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dentifying antibiotic resistance genes in clinical isolates of *Klebsiella pneumoniae* producing *IMP-1* and *TEM* β-lactamase

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Abstract

Aim and Background: *Klebsiella pneumoniae* is a common cause of β-lactamase-associated infections in hospitals. The present study aimed to determine the frequency of antibiotic resistance genes in *Klebsiella pneumoniae* strains producing IMP-1 and TEM β-lactamase.

Materials and methods: The present research identified 94 samples of *K. pneumoniae, using* antibiogram for the phenotypic confirmation of ESBLs. The antibiotic resistance of the isolates and the prevalence of *TEM* and *IMP-1* genes were determined using PCR method.

Findings: Of 94 samples, 77.6% were ESBL-positive and 22.3% ESBL-negative. A total of 4.1% of the samples carried the *IMP-1* gene and 43.8% the *TEM* gene, while 43.8% of the samples carried both genes.

Conclusion: Given that *TEM* and *IMP-1* genes were commonly present in a large number of the resistant samples, physicians are recommended to use therapeutic measures properly, and to prescribe antibiotics rationally.

Keywords: *Klebsiella pneumonia*, Extended-Spectrum Betalactamase (ESBL), *TEM, IMP-1*, Antibiotic Resistance.

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