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Original Article

Prevalence of Extended –Spectrum-Beta-Lactamase-Producing *Klebsiella Pneumonia* Isolates from Clinical Samples

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Abstract

Background and Objective: *Klebsiella pneumonia* (*K.pneumonia*) is one of the common causes of nosocomial infections. The aim of this research was to determine the prevalence of beta-lactamase genes and phenotypic confirmation of extended–spectrum-beta-lactamase (ESBL) producing *K.pneumonia* isolates from clinical samples.

Material and Methods: In this study, 122 *K.pneumonia* were isolated from clinical specimens of Khoramabad city and were confirmed by standard bacteriological tests. The presence of ESBL enzymes was detected by combined disk diffusion method. PCR assay with specific primers was used to determine bla_{SHV}, bla_{TEM}, $bla_{CTX\text{-}15}$ and $bla_{CTX\text{-}M}$ genes in the confirmed isolates.

Results: of 122 *K.pneumonia* isolates, 78 (64.18%) were positive for ESBL, using disk diffusion method. According to antibiogram results, 10.65% of isolates were resistant to cefotaxime, 3.27% to ceftazidime and 68.03% to both antibiotics. Ninety isolates (64.18%) considered as ESBLs isolates, at the same time, with being resistant to cefotaxime and ceftazidime were also sensitive to cefotaxime-clavulanic acid and ceftazidime-clavulanic acid. In PCR assays, blaCTX$_{-15}$, bla_{SHV}, $bla_{CTX\text{-}M}$ and bla_{TEM} genes were detected in 78.68%, 40.16%, 26.22% and 22.13% of isolates, respectively. Ten resistant patterns of genes were detected.

Conclusion: The significance percentage of antibiotic resistant genes of *K.pneumonia* isolates from clinical samples in Khoramabad city had ESBLs genes; CTX-M category was the most prevalent encoding genes of these enzymes.

Keywords: *Klebsiella Pneumonia*, Extended-Spectrum Beta-Lactamase, Antibiotic Resistance

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