Extended spectrum β-lactamase and plasmid mediated quinolone resistance in *Escherichia coli* fecal isolates from healthy companion animals in Algeria

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Abstract:
The aim of this study was to evaluate the rate of fecal carriage of *Escherichia coli* strains producing Extended-spectrum β-lactamases (ESBLs) and plasmid-mediated quinolone resistance (PMQR) isolated from healthy pets (dogs and cats) in Algeria.

Fecal samples from 171 healthy pets (102 dogs and 69 cats) in one veterinary practice and private owners were included. After isolates identification, antibiotic susceptibility was determined by disk diffusion procedure. ESBL were detected by combination disk tests. PCR and sequencing were used to characterize genes encoding ESBLs and PMQR. Transfer of ESBL and PMQR genes was assessed by conjugation experiments. Phylogenetic groups of *E. coli* were determined by PCR.

Of the 171 animals, 20 carried an ESBL producing *E. coli* giving a prevalence of ESBL fecal carriage of 11.7%. All isolates were susceptible to carbapenems, cefoxitin, piperacillin-tazobactam, amikacin and fosfomycine. For the rest of the tested β-lactams, susceptibility rates ranged from 35% to 70% for cefepime and amoxicillin-clavulanic acid respectively. Concerning the non-beta-lactams antibiotics, the rates of susceptibility ranged between 5% to trimethoprim and 95% for chloramphenicol.

The beta-lactamase genes identified in *E. coli* isolates were $bla_{\text{CTX-M-15}}$, $bla_{\text{CTX-M-1}}$, $bla_{\text{SHV-12}}$ and $bla_{\text{TEM-1}}$. The PMQR determinants *aac(6')-Ib-cr*, *qnrS1* and *qnrB5* genes were identified in 15 isolates. Transconjugants were obtained for two isolates. Phylogenetic analysis showed that *E. coli* isolates belong to commensal phylogroups of A and B1.

We reported here for the first time in Algeria ESBL and PMQR-producing *E. coli* in healthy cats and dogs.