

Título: GENOTYPIC CHARACTERIZATION OF A NEW VIRULENCE FACTOR DETECTED IN *Staphylococcus haemolyticus*

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Resumo:

Staphylococcus haemolyticus is the second most frequently specie isolated from human blood cultures among coagulase-negative staphylococci (CoNS), and has emerged as an important pathogen in human diseases. However, its pathogenic potential and virulence factors are still underexplored. Recently, genome sequencing of the *Staphylococcus aureus* ST239 strain revealed a novel gene, of previously unknown function, encoding a surface protein of 15kDa, named SasX. Another protein, named SesI, has been also found in *Staphylococcus epidermidis* RP62A strain. In both cases, the proteins demonstrated to be involved in pathogenesis, especially adhesion and invasion of host cell. The *sasX* and *sesI* genes, are in the same genetic environment, inserted into Φ SP β -like prophage 127.2 kb, on the chromosome in both species. The aim of the current study is to extend this research to *Staphylococcus haemolyticus*. For this, 62 *S. haemolyticus* strains were isolated from patients from the *Hospital Naval Marcílio Dias*, Rio de Janeiro, between 2006 and 2008. The presence of a gene encoding for a protein similar to SasX were analyzed by PCR. A fragment of the gene was detected in 33 samples (53.22%) and 2 of them were sequenced. The sequences were similar with *sasX* (95%) and *sesI* (98%), previously described in *S. aureus* and *S. epidermidis* respectively. Subsequently, the full sequence and the genetic context of the *sasX-like* gene in the *S. haemolyticus* genome were investigated from the design of new primers that included a fragment of prophage Φ SP β -like and subsequent sequencing of amplicons. Thus, we obtain the sequence of the novel gene described in *S. haemolyticus* and found the same genetic context which for the previously described *sasX* and *sesI* in 7 of the 33 samples. Among those who did not have confirmed genetic environment, we selected one strain (MD49) to sequence the complete genome. From the sequencing, we found a new genetic environment related to the gene, where it is not associated with a SP β -like prophage, and is flanked by an insertion sequence (IS). The bioinformatic analysis showed that the gene is located on chromosome. The description of a novel gene, which may encode a protein involved in the pathogenesis of *S. haemolyticus*, will be valuable for elucidating the virulence factors of the pathogen, and may be a new target for therapeutic action to provide the most promising developments. Furthermore, this study may provide a better understanding of the horizontal transfer of these genes between the species of genus *Staphylococcus*.