Molecular typing of *Staphylococcus aureus* causing community-acquired severe infections in an Italian tertiary-care paediatric hospital

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Background

Staphylococcus aureus (SA) causes a wide range of clinical manifestations, sometimes severe. Molecular typing of SA has been extensively used for epidemiological purposes, but often correlation between clinical findings and genotype is missing. Aim of this study is to evaluate the genetic background of SA causing community-acquired severe infections in a tertiary-care pediatric hospital in Rome, Italy, in the period January 2015 - August 2017.

Case Presentation Summary

SA isolated from clinical samples were retrospectively selected from community-acquired severe infections. Molecular analyses were performed for detection of genes encoding for *mecA* and Panton-Valentine leukocidin (PVL). MRSA strains were further investigated through the analysis of the SCCmec cassette and spa-typing. 24 SA strains were selected (source: blood 20; wound 3; nasopharyngeal aspirate 1). 14 strains were MSSA/PVL-; 5 MRSA/PVL+; 3 MRSA/PVL- and 2 MSSA/PVL+. Through spa-typing, the 16 MSSA were clustered in 11 groups. SCCmec IV-a was detected in 7 MRSA isolates. Interestingly, the 5 MRSA/PVL+ strains shared the same SCCmec (IV-a) and spa-type (t024). From a clinical perspective, among these five particular strains, 2 were responsible for severe wound infections, one for necrotizing pneumonia, one for liver abscesses in a neonate, one for hip osteomyelitis complicated by septic shock, multiple intramuscular abscess and necrotizing pneumonia.

Discussion

In our population, t024 was the most prevalent spa-type and was associated with MRSA/PVL+ strains, which caused severe diseases. It was not detected in MSSA strains. Molecular typing allows the monitoring of SA clusters and outbreaks, and in our experience it was also useful as a marker of severe disease. The circulation of this particular spa-type in patients not linked epidemiologically deserves further evaluation.

Distribution of spa types among MRSA strains

Distribution of spa types among MSSA strains