

Molecular characteristics of infection and colonization isolates of community-acquired methicillin-resistant *Staphylococcus aureus* (CA-MRSA)

ABSTRACT

Staphylococcus aureus is a gram-positive coccus that colonizes the skin and mucous membranes, particularly the anterior nares. Recently, community-acquired MRSA (CA-MRSA) has emerged as a cause of skin and soft-tissue infections in healthy individuals. These strains are sensitive to antimicrobials, carry genes for Panton-Valentine leukocidin (PVL) toxin, and feature the staphylococcal cassette chromosome mec (SCCmec) type IV or V. The suspected mode of transmission involves close contact with carriers, leading to skin or nasal colonization that results in subsequent active infection. This study was undertaken to determine the molecular characteristics of CA-MRSA isolates in children presenting with wound infections at Likas Hospital, Sabah, Malaysia, and the possible mode of transmission. The results showed that the majority of CA-MRSA infection isolates were from scalp abscesses (49%) in 1–5-year-old children (70%) in the Filipino (54%) community. The presence of the mec gene was detected in all isolates and the PVL virulence factor was found in 92% of the isolates. SCCmec typing revealed that 57% of the isolates were untypable, 35% harbored the SCCmecIVa element, and one each had SCCmecIVc, SCCmecV, or SCCmecII. Sixteen *S. aureus* strains were isolated from nasal swabs in 19 family members of index patients. Fourteen of these cultures were positive for catalase, coagulase, and DNAase. All of the colonization isolates carried the mecA gene and only a third were positive for the PVL toxin. SCCmec typing showed that 79% of the isolates were untypable and two had SCCmecIVa element and one had SCCmecV element. When five pairs of infection and colonizing isolates were compared by spa typing, only two pairs showed identical spa type with possible transmission between the patient and family contact. Further studies are necessary to establish CA-MRSA transmission by performing multiple-site cultures multiple times instead of one-time nares-only sample collection.