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Molecular characterization of Staphylococcus aureus isolates associated with nasal colonization among healthcare workers in a tertiary care facility

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Background: Nasal carriage of *Staphylococcus aureus* plays a key role in epidemiology, transmission and pathogenesis of staphylococcal infections in hospital settings. Previous work on *S. aureus* isolates from nasal colonization of young adults in Saudi Arabia revealed wide clonal diversity of methicillin sensitive *S. aureus* (MSSA) with carriage of different virulence genes that also can be seen in methicillin resistant *S. aureus* (MRSA). Healthcare workers (HCWs) may serve as a reservoir of infection for dissemination of *S. aureus,* particularly of MRSA. Data on the clonal distribution and virulence genes of *S. aureus* strains associated with nasal colonization among HCWs in Saudi Arabia are still rare. This study was carried out to characterize *S. aureus* isolates associated with nasal colonization among HCWs in a tertiary care hospital.

Material/methods: In March 2016, nasal swabs were collected from 93 HCWs at King Khalid University Hospital, Riyadh, Saudi Arabia. *S. aureus* identification was performed using standard laboratory techniques and MicroScan Walkaway 96 plus System (Siemens Healthcare Diagnostic Inc.) in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines. Methicillin resistance was confirmed on Mueller-Hinton agar using the disk diffusion method and by the Cepheid® MRSA GeneXpert test. Molecular characterization for all relevant targets of the isolates was carried out using the StaphyType DNA microarray.

Results: Twenty-nine HCWs (31%) had nasal colonization with *S. aureus* (MSSA=23; MRSA=6). The *S. aureus* isolates identified comprised of 16 clonal complexes (CC), eight of which were being described for the first time in Saudi Arabia. The MSSA isolates included three each for CC15, CC188, ST2867; two each for CC5, CC97, CC367; and one each for CC1, CC8, CC30, CC45, CC101, CC121, ST291/813, CC1153. The staphylococcal cassette chromosome recombinase genes *ccrA-1*; *ccrB-1* and the fusidic acid resistance gene *fus*C were observed in the CC1 and CC8 MSSA isolates. The six MRSA isolates belonged to CC5-MRSA-[VI+*fus*] (n=2) as well as one each of CC5-MRSA-V (sed/j/r + variant, previously described as West Australian MRSA-11/34/35/90/108); CC22-MRSA-IV (*tst1*+); CC80-MRSA-IV [PVL+] (“European caMRSA Clone”) and CC97-MRSA-[V+*fus*]. The Panton-Valentine leukocidin genes (*lukS*-PV and *lukF*-PV) were detected only in two isolates (MRSA: n=1; MSSA: n=1). The β-lactamase operon was present in the majority of MSSA (n/N=21/23) and all MRSA isolates. None of the isolates harboured the vancomycin and mupirocin resistance genes. A majority of the isolates harboured the staphylokinase (*sak*) and staphylococcal complement inhibitor (*scn*) genes (86% and 96% respectively) while 31% had the chemotaxis-inhibiting protein (*chp*) gene.

Conclusions: *S. aureus* isolates from nasal colonization of HCWs in Riyadh revealed a high diversity of clonal complexes with a low carriage of MRSA and PVL+ strains. MSSA isolates harbouring a combination of *ccrA-1, ccrB-1* and *fus*C genes in the mobile genetic environment of an SCC*mec* element were identified.