

ANTIMICROBIAL DRUG RESISTANT *Escherichia coli* FROM CATTLE AND POULTRY

(*Escherichia coli* RESISTENTE A ANTIMICROBIANOS ISOLADA DE BOVINOS E AVES)

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The antimicrobials used in animal production not only act against pathogenic bacteria, but also against commensal bacteria. These bacteria, especially those populations of the digestive tract, which are constantly exposed to the action of antimicrobial, develop resistance to survive. These microorganisms are still constantly excreted into the environment through feces spreading to other ecosystems. This study aimed to determine the levels of resistance of commensal bacterial populations in healthy cattle and poultry. Rectal swabs of 45 dairy cows and 80 cloacal swabs of broilers were collected. A total of 179 strains of *Escherichia coli* (91 birds and 88 cattle) were isolated and identified by biochemical tests and were tested for antimicrobial sensitivity (Koneman, 2008; NCCLS, 2003). The isolates from the digestive tract of birds were more resistant to the antibiotics erythromycin (96.7%), ampicillin (84.6%), streptomycin (79.1%), cephalothin (78.0%), trimethoprim+sulfa (68.1%) and tetracycline (67%). Furthermore, isolates from cattle were resistant to erythromycin (97.7%), cephalothin (95.5%), ampicillin (73.9%) and tetracycline (38.6%). The comparison of the resistance between populations showed that isolates from poultry were resistant to six of the nine antibiotics tested (ampicillin, Enrofloxacin, Streptomycin, Neomycin, Sulfa +Trimethoprim and Tetracycline), while the isolates from cattle showed greater resistance to 3 antibiotics (cephalothin, erythromycin and gentamicin). The greatest differences in resistance among populations were observed for Streptomycin (birds: 79.1%, cattle: 15.9%), sulfa+trimethoprim (birds: 68.1%, cattle: 10.2%) and tetracycline (birds: 67.0%, cattle: 38.6%). Populations of *E. coli* from the digestive tract of birds were more resistant to antimicrobials than the cattle populations. Additionally, results demonstrated that commensal bacterial populations can be a genetic reservoir of antimicrobial resistance that can spread resistant genes to other commensal and/or pathogenic bacteria.

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