Brief communication

Molecular characteristics of methicillin-resistant Staphylococcus aureus isolates from hospital and community environments in northeastern Brazil

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ABSTRACT

This study characterized 30 MRSA isolates from intensive care unit (ICU) environment and equipment surfaces and healthy children. The SCCmec types I, IVa and V were detected in HA-MRSA isolates while CA-MRSA showed the SCCmec type IVa and V. Most isolates were classified as agr group II. All isolates presented the sei gene, and only HA-MRSA were positive for etb and tst genes. Three genotypes were related to Pediatric (ST5/SCCmecIV) and Berlin (ST45/SCCmecIV) clones. The present study showed molecular similarity between CA- and HA-MRSA isolates in hospital and community settings in a Brazilian region.

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Staphylococcus aureus is an important human pathogen associated with a broad spectrum of infections in community and hospital settings worldwide. Currently, MRSA is the main cause of nosocomial infections in Latin America, and in many Brazilian hospitals the Brazilian Endemic Clone (BEC/ST239/CC8/SCCmecIII) remains the prevalent lineage in these settings. However, a number of studies report on a substitution of this well-established clone by the USA400 (ST1/CC1/SCCmecIV) lineage and the Pediatric clone (USA800/ST5/CC5/SCCmecIV). Meanwhile, the MRSA prevalence in community acquired infections continues to grow. The aim of the present study was to compare molecular characteristics of HA- and CA-MRSA isolates obtained from intensive care units (ICUs) environment and equipment surfaces and from healthy children in public day care centers (DCCs), from Vitória da Conquista, Brazil. Thirty isolates were identified as MRSA and had their genomic DNA extracted using the PureLink™ Genomic DNA...
In regards to virulence genes, the *sei* gene was present in all 30 MRSA isolates (Table 1). Despite that the *seq* (100%) and *sej* (64%; 7/11) genes were found to be associated only with CA-MRSA isolates (p-value < 0.05), the *etb* (63%; 12/19) (p-value < 0.05) and *tst* (21%; 4/19) genes were only detected among HA-MRSA isolates. The *eta* gene was present in CA-MRSA (27%) and HA-MRSA (10.5%) isolates. The *icaD* gene was related to both HA- and CA-MRSA, whereas *icaA/icaD* was detected only among HA-MRSA isolates (p-value < 0.05).

The epidemiology of MRSA infections is very dynamic and the substitution of well adapted hospital clones by community ones has been shown by several authors. However, there are few studies comparing HA- and CA-MRSA isolates in Brazilian studies.

A prevalence of SCoMec types IV and V, typically from the community, were reported in all CA-MRSA isolates, and were the main types found among HA-MRSA isolates (63%) as well. The distinction between MRSA isolates from community and healthcare facilities became cloudy with the replacement of HA-MRSA lineages by CA-MRSA in the hospital setting. In a study conducted in Brazil describing the molecular characteristics of isolates collected from healthy children, most isolates were related to SCoMec III and only three isolates showed the SCoMec type IV and one type V. On the other hand, Caboclo et al. showed dissemination of the USA400/SCoMec IV, a community lineage, at a military hospital in Rio de Janeiro. In Brazil, the report of isolates carrying the SCoMec type V is still rare, but in the present study this cassette type was present in both groups evaluated. The presence of both SCoMec types IV and V among healthy and hospitalized people seems to be related to the exposure of healthcare professionals, hospital staff, visitors, and patients to a wide range of pathogens.

The MLST revealed a wide diversity of STs in both environments. ST5, ST45 and ST2228 (single locus variant ST45) were found among CA-MRSA and HA-MRSA strains. The ST5 isolates has emerged in hospital and community isolates, while ST45 has most often been found in the CA-MRSA carrying SCoMec type IV. The spa typing also showed great genetic variation among the analyzed isolates. Most CA-MRSA isolates shared common spa types with HA-MRSA isolates.

The Clonal complexes – CC5 and CC45 – which represented 100% of HA-MRSA and 82% of CA-MRSA isolates in this study, are among the clonal groups known to be involved in a global pandemic caused by MRSA. Although CA-MRSA isolates usually have different molecular characteristics than HA-MRSA, most community isolates in this study shared the same genotype of those from hospitals, mainly in pulsotypes A and C (n = 14; 47%). The C and I clones were related to the Pediatric clone (ST5/CC5/SCoMecIV). The A1 and A2 subtypes were related to the Berlin clone (ST45/CC45-SCoMecIV). Thereby, both Pediatric and Berlin clones are present in children attending day care centers (55% and 18%, respectively) and on ICUs environmental surfaces (16% and 21% respectively), sharing the same genetic background. This similarity between genetic groups of CA- and HA-MRSA may indicate an eventual co-transmission between the community and hospital settings.

The MRSA clone (CC45), recently described in the northeast of Brazil among MSSA (2%) isolates from nosocomial infections, has the ability to cause high mortality in patients with
bloodstream infections and a large global spread capacity.\textsuperscript{18} On the other hand, the Pediatric clone (CC5) has emerged in Brazilian hospitals,\textsuperscript{19} and this is the first detection in healthy children and objects in ICUs and equipment surfaces, suggesting that this clone is spreading from Brazilian hospitals to the community, which can act as a reservoir and contribute to the spread of this pathogen.

The accessory gene regulator group I and II predominated in the community and hospital isolates. These groups have been associated with endocarditis and suppurative infections.\textsuperscript{20} This study revealed that enterotoxin genes were more prevalent in CA-MRSA isolates, a result also found by Xie et al.\textsuperscript{12} comparing HA- and CA-MRSA in hospital isolates in China, while the exfoliatin b (etb) gene predominated among HA-MRSA isolates. The presence of superantigen genes in MRSA isolates from hospital surfaces and healthy individuals implies the possibility of increased bacterial dissemination and more severe infections. Genes related to biofilm production were detected in all strains. The finding of this gene is important because infections associated with biofilm production are usually recurrent, aggravate nosocomial infections, and act as a barrier to antimicrobial action.

Our results demonstrated high genetic diversity among MRSA isolates, although most of the isolates are related to the CC5 and CO45 showing the importance of local studies to better understand the dynamics involved in the spread and pathogenicity of MRSA lineages.
In conclusion, the CA- and HA-MRSA isolates sharing similar molecular characteristics irrespective of their environment origin as well as the discovery of international clonal lineages demonstrate the dissemination ability of MRSA and the risk of community and hospital infections. It underscores the need for public health officials to monitor these populations, sites and to develop strategies to reduce the prevalence of these MRSA clones on hospital surfaces and DCCs. These environments could act as important reservoirs for future community and hospital infections.

Conflicts of interest
The authors declare no conflicts of interest.

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