

Molecular Detection Of Virulence Gene From Nosocomial Staphylococcus Infection In Hospital Kuala Lumpur, Malaysian-A Brief Report

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Citation

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Abstract

Methicillin-resistant Staphylococcus aureus (MRSA) remains as the most nosocomial pathogen and is now the emerging problem of community-associated infections. In the present study 100 nasal samples from pediatric patients were subjected to bacteriological and molecular tests for the identification drug resistant Staphylococcus organisms and detection of responsible genes. It revealed that out of 100 nares specimens examined 25% were Staphylococcus aureus, 65% were coagulase-negative Staphylococcus (CONS), and 10% were positive other than Staphylococcus. Among 25 Staphylococcus aureus isolates, only 1 identified as MRSA. The MRSA carrier strain was characterized through sequencing and it was observed that the strains possesses SCCmec type III, Spa type t037 and sequence type 239 with presence of sea and fnbA genes. In conclusion MRSA carrier strain can represent the clonal distribution of locally prevalent MRSA clone. Therefore, a study with large number of strains from many regions is needed to confirm the predominant clones circulating in Malaysia.

INTRODUCTION

Molecular methods have been proven to be cost-effective for the study of nosocomial pathogen especially Methicillin-resistant Staphylococcus aureus (MRSA) (Nordin, 2011). Methicillin-resistant Staphylococcus aureus (MRSA) remains as the most nosocomial pathogens and is now the emerging problem of community-associated infections mostly in developing countries. The use of molecular method in clinical microbiology opened a new horizon for the effective infection control program (Rahman, 2011). In the present study, Staphylococcus aureus isolated from the patients admitted to pediatric institute, Hospital Kuala Lumpur, Malaysia were subjected to analyze for MRSA and detection of responsible gene.

MATERIALS AND METHODS

A total number of 100 nares specimens were collected from the patients admitted to Pediatric Institute, Hospital Kuala Lumpur during 2010. The samples were examined following standard bacteriological procedure to identify Staphylococcus aureus (Nordin, 2011). Antibiotic susceptibility test was performed to determine Methicillin-resistant Staphylococcus aureus (Ibrahim et al, 2011)

Molecular technique polymerase chain reaction was

performed using published primer to determine mecA gene which is responsible for drug resistant character of the organisms (Nordin, 2011)

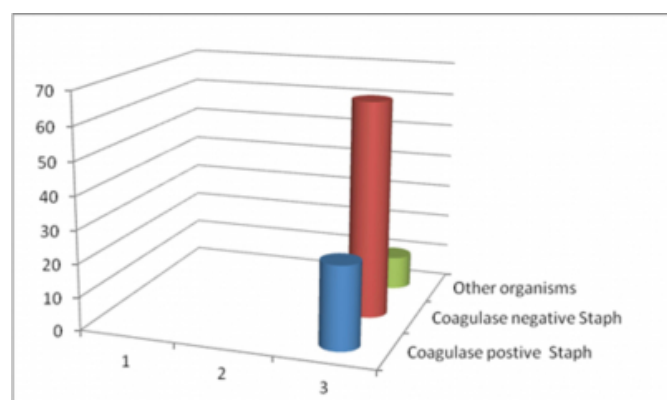
MRSA isolate was further subjected to staphylococcal protein A gene (Spa) sequencing, staphylococcal cassette chromosome mec (SCCmec) typing and multi-locus sequence typing (Ghaznav et al.2010)

RESULTS AND DISCUSSION

Out of 100 nares specimens examined 25% were Staphylococcus aureus, 65% were coagulase-negative Staphylococcus (CONS), and 10 % were other than Staphylococcus (Fig 1). Among 25 Staphylococcus aureus isolates, only 1 identified as MRSA. The patient from where the bacteria isolated is a 7 year-old boy who was hospitalized and suspected dengue fever and subsequently confirmed that too. The patient stayed in the hospital for 3 days.

Figure 1

Fig 1: Percent of Staphylococcus spp isolated from nosocomial infections



Forty six isolates were subjected to polymerase chain reaction (PCR) for the presence of *mecA* gene, out of which 14 were *mecA* positive. Of the 13 positive, 1 was from MRSA and 13 were from Coagulase negative *Staphylococcus aureus*. This result shows that a large number of coagulase negative staphylococcus that was not previously considered to be pathogens are carrier of *mecA* gene and a potential threat to hospital acquired infections.

In the further study of the one MRSA carrier strain, it was characterized through sequencing and it was observed that the strains possesses SCCmec type III, Spa type t037 and sequence type 239 with presence of *sea* and *fnbA* genes.

The results of the present study indicate that the percentage of MRSA nasal carriage among paediatric patients is low (1%) compared with those reported by other previous study (Noor et.al., 2008), but we believe that this figure does not reflect accurately the situation in Malaysia because the prevalence of MRSA colonization varies with time and geographical regions.

The study found that *mecA* gene is highly detected among Coagulase negative staphylococcus isolates. This finding is consistent with a study in India which showed 52% *mecA*

positive among isolated from NICU (Singh et.al.,2009)

One MRSA carrier strain was found to possess SCCmec type III, Spa type t037 and sequence type 239 with presence of *sea* and *fnbA* genes through sequencing . In Malaysia, the predominant MRSA strain that was recognized was SCCmec type III, Spa type t037, and sequence type 239 was also previously reported in 2010 (Neeela et.al. 2010). The study showed that *fnbA* and *sea* were among the commonly positive genes found in MRSA strains. The result of this study indicates that this clone is dominant in our country.

In conclusion the MRSA carrier strain can represent the clonal distribution of locally prevalent MRSA clone. Therefore, a study with large number of strains from many regions is needed to confirm the predominant clones circulating in Malaysia.

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