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