Common SCC*mec* genes among *S. aureus* and coagulase negative Staphylococci from the noses of healthy individuals with limited healthcare contact

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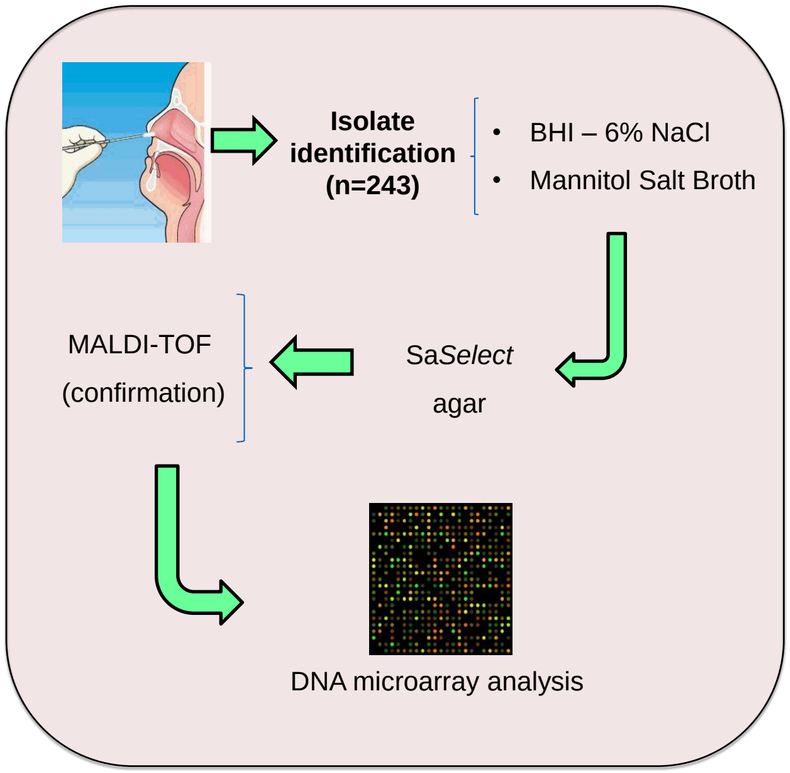
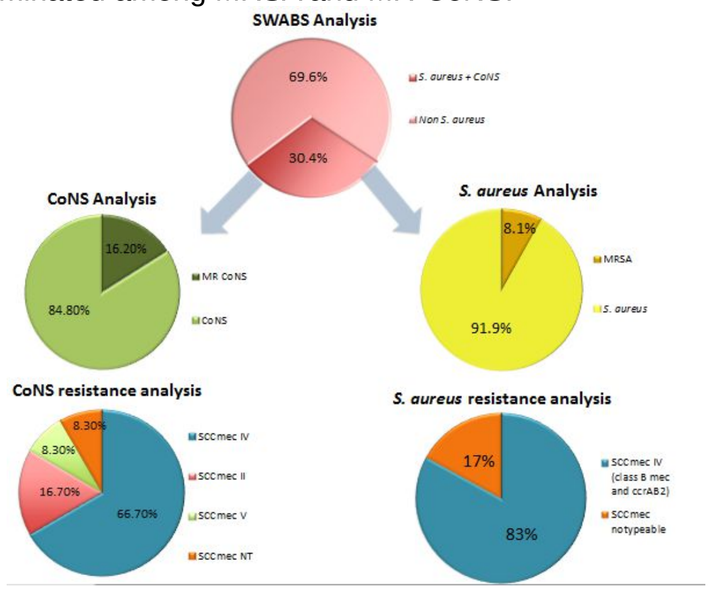
Introduction: *Staphylococcus aureus* colonises the nares of approximately 30% of healthy people but it is also a major cause of infection including skin and soft tissue and bloodstream infections. MRSA arises from the acquisition of either *mec*A or *mec*C, carried on mobile staphylococcal cassette 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.

Methods: Nasal swabs (eSwab Copan®) were obtained from 243 students without any previous hospital contact (ethical approval number REC949 by RCSI Research Committee). All the samples were screened using two step enrichment procedure to recover *S. aureus* (MRSA or MSSA), MRSE and other CoNS from the swab (Huber et al. 2011).

The swabs were enriched in Brain Heart Infusion (BHI) supplemented with 6% NaCl for 24 h at 37ºC followed by further enrichment in mannitol salt broth for 24 h at 37ºC. An aliquot (100 µl) of a 1/1000 dilution from this culture was spread onto SaSelect agar (Bio-Rad®, Hercules, CA, USA). The criteria for presumptive identification of different staphylococci growing on SaSelect were defined following the manufacturer instructions. DNA microarray was performed according to the manufacturer's instruction.



Results: Overall, class B mec (13/18) and *ccrAB*2 (14/18) were common to MRSA and MR-CoNS and SCC*mec* IV predominated among MRSA and MR-CoNS.



Conclusion: The occurrence of similar SCC*mec* elements among *S. aureus* and CoNS in healthy individuals, 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.

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