

Original Paper

Relationship between phylogenetic group and distribution of virulence genes of *Escherichia coli* isolated from patients with urinary tract infection

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Abstract

Background and Objective: Uropathogenic strains of *Escherichia coli* (UPEC) are the most common cause of urinary tract infections. UPEC strains possess an arsenal of virulence factors including *fimH*, *iucD*, *iroN* and *hlyA* which increase their ability to cause urinary tract infections. This study was done to determine the relationship between phylogenetic group and distribution of virulence genes of *Escherichia coli* isolated from patients with urinary tract infection.

Methods: This descriptive - analytic study was performed on 100 isolates *Escherichia coli* which collected from patients with UTIs. DNA was extracted from all isolates by the boiling method and subsequently DNA was used to determine the presence of genes encoding virulence factors by Multiplex-PCR. In addition, determination of phylogenetic group, A, B1, B2 and D, was performed by determination of present or absent of *yjaA* and *chuA* genes and DNA fragment TSPE4.C2 using Triple-PCR.

Results: The frequency of virulence factors, *fimH*, *iucD*, *iroN* and *hlyA* were 95%, 69%, 29% and 32%, respectively. In all isolates, the frequency of phylogeny of groups A, B1, B2 and D were 17%, 6%, 55% and 22%, respectively. A significant correlation was found between the presence of virulence encoding genes and the B2 phylogenetic group ($P < 0.05$).

Conclusion: Virulence genes were common in phylogenetic group B2 isolates among all phylogenetic groups.

Keywords: Infection, Urinary tract, *Escherichia coli*, Virulence genes, Phylogenetic group

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Received 7 Apr 2014

Revised 20 Jul 2014

Accepted 7 Oct 2014