











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

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Antimicrobial resistance to Critically Important Antibiotics (CIA) is a worldwide public health concern. The presence of multidrug resistance (MDR), among *Escherichia coli* isolated from livestock and animal-derived food, raises important questions due to the ubiquitous nature of this species, in the gut microbiota of most warm-blooded animals, and the possibility of horizontal gene transfer. Extended-spectrum beta-lactamase (ESBL) and production of plasmid-mediated AmpC beta-lactamase (PMAβ) enzymes have been increasing in *E. coli*.

The aim of this study was to determine the prevalence of resistance to CIA in *E. coli* isolates from food-producing animals, and characterize their antibiotic resistance genes.

METHODS

- 104 bovine and 162 swine *E. coli* isolates, with reduced susceptibility to third generation cephalosporins and cephamycins were obtained from cecal contents collected at slaughterhouses in the mainland Portugal and Azores islands;
- Antimicrobial susceptibility profile of the isolates was determined by Minimum Inhibitory Concentration (MIC) through the microdilution technique¹, using EUCAST epidemiological breakpoints²;
- Molecular characterization of ESBL/PMAβ³, plasmid-mediated quinolone (PMQR)⁴ and plasmid-mediated colistin resistance (PMCR)⁵-encoding genes, and integrons⁶ Class 1, 2 and 3 was carried out by multiplex PCR (Polymerase Chain Reaction) of selected multidrug-resistant isolates.

RESULTS

E. coli isolates with reduced susceptibility to third generation cephalosporins and cephamycins were grouped into MDR and non-MDR accordingly to their antimicrobial resistance profile (Fig. 1 and Fig. 2).

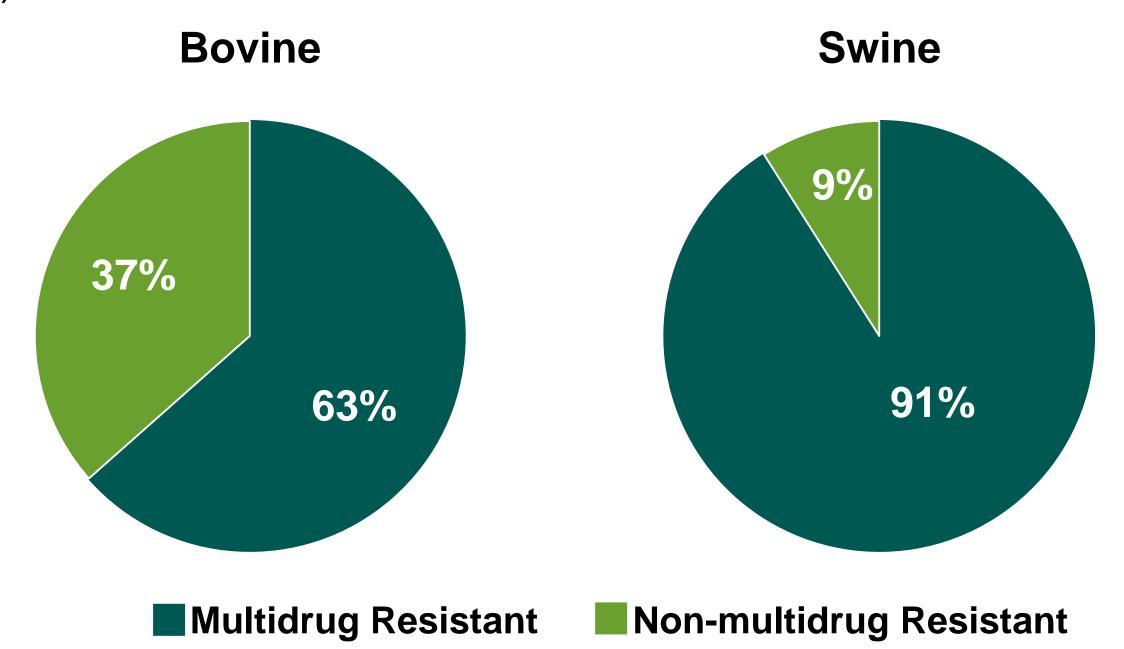


Fig. 1 Prevalence of multidrug resistant *E. coli* isolated from bovine and swine

Higher prevalence of MDR strains was detected in swine (91%) compared with bovine (63%). Furthermore, 18.5% of MDR isolates from swine were resistant to third generation cephalosporins, sulfonamides, fluoroquinolones and polymyxins (Fig. 2).

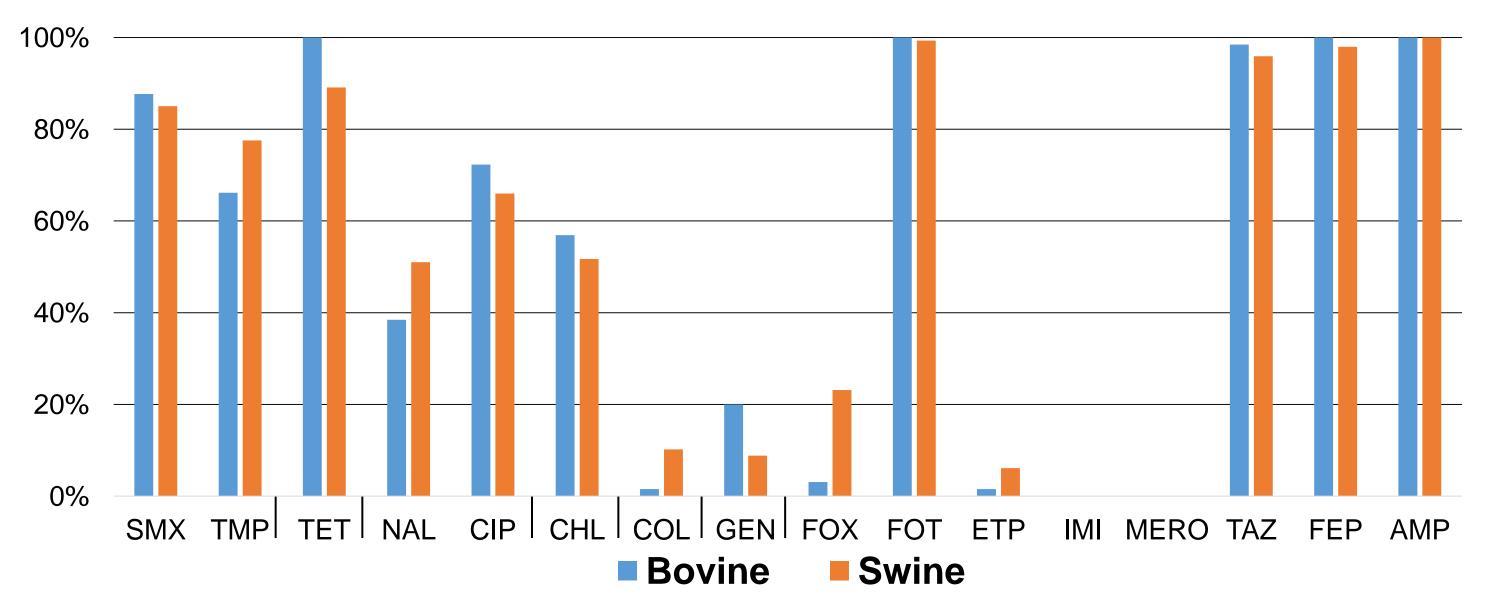


Fig. 2 Antibiotic resistance distribution of multidrug resistant swine and bovine isolates (SMX – sulphametoxazole, TMP – trimethoprim, TET – tetracycline, NAL – nalidixic acid, CIP – ciprofloxacin, CHL – chloramphenicol, COL – colistin, GEN – gentamicin, FOX – cefoxitin, FOT – cefotaxime, ETP – ertapenem, IMI – imipenem, MERO – meropenem, TAZ – ceftazidime, FEP – cefepime, AMP – ampicillin)

The prevalence of plasmid-mediated antimicrobial resistance genes of a representative sample of bovine (n=31) and swine (n=65) isolates (Fig.3), selected upon their susceptibility phenotype and slaughterhouse location, supported the following considerations:

- Resistance to third generation cephalosporins and cephamycins was mostly due to CTX-M Group 1-encoding genes and, occasionally, to coexistence of different ESBL-encoding genes in the same isolate;
- ✓ Among PMQR-encoding genes, only *qnrB* and *aac-6'lb-cr* were detected, the former being at higher frequency;
- ✓ PMCR-encoding gene *mcr-1* was found in all colistin resistant isolates;
- ✓ Type 1 integron is the most prevalent, specially in swine isolates; concomitant presence of Class 1 and 2 in the same isolate was observed.

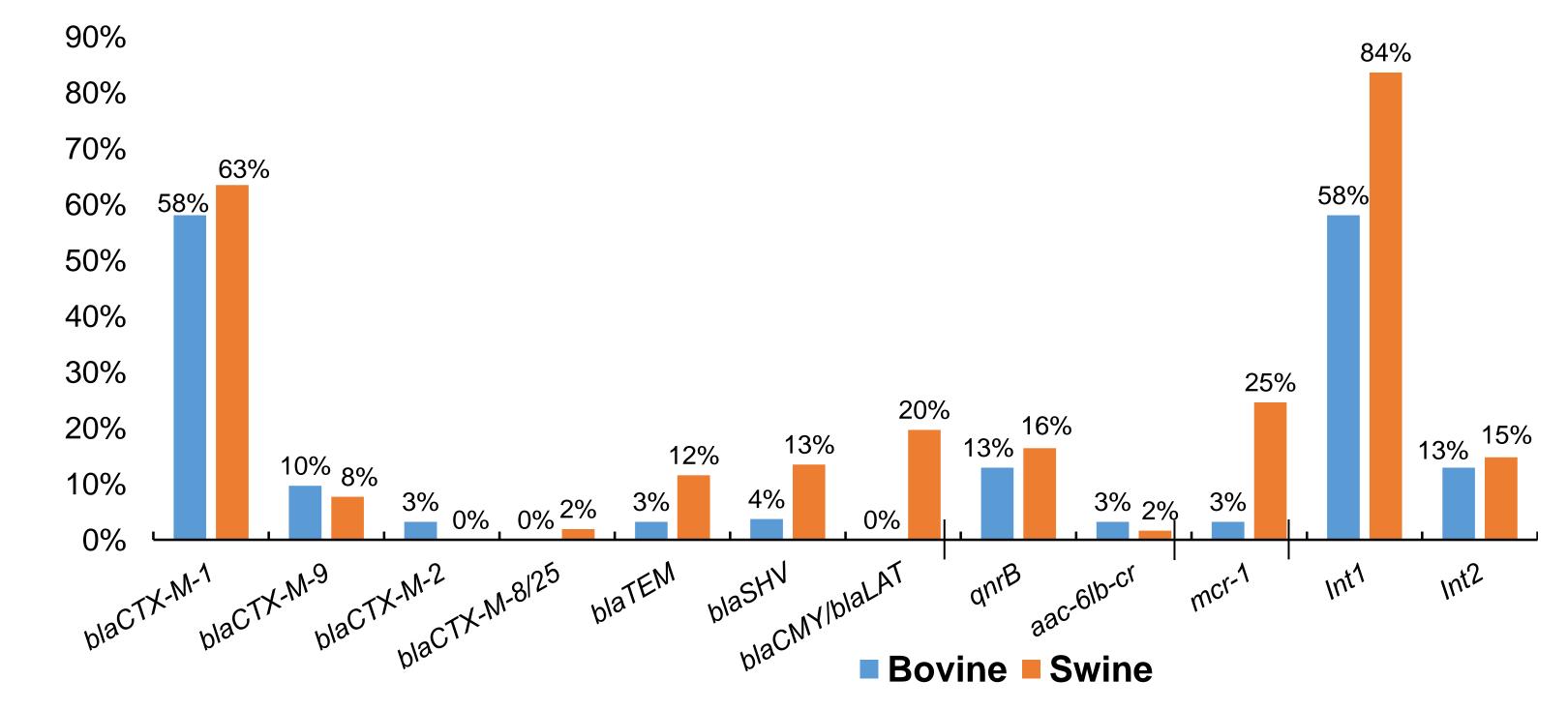


Fig. 3 Molecular characterization of multidrug resistant bovine and swine isolates.

Final Remarks:

- ✓ High prevalence of MDR was found in ESBL-producing *E. coli* isolated from bovine and swine.
- ✓ Plasmid-mediated 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.

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