

## 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

Mehdi Akbari\*<sup>1</sup>; Mohammad Hossein Maleki<sup>1</sup>; Sattar Mohamadi Darbidi<sup>1</sup>; Khairollah Asadollahi<sup>2</sup>; Sayad Bastaminajadi<sup>1</sup>; Mohammad Reza Nazari<sup>1</sup>; Morovat Taherikalani<sup>1</sup>; Setareh Soroush<sup>1</sup>; Mohammad Emaneini<sup>3</sup>

1-Department of Medical Microbiology, School of Medicine, Ilam University of Medical Sciences, Ilam, Iran

2-Department of Epidemiology, School of Medicine, Ilam University of Medical Sciences, Ilam, Iran

3-Department of Medical Microbiology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran

taherikalani@gmail.com

**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