

Abstract

Uropathogenic *Escherichia coli* is the main pathogen in urinary tract infections. These strains carry major virulence factors such as; invasins, siderophores and toxins, which helps to develop urinary tract infection. The first step to confront and inhibit of this pathogen is the identification of the major virulence factors. Phylogenetic studies have revealed that gene encoding Toxins an important role in the pathogenesis. The main objective of this study was to determine the frequency of virulence factors genes encoding, toxins(*cvi/cva*, *iss*, *vat*, *astA* and *cdtB*), Iron acquisition systems(*iutA*), Capsule Lipopoly Saccharides(*neuS* and *kpsII*) and Invasins(*ibeA* and *tsh*) determined using Multiplex PCR method. A total of the 100 *Escherichia coli* isolates, *iutA* gene with 99% highest frequencies and *cdtB* gene was not detected in any of the isolates the lowest frequency, respectively. Gene frequency for *kpsII*, *neuS*, *ibeA*, *iss*, *astA*, *cvi/cva*, *vat* and *tsh* genes were detected 98%, 96%, 67%, 47%, 29%, 19%, 18% and 1% respectively.

Keywords: Invasin, Siderophore, Toxin, Virulence genes, Uropathogenic *Escherichia coli* (UPEC)



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**Prevalence of Virulence Genes in
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Isolated from Patients with Urinary Tract
Infection in Sistan**

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