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Genetic diversity among circulating *Staphylococcus aureus* strains in a Western Nigerian hospital

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Introduction & Aim: African countries lack detailed and current surveillance information on circulating pathogenic *S. aureus* isolates because of limited resources. Preparedness to control outbreaks may therefore take longer. While Africa awaits uniform infectious diseases surveillance and reporting systems for the region, the sporadic contribution of research groups from the continent is noteworthy. Genotyping provides epidemiological data on circulating pathogens. Information on circulating S. aureus genotypes from western Nigeria is about eight years old. Previous sporadic *S. aureus* clones reported in Nigeria include sequence type (ST) 88, ST 5 and ST 8, a clone which is pandemic in Canada, several European countries and the United States. This study provides information on the circulating sequence types of selected *S. aureus* pulsotypes from western Nigeria.

Methods: Clinical *S. aureus* isolates were collected from a tertiary hospital in western Nigeria. Isolates were clustered into pulsotypes using pulsed field gel electrophoresis (PGFE). The sequence types as well as clonal complexes (CC) of selected pulsotypes were analysed using the multi locus sequence typing (MLST) method and the e BURST database respectively.

Results: The most prevalent clonal groups were the CC 15-ST 789 [31% (5/16) and CC 1-ST 8 [25% (4/16). Other circulating strains in the study were CC 1-ST 5, the Bengal Bay CC 1-ST 772, CC 9-ST 88 and CC 22-ST 152. The most prevalent clonal complex was CC 1 which includes ST 8, ST 5 and ST 772. Strains ST 772 and ST 789 have not been previously reported in western Nigeria.

Discussion & Conclusion: Pandemic and sporadic *S. aureus* strains belonging to ST 8, ST 88, ST 152 and ST 5 detected in this study, have been reported in previous studies in western Nigeria. The most prevalent ST 789 in this study has been previously reported in neighbouring Ghana while ST 772 is a transmitted strain reported in parts of the world including Saudi Arabia. Although patients history showed previous visits to these countries which may indicate possible source of transmission of these clones to Nigeria, further comparative genomic analysis will be required for confirmation.

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