

Dissemination of *Pseudomonas aeruginosa* producing bla_{IMP-1} and bla_{VIM-1} in Qazvin and Alborz educational hospitals, Iran

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Received: July 2015, Accepted: October 2015

ABSTRACT

Background and Objectives: *Pseudomonas aeruginosa* is a frequent opportunistic pathogen in health care associated infections that is highly resistant to the majority of β -lactams. The aims of this study were to access the antimicrobial susceptibility pattern of *P. aeruginosa* isolated from educational hospitals of Qazvin and Alborz provinces, to determine the prevalence of metallo- β -lactamase (MBL) among carbapenem non-susceptible isolates by combined disk (CD) method, and to detect the bla_{IMP} , bla_{VIM} , bla_{SIM} , bla_{GIM} , bla_{SPM} and bla_{NDM-1} -MBL genes.

Materials and Methods: In this cross-sectional study, 300 *P. aeruginosa* isolates were collected from different clinical specimens in two provinces of Qazvin and Alborz hospitals, Iran. After identification of isolates by standard laboratory methods, antimicrobial susceptibility was done against 17 antibiotics according to clinical and laboratory standards institute (CLSI) guideline. CD method was carried out for detection of MBLs and the presence of bla_{IMP} , bla_{VIM} , bla_{SIM} , bla_{GIM} , bla_{NDM-1} and bla_{SPM} -genes was further assessed by PCR and sequencing methods.

Results: In this study, 107 (35.66%) isolates were non-susceptible to imipenem and/or meropenem among those 56 (52.3%) isolates were metallo- β -lactamase producer. Twenty-four of 56 (42.85%) MBL-positive isolates were confirmed to be positive for MBL-encoding genes in which 14 (25%) and 10 (17.85%) isolates carried bla_{IMP-1} and bla_{VIM-1} genes either alone or in combination. Three (5.35%) isolates carried bla_{IMP} and bla_{VIM} genes, simultaneously.

Conclusion: Considering the moderate prevalence and clinical importance of MBL-producing isolates, rapid identification and use of appropriate infection control (IC) measures are necessary to prevent further spread of infections by these resistant organisms.

Keywords: *Pseudomonas aeruginosa*, Antibiotic resistance, Metallo- β -lactamase

INTRODUCTION

Pseudomonas aeruginosa is one of the most prevalent opportunistic human pathogen causing several clinical infections including wound infection, pneumonia, urinary tract infections, endocarditis, meningitis, brain abscess, and bacteremia (1-3). The increasing inappropriate use of broad-spectrum an-

tibiotics has increased the appearance of multidrug resistant *P. aeruginosa* (MDRPA) isolates which complicates the process of therapy and limits treatment options (4).

Multidrug resistant is defined as being resistant to at least 3 anti-pseudomonal antibiotic-groups including β -lactams, aminoglycosides, and fluoroquinolones (5). Carbapenems are antibiotics used for treatment of hospitalized patients infected with MDRPA (6). These antibiotics are a class of β -Lactam antibiotics with a broad spectrum of antibacterial activity and have the broadest antibacterial spectrum compared to other β -lactams such as penicillins and cephalosporins (7). However, the incidence

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of carbapenem resistance among clinical isolates of *P. aeruginosa* has been raised, predominantly due to production of carbapenemases, including the imipenem metallo- β -lactamase (IMP), VIM (Verona imipenemase), SPM (São Paulo metallo- β -lactamase), and GIM (German imipenemase) (3, 8).

MBLs were first formally categorized from serine β -lactamases in 1980 in molecular classification scheme proposed by Ambler (9). In 1989, Bush further classified MBLs into a separate group (group 3) according to their functional properties (10). The MBLs-mediated resistance is important emerging resistance mechanisms in *P. aeruginosa* and is therefore associated with significant morbidity and mortality (3, 11). MBL activity is inhibited by metal chelators, such as EDTA and THIOL compounds. These enzymes can hydrolyze most beta-lactam antibiotics including, penicillins, cephalosporins and carbapenems except monobactams (12, 13).

The *bla*_{IMP}, *bla*_{VIM}, *bla*_{SPM} and *bla*_{NDM-1}-encoding genes responsible for MBL production are horizontally transferable via plasmids and can rapidly spread to other bacteria (6). The first reported of mobile MBLs was with the discovery of *P. aeruginosa* strain GN17203 from Japan in 1988 (14). The IMP enzymes were originally detected in Asia, but later spread to Europe, to the United States and to Australia, while the VIM gene was first found in Europe, and shortly after emerged to other countries (3). The aims of this study were (i) to access the antimicrobial susceptibility of *P. aeruginosa* isolated from educational hospitals of Qazvin and Alborz provinces, (ii) to determine the prevalence of MBLs among carbapenem non-susceptible isolates by CD test, (iii) and to detect the *bla*_{IMP}, *bla*_{VIM}, *bla*_{SIM}, *bla*_{GIM}, *bla*_{SPM} and *bla*_{NDM-1} genes in MBL-producing isolates.

MATERIALS AND METHODS

Study design and identification. A total of 300 non-repetitive *P. aeruginosa* isolates were obtained from the different clinical specimens of patients admitted in Qazvin and Alborz educational hospitals. The bacterial isolates were collected from January of 2011 until November 2013. These isolates were identified by standard laboratory methods including bacteriologic and biochemical methods such as; Gram staining, oxidase test, growth at 42°C, growth

on cetrimide agar medium (Liofilchem, Italy), O/F (Oxidation-Fermentation) test and pigment production (15). The isolates were collected from various clinical specimens including tracheal aspirate, urine, sputum, blood, wound, and broncho alveolar lavage. These isolates were stored at -70°C in trypticase soy broth containing 20% glycerol and sub cultured twice prior to testing.

Antimicrobial susceptibility testing. This test was performed using Kirby-Bauer disc diffusion method according to the CLSI guideline (16). The following antibiotic discs were used: cefepime (30 μ g), amikacin (30 μ g), aztreonam (30 μ g), polymyxin B (10 μ g), imipenem (10 μ g), meropenem (10 μ g), gentamicin (10 μ g), piperacillin/tazobactam (100/10 μ g), piperacillin (100 μ g), ceftazidim (30 μ g), cefotaxime (10 μ g), ciprofloxacin (5 μ g), levofloxacin (5 μ g), ofloxacin (10 μ g), ticarcillin (10 μ g), carbenicillin (10 μ g) and tobramycin (10 μ g). Antibiotic discs were purchased from Mast (Mast Diagnostics Group Ltd, Merseyside, UK). *P. aeruginosa* ATCC 27853 was used as the quality control strain in antimicrobial susceptibility testing.

MBL screening and confirmation by phenotypic methods. Kirby-Bauer disk diffusion test was performed in order to screen MBL production using imipenem (10 μ g) and meropenem (10 μ g) disks. Isolates that were non-susceptible to carbapenem antibiotics in combined disc method, were used as a potential MBL producer. In brief a 0.5 M EDTA solution was prepared and then was added to 10 μ g imipenem disks to obtain a concentration of 750 μ g. The bacterial suspension equivalent to 0.5 McFarland turbidity was prepared and was inoculated onto plates of Mueller–Hinton agar as recommended by the CLSI. The imipenem and imipenem-EDTA disks were placed on the plate. The inhibition zones of these disks with and without EDTA solution were compared after 16–18 hours of incubation in air at 35°C. An increase of ≥ 7 in the zone diameter for imipenem in the presence of EDTA was considered as positive result (13).

Detection of MBL- encoding genes by PCR and sequencing. All MBL-producing isolates were subjected to PCR for detection of *bla*_{IMP-1}, *bla*_{IMP-2}, *bla*_{VIM-1}, *bla*_{VIM-2}, *bla*_{SPM}, *bla*_{SIM}, *bla*_{GIM} and *bla*_{NDM-1} genes, using specific primers (Table 1) (17-19).

Table 1. Oligonucleotide primers used in this study

Genes	Sequence (5'→3')	Reference
<i>bla</i> _{IMP-1} F	ACCGCAGCAGAGTCTTTGCC	17
<i>bla</i> _{IMP-1} R	ACAACCAGTTTTGCCTTACC	
<i>bla</i> _{IMP-2} F	GTTTTATGTGTATGCTTCC	17
<i>bla</i> _{IMP-2} R	AGCCTGTTCCCATGTAC	
<i>bla</i> _{VIM-1} F	AGTGGTGAGTATCCGACAG	17
<i>bla</i> _{VIM-1} R	ATGAAAGTGCCTGGAGAC	
<i>bla</i> _{VIM-2} F	ATGTTCAAACCTTTGAGTAAG	17
<i>bla</i> _{VIM-2} R	CTACTCAACGACTGAGCG	
<i>bla</i> _{SPM-1} F	GCGTTTTGTTTGTGCTC	17
<i>bla</i> _{SPM-1} R	TTGGGGATG TGAGACTAC	
<i>bla</i> _{GIM} F	TCGACACACCTTGGTCTG	18
<i>bla</i> _{GIM} R	AACTTCCAACCTTTGCCAT	
<i>bla</i> _{SIM} F	TACAAGGGATTCCGGCATCC	18
<i>bla</i> _{SIM} R	TAATGGCCTGTTCCCATG	
<i>bla</i> _{NDM-1} F	GGCGGAATGGCTCATCACGA	19
<i>bla</i> _{NDM-1} R	CGCAACACAGCCTGACTTTC	

Total DNAs were extracted by the DNA extraction kit (Bioneer Company-Korea). PCR amplifications were performed in a thermocycler (Applied Biosystems, USA) as follows: 95°C for 5min and 35 cycles of 1min at 95°C, 1min at specific annealing temperature for each primer and 1min at 72°C. A final extension step of 10 min at 72°C was performed. Amplification reactions were prepared in a total volume of 25µl (24µl of PCR master mix plus 1µl of template DNA) including 5ng of genomic DNA, 2.0U of Taq DNA polymerase, 10mM dNTP mix at a final concentration of 0.2mM, 50mM MgCl₂ at a final concentration of 1.5mM, 1µM of each primer, and 1X PCR buffer (final concentration). PCR products were electrophoresed on 1% agarose gel and then were stained with ethidium bromide solution and finally visualized using gel documentation system (UVtec, UK). The purified PCR products were sequenced by the Macrogen Company (Seoul, South Korea) and the sequence alignment and analysis were performed online using the BLAST program of the National Center for Biotechnology Information (www.ncbi.nlm.nih.gov).

Statistical analysis. Statistical data analysis was performed for descriptive statistics, including frequencies, cross tabulation of microbiological, clinical features and demographic characteristics us-

ing the computer software program SPSS version 16.

RESULTS

In this study, 96 (32 %) isolates were collected from the patients admitted to intensive care unit (ICU), 100 (33.3 %) infection diseases, 61 (20.3 %) internal medicine, 30 (10 %) surgery, 8 (2.7 %) neurosurgery and 5 (1.7 %) neurology wards. Our bacterial isolates were recovered from blood (108-36%), urine (91-30.33%), wound (34-11.33%), bronco alveolar lavage (23-7.66 %), trachea secretions (23-7.66%) and sputum (21-7%) samples. One hundred fifty-six patients (52%) were female and 144 (48%) were male. The mean age of the patients was 51.07±18.8 (range 18–90) years.

Antimicrobial susceptibility. The high rates of antibiotic resistance were against cefotaxime (92.7 %) and aztreonam (57.7%). Polymyxin B, amikacin and piperacillin/tazobactam revealed high susceptibility rates of 98.3%, 71.3% and 64.7 %, respectively. One hundred one (33.7%) isolates were characterized as MDRPA i.e., were intermediate or resistance to at least three different classes of antimicrobial agents including β-lactams, aminoglycosides and fluoroquinolones. In total, 107 (35.66%) isolates were

non-susceptible to imipenem and/or meropenem (Table 2).

Detection of MBL by CD and PCR methods.

Among 107 carbapenem non-susceptible *P. aeruginosa* isolates, 56 (52.3%) isolates were MBL producer. PCR and sequencing showed that 24 (42.85%) iso-

lates were positive for MBL genotypes among those 14 (25%) isolates and 10 (17.85%) isolates carried bla_{IMP-1} and bla_{VIM-1} genes either alone or in combination. Three (5.35%) isolates carried both the bla_{IMP-1} and bla_{VIM-1} genes, simultaneously. Isolates were negative for bla_{IMP-2} , bla_{VIM-2} , bla_{GIM} , bla_{SIM} , bla_{NDM-1} and bla_{SPM} genes (Table3).

Table 2. Antimicrobial susceptibility of *P. aeruginosa* isolated from hospitals of Qazvin and Alborz provinces

Antibiotics	Number (%)		
	Resistant	Intermediate	Susceptible
Cefotaxime	(7%.52)158	(40%)120	(3%.7)22
Aztreonam	(36%) 115	(21.7%) 65	(40%) 120
Carbenicillin	(7%.51)155	(7%.4)14	(7%.43)131
Levofloxacin	(7%.48)146	(2%)6	(3%.49)148
Ofloxacin	(47%)141	(7%.3)11	(3%.49)148
Ticarcillin	(3%.47)142	(3%.2) 7	(3%.50)151
Ciprofloxacin	(3%.43)130	(7%.3)11	(53%)159
Gentamicin	(7%.44)134	(3%.1)4	(54%)162
Tobramycin	(7%.42)128	(7%.1)5	(7%.55)167
Ceftazidime	(37%)111	(3%.5)16	(7%.57)173
Piperacillin	(3%.32)97	(7%.9)29	(58%)174
Meropenem	(35%)105	(3%.5)16	(7%.59)179
Imipenem	(31%)93	(7%)21	(62%)186
Cefepime	(33%) 99	(4%)12	(63%) 189
Piperacillin/tazobactam	(7%.25)77	(9.7%)29	(64.7%)194
Amikacin	(38.3%) 62	(8%)24	(71.3%) 214
Polymyxin B	(1.7%)5	0	(3%.98)295

Table 3. Case histories and characteristics of the 24 bla_{IMP} and bla_{VIM} -producing *P. aeruginosa* isolates collected from Qazvin and Alborz hospitals

Isolates	Age (yr)/ gender	Ward	Source	Antibiotic susceptibility profile	MBL genes
P.A 16	71/F	ICU	Blood	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= R, CIP= R, GM=R, PB= S, PTZ= R, OFX= R, TN= S, ATM=R, LEV=R, PRL=R, CPD= R	bla_{VIM-1}
P.A 26	32/M	Internal	Blood	IMP= R, MEM= R, CPM= R, AMK= S, CTX= I, CAZ= S, TC= R, CIP= R, GM=R, PB= S, PTZ= R, OFX= R, TN= S, ATM=I, LEV=R, PRL=R, CPD= R	bla_{VIM-1}
P.A 76	62/F	Infection	Urine	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= R, CIP= R, GM=R, PB= S, PTZ= I, OFX= R, TN= R, ATM=I, LEV=R, PRL=I, CPD= R	bla_{VIM-1}
P.A 77	47/M	Infection	Wound	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= R, CIP= R, GM=R, PB= R, PTZ= R, OFX= R, TN= R, ATM=R, LEV=R, PRL=R, CPD= R	bla_{VIM-1}
P.A 79	49/F	Infection	Urine	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= R, CIP= R, GM=R, PB= S, PTZ= R, OFX= R, TN= R, ATM=R, LEV=R, PRL=R, CPD= R	bla_{VIM-1}
P.A 92	29/F	ICU	BAL	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= R, CIP= R, GM=R, PB= S, PTZ= R, OFX= R, TN= R, ATM=R, LEV=R, PRL=R, CPD= R	bla_{IMP-1}

Table 3. Continued ...

P.A 113	30/M	Infection	Urine	IMP= R, MEM= I, CPM= S, AMK= S, CTX= R, CAZ= S, TC= R, CIP= S, GM= R, PB= S, PTZ= S, OFX= R, TN= R, ATM= S, LEV= R, PRL= S, CPD= R	<i>bla</i> _{VIM-1}
P.A 117	24/F	Infection	Blood	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= R, CIP= R, GM= R, PB= S, PTZ= R, OFX= R, TN= S, ATM= R, LEV= R, PRL= R, CPD= R	<i>bla</i> _{IMP-1} + <i>bla</i> _{VIM-1}
P.A 123	50/F	Surgery	Wound	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= R, CIP= R, GM= R, PB= S, PTZ= R, OFX= R, TN= R, ATM= R, LEV= R, PRL= R, CPD= R	<i>bla</i> _{IMP-1}
P.A 124	47/M	Infection	Urine	IMP= R, MEM= R, CPM= R, AMK= S, CTX= R, CAZ= R, TC= R, CIP= R, GM= R, PB= S, PTZ= I, OFX= R, TN= R, ATM= I, LEV= R, PRL= R, CPD= R	<i>bla</i> _{IMP-1}
P.A 159	33/F	Infection	Blood	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= R, CIP= R, GM= R, PB= S, PTZ= R, OFX= R, TN= R, ATM= R, LEV= R, PRL= R, CPD= R	<i>bla</i> _{IMP-1}
P.A 179	57/F	Internal	Urine	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= R, CIP= R, GM= R, PB= S, PTZ= R, OFX= R, TN= R, ATM= R, LEV= R, PRL= R, CPD= R	<i>bla</i> _{IMP-1} + <i>bla</i> _{VIM-1}
P.A 183	46/F	ICU	BAL	IMP= R, MEM= R, CPM= R, AMK= I, CTX= R, CAZ= R, TC= S, CIP= R, GM= R, PB= S, PTZ= S, OFX= S, TN= R, ATM= R, LEV= S, PRL= S, CPD= R	<i>bla</i> _{IMP-1}
P.A 196	24/F	Infection	Blood	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= R, CIP= R, GM= R, PB= S, PTZ= R, OFX= R, TN= R, ATM= R, LEV= R, PRL= R, CPD= R	<i>bla</i> _{IMP-1}
P.A 198	36/F	Internal	Blood	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= R, CIP= R, GM= R, PB= S, PTZ= R, OFX= R, TN= R, ATM= R, LEV= R, PRL= R, CPD= R	<i>bla</i> _{IMP-1}
P.A 207	42/F	ICU	Urine	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= R, CIP= R, GM= R, PB= S, PTZ= R, OFX= R, TN= R, ATM= R, LEV= R, PRL= R, CPD= R	<i>bla</i> _{IMP-1}
P.A 212	33/F	Internal	Blood	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= R, CIP= R, GM= R, PB= S, PTZ= I, OFX= R, TN= S, ATM= I, LEV= R, PRL= R, CPD= R	<i>bla</i> _{IMP-1}
P.A 224	61/M	Infection	Urine	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= R, CIP= R, GM= R, PB= S, PTZ= R, OFX= R, TN= R, ATM= R, LEV= R, PRL= S, CPD= R	<i>bla</i> _{IMP-1} + <i>bla</i> _{VIM-1}
P.A 241	39/M	Surgery	Blood	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= I, CIP= R, GM= R, PB= S, PTZ= R, OFX= R, TN= S, ATM= R, LEV= R, PRL= R, CPD= R	<i>bla</i> _{VIM-1}
P.A 242	59/F	ICU	Blood	IMP= R, MEM= R, CPM= R, AMK= I, CTX= R, CAZ= R, TC= R, CIP= R, GM= R, PB= S, PTZ= R, OFX= R, TN= R, ATM= R, LEV= R, PRL= I, CPD= R	<i>bla</i> _{IMP-1}
P.A 278	61/M	Infection	Urine	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= R, CIP= R, GM= R, PB= S, PTZ= S, OFX= S, TN= S, ATM= S, LEV= S, PRL= S, CPD= R	<i>bla</i> _{IMP-1}
P.A 283	74/F	ICU	Blood	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= R, CIP= R, GM= R, PB= S, PTZ= R, OFX= R, TN= R, ATM= R, LEV= R, PRL= R, CPD= R	<i>bla</i> _{IMP-1}
P.A 292	37/F	Internal	Urine	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= R, CIP= R, GM= R, PB= S, PTZ= I, OFX= R, TN= R, ATM= R, LEV= R, PRL= I, CPD= R	<i>bla</i> _{IMP-1}
P.A 295	77/M	Surgery	Wound	IMP= R, MEM= R, CPM= R, AMK= R, CTX= R, CAZ= R, TC= R, CIP= R, GM= R, PB= S, PTZ= I, OFX= R, TN= R, ATM= R, LEV= R, PRL= R, CPD= R	<i>bla</i> _{IMP-1}

R: Resistance; I: Intermediate; S: Susceptible; ATM: Aztreonam; CTX: Cefotaxime; CAZ: Ceftazidime; PIP: Piperacillin; TZP: Piperacillin-tazobactam; CPM: Cefepime; GEN: Gentamicin; CIP: Ciprofloxacin; LEV: Levofloxacin; AMK: Amikacin; MEM: Meropenem; IPM: Imipenem; PB: Polymyxin B; TN: Tobramycin; OFX: Ofloxacin; TC: Ticarcillin; PY: Carbenicillin

DISCUSSION

Despite the rapid development of antibiotics and improvement in supportive care, *P. aeruginosa* remains one of the most serious health care associated infections with high rate of mortality and morbidity. This

organism exhibits high rates of resistance to the several classes of antimicrobial agents (20). Carbapenems (imipenem and meropenem) are the most active agents for treating of nosocomial infections caused by *P. aeruginosa* isolates (3). However, the emergence of carbapenem resistant *P. aeruginosa* isolates has be-

come a serious clinical concern because of its intrinsic and acquired resistance mechanisms, limiting the treatment options (21). MBLs are increasingly widespread around worldwide as important mechanisms of carbapenem resistance among *P. aeruginosa* (3, 6, 22).

In the present study, antimicrobial susceptibility results showed that 33.7% isolates were MDRPA with significant rate of resistance against common used antibiotics. These findings are in agreement with results of previous studies in Iran, which reported that *P. aeruginosa* isolates are resistant to many classes of antibiotics (23, 24).

Overall, resistance to imipenem and/or meropenem was 35.66% which is higher than results of other studies have been reported by Shahcheraghi et al. (12.4%) and Japoni et al. (30%) in Iran (24, 25), but lower than that found in two previous studies carried out by Sepehriseresht et al. (56%) and Khosravi (41%) et al. in burn patients in Iran (26, 27). The varied range in susceptibility rate of carbapenems among *P. aeruginosa* isolates in different studies could be because of varied antibiotic usage profiles in different geographic regions. These results indicate that the available choices for the appropriate treatment of infection caused by MDRPA are currently limited.

In this study, 52.3% of carbapenem non-susceptible isolates were MBL producers which are higher than those reported by Khosravi et al. from Iran (19.5%) (27), Nagaveni et al. from India (20.8%) (28), Ellington et al. from UK (38.3%) (29) and Pitout et al. from Germany (46%) (30), indicating the MBL-producing *P. aeruginosa* is increasing. It should be noted that 48.7% of carbapenem resistant *P. aeruginosa* were MBL negative which suggest other mechanisms might alternatively be contributed in the carbapenem resistance, most importantly production of oxacillinase or deficiency in porin or reduced expression of outer membrane proteins (3). We previously reported that 31 (49%) of *A. baumannii* isolates were found to be MBL producers (31).

In the present study, of 56 MBL-producing isolates, 24 (42.85%) isolates were positive for MBL genotypes which 14 (25%) isolates and 10 (17.85%) isolates carried bla_{IMP-1} and bla_{VIM-1} genes either alone or in combination. In recent years, bla_{IMP} and bla_{VIM} -producing *P. aeruginosa* isolates have been reported in Asian countries. In a study from Iran, Sarhangi et al. reported that 8 (9.75%) and 10 (12.19%) of MBL-producing *P. aeruginosa* isolates were positive for bla_{IMP-1} and bla_{VIM-1} genes, respectively (32). In another study

from Iran, Khosravi et al. reported that 19.51% of clinical isolates of *P. aeruginosa* contained bla_{VIM} gene (27). In South Korea, Oh et al. reported that 82.85% and 5.71% of *P. aeruginosa* isolates harbored bla_{VIM-2} and bla_{IMP-1} genes, respectively (33). In another study from South Korea, Ryoo et al. reported that 15.6% of *P. aeruginosa* isolates harbored bla_{IMP-1} and 8.6% of isolates harbored bla_{VIM-2} (34). In Turkey, Ozqumus et al. reported that 9% and 1% of *P. aeruginosa* isolates were positive for bla_{IMP-1} and bla_{VIM} genes, respectively (35). In France, Pitout et al. showed that 43% and 2% of *P. aeruginosa* isolates carried bla_{VIM} and bla_{IMP} genes, respectively (30).

This study showed that most bla_{IMP-1} and bla_{VIM-1} -positive *P. aeruginosa* isolates were frequently collected from the patients admitted to intensive care and infection disease units. It seems that chronic underlying conditions, prolonged period of ICU stay and the use of invasive techniques and devices predispose patients to infection with these resistant isolates.

In conclusion, results of this study revealed the considerable prevalence of MBL-producing *P. aeruginosa* isolates in our hospital settings. Moreover, the MBL-encoding genes often carried by mobile genetic elements which can rapidly spread horizontally between different strains. However, early recognition of MBL-producing isolates and establishing tactful policies associated with infection control measures and appropriate antimicrobial therapy based on laboratory data are necessary to reduce further spread of these resistant bacteria in our hospitals.

ACKNOWLEDGMENT

This study was financially supported by the Cellular and Molecular Research Center and Research Deputy of Qazvin University of Medical Sciences, Qazvin, Iran.

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