

Prevalence of Methicillin-resistant *Staphylococcus aureus* Isolated from Clinical Samples by Phenotypic and Genotypic Methods

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Background & Objectives: Methicillin-resistant *Staphylococcus aureus* (MRSA) which one of the major causes of community and hospital-acquired infection, capable of producing a wide range of diseases from skin and soft tissue infection to life-threatening endocarditis, bacteremia and necrotizing pneumonia. This study was carried out on 279 *S. aureus* (SA) were collected from the clinical samples during 2011-2012. The aim of this study was to identify MRSA in phenotypic and genotypic methods in order to obtain information of the spread of this bacteria in patients, detection of the *mecA* gene and determine antibiotic resistance patterns to increase the accuracy of therapy.

Methods: Clinical strains were investigated for biochemical characterization like gram stain, catalase, coagulase, and carbohydrate fermentation to identify SA, then disk diffusion test was performed on SA based on CLSI to identify MRSA, in addition antibiotic sensitivity patterns were obtained using Vancomycin, Oxacillin, Tetracycline, linezolid, Penicillin G, Cefazolin, Gentamicin. PCR test was carried out by a pair of specific primers to detect the *mecA* gene in MRSA strains.

Results: A total of 279 strains, 62% were MRSA. The results of the sensitivity patterns to antibiotics used in this study of 279 samples showed that the greatest sensitivity was to linezolid and the highest resistance was to penicillin G. The results of molecular analysis revealed the presence of the *mecA* gene in MRSA.

Conclusion: More than 60% of SA strains were resistant to oxacillin, increasingly in comparison to previous reports. This research showed that there was a direct relationship between the *mecA* gene and drug resistance in MRSA.

Keywords: Methicillin-resistant *Staphylococcus aureus*; *MecA*; Vancomycin; Oxacillin