Survey of Aminoglycoside Acetyl Transferase Genes in Multi-Drug Resistance *Acinetobacter*

Abstract

*Acinetobacter baumannii* is a gram-negative, non-fermenting cocobacilli that its species are opportunistic pathogens and cause nosocomial infections. Bacteria achieve their resistance to the antibiotics through three mechanisms. Aminoglycoside acetyl transferase are member of GCN5 super family as AMEs for example AAC(3) and AAC(6) N acetylate aminoglycoside on the amine group on position 3and 6 amino hexose respectively. In this study we are survey present of AAC (3, 6) gen in *Acinetobacter baumannii* isolated from Iranian hospital patient. A total of 43 non-duplicated *Acinetobacter* clinical isolates were collected from the Tehran hospital in 2016. DNA extraction carried out by gram negative DNA extraction kit. Two target gens and their primers used for PCR amplification. Result show that aac (3) IIa gene with 740bp was 68.4% and in gentamicin resistant strain was 66.9% aac (6) Ib gene with 482bp present in 76% of resistant strain (43/33) and in amikacin resistant strain was 72.2% and in gentamicin resistant strain was 70.6%. Preview study showed presence of high variety of resistance gene especially aminoglycoside. This variety explains that other genes may be have role in *Acinetobacter* resistance for aminoglycoside. It believes that the ability of this pathogen to harbor diverse genetic elements parallels the experience with *P. aeruginosa*. Genome wide analysis will provide critical insights into this ability.

Key words: *Acinetobacter*; Aminoglycoside acetyl transferase; Aminoglycoside; PCR

Introduction

*Acinetobacter baumannii* is a gram-negative, non fermenting cocobacilli that its species are opportunistic pathogens and cause nosocomial infections among patients in intensive care unit (ICUs). This bacteria cause various infections such as pneumonia, meningitis, endocarditis, and urinary tract [1]. Three decades ago, *Acinetobacter baumannii* infections treated with traditional antibiotics but today it show resistance to major classes of antibiotics including aminoglycosides, tetracyclines, fluoroquinolones, carbapenems, cephalosporins, etc... At last year’s multidrug resistance (MDR) clinical isolates have shown global distribution [2]. Since Discovery and use of antibiotics, resistance to these agents has been observed. That has negative effect on the treatment of infectious disease [3]. Bacteria achieve their resistance to the antibiotics through three mechanisms:

1. Efflux of the antibiotic from the cell via membrane-associated pumping proteins.
2. Modification of antibiotic binding target molecule such as special protein or ribosomal RNA or by reprogramming of biosynthetic pathways.
3. By modifying enzymes that selectively modified and destroyed of antibiotic activity. These mechanisms require new programming by the cell in response to the presence of antibiotics [4]. Acetyl transfer, is a common mechanism for in activation of antibiotic that employed by bacteria. O-acetylation or N-acetylation is biologically stable. The aminoglycoside antibiotics bind to the A-site of the ribosome and as a result, impire the codon-anticodon decoding mechanism and blocking of translation fidelity. Aminoglycoside antibiotics bind to 16s rRNA molecule [5]. Aminoglycoside acetyl transferase are member of GCN5 super family of protein include the histon acetyl transferase that are classified based on their region specificity of acetyl transfer on the aminoglycoside structure. For example AAC (3) and AAC (6) N acetylate aminoglycoside on the amine group on position 3and 6amino hexose respectively. Genes encoding these enzymes are widespread in plasmids, transposons, and integrons (Figure 1) [6]. In this study we are survey present of AAC (3,6) gen in *Acinetobacter baumannii* isolated from Iranian hospital patient.

Figure 1: Reaction catalysed by AAGs.
Survey of Aminoglycoside Acetyl Transferase Genes in Multi-Drug Resistance Acinetobacter

Methods and Materials

A total of 43 non-duplicated Acinetobacter clinical isolates were collected from the Tehran hospital in 2016. Biochemical test were used for identification at the species level in 43 gram negative bacteria that had negative reaction on oxidase test and lack of lactose fermentation and TSI tests Alk/Alk [7-9]. The strains were isolated from trachea (60%) and sputum (40%). Multi drug resistance tests carried out for several antibiotics groups. Isolated Acinetobacter spp has high resistance to all groups of antibiotics. Aminoglycoside resistance for amikacin, was 95% and for gentamicin was 93%. Aac (3)IIa gene with 740bp was 68.4% and in gentamicin resistant strain was 66.9%. Aac (6)Ib gene with 482bp present in 76% of resistant strain (43/33) and in amikacin resistant strain was 72.2% and in gentamicin resistant strain was 70.6%. Figures 2 & 3 show result of PCR product electrophoresis the last sample from right related to negative control and sample without band related to negative sample for Acinetobacter and band show present of gene in bacteria first column from left related to DNA ladder band.

Discussion

Acinetobacter spp isolated were recovered from 43 patient that in ICUs and some other part of hospital. The strains were isolated from trachea (60%) and sputum (40%). Antibiotic susceptibility testing was performed using disk diffusion method (Kirby-bauer) on Muller Hinton agar. The criteria used were in accordance with the guidelines established by the Clinical and Laboratory Standards Institute (CLSI) [8]. DNA extraction carried out by gram negative DNA extraction kit. Two target gens and their primers used for PCR amplification are listed in Table 1.

100bp-1kb DNA ladder was used to assess PCR product size and treatment 10min with ethidium bromide and imaging with UV illuminator [9].

Table 1: Two target gens and their primers used for PCR amplification.

| Primer Name | Primer Sequence (5 to 3) | Genes | Bp | Reference |
|-------------|--------------------------|-------|----|-----------|
| aac(3)IIa   | CGAAGGCAATAAGGAG For     | Aac(3)IIa | 740 | [10]      |
|             | TGGACAGTAGCCTAGG4G Rev    |       |    |           |
| aac(6)Ib    | TGGGATGCTCTATGAGGCT For   | Aac(6)Ib | 482 | [11]      |
|             | CTGAAATGCGCTGGGCTTT Rev   |       |    |           |

Figure 2: aac(3)IIa gene present in Acinetobacter with 740bp.

Figure 3: aac(6)Ib gene present in Acinetobacter with 482bp.

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that other genes may be have role in Acinetobacter resistance for aminoglycoside. Resistance to so antibiotics perhaps the intrinsic impermeability of these outer membranes coupled with the close relationship of A. baumannii to the soil and aquatic environment has made it possible for these organisms to acquire highly effective resistance determinants in response to multiple challenges [16].

Conclusion

It believes that the ability of this pathogen to harbor diverse genetic elements parallels the experience with P. aeruginosa. Genome wide analysis will provide critical insights into this ability. Wasteful use of antibiotic cause to appearance of resistance strain of bacteria to the existence antibiotics and this makes treatment difficult also the cost and duration of treatment increased.

Acknowledgement

None.

Conflict of Interest

None.

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