Emerging Challenges: High frequency of Antiseptic Resistance Encoding Genes and Reduced Biguanide Susceptibility in Antibiotic-Resistant *Acinetobacter baumannii* in Iran

ABSTRACT:

Acinetobacter baumannii (*A. baumannii*) is a prevalent infectious agent regularly reported from hospital intensive care unit (ICU) patients. Annually, Multi-drug-resistant (MDR) isolates present a significant clinical challenge. The present study aimed to determine the prevalence of antiseptic resistance genes and the level of resistance to quaternary ammonium and biguanide compounds in *A. baumannii* isolates obtained from patients of north Khorasan province.All obtained *A. baumannii* isolates were examined for in vitro susceptibility to antiseptic agents and the presence antiseptic resistance encoding genes including *qac*E, *qac*EΔ1, and *bla*OXA-23.The broth microdilution method detected the Minimum Inhibitory Concentrations (MIC) against antiseptic compounds. The majority of *A. baumannii* infections were observed in ICU patients (n=63, 84%). MDR and extensively drug-resistant (XDR) phenotypes were present in 53.2% and 46.7% of cases, respectively. Among 75 isolates, 48 (64%) had at least one resistance gene. This includes 24 (32%) isolates with only the qacE gene and 5 (6.7%) isolates with the qacEΔ1 gene. Coexistence of qacE and qacEΔ1 genes were found in nine (25.3%) isolates. The mean minimum inhibitory concentration (MIC) of chlorhexidine digluconate (CHG) was statistically significantly higher in isolates harboring antiseptic resistance genes than in isolates without such genes (81.4 µg/ml versus 27.9 µg/ml, *P=0.001*).

The increased MIC against antiseptic agents among *A. baumannii* isolates is a big medical concern. The presence of antiseptic-resistant genes and increased minimum inhibitory concentration (MIC) levels against antiseptic agents in MDR and XDR *A. baumannii* emphasizes the critical need for comprehensive monitoring of all *A. baumannii* isolates in hospital settings to ensure efficient infection control.

Keywords

Acinetobacter baumannii, Multi Drug Resistant, Antiseptic resistance, Biguanide compound, *qac*E*, qac*EΔ1

Introduction:

Acinetobacter baumannii is a colonizer of the human ecosystem and a nosocomial infectious agent simultaneously (1). It causes different infections in the hospital setting including pulmonary infection, urinary tract infection, and meningitis. Multi-Drug Resistance (MDR) and carbapenems resistance among *A. baumannii* isolates from Intensive Care Units (ICU) is a universal dilemma (2). Resistance against carbapenems that result from genes such as those encoding oxicillinase (OXAs) withdrew this class of antibiotics from the first-line drugs of choice for *A. baumannii* infection treatment (3). Inserted gene sequences in upstream regions of *bla*OXA-23 genes regulate the resistance against carbapenems among *A. baumannii* (4) . It highlights the importance of choosing effective prevention strategies against this microbial species in hospitals.

In healthcare settings, disinfectants containing quaternary ammonium compounds (QAC) such as benzethonium chloride (BTC) and benzalkonium chloride (BKC), as well as biguanide compounds like chlorhexidine digluconate (CHG), are widely employed to prevent nosocomial infections. The action characteristics of chlorhexidine and QAC, such as cytoplasmic membrane disruption and damaging the phospholipid bilayer, further underline their efficacy (5). However, it's important to note that extended use of these antiseptic agents can induce resistance in *A. baumannii* by acquiring genes such as *qac*A/B, *qac*C/D, and *qac*E (6). Gram-negative bacteria that harbor *qac*E and *qac*EΔ1 genes are resistant against QAC (7). The acquisition of antiseptic resistance genes by already otherwise antibiotic-resistant bacteria is an evolving issue in hospitals, demanding attention and action (8,9).

In the current study, to determine the possible relation between the presence of antiseptic resistance genes and increased resistance phenotype against main antiseptic agents, we investigated the prevalence of antiseptic resistance genes (according to most famous resistance genes) and the Minimum Inhibitory Concentrations (MIC) of quaternary ammonium compounds and biguanide compounds in *A. baumannii* isolates obtained from various infections in hospitalized patients at the Imam Hassan Hospital (the primary and referral teaching and care facility in the North Khorasan province, Iran.

MATERIAL AND METHODS:

Study samples:

During the study period, all *A. baumannii* isolates responsible for infections in hospitalized patients at Imam Hassan Hospital in North Khorasan Province, Iran, were identified to the species level in the hospital laboratory. This identification was further validated in the microbiology laboratory at the Faculty of Medicine using Gram staining, oxidase testing, motility testing, and assessing their ability to grow at 42°C, following the Clinical and Laboratory Standard Institute (CLSI) guidelines. All isolates were confirmed at the gene level as *A. baumannii* by *Bla*OXA51-like PCR. All specimens were kept at -30°C in Trypticase Soy Broth (TSB) with 20% glycerol added. Chromosomal DNA was isolated using a DNA extraction kit from Poyagene Azma, Iran, per the manufacturer's guidelines for subsequent molecular analyses.

Antiseptic susceptibility testing

Susceptibility to QACs and biguanide compounds (CHG; Sigma-Aldrich, Steinheim, Germany) was assessed using the Mueller–Hinton broth microdilution method (BMD).

Antibiotic susceptibility testing

Antimicrobial susceptibility testing (AST) was conducted on Mueller–Hinton agar from Merck, Germany, utilizing the disk diffusion (Kirby–Bauer) method. The interpretation of zone sizes was based on CLSI guidelines. The following 11 antimicrobial agents were used to differentiate the isolates of *A. baumannii*: cephalosporins (Cefepime, Ceftazidime), carbapenems (Doripenem, Meropenem, Imipenem), tetracyclines (Tigecycline), b-lactamase inhibitors (Ampicillin+Sulbactam, Piperacillin+Tazobactam), aminoglycosides (Amikacin, Tobramycin) and fluoroquinolones (ciprofloxacin). We classified isolates as extensively drug-resistant (XDR) if they showed resistance to one or more antimicrobial agents in at least six categories or if they were resistant to all antibiotics except one or two. Bacteria were grouped as multi-drug resistant (MDR) if they resisted one or more agents in three or more categories.

Detection of genes

All collected samples were screened using previously established methods for the presence of antiseptic and antibiotic resistance genes, such as *qac*E, *qac*EΔ*1*, and *bla*OXA-23 genes (8). The used primers are provided in Table 1.

Statistics

SPSS 17 for Windows (SPSS Inc., Chicago) software was used for data analysis. Differences among the isolates were determined using One-way ANOVA and *P*-values <0.05 were considered statistically significant.

RESULTS:

Out of 87 documented *A. baumannii* infections, 75 *A. baumannii* isolates were available and included in the present study. The *A. baumannii* isolates were collected from various

clinical specimens, including urine (2 isolates, 2.6%), wounds (5 isolates, 6.6%), blood (4 isolates, 5.3%) and tracheal aspirates (63 isolates, 87%) (Table 2).

Among the infected patients, 60% were male (n=45/75). The mean age of the infected patients was 65.4 (22-92) years with 67.7 (22-92) years for males and 63.1 (22-83) years for females (Table 2). The vast majority of the *A. baumannii* infections occurred in the ICU (n=63, 84%), comprising ICU I (n=46, 61.3%), ICU II (n=16, 21.3%), and ICU III (n=1, 1.3%). The rest of the *A. baumannii* infections were detected in the Neurology ward (n=4, 5.3%), the Emergency ward (n=4, 5.3%), the infectious diseases ward (n=3, 4%), followed by the Cardiology ward (n=1, 1.3%). The main isolation sites of *A. baumannii* isolates were the lungs (84%) followed by wounds (6.6%), blood (5.3%), urine (2.6%), and other (1.3%) (Table 2).

Antibiotic susceptibility test (AST):

Overall, the *A. baumannii* isolates expressed resistance against nine out of twelve antibiotics (96%). The highest and lowest resistance rates were against CAZ (98.7%) and TGC (34.7%), respectively.

We found Five antibiotic resistance patterns(A-E). Four of them contained XDR phenotypes except for pattern A (Table 3). It was the dominant resistance pattern detected among 31 isolates (41.3%). *A. baumannii* showing pattern A expressed resistance against ten antibiotics (Table 3). XDR isolates were spotted among Pattern B (11 antibiotics) (N=19, 25.3%), pattern C (nine antibiotics) (N=12, 16%), pattern D (10 antibiotics) (N=6, 8%), and pattern E (11 antibiotics) (N=3, 4%) (Table 2). Four isolates showed a unique resistance pattern.

The ICU patients saw the highest number of A. baumannii infections (75 patients total, with 63 infections, making up 84%. Among these patients were 36 males (57%) and 27 females (43%). Most cases showed MDR XDR phenotypes, with 62 cases (98.4%) demonstrating these traits (53.2% MDR and 46.7% XDR).

Antiseptic resistance gene distribution:

Out of 75 isolates, 48 (64%) were found to have at least one antiseptic resistance gene. This included 24 isolates (32%) with the *qacE* gene, five isolates (6.7%) with the *qacEΔ1* gene, and nine isolates (25.3%) where both *qacE* and *qacEΔ1* genes were detected simultaneously.

The highest prevalence of antiseptics resistance genes (*qac*E and *qac*EΔ1) was detected in overall antibiotic resistance pattern D (100%), followed by pattern B (68.4%), pattern A (64.5%), and pattern C (58.3%). The most frequent single occurrence of *qac*E (83.3%) and *qac*EΔ1 (66.7%) genes was in pattern D. In pattern D, there was a simultaneous occurrence of resistance genes at the highest rate of 50%.

Antibiotic resistance gene distribution:

The *Bla*OXA-23 gene was spotted in 63 (84%) isolates. The majority of *Bla*OXA-23 gene positive isolates had at least one antiseptic resistance gene as well (n=41/63, 65%). The highest occurrence of the *Bla*OXA-23 gene was among pattern D (100%), following pattern B (89.4%), pattern A, and pattern C (83.3%) isolates (Table 3).

MICs for antiseptics:

Notably, there was no significant difference among isolates for BTC and BKC resistance levels, indicating a uniformity in resistance patterns. The MICs for different antiseptics were 3.9 to 31.2 µg/ml for BTC, 3.9 to 62.5 µg/ml for BKC, and 31.2 to 250 µg/ml for CHG.

The mean MIC for CHG in isolates harboring antiseptic resistance genes was significantly higher than in isolates without these genes (81.4 µg/ml versus 27.9 µg/ml, P=0.001). Furthermore, there was a statistically significant difference in mean MICs for CHG among isolates harboring *qacE* (63.8 µg/ml), *qacEΔ1*(56.2 µg/ml), and q*acE+qacEΔ1* (111.8 µg/ml) in comparison to those not possessing these genes (27.9 µg/ml, *P*=0.001). Among the isolates, 63/75 (97.3%) isolates had *bla*OXA-23 gene, comprising 41/63 (65%) isolates with *bla*OXA-23 gene and at least an antiseptic resistance gene (Table 4).

DISCUSSION:

The current study results illustrate the correlation between the antiseptic resistance genes (*qac*E and *qac*EΔ1) and MICs against CHG.

The prevalence of MDR and XDR (94.6%) is higher than reported from other parts of Iran. The MDR prevalence ranges between 32.7% to 93% (2001 to 2011 among Iranian *A. baumannii* isolates reported by seven studies) (10). A recent study by Mirzayi and colleagues (2020) reported 74.8% and 73.1% prevalence of MDR and XDR, respectively (11). The MDR phenotype rate was reported from 50% - 85% from Latin American countries, Africa, Asia, and North American countries (12). The high prevalence of MDR isolates isolated from ICU wards noted in this study aligns with findings from other research, except in North American countries (12).

Resistance against carbapenems detected in the current study was reported differently in European and Arabian countries (13). Elevated resistance against carbapenems was reported in Iran as well (14).

The prevalence of the *qac*EΔ1gene reported in the present study is much lower than in several other studies in Iran (49.5%, 59%, and 91%) and other countries (63% - 96.07%

(15,16). Some studies in Iran reported a higher frequency of the *qac*E gene (40% - 47.5%) (17,18), while its rate was reported to be lower (4% - 17%) in the other studies (19). The prevalence of the *qacE* gene among *A. baumannii* isolates was reported to be higher in other countries (33.3% from Saudi Arabia) (20), 45.5 and 52% from Egypt (21), and 73% from Malaysia (22). However, there is a reportedly lower prevalence in China (30.48% and 31.37%) (8,16).

The elevated prevalence of the *bla*OXA-23 gene and its carbapenems resistant phenotype documented here is interesting (23). The co-occurrence of antiseptic and antibiotic resistance in our isolates, likely attributable to their co-location within the same class I integron, is a significant concern. This discovery highlights the potential difficulties in eliminating these isolates, emphasizing the need for further research in this critical area (24). Frequent detection of antiseptic resistance genes among the *bla*OXA-23 harboring isolates makes eradication of these isolates more difficult.

We detected a statistically significant increase in the MIC against CHG among *qac*E and *qac*EΔ1 gene positive *A. baumannii* isolates Guo and colleagues documented a statistically significant increase in the MIC against CHG in qacE-positive isolates in China (16). Liu and colleagues noted a non-statistically significant increase in MIC against BKC among *qac*E positive *A. baumannii* isolates only (8). In studies conducted in Saudi Arabia (20) no increase in MIC value among *A. baumannii* isolates against CHG and BTC were reported (8).

CONCLUSION:

Fortunately, the recommended concentration of use for CHG in commercial disinfectants (5000 µg/ml) is still higher than the highest measured MIC in the current study (25). Still,

the increased MIC among *A. baumannii* isolates from our region is a significant clinical concern. *A. baumannii* with MDR and XDR phenotypes having antiseptic resistance genes and elevated MIC against antiseptic agents highlights the importance of close monitoring of all *A. baumannii* isolates in hospitals.

ACKNOWLEDGEMENT

We take this opportunity to thank Mrs. Shabnam Shirazii staff of diagnostic laboratory of Imam Hassan Hospital Bojnurd for kindly providing all isolates.

Authors' contributions

HGM; Conceptualization, Project Administration, Writing – Original Draft Preparation

M R; Investigation and laboratory works, NF; Investigation and Resources

MM; Project Administration, AA; Investigation and Resources, and AvB. Writing – Review and Editing, scientific advice.

Funding

This project was supported by Islamic Azad University, Damghan, Iran (ethics code: IR.IAU.DAMGHAN.REC.1401.001.).

Data availability

The raw data supporting the conclusions of this article will be made available by the authors, without undue reservation.

Declarations

Conflict of interest

The authors have no relevant financial or non-financial interests to disclose.

Ethical approval

Sample collection was performed in strict compliance with the guidelines approved by the Ethical Committee of Islamic Azad University, Damghan, Iran (ethics code: IR.IAU.DAMGHAN.REC.1401.001.).

REFERENCES:

1. Antunes LCS, Visca P, Towner KJ. Acinetobacter baumannii: Evolution of a global pathogen. Pathog Dis. 2014;71(3):292–301.
2. Lima WG, Silva Alves GC, Sanches C, Antunes Fernandes SO, de Paiva MC. Carbapenem-resistant Acinetobacter baumannii in patients with burn injury: A systematic review and meta-analysis. Burns. 2019;45(7):1495–508.

3. Hamidian M, Nigro SJ. Emergence, molecular mechanisms and global spread of carbapenem-resistant acinetobacter baumannii. Microb Genomics. 2019;5(10).

4. Hussain EA, Qasim Hameed H, Mujahid Al-Shuwaikh A, Mujahid Abdullah R. Detection of the aadA1 and aac (3)-1V resistance genes in Acinetobacter baumannii. Arch Razi Inst. 2022;77(3):959–66.

5. Mcdonnell G, Russell AD. Antiseptics and disinfectants: Activity, action, and resistance. Clin Microbiol Rev. 1999;12(1):147–79.

6. Correa JE, De Paulis A, Predari S, Sordelli DO, Jeric PE. First report of qacG, qacH and qacJ genes in Staphylococcus haemolyticus human clinical isolates. J Antimicrob Chemother. 2008;62(5):956–60.

7. Paulsen IT, Littlejohn TG, Radstrom P, Sundstrom L, Skold O, Swedberg G, et al. The 3’ conserved segment of integrons contains a gene associated with multidrug resistance to antiseptics and disinfectants. Antimicrob Agents Chemother. 1993;37(4):761–8.

8. Liu WJ, Fu L, Huang M, Zhang JP, Wu Y, Zhou YS, et al. Frequency of antiseptic resistance genes and reduced susceptibility to biocides in carbapenem-resistant Acinetobacter baumannii. J Med Microbiol. 2017;66(1):13–7.

9. Nima F, Foroughi Borj H, Ziaali N, Tavakoli Kareshk A, Ahmadinejad M, Shafiei R. Genetic Diversity of Toxoplasma gondii by Serological and Molecular Analyzes in Different Sheep and Goat Tissues in Northeastern Iran. Iran J Parasitol. 2023;18(2):217–28.

10. Moradi J, Hashemi FB, Bahador A. Antibiotic resistance of Acinetobacter baumannii in Iran: A systemic review of the published literature. Osong Public

Heal Res Perspect. 2015;6(2):79–86.

11. Mirzaei B, Bazgir ZN, Goli HR, Iranpour F, Mohammadi F, Babaei R. Prevalence of multi-drug resistant (MDR) and extensively drug-resistant (XDR) phenotypes of Pseudomonas aeruginosa and Acinetobacter baumannii isolated in clinical samples from Northeast of Iran. BMC Res Notes. 2020;13(1):1–6.

12. Lob SH, Hoban DJ, Sahm DF, Badal RE. Regional differences and trends in antimicrobial susceptibility of Acinetobacter baumannii. Int J Antimicrob Agents. 2016;47(4):317–23.

13. Moghnieh RA, Kanafani ZA, Tabaja HZ, Sharara SL, Awad LS, Kanj SS. Epidemiology of common resistant bacterial pathogens in the countries of the Arab League. Lancet Infect Dis. 2018;18(12):e379–94.

14. Abbasi E, Goudarzi H, Hashemi A, Chirani AS, Ardebili A, Goudarzi M, et al. Decreased carO gene expression and OXA-type carbapenemases among extensively drug-resistant Acinetobacter baumannii strains isolated from burn patients in Tehran, Iran. Acta Microbiol Immunol Hung. 2021;68(1):48–54.

15. Gomaa FAM, Helal ZH, Khan MI. High prevalence of blandm-1, blavim, qace, and qace∆1 genes and their association with decreased susceptibility to antibiotics and common hospital biocides in clinical isolates of acinetobacter baumannii. Microorganisms. 2017;5(2):18.

16. Guo J, Li C. Molecular epidemiology and decreased susceptibility to disinfectants in carbapenem-resistant Acinetobacter baumannii isolated from intensive care unit patients in central China. J Infect Public Health. 2019;12(6):890–6.

17. Khosravi AD, Montazeri EA, Maki SR. Antibacterial effects of Octenicept, and

benzalkonium chloride on Acinetobacter baumannii strains isolated from clinical samples and determination of genetic diversity of isolates by RAPD-PCR method. Mol Biol Rep. 2021;48(11):7423–31.

18. Mahzounieh M, Khoshnood S, Ebrahimi A, Habibian S, Yaghoubian M. Detection of antiseptic-resistance genes in Pseudomonas and Acinetobacter spp. isolated from burn patients. Jundishapur J Nat Pharm Prod. 2014;9(2).

19. Keshavarz-Hedayati S, Shapouri R, Habibollah-Pourzereshki N, Bigverdi R, Peymani A. Molecular Investigation of Resistance to Disinfectants in Acinetobacter Baumannii Isolates Collected From Qazvin Hospitals, Iran (2017). J Qazvin Univ Med Sci. 2019;23(1):2–13.

20. Vijayakumar R, Sandle T, Al-Aboody MS, AlFonaisan MK, Alturaiki W, Mickymaray S, et al. Distribution of biocide resistant genes and biocides susceptibility in multidrug-resistant Klebsiella pneumoniae, Pseudomonas aeruginosa and Acinetobacter baumannii — A first report from the Kingdom of Saudi Arabia. J Infect Public Health. 2018;11(6):812–6.

21. Elkhatib WF, Khalil MAF, Ashour HM. Integrons and Antiseptic Resistance Genes Mediate Resistance of Acinetobacter baumannii and Pseudomonas aeruginosa Isolates from Intensive Care Unit Patients with Wound Infections. Curr Mol Med. 2019;19(4):286–93.

22. Babaei MR, Sulong A, Hamat RA, Nordin SA, Neela VK. Extremely high prevalence of antiseptic resistant quaternary ammonium compound E gene among clinical isolates of multiple drug resistant acinetobacter baumannii in Malaysia. Ann Clin Microbiol Antimicrob. 2015;14(1):1–5.

23. Wong MH yin, Chan BK wai, Chan EW chi, Chen S. Over-Expression of ISAba1-Linked Intrinsic and Exogenously Acquired OXA Type Carbapenem-Hydrolyzing-Class D-ß-Lactamase-Encoding Genes Is Key Mechanism Underlying Carbapenem Resistance in Acinetobacter baumannii. Front Microbiol. 2019;10:486957.

24. Sabbagh P, Rajabnia M, Maali A, Ferdosi-Shahandashti E. Integron and its role in antimicrobial resistance: A literature review on some bacterial pathogens. Iran J Basic Med Sci. 2021;24(2):136–42.

25. Taheri N, Ardebili A, Amouzandeh-Nobaveh A, Ghaznavi-Rad E. Frequency of antiseptic resistance among Staphylococcus aureus and coagulase-negative staphylococci isolated from a university hospital in Central Iran. Oman Med J. 2016;31(6):426–32.

٣٢٩

٣٣٠

٣٣١

٣٣٢

٣٣٣

٣٣٤

٣٣٥

Table 1: Primer sequence for studied genes.

NO	Oligo Name	Seq(5-3)
1	*bla OXAlike-51F*	TAATGCTTTGATCGGCCTTG
2	*bla OXAlike-51R*	TGGATTGCACTTCATCTTGG
3	*qac E F*	ATGAAAGGCTGGCTT
4	*qac E R*	TCACCATGGCGTCGG
5	qacEΔ1 *F*	TAGCGAGGGCTTTACTAAGC
6	qacEΔ1 *R*	ATTCGAAATGCCGAACACCG

Table 2**:** Demographic data of *A. baumannii* infections

Gender	Age(year)	Ward							Site of infection				
		No./percent							No./percent				
No.(%)	Mean	ICU											
	Rang	I	II	III	NERO	EMR	INF	CARD	LC	WC	BC	UC	other
Male	67.7	30	6	0	3	3	2	1	36	3	4	2	0
45(60)	22-92	40	8	0	4	4	2.6	1.3	48	4	5.3	2.6	0
Female	63.1	16	10	1	1	1	1	0	27	2	0	0	1
30 (40)	22-83	21.3	13.3	1.3	1.3	1.3	1.3	0	36	2.6	0	0	1.3
Total	65.4	46	16	1	4	4	3	1	63	5	4	2	1
75	22-92	61.3	21.3	1.3	5.3	5.3	4	1.3	84	6.6	5.3	2.6	1.3
(100)													

ICU: Intensive care unit , CARD: Cardiology, EMR: Emergency, INF: Infectious diseases, NERO: Neurology, LC: tracheal aspirate culture, BC: blood culture, UC: urine culture, WC: wound culture

Table 3: Antibiotic resistance patterns versus antiseptic and antibiotic resistance gene distribution among *A. baumannii* isolates

Pattern No. (%)	Resistant to antibiotic	Sensitive	having at least a gene	*qac*E	*qac*EΔ 1	*qac*E+ *qac*EΔ1	*Bla*OXA -23
			No.(%)				
A(MDR) 31(41.3)	SAM, FEP, AMI, TOB, PI+TZ, CAZ, MEM, IMI, DOR, CIP 10	TGC 1	20 64.5	17 54.8	12 38.7	9 29	26 83.8
B (XDR) 19 (25.3)	SAM, FEP, AMI, TOB, PI+TZ, CAZ, MEM, IMI, DOR, CIP, TGC 11	- 0	13 68.4	13 68.4	5 26.3	5 26.3	17 89.4
C (XDR)		SAM, TGC	7	6	3	2	10

12 (16)	FEP, AMI, TOB, PI+TZ, CAZ, MEM, IMI, DOR, CIP 9	2	58.3	50	25	16.6	83.3
D (XDR) 6 (8)	FEP, AMI, TOB, PI+TZ, CAZ, MEM, IMI, DOR, CIP, TGC 10	SAM, 1	6 100	5 83.3	4 66.7	3 50	6 100
E (XDR) 3 (4)	SAM, FEP, AMI, TOB, PI+TZ, CAZ, MEM, IMI, DOR, CIP, TGC 11	- 0	1 33.3	1 33.3	0	0	1 33.3

Doripenem(DOR)(10mg), Meropenem(MEM)(10mg), Tigecycline(TGC)(15mg), Imipenem(IMI)(10mg), Ceftazidime(CAZ)(30mg), Ampicillin+Sulbactam (SAM) (20mg), Cefepime(FEP)(30mg), Amikacin(AMI)(30mg) ,Tobramycin(TOB)(10mg), Ciprofloxacin (CIP), Piperacillin+Tazobactam (PI+TZ)

Table 4: distribution of antiseptic resistance genes and MIC level among *A. baumannii* isolates

gene	BTC		BKC		CHG		resistance gene	BTC	BKC	CHG	*Bla*OXA-23
	Mean (µg/ml) rang	*P*	Mean µg/ml Rang	*P*	Mean µg/ml rang	*P*	distribution pattern	Mean (µg/ml)			
							no. (%)		rang		no.(%)
Positive 48 (64%)	14.4 3.9-31.2	0.276	20.2 3.9-62.5	0.41	81.4 31.2-250	**0.001**	*qac*E 24 (50%)	13.02 (3.9-31.2)	18.8 (7.8-31.2)	62.5 (31.2-125)	20 49.3
							*qac*EΔ1 5 (10.4%)	16.4 (3.9-31.2)	16.4 (3.9-31.2)	56.2 (31.2-62.5)	5 28.7
							*qac*EΔ1+*qac*E 19 (39.5%)	15.6 (7.8-31.2)	22.8 (3.9-62.5)	111.8 (62.5-250)	16 21.9

Negative 27 (36%)	11.5 3.9-31.2		14.6 1.9-62.5		27.9 1.9-62.5			11.5 (3.9-31.2)	14.6 (1.95-62.5)	27.9 (1.9-62.5)	
*Bla*OXA-23: Antibiotic resistance gene , P: One way ANNOVA test , bold text: significant											