

# EPIDEMIOLOGICAL AND GENOMIC PATTERNS OF METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS ISOLATES OBTAINED FROM PATIENTS SEEKING TREATMENT IN NAKURU COUNTY REFERRAL AND TEACHING HOSPITAL, KENYA

## BACKGROUND:

- Staphylococcus aureus is a global cause of both community and hospital-acquired infections, posing a serious threat of antimicrobial resistance.
- Staphylococcus aureus is a pathogenic bacterium that can evolve rapidly to Methicillin Resistant Staphylococcus aureus (MRSA).
- MRSA is a global health concern that is associated with significant morbidity and mortality.



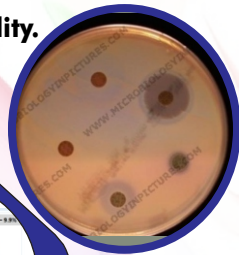
## OBJECTIVES

- To determine the epidemiological and genomic patterns observed from MRSA isolates obtained from patients seeking treatment in Nakuru County Referral and Teaching Hospital.
- To determine the prevalence of MRSA isolates obtained from patients seeking treatment in Nakuru County Referral and Teaching Hospital.
- To determine the resistance pattern to commonly prescribed antibiotics on staphylococcus aureus in Nakuru County Referral and Teaching Hospital.
- To determine the genotype and virulence factors of MRSA isolates in Nakuru County Referral and Teaching Hospital.
- To determine the patient-level factors (length of hospital stay, antibiotic use and surgical intervention) associated with MRSA in Nakuru County Referral and Teaching Hospital.



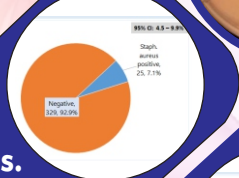
## METHODOLOGY:

Bacterial culture and sensitivity  
Whole Genome Sequencing

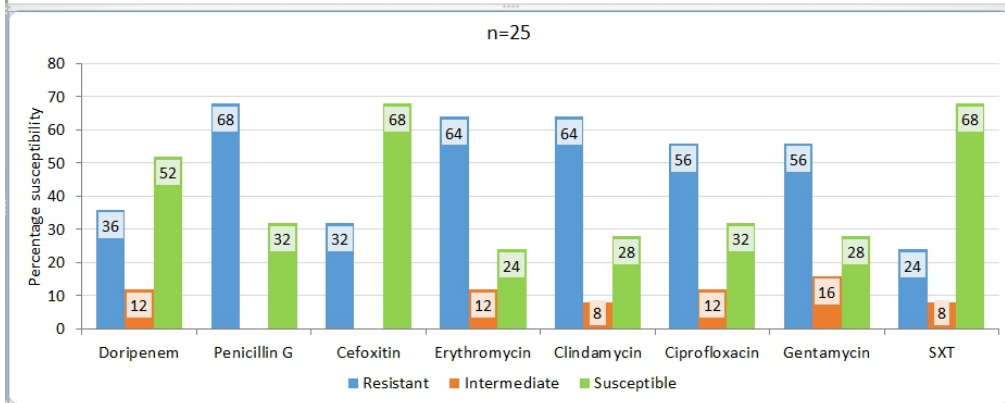


## RESULTS

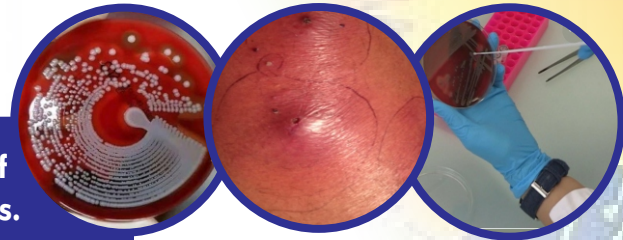
Prevalence of Staphylococcus Aureus.



Resistance pattern to commonly prescribed antibiotics on Staphylococcus aureus



Prevalence of MRSA isolates.



## CONCLUSION & RECOMMENDATION

Prolonged hospitalization and prior antibiotic use were significant risk factors. These findings highlight the need for strengthened genomic surveillance and targeted antimicrobial stewardship to improve MRSA control in the region

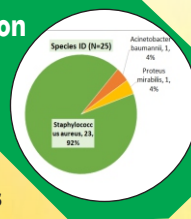
## REFERENCES

- CDC 2019, 2022-2025
- Clinical and Laboratory Standards Institute. (2017)
- GARDP (Global Antibiotic Research & Development Partnership). (2024)
- WHO 2014 and 2021

## ACKNOWLEDGEMENT

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## Genotypic identification of Staphylococcus Aureus

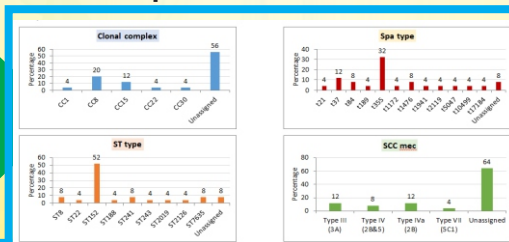


Comparison between resistance in AST versus Genotype profiles

Drugs	AST profile		Genotyping profile	
	n (%)	95% CI	n (%)	95% CI
Doripenem*	9 (36.0)	20.0-56.0	1 (4.0)	0-12.0
Penicillin G	16 (64.0)	44.0-84.0	20 (80.0)	64.0-96.0
Cefoxitin	8 (32.00)	16.0-52.0	9 (36.0)	16.0-56.0
Erythromycin	16 (64.0)	48.0-84.0	9 (36.0)	16.0-56.0
Clindamycin*	16 (64.0)	44.0-80.0	1 (4.0)	0-12.0
Ciprofloxacin	14 (56.0)	36.0-76.0	6 (24.0)	8.0-40.0
Gentamycin*	14 (56.0)	36.0-76.0	4 (16.0)	4.0-32.0
SXT*	6 (24.0)	8.0-43.9	20 (80.0)	64.0-96.0

\*Significantly different because the 95% CI for the proportions did not overlap

## Population Structure



## Virulence Profile

