

Can *Escherichia coli* resistant to broad-spectrum cephalosporins isolated from feedlot lambs act as meat contaminant?

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ABSTRACT:

Escherichia coli colonize the gastrointestinal tract (GIT) of animals and humans, and the ones that present resistance to β -lactams are a public health concern. The overuse of antimicrobials in food-producing animals could select resistant strains that can reach humans through food chain. Sheep farming has increased in recent years in Brazil, and research on resistant bacteria from feedlot lambs is a still neglected field. Therefore, the objective of this study was to evaluate genes codifying resistance third-generation cephalosporins (3GC) in *E. coli* isolated from feedlot lambs. Stools from 100 feedlot lambs and swabs on their carcasses just after slaughtering were sampled in 2017. *E. coli* were selected on MacConkey agar supplemented with 4 mg/L of ceftiofur, identified by commercial biochemical tests, and submitted to antimicrobial susceptibility test. 3GC-resistance genes and phylogenetic group were detected by PCR. Genetic similarity was accessed by *Xba*I-PFGE. Fifty 3GC-resistant *E. coli* were recovered from feces of 43 animals and four from four different carcasses. Resistance to tetracycline was detected in 90.7% of the isolates, resistance to phenicols and trimethoprim/sulfamethoxazole in 66.7%, to quinolones in 59.3%, and to aminoglycosides in 29.7%. All antimicrobial classes tested are approved for use in sheep. *bla*_{CTX-M} and *bla*_{CMY-2} genes were detected in isolates from feces and carcasses. Variants of *bla*_{CTX-M} groups 1, 2 and 8 were detected in 57.4%, 13% and 11.1% of isolates, respectively, and 18.5% presented *bla*_{CMY-2}. Since it is know the prevalence of *bla*_{CTX-M-2}, *bla*_{CTX-M-8}, and *bla*_{CMY-2} genes in food-producing animals in Brazil, it is remarkable the high proportion of *bla*_{CTX-M-1}-like genes detected. Moreover, those genes are often associated to human infections and worldwide disseminated clones. However, almost all isolates belonged to phylogroup B1 and A, and only 2 were classified as D or B2, which illustrates those 3GC-resistance genes spread through commensal strains in feedlot lambs. Instead of most isolates are considerably genetic distinct, it was outstanding that one isolate obtained from carcass presented 97.1% of similarity with another isolated from stool, which demonstrates that antimicrobial resistant *E. coli* selected in the GIT contaminate the products from animals, such as meats, could reach humans and cause hard-to-treat infections.

Keywords: *Escherichia coli*, Gastrointestinal tract, Beta – lactamases, Sheep, Bacterial resistance, PCR

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