DETECTION OF ANTIBIOTIC RESISTANCE GENES IN *Escherichia coli* ISOLATES FROM CYSTITIS-PYELONEPHRITIS CASES OF SOWS

Reck, C.[1]; Portes, V.M.[2;3]; Menin, A.[3*]

[1] VERTÁ – Instituto de Pesquisa e Diagnóstico Veterinário (Avenida Lions, n° 1286, CEP: 89520-000, Curitibanos, SC). [2] Epagri/CEPAF - Centro de Pesquisa para Agricultura Familiar (Servidão Ferdinando Tusset, S/N, CxP.:791, 89801-970, Chapecó, SC). [3]UFSC – Universidade Federal de Santa Catarina - Campus Curitibanos (Rodovia Ulysses Gaboardi, km 3, Área rural, Curitibanos, SC. CEP: 89520-000). *E-mail: alvaro.menin@ufsc.br

Bacterial resistance to antibiotics is recognized as a serious worldwide public health problem. The intensive use of antibiotics to treat infections in animals and humans supports bacterial resistance mechanisms, however, in Brazil, there are no policies aimed at monitoring and control of bacteria resistance to antibiotics in human or veterinarian. *E. coli* is a constituent of the urogenital and enteric microflora of humans and animals. It is widely distributed in the environment, considered water and food contamination marker and important indicator of susceptibility to antibiotics. The objective of this study was to detect the antibiotic resistance genes in *E. coli* isolates associated with cystitis-pyelonephritis infection of sows using PCR - multiplex (mPCR). It was conducted bacteriological examination of 358 urine samples from sows, of different phases of the reproductive cycle, with clinical signs of cystitis-pyelonephritis. The samples were collected in farms of different regions of the state of Santa Catarina. From the samples, the 208 isolates identified by morphological and biochemical characteristics as *E. coli* were subjected to DNA extraction and detection of genes of different classes / groups of antibiotics by assay based on polymerase chain reaction (PCR). Resistance genes studied were sulfonamides (*sfn*), tetracycline (*tet*), aminoglycosides (*aag*), β-lactam (*lac*) and quinolones (*qn*l). All groups are used to treat infections in animals and humans. The resistance genes to antibiotics most frequently detected *tet* were 86.1% (179/208) and lac 71.2% (148/208). The *aac* gene was detected in 2.9% (6/208) of isolates. Together the findings presented here reveal the need to implement rational strategies of surveillance of antibiotic resistance, to guide policy for antibiotics in animals, since the evolution of resistance mechanisms and dissemination of the factors is permanent and progressive.

Keywords: bacterial infection, environmental contamination, infection diseases.