

## Abstract

**Background:** *Escherichia coli* (*E.coli*) is one of the most common bacterial causes of urinary tract infection (UTI). *E.coli* fimbriae increases invasion ability of bacteria to renal tissues. Phylogentic analyses of *E.coli* indicate that these isolates distributed in four main phylogroups A, B1, B2 and D. Phylogentic groups differ in their Virulence genes and antibiotic resistance properties.

**Methods:** One hundred eighty five urine samples were obtained from patients with urinary tract infection in Sistan. samples were cultured for isolation *E.coli* and was confirmed by biochemical tests. from the cultured samples, 100 *E.coli* isolates were obtained. DNA was extracted from all of isolates by boiling method, examined for detection of Phylogentic groups and also for determination of *fim*, *sfa*, *pap*, *foc* and *afa* genes by using PCR technique.

**Results:** A total of the 100 *Escherichia coli* isolates, *fim* gene with 95% and *afa* with 12%, respectively were the highest and lowest frequencies. Gene frequency for *sfa*, *pap*, and *foc* genes were detected 81%, 57% and 16%, respectively. About 55, 22, 17 and 14, isolates respectively belonged to B2, D, A and B1 phylogeny groups. The highest of the virulence gene distribution was observed in group B2 and the lowest in groups B1. The most significant association between the phylogeny groups and virulence genes was observed in isolates belonging to groups A and B2. ( $P$  value  $\leq 0.05$ ). Group B1 and D isolates had no significant correlation with the distribution of any genes ( $P$  value  $\geq 0.05$ ).

**Conclusion:** The results of this study showed that genes *fim*, *sfa* and *pap* most common genes encoding fimbriae in *Escherichia coli* isolated from urinary tract infections in the Sistan region. This can be important information in relation to the pathology of urinary tract infection, UTI management and treatment strategies provided.

**Key words:** Urinary Tract Infection (UTI), fimbriae, *Escherichia coli*, virulence genes, Phylogeny groups



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**Prevalence of virulence genes fimbriae in  
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