

# Antimicrobial Resistance Gene Distribution in ESBL-Producing *Escherichia coli* Isolates from Animals in Greece

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## Abstract:

The increasing prevalence of multidrug resistant, extended spectrum  $\beta$ -lactamase (ESBL)-producing *Enterobacteriaceae* is a constantly growing and evolving worldwide challenge. Livestock and wildlife animals play an important role as a reservoir of such potentially pathogenic and (multi)-resistant bacteria. The present study aimed to provide an overview of the multidrug resistance phenotype and correlating genotype of ESBL-producing *Escherichia coli* isolates of livestock and wild bird origin in Greece. Nineteen phenotypically confirmed ESBL-producing *E. coli* strains isolated from fecal samples of pigs ( $n = 11$ ), cattle ( $n = 7$ ) and an eurasian magpie that presented resistance to at least one class of non  $\beta$ -lactam antibiotics, were selected and genotypically characterized. A DNA microarray-based assay was used, which allows the detection of various relevant genes associated with antimicrobial resistance. Allelic variants of *bla*CTX-M-1/15 were found in all strains, while *bla*TEM was co-detected in 13 of them. Resistance genes were also reported for aminoglycosides in all 19 isolates, for quinolones in six, for sulfonamides in 17, for trimethoprim in 14, and for macrolides in eight. The *int11* and/or *tnp1SEcp1* genes, associated with mobile genetic elements, were identified in all but two isolates. This study describes the first detection of multidrug resistance genes among ESBL-producing *E. coli* strains retrieved from feces of cattle, pigs, and a wild bird in Greece, underlining their dissemination in diverse ecosystems and emphasizing the need for a One-Health approach when addressing the issue of antimicrobial resistance.