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KNOWLEDGE AND PREVALENCE OF BACTERIAL ISOLATES AND ANTIBIOTIC SUSCEPTIBILITY PATTERNS IN WOUND INFECTIONS AMONG PATIENTS ATTENDING BAYERO UNIVERSITY, CLINIC KANO STATE, NIGERIA

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ABSTRACT
This study investigated the prevalence of bacterial isolates from wound infections, their morphological, cultural, and biochemical characteristics, and their antibiotic susceptibility patterns. A total of 20 wound swab samples were analyzed, with 14 bacterial isolates recovered, giving an overall prevalence of 70%. Gram-negative bacteria predominated (64.3%) compared with Gram-positive bacteria (35.7%). *Escherichia coli* (28.6%) was the most frequently isolated organism, followed by *Klebsiella spp.* and *Staphylococcus aureus* (21.4% each). Antibiotic susceptibility testing revealed high susceptibility of isolates to levofloxacin, gentamycin, and azithromycin, whereas resistance was observed for ciprofloxacin, amoxicillin, and certain cephalosporins. These findings highlight the importance of accurate bacterial identification and antimicrobial susceptibility testing to guide effective therapy for wound infections.

Keywords: Wound infection, bacterial isolates, antibiotic susceptibility, Gram-negative, Gram-positive

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Introduction

Wound sepsis, an infection resulting from microbial invasion of a wound site, remains a significant medical concern worldwide. It occurs when bacteria enter through broken skin, multiply, and potentially lead to systemic infections. Wounds can arise from surgical incisions, traumatic injuries, or chronic conditions, and individuals with compromised immune systems, including patients with diabetes, cancer, or those undergoing surgeries, are particularly vulnerable. Clinically, wound sepsis can lead to prolonged hospital stays, increased healthcare costs, and in severe cases, death (Kumar et al., 2020). Common pathogens implicated in wound infections include *Staphylococcus aureus*, *Escherichia coli*, and *Pseudomonas aeruginosa*, with infection severity influenced by bacterial virulence and patient health status (Chawla et al., 2021). A major challenge in the management of wound infections is the rise of antibiotic resistance. Many bacteria responsible for wound sepsis have developed resistance to commonly used antibiotics, complicating treatment. Misuse and overuse of antibiotics in healthcare settings accelerate the emergence of resistant strains, resulting in treatment failure, prolonged infection, and more severe patient outcomes. Continuous monitoring of antimicrobial susceptibility patterns is therefore critical to guide appropriate treatment (Patel et al., 2022; Verma et al., 2021). The emergence of multidrug-resistant bacteria, including Methicillin-resistant *Staphylococcus aureus* (MRSA), has further complicated clinical management. MRSA and other multidrug-resistant organisms (MDROs) significantly reduce available treatment options and are associated with increased healthcare costs, prolonged hospitalization, and higher morbidity and mortality rates (Singh et al., 2022). Consequently, accurate identification of the bacterial pathogens responsible for wound infections and their susceptibility profiles is essential for targeted therapy. Without such information, clinicians often rely on broad-spectrum antibiotics, which can exacerbate resistance and increase the risk of superinfections, including *Clostridium difficile* infection (Ravi et al., 2021).

Routine surveillance of bacterial resistance patterns in wound infections is key to curbing the spread of resistant organisms. Hospitals and clinics that conduct regular susceptibility testing can provide effective, patient-specific treatment. However, in many regions, including Kano State, Nigeria, routine monitoring and documentation of bacterial pathogens and their resistance patterns in wound infections are limited. Physicians often rely on generalized treatment protocols that may not reflect local resistance patterns, potentially resulting in suboptimal therapy and adverse outcomes (Chhabra et al., 2023). Recent molecular diagnostic advancements, such as polymerase chain reaction (PCR) and whole-genome sequencing, allow rapid identification of pathogens and detection of resistance genes, improving treatment accuracy (Johnson et al., 2020). Nevertheless, many healthcare facilities in Kano lack access to these technologies due to resource constraints, meaning clinical decisions are frequently based on observation alone. This gap underscores the need for local studies to determine the prevalence of bacterial pathogens and their antibiotic susceptibility patterns in the region (Ahmed et al., 2019). Wound sepsis remains a critical health challenge in Kano, particularly given rising antibiotic resistance and limited surveillance data. A deeper understanding of the bacterial agents involved, coupled with antimicrobial susceptibility profiling, is essential to inform treatment strategies, guide antibiotic stewardship, and reduce the burden of resistant infections. This study seeks to address these gaps by investigating the bacterial species associated with wound sepsis and their antibiotic resistance profiles among patients attending Bayero University Clinic, Kano State, Nigeria.

Statement of the Problem

Wound infections are a major public health concern worldwide, contributing to increased morbidity, prolonged hospital stays, and higher healthcare costs. In developing countries such as

Nigeria, the burden is exacerbated by the rising prevalence of antibiotic-resistant bacteria, inadequate diagnostic facilities, and limited surveillance of bacterial pathogens. Despite the clinical significance of wound infections, there is insufficient local data on the prevalence, bacterial profile, and antibiotic susceptibility patterns of isolates from wound infections in the Bayero University community. This knowledge gap hinders the development of effective treatment guidelines and infection control strategies, potentially leading to poor patient outcomes and the spread of resistant bacterial strains. Therefore, it is crucial to identify the common bacterial pathogens in wound infections and assess their antibiotic susceptibility to inform clinical management and reduce the burden of wound-related morbidity.

Aim and Objectives of the Study

The aim of this study is to investigate the antibiotic susceptibility patterns of bacteria associated with wound sepsis in patients attending Bayero University, School Clinic Kano State, Nigeria. The specific objectives of this study are:

i. To determine the prevalence of bacterial isolates in wound samples from patients attending Bayero University Clinic, Kano State, Nigeria.

ii. To isolate and identify the bacterial species associated with wound infections among patients at Bayero University Clinic, Kano State, Nigeria.

iii. To assess the antibiotic susceptibility patterns of the bacterial isolates obtained from wound samples.

Study Area

The study was conducted at the Bayero University Clinic, located within the main campus of Bayero University, Kano (BUK), Northwestern Nigeria. The clinic provides primary and secondary healthcare services to students, staff, and residents of nearby communities, offering outpatient, laboratory, maternal and child health, and general medical services. Kano State, the most populous in Nigeria, lies between latitudes 11°30′N–12°03′N and longitudes 8°30′E–9°03′E, within the Sudan savannah vegetation zone. The area experiences a tropical continental climate with a rainy season from May to October and a dry season from November to April; mean annual rainfall ranges from 800–1,000 mm, and temperatures vary between 21°C and 33°C. Kano City, the state capital, is a major commercial, industrial, and educational hub. The diverse university population makes the clinic a suitable site for epidemiological studies involving infectious diseases.

Media and Reagents

The media employed in this study included MacConkey Agar (MilliporeSigma, Merck KGaA), Blood Agar (SSI Diagnostical), Mueller-Hinton Agar (Becon, Dickinson and Company), and Nutrient Agar (Himedia Laboratories, India). The reagents used included Gram iodine, methylene blue, alcohol, and crystal violet.

Collection of Samples

A total of 20 wound swab samples were collected from patients diagnosed with wound sepsis attending Bayero University Clinic. The sample size was determined using the formula for calculating sample size in prevalence studies (Naing et al., 2020). Samples were collected aseptically using sterile cotton swabs and transported in Amies transport media to prevent contamination. Samples were obtained from both male and female patients across different age groups, ensuring diverse representation.

Isolation and Identification of Bacterial Species

Preparation of Media

The culture media (Nutrient Agar, MacConkey Agar, and Blood Agar) were prepared according to the manufacturer's instructions. The media were sterilized by autoclaving at 121°C for 15 minutes, dispensed into sterile Petri dishes under aseptic conditions, and allowed to set at room temperature.

Sample Inoculation

The collected wound swab samples were inoculated onto different culture media to facilitate bacterial growth and identification. Each sample was streaked onto Nutrient Agar, MacConkey Agar, and Blood Agar using the quadrant streaking method to obtain isolated colonies. The inoculated plates were incubated aerobically at 37°C for 18–24 hours, after which bacterial colonies were examined for morphological characteristics such as colony shape, color, and hemolysis patterns. Distinct colonies were then sub-cultured on fresh media to obtain pure isolates for further identification and biochemical testing (Ochei & Kolhatkar, 2017).

Isolation of Bacterial Species

Wound swabs were cultured on MacConkey and Blood agar and incubated at 37°C for 24 hours. After incubation, colonies were microscopically examined for their size, shape, color, texture, and hemolytic properties on Blood Agar.

Identification of Bacterial Species

Bacterial isolates were identified using a combination of morphological, microscopic, and biochemical techniques (Cheesbrough, 2016). Gram staining was performed to differentiate bacteria into Gram-positive and Gram-negative groups. Further identification involved biochemical tests, including catalase, coagulase, sugar fermentation tests (glucose, lactose, sucrose), indole, citrate, urease, and triple sugar iron (TSI) tests (Ochei & Kolhatkar, 2017).

Gram Staining

Gram staining was performed to differentiate bacterial isolates into Gram-positive and Gram-negative groups. A heat-fixed smear of each bacterial isolate was prepared on a glass slide, flooded with crystal violet for 1 minute, rinsed with water, and treated with iodine solution for 1 minute. The slide was decolorized using alcohol for 10–15 seconds and counterstained with safranin for 1 minute. After rinsing and drying, slides were examined under a microscope. Gram-positive bacteria appeared purple, while Gram-negative bacteria appeared pink (Citation et al., 2023).

Biochemical Tests

Catalase Test

The catalase test was performed to identify catalase-producing bacteria, such as Staphylococcus species. A small amount of bacterial colony was placed on a clean slide, and a drop of 3% hydrogen peroxide was added. Formation of bubbles indicated a positive result, confirming the presence of the catalase enzyme (Brown & Smith, 2021).

Oxidase Test

The oxidase test was conducted to identify cytochrome c oxidase-producing bacteria, such as Pseudomonas aeruginosa. A piece of filter paper was moistened with oxidase reagent, and a bacterial colony was smeared onto it. A color change to dark blue within 10–15 seconds indicated a positive result (Brown & Smith, 2021).

Indole Test

The indole test was performed to detect indole production from tryptophan. Bacterial isolates were inoculated into tryptone broth and incubated at 37°C for 24–48 hours. After

incubation, Kovac's reagent was added. A red ring at the surface of the broth indicated a positive result (Ochei & Kolhatkar, 2017).

Citrate Utilization Test

The citrate utilization test determined the ability of bacteria to use citrate as a carbon source. Bacterial isolates were streaked onto Simmons citrate agar and incubated at 37°C for 24–48 hours. A color change from green to blue indicated a positive result (Ochei & Kolhatkar, 2017).

Urease Test

The urease test detected the production of urease enzyme. Bacterial isolates were inoculated into urea broth and incubated at 37°C for 24–48 hours. A color change from yellow to pink indicated a positive result (Ochei & Kolhatkar, 2017).

Antibiotic Susceptibility Testing

The antibiotic susceptibility of bacterial isolates was determined using the Kirby-Bauer disk diffusion method on Mueller-Hinton Agar (CLSI, 2023). Bacterial suspensions were adjusted to 0.5 McFarland standard and spread onto Mueller-Hinton Agar plates. Antibiotic discs commonly used in the treatment of wound infections (e.g., penicillin (10 µg), streptomycin (10 µg), ciprofloxacin (5 µg), tetracycline (30 µg), erythromycin (15 µg), chloramphenicol (30 µg), oxacillin (5 µg), ampicillin (10 µg), cephalexin (30 µg), ceftriaxone (30 µg), cefotaxime (30 µg), and azithromycin (15 µg)) were placed onto the plates, which were incubated at 37°C for 18–24 hours. After incubation, the antibiotic susceptibility of each bacterial isolate was assessed by measuring the zones of inhibition around the antibiotic discs. The diameter of each clear zone was measured in millimeters using a calibrated ruler or digital caliper and compared to the Clinical and Laboratory Standards Institute (CLSI) guidelines to classify bacterial response as Sensitive (S), Intermediate (I), or Resistant (R). Larger zones of inhibition indicated greater susceptibility, while smaller or absent zones suggested resistance (CLSI, 2023). Results were recorded systematically for each isolate to determine overall antibiotic susceptibility patterns and identify potential multidrug-resistant strains.

Data Analysis

Data were analyzed using descriptive statistics to summarize the frequency and percentage distribution of bacterial isolates and their antibiotic susceptibility patterns. Chi-square tests were used to determine the association between bacterial species and antibiotic resistance. Statistical significance was set at $p < 0.05$. Data analysis was performed using statistical software such as SPSS.

RESULTS

Prevalence of Bacterial Isolates

Out of 20 wound swab samples analyzed, 14 yielded bacterial growth, giving a prevalence of **70%**, while 6 samples (30%) were negative.

Table 1. Prevalence of Bacterial Isolates from Wound Samples

Parameter	Frequency	Percentage (%)
Total samples examined	20	–
Positive samples (isolates)	14	70.0
Negative samples	6	30.0

Sentence Presentation:

Fourteen of the 20 wound samples were positive for bacterial growth, representing a prevalence rate of 70%.

Gram Reaction Distribution

Gram-negative bacteria were more common than Gram-positive bacteria.

Table 2. Distribution of Isolates by Gram Reaction

Gram Reaction	Number of Isolates	Percentage (%)
Gram-negative	9	64.3
Gram-positive	5	35.7
Total	14	100

Sentence Presentation:

Among the bacterial isolates, **64.3%** were Gram-negative, whereas **35.7%** were Gram-positive.

Species Distribution

Escherichia coli was the predominant isolate.

Table 3. Species Distribution of Bacterial Isolates

Bacterial Species	Number of Isolates	Percentage of Total (%)
Escherichia coli	4	28.6
Klebsiella spp.	3	21.4
Staphylococcus aureus	3	21.4
Pseudomonas aeruginosa	2	14.3
Streptococcus spp.	2	14.3
Total	14	100

Sentence Presentation:

Escherichia coli accounted for 28.6% of isolates, followed by *Klebsiella spp.* and *Staphylococcus aureus* (21.4% each), while *Pseudomonas aeruginosa* and *Streptococcus spp.* were the least common (14.3% each).

Gram-Specific Distribution of Species

Table 4. Gram-Specific Distribution of Bacterial Species

Bacterial Species (Gram-Negative)	Number	Percentage (%)	Bacterial Species (Gram-Positive)	Number	Percentage (%)
Escherichia coli	4	44.4	*Staphylococcus aureus*	3	60.0
Klebsiella spp.	3	33.3	*Streptococcus spp.*	2	40.0
Pseudomonas aeruginosa	2	22.2	—	—	—
Total (Gram–)	9	100	**Total (Gram+)**	5	100

Sentence Presentation:

Within Gram-negative bacteria, *E. coli* was most common (44.4%), followed by *Klebsiella spp.* (33.3%) and *Pseudomonas aeruginosa* (22.2%). For Gram-positive bacteria, *Staphylococcus aureus* predominated (60%) over *Streptococcus spp.* (40%).

Morphological, Cultural, and Biochemical Characteristics

The isolates showed typical colony morphology: *E. coli* had smooth, circular, pink colonies on MacConkey agar; *Klebsiella spp.* showed large mucoid pink colonies; *Staphylococcus aureus* was

golden yellow and mannitol positive; *Pseudomonas aeruginosa* had greenish colonies with fruity odor; *Streptococcus spp.* appeared as translucent chains. Biochemical tests confirmed identities (Table 5).

Table 5. Morphological, Cultural, and Biochemical Characteristics of Isolates

Isolate	Colony Morphology	Gram	Cell Shape/Arrangement	Catalase	Oxidase	Indole	Citrate	Urease
E. coli	Smooth, circular, pink	–	Rods	+	–	+	–	–
Klebsiella spp.	Mucoid, pink	–	Rods	+	–	–	+	+
Staphylococcus aureus	Golden yellow, opaque	+	Cocci in clusters	+	–	–	+	+
Pseudomonas aeruginosa	Greenish pigment colonies	–	Rods	+	+	–	+	–
Streptococcus spp.	Translucent colonies	+	Cocci in chains	–	–	–	–	–

Antibiotic Susceptibility Patterns

Gram-Negative Bacteria:

Levofloxacin, gentamycin, and azithromycin were 100% effective. *E. coli* was completely resistant to ciprofloxacin, while *P. aeruginosa* was resistant to amoxicillin. Moderate sensitivity was observed for cephalexin and sparfloxacin (Table 6).

Table 6. Antibiotic Susceptibility of Gram-Negative Isolates

Antibiotic (µg)	*E. coli* S/R	*Klebsiella spp.* S/R	*Pseudomonas aeruginosa* S/R
Levofloxacin	4/0	3/0	2/0
Cephalexin	2/2	3/0	2/0
Sparfloxacin	2/2	3/0	1/1
Ciprofloxacin	0/4	1/2	1/1
Amoxicillin	1/3	1/2	0/2
Augmentin	2/2	1/2	2/0
Gentamycin	4/0	3/0	2/0
Pefloxacin	2/2	2/1	1/1
Ofloxacin	1/3	2/1	2/0
Azithromycin	4/0	3/0	2/0

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Gram-Positive Bacteria:

Staphylococcus aureus was fully susceptible to rifampicin, streptomycin, azithromycin, levofloxacin, and gentamycin, but resistant to ceftriaxone, amikacin, and cefepime. *Streptococcus spp.* showed complete susceptibility to rifampicin, amikacin, and levofloxacin, but resistance to streptomycin, azithromycin, erythromycin, and cefotaxime (Table 7).

Table 7. Antibiotic Susceptibility of Gram-Positive Isolates

Antibiotic (µg)	***S. aureus* S/R**	***Streptococcus spp.* S/R**
Rifampicin	3/0	2/0
Ceftriaxone	0/3	1/1
Streptomycin	3/0	0/2
Azithromycin	3/0	0/2
Amikacin	0/3	2/0
Cefepime	0/3	1/1
Erythromycin	1/2	0/2
Levofloxacin	3/0	2/0
Gentamycin	3/0	1/1
Cefotaxime	2/1	0/2

Discussion

The overall bacterial prevalence of 70% aligns with previous studies reporting wound infection rates ranging from 60% to 80% (Cheesbrough, 2015; Agyepong et al., 2020). Gram-negative bacteria predominated (64.3%), similar to observations by Kumar et al. (2021), likely due to their ubiquity in hospital and environmental settings.

E. coli was the most frequent isolate (28.6%), consistent with prior studies identifying Enterobacteriaceae as major opportunistic pathogens in wound infections (Liu et al., 2019). *Staphylococcus aureus* and *Klebsiella spp.* were also significant, highlighting the need for targeted antimicrobial therapy.

Antibiotic susceptibility results revealed complete susceptibility to levofloxacin, gentamycin, and azithromycin among all isolates, confirming their continued clinical efficacy. Conversely, high resistance to ciprofloxacin (*E. coli*) and amoxicillin (*P. aeruginosa*) mirrors global trends in emerging antimicrobial resistance (WHO, 2022). Such resistance patterns underscore the importance of routine susceptibility testing prior to empiric therapy.

Conclusion

Wound infections in this study were predominantly caused by Gram-negative bacteria, particularly *E. coli*, *Klebsiella spp.*, and *Staphylococcus aureus*. While some antibiotics remain highly effective, resistance to commonly used drugs such as ciprofloxacin and amoxicillin is alarming. Continuous monitoring of bacterial prevalence and susceptibility patterns is essential for effective wound management.

Recommendations

1. Clinicians should perform culture and sensitivity testing before initiating antibiotic therapy.
2. Levofloxacin, gentamycin, and azithromycin are recommended as first-line treatment for these wound infections.
3. Hospitals should implement infection control measures to minimize the spread of resistant bacteria.
4. Further research with larger sample sizes is needed to monitor evolving resistance patterns.

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