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Abstracts

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ANTIBIOTIC-RESISTANCE PROFILES IN RELATION TO VIRULENCE FACTORS, AND PHYLOGENETIC GROUP OF UROPATHOGENIC *ESCHERICHIA COLI* ISOLATED FROM DOGS AND CATS

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SUMMARY - In this study we assessed the association among antibiotic resistance profiles, virulence genotype and phylogenetic group within a collection of *Escherichia coli*. Forty uropathogenic *E. coli* strains isolated from dogs and cats with urinary tract infection were analysed by disk diffusion method and by PCRs. Results suggest that clinical isolates with a number ≥ 3 of virulence factors belong on the whole to phylogroup B2 (90.5%) and *E. coli* strains with a number < 3 of virulence genes were distributed in all phylogenetic groups. Considering virulence factors association with antimicrobial resistance, no statistically significant results were obtained ($P > 0.05$). Only gene *iutA* showed a trend of association with MDR ($P = 0.055$). Resistant strains were distributed in all phylogenetic groups (57%, B2; 43%, non-B2), in contrast *E. coli* isolates susceptible were associated with group B2 (90%) and with group D (10%).