

Diversity of Aminoglycoside Modifying Enzyme Genes Among Multidrug Resistant *Acinetobacter baumannii* Genotypes Isolated From Nosocomial Infections in Tehran Hospitals and Their Association with Class 1 Integrons

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Background & Objectives: The aim of the present study was to investigate, for the first time, the diversity of the genes encoding aminoglycoside-modifying enzymes (AME) and their association with class 1 integrons in Iranian *Acinetobacter baumannii* strains.

Methods: A total of 100 multidrug resistant *A. baumannii*, isolated from eight distinct hospitals in Tehran, were enrolled in this study. Susceptibility of these isolates to antimicrobial agents including gentamicin and amikacin was determined by E-test. Aminoglycoside resistant isolates were then tested by PCR for AME genes, including aphA6, aacC1, aacC2, aacA4, aadB, aadA1, classes 1 integron, 5_-CS-3_ and typed by RAPD PCR. The rate of resistance to imipenem, meropenem, gentamicin and amikacin were 39%, 39%, 38% and 32%, respectively. Intermediate resistance phenotype to gentamicin and amikacin was observed in 2% and 5% of all the isolates, respectively.

Results: After aph6 with 90% (n = 36/40), aadA1, aacC1 and aadB with 82.5% (n = 33/40), 65% (n = 26/40) and 20% (n = 8/40) were the most prevalent AME genes among aminoglycosides resistant *A. baumannii* isolates. A combination of two to four different resistance genes was observed in 39 of 40 strains (97.5%), with a total of 7 different combinations. PCR of integrase genes revealed that AME gene was associated with 67% of class 1 integrons. RAPD analysis showed three predominant genotypes A (n=20), B (n = 10) and 10 unrelated genotypes.

Keywords: AME Genes; Aminoglycoside Resistance; *A. Baumannii*; Tehran