

## Abstract

Uropathogenic *Escherichia coli* is the main pathogen in urinary tract infections. These strains carry major virulence factors such as; adhesion, siderophore 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 these bacteria fall into four groups A, B1, B2 and D, and the phylogroup type of these microorganisms plays an important role in the pathogenesis. The main objective of this study was to determine the frequency of virulence factors genes encoding, toxins(*hlyA* and *cnf1*), Iron acquisition systems(*iucD*,*iroN* and *irp2*), adhesions(*fimH* and *iha*) and outer membrane protease(*ompT*), and also the type of phylogenetic groups was determined using Multiplex PCR method. A total of the 100 *Escherichia coli* isolates, *fimH* gene with 95% and *cnf1* with 28% were the highest and lowest frequencies, respectively. Gene frequency for *hlyA*, *iroN*, *iucD*, *iha*, *irp2* and *ompT* genes were detected 32%, 29%, 69%, 29%, 89% and 67%, respectively. About 55, 22, 17 and 14 isolates belonged to B2, D, A and B1 phylogenetic groups, respectively. The highest of the virulence gene distribution was observed in group B2 and the lowest in groups B1 and A. The most significant association between the phylogenetic groups and virulence genes was observed in isolates belonging to groups A and B2, respectively. Group B1 isolates had no significant correlation with the distribution of any genes( $P \text{ value} \leq 0.05$ ). This study showed that genes *ompT*, *iucD*, *irp2*, *fimH* and phylogenetic group B2 are more abundant and important in isolates of Sistan region.

**Keywords:** Uropathogenic *Escherichia coli*, Urinary tract infection, Virulence factors, Phylogenetic groups



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**Prevalence of Virulence Genes in  
Uropathogenic *Escherichia coli* Strains  
Isolated from Patients with Urinary Tract  
Infection in Sistan**

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