ARE HEALTHY DOGS A RESERVOIR OF ANTIMICROBIAL RESISTANT-EXTRAINTESTINAL PATHOGENIC *ESCHERICHIA COLI*?

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Introduction: Phylogenetic analysis has shown that *Escherichia coli* is composed of four main phylogenetic groups (A, B1, B2, and D) and that virulent extra-intestinal strains (ExPEC) mainly belong to groups B2 and D. Do canine commensal gastrointestinal *E. coli* represent a reservoir of antimicrobial resistance and virulence, particularly strains that cause urinary tract infection? The aim of this study was to detect and characterize ExPEC *E. coli* isolated from healthy dogs (under no antimicrobial pressure) regarding antimicrobial resistance, phylogenetic group, pathogenicity islands and virulence profiles.

Material/methods:

In this study 126 *E. coli* were isolated from faeces from healthy dogs. Susceptibility testing was performed by the disk diffusion method. Resistant to third-generation cephalosporin (3GC) *E. coli* were screened for extended-spectrum β-lactamases (ESBL) and plasmid-mediated AmpC genes by PCR and sequencing. Determination of phylogenetic groups, 8 pathogenicity islands markers and *papEF*, *sfaDE*, *afaBC*, *hlyA*, *cnf1*, *iucD*, *usp*, *ecp*A virulence genes was done by PCR. Associations between phylogroups and ESBLs and pAmpC genes were investigated by Fisher´s exact test (2-tailed) and differences were considered relevant if $p \leq 0.05$.

Results/conclusion

E. coli isolates were resistant to amoxicillin 39% (n=49/126), 23% (n=29/126) to amoxicillin/clavulanate, 25% (n=31/126) to 3CG, 29% (n=37/126) to trimethoprim/sulfamethoxazole, 17% (n=21/126) to fluoroquinolones, and 3% (n=3/126) to aminoglycosides. *E. coli* isolates belonged mainly to B1 filogenetic group (34.2 %, n=43/126) followed by group-B2 (28.0%, n=35/126), group-A (24.0%, n= 30/126) and group-D (14.5%, n=15/126). Among beta-lactam resistant isolates, 21% (n=26/124) were pAmpC beta-lactamases producers and 17 % (n=22/126) were ESBL-producers. The majority of ESBLs and AmpC-producing *E. coli* isolates belonged to the phylogenetic group-D ($bla_{\text{CTX-M-1}}$ n=2, $bla_{\text{CTX-M-15}}$ n=3, $bla_{\text{CTX-M-9}}$ n= 2, $bla_{\text{CTX-M-9 like}}$ n= 1, $bla_{\text{CTX-M-32}}$ n=1, $bla_{\text{CMY-2}}$ n= 11), followed by group-B1 ($bla_{\text{CTX-M-32}}$ n =3, $bla_{\text{CTX-M-1}}$ n= 2 and $bla_{\text{CTX-M-9like}}$ n=1, $bla_{\text{CMY-2}}$ n=7, $bla_{\text{CMY-2like}}$ n=1), group-B2 ($bla_{\text{SHV-12}}$ n=1, $bla_{\text{CTX-M-32}}$ n=3, $bla_{\text{CMY-2like}}$ n=1, $bla_{\text{DHA-1}}$ n=1) and group-A ($bla_{\text{CTX-M-15}}$ n=2, $bla_{\text{CTX-M-32}}$ n=1 and $bla_{\text{CMY-2}}$ n=5). ESBLs and pAmpC - producing *E. coli* were mainly associated with group D (p =0.005, p= 0.002, respectively). Pathogenicity profiles and virulence-associated genes of group-B2 and D *E.coli* belonged mostly to pathogenicity islands PAI IV_{536} PAI II_{536} PAI II_{J96} PAI I_{CFT073}, *ecpA-hly*A-*cnf1-sfaDE-papEF*, and PAI IV_{536} PAI I_{CFT0T3}, *ecp*A-*pap*, respectively.

This study demonstrates that healthy dogs are reservoirs of ExPEC *E. coli* strains resistant to oxyimino-cephalosporins like cefotaxime and cefamicins like cefoxitin and that the majority of the *E. coli* strains belonged to virulent groups B2 and D. This may have impact on human health due to the close and direct contact between pets and their owners.

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