

## Differential between multi-drug resistance pattern of extended spectrum b- Lactamases producing *E. coli* and *K. pneumoniae*

### ABSTRACT

The current study aimed to determine the prevalence of Extended-Spectrum b-Lactamases (ESBLs) in *Escherichia coli* (*E. coli*) and *Klebsiella pneumoniae* (*K. pneumoniae*) strains isolated from patients with Urinary Tract Infections (UTIs), to study the association between presence of ESBL enzyme and multi-drug resistance strains and finally, and to investigate the predominant ESBL gene in *E. coli* and *K. pneumoniae*. The strains were examined for the presence of ESBL as a Clinical Laboratory Standards Institute (CLSI) guideline. Among 284 clinical isolates, 52.8% (n = 150) and 47.2% (n = 134) were *E. coli* and *K. pneumoniae*, respectively, and 110 strains were ESBL producer, which 68 strains were *K. pneumoniae* and 42 strains were *E. coli*. Significant difference observed between the TEM gene and ciprofloxacin resistant in *E. coli* ( $P < 0.05$ ) while no significant difference observed between CTX-M, SHV genes and the other multi-drug resistant *E. coli*. No significant difference observed between CTX-M, TEM, and SHV genes and multi-drug resistant *K. pneumoniae*. In conclusion, spreading of ESBL-producing strains is a concern, as it causes limitations to the antimicrobial agents for optimal treatment of patients. Prevalence of ESBLs was more observed in *K. pneumoniae* than *E. coli*. In addition, TEM gene was more prevalent in *E. coli* and resistance to ciprofloxacin was predominant in *E. coli*.

**Keyword:** Multi-drug resistant; ESBLs; Urinary tract infection