

Abstract:

Objective: To investigate virulence associated characteristics in uropathogenic *Escherichia coli* isolates derived from urine specimens, and to investigate the distribution of the pathogenicity islands virulence markers (PAIs) among the isolates.

Methods: In this study, 150 *E.coli* strains isolated from patients with symptoms of urinary tract infections were collected and all of them were confirmed by biochemical tests and molecular techniques. PCR was conducted by specific pair primers in order to determine the prevalence of pathogenicity islands markers.

Results: Among the 150 examined isolates, distribution of PAI in commensal and Pathogenic isolates were PAI II536 (41/26%, 57/47%) ,PAI III536 (58/73%, 73/56%),PAI IV536(84%, 85/5%)PAI ICFTO73 (23/80%, 56/32%).

Conclusion:Pathogenicity island markers cause horizontal transfer of genes. Many virulence genes are present in the pathogenicity islands regions in such a way that by deletion and/or mutation of these genes, the bacteria would lose its pathogenicity. Knowledge of the molecular details of uropathogenic *E. coli* is useful to develop successful strategies for the treatment of urinary tract infection and complications associated with urinary tract infections in human.

Keywords: Pathogenicity island. urinary tract infections. Uropathogenic *Escherichia coli*