

Título: Genetic Variability of *Staphylococcus* spp. with Vancomycin Intermediate Heteroresistance (hVIS) in a hospital in south of Brazil

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Resumo:

Staphylococcus spp. showing positive phenotype of intermediate heteroresistance for vancomycin (hVIS) is among the leading causes of nosocomial infections in worldwide. Recent studies have demonstrated the presence of prevalent epidemic clones over time, and because the account this new type heterogeneous and intermediate resistance there is the possibility of evolution of these clones should be evaluated. The objective was to study the epidemiology of infections by *Staphylococcus* spp. in a teaching hospital in south of Brazil. In this study we analyzed by molecular and phenotypic methods and relate the outcome of antimicrobial therapy in the period of 36 months (August 2012 to March 2015). Antimicrobial susceptibility was performed using disc diffusion and vancomycin minimum inhibitory concentration (MIC) was analyzed by broth microdilution (CLSI). Polymerase chain reaction (PCR) assays evaluated *mecA* and *hld* gene, Panton-Valentine leukocidin (PVL), *SCCmec* and *agr* typing. The AUC was determined for each test isolate and compared to the AUC of the reference strain Mu3 (ATCC700698). The test isolate was considered an hVISA if the population analysis profile area under the curve (PAP-AUC) ratio of the test isolate to Mu3 was >0.9 as previously described by Wootton. 200 isolates of *Staphylococcus* spp. from infection were analyzed, and no isolate was characterized as VISA. We obtained 34 samples of *Staphylococcus* heteroresistant intermediate to vancomycin (hVIS) and 70.58% of them resistant to methicillin (MRSA). Minimal inhibitory concentrations (MIC) by microdilution broth and Etest method ranging between 1 and 2 µg/mL ($p=0.007$). The clonality measured by PFGE demonstrated two clones among hVIS in patients who had not suffered multiple episodes of bacteremia. The dysfunctional *agr* was more frequent hVIS isolates. The results of molecular typing indicate that hVIS isolated from our hospital has genetic diversification, giving indication of a possible evolution and not spread.

Palavras-chaves: *Staphylococcus* spp., Vancomycin, Epidemiology

Agências de fomento: CNPq, FAPERGS