Prevalence of agr specificity groups among *Staphylococcus aureus* strains colonizing hospitalized patients in tertiary hospital centre

Institute of Public Health

Blerta (Kika) Brati[1], Erjona Abazaj[1] Oltiana Petri[1]; Andi Koraqi[2]

1. Institute of Public Health, Tirana, Albania

2. Medicine University of Tirana, Faculty of Medicine, Tirana, Albania

Abstract

Introduction

Methicillin resistant *Staphylococcus aureus* (MRSA) is a major pathogen in humans (1), and the regulator of virulence factors in *S. aureus* is accessory gene regulator (*agr*) quorum sensing system (2,3). This study aims to investigate the prevalence of the MRSA and frequency of virulence genes in hospitalized patients in tertiary hospital centre in Tirana, Albania.

Methodology

Latex agglutination kit for the rapid detection of PBP2 and the cefoxitin disk screen test were used for detection of MRSA in 452 samples. PCR assays were used to detect gene`s content (agr groups I-IV) in 150 clinical samples isolates.

Table 1. Primers used for aplification of agrI; agrII; agrIII; agr IV

Gene	Sequence	Size of Product
agr I	**5'**_CCAGCTATAATTAGTGGTATTAAGTACAGTAAACT **3'**_AGGACGCGCTATCAAACATTTT	441 bp
agr II	**5'**_CAATAGTAACAATTTTAGTGACCATGATCA **3'**_GCAGGATCAGTAGTGTATTTTCTTAAGTT	575 bp
agr III	**5'**_CATTATAACAATTTCACACAGCGTGTT **3'**_GCAAGTGCATAAGAAATTGATACATACA	323 bp
agr IV	**5'**_GAGTTCTCAAAAAGATTAGCTCATCATATC **3'**_TAGCTTCATCCGAGTTTATTTGAGAAT	659 bp

Results

Samples were collected from blood stream and catheter-associated infections 31.2%; 27.9% from urine infections; 16.2% from skin and soft-tissue infections cases; 14% from wounds and 10.75% from nasal area. The prevalence of methicillin-resistant *S. aureus* (MRSA) resulted 33.2% and 12% of them demostreted multi-drug resistant with resistance to six classes of antibiotics. The most predominated agr specificity group was agr I 43%, agr II was 28%, agr III 19%, dhe agr IV 7%. It wasn`t find association between *agr* group with gender, age and samples origin, p value resulted >0.05.

Conclusion

There is lack of data associate to agr group in MRSA in Albania population and this study aims to clarify the prevalence of *agr* groups. The majority of isolates were classified as *agr* group I. The obtained results do not allow us to establish a direct relationship between virulence of agr groups and some of *S. aureus* infection factors. So more expanded surveillance studies are needed to apply in the future for better estimation of agr virulence.

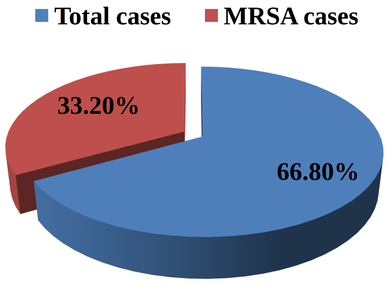


Figure 1. Prevalence of MRSA

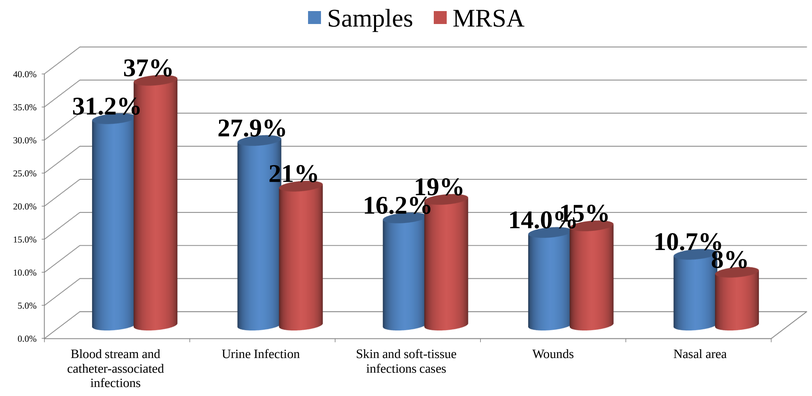


Figure 2. Sample collection and prevalence of MRSA

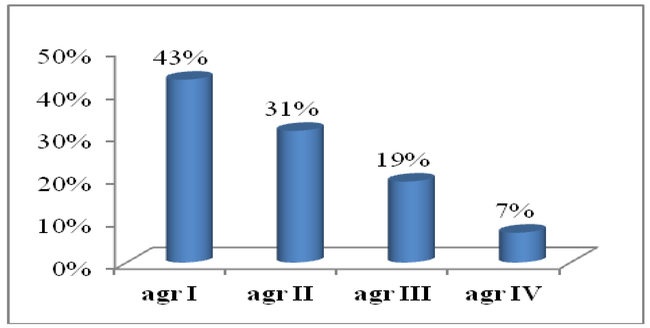


Figure 3. Prevalence of agr specificity group

Key words: MRSA, hospitalized patients, agr groups, PCR

Rererence

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