

MOLECULAR EPIDEMIOLOGY OF METHICILLIN RESISTANT

***STAPHYLOCOCCUS AUREUS* IN PATIENTS WITH SURGICAL SITE INFECTIONS AT**

MULAGO HOSPITAL, KAMPALA – UGANDA



JEREMIAH SENI (MD, Dar)

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ABSTRACT

Background

Surgical site infections (SSI) are globally the third most common type of nosocomial infections with *Staphylococcus aureus* being the most common causative agent. SSI are difficult to treat and are associated with substantial longer hospital stay, higher cost, morbidity and mortality particularly when the etiological agent is Methicillin resistant *Staphylococcus aureus* (MRSA). In a recent study, MRSA accounted for 31.5% of *Staphylococcus aureus* isolates in patients with SSI at Mulago National Hospital, however, MRSA lineages circulating in Mulago surgical patients are not known. Further, it is not known whether there is clonal spread of the strains. Therefore, this study aimed at determining MRSA lineages in Mulago surgical patients using SCCmec and *spa* genotyping techniques. Data herein will also be helpful in guiding infection control at Mulago National Hospital.

Materials and methods

A cross sectional study was conducted from September 2011 to April 2012 and involved 314 patients with SSI in the general surgery, orthopedic surgery and obstetrics & gynaecology wards at Mulago National Hospital. Microbiological and Molecular procedures were performed in the Bacteriology and Molecular laboratories of the Department of Medical Microbiology, Makerere University College of Health Sciences. Pus swabs were taken from SSI and processed with conventional phenotypic methods to identify MRSA, which were confirmed by PCR-detection of the *mecA* gene. MRSA were also screened for presence of *pvl* gene, and further genotyped by multiplex PCR to determine SCCmec types. Then, *spa* sequence based genotyping was done on all *S. aureus* isolates to determine their genetic lineages.

Results

Of the 314 patients with SSI, *Staphylococcus aureus* accounted for 20.4% (64/314), of which 37.5% (24/64) were MRSA. The predominant SCC*mec* types were type V 33.3% (8/24) and type I, 16.7% (4/24). Based on spa genotyping, the predominant lineages were t645 in 17.2% (11/64) and t4353 in 15.6% (10/64), of these MRSA accounted for 8.3% (2/24) and 4.2% (1/24) respectively. These spa lineages were found to be clonally circulating in all surgical wards. Conversely, lineages t064, t355, and t4609 were confined to the obstetrics and gynecology wards. Moreover, a new spa type namely t10277 was identified in this study. MRSA SSI was strongly associated with multidrug resistance, inducible clindamycin resistant (p-value 0.002), infections involving organ (0.005) and cancer comorbid (0.022) as compared to MSSA SSI. The finding of VRSA isolate in this study may be the first in the region.

Conclusions

In this study, SCC*mec* types V and I are the most prevalent MRSA genotypes. The predominant spa lineages (t645 and t4353) were found to be clonally circulating in all surgical wards.

Recommendations

The finding of predominant spa types circulating in all surgical wards calls for strengthening of infection control practices at Mulago National Hospital.