ANTIMICROBIAL RESISTANCE AND VIRULENCE IN *ESCHERICHIA COLI* FROM BROILERS: GENETIC INSIGHTS FOR ONE HEALTH

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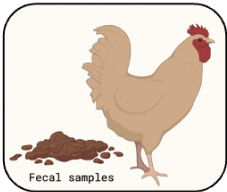
01 INTRODUCTION

The widespread use of antibiotics in livestock has contributed significantly to the emergence and spread of antimicrobial-resistant bacteria, posing a risk for zoonotic transmission. The presence of multidrug-resistant *Escherichia coli* in poultry emphasizes the need for a One Health approach in monitoring antimicrobial resistance.

02 AIMS

The aim of this study was to characterize the antimicrobial resistance profiles of *E. coli* isolated from broiler fecal samples and to evaluate their genetic characteristics, including resistance genes, virulence factors, integrases, and phylogenetic groups.

03 METHODOLOGY

Genomic DNA was extracted from 19 *E. coli* isolates obtained from broiler fecal samples collected at Savinor (Trofa, Portugal) using the boiling method. Resistance genes, integrases, virulence factors, and phylogenetic groups were identified by PCR.

Fecal samples

Escherichia coli

04 RESULTS

GENES	(+) ISOLATES
ampC	17
tetA	12
blaCTX-M	11
qnrS	7
blaSHV, blaTEM, blaVIM, aadA1, aadA5, sul1, sul2, strB, aac(3)-II	1

PHYLOGENETIC GROUPS

Group D (2)
Group B1 (5)
Group A (12)
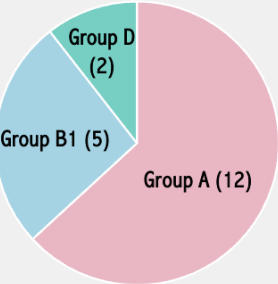
VIRULENCE FACTORS AND INTEGRASES

int1 6
aer 5
fimA 19

05 CONCLUSIONS

This study reveals the high prevalence of antibiotic-resistant *E. coli* in broilers in Portugal, underscoring the importance of regional surveillance. The combined analysis of resistance, virulence factors, and phylogenetic groups provides a broader understanding of the genetic traits that may enhance zoonotic potential. Resistance was mainly observed in typically commensal phylogroups, suggesting adaptation to selective pressure in poultry environments. Stronger antimicrobial stewardship, including restricting critically important antibiotics, promoting alternatives like probiotics and vaccination, and improving farm hygiene, is crucial. Future research should focus on tracking resistance gene mobility and transmission pathways to inform public health strategies within a One Health framework.