

Phylogenetic Associations of Virulence and Antibiotic Resistance of Uropathogenic Escherichia coli from Humans and Dogs

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Urinary tract infections (UTIs) caused by multi-drug resistant (MDR) uropathogenic *Escherichia coli* (UPEC) is a significant health concern. The pathogenicity of UPEC is mediated through plasmid mediated virulence factors which coexist with antimicrobial resistant genes. The association of virulence factors and antimicrobial resistance with the phylogenetic background of *E. coli* isolated from humans and dogs was evaluated in this study. A total of 65 isolates confirmed as *E. coli* by PCR (human=55, canine=10) were included in the study. Antibiotic susceptibility to 12 antibiotics was determined following EUCAST guidelines. Virulence properties (haemolytic activity, serum resistance, curli fimbriae expression) were assessed using standard procedures, and phylogroups and presence of plasmid-mediated virulence genes, (*traT*, *cvaC*, and *cdtB*) were determined by PCR. Phylogenetic analysis revealed 57% of isolates in phylogroup B2, 22% in group E, 12% in group A, and 9.2% in group B1. Phylogroups A, B1, and B2 exhibited over 50% MDR, while only 36% in group E were MDR. Phylogroup-specific antibiotic resistance patterns were observed, with notable resistance rates in phylogroup B1 to clavulanate amoxicillin (83%), B2 to quinolones (86%), and A to trimethoprim-sulfamethoxazole (75%). Serum resistance varied among phylogroups (100%-67%), with all phylogroup A isolates being serum resistant. Hemolysin ability was seen in 26% of isolates, notably higher in phylogroup A. Curli fimbriae expression was prevalent in B2 (89%), B1 (83%), E (71%), and A (69%). The dominant gene was *traT*, present in over 86% of B2, E, and B1 isolates. *CvaC* was detected in 4.6% of isolates, while *cdtB* was absent in all isolates. Antibiotic resistance showed a link to phylogroups and virulence-related factors; serum resistance, curli fimbriae, and *traT* gene were common in all isolates but high among B2. Further studies with more isolates and other virulent factors are needed to depict the association.

Keywords: *E. coli*, virulence, antibiotic resistance, phylogeny, UPEC

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