Abstract

Introduction

Despite of the development of new antimicrobial agents, aminoglycosides continue to play an important role in the treatment of illnesses caused by *Acinetobacter baumannii*. However, *A.baumannii* often uses different mechanisms to overcome the activity of aminoglycosides.

This study aimed to investigate the role of various aminoglycoside resistance mechanisms in *A. baumannii*.

Material and Methods

Eighty-seven isolates of *A. baumannii* were collected from different hospitals in Tabriz and Urmia. All isolates were identified using both phenotypic and genotypic methods. Clonal relatedness of isolates to Epidemic clones was investigated using Sequence group typing. Minimum inhibitory concentration of gentamicin, amikacin, kanamycin, netilmicin and tobramycin were determined using E-test strips. Amplification of the genes encoding the following AMEs: APH(3′)-Ia, APH(3′)-VIa, AAC(3′)-Ia, AAC(3′)-IIa, AAC(6′)-Ib, AAC(6′)-Ih, ANT(2′)-Ia, and ANT(3′)-Ia, as well as 16S rRNA methylase (ArmA, RmtB and RmtC) were performed. Real time PCR was performed for measuring the expression level of AdeABC and AbeM pumps.

Results

Sequence group typing revealed that 39%, 33.3% and 12.6% of isolates belonged to SG1, SG2 and SG3 clones, respectively. Ninety-four percent of isolates were positive for AME genes. The genes coding for *aph(3')-VI* و *aac(3')-Ia* (detection rates of 62% and 49.2%, respectively) were the most detected AME genes and conferred resistance to a certain class of aminoglycosides. ArmA coding gene was detected in 34.4%, 34.2%, 29.2%, 40.3% and 64.2% of groups showing non-susceptibility to gentamicin, amikacin, kanamycin, tobramycin and netilmicin, respectively. Amikacin non-susceptibility was correlated with over production of *adeB*.

Conclusion

The results represented a definitive correlation between presence of AME genes as well as *armA* and aminoglycosides resistance in *A. baumannii*. On the other hand, the up-regulation of AdeABC and AbeM systems was found to have only the partial role in development of aminoglycoside resistance.

Keywords: *Acinetobacter baumannii*, Aminoglycoside, Aminoglycoside modifying enzyme, Methylase, Efflux pump