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Identification and characterisation of *Staphylococcus aureus* isolated from nasal swabs obtained from patients and healthcare workers at a tertiary hospital in Nigeria

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Introduction: Invasive *Staphylococcus aureus* infections are associated with initial colonisation especially of the nostrils. Individuals that are at risk due to health status or hospital exposure require nasal screening to prevent transmission. Bacteriological screening of nasal swabs is a quick and non invasive method of assessing the colonisation of pathogenic *S. aureus*. Newer methods such as MALDI-TOF MS and M-PCR are more specific and sensitive than culturing. The use of culture followed by biochemical testing in isolation may miss important information such as the carriage of mecA and PVL toxin genes which are associated with antibiotic resistance and virulence in *S. aureus* isolates. The purpose of this study was to characterise *S. aureus*/methicillin-resistant *S. aureus* (MRSA) isolates from the nasal swabs obtained from patients and healthcare workers at a tertiary hospital using culturing and newer characterisation assays.

Method: Two hundred and fifty nasal swabs were collected from patients and healthcare workers in the surgical, gynaecology, ICU and outpatient wards of the hospital. Selective chromogenic MRSA/*S. aureus* ID media was used for isolation. Presumptive *S. aureus* isolates were identified with MALDI-TOF MS analysis with detection of MRSA using Vitek 2 system and further characterisation with M-PCR assay targeting the 16S RNA (genus specific), nuc (species specific), mecA (methicillin resistance) and PVL toxin gene. Prevalence of mecA and PVL positive *S. aureus* isolates was calculated in percentage for each ward.

Results: The selective media identified 169 presumptive MRSA/*S. aureus* isolates. The MALDI-TOF MS analysis confirmed only 56% (95/169) as *S. aureus*. A total of 38% (36/95) and 22% (21/95) were confirmed as mecA and PVL positive respectively using M-PCR assay. Vitek 2 automation system detected MRSA with oxacillin resistance among 38% (36/95) of the *S. aureus* isolates. The surgical [46% (18/39)] and outpatient [48 (18/39)] wards had more colonised patients and healthcare workers than other wards.

Conclusion: Selective media showed a higher percentage of false positive results and was not sensitive enough when used in isolation to identify *S. aureus*/MRSA from swab specimen. Additional information such as the carriage of resistance and pathogenic genes were only provided by MALDI-TOF, Vitek 2 phenotypic systems and molecular M-PCR assay characterisation. These methods are encouraged for the screening of patients and healthcare workers for virulent *S. aureus* colonisation. Nasal decolonisation is advised for colonised individuals in high prevalence wards in this study to prevent the transmission of virulent isolates in the hospital.

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