

Abstract

Uropathogenic *Escherichia coli* is the most common cause of urinary tract infection (UTI). The ability of *E. coli* to cause UTI is associated with specific virulence determinants, some of which are encoded on *pathogenicity islands markers* (PAI). The first step to confront and inhibit this pathogen is the identification of genetic traits associated with the pathogenicity of *pathogenicity islands markers*, virulence genes. The main objective of this study was to determine the frequency of pathogenicity islands. PAI of I536, II536, ICFT073, IJ96, IJJ96 which encoded the α -hemolysin and PAI of IJ96, ICFT073, IICFT073 that are fimbriae encoder, virulence genes include: traT Encoding outer membrane, lipoprotein Iron acquisition systems gene *fyuA*, and Aerobactin receptor *iutA*, Serum resistance genes (*K1*, *traT*, *kpsII*) and gene encoding colicin V which called *cvaC* gene and also the type of phylogeny groups was determined using Multiplex PCR method. A total of the 100 *Escherichia coli* isolates, pathogenicity islands PAI IV536 with 84% highest prevalence and pathogenicity islands PAI IJ96, PAI I536 do not exist, respectively. Frequency of pathogenicity islands for islands PAI IJJ96, PAI IICFT073, PAI ICFT073, PAI II536 were detected 9%, 30%, 44%, 16% respectively. Gene frequency for *fyuA*, *iutA*, *K1*, *kpsII*, genes were detected 79%, 76%, 15% and 68%, respectively. About 55, 22, 17 and 6 isolates belonged to B2, D, A and B1 phylogeny 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 phylogeny groups and pathogenicity islands 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 value ≤ 0.05). Generally, results of this study showed that *Pathogenicity island* PAI IV536 and genes *fyuA*, *kpsII*, *iutA*, *traT* are more abundant and important in isolates of Sistan region.

Key words: Uropathogenic *Escherichia coli*, Urinary tract infection, *Pathogenicity island markers*, Virulence genes, Phylogeny groups



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