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ePoster Viewing

Resistance surveillance & epidemiology: Gram-negatives

Antibiotic susceptibility profile and molecular characterization of extended spectrum beta lactamases (ESBL) in uropathogenic Escherichia coli (E.coli) in a tertiary care hospital in Pakistan

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Background: *Escherichia coli* (*E.coli*) is the most common gram negative organism causing both community as well as hospital acquired Urinary Tract Infection (UTI). This study was conducted in a tertiary care hospital in Pakistan to find out the prevalence of uropathogenic *E.coli* and to demonstrate ESBL phenomenon and their antimicrobial susceptibility patterns. The genetic characterization of ESBL producing isolates was also done to demonstrate the genes conferring drug resistance to these organisms in our institution using conventional PCR

Material/methods: This research was a prospective, non-randomized, descriptive study. A proforma was used as a tool for data collection. The study was conducted in the Microbiology laboratory, Department of Pathology, Pakistan Institute of Medical Sciences, Shaheed Zulfiqar Ali Bhutto Medical University, Pakistan for 8 months. 140 urine non duplicate samples of patients with UTI yielding growth of *E.coli* were selected and their susceptibility profile was determined. Their molecular characterization was done using the conventional PCR targeting CTX-M, TEM and SHV genes.

Results: Urine samples of 140 (one hundred and forty) patients yielding *E.coli* were enrolled in the study. There were 81 (58%) females and 59 (42%) males. Patients included in the study were from 12-86 years of age. The ESBL phenomenon was confirmed by double disc method which demonstrated that 80 (57%) samples were positive and 60 (43%) were negative. The antimicrobial Susceptibility profile is illustrated in the table at the end of the abstract. In our study, the dissemination of ESBL encoding genes was as following: CTX-M, TEM and SHV 75%, 60%, 25% respectively. In 10% isolates, all three were present together. Group of TEM+SHV, TEM+CTX and SHV+CTX were 10%, 35% and 5% respectively in isolates. In 10% of isolates, none of the above genes were detected.

Conclusions: Our results showed emergence of multidrug resistant ESBL producing *E.coli* in our set up in Pakistan which is a very serious problem. CTX-M is the most prevalent genes encoding for ESBL in *E.coli* followed by TEM and SHV. Nitrofurantoin and Fosfomycin may be used as first line oral drugs and that Carbapenems can be safely but must be judiciously used in UTI caused by ESBL positive *E.coli*.

Susceptibility Pattern of ESBL- Producing *E.coli* (n=80).

