

Título: Molecular epidemiology and characterization of resistance genes of methicillin-resistant *Staphylococcus aureus* isolates in Brazilian tertiary hospital

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Resumo:

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a major cause of nosocomial infections worldwide and is a serious source of concern due to the fact that multi-drug resistance is critically important to antimicrobials. The aim of this work was to evaluate the antimicrobial susceptibility of MRSA strains isolates from infections in a Brazilian tertiary hospital and determinate the presence of molecular resistance markers, SCC*mec* types, genotypic diversity and clonal complex. A total of 91 samples of MRSA, obtained consecutively between 2005 and 2010, were evaluated. The antimicrobial susceptibility patterns were determined by disk-diffusion method. The occurrence of molecular resistance makers (*aacA-aphD*, *ermA*, *ermB*, *ermC*, *vatA*, *vatB*, *vatC*, *tetK*, *tetM*, *msrA* and *mef*) was performed by PCR. The determination of the SCC*mec* types was performed by PCR and the strains were typed by PFGE. High percentage of antimicrobial resistance was observed for clindamycin, erythromycin and azithromycin (100%), levofloxacin (97.8%), gentamicin (94.5%), tetracycline and rifampicin (84.6%), trimethoprim/sulfamethoxazole (78%) and an intermediate antimicrobial resistance rate was observed for chloramphenicol (61.5%). Regarding the research of resistance markers, the *aacA-aphD*, *ermA*, *tetM*, *ermC*, and *msrA* were detected in 96.7%, 93.4%, 70.3%, 7.6% and 1.1% of strains, respectively. The *ermB*, *vatA*, *vatB*, *vatC*, *tetK* and *mef* genes were not detected. SCC*mec* types III (77%), II (11%), and IV (7.6%), I (2.2%) were found. Most (77%) of the isolates were related to the Brazilian Epidemic Clone (BEC), whereas the USA100/CC5/SCC*mec* II lineage emerged in 2007 and was more frequent in 2009 and 2010. Isolates carrying the SCC*mec* type IV (USA400/CC1 and USA800/CC5 lineages) and I (USA500/CC5) were also detected. Our data are highly relevant for surveillance systems and to map on a wider scale the dynamics of circulation of MRSA and raise discussions on containment strategies and rational use of empiric chemotherapy.

Palavras-chaves: MRSA, antimicrobial resistant, SCC*mec*, clonality

Agência Fomento: CNPq, CAPES, FAPEMIG