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COMPARATIVE MOLECULAR ANALYSIS OF MRSA ISOLATES FROM INFECTION SITES AND CARRIER COLONIZATION SITES

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Purpose: Methicillin resistant *Staphylococcus aureus* (MRSA) constitutes a major global health concern causing hospital and community acquired infections. A wide diversity of MRSA genotypes are circulating in geographically related regions. Therefore understanding the genetic spectrum of MRSA is fundamental to design control and clearance measures.

Methodology: A total of 106 MRSA isolates from infection (51) and carrier colonization sites (55) are characterized genetically based on SCCmec and MLST genotyping methods in addition to detection of Panton-Valentine Leukocidin (PVL), Toxic shock syndrome toxin-1 (TSST-1) and enterotoxins.

Results: Staphylococcal cassette chromosome *mec* (SCCmec) IV was the most frequently detected genotype (77.3%) followed by genotype V (13.2%) and III (9.4%). SCCmec IVa was more prevalent among the carrier group (p value 0.002). CC80 was the most commonly identified clonal complex (CC). CC6 and CC22 were significantly more prevalent among the carrier group (p value 0.02 and 0.01, respectively). PVL was highly prevalent among the isolates (58.5%). All strains were sensitive to vancomycin; however, MRSA strains isolated from infection sites had significantly higher minimum inhibitory concentrations (MICs) compared to strains isolated from carrier colonization sites (p value 0.021). Five new sequence types mainly from the carrier group were identified and described in the study.

Conclusion: MRSA population is genetically very diverse among carriers and infected individuals. Particular strains are more prevalent among carriers. With SCCmec type IV being most prevalent, this suggests a community origin of most MRSA strains. Therefore very well designed surveillance and clearance strategies should be prepared to prevent emergence and control spread of MRSA in the community

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