Relationship between the resistance genes to quaternary ammonium compounds and antibiotic resistance in staphylococci isolated from surgical site infections

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Background: We aimed to investigate the prevalence of disinfectant resistance genes (qacA/qacB,qacC) and the aminoglycosides resistance genes [(aac(6')aph(2''),aph(3')-IIIa,ant(4')-Ia)] in both S. aureus and coagulase-negative staphylococcal strains (CoNS) isolated from surgical site infections.

Material/Methods: Totally, 130 staphylococcal strains isolated from surgical site infections between January 2012 and February 2013 were included in the study. The PCR technique was employed to verify any presence of methicillin resistance gene (mecA), aminoglycoside resistance genes [(aac(6')/aph (2''), aph(3)-III a ant (4')-Ia)], and disinfectant resistance genes (qacA/qacB,qacC) in staphylococci.

Results: MecA gene was determined in 58 (44.6%) of 130 staphylococcal isolates. A total of 28 (73.7%) of 38 S. aureus isolates were found to be positive for the mecA gene, and 4 (12.9%) of 31 isolates sensitive to amikacin were sensitive to methicillin. Eighteen (47.4%) of 38 amikacin-resistant S. aureus isolates were found to be positive for qacA/qacB genes and 11 (8.9%) of them were positive for qacC gene. Both mecA and qacA/qacB genes were found to be positive at the same time in 19 amikacin-resistant S. aureus strains. Seven (18.4%) S. aureus isolates were determined to be positive for qacA/qacB and qacC genes. Frequency of qacA/B genes was found to be 47.4% among amikacin-resistant S. aureus strains, while qacC gene was found to be 28.9% (p<0.05). The ratio of qacA/B and qacC genes in CoNS was found to be 37.9% and 20.7%, respectively (p<0.05).

Conclusions: Quaternary ammonium resistance genes were found to be positive at a remarkable ratio in the staphylococcal isolates from surgical wounds. Especially, the high rates of aminoglycosides and methicillin-resistance gene was remarkable in S. aureus isolates. Quaternary ammonium resistance genes were found to be positive.

MeSH Keywords: Surgical Site Infections • Staphylococcal Infections • Disinfectant Resistance • Drug Resistance, Microbial – drug effects • Staphylococcal Infections

Full-text PDF: http://www.medscimonit.com/download/index/idArt/890177
**Background**

Mostly caused by staphylococci, surgical site infections are the most common complications occurring after surgery. Staphylococci can cause infections ranging from skin and soft-tissue infections to deep tissue infections such as osteomyelitis, bacteremia, and endocarditis. Recently, methicillin and antibiotics resistance for various antibiotics have seemed to develop in both nosocomial *S. aureus* and coagulase-negative staphylococcal strains [1,2].

Very high resistance rates have been reported to develop against widely used antimicrobial agents and disinfectants in both *S. aureus* and coagulase-negative staphylococci. Combined antibiotics may often be required for the treatment of these kinds of infections caused by resistant bacterial strains. Due to their synergistic effects with many antibiotics, aminoglycosides are often administered in combination with other antibacterial agents in the treatment of staphylococcal infections [2].

As in all other antibiotic groups, resistance to antibiotics is a serious problem for aminoglycosides. The main mechanism of aminoglycoside resistance in staphylococci is based on the drug inactivation by aminoglycoside-modifying enzymes (AMEs). The most common AMEs among staphylococci is 6′-N-acetyltransferase-2′′-O-phosphotransferase [aac(6′)-aph(2′′)]. It is encoded by aac(6′)-aph-ie (2′′) gene. This enzyme fulfills the inactivation of gentamycin, kanamycin, tobramycin, neomycin, and amikacin. Additionally, 4′-O-Adenyltransferase I [ant(4′)-I] is encoded by ant(4′)-la gene, and it inactivates kanamycin, neomycin, tobramycin, and amikacin. Another enzyme is 3′-O-phosphotransferase III[aph(3′)-III], which inactivates kanamycin and amikacin and is encoded by aph (3′)-IIIa gene [3–7].

To control nosocomial infections, it is essential to secure hygienic conditions in hospitals. Of vital importance is the efficacy of disinfectants used for hand washing and surface disinfectants extensively used in hospitals against microorganisms. Nowadays, the most commonly used disinfectant agents in hospitals are quaternary ammonium compounds [8]. Recently, *qac* genes (*qacA/qacB* and *qacC* or *smr*), which are the resistance genes to quaternary ammonium compounds, have appeared more frequently in Staphylococcal isolates [9,10].

In this study, we aimed to investigate the prevalence of disinfectant resistance genes (*qacA/qacB, qacc*) and the aminoglycosides resistance genes ([*aac(6′)aph(2′), aph(3′)-IIla, ant(4′)-Ia*]) in *S. aureus* and coagulase-negative staphylococcal strains isolated from surgical site infections. We also tried to determine, the relationship, if any, between the disinfectant resistance genes and the aminoglycosides resistance genes.

**Material and Method**

The study included a total of 130 staphylococcal strains isolated from surgical site infections between January 2012 and February 2013. Polymerase chain reaction (PCR) technique was employed to verify any presence of methicillin resistance gene (*mecA*), aminoglycoside resistance genes ([*aac(6′)/aph(2′), aph(3′)-IIIa and ant(4′)-Ia*]), and disinfectant resistance genes (*qacA/qacB, qacc*) in staphylococci.

**Bacterial isolates**

The study involved a total of 130 consecutive isolates of staphylococci collected from Mustafa Kemal University Research Hospital, Department of General surgery. Bacterial isolates were obtained postoperatively from various infected wounds. To isolate staphylococci, samples were inoculated onto sheep blood agar plates and phenol-red mannitol salt agar plates. The plates were incubated at 37°C for 48 h. Identification of staphylococci was based upon colony morphology, biochemical activities, and coagulase test results [11]. If necessary, further confirmatory tests were done with the Vitek-2 automated microbiology system (bioMerieux, France).

**Susceptibility testing**

**Disc diffusion method**

Antimicrobial susceptibilities of the isolates to amikacin were tested by the agar disk diffusion method on Mueller-Hinton agar (Tiantan Biotechnology, PR China) according to the Clinical and Laboratory Standards Institute (CLSI) guidelines [12]. All antibiotic discs [oxacillin (1 µg) and amikacin (10 µg)], were obtained from Oxoid. Mueller-Hinton broth was used as the growth medium. Plates were incubated aerobically at 35°C and 37°C for 24 h in oxacillin and amikacin susceptibilities tests, respectively. The diameter of each zone was measured in millimeters.

**Quality control organisms**

*S. aureus* ATCC 29213 and *S. aureus* ATCC (43300) were chosen as the negative and positive control strains, respectively.

**Broth microdilution susceptibility tests**

The minimum inhibitory concentrations (MICs) of chlorhexidine were determined by the reference broth microdilution procedure recommended by the CLSI. At the end of incubation, the MIC was defined as the lowest concentration of an antibiotic that produced no growth [13].
PCR method for ica A and ica D

Primers specific for mecA, femA, aac(6′)/aph(2′′), aph(3′)-IIIa, and ant(4′)-Ia were selected from the studies of Strommenger et al. [14], Martineau et al. [15], and Duran et al. [16] (Table 1). The oligonucleotide primers for the qacA/qacB and qacC genes were selected based on the study by Zmantar et al. (Table 1) [17].

Multiplex PCR assay was carried out for the detection of mecA, femA, aac(6′)/aph(2′′), aph(3′)-IIIa, ant(4′)-Ia, qacA/qacB, and qacC genes in all staphylococcal strains. PCR amplification was carried out in a total volume of 25 µl. PCR amplification was achieved as follows: 5 µl of genomic DNA (approximately 50 ng) sample was added to 20 µl of PCR mixture (20 mmol/L Tris-HCl, pH 8.4; 50 mmol/L KCl, 10 mmol/L MgCl2) and 200 µmol/L each of deoxynucleoside triphosphates (dNTPs), 0.6 µmol/L each primer and 1 U Taq DNA polymerase. The amplification process for mecA, femA, aac(6′)/aph(2′′), aph(3′)-IIIa, ant(4′)-Ia, qacA/qacB, and qacC genes was started with an initial denaturation step (94°C, 4 min). Each cycle consists of 3 steps: denaturation, annealing, and extension. Each PCR reaction consisted of 30 cycles of amplification. Amplification consisted of denaturation at 94°C for 45 s, annealing at 52°C for 30 s, and DNA chain extension at 72°C for 1 min.

The amplification process for qacA/qacB and qacC was started with an initial denaturation step (94°C, 5 min). Each cycle consists of 3 steps: denaturation, annealing, and extension. Each PCR reaction consisted of 30 cycles of amplification. Amplification consisted of denaturation at 94°C for 1.5 min, annealing at 56°C for 30 s, and DNA chain extension at 72°C for 1.5 min. A final extension cycle was performed at 72°C for 7 min.

After the amplification of the slime and adhesin genes, 10 µl volumes of PCR samples were mixed with 3 µl of loading buffer (10%, w/v, Ficoll 400; 10 mmol/L Tris-HCl, pH 7.5; 50 mmol/L EDTA; 0.25% bromophenol blue). The PCR products were analyzed in a 2% (w/v) agarose gel in 1xTAE buffer (40 mmol/L Tris-acetate, 1 mmol/L EDTA; 0.25% bromophenol blue). The PCR products were analyzed using gel imaging system (Wealtex, Dolphin-View, USA).

Statistical analysis

Statistical analysis was performed using the chi-square test and p values less than 0.05 were considered statistically significant. The statistical analyses were performed using Statistical Package for Social Sciences (SPSS, ver. 17.5, Chicago, USA) software.

Results

We found that 69 of the isolates (53.1%) were coagulase positive. MecA gene was determined in 58 (44.6%) of 130 staphylococcal isolates. A total of 28 (73.7%) of 38 S. aureus isolates were positive for the mecA gene, and 4 (12.9%) of 31 isolates sensitive to amikacin were sensitive to methicillin. Eighteen (47.4%) of 38 amikacin-resistant S. aureus isolates were positive for qacA/qacB genes and 11 (%8.9%) were positive for qacC gene. mecA and qacA/qacB genes were positive at the same time in 19 amikacin-resistant S. aureus strains, and 7 (18.4%) S. aureus isolates were positive for qacA/qacB and qacC genes (Table 2).

In addition, 20 (69.0%) of 29 amikacin-resistant coagulase-negative staphylococci were found to carry mecA gene, while

Table 1. Primer sequences and predicted sizes used in the multiplex PCRs for fem-A, mecA, aac(6′)/aph(2′′), aph(3′)-IIIa, ant(4′)-Ia, qacA/qacB and qacC.

| Gene            | Primers            | Oligonucleotide sequence (5′-3′)                      | Size of amplified product (bp) |
|-----------------|--------------------|------------------------------------------------------|-------------------------------|
| mecA            | mecA-1             | ACTGCTATCCACCCCTCAAC                                 | 163                           |
|                 | mecA-2             | CTGGTGAAGTGTAACTGG                                   |                               |
| aac(6′)/aph(2′′)| aph(3′)-IIIa-1     | 5′-GAAGTACGCAGAAGAGA-3′                               | 491                           |
|                 | aph(3′)-IIIa-2     | 5′-ACATGGCAAGCTCTAGGA-3′                              |                               |
| ant(4′)-Ia      | ant(4′)-1a-1       | 5′-AAATACCGCTGGCCTA-3′                                | 242                           |
|                 | ant(4′)-1a-2       | 5′-GCACCTGCAATGCTA-3′                                 |                               |
| qacA/qacB       | qacA/qacB-1        | 5′-TCCTTTAAATGCTGGCTATTACCC-3′                        | 220                           |
|                 | qacA/qacB-2        | 5′-AGCCTACCGTCGATCACTA-3′                             |                               |
| qacC            | luk PVL-1          | 5′-GGCTTTCAAATTTATACCCCTCC-3′                         | 249                           |
|                 | luk PVL-2          | 5′-ATGGCAGATGTCGCAAATGT-3′                            |                               |
6 (18.8%) of 32 amikacin-sensitive isolates carried the methicillin resistance gene. Eleven (37.9%) and 6 (20.7%) of 29 amikacin-resistant coagulase-negative staphylococci were positive for qacA/qacB genes and qacC genes, respectively. In addition, 4 (13.8%) and 2 (6.9%) of these strains were positive for mecA and qacA/qacB genes, and mecA and qacC genes, respectively (Table 2). Aminoglycoside resistance genes were detected by PCR method in all of the 38 S. aureus strains, which were phenotypically determined to have amikacin resistance, while 3 (9.7%) of the 31 S. aureus strains sensitive to amikacin were found to carry aac(6')/aph(2'') genes. The aph(3')-Ila gene was identified in 1 strain (3.2%). Similarly, all 29 amikacin-resistant coagulase-negative strains had at least 1 aminoglycoside-resistant gene, while aac(6')/aph(2'') genes, aph(3')-Ila, and ant(4')-Ia genes were 6.3% (2/32), 9.4% (3/32) and 3.1% (1/32) positive, respectively, in the 32 strains found to be phenotypically susceptible to amikacin (Table 2).

The occurrence of mecA gene among amikacin-resistant S. aureus strains was determined as 73.7%, and this ratio was 12.9% among amikacin-sensitive S. aureus strains. There was a statistically significant difference among the methicillin-sensitive and -resistant strains in amikacin resistance (p<0.001). This difference was also recognized among coagulase-negative strains. Occurrence of methicillin resistance genes among amikacin-resistant S. aureus strains was 69.0%, and the same ratio was 18.8% among coagulase-negative strains (Table 2).

Frequency of qacA/B genes was 47.4% among amikacin-resistant S. aureus strains, while qacC gene was 28.9% (p<0.05). The ratio of qacA/B and qacC genes in CoNS was 37.9% and 20.7%, respectively (p<0.05).

At least 1 of the amikacin resistance genes existed in all of the amikacin-resistant S. aureus strains. The aac(6')/aph(2'') resistance gene positivity (48.6%) was highest, followed by aph(3')-Ila (28.9%) and ant(4')-Ia (26.3%) genes. As in S. aureus isolates, at least 1 or more resistance genes existed in all of the amikacin-resistant CoNS. Two amikacin-sensitive CoNS had aac(6')/aph(2'') gene, while 3 CoNS had aph(3')-Ila gene (Table 3). It was observed that 2 amikacin-sensitive CoNS had aac(6')/aph(2'') gene, while 3 CoNS had aph(3')-Ila gene (Table 3).

### Table 2. Correlation between antibiotics resistance and quaternary ammonium compounds resistance genes (qacA/qacB and qacC).

| Isolates | Amikacin resistance | Methicillin resistance gene | Quaternary ammonium resistance genes |
|----------|---------------------|----------------------------|--------------------------------------|
|          |                     | mecA | qacA/qacB | qacC |
|          |                     | n   | %      | n   | %      | n   | %      |
| I – S. aureus | 38 (resistant) | 28  | 73.7   | 18  | 47.4   | 11  | 28.9   |
| II – S. aureus | 31 (sensitive) | 4   | 12.9   | 6   | 19.4   | 2   | 6.5    |
| III – CoNS | 29 (resistant) | 20  | 69.0   | 11  | 37.9   | 6   | 20.7   |
| IV – CoNS | 32 (sensitive) | 6   | 18.8   | 3   | 9.4    | 0   | 0.0    |
| Total      | 130                | 58  | 44.6   | 38  | 29.2   | 19  | 14.6   |

p values for mecA: I–II: 0.000, I–III: NS, I–IV: 0.000, II–IV: <0.05; p values for qacA/qacB: I–II: 0.000, I–III: <0.05, I–IV: 0.000, II–IV: 0.01; p values for qacC: I–II: 0.000, I–III: <0.05, I–IV: 0.000, II–IV: 0.00; NS – non-significant.

### Table 3. The relation between amikacin resistance and amikacin resistance genes [aac(6')/aph(2''), aph(3')-Ila, ant(4')-Ia].

| Isolates | Amikacin resistance | Amikacin resistance genes | Number of PCR negative isolates |
|----------|---------------------|---------------------------|---------------------------------|
|          |                     | aac(6')/aph(2'')         | aph(3')-Ila | Ant(4')-Ia | n | % |
| I – S. aureus | 38 (resistant) | 17  | 48.6   | 11  | 28.9   | 10 | 26.3 | 0  | 0.0 |
| II – S. aureus | 31 (sensitive) | 3   | 9.7    | 1   | 3.2    | 0  | 0.0  | 27 | 87.1 |
| III – CoNS | 29 (resistant) | 13  | 44.8   | 11  | 37.9   | 7  | 24.1 | 0  | 0.0 |
| IV – CoNS | 32 (sensitive) | 2   | 6.3    | 3   | 9.4    | 1  | 3.1  | 26 | 81.3 |
| Total      | 130                | 35  | 100.0  | 26  | 100.0  | 18 | 100.0| 53 | 100.0|

p values for aac(6')/aph(2''): I–II: 0.000, I–III: NS, I–IV: 0.000, II–IV: <0.05; p values for aph(3')-Ila: I–II: 0.000, I–III: NS, I–IV: 0.00, II–IV: 0.01; p values for Ant(4')-Ia: I–II: 0.000, I–III: NS, I–IV: 0.000, II–IV: NS; NS – non-significant.

### Table 4. Quaternary ammonium resistance genes (qacA/qacB and qacC).

| Number of PCR negative isolates | qacA/qacB | qacC |
|--------------------------------|-----------|------|
| I – S. aureus                  | 11  | 28.9 |
| II – S. aureus                 | 2   | 6.5  |
| III – CoNS                     | 6   | 9.4  |
| IV – CoNS                      | 0   | 0.0  |
| Total                          | 19  | 14.6 |
We found that mecA gene and qacA/B genes were both positive in 27 (20.8%) staphylococcal isolates, while mecA and qacC occurred in 10 (7.7%) of the isolates. Methicillin and qacA/B genes positivity were determined in 50% of 38 amikacin-resistant S. aureus isolates, while qacC gene was detected in 18.4% of them. Of a total of 38 S. aureus isolates, 68.4% carried both methicillin and disinfectant resistance genes. Similarly, qacA/B genes were positive in 14.8% of 29 amikacin-resistant CoNS, while qacC gene was observed in 2 (6.9%) isolates. There was a significant difference between S. aureus isolates carrying mecA genes and CoNS carrying mecA genes containing the disinfectant resistance genes. Methicillin and disinfectant resistance genes were detected in 20.7% of amikacin-resistant CoNS. mecA plus qacA positivity was detected as 9.7% of the 31 S. aureus strains that were resistant to amikacin. No common positivity for mecA and qacA was found (p<0.01) among the amikacin-sensitive S. aureus strains. One isolate was positive for mecA and qacA/B genes among amikacin-sensitive CoNS, and 1 isolate was positive for mecA plus qacC genes (Table 4).

Chlorhexidine MIC values were determined as 0.5–8 mg/l. Chlorhexidine resistance was 50.7% among S. aureus isolates carrying qacA/B genes, while the same ratio was 29.5% among CoNS isolates (p<0.01). Chlorhexidine resistance was detected in all of the 24 S. aureus strains whose qacA/B genes were positive, while chlorhexidine resistance was positive in 11 of 13 qacC genes (84.6%) (p<0.05). Chlorhexidine resistance was determined in 13 (92.3%) of 14 isolates among CoNS strains that were detected with qacA/B gene, while chlorhexidine resistance was observed in 5 of 6 CoNS strains (83.3%) with qacC gene positivity (Table 5).

**Discussion**

A number of disinfectant agents are used for both hand hygiene and the prevention of nosocomial infections. It has been reported that qacA/B and qacC (or smr) genes transmitted by plasmids are responsible for the development of resistance in staphylococci against cationic antiseptic agents. Medically,
S. aureus and CoNS are remarkable microorganisms, which may cause diseases of skin and soft-tissue, as well as bacteraemia and endocarditis. Staphylococci can readily develop resistance to most antimicrobial agents, including antiseptic and disinfectants [18,19].

Quaternary ammonium compounds are disinfectants frequently used for controlling nosocomial infections. Recently, resistance to quaternary ammonium compounds has frequently appeared among clinical staphylococcal strains. In a study exploring the relation between the antiseptic resistance genes (qacA/B, qacC) and antibiotic resistance in clinical S. aureus isolates, it was observed that qacC genes occurred at a higher ratio than did qacA/B genes. Presence of qacC gene was positive in 36% of MRSA isolates. No qacA/C resistance gene could be detected in MSSA isolates, but qacA/B gene was positive in them at the rate of 4%. In that study, smr resistance gene was detected only in MRSA isolates, while qacA/B genes were determined in MRSA isolates at lower rates [20]. Unlike this study, qacA/B ratio in MRSA isolates was found to be statistically significantly higher than qacC ratio (p<0.01) in our study. In contrast, in our research qacC resistance gene was detected both in MRSA and methicillin-sensitive CoNS isolates. In addition, qacA/B and qacC resistance genes were found positive in 8.2% (5/61) and 4.9% (3/61) CoNS, respectively.

Previous studies have reported that the frequency of occurrence of disinfectant resistance genes varied from country to country and even from hospital to hospital. Noguchi et al. studied the frequency of disinfectant genes in MRSA strains. For this purpose, they used clinical MRSA isolates from different countries. QacC gene frequency among MRSA isolates from Indian isolates was 31.6%, while the same values were 1.9% in Asian samples. QacA/B frequency in Asian isolates was reported to be 41.6% and these isolates were found resistant to acriflavine at the rate of 57.7%. In the study, it was pointed out that qacA/B genes were widespread in MRSA isolates in Asia and that qacA/B play role in resistance to disinfectants [21]. In our study, the frequency of qacA/B genes with Asian roots was rather high. Chlorhexidine resistance was found in 28.5% of the isolates carrying qacA/B genes.

In a study by Zhanq et al., [22], the relation between efflux proteins was encoded by qac genes and biocide resistance. They investigated the prevalence of antiseptic resistance genes (qacA/qacB qacC) in staphylococci colonized in medical staff and nurses and found that qacA/B and qacC genes were related to the presence of mecA genes. In addition, rather high antibiotic resistance was detected in S. aureus strains where presence of qac genes was verified and in all qac gene-positive isolates, and quite high MIC and MBC values were found against antiseptics [22].

In our study, qacA/B ratio was 20.8% in 27 isolates in which presence of mecA gene was verified, while qacC genes existed at the rate of 7.7%. We also found a high chlorhexidine resistance value in isolates in which qacA/qacB and qacC resistance genes were verified. Our findings are in line with the results of Zhang and et al. [22].

In a study conducted in Malaysia in 2012 to investigate the frequency of antiseptic resistance genes in MRSA strains, it was determined that antiseptic resistance genes qacA/B and qacC occurred in 83.3% and 1.6% of the isolates, respectively. It was established in the study that qacA/B genes carriage leads to decline in chlorhexidine digluconate and benzethonium sensitivity. It was reported that MIC values were 0.5 to 2 mg/l against 3 disinfectant agents (benzalkonium chloride, benzethonium chloride, and chlorhexidine digluconate) in MRSA strains. The presence of antiseptic resistance genes was reported to be related to rising resistance values against disinfectant agents [23]. In our study, chlorhexidine MIC value was determined as 0.5–8 mg/l in isolates in which qacA/B and qacC genes were detected, and MIC value was <1 mg/l in strains where no resistance genes were detected.

Chlorhexidine is among the most widely used disinfectants for controlling nosocomial infections. Although chlorhexidine-impregnated catheter practice is reported to reduce catheter-related infections, chlorhexidine resistant S. aureus isolates have been found in recent years. In a study investigating MRSA isolates, the efficiency of chlorhexidine resistance genes (qacA and qacA/B), and chlorhexidine-impregnated catheters, MIC values against chlorhexidine in qacA/B genes carrying S. aureus isolates were >2 mg/l, while the MIC values in isolates not carrying qacA/B genes were >1 mg/l. It was also found out that MIC values were 1 mg/l in MSSA isolates and 2 mg/l in MRSA isolates, and qacA/B prevalence in MRSA and MSSA isolates was 57.7% and 3.3%, respectively. The prevalence of qacC gene in MRSA and MSSA isolates was 5% and 7%, respectively [24]. As in this study, MIC values against chlorhexidine were found to be high (>2–8) in our study.

In a study of 522 S. aureus isolates from a hospital in Japan, qacA and qacB genes were investigated; the presence of qacA/B in MRSA isolates was 32.6% and that of qacA/B genes was 7.5% among MSSA isolates. The presence of qacC in MRSA and MSSA isolates was 3.3% and 5.9%, respectively. Among S. aureus isolates, qacA/B gene frequency was widespread. In qacA/B-positive isolates, qacA and qacB genes were positive at the rate of 59.3% and 40.7%, respectively [25]. As in our study, qacA/B genes were more frequent among MRSA isolates.

In a study carried out with 98 methicillin-resistant clinical isolates, distribution and sensitiveness to antiseptics of
antiseptic resistance genes (qacA and qacC) were investigating. Frequencies of qacA and qacC were 20.2% and 20.4%, respectively [26].

In our study, qacC gene prevalence was at a lower level than in the study by Noguchi et al. [26]. The disinfectant resistance genes (qacA/B, qacC) frequency was determined as a remarkably high ratio in this first study conducted in our region. In our hospital, the prevalence of qacA/B genes was higher than that of qacC gene. There was a statistically significant difference between the qacA/B gene-positive and qacA/B gene-negative groups in chlorhexidine resistance. Similarly, resistance to chlorhexidine was significantly higher in presence of qacC gene.

In our study, 68.7% of the isolates in which antiseptic resistance genes were detected had amikacin resistance, while in the isolates lacking disinfectant resistance genes, amikacin resistance was 31.3%.

Conclusions

Rather high resistance to chlorhexidine was determined in the isolates found to carry qacA/B and qacC antiseptic resistance genes. Our findings indicate a significant relation between the presence of qacA/B and qacC resistance genes and amikacin and methicillin resistance.

Quaternary ammonium resistance genes were found to be positive at a remarkable ratio in the staphylococcal isolates from the surgical wounds. The rates of aminoglycoside- and methicillin-resistance genes were remarkably high in S. aureus isolates, especially when quaternary ammonium resistance genes were positive.

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