

Genotypic characterization of MRSA from patients during the period 2012 to 2022 at two tertiary hospitals in Thailand

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ABSTRACT

Background: Methicillin-resistant *Staphylococcus aureus* (MRSA) is an important bacterial pathogen in humans. MRSA infections increased mortality and morbidity. The MRSA strains have decreased susceptibility to many antibiotics, particularly vancomycin, leading to failure of treatment. The isolates from two tertiary hospitals including Thammasat University Hospital and Songklanakarind Hospital have not been scrutinized in details at molecular level.

Objective: This study aimed to investigate genetic characteristics and antibacterial susceptibility of MRSA strains isolated from patients during the period 2012-2022 at Thammasat University Hospital and Songklanagarind Hospital during 2019-2020.

Methods: Antibacterial susceptibility test was performed by disk diffusion method and broth dilution method. One-point population was carried out to examine hVISA strains. Genotypic analysis was analyzed by whole genome sequence data.

Results: Most isolates from Thammasat University Hospital during 2012-2022 were resistant to erythromycin, clindamycin and azithromycin. Only one out of 48 isolates from Songklanagarind Hospital was resistant to all tested antimicrobial agents. All isolates (n=169) were susceptible to vancomycin (MIC = 0.25-2 µg/ml). 32 out of 101 isolates (2012-2015) from Thammasat University Hospital and 6 out of 48 isolates from Songklanagarind Hospital were vancomycin MIC creep (1.5-2 µg/ml). The MRSA with vancomycin reduced susceptibility were hVISA detected from Thammasat University Hospital (31.25%) and Songklanagarind Hospital (16.67%). The vancomycin MIC creep and hVISA strains were significant predictor of treatment failure. During the period 2019-2022, most of the strains from Thammasat University Hospital belonged to ST22 (30.8%) while ST239 (25.7%), the most common found in Thailand, was mostly found from Songklanagarind Hospital. SCC mec Type IIa (2012-2015) and IVa (2019-2022) strains were mostly detected from the strains from Thammasat University Hospital at 40.6% and 61.5%, respectively. SCC mec Type IV (22.9%) was also found in Songklanagarind Hospital. This indicated that these strains were CA-MRSA which caused infections in patients at the two tertiary hospitals during the period 2019-2022.

Conclusion: The results would provide an insightful detail information for surveillance and control of MRSA strains. Medical personnel would be alert for effective prevention of the spread from infected patients to other patients in Hospital.

BIOGRAPHY

Lalita Narachasima has current research study on Methicillin-resistant *S. aureus* in the aspects of genetic diversity, mutation of genes associated with reduced susceptibility and resistant strains of MRSA and epidemiology of MRSA in tertiary hospitals. The detailed information of MRSA characterization study will be useful for tracking sources of infections, implementing preventive control measures, and providing effective treatment of the infections.

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