

Title: VIRULENCE PROFILE AND GENOTYPING OF *Staphylococcus aureus* HARBORING PANTON – VALENTINE LEUKOCIDIN (PVL) GENES

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Abstract:

Staphylococcus aureus is an important cause of nosocomial infections in worldwide. *LukS-PV* and *lukF-PV* genes encode the Pantone-Valentine Leukocidin (PVL) which is an important virulence factor produced by this pathogen. The mechanism of action is related to lysis of leukocytes and phagocytes facilitating installation of infections with variable severity. The aim of this study was to analyze resistance and virulence profile and genotyping of *S. aureus* clinical isolates harboring the *lukS/F-PV* genes. One hundred isolates were analyzed among January/2012 and January/ 2014 and 22 presented these genes. The detection of the *mecA* gene, SCC*mec* typing and five adhesin genes (*ebpS*, *bbp*, *fnbA*, *fnbB* and *cna*) and four toxin genes (*sea*, *sec*, *see*, and *tsst*) were made by PCR. The analysis of fragmentation patterns of chromosomal DNA was performed using *Sma*I enzyme and subsequent pulsed field gel electrophoresis (PFGE). Five isolates were sensible (MSSA) and 17 resistant to methicillin (MRSA) due to *mecA* gene presence. These 17 isolates were submitted to SCC*mec* typing and 11 belonged SCC*mec*IV, three SCC*mec*II and three were nontypeable. The eight different virulence profiles were detected. PFGE analysis showed four distinct lineages among all 22 isolates (A-D). Prevalent lineage A was found in 13 of them, all presented SCC*mec*IV and three virulence profiles (P): P1: *fnbB* and *fnbA* genes; P2: *ebpS* and *fnbB* and P3: only *fnbB* gene. Four isolates presented lineage B, SCC*mec*II and virulence profile characterized only by *ebpS* gene (P4). Genotype C, involved four MSSA isolates and showed the most virulent profiles: P5: *cna*, *bbp*, *ebpS*, and *fnbA* genes; P6: *cna*, *bbp*, *ebpS*, *fnbA* and *sea*; and P7: *cna*, *bbp*, *ebpS*, and *sea* genes. The genotype D was present in only one MSSA isolated and was characterized by absence of virulence genes beyond *lukS/F-PV*. This study showed a high prevalence of one lineage harboring PVL genes and a low presence of others virulence genes. PVL was more common in MRSA-SCC*mec*IV, but MSSA isolates presented more virulent profile. Our results contributed to increase the understanding of epidemiology of MRSA harboring PVL isolates.

Key-words: *Staphylococcus aureus*, Pantone-Valentine Leukocidin, Virulence.

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