Molecular typing of methicillin resistant *Staphylococcus aureus* clinical isolates on the basis of protein a and coagulase gene polymorphisms

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Increased frequency of methicillin-resistant *Staphylococcus aureus* (MRSA) in hospitalized patients requires rapid and reliable characterization of isolates for control of MRSA spread in hospitals. This study evaluated polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) as a molecular typing technique for MRSA strains on the basis of protein A (spa) and coagulase (coa) gene polymorphisms to verify their ability in assessing the relatedness of isolates. Seventy five MRSA isolates, from different ICUs of Alexandria University Main Hospital, were characterized using antibiotyping and PCR-RFLP analysis of coa and spa genes. Thirty two antibio types were identified. Coa gene PCR generated 3 types and 10 subtypes band patterns. *HaeIII* restriction digestion of amplified coa gene products produced 5 major banding patterns and 12 subtypes. Spa gene PCR products generated 4 major and 11 minor types, and their *HaeII* restriction digestion showed 5 major and 12 minor banding patterns. The combined coa and spa RFLP patterns generated 22 combined R types. Typing using coa PCR and PCR-RFLP had the same Discriminatory index (DI) value (0.64), which was comparable to that of both spa PCR and PCR-RFLP techniques (0.68). The combined grouping increased the DI value to 0.836. The current study revealed that testing for multiple gene polymorphisms is more useful for local epidemiologic purposes.

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