

ABSTRACT

Molecular Epidemiology and Characterization of *Staphylococcus aureus* infection in Trinidad and Tobago.

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Few reports are available regarding *Staphylococcus aureus* (whether methicillin sensitive - MSSA or methicillin resistant - MRSA) infections in Trinidad and Tobago. Previous studies regarding *Staphylococcus aureus* in Trinidad and Tobago has so far been conducted mainly on MRSA isolates. There is the need therefore to expand current knowledge as well as determine current status *Staphylococcus aureus* infections in the country.

This study was therefore designed to determine the unique molecular epidemiology and characteristics of *Staphylococcus aureus* infections both in the community and hospitals in Trinidad and Tobago. Additionally, to determine the toxins and proteins commonly associated with the organisms, identify the epidemiological factors involved and evaluate the antimicrobial susceptibility pattern of the *Staphylococcus aureus* isolates.

During a 10 month period, 385 isolates derived from persons who had infections caused by *Staphylococcus aureus* were analyzed. Standardized questionnaires

were utilized for obtaining demographic data of individuals with *Staphylococcus aureus* infections from three study sites namely Eric Williams Medical Sciences Complex – EWMSC; San Fernando General Hospital – SFGH; and Scarborough General Hospital Tobago – SGHT.

Standard and molecular microbiological methods including DNA microarray and multi locus sequence typing (MLST) analysis were performed on 309 clinical *Staphylococcus aureus* isolates recovered from these individuals who attended three of the country’s main health institutions.

Skin and soft tissue infections (SSTI) was the most prevalent type of infections and yielded the largest number of *Staphylococcus aureus* isolates. This was followed by blood system, urogenital tract and respiratory tract infections. *Staphylococcus aureus* isolates from the paediatric ward produced the greatest rate of susceptibility among hospital acquired (HA) infection sites, while the Accident and Emergency cases and isolates displayed the greatest susceptibilities among community acquired (CA) infection cases. The results also revealed that surgical, paediatric and medical wards provided the majority of hospital acquired (HA) infections and isolates from all study sites. Thirteen of 19 antimicrobials tested against *Staphylococcus aureus* exhibited susceptibilities of 75% and over and over with the most susceptible being Nitrofurantoin, Rifampin and Trimethoprim/sulfamethoxazole and least susceptible being Ampicillin and penicillin.

The study revealed *Staphylococcus aureus* clonal complexes diversity among the population studied which possibly may be due to high influx of visitors as well as proximity to the main land of South America. The CC8 was the most prevalent clonal complex with CC8-MSSA, PVL⁺ being the most common strain. Pantone-Valentine Leukocidin (*PVL*) rate was found to be 47% while MRSA now stands at 13.6%. The most prevalent MRSA strains were ST239-MRSA III and ST8-MRSA IV (USA300).

In conclusion, this study shows a high diversity of infections by *Staphylococcus aureus* clonal complexes in Trinidad and Tobago and the *PVL* gene which was considered rare is highly prevalent. Methicillin resistance though slightly higher than previously reported does not represent a significant increase. Efforts should therefore continue to be directed to eliminate any possibility of outbreak of *Staphylococcus aureus* infections in the country as currently experienced by several other countries.

Keywords: *Staphylococcus aureus*, MSSA, MRSA, Trinidad and Tobago, clonal complexes, MLST, PVL, ST239-MRSA III, ST8-MRSA IV, USA300