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Prevalence and antimicrobial susceptibility of methicillin-resistant *Staphylococcus aureus* clones: A study at Taksin Hospital, Bangkok, Thailand

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ABSTRACT: Methicillin-resistant *Staphylococcus aureus* (MRSA) is a common pathogen in human diseases. Thirty-seven clinical clones from different patients were tested for a molecular study of the *mecA* gene and multilocus sequence types (ST). Total genomic extraction, followed by a polymerase chain reaction (PCR) for DNA amplification with specific primers for *mecA*, and specific primers for various ST were used. Molecular typing for the study of genetic relationships among clones was performed by enterobacterial repetitive intergenic consensus (ERIC)-PCR. Antimicrobial susceptibility testing for all clones to 9 drugs was performed by the disk diffusion and vancomycin E-test. The presence of *mecA* was detected in all clones. The most common ST was MRSA-ST30, accounting for 81.1% of all MRSA tested, followed by MRSA-ST8/ST97/ST779 (8.1%), MRSA-ST239 (2.7%) and MRSA-nontypeable clones (8.1%). Molecular typing by ERIC-PCR demonstrated DNA fingerprints with corresponding results with sequence types. All clones were susceptible (70–100%) to fosfomycin, fusidic acid, gentamicin, tetracycline, trimethoprim-sulfamethoxazole and vancomycin [minimal inhibitory concentration (MIC) range, MIC_{50} and MIC_{90} were 0.25–1.0, 0.5 and 0.75 μg/ml, respectively by using E-test] but resistant to ciprofloxacin, clindamycin and erythromycin. Inducible macrolide, lincosamide-type B streptogramin resistance (iMLSB) phenotype was 5.4% while constitutive MLSB phenotype was 91.9%. For MRSA-ST30 clones, 96.7% were multi-drug resistant (MDR) with the most common pattern being resistant to ciprofloxacin, clindamycin and erythromycin. These results suggest the importance of MRSA in the field of epidemiology at a hospital in Thailand.

KEYWORDS: MRSA, *Staphylococcus aureus*, ST239, ST30, Thailand

INTRODUCTION

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a pathogen that poses a serious threat to public health and hospital resources due to its resistance to several antimicrobial agents [1]. Its resistance is associated with the acquisition of a mobile genetic element called staphylococcal cassette chromosome *mec* that carries the *mecA* gene which encodes for the low-affinity penicillin-binding protein 2a [2]. Infections caused by multidrug-resistant (MDR) clones lead to prolonged hospital stays and increased mortality. The spread of MRSA in hospitals is a serious health threat and a danger to the global economy [3]. MRSA is highly prevalent in hospitals worldwide with high rates (> 50%) reported in Asia, Malta, North America, and South America [4]. A review of 15 studies showed that between 13% and 74% of worldwide *S. aureus* infections were MRSA [5]. In Thailand, data from two-multi-center studies revealed MRSA prevalence of 57%, with most cases being hospital-acquired MRSA [6]. At Thammasat University Hospital, Pathum Thani Province (adjacent to Bangkok) the prevalence of MRSA was reported to be 46% [7]. In a recent study, Chulalongkorn Memorial Hospital (a tertiary care university hospital in Bangkok) reported MRSA prevalence of 17% [8]. Two other provinces located outside Bangkok, Sa Kaeo Province (in eastern Thailand, near the Cambodian border) and Nakhon Phanom Province (in northeastern Thailand, near the border with Laos), reported MRSA prevalence of 10% [9]. Hospital-acquired MRSA from 12 Asian countries from Saudi Arabia to Philippines was identified by multilocus sequence typing [10]. Due to the high frequency of MRSA in Asia, data from the region suggests that at least 90% of hospital-acquired MRSA accounts for > 60% of MRSA in the world and can be traced to a single clone (ST239 or multilocus sequence type 239) [10–12]. The ST239 sequence has also been found in 26 countries outside Asia [12]. The global dissemination of ST239 is consistent with high transmissibility. ST239 evolved from DNA recombination involving the import of DNA from ST30 into ST8. However, ST239 has been recently replaced by other clones in several countries [12, 13]. As for Thai MRSA, all four isolates tested in 2006 belonged to ST239 [11]. In 2008, 90% of MRSA, from northeast Thailand were linked to ST239 [12]. For other multilocus sequence types of MRSA, many studies have been conducted around the world. In 2019, a study from Northwestern China