

VIRULENCE FACTORS AND MOLECULAR EPIDEMIOLOGY OF UROPATHOGENIC *ESCHERICHIA COLI* ISOLATED FROM PAIRED URINE AND RECTAL SWAB SAMPLES OF PATIENTS WITH URINARY TRACT INFECTIONS IN THAILAND

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Abstract. The role of uropathogenic *Escherichia coli* (UPEC) pathotypes and genotypes, including their specific virulence factors, in the pathogenesis of infection remains unclear. We aimed to find the role of UPEC in the pathogenesis of the patients with urinary tract infections. Ninety urine and corresponding rectal swab *E. coli* samples from patients with community-acquired (CAI), hospital-acquired (HAI) and asymptomatic (AUTI) urinary infections ($n = 30$ per group) admitted to a hospital in Thailand were subjected to characterization of virulence phenotypes and genotypes. Serogroup O25 was most prevalent (18%) among 6 serogroups (including O1, O6, O8, O18, and O15) and phylogenetic group B2 (39%) among 4 groups (including A, B1 and D) of *E. coli* isolates, with those from urine significantly higher than in rectal swab from all three types of UTIs. Three virulence-associated gene profiles (*fimH*⁺, *fimH*⁺*aer*⁺ and *fimH*⁺*aer*⁺*usp*⁺) were the most common in *E. coli* strains isolated from both urine and rectal swab samples of all three UTIs. Six out of eight randomly amplified polymorphic DNA patterns of paired urine and rectal swab *E. coli* strains with identical serogroup, phylogenetic group and virulence-associated gene profile isolated from AUTI, CAI and HAI groups (two in each group) showed the same pattern. These findings should contribute to a better understanding of the transmission of commensal *E. coli* through the urethral route.

Keywords: uropathogenic *Escherichia coli*, phylogenetic group, RAPD profiling, serogroup, virulence-associated gene

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