosporins (3rd gen.)	Fluoroquinolones	Penicillins	Phenolics	Sulfonamides	Tetracycline	Trimethoprim
VS3367	●	●	●	●		●	●	●
VS3368	●	●	●	●		●	●	●
VS3369	●			●	●	●		●
VS3370	●			●		●	●	●
VS3371	●			●	●	●	●	●
VS3372	●		●	●		●	●	●

Figure 1. Phenotypic antimicrobial resistance profiles of *K. pneumoniae* isolates recovered from healthy meat rabbits.

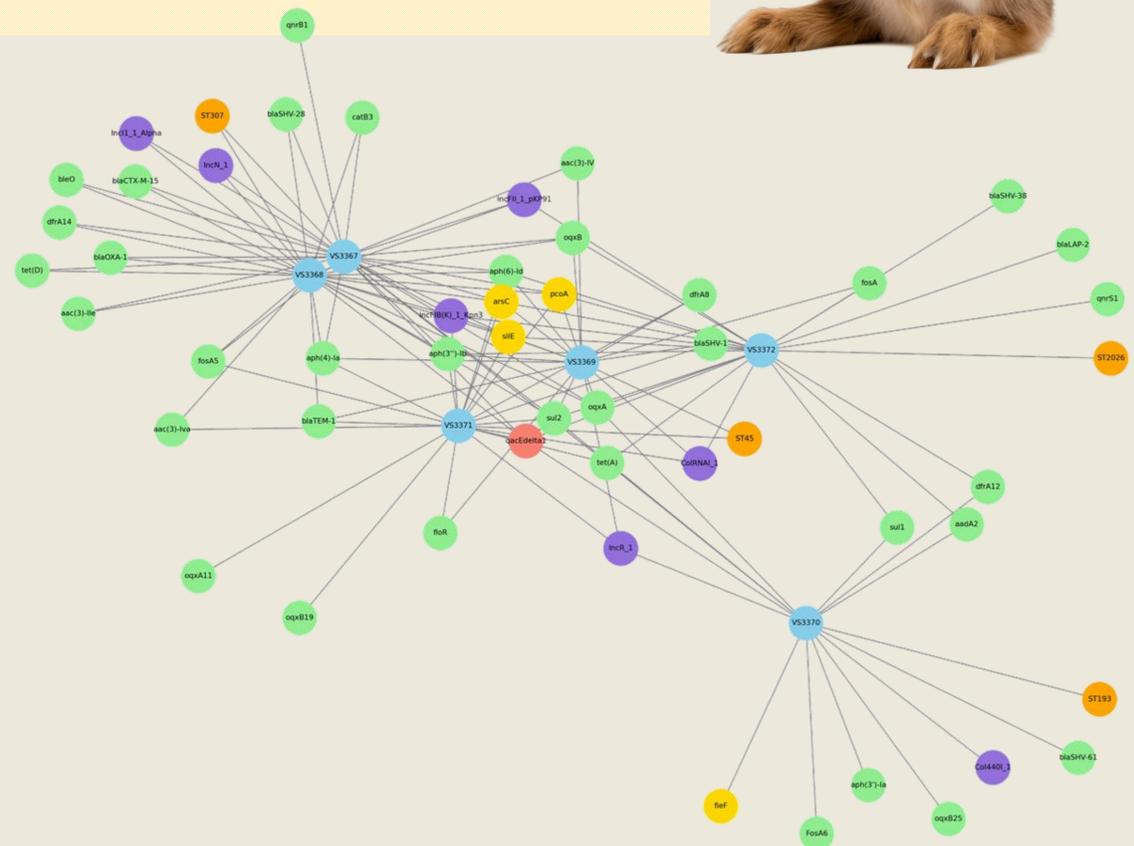


Figure 2. Network of *K. pneumoniae* isolates and associated genetic elements. Nodes represent isolates (blue), resistance genes (green), plasmids (purple), sequence types (orange), and resistance to metals (yellow) or biocides (red). Connections indicate the presence of each element in a given isolate.

Conclusions

These findings reinforce the need for continuous monitoring of antimicrobial resistance in *K. pneumoniae* from food-producing animals, as their potential role in the spread of resistance genes poses a risk to public health

