

Comparison between phenotype and molecular resistance characteristic in *Staphylococcus epidermidis* isolates from wound infections in Al-Basrah province, Iraq

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ABSTRACT

Background: *Staphylococcus epidermidis* is considered the upper respiratory tract's human skin flora and mucosal membrane and displays low pathogenic capacity in healthy individuals. Drug-resistant strains can be identified as a natural result of the microflora through antibiotic therapy and are a possible cause of pathogenic strain resistance genes. **Methods:** Culture, biochemical analysis and Vitek[®]2 Utilizing for identified the One hundred and fifty swab sample was collected from different wounds infected. *S. epidermidis* strain's ability to resist antibiotics was tested using a disk diffusion method. Result of antibiotic sensitivity test was confirmed and supported by Vitek[®]2 system. Also, the PCR antibiotic resistance gene was detected.

Results: Out of 150 swab samples, twelve were positive for *S. epidermidis*. Disc method was shown the 75%,66.7%,83.3% and 58.3% harboured highest prevalence of antimicrobial resistance against penicillin, oxacillin, cefoxitin and erythromycin respectively. While the moderate prevalence 50.7%,41.7% and 33.3% of resistance against tetracycline,clandomycin and ciprofloxacin respectively. Furthermore, lowest incidence was shown the 25% for both of resistance against rifampin, and gentamycin. The Vitek[®]2 system was confirmed and support antibiotic sensitivity test. A most frequently found antibiotic resistance genes amongst *S. epidermidis* strains, according to the findings, were *mecA* (91.7%), *blaZ* (91.7) , *ermA* (16.7%),*ermB* (25%),*ermC* (25%), *tetM* (25%), *tetK* (33.3 %) and *aacA-aphD* (41.7%) respectively. All *S. epidermidis* strain doesn't have ,*vanA* and *vanB* antibiotic resistance gene.

Conclusion: Frequency of resistance to antibiotic should be detected more than one method , and used the Vitek[®]2 system detected the antibiotic resistance gave better support for result. Additional PCR technique, actually very important to detect antibiotic resistance genes of *S. epidermidis* strains.

Keywords: *Staphylococcus epidermidis*; antibiotic resistant characteristic; resistant genes; wound infection..

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1. Introduction

Staphylococci are popular bacterial colonizers of human and other mammalian skin and mucosal membranes. It major Gram-positive opportunistic bacteria that have a variety of pathogenic species [1-2]. As essential nosocomial pathogens, coagulase-negative staphylococci have been increasingly recognized [3]. Primarily *Staphylococcus epidermidis*, are associated with human skin flora and upper respiratory tract mucosal membranes, and have in stable individuals, commensals have a low pathogenic risk [4].

Even then, in immunocompromised patients, *S. epidermidis* can be responsible for some serious infection [5]. Furthermore, drug-resistant pathogens can be selected as a normal part of the microflora during antibiotic therapy and are a possible reservoir for pathogenic strains resistance genes [6-7-8-9]. Infections of the prosthetic bone, artery graft, surgical site, central nervous system shunt, operation wounds, and heart system, among other things, have been linked to *S. epidermidis* [2].

There is no clear genetic difference between pathogenic and commensal *S. epidermidis* strains, and nosocomial strains are rich in virulence and antibiotic resistance genes. It has been indicated that such genes are mobilized between and within species inside the companion genome pool [10-11]. There is few available information on the molecular epidemiology of *S. epidermidis* strains existing in Iraq. Therefore, The current study looked into the incidence rate, antimicrobial resistance properties, and the distribution of *S. epidermidis* virulence factors. Isolated wound infection strains from Al-Basrah province, Iraq.