MOLECULAR ANALYSIS AND ANTIMICROBIAL SUSCEPTIBILITY OF METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS IN ONE OF THE HOSPITALS OF TEHRAN UNIVERSITY OF MEDICAL SCIENCES: HIGH PREVALENCE OF SEQUENCE TYPE 239 (ST239) CLONE

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Methicillin-resistant Staphylococcus aureus (MRSA), particularly the multi-drug-resistant clones, is an increasing worldwide problem. The average incidence rate of MRSA in Tehran was found to be over 40%. A total of 140 MRSA isolates obtained from patients attending a teaching hospital in Tehran, from May 2009 to December 2009, were included in this study. The antimicrobial susceptibility profile of MRSA isolates was determined by the agar disk diffusion method. Molecular analysis of MRSA strains was accomplished by Pulsed-Field Gel Electrophoresis (PFGE) and Multi-locus sequence typing (MLST). Detection of mecA gene was used to confirm resistance to methicillin among the MRSA isolates. All the MRSA isolates were susceptible to chloramphenicol, teicoplanin, tigecycline and vancomycin. All MRSA isolates were resistant to oxacillin, whilst 139 strains showed resistance against ciprofloxacin, erythromycin, gentamicin, tetracycline and trimethoprim-sulfamethoxazole. PFGE analysis of all the 140 MRSA isolates produced five distinct pulsortypes designated as pulsortypes A–E. Most of the isolates (n=132) were clustered into pulsortype A. The most prevalent sequence type (ST) was ST 239 (pulsortype A) found in 82% (37/45) of the tested isolates. The second most prevalent type was ST 1238 (pulsortypes B, C and D) found in 15% (7/45) of the isolates. The remaining type, ST 8 (pulsortype E) was found in a single isolate. The results of this study indicated that the MRSA clone ST