Title: IDENTIFICATION OF VIRULENCE FACTORS AND ANTIBIOTIC RESISTANCE PROFILE OF *ESCHERICHIA COLI* ISOLATED FROM A DIARRHEA OUTBREAK IN A RABBITRY IN PIRASSUNUNGA, SP, BRAZIL

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Abstract:

Escherichia coli is a commensal inhabitant of the intestinal tracts of healthy humans and many animal species, but it can also cause a wide range of diseases, ranging from diarrhea to extraintestinal infections. Although usually harmless, various strains of *E. coli* have acquired genetic determinants (virulence factors) rendering them pathogenic for both humans and animals. Diarrheagenic strains of *E. coli* can be divided into at least six different categories with corresponding distinct pathogenic schemes. Additionally, in the veterinary area, the alarming state of bacterial antibiotic resistance is seen in examining the *E. coli* isolates, where attention has been given especially to food-producing animals as rabbit (*Oryctolagus cuniculus*), a species of little livestock interest in Brazil. The purpose of this study was to investigate an outbreak of diarrheagenic disease in the rabbitry of the Campus of the University of São Paulo in Pirassununga, São Paulo, Brazil. In the last five months, 24 out of 155 raised rabbits have died showing typical symptoms of diarrhea. Samples of intestinal content from the small intestine of a necropsied animal were collected, plated onto MacConkey agar plates and incubated aerobically at 37°C for 48h. *Escherichia coli* was identified according to morphology, gram-stain, and biochemical properties. Antibiotic susceptibility was tested by disk diffusion method on Mueller Hinton agar. *E. coli* isolate was only resistant to amikacin. A multiplex PCR was performed to determine the presence of six virulence factors (*ST1*, *LT1*, *LT2*, *VT1*, *VT2* and *eae*) and Pho gene, and a duplex PCR was carried out targeting *Einv* e *Eagg* genes. For the *E. coli* isolate, PCR amplifications were obtained for *Pho A*, *ST1*, *eae* and *Eagg* genes. In this context, an unusual simultaneous detection of *ST1*, *eae and Eagg* genes requires further investigations for better characterization of this isolate. We believe that this report can contribute to a better understanding of the epidemiology of pathogenic *E. coli* in farm rabbits in the central-eastern region of the state of São Paulo.

Keywords: *Escherichia coli*, diarrhea, rabbit, PCR multiplex, virulence genes