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PREVALENCE OF MRSA AND AGR SPECIFICITY GROUPS AMONG STAPHYLOCOCCUS AUREUS STRAINS COLONIZING HOSPITALIZED PATIENTS IN TERTIARY HOSPITAL CENTRE

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ABSTRACT

Methicillin resistant *Staphylococcus aureus* (MRSA) is a major pathogen that causes a broad range of serious diseases in humans, but the regulator of virulence factors in *S. aureus* is orchestrated by accessory gene regulator (*agr*) quorum sensing system. The objective of this study was to investigate the prevalence of the MRSA and frequency of virulence genes among clinical samples hospitalized in tertiary hospital centre in Tirana, Albania. Methods. About 452 clinical specimens were collected during three years in hospitalized patients. The min age of patients were 18 years and the max 89 years old. To detect the presence of MRSA in samples, we have used a slide latex agglutination kit for the rapid detection of PBP2 and the cefoxitin disk screen test. PCR assays were used to detect gene`s content (*agr* groups) in 150 clinical samples isolates. Four reverse primers specific for amplification were used for each single *agr* group (*agrI-IV*). Results. Patients enrolled in this study were hospitalized in different wards and samples are collected from blood, urine, sputum, throat swab, wound, abscess, pus/exudates, skin and soft tissue swab, and indwelling medical devices. The prevalence of methicillin-resistant *S. aureus* (MRSA) was 33.2% (150/452) cases. Of the MRSA isolates identified in this study 36 (24%) were susceptible to antibiotics 10 (7%) demonstrated intermediate resistance and 9 (6%) were multi-drug resistant with resistance to six classes of antibiotics. *agr I* was the most isolates of our samples 45%. *agr II* resulted in 28% of samples, *agr III* in 10%, dhe *agr IV* in 19%. In our study we were not observed association for *agr* group with gender, age and wards. Conclusion. This is the first study conducted in Albania for prevalence of *agr* groups among *S. aureus* strains. The majority of *S. aureus* isolates in this study were classified as *agr* group I. The obtained results do not allow us to establish a direct relationship between the *agr* group and some of factors of *S. aureus* infection. To be more effective for infection control need to do future surveillance studies in order to understand distribution and relationship of *agr*.

Key words: *S. aureus*, MRSA, *agr* groups, hospitalized patients