

JOINT EVENT

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## Impact of sequential passage on overall protein expression using proteomic analysis

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**Background:** *Escherichia coli* (*E. coli*) is the main causative agent of 80-90% of community-acquired infection, about 40% of nosocomial urinary tract infections (UTI), and 25% of recurrent infections. The field of proteomics has emerged as a great tool to analyze expressed proteins and to identify possible biomarkers associated with many pathological states, and to the same extent those associated with bacterial pathogenesis and their ability to cause recurrent infections. However, protein profiles could vary due to environmental stress created and can be simulated by subculturing; here we investigated the effects of sequential passaging on protein profiles of *E. coli* from patients with recurrent UTIs.

**Method:** Four urine samples were collected from individuals with recurrent UTI, and sequentially subcultured. Protein samples were prepared by sonicating bacterial pellets and analyzed using one- and two-dimensional gel electrophoresis. Protein spots of interest arising from changes in the protein profile were analyzed using Liquid Chromatography-Mass Spectrometry and matched against known data bases to identify related proteins.

**Result:** No major differences were observed using 1-D gel electrophoresis except for one sample. However, 2-D gel electrophoresis identified ATPB\_ECOBW, ASPA ECOLI, DPS ECOL6 and DCEB ECOLI as proteins associated with higher passaging.

**Conclusion:** Passaging resulted in identifiable changes in the protein profile of *E. coli*, namely proteins that are associated with ferocity and virulence of bacteria and suggestive of factors contributing to antibiotic resistance and recurrent UTIs.

### Biography

Mohammed S. Alhajouj is a Master student who is doing his research works on Clinical Chemistry in the Clinical Laboratory Science College of Applied Medical Science, King Abdulaziz University.

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