

Molecular characterization of methicillin resistant *Staphylococcus aureus* isolates from the United Arab Emirates: An updated view post pandemic

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Introduction

Infections caused by methicillin resistant *Staphylococcus aureus* (MRSA) contribute significantly to the burden of antimicrobial resistance in the United Arab Emirates (UAE)

MRSA isolates associated with clinical infections in the UAE show :

- Wide clonal diversity
- Presence of rare clonal complexes
- Emergence of novel variant strains

The molecular epidemiology of MRSA in the UAE in the Aftermath of the COVID-19 pandemic remains unknown

Objectives

To determine the molecular characterization of MRSA isolates associated with clinical infections in the UAE and the impact of the COVID-19 pandemic

Methods

Setting:

- ▶ Rashid Hospital, Dubai
- ▶ Mediclinic City Hospital, Dubai
- ▶ Dubai Hospital, Dubai
- ▶ Burjeel Medical City, Abu Dhabi
- ▶ Sheikh Khalifa General Hospital, Umm Al Quwain

Bacterial isolates:

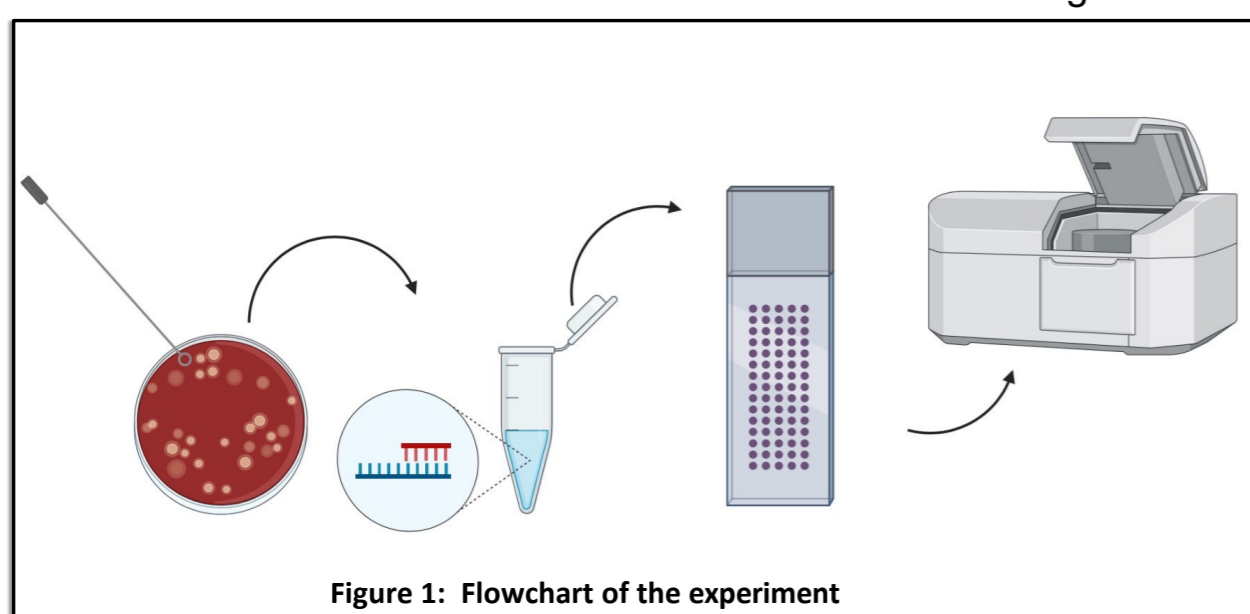
- ▶ From February to June 2022
- ▶ non-duplicate MRSA isolates identified at participating centers were obtained
- ▶ Isolates associated with clinical infections only

MRSA identification & confirmation of methicillin resistance:

- ▶ Standard laboratory techniques according to CLSI guidelines
- ▶ Full antibiotic susceptibility profile

Molecular genotyping:

- Carried out using DNA microarray-based assays (Inter-Array GmbH, Bad Langensalza, Germany) (Figure 1)
- Assignment to clonal complexes (CC) and distinct strains
- Identification of virulence and antimicrobial resistance genes



Results

- 77 isolates were identified, predominantly from wound swabs
- 18 Clonal Complexes and 40 strain assignments (Figure 2)

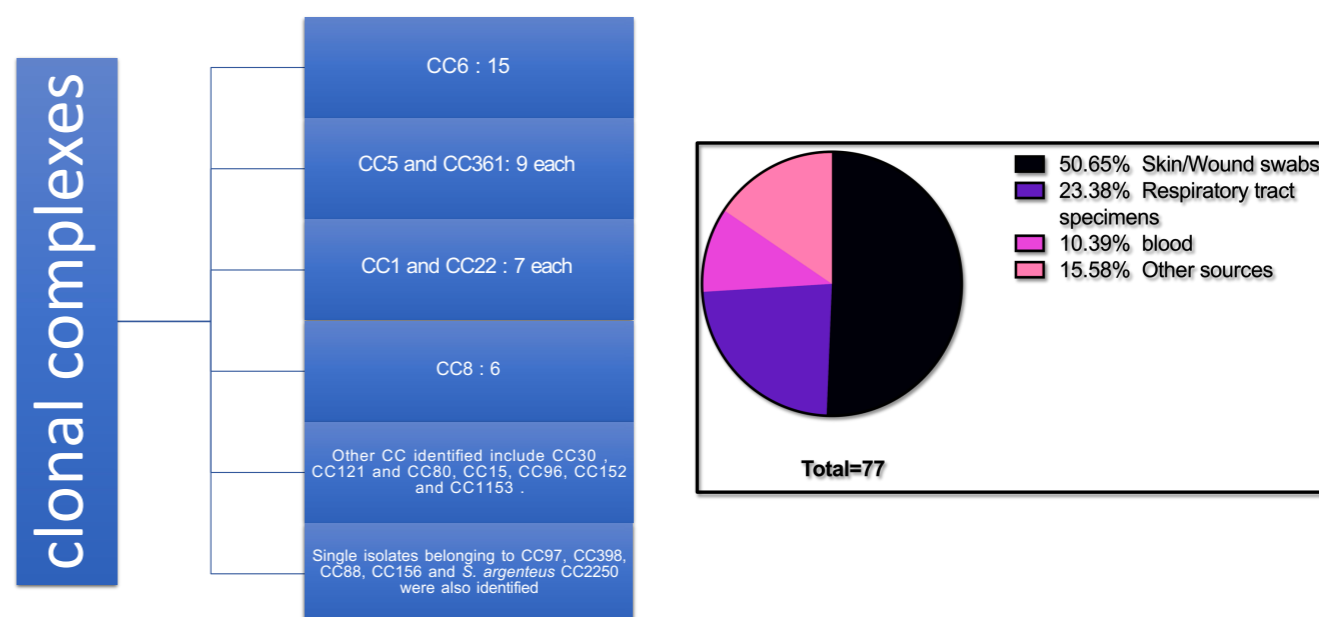


Figure 2: Isolates distribution based on Clonal Complex and origin of swab

Strains identified for the first time in UAE

- ▶ CC8-MRSA-IV+*ccrA/B-4* Irish AR43 strain
- ▶ CC5-MRSA-IV (*se/d/j-*, *tst-*, *PVL-*, *edinA-*) Paediatric clone/WA MRSA-74
- ▶ mutated CC121-MRSA-[V/VT+*fusC*] (*PVL+*) strain with missing Orf CM14 gene

Virulence genes identified (Figure 3) :

- ▶ High carriage of Panton-Valentine leukocidin genes (*lukS-PV* and *lukF-PV*) (31.1% of isolates).
- ▶ Toxic shock syndrome (*tst-1*) gene was present in 16.9% of isolates.

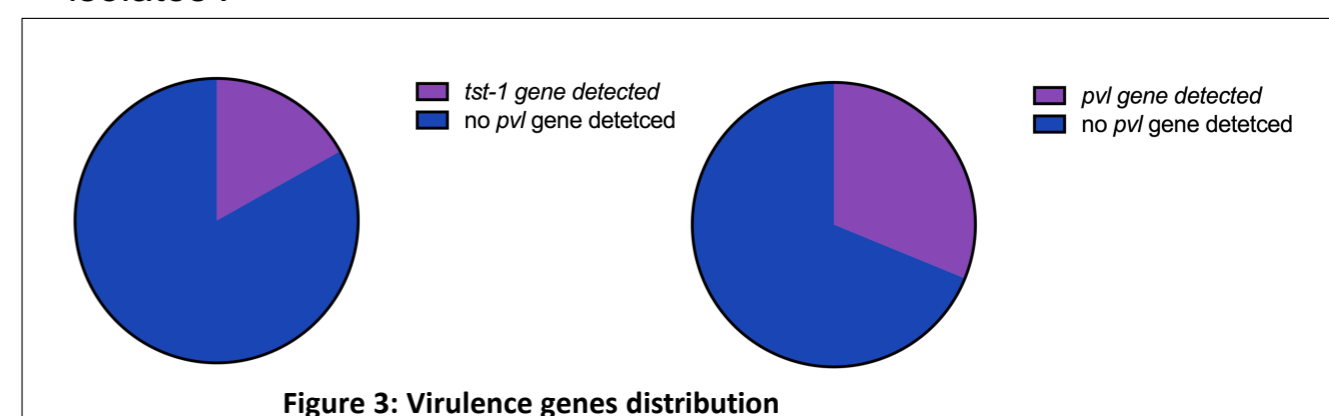


Figure 3: Virulence genes distribution

Isolates exhibited high carriage of fusidic acid resistance (*fusC*) with 37.6% isolates (Figure 4)

- Other antibiotic resistance genes identified:
 - ▶ Erythromycin/clindamycin resistance (*ermC*)
 - ▶ Gentamicin resistance (*aacA-aphD*)
 - ▶ Mupirocin resistance *mupA* gene was detected in 1 isolate
- No vancomycin resistance gene detected

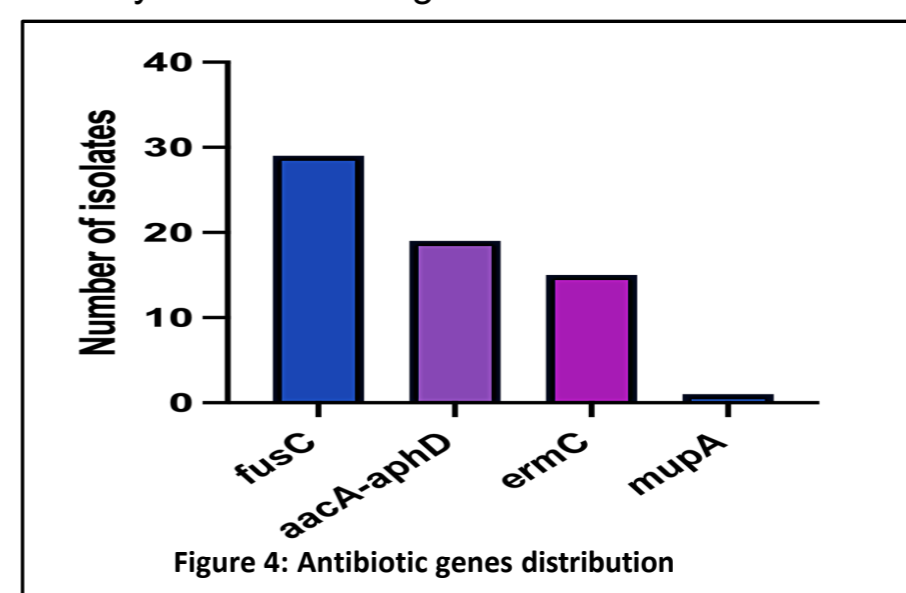


Figure 4: Antibiotic genes distribution

Conclusions

The wide clonal diversity and identification of MRSA strains previously not reported from the UAE suggests ongoing trafficking of MRSA despite pandemic restrictions. Continued surveillance for tracking community dissemination of MRSA strains is needed.