

Antibiotic Resistance in *Escherichia coli* Isolates from Poultry, Swine and Bovine Meat, Portugal (2016-2017)

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Background: Antibiotic resistant bacteria are a public health concern worldwide, being the food chain a potential source of transmission to humans. Understanding the molecular mechanisms behind this phenomenon is a key step towards an efficient control. Thus, this study aims to characterize the molecular mechanisms involved in resistance to third-generation cephalosporins or cephamycins, quinolones and colistin in *Escherichia coli* isolates from bovine, swine and poultry meat.

Methods: We studied 109 *E. coli* isolates, from bovine ($n=26$), swine ($n=23$) and poultry ($n=60$) meat, by assessing the antimicrobial susceptibility profile through the determination of Minimum Inhibitory Concentrations (MIC), and interpretation of results according to EUCAST epidemiological breakpoints. Resistance to third generation cephalosporins and/or cephamycins was screened by multiplex polymerase chain reaction (mPCR), for the presence of extended spectrum β -lactamases (ESBLs) and/or plasmid-mediated AmpC β -lactamases (PMA β)-encoding genes. Additionally, isolates resistant to fluoroquinolones and colistin were studied by mPCR for the presence of plasmid-mediated quinolone resistance (PMQR) and plasmid-mediated colistin resistance (PMCR)-encoding genes, respectively.

Results: Antimicrobial susceptibility profile revealed a high percentage of multidrug-resistant (MDR) isolates in bovine (84%), swine (87%) and poultry (95%). In 91 isolates exhibiting an ESBL phenotype, *bla*_{CTX-M-1-type} ($n=44$), *bla*_{CTX-M-9-type} ($n=17$), *bla*_{TEM-type} ($n=14$) and *bla*_{SHV-type} ($n=21$), were detected as single genes or associated. In 21 isolates showing a PMA β profile, *bla*_{CMY-type} genes ($n=8$) were identified. Resistance to colistin ranged between 15% (bovine), 5% (poultry) and 4% (swine); overall, *mcr-1* type gene was detected in 7 isolates. In 86 isolates resistant to fluoroquinolones, *qnrB* ($n=16$) and *aac(6')-Ib* ($n=5$) genes were identified.

Conclusion: The food chain is an important reservoir of antimicrobial resistant bacteria, requiring a multisectorial One Health approach to control its spread. Integrated surveillance of antimicrobial resistance in foodborne bacteria from humans, animals, and food and prudent use of antibiotics in human and animals is recommended by competent authorities.

Keywords: antimicrobial resistance; food; *Escherichia coli*; *bla* genes; *mcr-1*

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