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Genotypic and phenotypic characterization of methicillin resistant *staphylococcus aureus* in Kiambu county Kenya

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Methicillin resistant *Staphylococcus aureus* causes illness to people in both healthcare facilities and surrounding environment leading to high rate of morbidity and mortality. Resistance to *S. aureus* is mainly caused by resistance gene PBP2a found in antibiotic with β -lactam antibiotics such as penicillins, cephalosporins and carbapenems. Samples from wound swabs were collected from patients attending Kiambu and Thika Level-5 hospitals. Out of 138 samples, 54 (39.1%) were culture positive for *S. aureus*. There was no significant association between *S. aureus* prevalence and the gender of patients from the study (Chi Square = 3.00; degree of freedom = 1; $p = 0.08$). Twenty two (22) samples tested positive for MRSA based on Cefoxitin susceptibility test, indicating a prevalence of 15.9% (22/138; 95% CI = 9.4 - 22.1). Susceptibility to 9 common antibiotics ranged from 15% to 85% in the 54 isolates. A total of 27 isolates with MRSA infection were obtained based on the genotypic analysis which is a prevalence of 19.6% (27/138; 95% CI = 13.8-25.4). Out of the 54 *S. aureus* isolates, 14 (25.9%; 95% CI = 11.9-38.9) had *mecA* gene and 14 (25.9%; 95% CI = 11.9-38.1) had Panton-Valentine Leucocidin (PVL) genes. DNA sequencing revealed 18 different *spa* types circulating in the study area with the most frequent being t355 at 50%. More data on these findings, which have a huge impact on the rational use of antibiotics in Kenya, will be presented.

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