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Optimization of Sample Sites for MRSA Colonization Detection and Prevalence of SCCmec Types II and V among People Living with HIV/AIDS at Irrua Specialist Teaching Hospital, Edo State, Nigeria

Ogbue Itohan Joan[1,2], Samuel Olowo Sunday[1,2], Adewuyi Gbolagade Morufu[1,2]

[1]Department of Medical Microbiology and Parasitology, Irrua Specialist Teaching Hospital, Irrua, Edo State, Nigeria
[2]Department of Medical Microbiology and Parasitology, Ambrose Alli University, Ekpoma Edo State, Nigeria

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***Corresponding Author:** Adewuyi Gbolagade Morufu

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Abstract **Original Research**

Background: Accurate Methicillin-resistant *Staphyloccus aureus* (MRSA) colonization surveillance depends critically on anatomical site selection. Conventional protocols prioritize nasal swabbing, but evidence from immunocompetent populations may not apply to people living with HIV/AIDS (PLWH), who exhibit atypical cutaneous colonization patterns. Concurrently, the staphylococcal cassette chromosome mec (SCCmec) type — the principal molecular classifier distinguishing healthcare-associated from community-associated MRSA lineages — has not been characterised in any PLWH cohort from Edo State, Nigeria. This study evaluates the diagnostic yield of different anatomical swabbing strategies and characterizes the prevalence and co-carriage of SCCmec types II and V among MRSA isolates from PLWH at ISTH.

Methods: 230 MRSA isolates from nasal, axillary, and groin swabs of 176 PLWH were subjected to multiplex PCR for SCCmec types II and V (Zhang protocol). Site-specific MRSA positivity rates and incremental mecA-positive detection yields of all single-site and multi-site swabbing combinations were calculated. Chi-square, phi coefficient ($\varphi = \sqrt{\chi^2/n}$), Spearman rank correlation (continuous variables), and logistic regression assessed SCCmec associations.

Results: Groin had the highest specimen positivity rate (53.4%, 94/176), exceeding nasal (40.3%, 71/176) and axilla (36.9%, 65/176). A nasal-only protocol captured 31.7% of mecA+ isolates; nasal+groin captured 71.5%; all three sites captured 100%. SCCmec type II was detected in 105 isolates (45.7%) and type V in 108 (47.0%). Both co-occurred in 88 isolates (38.3%; φ=0.668, χ^2=102.64, p<0.001, OR=27.2, 95%CI 13.4–55.1). SCCmec distribution was uniform across sites (all p>0.88). Underlying disease independently predicted SCCmec II positivity (aOR=0.35, p=0.017); hand covering while sneezing predicted SCCmec V positivity (aOR=2.18, p=0.022).

Conclusion: Groin is the highest-yield single MRSA site in PLWH. A nasal+groin two-site strategy captures 71.5% of mecA+ isolates; three-site swabbing achieves 100%. The near-equal co-predominance of SCCmec types II and V with large-magnitude phi concordance (φ=0.668) is consistent with a dual-cassette MRSA complex circulating in this ART clinic setting.

Keywords: SCCmec type II, SCCmec type V, MRSA, anatomical site optimization, swab yield, PLWH, HIV, groin colonization, nasal swab, Nigeria, Edo State, phi coefficient, site combination

Introduction

The selection of anatomical swab sites is a foundational methodological decision in Methicillin – resistant *Staphyloccus* aureus (MRSA) colonization surveillance, with direct consequences for prevalence estimates, decolonization targeting, and infection control resource allocation.[1,2] *Staphylococcus aureus* colonizes multiple body surfaces, including the nasal vestibule, axillary folds, groin, perineum, pharynx, and umbilicus, but these sites do not contribute equally to detection yield in all populations or settings.[3] Conventional MRSA screening protocols, developed primarily in acute hospital and surgical settings, prioritize nasal swabbing based on its established role as the dominant *S. aureus* reservoir in the general population.[4,5] However, protocol design based on immunocompetent populations may systematically underestimate MRSA carriage in groups such as people living with HIV/AIDS (PLWH), whose cutaneous ecology differs in ways that may shift the anatomical burden of colonization away from the nose.[6]

Several HIV-specific pathophysiological factors create conditions favoring extra-nasal MRSA colonization among PLWH. HIV-associated eosinophilic folliculitis, pruritic papular eruption, and seborrheic dermatitis preferentially affect intertriginous areas, including the axillary folds and groin, generating microabrasions that breach the epidermal barrier and facilitate cutaneous staphylococcal entry.[7,8] Chronic HIV-associated pruritus leads to repetitive scratch trauma at these sites. Furthermore, prolonged ART clinic attendance involving repeated skin puncture for venepuncture and immunization provides localized entry points beyond the nasal mucosa. These factors collectively suggest that a nasal-centric surveillance strategy may miss a disproportionate share of the MRSA burden specifically in PLWH.

Independent of site selection, the Staphyloccal Cassette Chromosome Mec (SCCmec) cassette type carried by each MRSA isolate provides critical information about its likely origin, whether healthcare-associated or community-acquired, and its antibiotic resistance breadth. SCCmec types I, II, and III, which encode multiple non-beta-lactam resistance determinants in addition to mecA, are the hallmark elements of Healthcare-associated MRSA (HA-MRSA) lineages that dominate hospital transmission chains.[9,10] Types IV and V, by contrast, are smaller cassettes with fewer accessory resistance genes, characteristic of Community-associated MRSA (CA-MRSA) strains that emerged globally during the 1990s and continue to spread through community settings in sub-Saharan Africa.[11,12] Understanding which SCCmec types predominate in an ART clinic MRSA population is therefore a distinct and clinically meaningful question from characterizing mecA prevalence alone: two populations with identical mecA rates may carry entirely different SCCmec profiles, have different multidrug resistance burdens, and require different treatment and decolonization approaches.

This paper addresses which anatomical swabbing strategy provides the best diagnostic yield for MRSA colonization detection in PLWH, and what is the prevalence, anatomical distribution, co-carriage architecture, and clinical determinants of SCCmec types II and V. The findings have direct implications for MRSA surveillance protocol design and MRSA lineage characterization in Nigerian ART clinic settings.

METHODS

Study design, site, and participants

This study was conducted at the Department of Medical Microbiology and Parasitology, Irrua Specialist Teaching Hospital (ISTH), Irrua, Edo State, Nigeria. ISTH operates an ISO 9001-certified Medical Microbiology Laboratory and one of the South-South zone's largest Antiretroviral (ART) clinics, with 7,903 attendances recorded in 2019. A cross-sectional hospital-based study enrolled 176 PLWH on ART for ≥6 months by systematic random sampling. Three rayon swabs per participant were collected from the nasal vestibule, axillary fold, and groin (528 specimens). MRSA was confirmed by cefoxitin disc diffusion per

(Clinical Laboratory Standard Institute) CLSI 2021 guidelines; 131 participants (74.43%) were MRSA-positive, yielding 230 confirmed MRSA isolates from three sites.

Sample size and sampling

Sample size was calculated using the standard formula for proportions in large populations (N > 10,000): $N = Z^2pq/d^2$. Using Z = 1.96 (95% confidence interval), p = 0.161 (prevalence of MRSA in PLWH reported from Port Harcourt, Nigeria[19], used as the best available Nigerian estimate), q = 0.839, and d = 0.05 (precision), the calculation yielded N = 207.6. An additional 10% was added to account for attrition (n = 20.76), resulting in a minimum sample size of 228.36, rounded up to 230.

Participants were recruited by systematic random sampling with a k-value of 5.4, calculated from the average number of ART clinic patients per three-month study period (approximately 1,248) divided by the target sample size (230). In practice, every fifth eligible patient was enrolled. The starting point was selected by ballot (number 3), and subsequent patients were selected at five-patient intervals across four clinic days per week.

Eligibility criteria

Inclusion criteria: PLWH aged 2 years and above, attending the ART clinic, and on antiretroviral therapy for six months or longer, regardless of sex.

Exclusion criteria: Patients on Highly Active Antiretroviral Therapy (HAART) for less than six months at the time of enrolment. This cut-off was applied to ensure a minimum period of immunological reconstitution and to exclude early-treatment immune dysregulation that might confound MRSA acquisition risk.

Ethical considerations

Ethical approval was obtained from the Ethics and Research Committee of Irrua Specialist Teaching Hospital before commencement. Written informed consent was obtained from all adult participants before enrolment. For paediatric participants (age <18 years), written parental/guardian consent and child assent were obtained. All participants were interviewed in a private, screened examination room to ensure confidentiality and minimise stigmatisation. Participant identities were replaced with numeric codes throughout data collection and analysis. No personal identifiers were retained in the research database. All COVID-19 infection control measures were maintained throughout the study period. Research costs were fully borne by the investigators.

Bacterial culture and DNA extraction

MRSA isolates were stored at −70°C in 16% glycerol broth immediately after primary identification. For PCR analysis, each isolate was sub-cultured from glycerol stock onto mannitol salt agar (MSA) and incubated aerobically at 35°C for 18–24 hours to obtain viable single colonies. A single well-isolated colony morphologically consistent with S. aureus (golden-yellow, mannitol-fermenting) was selected and inoculated into 1 mL of tryptic soy broth, then incubated overnight at 35°C on an orbital shaker at 150 rpm to obtain a bacterial suspension of adequate density for DNA extraction.

DNA was extracted from 1 mL of overnight broth culture using the Norgen Biotek Bacteria and Fungi Genomic DNA Purification Kit (Norgen Biotek Corp., Thorold, Canada) following the manufacturer's standard protocol for Gram-positive organisms. Briefly, this involved enzymatic cell lysis with lysozyme (50 mg/mL) at 37°C for 30 minutes, followed by proteinase K digestion, binding to a silica spin column, washing with proprietary wash buffers to remove inhibitors, and elution with 50 µL of RNase-free elution buffer. Extracted DNA quantity and purity were assessed spectrophotometrically using a NanoDrop instrument; samples with A260/A280 ratios between 1.7 and 2.0 were accepted for PCR. Extracted DNA was stored at −20°C until use.

mecA PCR protocol

Polymerase Chain Reaction (PCR) amplification of the mecA gene was performed in a final volume of 25 µL comprising: 5 µL of 5X FIREPol Blend Master Mix (Solis Biodyne, Tartu, Estonia; containing 1.5 mM $MgCl_2$, dNTPs at 200 µM each, and 2 units of Hot FIREPol DNA polymerase), 25 pmol of each primer (mecA forward: 5'-GTGAAGATATACCAAGTGATT-3'; mecA reverse: 5'-ATGCGCTATAGATTGAAAGGAT-3'; expected amplicon 147 bp), 5 µL of extracted template DNA, and nuclease-free water to volume.

Amplification was performed in an Eppendorf Vapo Protect Nexus Series thermocycler with the following programme: initial denaturation at 95°C for 5 minutes; 30 amplification cycles of denaturation at 95°C for 30 seconds, annealing at 52°C for 60 seconds, and extension at 72°C for 90 seconds; followed by a final extension at 72°C for 10 minutes and a hold at 4°C. Each PCR batch included a positive control (S. aureus ATCC 700699, mecA-positive) and a negative control (S. aureus ATCC 29213, mecA-negative). Batches in which either control failed were invalidated and repeated.

Gel electrophoresis

PCR products were resolved on 1.5% agarose gels prepared in 1× TAE buffer (40 mM Tris, 20 mM acetic acid, 1 mM EDTA, pH 8.0), cast in a horizontal electrophoresis tank at room temperature. A 100-bp DNA ladder (Solis Biodyne, Tartu, Estonia) was loaded in the first lane as molecular weight reference. Electrophoresis was conducted at 80 V for 90 minutes. Gels were stained with ethidium bromide (0.5 µg/mL) for 20 minutes and de-stained in distilled water for 15 minutes before visualisation under UV transillumination. Band sizes were confirmed against the 100-bp ladder; a band at 147 bp was recorded as mecA-positive.

SCCmec typing PCR

SCCmec types II and V were detected using the validated multiplex PCR protocol of Zhang et al. (2005).[7] Reactions used Solis Biodyne 5X FIREPol Blend Master Mix in 25-µL volumes (1.5 mM $MgCl_2$, 200 µM dNTPs, 2 units Hot FIREPol polymerase, 25 pmol each primer). Two-stage thermal cycling (Techne 3 Prime thermocycler): initial denaturation 95°C 5 min; 10 cycles [95°C 45 s, 65°C 45 s, 72°C 90 s]; 25 cycles [95°C 45 s, 55°C 45 s, 72°C 90 s]; final extension 72°C 10 min. Expected amplicons: SCCmec type II = 398 bp; type V = 325 bp. Products were resolved on 1.5% agarose gels (80V, 90 min) with ethidium bromide staining. Each run included mecA-positive (ATCC 700699) and mecA-negative (ATCC 29213) controls; batches with control failure were invalidated and repeated.

Site yield analysis

The primary site optimization metric was the proportion of mecA-positive isolates captured by each anatomical site or site combination, with the full three-site protocol serving as the 100% reference. MRSA specimen positivity rate (MRSA-positive specimens per 176 collected at each site) and mecA detection yield (mecA+ isolates captured as a proportion of all 123 mecA+ isolates in the three-site dataset) were computed and treated as distinct metrics: the former reflects the colonization burden at each body surface; the latter reflects the diagnostic sensitivity of each surveillance strategy.

Statistical analysis

SCCmec type positivity rates were expressed as proportions with exact binomial 95% confidence intervals. Site-specific differences were assessed by Pearson chi-square. SCCmec II×V concordance was quantified by the phi coefficient ($\varphi = \sqrt{\chi^2/n}$), the appropriate effect size measure for 2×2 binary associations, equivalent to Cramér's V for 2×2 tables, and expressed alongside odds ratios (OR) with 95% CI. Associations between SCCmec status and continuous variables (CD4+ count, age) used Spearman rank correlation, given non-normal distributions (Shapiro-Wilk $p<0.001$ for both).

Logistic regression identified independent predictors of SCCmec II and V positivity; variables with univariable $p<0.20$ were entered simultaneously into the multivariable model. Model fit was assessed by AIC and McFadden pseudo-R^2. All analyses used SPSS v27.0 (IBM Corp., Armonk, NY, USA) at $\alpha=0.05$ (two-tailed).

RESULTS

Site-specific MRSA positivity rates and swabbing strategy yield

Table 1 and Figure 1 present site-specific MRSA positivity data and the incremental yield of different swabbing strategies. The groin demonstrated the highest specimen positivity rate: 94 of 176 groin specimens (53.4%) were MRSA-positive, substantially exceeding nasal positivity (71/176, 40.3%) and axillary positivity (65/176, 36.9%).

Overall specimen-level positivity across all 528 specimens was 43.6% (230/528). In terms of mecA+ isolate capture, a groin-only protocol yielded 39.8%, outperforming both nasal-only (31.7%) and axilla-only (28.5%) single-site strategies. Among two-site combinations, nasal+groin achieved the highest yield (88/123, 71.5%), followed by axilla+groin (84/123, 68.3%) and nasal+axilla (74/123, 60.2%). The three-site protocol captured all 123 mecA+ isolates (100%).

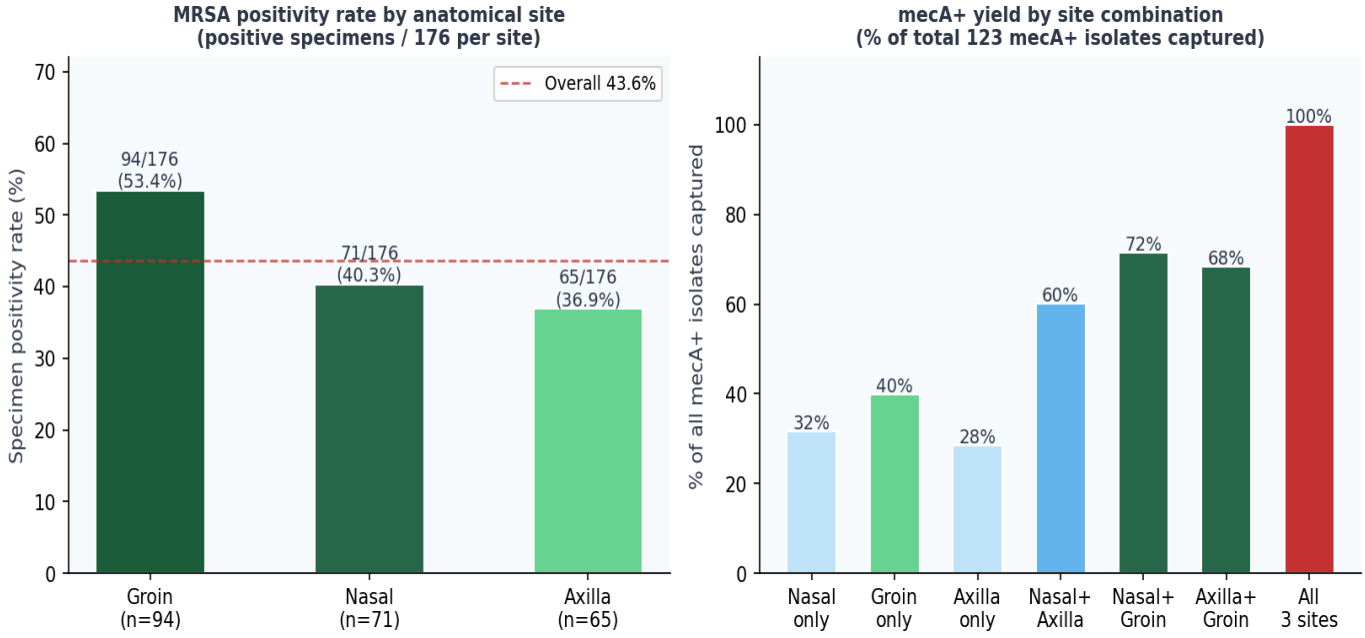

Figure 1. Site-specific MRSA positivity and mecA detection yield by swabbing strategy. Left: MRSA specimen positivity rates per anatomical site (denominator = 176 specimens per site); dashed line = overall positivity 43.6%. Right: mecA+ isolate capture yield by site combination; nasal+groin achieved 71.5%; three-site protocol = 100%.

Table 1. MRSA Positivity Rates and mecA Yield by Anatomical Site and Combination (N=176 Participants)

Site / Combination	MRSA+ specimens	% of 176 per site	mecA+ isolates captured (%)
Single-site strategies			
Groin only	94	53.4%	49/123 (39.8%)
Nasal only	71	40.3%	39/123 (31.7%)
Axilla only	65	36.9%	35/123 (28.5%)
Two-site strategies			
Nasal + Groin	165	—	**88/123 (71.5%)**
Axilla + Groin	159	—	84/123 (68.3%)
Nasal + Axilla	136	—	74/123 (60.2%)
Three-site strategy (reference)			
Nasal + Axilla + Groin	230	—	**123/123 (100%)**

mecA yield = mecA+ isolates captured ÷ 123 total mecA+ isolates in three-site dataset. Positivity rate = MRSA+ specimens ÷ 176 specimens per site. These are distinct metrics serving different purposes.

SCCmec type prevalence and anatomical distribution

SCCmec type II was detected in 105 of 230 isolates (45.7%; 95%CI 39.2–52.4%) and type V in 108 (47.0%; 95%CI 40.4–53.7%). Figure 2 illustrates the overall prevalence and site distribution. SCCmec type distribution was nearly identical across all three anatomical sites: type II positivity was 45.1% (nasal), 47.7% (axilla), and 44.7% (groin) (χ^2=0.154, p=0.926); type V positivity was 45.1%, 49.2%, and 46.8% (χ^2=0.237, p=0.888). No site-specific enrichment for either cassette type was observed.

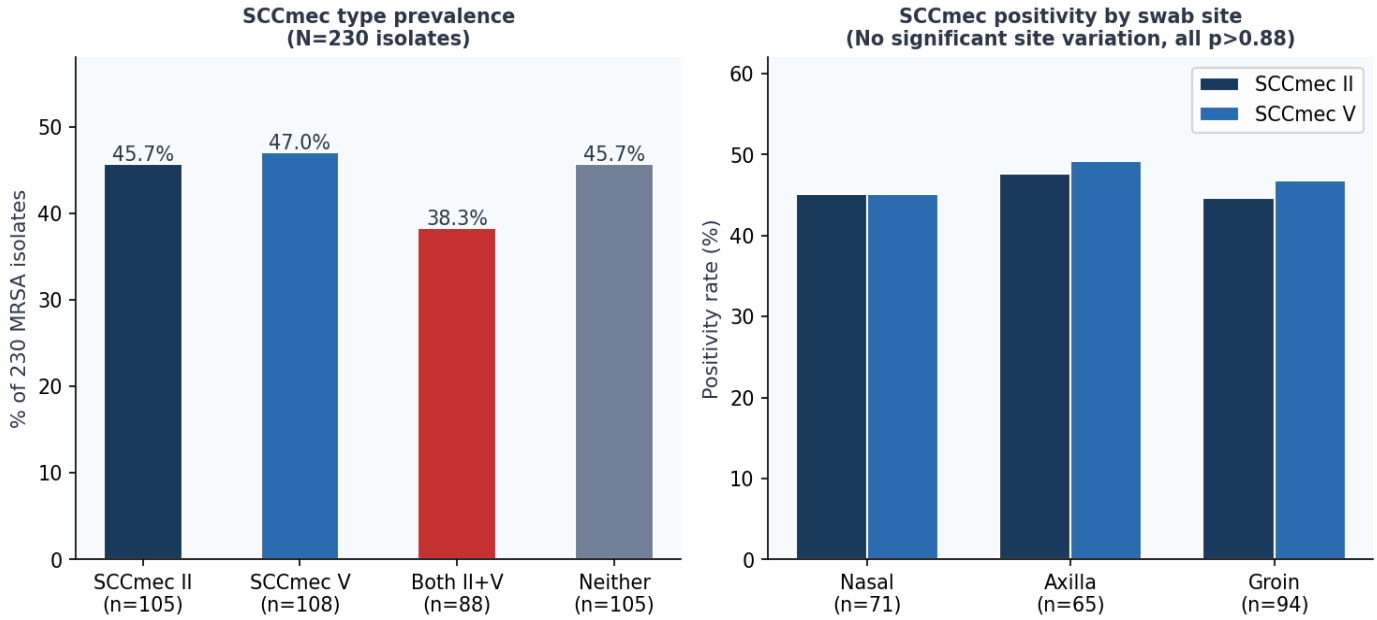

Figure 2. SCCmec type II and V prevalence. Left: overall prevalence among 230 MRSA isolates — types II and V present at near-equal rates (45.7% and 47.0%). Right: positivity by anatomical site — no significant variation across nasal, axillary, and groin sites (SCCmec II p=0.926; SCCmec V p=0.888).

SCCmec type co-carriage and concordance

Of 230 isolates, 88 (38.3%) co-carried SCCmec types II and V simultaneously, 17 (7.4%) carried type II alone, 20 (8.7%) carried type V alone, and 105 (45.7%) carried neither (Figure 3). The phi coefficient quantifying SCCmec II×V concordance was $\varphi=0.668$ ($\chi^2=102.64$, $p<0.001$, OR=27.2, 95%CI 13.4–55.1), representing a large-magnitude association. Among SCCmec II-positive isolates, 83.8% (88/105) also carried type V; among type V-positive isolates, 81.5% (88/108) also carried type II.

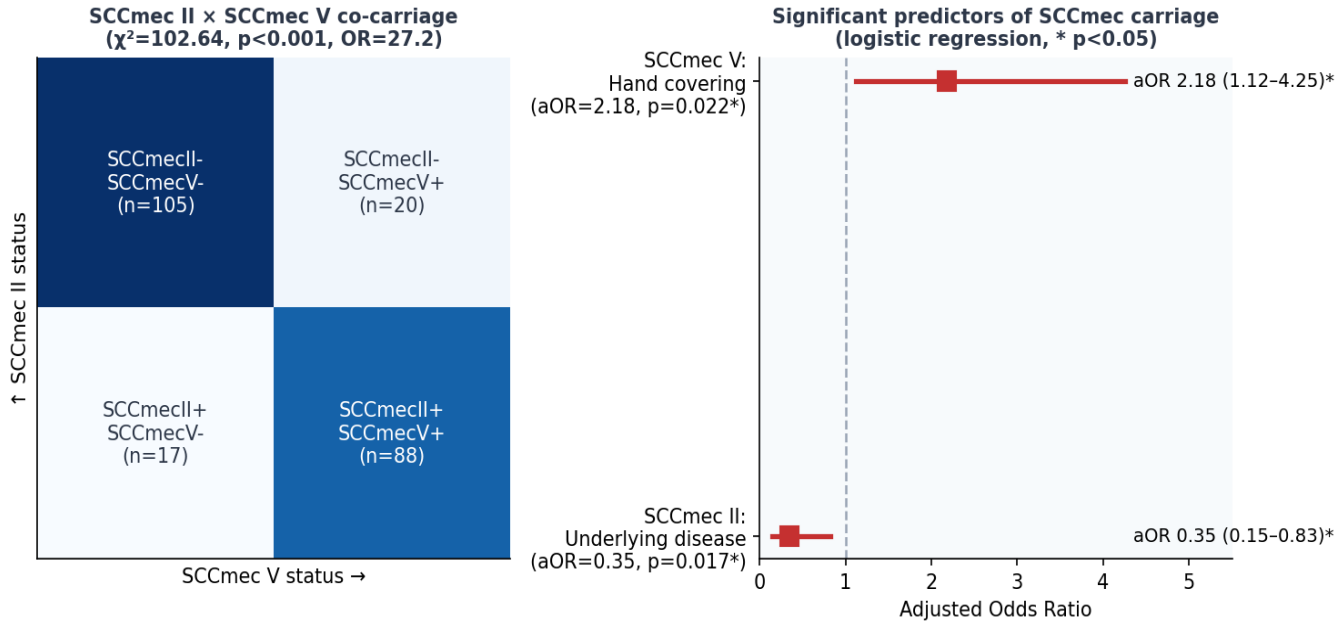

Figure 3. SCCmec II × SCCmec V co-carriage matrix and determinants. Left: 2×2 concordance — 88 co-positive, 105 co-negative, only 37 discordant isolates (φ=0.668, OR=27.2, p<0.001). Right: independent SCCmec carriage predictors from logistic regression.

Table 2. SCCmec Type Prevalence, Site Distribution, and Co-Carriage (N=230)

Variable	Overall	Nasal	Axilla	Groin	p-value
SCCmec type II					
Positive n (%)	105 (45.7%)	32 (45.1%)	31 (47.7%)	42 (44.7%)	0.926
Negative n (%)	125 (54.3%)	39 (54.9%)	34 (52.3%)	52 (55.3%)	—
SCCmec type V					
Positive n (%)	108 (47.0%)	32 (45.1%)	32 (49.2%)	44 (46.8%)	0.888
Negative n (%)	122 (53.0%)	39 (54.9%)	33 (50.8%)	50 (53.2%)	—
SCCmec II × SCCmec V co-carriage					
Both positive	**88 (38.3%)**	—	—	—	—
Type II only (V negative)	17 (7.4%)	—	—	—	—
Type V only (II negative)	20 (8.7%)	—	—	—	—
Neither type	105 (45.7%)	—	—	—	—
φ=0.668, χ²=102.64, p<0.001, OR=27.2 (95%CI 13.4–55.1)					
p-values from Pearson chi-square across three sites. φ=√(χ²/n); equivalent to Cramér's V for 2×2 tables; φ≥0.50 = large effect (Cohen, 1988). OR = odds ratio for SCCmec II×V co-carriage.					

Determinants of SCCmec type II and V positivity

Table 3 presents logistic regression results for SCCmec types II and V. For SCCmec type II, significant univariable predictors included underlying disease (cOR=0.32, 95%CI 0.16–0.61, p=0.001), any current medication (cOR=0.49, p=0.033), and active skin infection at visit (cOR=0.38, p=0.047). In the multivariable model (AIC=309.5, McFadden R^2=0.112), underlying comorbid disease was the sole significant independent predictor (aOR=0.35, 95%CI 0.15–0.83, p=0.017).

For SCCmec type V, hand covering while sneezing was the sole significant independent predictor in the multivariable model (aOR=2.18, 95%CI 1.12–4.25, p=0.022; AIC=314.2, R^2=0.100). CD4+ count was not independently associated with either SCCmec type (SCCmec II: Spearman rho, p=0.727; SCCmec V: p=0.466).

Table 3. Logistic Regression: Determinants of SCCmec Type II and V Positivity (N=230)

Variable	SCCmec II cOR	SCCmec II aOR	p (II)	SCCmec V cOR	SCCmec V aOR	p (V)
Underlying disease (ref: No)	0.32 (0.16–0.61)	**0.35 (0.15–0.83)**	**0.017***	0.50 (0.27–0.93)	0.78 (0.34–1.78)	0.551
Hand covering (ref: No)	1.18 (0.55–2.52)	1.32 (0.68–2.57)	0.412	1.78 (1.00–3.16)	**2.18 (1.12–4.25)**	**0.022***
Any medication	0.49 (0.26–0.91)	0.97 (0.41–2.33)	0.951	0.50 (0.27–0.93)	0.64 (0.26–1.58)	0.335
Skin infection at visit	0.38 (0.15–0.93)	0.47 (0.17–1.32)	0.151	0.75 (0.28–1.97)	0.56 (0.19–1.64)	0.291
CD4+ count (continuous)	Ref.	1.000 (0.999–1.001)	0.727	Ref.	1.001	0.466
Age (per year)	1.00 (0.98–1.02)	1.01 (0.99–1.04)	0.521	0.99 (0.97–1.01)	1.00 (0.98–1.02)	0.641

**p<0.05. cOR=crude OR; aOR=adjusted OR. CD4 associations by Spearman rank correlation given non-normal distribution (Shapiro-Wilk p<0.001).*

Discussion

The groin-predominant MRSA positivity (53.4%) and the diagnostic yield analysis have important practical implications for MRSA surveillance in Nigerian ART clinic settings. Conventional MRSA screening in many West African healthcare facilities relies exclusively on nasal swabs, a practice our data show captures only 31.7% of mecA-positive MRSA in PLWH, giving a miss rate of 68.3% relative to three-site swabbing. A protocol that detects fewer than one in three resistant isolates cannot accurately estimate institutional MRSA burden and leaves the majority of colonized patients unidentified and unmanaged.

The superiority of groin swabbing over nasal swabbing in this cohort is plausible. The inguinal and perineal region in PLWH is disproportionately affected by HIV-associated dermatoses, including pruritic papular eruption, folliculitis, and tinea cruris, which generate persistent microtrauma and epidermal barrier disruption that facilitate *S. aureus* colonization.[13] Farley et al.[14] similarly found that groin and perirectal sites contributed substantially to MRSA detection among HIV-positive adults in the United States, with nasal-only protocols missing over 40% of carriers. Kapali et al.[15] further showed that skin colonization at non-nasal sites frequently precedes clinically apparent infection, supporting the view that extra-nasal sites are independent rather than merely secondary reservoirs.

The near-equal prevalence of SCCmec types II (45.7%) and V (47.0%) was similar to findings from Makgotlho et al.[16] found it in 67.0% of hospital MRSA in South Africa, while community-onset MRSA in West Africa more commonly carries type V, as documented by Obasuyi et al.[17] in Edo state.

The strong SCCmec II×V co-carriage concordance (φ=0.668, OR=27.2) most likely reflects physical co-carriage of both cassette elements on a single MRSA chromosome, through composite cassette formation at the attBscc chromosomal integration locus.

The inverse association between underlying comorbid disease and SCCmec type II carriage (aOR=0.35) likely reflects antibiotic selection pressure: patients with active comorbidities tend to receive more intensive empirical antibiotic regimens that selectively suppress HA-MRSA strains carrying type II, allowing mecA-negative or type V strains to persist. The positive association between hand covering while sneezing and SCCmec type V carriage (aOR=2.18) likely reflects a healthcare engagement proxy — clinic-engaged PLWH are more likely to have internalized health promotion messages and simultaneously more likely to have incurred the healthcare contacts associated with CA-MRSA acquisition.

This study has several limitations. The cross-sectional design means that colonization at all three sites was assessed at a single time-point; whether groin predominance is stable over time or varies with ART duration remains unknown. Only SCCmec types II and V were characterised, and the contribution of other types cannot be excluded. The site optimization results apply to a tertiary-level ART clinic population and may not generalize to primary care HIV settings.

Conclusion

Groin swabbing yielded the highest single-site MRSA positivity rate (53.4%) in PLWH at ISTH, and a nasal-only surveillance strategy captured only 31.7% of mecA+ isolates. A nasal+groin two-site protocol captured 71.5%, and three-site swabbing achieved complete 100% detection. SCCmec types II and V co-predominated at near-equal rates (45.7% and 47.0%) with a large-magnitude phi coefficient concordance (φ=0.668, OR=27.2), consistent with dual-cassette MRSA co-circulation in this ART clinic setting.

Three-site swabbing — nasal, axillary, and groin — is recommended as the standard MRSA screening protocol for PLWH in Nigerian ART facilities, and whole-genome sequencing is needed to resolve the molecular architecture of the dual SCCmec co-carriage observed here.

AUTHORS' CONTRIBUTIONS

Ogbue Itohan Joan conceived the idea and conceptualized the study. She was actively involved in all aspects of the study including, literature search, development of research proposal, samples collection and analysis, data collection and analysis, manuscript drafting and publishing. Adewuyi GM and Samuel OS were supervising Consultants for the project and actively participated at all stages of the study. In addition, Adewuyi GM is the Head of the Department of HIV/AIDS, ISTH.

DECLARATIONS

Conflict of interest: There is no conflict of interest.

Funding: Research costs were self-funded by the investigators.

Ethics: Ethics and Research Committee, Irrua Specialist Teaching Hospital (Ref:

NHREC/29/03/2017)

Data availability: Available from the corresponding author on reasonable request.

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