

## **Evaluation of Antibiotic Resistance and Virulence Genes among Clinical Isolates of *Pseudomonas aeruginosa* from Cancer Patients**

### **ABSTRACT**

**Objectives:** The objectives of this study were to evaluate *P. Aeruginosa* isolates from cancer patients for the phenotypic pattern of antibiotic resistance and to detect the gene responsible for virulence as well as antibiotic resistance. **Methods:** A total of 227 *P. aeruginosa* isolates were studied and 11 antibiotics were applied for susceptibility testing. PCR detection of the genes BIC, TEM, IMP, SPM, AIM, KPC, NDM, GIM, VIM, OXA, *toxA* and *oprI* was done. Finally, the carbapenem resistant isolates were tested for phenotypic identification of carbapenemase enzyme by Modified Hodge test. **Results:** The results showed that the isolates were resistant to imipenem (95%), cefipime (93%), meropenem (90%), polymixin B (71%), gentamicin (65%), ciprofloxacin (48%), ceftazidime (40%), levofloxacin (39%), amikacin (32%), tobramycin (28%) and tazobactam (24%). The PCR detection of the carbapenem resistant genes showed 51% isolates were positive for IMP, GIM and VIM, 38% for AIM and SPM, 30% for BIC, 20% for TEM and NDM, 17% for KPC and 15% for OXA. However, *toxA* and *oprI* genes were not detected. 154 carbapenem resistant isolates were found positive phenotypically for carbapenemase enzyme identification by Modified Hodge test. **Conclusion:** The co-existence of multiple drug-resistant bodies and virulent genes has important implications for the treatment of patients. This study provides information about treating drug-resistant *P. Aeruginosa* and the relationship of virulent genes with phenotypic resistance patterns.