Novel molecular analysis for characterization of staphylococcal cassette chromosome in a methicillin-resistant staphylococcus aureus isolated from Malaysian hospital.

ABSTRACT

Methicillin-resistant Staphylococcus aureus strains have appeared in countries worldwide and continue to be one of the most common hospital pathogens and it has become increasingly prevalent in community-acquired infections and provided strong evidence for the independent origins of health care-associated Methicillin-resistant Staphylococcus aureus and community-acquired. It has been shown that methicillin-susceptible S. aureus strains become MRSA strains by the acquisition of a staphylococcal cassette chromosome mec element carrying the mecA gene, which is responsible for methicillin resistance and has become essential for the characterization of Staphylococcus aureus clones in epidemiological studies. The objective of this study to identify the staphylococcal cassette chromosome mec types of methicillin-resistant Staphylococcus aureus isolated from different Malaysian Hospitals. PCR amplification and sequencing analysis were performed to determine the SCCmec type of MRSA. The present research successfully established molecular characteristics of local MRSA contribute as initial database of these isolates in order to fully understand the epidemiology, microbiology and pathophysiology of these infections.

Keyword: Methicillin-resistant staphyloccus aureus (MRSA); Staphylococcal cassette chromosome (SCC); Community-acquired MRSA (C-MRSA); Mutation; Polymerase chain reaction (PCR); Malaysia.