

Prevalence of Extended Spectrum Beta Lactamase Genotypes in *Klebsiella pneumoniae* from Respiratory Tract Infections at Tertiary Care Hospital

Title: Prevalence of Extended Spectrum Beta Lactamase Genotypes in *Klebsiella pneumoniae* from Respiratory Tract Infections at Tertiary Care Hospital

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Description: **Background:** Extended Spectrum Beta Lactamases (ESBLs) are rapidly evolving group of β -lactamase enzymes that are of particular concern to clinicians and epidemiologists. Most ESBLs have been evolved by genetic mutation from blaTEM and blaSHV genes, and are well described in *Klebsiella pneumoniae*. **Aim and Objective:** To investigate the ESBL genotypes in *K. pneumoniae* isolates from Respiratory Tract Infections (RTIs). **Material and Methods:** Clinical isolates of *K. pneumoniae* were obtained from RTI -sputum samples. Antimicrobial susceptibility was determined by Kirby- Bauer disc diffusion method. ESBL was detected phenotypically and multiplex Polymerase Chain Reaction (PCR) specific for blaTEM, blaSHV and blaCTX-M genes was performed to identify genotypes. **Results:** During the 19 months period, a total of 212 of *K. pneumoniae* were found from RTIs. Of these 212 isolates, 60 isolates (28.3%) were ESBL producers by phenotypic method. Of these 212 isolates, 96 were randomly selected for multiplex PCR for blaTEM, blaSHV and blaCTX-M genes. The findings of multiplex PCR showed that 24 isolates (25%) possessed blaTEM gene and only 4 isolates (4.1%) possessed each blaSHV and blaCTX-M gene alone. Isolates having both blaTEM+blaSHV genes were 20 (20.8%), and both blaTEM+blaCTX-M genes were 12 (12.5%); and isolate possessing all three blaTEM+blaSHV+blaCTX-M genes were 20 (20.8%). The overall prevalence of blaTEM, blaSHV and blaCTX-M genes in this study was 79.1%, 45.8% and 37.5% respectively. Imipenem was most effective antibiotic. **Conclusion:** Spread of ESBL producing *K. pneumoniae* is a major concern, as it causes limitations to optimal treatment. Multiplex PCR can be used as a rapid method to identify ESBL genotypes in *K. pneumoniae*. It will prove valuable for surveillance and establishing the treatment line against drug resistant organisms, thus saving precious time and resources. In our study blaTEM genotype was most prevalent.

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