



Erythromycin Resistance Genes among Coagulase-negative Staphylococci Isolated from Humans in Basrah, Iraq

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ABSTRACT

Aims In recent years, the global incidence of infections caused by gram-negative bacteria resistant to antibiotics has increased. This study aimed to investigate the presence and frequency of coagulase-negative Staphylococci in contact between animals and people and determine the phenotypic antimicrobial resistance profiles of coagulase-negative Staphylococci isolates from these sources.

Materials & Methods 80 samples were collected from humans in different areas of Basrah Province, including 40 samples from human hand swabs and 40 from nasal swabs. The samples were inoculated onto mannitol salt agar and blood agar and then incubated at 37°C for 24 hrs. Antibiotic susceptibility testing was performed using the disc diffusion method. A molecular study was done using the PCR technique.

Findings 37 samples (46.25%) were positive for staphylococcal infection. Five species, including *S. sciuri*, *S. lentus*, *S. gallinarum*, *S. chromogen*, and *S. haemolyticus* were identified, according to Vitek 2 kit. Staphylococci were resistant to several different antibiotics. Out of 20 amplification samples, only 12 positive samples were purified for the *ermA* gene region with a PCR product of 190 bp. The results also showed the presence of an *ermC* band with a size of 299 bp, which represents the correct expected band in 8 isolates out of all isolates.

Conclusion Gram-positive organisms are increasingly identified as the source of acute clinical infection in animals and humans. Some isolates are resistant to several different antibiotics. The *ermC* gene, *ermA* gene, and both *ermA* and *ermC* genes are present in the genome of these bacteria.

Keywords Erythromycin; Antibiotic Resistance; Bacterial Genes; Staphylococcus; Human; PCR

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