

TITLE: MOLECULAR TYPING OF CLINICAL METHICILLIN RESISTANT *Staphylococcus aureus* ISOLATES FROM SANTA CATARINA STATE

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ABSTRACT:

Methicillin-resistant *Staphylococcus aureus* (MRSA) are one of the most important pathogens due to their incidence and severity of infections as well as their multiresistance to various antimicrobials. The ability to cause infection is closely linked to the expression of virulence genes encoding molecules associated to colonization, tissue damage and evasion to the host immune defense. In the State of Santa Catarina (SC), only one published study regarding the characterization of MRSA isolates was found and only partial molecular typing was performed. In this previous study, isolates from two main cities presented a low prevalence (2-8%) of MRSA when compared to other Brazilian regions (~30-60%). In order to better characterize MRSA strains isolated from SC to help to understand more about the differential epidemiology from the region, the present study performed a molecular typing of 55 MRSA strains isolated from all SC. SCC*mec* typing, Multilocus Sequencing Typing (MLST) and detection by Polymerase Chain Reaction (PCR) of the virulence genes encoding for leukocidins (LukDE and Panton-Valentine; PVL), enterotoxins G and H (SEG and SEH) and Toxic Shock Syndrome Toxin-1 (TSST-1) were performed. These characteristics were also compared to MRSA strains isolated in other Brazilian states and countries using genome analyzes (*in silico*). SCC*mec* typing showed most of the isolates harboring SCC*mec* type II (43.6%) and IV (49.1%). So far, MLST was performed for only one clinical isolate, that was classified as ST105-SCC*mec* II lineage, related to the USA100 clone (commonly found in Brazil). The detection of virulence genes was as follows: 90.7% of the strains harbored the genes encoding for LukDE; 23.6% harbored genes encoding for PVL; 7,3% presented the genes encoding for SEG; 7,3% the genes encoding for TSST-1 and none harbored the gene encoding for SEH. To our knowledge, this is the first study reporting the MLST and virulence genes from MRSA-SC isolates. In addition to literature review and the *in silico* analysis, the MRSA-SC isolates seem to be following, at least in part, the Brazilian tendency regarding the predominant MRSA lineages and virulence genes profile. So far, the study could not find differential characteristics from MRSA-SC which could justify the differential epidemiological cenario previously observed. More studies (including gene expression and *fitness* investigation), are needed to better understand the low incidence of MRSA in Santa Catarina.

Keywords: *Staphylococcus aureus*; MRSA; molecular typing; virulence; santa catarina

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