Title:VIRULENCE AND GENOTYPIC DIFFERENCES AMONG NASAL COLONIZATION AND INFECTION SAMPLES ISOLATED FROM PUBLIC AND PRIVATE HOSPITALS

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ABSTRACT: Methicillin-resistant *Staphylococcus aureus* (MRSA) is a pathogen responsible for colonization and different types of infections in humans. Hospitalizations related to this pathogen have been increasing lately. This microorganism is responsible for the increase in morbimortality, costs of hospitalization and general health care services. The aim of this study is to compare the molecular profile of MRSA isolates that cause nasal colonization and infection among patients treated at two major public and private Niterói hospitals in Brazil. Isolates were collected, from March 2013 to December 2015, phenotyped and genotyped to detect *mec*A gene, Panton-Valentine Leucocidin (PVL) gene, biofilm forming (*icaC* and *icaR*), arginine catabolic mobile element (ACME) and alpha-hemolysin (*hla*) genes, by Polymerase chain reaction (PCR). Moreover, genotyping of the staphylococcal chromosome cassette *mec* (SCC*mec*) was done by multiplex PCR and analysis of the clonal profile was performed by SPA typing and Multilocus sequencing typing (MLST). A total of 85 samples of nasal colonization and 62 of infection were collected from several anatomical sites. Colonization and infection isolates were more frequent among patients over 60 years. A larger number of multiresistant samples were found within the infection group of isolates. All isolates were positive for the presence of *mec*A gene. In the colonization group, the SCC*mec* Type IV was prevalent, while within the infection group, SCC*mec* Type II was the most found. ST5 and ST30 were the most prevalent genotypes found among colonization isolates and ST5 and ST239 were the most frequent clones in infection sites. It was really important to find a number of isolates carrying the ACME gene, which has been known to increase the isolates virulence, as can be observed in infections caused by the strain USA300. Infection samples presented a multi drug resistance profile, when compared to colonization isolates. New clones have been emerging in hospitals, different from the Brazilian Epidemic Clone (BEC). Also, virulence profile has been changing among these isolates, as ACME genes type I and II were also identified within this study.

Key words: MRSA, virulence, PCR, genotyping

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