

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

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## Introduction

- Nasal carriage of *Staphylococcus aureus* plays a key role in epidemiology, transmission & pathogenesis of staphylococcal infections
- Colonized healthcare workers (HCWs) may serve as a reservoir of infection
- *S. aureus* isolates from nasal colonization of young adults in Saudi Arabia has revealed:
  - wide clonal diversity of methicillin sensitive *S. aureus* (MSSA)
  - MSSA isolates with virulence genes typically seen in methicillin resistant *S. aureus* (MRSA)
- Paucity of data on clonal distribution & virulence genes of *S. aureus* from HCW in Saudi Arabia

## Objectives

To characterize *S. aureus* isolates associated with nasal colonization among HCWs in a tertiary care facility in Saudi Arabia

## Methods

- **Setting:**
  - King Khalid University Hospital, Riyadh Saudi Arabia
- **Subjects:**
  - In March 2016, nasal swabs were obtained from HCWs in the hospital.
- ***S. aureus* identification & confirmation of methicillin resistance:**
  - Standard laboratory techniques according to CLSI guidelines
  - Cepheid® MRSA GeneXpert test
- **Molecular genotyping:**
  - Carried out using StaphyType DNA microarray (Alere Technologies, Jena, Germany) (Figure 1).

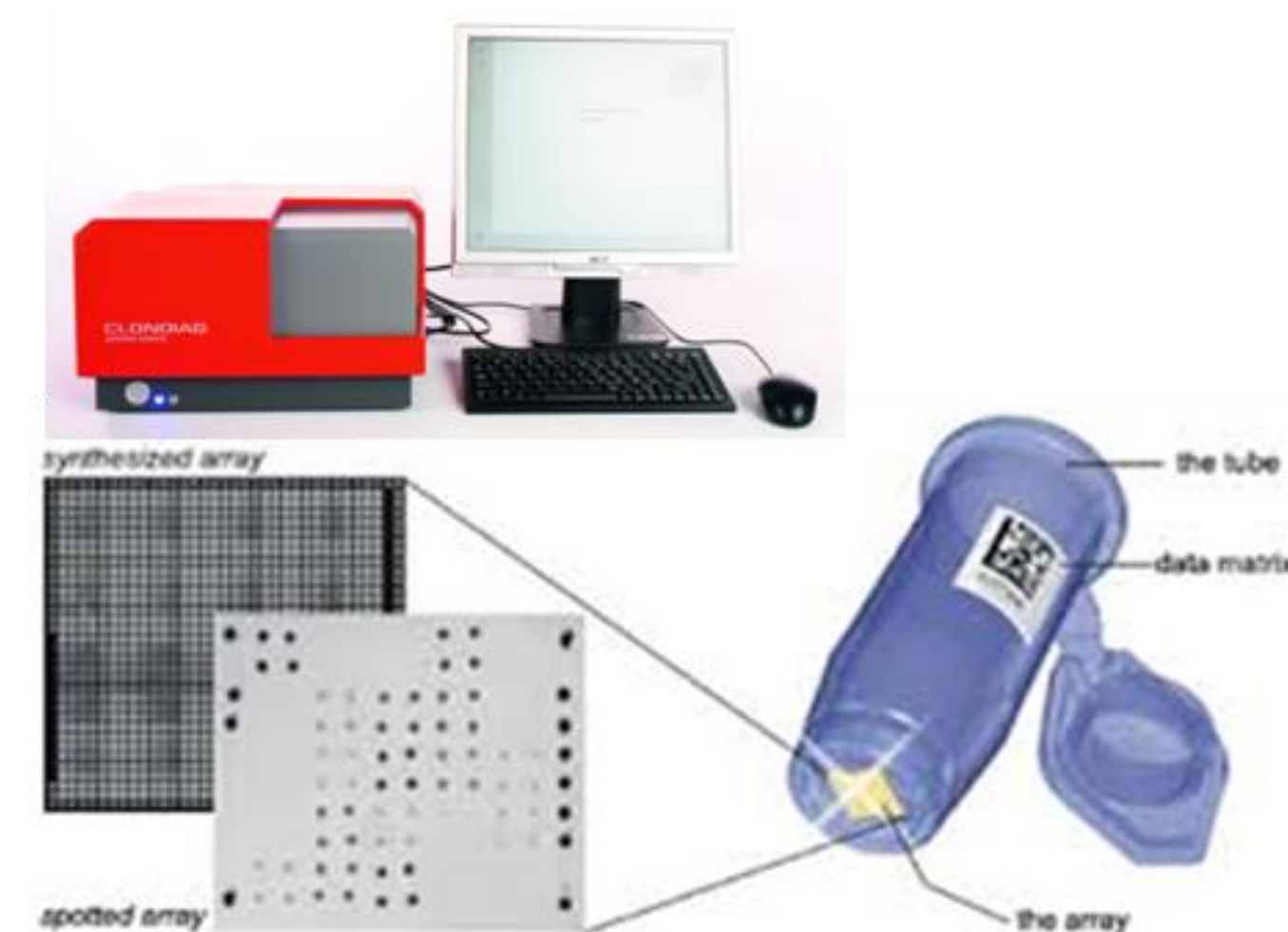


Figure 1

## 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 *pvf*<sup>+</sup> strains
- MSSA isolates harbouring a combination of *ccrA-1*, *ccrB-1* and *fusC* genes in the mobile genetic environment of *S. aureus mec* element were identified

## Results

- 93 HCWs were screened. Figure 2 shows the distribution of HCWs.
  - 29 HCWs (31%) had nasal colonization with *S. aureus*.
- 16 clonal complexes (CC) were identified

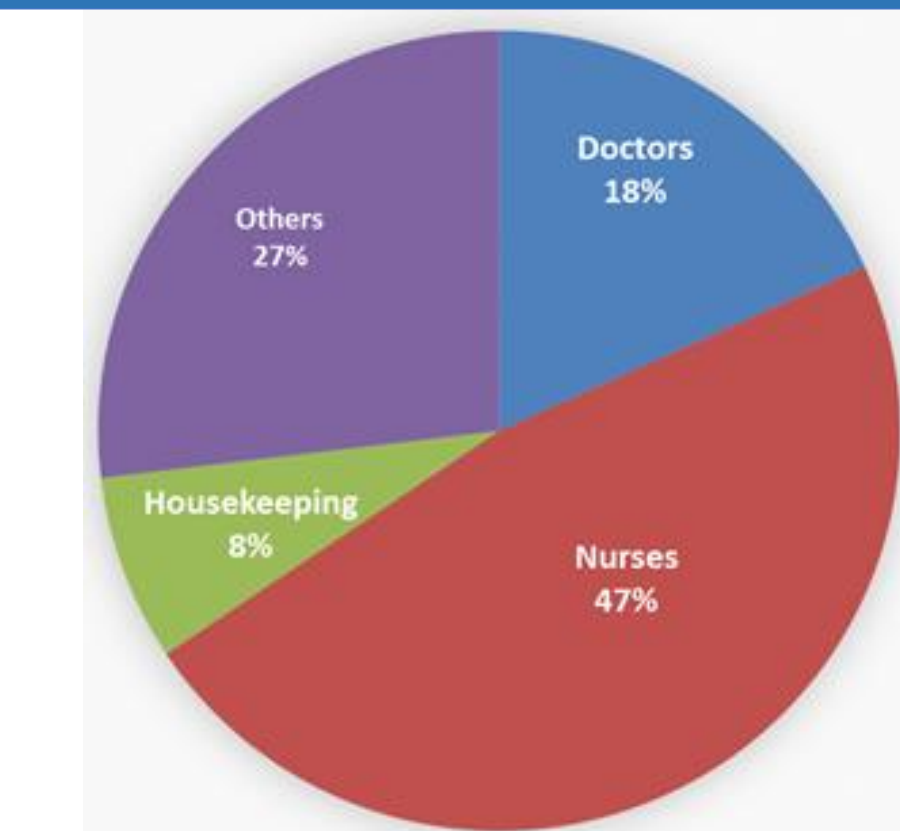


Figure 2

### Distribution of *S. aureus* Clonal Complexes

MSSA isolates (n=23):

- three each for CC15, CC188, ST2867
- two each for CC5, CC97, CC367
- one each for CC1, CC8, CC30, CC45, CC101, CC121, ST291/813, CC1153

MRSA isolates (n=6):

- CC5-MRSA-[VI+*fus*] (n=2)
- 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")
- CC97-MRSA-[V+*fus*].

- The staphylococcal cassette chromosome recombinase genes *ccrA-1*; *ccrB-1* were found in CC1 and CC8 MSSA isolates
- Virulence and antibiotic resistance genes
  - The Pantone-Valentine leukocidin genes (*lukS-PV* and *lukF-PV*) were detected only in two isolates (MRSA: n=1; MSSA: n=1). Figure 3 shows the distribution of some virulence genes
  - Fusidic acid resistance gene were seen in two isolates (CC1 & CC8 MSSA)
  - No vancomycin or mupirocin resistance gene was detected

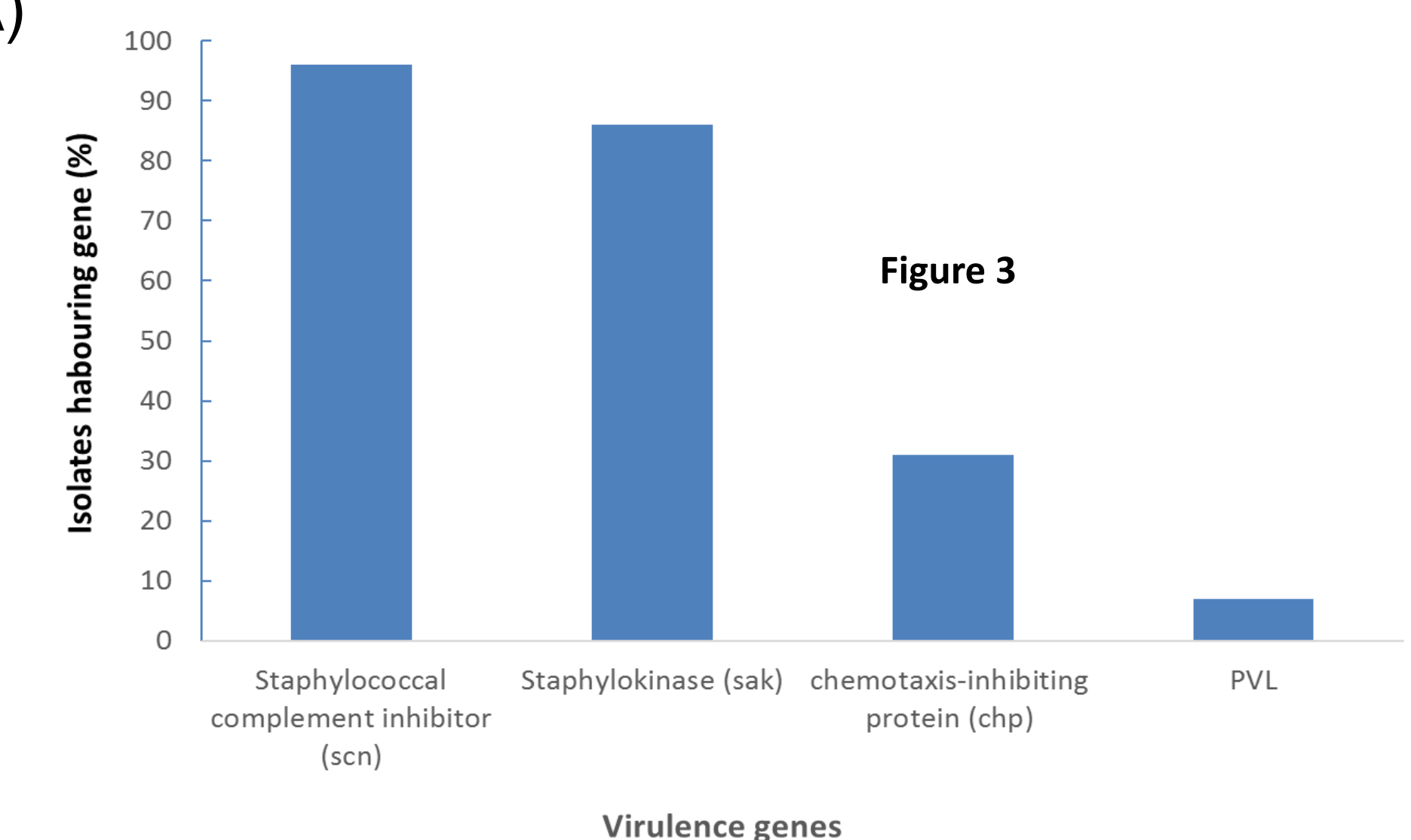


Figure 3