

TITLE: EVALUATION OF CLINICAL STRAINS OF *Staphylococcus aureus* FROM UNIVERSITARY HOSPITAL

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ABSTRACT:

The *Staphylococcus aureus* is considered a human opportunistic pathogen and the phenotype methicillin resistant *Staphylococcus aureus* (MRSA) is one of the main human pathogens causing nosocomial infection worldwide and its resistance and virulence has been the focus of numerous surveillance studies over the past few years. The objective was to determine the presence of the *mecA* gene in clinical strains of *S. aureus* and its relation with resistance to antibiotics and virulence genes. The strains of *S. aureus* used in this study were recovered from university hospital in Minas Gerais. The *mecA* gene and virulence genes were investigated using the Polymerase Chain Reaction technique in oxacillin-resistant samples determined by the hospital microbiology laboratory using the Vitek®2 automated system. There was a predominance of *S. aureus* infections in the Medical Clinic (29.1%), most of the MRSA samples were obtained from blood collection and tracheal secretion (32.3% and 20.5%, respectively) and 51.3% of strains were resistant to antibiotics Lincosamide, Macrolide and Penicillin. The *mecA* gene was found in most samples (91.1%), the *fnbB* gene in 8.8%, and the *clfA* gene appeared in almost half of them (44.1%) and all samples were negative for the *lukS* gene. Profile antibiotic multiresistant R1 and R2 showed a positivity relation of the virulence genes, being: 24.1% R1 and *clfA* +, 3.4% R1 and *fnbB*+, and 27.5% R2 and *clfA*+. The frequency of MRSA was high (46.0% - 34/74), all of them were positive for the *clfA* genes and only 3.2% were also positive for the *fnbB* gene. The association of the virulence genes and resistance to antibiotics causes the patient's clinical condition to complicate, increase the symptomatology, make it difficult and increase the cost for the treatment.

Keywords: Hospital infection. *Staphylococcus aureus*. MRSA. Virulence.

Development Agency: Fundação de Amparo à Pesquisa do Estado de Minas Gerais