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FREQUENCY OF AMINOGLYCOSIDES RESISTANCE GENES (ANT(4’)-IA, APH(3’)-IIIA, AAC-(6’)-IE-/APH]2) IN STAPHYLOCOCCUS AUREUS ISOLATED FROM SURGICAL AND RESPIRATORY SITE INFECTIONS

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Abstract

Background: *Staphylococcus aureus is the most common bacterial cause of surgical wound infections. Aminoglycoside antibiotics are often used in combination with beta-lactams or glycopeptides to treat Staphylococci. The main mechanisms of resistance to aminoglycosides in staphylococcal species include aminoglycoside acetyltransferases AACs, aminoglycoside phosphoryltransferase APHs, aminoglycoside nucleotidyltransferases ANTs. The purpose of the present study is to determine the frequency of [aac (6’)-Ie-aph (2’)], ant (4’)-Ia, and aph (3’)-IIIa genes encoding aminoglycoside modifying enzymes by PCR method in Staphylococcus aureus isolated from surgical wounds.*

Materials and methods*: In the present study, 77 isolates of Staphylococcus aureus were collected from patients with surgical wound and respiratory site infections hospitalized in Yasuj hospitals. Antibiotic sensitivity pattern was determined by disc diffusion method according to CLSI guidelines for gentamicin, kanamycin, tobramycin, amikacin, and neomycin antibiotics. PCR method was used to identify aminoglycoside resistance genes ant(4’)-Ia, aph(3’)-IIIa, aac-(6’)-Ie-/aph]2.*

Findings*: The highest rate of resistance to aminoglycosides was 68.8% amikacin, 64.9% gentamicin, 64.9% tobramycin, 61% kanamycin, and 57.1% neomycin. The frequency of aminoglycoside antibiotic-resistance genes (ant(4’)-Ia, aph(3’)-IIIa, aac-(6’)-Ie-/aph]2) in isolates resistant to amikacin antibiotic respectively 13.2%, 18.6%, and 16.4% were reported.*

Conclusion*: Due to the increase in the prevalence of antibiotic resistance during the clinical use of these drugs, Fast diagnosis and timely identification of resistant strains seem essential in order to choose appropriate treatment options and prevent the spread of resistance. Therefore, the identification of aminoglycoside antibiotic-resistance genes can play an important and effective role.*

Keywords: *staphylococcus aureus, [aac (6’)-Ie-aph (2”)], ant (4’)-Ia and aph (3’)-II*I

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