Whole genome sequencing of Methicillin-resistant *Staphylococcus aureus* (MRSA) bacteraemia strains delineating changing lineages associated with specific drug resistance in Hong Kong, 2009-2024.

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Introduction

Methicillin-resistant *Staphylococcus aureus* (MRSA) is endemic in hospitals across Hong Kong. MRSA infections complicate treatment options and are linked to high morbidity, mortality, and healthcare costs. The prevalence of MRSA poses significant challenges for infection control measures and requires ongoing surveillance to mitigate its impact on public health.

Objective

To characterize the sequence type structure and temporal dynamics of MRSA bloodstream isolates in Hong Kong 2009-2024

Methods

Whole genome sequencing was performed on MRSA strains isolated from individual patients diagnosed with bacteraemia in a 1350-bed teaching hospital from 2009 to 2024. MRSA strains were stored in agar slants at room temperature or in glycerol-BHI broth at -80ºC. They were subcultured on conventional media and their identity confirmed using MALDI-TOF (Bruker), prior to DNA extraction with the QIAamp 96 DNA QIAcube HT kit (Qiagen). A DNA library was prepared according to the manufacturer's protocol (Twist 96-Plex Library Prep Kit, Twist Bioscience) and sequenced using the NextSeq 500 high-output platform (Illumina).

Results

The median age of the patients was 78 years. A total of 69.3% were male and 30.7% were female.

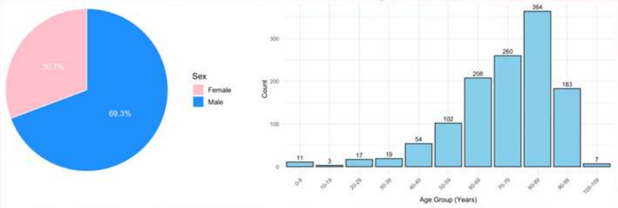


Figure 1. Demographic Characteristics of the Study Population

A total of 1183 MRSA genomes for the 16-year period were analysed. Multi-locus sequence typing (MLST) analysis revealed four major sequence types: ST22, ST45, ST1774, and ST1047, accounting for 82.5% of all isolates.

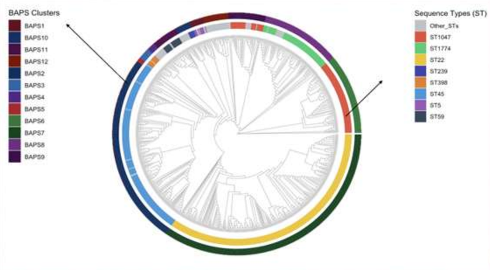


Figure 2. Midpoint-rooted maximum likelihood tree showing the phylogenetic relationships of MRSA genomes

Throughout the duration of the study, ST22 and ST45 were consistently the most prevalent strains, demonstrating persistence over the entire period. Conversely, ST1047 exhibited a notable increasing trend, while ST1774 experienced a decline over time.

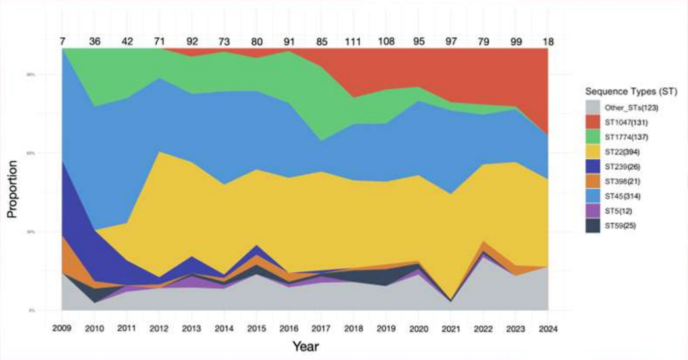
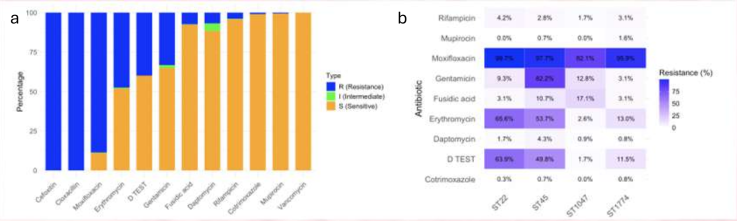


Figure 3.Yearly distribution of the proportion of major STs across the entire population throughout the study period. The number of isolates per year is shown at the top.

Resistance rates were highest for moxifloxacin and erythromycin, while most strains remained susceptible to cotrimoxazole, mupirocin, daptomycin, and vancomycin. An association between a high gentamicin resistance rate in ST45 (82.2%) and fusidic acid resistance rate in ST1047 (17.1%) was noted.



	ST22	ST45	ST1047	ST1774
Rifampicin	4.2%	2.8%	1.7%	3.1%
Mupirocin	0.0%	0.7%	0.0%	1.6%
Moxifloxacin	99.7%	97.7%	82.1%	95.3%
Gentamicin	9.3%	82.2%	12.8%	3.1%
Fusidic acid	3.1%	10.7%	17.1%	3.1%
Erythromycin	65.6%	53.7%	2.6%	13.0%
Daptomycin	1.7%	4.3%	0.9%	0.8%
D TEST	63.9%	49.8%	1.7%	11.5%
Cotrimoxazole	0.3%	0.7%	0.0%	0.8%

Figure 4. a. The overall rates of antibiotic resistance (R), intermediate susceptibility (I), and susceptibility (S). b. The resistance rate of eight antibiotics in dominant lineages.

Conclusion

Predominant and evolving lineages of MRSA types associated with specific antibiotic resistance were identified in patients with MRSA bacteraemia.

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