Summary

Escherichia coli are a diverse bacterial species found naturally in the intestinal tract of humans and many other animal species. However, some strains are pathogenic and cause a wide variety of different intestinal as well as extra-intestinal diseases. Extra-intestinal pathogenic *E. coli* (ExPEC) isolates are a medically important group of pathogens responsible for significant morbidity, mortality and cost of the healthcare system as a result of urinary tract infections (UTIs), diverse intra-abdominal infections, pneumonia, surgical-site infections, meningitis, osteomyelitis, skin and soft-tissue infections (SSTIs) and bacteremia.

All ExPEC strains have a common phylogenetic background deriving typically from phylogenetic groups B2 and D, and share the same spectrum of virulence determinants**.**

ExPEC strains differ significantly from both intestinal pathogens and commensal strains, as they possess typical virulence determinants these include adhesins (e.g. type 1 fimbriae and P-pili), toxins (e.g. haemolysin and cytotoxic necrotizing factor), polysaccharide capsules (e.g. K1 and K5), and siderophores (e.g. iron transport systems aerobactin and novel catecholate siderophore *E. coli*)**.**

This study compared the phylogenicity, drug resistance patterns and virulence related genes of ExPEC isolated from UTI and skin and soft tissue infections patients (SSTIs).

The present study was conducted on 250 patients (150 patients have skin and soft tissue infections and 100 patients with urinary tract infections).

Mid-stream urine sample collected with standard precautions from patients of suspected urinary tract infection and examined for presence of *E .coli*.

Wound swabs were collected from the infected burn wound (75 patient),infected surgical incision (40 patients) , Infected traumatic wound (20 patients). Also Pus samples of skin abscess (15 patients) was obtained by sterile syringes. All samples examined for presence of *E. coli*.

All the samples were cultured by inoculating on MacConkey's agar media and identified as *E .coli* on microbiological basis. *E. coli* strains were found in 80 (32%) of the collected samples (50 urinary isolates and 30 skin and soft tissue isolates).

E. coli isolates were tested for antibiotic sensitivity by Kirby-Bauer –disc diffusion method on MHA plates. Antibiotic sensitivity reveal that all isolates showed no resistance to amikacin in both urinary and skin and soft tissue isolates. Also the isolates showed higher resistance among SSTIs to ampicillin and ciprofloxacin (96.7%) (70%) than UTI isolates (82.0) (4%) respectively .MDR is very frequent in SSTIs and UTI caused by *E. coli*.

A triplex PCR was performed for assigning each *E. coli* isolate to one of four phylogenetic groups (A, B1, B2 and D). Phylogenetic groups distribution of UTI isolates was as follows most of the isolates were grouped into the B2 group (50%) , (40.0%) fell in group D, (10.0%) to group A. However Phylogenetic groups distribution of SSTIs was as follow (50%) were classified as phylogenetic group B2, (43.3%) grouped into D group, (6.7%) to group A.

Multiplex PCR was performed for detection of four virulence genes (Cytotoxic necrosis factor **(***Cnf-1*), hemolysin A (*hlyA*) , outer membrane protease (*omp T*) and iron uptake, Aerobactin synthesis (*aer 1*) gene). We compared the presence of the four genes in urinary tract isolates and skin and soft tissue isolates and we found that the VF profile of both was similar but SSTI exhibited a higher prevalence of *(Omp T)*, *(aer1*) 56.7% and 90% than UTI isolates 34.0% and 44.0% respectively. The rates of the prevalence of *cnf1* and *hlyA* were similar in both SSTI and UTI isolates.

Our results showed greater association of traditionally recognized uropathogenic virulence factors and SSTIs virulence factors (e.g. *hly*) with groups D and B2 as compared with A and B1 but statistical analysis revealed insignificant association between virulence and phylogenetic group in both UTI isolates and SSTI isolates that might be due to low number of our tested isolates.

A correlation between virulence potential and antibiotic susceptibility/resistanc for cefixime , ampicillin , amoxicillin clavuronic acid and Cefoperazone was studied the most prevalent antibiotic resistance patterns among the studied isolates revealed that group D and group B2 isolates were highly resistant to these drugs. Most resistant strains to these drugs of urinary and soft tissue isolates possessed a high percentage of studied virulence factors.

We recommend a judicious use of antibiotics. A good antibiotic policy is necessary to limit the emergence and spread of antibiotic resistance in bacteria. Further analysis of VF profiles, phylogenetic group, and their resistance to antibiotics, on larger scale of Extra-

intestinal pathogenic *E. coli* to is important for better diagnosis and treatment of these infections.