

TITLE: Third-generation cephalosporin-resistant *Escherichia coli* remain all over a year in feedlot without food-producing animals

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Food-producing animals are well known as reservoirs of bacteria associated to hard-to-treat infections in humans, which can be transferred through the food chain. It is also reported that use of antimicrobials in such animals has an important role in selection of resistance genes or strains. Thus, the aim of this study was to investigate the clonal relationship of and the presence of third-generation cephalosporins (3GC)-resistant *Escherichia coli* obtained from feces of healthy lambs during feedlot and their carcasses in subsequent years, 2017 and 2018. For this, feces were collected on the first and last days of animals in the feedlot, and swabs on carcasses were collected just after slaughtering. Isolates were selected in MacConkey agar supplemented with 4 mg/L of ceftiofur and identified by biochemical methods. *E. coli* were submitted to antimicrobial susceptibility test by disc-diffusion and screened for genes codifying resistance to 3GC by PCR. Clonality was accessed by *Xba*I-PFGE, considering similarity as $\geq 90\%$. Fifty-four *E. coli* were isolated in 2017, and 50 in 2018. As expected, all 104 isolates presented resistance to 3GC, and the majority (92.3%) was classified as multidrug-resistant (MDR) considering other antimicrobial classes. Variants of *bla*_{CTX-M} gene were detected in 85.6% of the isolates, and *bla*_{CMY-2} in 14.4%, both in 2017 and 2018. *bla*_{CTX-M-1}-like genes prevailed in both years, with 69.7% positive isolates, followed by *bla*_{CTX-M-2}-like (16.8%). *bla*_{CTX-M-8} was detected only in 2017 (9.0% of the isolates), and *bla*_{CTX-M-9}-like only in 2018 (4.5%). Isolates recovered on first and last days of feedlotting and from carcasses in 2018 clustered, all carrying the same *bla*_{CTX-M} variant, which illustrates the potential contamination of retail meat with 3GC-resistant *E. coli*. Remarkably, some isolates collected in 2017 and 2018 also clustered, even some obtained from feces and carcasses. This study demonstrates that MDR *E. coli* remain at the feedlotting site for consecutive years, which might be due to the existence of different animals in the surroundings or the same workers who handle the animals. In special, the worldwide spread *bla*_{CTX-M-1}-like genes prevailed and remained, but further studies are required to understand why. Therefore, we show that such antimicrobial resistant bacteria disseminate in food-producing animals set on the same place, and is a feasible way to spread resistance through the food chain and reach meat consumers.

Keywords: *Escherichia coli*, food-producing animals, lambs, antimicrobial resistance

Development Agency: São Paulo Research Foundation –FAPESP (FAPESP Process N° 2018/02691-4, 2018/16343-8, 2018/16147-4)