

Multidrug Resistant *Escherichia coli* with Reduced Susceptibility to Third Generation Cephalosporins and Cephamycins Isolated from Bovine and Swine

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Background: Antimicrobial resistance to critically important antibiotics is being found in livestock and animal-derived foods. Bacterial resistance resulting from the production of extended-spectrum beta-lactamase (ESBL)/plasmid-mediated AmpC beta-lactamase (PMA β) has been increasing during the last years among *Escherichia coli*. Therefore, the aim of this study was to determine the prevalence of resistance to critically important antibiotics among ESBL/PMA β -producing *E. coli* isolated from bovine and swine cecal contents, and characterize the antibiotic resistance genes.

Methods: Antimicrobial susceptibility profile of ESBL/PMA β producing *E. coli* isolated from bovine (n=104) and swine (n=162) samples, in 2017, was determined by the Minimum Inhibitory Concentration, through the microdilution technique, using the EUCAST epidemiological breakpoints. Molecular characterization of ESBL/PMA β , plasmid-mediated quinolone (PMQR) and plasmid-mediated colistin resistance (PMCR)-encoding genes was achieved by using multiplex PCR on selected multidrug-resistant (MDR) isolates (bovine, n=30; swine, n=66).

Results: The prevalence of MDR strains was higher in swine (91%) than bovine (63%). Resistance levels to tetracyclines (100% vs 88%), sulfonamides (87% vs 85%), quinolones (77% vs 76%), amphenicols (48% vs 36%), aminoglycosides (29% vs 8%) and polymyxins (3% vs 23%) were found in bovine and swine, respectively. Furthermore, in swine, 18.5% of MDR isolates were resistant to third generation cephalosporins, sulfonamides, fluoroquinolones and polymyxins. Of note, a diversity of ESBL/PMA β -encoding genes as single genes or associated was identified: *bla*_{CTX-M-1-type} (n=51), *bla*_{CTX-M-2-type} (n=1), *bla*_{CTX-M-9-type} (n=7), *bla*_{CTX-M-8/25-type} (n=1), *bla*_{TEM-type} (n=7), *bla*_{SHV-type} (n=8) genes and *bla*_{CMY-type} (n=12). All colistin resistant isolates showed a *mcr-1* type gene (n=16). In ciprofloxacin resistant isolates, *qnrB* (n=14) and *aac(6')-Ib-cr* (n=2) genes were identified.

Conclusion: High prevalence of MDR was found in ESBL-producing *E. coli* recovered from bovine and swine isolates. Co-resistance to third generation cephalosporins, fluoroquinolones and polymyxins in *E. coli* isolates from animals is of major importance in the One Health concept and warrants further investigation.

Keywords: Food-producing animals; *Escherichia coli*; MDR; ESBL/PMA β

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