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Research Article

Bacterial Etiology and Antimicrobial Resistance Patterns of Skin Infections in a Primary Healthcare Setting in Northeastern Nigeria

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Abstract

Skin and soft tissue infections (SSTIs) constitute a significant global health burden, particularly in sub-Saharan Africa where climatic, socioeconomic, and healthcare factors converge to facilitate high prevalence rates. In Northeastern Nigeria, protracted humanitarian crises and healthcare system disruption have compounded the challenge of managing bacterial skin infections. However, limited data exist on the etiological spectrum and antimicrobial resistance patterns specifically within primary healthcare settings in this region. This study aimed to characterize the bacterial etiology and antimicrobial resistance profiles of skin infections presenting to a primary healthcare facility in Northeastern Nigeria. A cross-sectional laboratory-based investigation was conducted at Sangere Clinic, Adamawa State. Twenty pus samples from patients with skin infections were aseptically collected and processed using standard microbiological techniques. Bacterial isolates were identified through Gram staining, cultural characteristics, and biochemical tests. Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method following Clinical and Laboratory Standards Institute (CLSI) guidelines. A total of 18 bacterial isolates were recovered. Staphylococcus aureus was the most predominant organism (44.4%), followed by Escherichia coli (22.2%), Klebsiella pneumoniae (16.7%), Pseudomonas aeruginosa (11.1%), and Streptococcus spp. (5.6%). Meropenem demonstrated the highest overall susceptibility (≥85%), while ampicillin exhibited the lowest susceptibility and the highest resistance rate (>80%). Gentamicin and ciprofloxacin showed considerable activity against both Gram-positive and Gram-negative isolates. S. aureus remains the predominant pathogen, but the substantial isolation of Gram-negative organisms signals an important epidemiological shift. Ampicillin is no longer effective for empirical therapy; ciprofloxacin or ceftriaxone may serve as first-line agents. These findings underscore the urgent need for context-appropriate treatment algorithms, enhanced laboratory capacity, and robust antimicrobial stewardship programmes in primary healthcare settings.

Keywords: *Bacterial skin infections; antimicrobial resistance; primary healthcare; Staphylococcus aureus; Antimicrobial resistance.*

Introduction

Skin and soft tissue infections (SSTIs) constitute a substantial proportion of the global burden of infectious diseases, ranking among the most frequent reasons for outpatient consultations across all levels of healthcare delivery (Deng *et al.,* 2025). In sub-Saharan Africa, where tropical climates, high population densities, and limited access to clean water and sanitation converge, the epidemiology of bacterial skin infections assumes particular significance (Ahmad *et al.,* 2025). These infections range from superficial pyodermas such as impetigo and folliculitis to deeper-seated conditions including cellulitis, abscesses, and chronic wound infections, all of which carry the potential for significant morbidity, disability, and, in severe cases, mortality. The interplay of environmental, socioeconomic, and healthcare-related factors in regions such as Northeastern Nigeria creates a uniquely conducive milieu for the high prevalence and recurrence of bacterial skin

infections, rendering them a persistent public health challenge that demands systematic investigation (Abdulgafar *et al.,* 2025).

The bacterial etiology of skin infections is well-characterized globally, with *Staphylococcus aureus* and *Streptococcus pyogenes* predominating as the primary Gram-positive pathogens, alongside an increasing recognition of Gram-negative organisms such as *Pseudomonas aeruginosa*, *Escherichia coli*, and *Klebsiella pneumoniae* in wound-related infections. In Nigeria, studies across various geopolitical zones have consistently identified *S. aureus* as the most frequently isolated organism from skin and wound infections (Nwafia *et al.,* 2024). A systematic review and meta-analysis of wound, skin, soft tissue, and surgical site infections across Central, Eastern, Southern, and Western Africa reported *S. aureus* isolation rates of approximately 29%, with *P. aeruginosa* and *K. pneumoniae* likewise emerging as significant contributors, particularly in healthcare-associated and chronic wound infections (Ngoshe *et al.,* 2023). The spectrum of causative organisms, however, exhibits considerable geographic and institutional variation, underscoring the necessity for region-specific etiological data to inform empirical treatment guidelines and antimicrobial stewardship programmes.

Perhaps the most concerning dimension of bacterial skin infections in contemporary practice is the accelerating trajectory of antimicrobial resistance (AMR). The World Health Organization has identified AMR as one of the most pressing threats to global health, with mortality attributable to bacterial AMR being disproportionately high in African regions. In Nigeria, the prevalence of multidrug-resistant (MDR) organisms in superficial skin samples has been estimated at 69% (Adegbite *et al.,* 2023), with methicillin-resistant *S. aureus* (MRSA) accounting for over 40% of isolates in some settings (Ezeh *et al.,* 2023). Alarmingly high resistance rates have been documented for commonly prescribed antibiotics: *S. aureus* isolates have shown resistance to penicillin approaching 82%, to ampicillin reaching 68%, and to amoxicillin exceeding 74% (Ezeh *et al.,* 2023). Gram-negative pathogens have fared no better, with *E. coli* and *K. pneumoniae* demonstrating substantial resistance to first-line agents (Alabi *et al.,* 2025). These patterns are driven by a complex nexus of factors including indiscriminate antibiotic use, inadequate healthcare infrastructure, limited diagnostic capacity, and unregulated access to antimicrobial agents without prescription (Otorkpa *et al.,* 2025; Alabi *et al.,* 2025).

Northeastern Nigeria presents a particularly challenging context for the management of bacterial skin infections. The region has endured prolonged humanitarian crises, population displacement, and substantial disruption of healthcare services, factors that collectively exacerbate the burden of infectious diseases and compromise infection prevention and control measures. Studies from Maiduguri, the regional capital, have reported a recovery rate of 16.2% for *P. aeruginosa* from wound samples, with all isolates demonstrating resistance to ceftazidime and 44.1% exhibiting multidrug resistance (Ngoshe *et al.,* 2023). *S. aureus* has been identified as the major organism isolated from skin sepsis-associated conditions in northern Nigeria (Mohammed *et al.,* 2024). The prevalence of healthcare-associated infections in Nigeria, including SSTIs, stands at 15.75%, a figure that likely underestimates the true burden in conflict-affected settings where surveillance systems are fragmented, and healthcare access is severely constrained (Nwafia *et al.,* 2024). These realities underscore the urgent need for robust, locally generated evidence to guide clinical decision-making in this resource-limited environment.

Despite the recognized importance of bacterial skin infections in primary healthcare, there remains a conspicuous gap in the literature concerning their etiological spectrum and antimicrobial resistance patterns specifically within primary healthcare settings in Northeastern Nigeria. The majority of existing studies have been conducted in tertiary or specialist hospitals, which serve populations that may not be representative of the broader community and where the epidemiology of infections may be skewed by referral bias and nosocomial acquisition (Ngoshe *et al.,* 2023; Nwafia *et al.,* 2024). Primary healthcare facilities, which constitute the first point of contact for most Nigerians seeking medical care, operate under distinct constraints, limited laboratory capacity, restricted formularies, and high patient volumes, that shape both the presentation of skin infections and the patterns of antibiotic prescribing. The absence of systematic data from this level of care perpetuates a cycle of empirical prescribing based on outdated or extrapolated guidelines, thereby fueling further resistance (Alabi *et al.,* 2025). This study, therefore, seeks to address this critical knowledge gap by characterizing the bacterial etiology and antimicrobial resistance profiles of skin infections presenting to primary healthcare facilities in Northeastern Nigeria, to provide evidence to inform context-appropriate treatment algorithms, strengthen antimicrobial stewardship, and ultimately improve patient outcomes in this underserved region.

Materials and Methods

Study Area and Population

This cross-sectional laboratory-based investigation was conducted at Sangere Clinic, located within Girei Local Government Area of Adamawa State, Northeastern Nigeria. Girei, one of the 21 Local Government Areas in the state, lies within the Adamawa Central Senatorial District, positioned approximately between Latitude 9°22'11.83" N and Longitude 12°33'0.74" E. Sangere Metropolis, situated about 2 km from Girei, had an estimated population of approximately 15,000 residents as of 2021, comprising a diverse demographic of ethnicities, religions, and occupational groups. Sangere Clinic serves as a primary healthcare facility providing outpatient medical services, diagnostic evaluation, and therapeutic interventions for a broad spectrum of health conditions affecting the local population.

Culture Media Preparation

Microbiological culture media employed in this study comprised Nutrient agar, Blood agar, and MacConkey agar, all of which were prepared strictly according to the manufacturers' specifications and standard laboratory protocols (Cheesbrough, 2015).

Sample Collection and Processing

A total of 20 clinical samples were obtained from patients presenting with signs and symptoms suggestive of bacterial skin infections at Sangere Metropolis. Before sample collection, written informed consent was obtained from all participants or their legal guardians following a detailed explanation of the study objectives and procedures. Pus specimens from abscesses, boils, and purulent skin lesions were aseptically collected using sterile cotton swabs pre-moistened with sterile normal saline to minimize surface contamination. For deeper-seated infections, sterile needles and syringes were employed to aspirate purulent material. All collected specimens were promptly transferred into sterile transport media, appropriately labelled, and transported to the laboratory for microbiological analysis (Abaka *et al.,* 2024).

Upon arrival at the laboratory, specimens were initially examined for volume, color, and consistency before inoculation. Using standard aseptic techniques, each sample was streaked onto Blood agar, MacConkey agar, and Nutrient agar plates. The inoculated plates were subsequently incubated aerobically at 37°C for 24 hours. Following incubation, bacterial growth was assessed based on colonial characteristics including size, shape, pigmentation, and hemolytic activity (Abaka *et al.,* 2025). For microscopic examination, Gram-stained smears were prepared from isolated colonies and examined under oil immersion at ×100 magnification to determine Gram reaction, cellular morphology, and arrangement (Owama, 2015).

Biochemical Identification

Gram Staining: A smear was prepared by emulsifying a bacterial colony in a drop of sterile distilled water on a clean, grease-free glass slide. The smear was air-dried and heat-fixed by gentle flaming. The fixed smear was flooded with crystal violet for 1 minute, rinsed with distilled water, and then treated with Gram's iodine for 1 minute. After decolorization with ethyl alcohol, the smear was counterstained with safranin for 30 seconds, washed, air-dried, and examined microscopically under oil immersion at ×100 objective lens following the procedure described by Owama (2015).

Sugar Utilization Test: Triple Sugar Iron (TSI) agar slants were inoculated by stabbing the butt and streaking the surface using a sterile inoculating needle. The inoculated slants were incubated at 37°C for 24 hours, after which the pattern of glucose, lactose, and sucrose utilization was interpreted according to the method described by Redmond (2003).

Catalase Test: A small amount of bacterial growth from each isolate was emulsified in 2–3 ml of hydrogen peroxide solution. The production of effervescence (bubbles) indicated a positive catalase reaction, while the absence of bubbles denoted a negative result (Cheesbrough, 2015b).

Citrate Utilization Test: A dense suspension of each bacterial isolate was prepared in sterile physiological saline and a citrate tablet was added. The tubes were incubated overnight at 35–37°C. A color change to red indicated a positive reaction, whereas a yellow-orange colour signified a negative result (Dominic *et al.,* 2025).

Coagulase Test: Three test tubes were each prepared with 0.2 ml of plasma. The first tube received 0.8 ml of the test culture, the second tube (positive control) received *Staphylococcus aureus* suspension, and the third tube (negative control) received sterile broth. Following gentle mixing, all tubes were incubated at 37°C. Clot formation observed within 1 hour was interpreted as a positive coagulase test (Dominic *et al.,* 2025).

Indole Test: Each bacterial isolate was inoculated into 0.5 ml of sterile saline, and three drops of Kovac's reagent were subsequently added. The tubes were incubated at 37°C for 24 hours. A blue or violet colour development signified a positive indole reaction, while a yellow or green colour indicated a negative result (Dominic *et al.,* 2025).

Oxidase Test: A piece of filter paper was placed in a Petri dish and moistened with two drops of freshly prepared oxidase reagent. Using a sterile inoculating rod, a single bacterial colony was smeared onto the reagent-soaked paper. The development of a blue-purple color within 10–30 seconds indicated a positive oxidase reaction, whereas the absence of color change signified a negative result (Abaka *et al.,* 2025).

Urease Test: The urease test was performed by inoculating each bacterial isolate onto a slope of Christensen's urea agar medium. The inoculated slants were incubated at 35–37°C for 24 hours. A color change from yellow to pink or purple indicated a positive urease reaction, indicative of urease enzyme production, whereas the absence of color change signified a negative result (Osei and Addo, 2020).

Determination of Antimicrobial Susceptibility Pattern

Standardization of Inoculum

The bacterial inoculum was standardized to ensure reproducibility and accuracy of susceptibility testing. Nutrient broth (5 mL) was dispensed into a sterile test tube, and three isolated colonies from a 24-hour pure culture grown on solid media were aseptically transferred into the broth using a sterile inoculating loop. The suspension was thoroughly mixed using a vortex mixer to achieve a homogeneous dispersion of bacterial cells. The turbidity of the suspension was then adjusted to match the 0.5 McFarland standard, which corresponds to an approximate bacterial density of 1.5×10^8 CFU/mL (CLSI, 2023).

Antimicrobial Susceptibility Testing (AST)

Antimicrobial susceptibility of the bacterial isolates was determined using the Kirby–Bauer disk diffusion method on Mueller–Hinton agar (MHA), in accordance with the guidelines established by the Clinical and Laboratory Standards Institute (CLSI, 2023). The standardized inoculum was uniformly spread across the surface of the MHA plates using a sterile cotton swab to ensure confluent growth. Commercially available antibiotic discs were then aseptically placed onto the inoculated agar surface within 15 minutes of swabbing. The plates were incubated at 37°C for 18–24 hours. Following incubation, the diameters of the zones of inhibition surrounding each disc were measured in millimetres using a calibrated ruler. The results were interpreted as susceptible, intermediate, or resistant based on the CLSI (2023) interpretive criteria and breakpoint tables.

Quality Assurance

Quality control measures were implemented throughout the study to ensure the validity and reliability of the results. Standard reference strains were included as positive and negative controls for all biochemical tests and antimicrobial susceptibility testing, as recommended by CLSI guidelines (CLSI, 2023).

Statistical Analysis

Data obtained from the study were recorded, collated, and analyzed using descriptive statistics. Categorical variables, including the frequency and proportion of bacterial isolates, were summarized as counts and percentages. The antimicrobial susceptibility patterns were presented as frequencies and percentages of susceptible, intermediate, and resistant isolates for each antibiotic tested, based on the zone of inhibition diameters interpreted according to the Clinical and Laboratory Standards Institute breakpoint criteria. For the antibiotic susceptibility testing, the mean zone diameters and standard deviations were calculated for each organism-antibiotic combination to provide a measure of central tendency and dispersion of the inhibition zone sizes. The overall susceptibility and resistance rates were expressed as percentages of the total isolates tested against each antimicrobial agent (Mahmud *et al.,* 2023)

All data were entered into Microsoft Excel (version 2019) for systematic organization and subsequent analysis. No inferential statistical tests were performed, as the primary objective of this study was descriptive, aimed at characterizing the frequency distribution of bacterial isolates and their antimicrobial resistance patterns. Results were presented using tables and figures to facilitate visual interpretation and clarity of findings. Quality control was maintained by including standard reference strains (*Staphylococcus aureus* ATCC 25923, *Escherichia coli* ATCC 25922, and *Pseudomonas aeruginosa* ATCC 27853) in all antimicrobial susceptibility testing runs to ensure accuracy and reproducibility of the results, as recommended by CLSI guidelines (CLSI, 2023). Any results falling outside the acceptable quality control ranges were discarded, and the testing was repeated to ensure reliability.

Ethical Considerations

This study was conducted in accordance with the ethical principles outlined in the Declaration of Helsinki. Ethical approval was obtained from the relevant institutional review board, and written informed consent was secured from all participants before sample collection.

Results

Frequency Distribution of Bacterial Isolates from Skin Infections

A total of 18 bacterial isolates were recovered from the clinical samples collected from patients presenting with skin infections at Sangere Clinic. The frequency distribution of the isolated organisms is presented in Table 1. *Staphylococcus aureus* was the most predominantly isolated organism, accounting for 8 isolates (44.4%), followed by *Escherichia coli* with 4 isolates (22.2%). Other organisms identified included *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*, among others. *Streptococcus* spp. was the least frequently isolated organism, with only 1 isolate (5.6%) recovered from the samples.

Antibiotic Susceptibility and Resistance Patterns of Gram-Positive Bacterial Isolates

The antimicrobial susceptibility and resistance profiles of the Gram-positive bacterial isolates are presented in Table 3. Among the Gram-positive organisms, *Streptococcus* spp. demonstrated the highest overall susceptibility to the antibiotics tested, showing sensitivity to Rocephin (ceftriaxone), ciprofloxacin, azithromycin, erythromycin, and pefloxacin. In contrast, *Staphylococcus aureus* exhibited the lowest susceptibility rates, with notable resistance observed against multiple antibiotics, including ampicillin and penicillin. A considerable proportion of *S. aureus* isolates displayed multidrug resistance phenotypes.

Antibiotic Susceptibility and Resistance Patterns of Gram-Negative Bacterial Isolates

Table 4 summarises the antimicrobial susceptibility and resistance patterns of the Gram-negative bacterial isolates. *Klebsiella pneumoniae* showed the highest susceptibility rates, particularly to sparfloxacin, ciprofloxacin, augmentin (amoxicillin-clavulanate), and pefloxacin. Conversely, *Escherichia coli* and *Pseudomonas aeruginosa* demonstrated the highest levels of resistance across the panel of antibiotics tested. Resistance was most pronounced against ampicillin, amoxicillin-clavulanate, and tetracycline among the Gram-negative isolates.

Overall Percentage Susceptibility and Resistance of Bacterial Isolates to Antimicrobial Agents

The overall percentage susceptibility and resistance of all bacterial isolates to various antibiotics are summarized in Table 5. Among the antibiotics evaluated, meropenem exhibited the highest susceptibility rate, with the majority of isolates showing sensitivity to this carbapenem agent. Gentamicin also demonstrated comparatively high activity against the isolates. In contrast, ampicillin recorded the lowest susceptibility and concurrently the highest resistance rate among all antibiotics tested. Resistance to ampicillin was observed in over 80% of isolates. Meropenem and gentamicin showed the least resistance, with resistance rates below 15%. Other antibiotics, including tetracycline and amoxicillin-clavulanate, showed intermediate susceptibility and resistance profiles.

Table 1. Cultural and biochemical characteristics of probable bacterial isolates

Probable bacterial isolate	Frequency (n)	Cultural characteristics	Gram reaction	Catalase	Coagulase	Oxidase	Indole	Citrate	Urease
Staphylococcus aureus	8	Golden-yellow, round colonies on Blood agar	Gram-positive cocci	+	+	−	−	−	−
Pseudomonas aeruginosa	2	Large, mucoid colonies on MacConkey agar	Gram-negative rods	+	−	+	−	+	+
Escherichia coli	4	Dry, greenish colonies	Gram-negative rods	+	−	−	+	−	−
Klebsiella pneumoniae	3	Flat, spreading colonies	Gram-negative rods	+	−	−	−	+	+
***Streptococcus* spp.**	1	Small, circular colonies on MacConkey agar	Gram-positive cocci	−	−	−	−	−	+
Total isolates	**18**								

Key: BA = Blood agar; MA = MacConkey agar; Catalase (Ca); Coagulase (Coa); Oxidase (Oxi); Indole (Ind); Citrate (Cit); Urease (Ur); (+) = Positive reaction; (−) = Negative reaction; spp. = species.

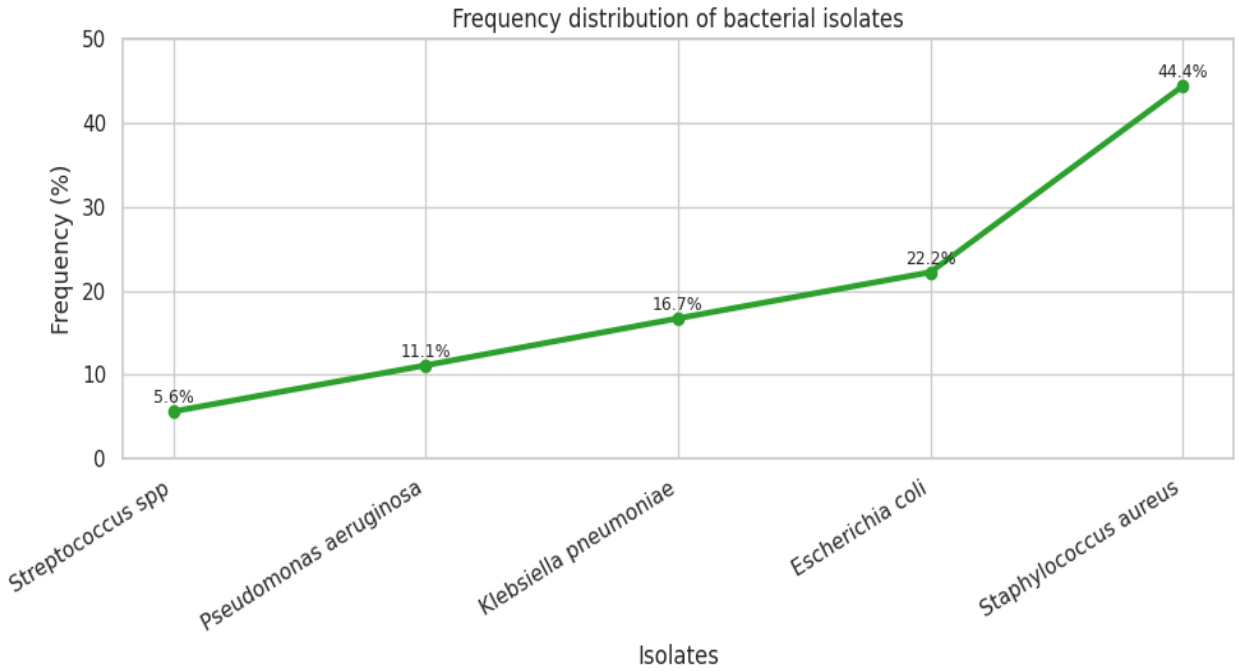

Figure 1: Frequency distribution of bacterial isolates

Table 2. Antibiotic susceptibility pattern of Gram-positive bacterial isolates (zone of inhibition, mm)

Isolate	Replicate	Ampicillin (AMP)	Ciprofloxacin (CIP)	Ceftriaxone (CRO)	Gentamicin (GEN)	Erythromycin (ERY)	Meropenem (MEM)
Staphylococcus aureus	1	10 (R)	22 (S)	20 (S)	16 (R)	14 (R)	28 (S)
	2	12 (R)	19 (S)	18 (S)	15 (R)	10 (R)	27 (S)
	3	11 (R)	23 (S)	21 (S)	17 (R)	12 (R)	29 (S)
Streptococcus spp.	1	19 (S)	23 (S)	25 (S)	14 (R)	24 (S)	22 (S)

Key: AMP = Ampicillin; CIP = Ciprofloxacin; CRO = Ceftriaxone; GEN = Gentamicin; ERY = Erythromycin; MEM = Meropenem; **R** = Resistant; **S** = Susceptible.

Interpretation: Zone of inhibition **0–17 mm = Resistant (R); ≥18 mm = Susceptible (S)** according to the **Clinical and Laboratory Standards Institute (CLSI, 2021).**

Table 3. Antibiotic susceptibility pattern of Gram-negative bacterial isolates (zone of inhibition, mm)

Isolate	Ampicillin (AMP)	Ciprofloxacin (CIP)	Ceftriaxone (CRO)	Gentamicin (GEN)	Erythromycin (ERY)	Meropenem (MEM)
Escherichia coli	9 (R)	18 (S)	18 (S)	23 (S)	15 (R)	10 (R)
Klebsiella pneumoniae	0 (R)	21 (S)	21 (S)	17 (R)	20 (S)	12 (R)
Pseudomonas aeruginosa	8 (R)	20 (S)	17 (R)	18 (S)	9 (R)	27 (S)

Key: AMP = Ampicillin; CIP = Ciprofloxacin; CRO = Ceftriaxone; GEN = Gentamicin; ERY = Erythromycin; MEM = Meropenem; **R** = Resistant; **S** = Susceptible.

Interpretation: Zone of inhibition **0–17 mm = Resistant (R); ≥18 mm = Susceptible (S)** according to the **Clinical and Laboratory Standards Institute (CLSI, 2021).**

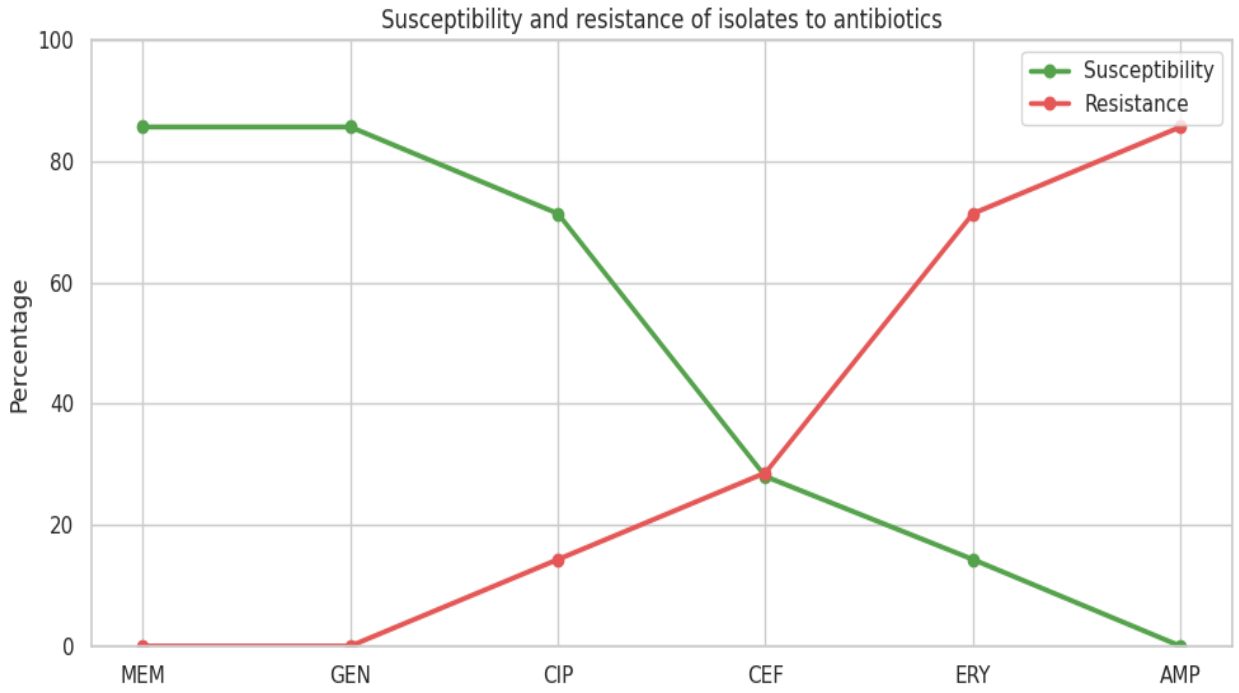

Figure 2: Percentage of susceptibility and resistance of isolates to antibiotics

KEY: MEM= Meropenem, GEN= Gentamycin, CIP= Ciprofloxacin, CEF= Ceftriaxone, ERY= Erythromycin, AMP= Ampicillin.

Discussion

The human skin microbiome represents a complex and dynamic ecosystem comprising diverse microbial communities, including bacteria, fungi, and viruses, that reside on the cutaneous surface. This intricate biological network plays an essential role in maintaining skin homeostasis, modulating host immune responses, and protecting against pathogenic colonization (Byrd *et al.,* 2018). The composition of this microbial community is shaped by multiple interrelated factors, including the anatomical site-specific microenvironment, host genetic predisposition, dietary habits, hygiene practices, and environmental exposures (Gao *et al.,* 2017). In the present study, we aimed to isolate and characterize bacterial species from the skin microbiome of patients presenting with skin infections at a primary healthcare facility in Northeastern Nigeria. A total of 18 bacterial isolates were recovered, with *Staphylococcus aureus* being the most predominant organism (44.4%), followed by *Escherichia coli* (22.2%), *Klebsiella pneumoniae* (16.7%), *Pseudomonas aeruginosa* (11.1%), and *Streptococcus* spp. (5.6%).

The preponderance of *Staphylococcus aureus* observed in this study corroborates findings from previous investigations, which have consistently identified this organism as the leading bacterial pathogen associated with skin and soft tissue infections globally (Gao *et al.,* 2017; Bessa *et al.,* 2016). As a Gram-positive coccus, *S. aureus* is a well-documented opportunistic pathogen capable of causing a spectrum of cutaneous infections, ranging from superficial conditions such as impetigo and folliculitis to more severe manifestations including furuncles, carbuncles, and cellulitis (Bessa *et al.,* 2016). The organism's pathogenic potential is attributed to its extensive arsenal of virulence factors, including surface proteins that facilitate adhesion to host tissues, enzymes such as coagulase and catalase that enable immune evasion, and toxins that cause tissue destruction (Martin, 2022). Furthermore, the ability of *S. aureus* to colonise intact skin and subsequently invade through breaches in the epithelial barrier renders it a formidable pathogen, particularly in individuals with compromised immune function or underlying dermatological conditions. The high isolation rate of *S. aureus* in our study population underscores the organism's clinical significance and the need for effective preventive and therapeutic strategies in this setting.

The emergence of Gram-negative organisms as significant etiological agents in skin and soft tissue infections represents a notable epidemiological shift, as historically these infections were predominantly attributed to Gram-positive pathogens (Gupta & Batra, 2021). In our study, *Escherichia coli* was the second most frequently isolated organism, accounting for 22.2% of all bacterial isolates. The presence of *E. coli* on the skin surface is often indicative of faecal contamination, poor personal hygiene, or inadequate sanitation practices, as this organism is a commensal of the gastrointestinal tract

(Ofoefule *et al.,* 2019). Its isolation from skin lesions may be associated with wound contamination, surgical site infections, or infections in immunocompromised hosts (Gupta and Batra, 2021). Similarly, *Pseudomonas aeruginosa* and *Klebsiella pneumoniae*, both opportunistic Gram-negative pathogens, were recovered from a proportion of our samples, reflecting the growing role of these organisms in cutaneous infections, particularly in healthcare-associated settings and chronic wounds (Ngoshe *et al.,* 2023). The presence of these organisms in primary healthcare settings is concerning and may reflect a combination of factors including environmental contamination, limited access to clean water, and suboptimal infection prevention practices.

Antimicrobial susceptibility testing revealed that the majority of bacterial isolates demonstrated sensitivity to meropenem, ceftriaxone, and ciprofloxacin, particularly among the Gram-positive isolates including *S. aureus* and *Streptococcus* spp. These findings are consistent with previous reports indicating the continued clinical efficacy of carbapenems and third-generation cephalosporins against skin pathogens in the Nigerian setting (Ezeh *et al.,* 2023). Meropenem, a broad-spectrum carbapenem, exhibited the highest overall efficacy, with resistance rates below 15%, suggesting its potential role as a reserve antibiotic for severe or multidrug-resistant infections. Gentamicin also demonstrated considerable activity against the isolates, with low resistance rates observed. Conversely, ampicillin showed the lowest susceptibility, with over 80% of isolates displaying resistance, a finding that aligns with the well-documented high resistance rates to penicillins among both Gram-positive and Gram-negative organisms in Nigeria (Alabi *et al.,* 2025). The observed resistance to ampicillin, as well as to amoxicillin-clavulanate and tetracycline, may be attributed to the widespread and indiscriminate use of these agents in community settings, often without proper prescription or microbiological guidance (Otorkpa *et al.,* 2025).

Among the Gram-negative isolates, *Klebsiella pneumoniae* exhibited the highest susceptibility to sparfloxacin, ciprofloxacin, and Augmentin, suggesting that fluoroquinolones and amoxicillin-clavulanate may still be effective therapeutic options for infections caused by this organism. However, *E. coli* and *P. aeruginosa* displayed the most extensive resistance profiles, with notable resistance to ampicillin, tetracycline, and amoxicillin-clavulanate. The resistance patterns observed in this study likely reflect the selective pressure exerted by antimicrobial overuse and misuse, which is a pervasive challenge in Nigeria and other resource-limited countries (Nwafia *et al.,* 2024). Factors such as over-the-counter antibiotic availability, incomplete treatment courses, and the use of substandard or counterfeit medications contribute to the escalating resistance crisis (Otorkpa *et al.,* 2025). The lower resistance rates observed for meropenem, gentamicin, and ciprofloxacin suggest that these agents may remain viable treatment options; however, judicious use is imperative to preserve their long-term efficacy. Overall, the bacterial isolates in this study demonstrated greater susceptibility than resistance to the antibiotics tested, indicating that effective therapeutic options remain available. Nevertheless, the resistance patterns identified warrant ongoing surveillance to monitor trends and inform evidence-based antimicrobial stewardship programmes.

Conclusion

This study provides critical baseline data on the bacterial etiology and antimicrobial resistance patterns of skin infections presenting to a primary healthcare facility in Northeastern Nigeria, addressing a significant gap in the literature from this underserved region. The findings demonstrate that *Staphylococcus aureus* remains the predominant pathogen associated with skin infections in this setting, accounting for 44.4% of all isolates, consistent with global and regional epidemiological patterns. However, the substantial isolation of Gram-negative organisms, particularly *Escherichia coli* (22.2%), *Klebsiella pneumoniae* (16.7%), and *Pseudomonas aeruginosa* (11.1%), signals an important epidemiological shift that has significant implications for empirical treatment decisions in primary care. The presence of these enteric organisms on the skin surface likely reflects underlying challenges related to hygiene, sanitation, and healthcare access that are particularly pronounced in conflict-affected settings such as Northeastern Nigeria. These findings underscore the necessity for healthcare providers to maintain a high index of suspicion for Gram-negative pathogens when managing skin infections, especially in patients with chronic wounds, underlying comorbidities, or exposure to healthcare environments.

The antimicrobial susceptibility patterns observed in this study carry important therapeutic and policy implications for primary healthcare delivery in the region. Meropenem, gentamicin, and ciprofloxacin demonstrated the highest efficacy against the bacterial isolates, while ampicillin exhibited alarmingly high resistance rates exceeding 80%, rendering it ineffective for empirical therapy. The susceptibility of *Streptococcus* spp. and *K. pneumoniae* to multiple antibiotics, juxtaposed with the extensive resistance profiles of *S. aureus*, *E. coli*, and *P. aeruginosa*, highlights the need for species-specific treatment approaches guided by local resistance data. The lower resistance rates observed for meropenem and gentamicin suggest that these agents may remain valuable options for severe or recalcitrant infections; however, their use must be judiciously reserved to preserve their long-term efficacy and prevent the emergence of further resistance. Given the constraints of primary healthcare settings, including limited laboratory capacity and restricted formularies, the findings support the empirical use of ciprofloxacin or ceftriaxone as first-line agents for skin infections in this context, with gentamicin as a second-line option for more severe cases. Nevertheless, the resistance patterns identified in this study warrant ongoing surveillance and the establishment of robust antimicrobial stewardship programmes at the primary

healthcare level. Future research should employ molecular typing techniques to characterize resistance determinants, expand sample sizes across multiple primary healthcare facilities, and include longitudinal surveillance to track emerging resistance trends. Ultimately, this study contributes essential evidence to inform context-appropriate treatment algorithms, strengthen infection prevention and control measures, and improve patient outcomes in Northeastern Nigeria's primary healthcare system.

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