Background and Objectives: Urinary Tract Infection (UTI) is one of the most common infectious diseases and the major agent of UTI is Uropathogenic Escherichia coli (UPEC). In our research, a genetic construct for inducing of cellular immune system was designed and immune response of immunized mice was evaluated. Moreover, an optimized genetic cassette was designed according to eukaryotic cell codon usage. Beside our survey, fimH gene variation was assessed to evaluation of conserved domains and prevalence of six virulence factors were assigned.

Materials and Methods: Chromosomal DNA extracted from E. coli 35218 and fimH gene amplified by PCR. The amplicon inserted to cloning vector and sequenced. Then, the fimH gene sub cloned to pVax eukaryotic expression vector. Also, an optimized fimH sequence according to eukaryotic codon usage was inserted to pVax. The expression of cassettes in COS7 cell line, assessed by RT_PCR. Three groups of BALB/c mice immunized with recombinant DNA construct and all mice challenged later. Additionally, Genomic DNA of 30 clinical samples were extracted and fimH gene was amplified. The gene sequence analysis was carried out using MEGA4, ClustalW and CLC Bio software. Moreover, specific primers were designed to detection of vat, sat, hlyA, cnf1, iutA and ent genes.

Results: The result of challenge showed 100 times reduction of E. coli colonization in bladder tissue of first group mice. Additionally, IFN-titer got rise in first group on compression with others groups. Moreover, fimH sequence of clinical samples in C-terminal had insignificant mutations. The prevalence of vat, sat, hlyA, cnf1, iutA and ent genes were 36, 75, 61.4, 48.5, 70.5, 65.9% , respectively.

Conclusion: Induction of cellular immune response was showed by increasing of INF-gammatitration in immunized mice. Insignificant mutation in C-terminal leads to the formation of truncated FimH, which can affect the attachment of feces strains to urotheilial cell; however, attachment factor has no role in Uropathogenic Escherichia coli pathogenic by itself. Also, molecular identification of uropathogenic E.coli according to sat and iutA genes seems to be valid.

Uropathogenic E.coli, Vaccine, Virulence factors

Presentation: Poster