TITLE: PHENOTYPICAL AND GENOTYPICAL CHARACTERIZATION OF STAPHYLOCOCCUS AUREUS RESISTANT OF THE BANK OF SAMPLES OF THE CENTRAL LABORATORY OF BRASILIA (LACEN-DF)

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ABSTRACT:

Staphylococcus aureus (S. aureus) are microorganisms present in the human microbiota on the skin, mucosa of the upper air tract and in small amounts in the gastro-intestinal tract and rectum. These micro-organisms break down the skin barrier and / or mucosa can trigger a pathological process from a simple dermatitis to a serious pneumonias leading to death. S.aureus is by far the main causative agent of hospital infections as its treatment is becoming increasingly difficult. Some strains of S. aureus have been able to develop resistance mechanisms against beta-lactam antibiotics through the Mec A gene, but some strains have the Luk S or Luk F gene that are responsible for producing the Panton-Valentine Leucocidin (PVL) toxin responsible for creating pores on the membranes of monocytes. This research aimed to identify the bacteria, resistance to cefoxetin and the search of Mec A and Luk F / S genes. The bacteria from the LACEN-DF sample bank were confirmed by the 16S gene, from 31 S.aureus samples, 28 (90.3%) showed resistance to cefoxethin (Minimal inhibitory concentration (MIC) <21mm) and only 3 (9.7%) Were drug sensitive (MIC> 22mm). The samples that were resistant to cefoxethin had the Mec A gene in their structures and those that were sensitive did not present Mec A in their DNA. Of the 28 samples that possessed the Mec A gene, 3 (10.7%) had the Luk F / S gene and the samples that were sensitive did not present the Luk F / S gene. Gene expression assays were confirmed from the Polymerase Chain Reaction (PCR) assay where the Mec A gene has 310 base pairs (bp), the Luk F / S gene 433 bp and the 16S 756 bp gene. It could be verified that the MecA gene is interconnected to samples that are resistant to cefoxethin and to amotrans with PVL positive.

KEYWORDS: Microbial Resistance to Medications, Polymerase Chain Reaction, Bacterial Genes

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