

TITLE: MOLECULAR CHARACTERIZATION OF METHICILIN RESISTANT *Staphylococcus aureus* ISOLATES FROM SANTA CATARINA STATE

AUTHORS: DOMINSKI, B. H.; RAITZ, M. F.; SILVEIRA, A. C. O.; SINCERO, T. C. M.; FERREIRA, F. A.;

INSTITUTION: UNIVERSIDADE FEDERAL DE SANTA CATARINA, FLORIANÓPOLIS, SC (Laboratório de Genética Molecular de Bactérias, CCB/MIP – 2º andar, sala 215. CEP: 88.040-970, Florianópolis-SC, Brasil)

ABSTRACT:

Methicillin-resistant *Staphylococcus aureus* (MRSA) are gram-positive bacteria and one of the most important hospital 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 with the expression of virulence genes encoding molecules associated with colonization, tissue damage to host cells, and biofilm formation. In the State of Santa Catarina, only one published non-randomized characterization study of MRSA isolates was found and only partial molecular typing was performed, without investigating virulence characteristics. It also reported a low prevalence (2-8%) of MRSA isolated in Santa Catarina compared to other regions of Brazil and other Latin American countries. However, it is suggested that circulating MRSA in SC are highly pathogenic, since they were predominantly associated with invasive clinical infections in patients. As the balance between fitness and virulence potential seems to be of great importance in the dynamics of MRSA strains prevalence, leading to the success of some strains over others, the present study suggested the hypothesis that circulating MRSA in Santa Catarina (MRSA-SC) have a higher biological cost compared to other strains. To assess this hypothesis, molecular typing experiments (SCCmec and MLST typing) and detection of virulence genes were performed. These characteristics were compared with other strains of MRSA isolated in other countries through in silico analyzes. 55 samples of MRSA isolated from several hospitals in Santa Catarina were molecularly characterized; with a higher incidence of SCCmec type II with 49.09% (27/55) and 43.60% (24/55) type IV. The presence of two virulence genes was verified, leucocidins encoding by *lukDE* genes and Panton-Valentine leukocidin, with 90.74% (49/55) and 23.63% (13/55) of the isolates bearing these genes, respectively. The MLST of a clinical isolate was performed, indicating the ST105-SCCmec II lineage, which is genetically related to the NY/J clone, belonging to the ST5-SCCmecII lineage. To our knowledge, this is the first study to report the MLST and virulence genes from MRSA-SC isolates. It is possible to observe that the MRSA-SC isolates seem to be following, at least in part, the Brazilian tendency regarding molecular typing and virulence genes analyzed. However, more studies are needed to better understand the low incidence and high virulence of MRSA in Santa Catarina.

Keywords: *Staphylococcus aureus*; MRSA, virulence; molecular typing;

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