

TITLE: ANTIBIOTIC RESISTANT GENES IN MULTIDRUG-RESISTANT *KLEBSIELLA PNEUMONIAE* ISOLATED FROM DIFFERENT HOSPITAL SETTINGS.

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Multidrug-resistant *Klebsiella pneumoniae* is one of the most important pathogen in nosocomial infections responsible for several diseases including pneumonia, wound, hepatic, blood and urine infections, bacteremia and neonatal septicemia. Treatment of infections is complicated due to their high potential of dissemination in health care units and its ability to acquire multiple drug resistance genes via mobile genetic elements. The aim of this study was to analyze MDR *K. pneumoniae* resistant genes coding for ESBL, PMQR, AME and carbapenems recovered from different patients attending a university hospital. Seventeen isolates were recovered from different clinical specimens: blood, urine, tracheal secretion, sputum, pleural fluid, tracheal aspirate and oropharynx swab. Antimicrobial susceptibility testing was done by the disc diffusion method, and were used PCR to investigate the presence of resistance genes. Eight (47.1%) multidrug-resistant (MDR) *K. pneumoniae* isolates were detected, showing resistance to three or more antimicrobial agent classes. All *K. pneumoniae* isolates were subjected to PCR assays and had at least one of the resistance genes investigated: 12 isolates (70.5%) had PMQR genes followed by nine isolates (52.9%) with at least one ESBL gene and three isolates (17.6%) with one AME gene. Considering the species ability to transfer and disseminate resistance genes in hospital settings, our results reinforce that control measures including adapting treatments and isolating infected patients are effective tools for screening of MDR pathogens and must be priority.

Key words: *Klebsiella pneumoniae*; multidrug-resistance; resistance genes; hospital settings