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MRSA - one health worldwide

Common SCCmec genes among S. aureus and coagulase-negative staphylococci from the nares of healthy individuals with limited healthcare contact

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Background: *Staphylococcus aureus* colonises the nares of approximately 30% of healthy people but it is also a major cause of infection including skin and soft tissue and bloodstream infections. MRSA arises from the acquisition of either *mec*A or *mec*C, carried on mobile staphylococcal cassette chromosome *mec* (SCC*mec*) elements by methicillin-susceptible *S. aureus* (MSSA) clones. There is convincing evidence that *mec* and SCC*mec* originated in coagulase-negative staphylococci (CoNS), which also colonise the nares, throat and skin of healthy individuals.

Material/methods: We investigated staphylococcal species from the nares of healthy individuals for carriage of similar SCC*mec* genes. Nasal swabs (eSwab Copan®) from 243 individuals with little hospital contact were screened using a two-step enrichment procedure and growth on SA select agar (Bio-Rad®) to recover staphylococci. Species identity was confirmed using a MALDI Biotyper (Brüker). Where more than one staphylococcal species was recovered from the same swab, genomic DNA from each species was analysed using the StaphyType kit (Alere, Germany) for detection of antibiotic resistance and virulence genes, including SCC*mec*, and for genotyping *S. aureus*.

Results: In total, *S. aureus* and CoNS were recovered from 74/243 (30.4%) swabs (68 *S. aureus*/*Staphylococcus epidermidis*, six *S. aureus*/*Staphylococcus saprophyticus*). Of these, 6/74 (8.1%) of *S. aureus* isolates were MRSA (all CC59), 11/68 (16.1%) were methicillin-resistant (MR) *S. epidermidis* and 1/6 (16.6%) were MR *S. saprophyticus*. Among MRSA, 5/6 (83%) carried SCC*mec* IV (class B *mec* and *ccr*AB2) and 1/6 was non-typeable (NT) (only *mec*A gene detected). Among MR *S. epidermidis*, 7/11 (63%) were SCC*mec* IV, 2/11(11.6%) were SCC*mec* II (class A *mec* and *ccr*AB2), 1/11 (5.8%) was SCC*mec* V (class C *mec* and *ccr*C) and 1/11 (5.8%) was NT (*mec*A, *ugp*Q, *ccr*AA). The single MR *S. saprophyticus* was SCC*mec* IV. Overall, class B *mec* (13/18) and *ccr*AB2 (14/18) were common to MRSA and MR-CoNS and SCC*mec* IV predominated among MRSA and MR-CoNS.

Conclusions: The occurrence of similar SCC*mec* elements among *S. aureus* and CoNS in healthy individuals, with limited exposure to the healthcare environment, supports the evidence that CoNS are a reservoir of mobile genetic elements including SCC*mec* that may contribute to the *S. aureus* gene pool even in the absence of significant antibiotic selective pressure. Further studies will include analysis of the entire DNA sequence of these SCC*mec* elements from MRSA and MR-CoNS to determine the full extent of their similarity.