

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

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Background:

Infections caused by methicillin resistant *Staphylococcus aureus* (MRSA) contribute significantly to the burden of antimicrobial resistance (AMR) in the United Arab Emirates (UAE). Previous work in the pre-pandemic era identified a wide clonal diversity, presence of rare clonal complexes and emergence of novel variant strains among MRSA isolates associated with clinical infections in the UAE. It has been suggested that the high usage of antibiotics during the COVID-19 pandemic might contribute to worsening of the AMR

crisis. This study was carried out to identify the molecular epidemiology of MRSA strains circulating in our setting in the post pandemic period.

Methods:

Between February to June 2022, we obtained MRSA isolates identified from clinical samples in diagnostic laboratories of five hospitals across three Emirates. Only isolates associated with clinical infections were obtained and only one isolate per patient was included. Molecular characterization was carried out using DNA microarray-based assays (Inter-Array GmbH, Bad Langensalza, Germany).

Results:

A total of 77 MRSA isolates predominantly from skin/wound swabs (n/N= 39/77), respiratory tract specimens (n/N=18/77), blood (n/N=8/77) were studied. The isolates belonged to 18 clonal complexes (CC) with 40 strain assignments. The predominant CCs were CC6 (n/N: 15/77), CC5 and CC361 (n/N: 9/77 each), CC1, CC8 and CC22 (n/N: 7/77 each). Other CC identified include CC30 (n=4), CC121 and CC80 (n=3 each) as well as CC15, CC96, CC152 and CC1153 (n=2 each). Single isolates belonging to CC97, CC398, CC88, CC156 and *S. argenteus* CC2250 were identified. The findings also demonstrated the first report of the CC8-MRSA-IV+*ccrA/B-4* Irish AR43 strain, CC5-MRSA-IV (*se/d/j-*, *tst-*, *PVL-*, *edinA-*) Paediatric clone/WA MRSA-74, and a mutated CC121-MRSA-[V/VT+*fusC*] (PVL+) strain with missing *Orf CM14* gene in the UAE. The Panton Valentine leukocidin (*pvl*) genes were present in 31.5% (n=24) of the isolates while 17.1% (n=13) were positive for the toxic shock syndrome (*tst-1*) gene. There was high carriage of SCC-borne fusidic acid resistance (*fusC*) (n = 29), erythromycin/clindamycin resistance (*ermC*) (n = 15) and gentamicin resistance (*aacA-aphD*) (n = 19) genes. Although none of the isolates harboured vancomycin resistance genes, one isolate with the plasmid mediated high level mupirocin resistance *mupA* gene was identified.

Conclusion:

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.