Abstract

Uropathogenic E. coli cause urinary tract infection and urinary tract infection is a major part of. Depending on the amount and type of bacteria pathogenic factors, geographic area and type of host variable that can diagnose and treat diseases caused by these bacteria make you worry and trouble. The first step is to confront and contain this pathogen identify important factors it. The main objective of this study was to determine the frequency of virulence factors genes encoding *fepC ,modD, prrA ,ye73 ,hlyB ,hlyC, hlyD and* Iron acquisition systems *feoBA fyuA , ireA* using Multiplex PCR method. A total of the 100 *Escherichia coli* isolates, *fyuA* gene with 63% highest frequencies and *hlyD* gene was not detected in any of the isolates the lowest frequencie, respectively. Gene frequency for, *hlyC, , prrA، cy73، modD ، feoB fepC،hlyB and ireA* genes were detected 40%, 9%,27%, 19%, 53%, 53%, 37% and10% respectively. In this study revealed the gene distribution Most pathogens are present in the Islands PAI IV536 fyuA number of islands in gene PAI IV536 were more pathogenic, causing disease by knowing which genes are islands can be effective strategies for treatment, thereby taking into account the fyuA most frequent pathogenic gene in samples showed Sistan region. The results are good in terms of epidemiological and produce effective vaccine available to researchers for further studies next place.

Keywords: Islands Uropathogenic coli, pathogenic factors**,** urinary tract infection, iron transporter genes**.**

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Prevalence of Virulence Genes iron transport on the islands in Uropathogenic *Escherichia coli*

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