

ABSTRACT

METHICILLIN-RESISTANT *STAPHYLOCOCCUS AUREUS* (MRSA) A MOLECULAR EPIDEMIOLOGICAL STUDY IN TRINIDAD AND TOBAGO

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In Trinidad and Tobago, molecular epidemiology of methicillin resistant *Staphylococcus aureus* (MRSA) isolates has not been studied, although its prevalence rates has previously been reported by other researchers. Knowledge of molecular epidemiology of MRSA is crucial in the control of spread of MRSA infections in any health institution or country. Hence, this prospective cross-sectional study was conducted at three major regional hospitals in the country to determine the (a) presence of *nuc* and *mecA* genes (b) prevalence and antibiotic susceptibility patterns (c) genetic relatedness and (d) effectiveness of two rapid commercial detection systems in comparison to traditional methods in terms of cost, specificity, sensitivity and time, of all MRSA isolates

Between January 2000 and December 2001, a total of 1912 clinical isolates of *S. aureus* were collected from three major regional hospitals distributed in the northwest, north central and southern Trinidad. Standard microbiological procedures were used to identify the *Staphylococcus aureus* isolates and the Latex agglutination (Denka Seiken) method was used to screen for the oxacillin (methicillin) resistance. Antimicrobial susceptibility tests were performed on the isolates using: E-test and Kirby Bauer disk diffusion methods according to the Clinical Laboratory Standards Institute (CLSI) guidelines.

Multiplex polymerase chain reaction (PCR) was used to detect the presence of *nuc* and *mecA* genes while pulsed field gel electrophoresis (PFGE) was used to determine the

clonal relatedness of the MRSA isolates. Statistical analysis was carried out using Epi Info 3.3 software (CDC, Atlanta, GA, USA).

A total of 244 isolates of the *S. aureus* strains were identified from routine clinical specimens received as methicillin resistant *S. aureus*, giving a prevalence rate of 12.8% (244/1,912) MRSA in the country. There was statistically no significant difference of these MRSA isolates in both sexes (49.6% vs. 50.4%, $p=1.00$). Age groups 40-49 had the highest prevalence rate of 25.0% while 10-19 age groups had the least, 6.1%. The highest prevalence of MRSA was found in the surgical wards (63.2%) and the least, in Obstetrics and Gynaecology wards (1.6%). Wound swabs yielded the highest (86.9%) number of the MRSA isolates, while urine samples yielded the least (0.4%). The antimicrobial susceptibility pattern of the 244 isolates revealed a 100% resistance to penicillin, oxacillin (methicillin), ceftriaxone, gentamicin and erythromycin while there was 100% sensitivity to rifampin, chloramphenicol, and vancomycin. The PCR detected *nuc* and *mecA* genes in all the MRSA isolates, and the pulsed field gel electrophoresis (PFGE) analysis after *Sma*I digestion of 60 randomly selected MRSA strains from the various wards of the three hospitals showed similar banding patterns.

The prevalence of MRSA in the country is low in comparison to that of other countries and antimicrobial sensitivity of the MRSA isolates is still very high to commonly used and available drugs in the country. The relatedness of the MRSA isolates examined suggests that all these strains were from the same epidemic MRSA clone prevailing in the country. While PFGE analysis was valuable in clarifying the molecular epidemiology of

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the MRSA, latex agglutination MRSA-Screen method appears to be the most cost effective method to determine MRSA in our setting.

Key words: methicillin-resistant *Staphylococcus aureus* (MRSA), Trinidad & Tobago, Pulsed-field gel electrophoresis (PFGE), Polymerase chain reaction (PCR), regional hospitals, *Sma*I digestion, *mecA* and *nuc* genes.