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

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INTRODUCTION

Antibiotic resistant bacteria are a public health concern worldwide. Food-producing animals, like bovine, swine and poultry, are considered large reservoirs of multidrug-resistant bacteria (MDR). *Escherichia coli* is a natural colonizer of the gut micro-flora of most warm-blooded species and has been associated with antibiotic resistance (ABR), namely to critically important antibiotics. One of the most important approaches to control the spread of ABR is to understand the molecular mechanisms behind this phenomenon.

AIM OF STUDY: To characterize the molecular mechanisms involved in resistance to third-generation cephalosporins and/or cephamycins, quinolones and colistin, in *E. coli* isolates from bovine, swine and poultry retail meat.

MATERIALS AND METHODS

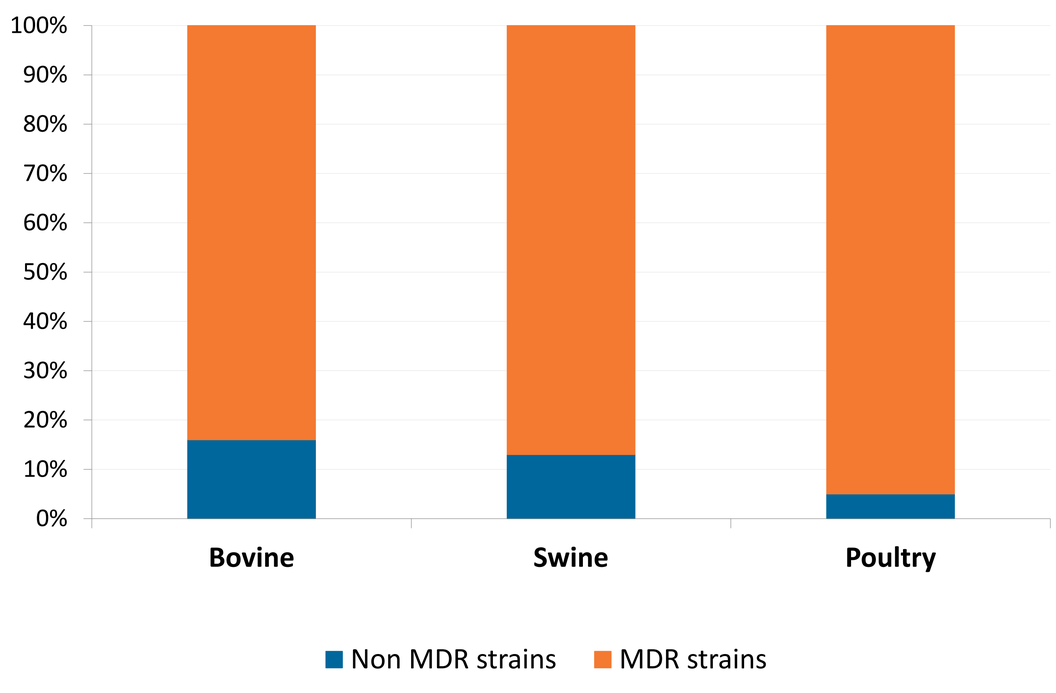
We analysed 109 *E. coli* strains with reduced susceptibility to cephalosporines and cephamycins isolated from bovine (*n*=26), swine (*n*=23) and poultry (*n*=60) retail meat in 2016 and 2017.

Antimicrobial susceptibility testing and Minimum Inhibitory Concentrations (MIC) were performed using EUVSEC® and EUVSEC2® microplates. Results were interpreted according to EUCAST epidemiological breakpoints[1].

Extended spectrum β-lactamases (ESBLs), plasmid-mediated AmpC β-lactamases (PMAβ), plasmid-mediated quinolone and colistin resistance (PMQR; PMCR)-enconding genes and integrons, class 1, 2 and 3, were screened by multiplex polymerase chain reaction (mPCR)[2-6].

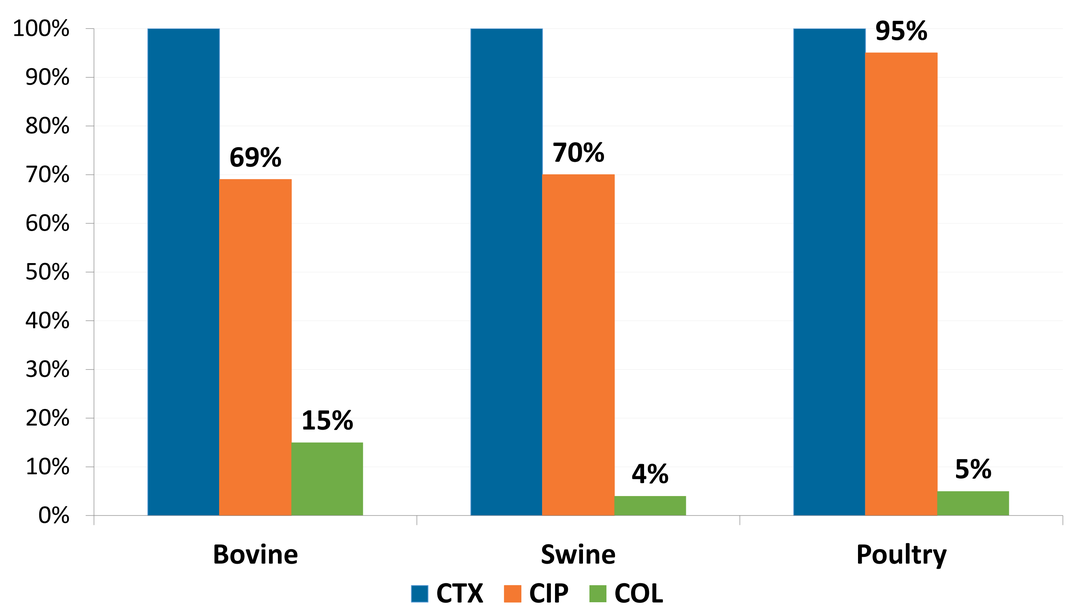
RESULTS

Results of antimicrobial susceptibility profiles revealed a high percentage of multidrug-resistant (MDR) strains in bovine (84%), swine (87%) and poultry (95%), as shown in Graph 1.



Graph 1 Prevalence of multidrug resistant (MDR) *E. coli* strains

Apart of cefotaxime (CTX) resistance, these strains also showed decreased susceptibility to other critically important antibiotics, namely ciprofloxacin (CIP) and colistin (COL) (Graph 2).



Graph 2 Prevalence of *E. coli* strains resistant to critically important antibiotics: cefotaxime (CTX); ciprofloxacin (CIP); and colistin (COL)

MDR strains detected phenotypically were further characterized at molecular level and the following determinants were detected: $bla_{\text{CTX-M-1-type}}$, $bla_{\text{CTX-M-9-type}}$, $bla_{\text{SHV-type}}$, $bla_{\text{TEM-type,}}$ $bla_{\text{OXA-type}}$, $bla_{\text{CMY-type}}$, *qnrB*, *aac(6')-Ib* and *mcr-1* genes. Mobile genetic elements, Class 1 and Class 2 integrons were present alone or in association. Class 3 integron was not found. Results are shown in Table 1.

Table 1 Prevalence of ESBL, PMAβ, PMQR and PMCR enconding-genes and integrons

Molecular mechanism	Resistance enconding-genes	Bovine (n)	Swine (n)	Poultry (n)	Total isolates (n)
ESBL	$bla_{\text{CTX-M-1-group}}$	11	12	21	44
	$bla_{\text{CTX-M-9-group}}$	8	6	4	18
	$bla_{\text{SHV-type}}$	3	0	17	20
	$bla_{\text{TEM-type}}$	3	0	17	20
	$bla_{\text{OXA-type}}$	0	0	1	1
PMAβ	$bla_{\text{CMY-type}}$	4	4	1	9
PMQR	*qnrB*	1	2	12	15
	aac(6')-Ib	4	1	0	5
PMCR	*mcr-1*	3	1	3	7
Mobile genetic elements					
Integrons	Class 1	17	13	46	76
	Class 2	3	3	4	10

FINAL REMARKS

- **High prevalence of multidrug resistant *E. coli* strains from retail meat particularly in poultry,**
- **The food chain is an important reservoir of isolates carrying ESBL/PMAβ, PMQR and PMCR-encoding genes, which might be transmissible to humans, and a potential source for human pathogens to acquire these resistance genes,**
- **The spread of resistance enconding-genes is eminent and requires a multisectorial One Health approach to minimize its impact.**

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