

P-107 - INTESTINAL COLONIZATION OF HEALTHY COMPANION ANIMALS WITH MULTI-DRUG RESISTANT (MDR) CTX-M-15-PRODUCING ESCHERICHIA COLI WITH TRANSFER ABILITY IN THE NORTH OF PORTUGAL

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Background

Companion animals share a common bacterial flora with Humans and nowadays there is a large overlap of antibiotic used in both human and veterinary clinic. These arguments validate the idea that companion animals could be a source of dissemination of resistant bacteria to humans, as well as enable horizontal transmission of resistance genes between bacteria. The ubiquitous character of *E.coli*, makes the resistant isolates a worldwide problem. This way, MDR *E.coli* encoding CTX-M-type extended-spectrum β -lactamases (ESBL), namely CTX-M-15-producers, are a raising concern as they represent an emerging problem in human and animal healthcare worldwide. The aim of this study was the detection of MDR ESBL-producing *E.coli* in intestinal colonization of healthy companion animals in Portugal.

Method

Fifty-six healthy companion animal fecal samples were enriched in TSB. Selection was performed in MacConkey agar with antibiotics. Antimicrobial susceptibility was determined by disk-diffusion-method by EUCAST. ESBL producers were detected by the double-disk-synergy-test. Presumptive identification was done by CHROMagar orientation. ESBL-producing *E.coli* (EC-ESBL) were selected for conjugation assays, screening for *bla*_{CTX-M} groups (group1 positives were screened for *bla*_{CTX-M-15}), *bla*_{TEM}, *bla*_{OXA} and *bla*_{SHV} by PCR.

Results & Conclusions

A total of 79 *E.coli* were selected, showing high resistance profile: 91% resistant to amoxicillin, 24% to amoxicillin+clavulanic acid, 29% to cefotaxime, 30% to ciprofloxacin and 24% to sulphamethoxazole+trimethoprim. Thirty-nine (81%) isolates showed a MDR profile. A total of 24 isolates were MDR-EC-ESBL, of these, 15 carried the *bla*_{CTX-M-15} gene, from those, 4 had conjugative ability of transferring the CTX-M 15 codifying gene. The results substantiate the occurrence and ongoing spread of *bla*_{CTX-M-15} mainly associated with the high-risk *E.coli* sequence type 131 (ST131) clonal group, representing a threat to animal and human health. Moreover, helps to confirm the possibility of transfer of resistance genes between colonizing bacteria of animals and Human commensal bacteria. These findings highlight the idea that antibiotic resistance is a public health problem that needs to be managed in a one-health perspective.

References & Acknowledgments

ARGUDÍN, Maria Angeles, et al. Bacteria from Animals as a Pool of Antimicrobial Resistance Genes. *Antibiotics*, 2017, 6.2: 12.

EWERS, Christa, et al. Emergence of human pandemic O25: H4-ST131 CTX-M-15 extended-spectrum- β -lactamase-producing *Escherichia coli* among companion animals. *Journal of antimicrobial chemotherapy*, 2010, 65.4: 651-660.

ROCHA-GRACIA, R. C., et al. Faecal *Escherichia coli* isolates from healthy dogs harbour CTX-M-15 and CMY-2 β -lactamases. *The Veterinary Journal*, 2015, 203.3: 315-319.