



Nasal carriage of methicillin-resistant *Staphylococcus sciuri* by residents of an urban informal settlement in Kenya



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A. INTRODUCTION

> *Staphylococcus sciuri*

- Gram +ve, coagulase -ve, clustered cocci
- Zoonotic in nature
- Colonizes human nasopharynx and skin
- Can cause (among others):
 - endocarditis
 - urinary tract infections,
 - pelvic inflammatory disease
 - wound infections.
- Methicillin-resistant (MRSS) strains have emerged

> MRSS

- Can move from animals to humans
- Are reservoirs of *mecA* and *mecC* genes
 - confer resistance to methicillin
 - are transferable to pathogenic *Staph* sp.

❖ **Knowledge gap:** MRSS carriage and circulation in Kenya is not documented.

STUDY GOAL

❑ To characterize the distribution and antibiotic resistance profiles of MRSS group bacteria isolated from healthy persons in Kibera informal settlement to address:

- How commonly do these bacteria colonize healthy persons?
- Which species circulate within the Kenyan population?
- What are their resistance patterns to different antibiotics?
- Do they carry *mecA* and/or *mecC* genes?

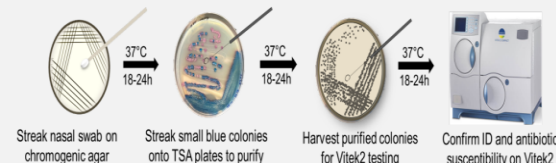
B. METHODS

I. Field sampling

- Study design for parent study

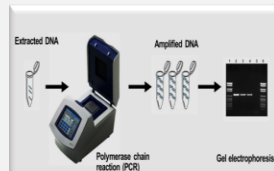
Sampling units	Households
Target population	<5 years, ≥18 years
Site sample sizes	768 (<5 y), 768 (≥18 y)
Sampling strategy	Cluster randomized
Target samples	Stool, nasal swabs

- Step 1: Bacterial isolation and susceptibility testing



II. Laboratory procedures

- Step 2: DNA extraction and PCR



C. RESULTS

1: How commonly does MRSS colonize healthy persons?

- Nasal swabs tested: 384
- Samples with presumptive MRSS isolates: 37 (10%)
- Confirmed MRSS (Vitek2): 16 (4%)

2: Which species circulate in Kenya?

- Species distribution (n = 16)
 - S. sciuri*: 8 (50%)
 - S. lentus*: 5 (31%)
 - S. vitulinus*: 3 (19%)

3: What are MRSS group resistance patterns to different antibiotics?

Antibiotic tested	<i>S. sciuri</i> (n = 8)	<i>S. lentus</i> (n = 6)	<i>S. vitulinus</i> (n = 4)	<i>S. sciuri</i> gp (n = 16)
Clindamycin	6 (75%)	4 (67%)	0 (0%)	10 (63%)
Daptomycin	1 (13%)	2 (33%)	0 (0%)	3 (19%)
Doxycycline	1 (13%)	0 (0%)	0 (0%)	1 (6%)
Erythromycin	7 (88%)	0 (0%)	2 (50%)	9 (56%)
Linezolid	1 (13%)	0 (0%)	0 (0%)	1 (6%)
Rifampicin	2 (25%)	0 (0%)	0 (0%)	2 (13%)
Sulfamethoxazole-trimethoprim	3 (38%)	1 (17%)	0 (0%)	4 (25%)
Tetracycline	6 (75%)	0 (0%)	4 (100%)	10 (63%)
Vancomycin	1 (13%)	0 (0%)	0 (0%)	1 (6%)

4: Do MRSS carry *mecA* and/or *mecC* genes?

- Total isolates tested: 16
 - Isolates with *mecA*: 12 (75%);
 - Isolates with *mecC*: 8 (50%)

<i>mecA</i> gene only	<i>mecC</i> only	<i>mecA</i> and <i>mecC</i>	Neither gene
7 (44%)	3 (19%)	5 (31%)	1 (6%)

D. CONCLUSIONS

- MRSS colonization prevalence appears low among the population studied.
- Nevertheless, they are resistant to medically important antibiotics and carry important resistance genes presenting a potential AMR threat
- Larger studies that address the prevalence and risk factors for MRSS colonization and infection in hospital and community settings to complement surveillance efforts.

Study limitations

- Narrow scope of the study
- Selected population may not represent other Kenyan populations
- Limited livestock contact in selected population

References

- Couto I, et al. J Clin Microbiol. 2000;38(3):1136-43.
- Severin JA, et al. Antimicrob Agents Chemother. 2010;54(12):5413-7.
- Paterson GK, et al. Trends Microbiol. 2014;22(1):42-7.

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One Health Relevance

The spread of resistant bacteria and resistance determinants within and between people, domestic animals and the environment needs to be addressed while combating antimicrobial resistance. *Staphylococcus sciuri* group – a zoonotic, opportunistic and pathogenic bacteria, can be isolated from the environment, animals and humans and are known reservoirs of resistance genes that are transferable to other pathogenic bacteria that circulate within the different ecological niches. This necessitates the need for an integrated and holistic multisectoral One Health approach in the management of this group of bacteria while addressing AMR.