The Bioscientist Journal Vol. 14 (1): 95 – 109, March 2026
Journal of the Faculty of Biosciences, Nnamdi Azikiwe University, Awka, Nigeria
Available online at http://www.bioscientistjournal.com
DOI 10.54117/the_bioscientist.v14i1.207



OPEN ACCESS

Full Length Research Article

Antibiotics Resistant Patterns of Bacteria from Patients with Wounds in a Tertiary Hospital, Southeast Nigeria.

*[1]Ekwealor, C. C., [1]Onyekachi C. R., [1]Anaukwu C. G., [1]Umunna V. C., [1]Anakwenze V. N, and [1]Anyaoha V. I.

[1]Department of Applied Microbiology & Brewing, Nnamdi Azikiwe University, Awka, Anambra State, Nigeria.

*Corresponding author: c.ekwealor@unizik.edu.ng

***Article History**: Received: 28th January, 2026 Accepted: 24th March, 2026*

ABSTRACT

Antibiotics resistant organisms involved in wound infection play an important role in delaying wound healing. This study aimed to determine antibiotics resistant patterns of bacteria from patients with wound infections in Alex Ekwueme University Teaching Hospital, Abakiliki. One hundred and two wound swabs collected from 95 patients between December, 2024 and February, 2025 were cultured on MacConkey agar, Blood agar, Nutrient agar and Mannitol salt Agar and isolates identified. Demographic data were obtained using structured questionnaires. Susceptibility of isolates to antibiotics was determined by Kirby Bauer disc diffusion method. Seventy six (74.51%) of the wound swabs yielded positive growth with 93 bacteria isolates: 30 (32.3%) *Klebsiella* spp., 10 (10.7%) *Pseudomonas aeruginosa,* 10 (10.7%) *Proteus mirabilis,* 5 (5.4%) *Escherichia coli,* 36 (38.7%) *Staphylococcus aureus* and 2 (2.2%) *Streptococcus* spp ($p < 0.05$). Fifty nine (77.63%) specimens recorded single microbial infections while seventeen (22.37%) had poly-microbial infections constituted with two species ($p < 0.05$). Infection was more prevalent among 31-40 years age group (74.2%), males (68.4%), widows (100%) and the retired (70%). No significant association was recorded with any of the variables. High resistance by all the gram-negative organisms was observed with Erythromycin (60 – 93.3%), Cefixime (60 – 90%), Gentamycin (50 – 93.3%) and Imipenem (50 – 60%); and by all the gram-positive organisms with Gentamycin (50 – 63.9%), Cefixime (50 – 83.3%), Cefotaxime (50 – 77.8%) and Levofloxacin (50%). This study shows the need for urgent targeted antimicrobial resistant intervention in Southeast, Nigeria.

Keywords: Antibiotics, resistance, wounds, susceptibility test.

Introduction

Antibiotics resistance bacteria are those bacteria that have the ability to resist antibiotics used to efficiently treat them. This resistance makes it very difficult to eradicate infections caused by them, as most drugs become less effective (Colson *et al*., 2021). Antibiotic resistance is already ranked a global concern to medical practice and public health systems (WHO, 2025); and it was recorded that one in six bacterial infections globally were antibiotic resistant in 2023. According to Wise (2025), antibiotic resistance rose by over 40% from 2018 – 2023, with low and middle income countries where healthcare system is poor being most affected. Antibiotics resistant microorganisms may survive for long periods of time, multiply in the presence of minimal nutrients and have the capability of colonizing injured skin. Antibiotic resistance occurs among bacterial species due to the attainment of plasmids through the transfer of resistance genes (Breijyeh *et al*., 2020), development of special mechanisms like efflux pumps, less permeability of the lipopolysaccharide layer, secretion of degrading enzymes, and alteration of targets (Cox and Wright, 2013). However, random and broad use of antibiotics, self-medication, poor training and prescribing skills, lack of antibiotic use regulations, prolonged hospitalization, inadequate surveillance and poor hygiene have been associated to the rapid emergence of antibiotic resistant bacteria in Africa (Diop *et al*., 2025).

Wound infections often emerge as a result of break in /or injured skin surface either by trauma or accident followed by invasion of bacterial pathogens into the skin gap either from other body sites or environmental sources, with the potential of involving other tissues (Tom *et al*., 2019).

Wound supplies conducive environment for bacteria invasion. Once settled, these pathogens survive and multiply within the necrotic and devitalized tissues of the wound, exacerbating and disseminating the infection (Kadam and Shahane, 2019). It has been established that infected wounds have long-term inflammation, bacterial load and unbalanced cellular defense mechanism (Zhao and Zhao, 2020). The common bacterial pathogens associated with wound infection include *Proteus* spp., *Escherichia coli, Mycobacterium tuberculosis, Pseudomonas aeruginosa, Klebsiella pneumonia, Staphylococcus aureus*, *Streptococcus pyogenes, Enterococcus* spp. and *Bacillus cereus* (Wang *et al*., 2024; Hussein *et al*., 2025).

The conventional approaches for combating bacterial infections in wound are primarily based on antibiotics use (Hassan *et al*., 2022). Antibiotics like Gentamycin, Levofloxacin, Ciprofloxacin, Erythromycin and Azithromycin are considered as first line drugs for the treatment of wound infections (Isomah *et al.,* 2023). Unfortunately, many bacteria from wound infections have been implicated in resistance to these antibiotics due to extensive, uncontrolled and empirical use of broad spectrum antibiotics by clinicians (Hassan *et al*., 2022). Studies conducted in many developing nations, including Nigeria, have shown that the presence of antimicrobial resistant bacteria can complicate and reduce the effectiveness of treatments for common wound infections (Wang *et al*., 2024; Onsando *et al*., 2025) thereby, leading to treatment failure, prolonged hospitalization, patients' debility, increased treatment cost and mortality (Ilyas *et al*., 2024). There is therefore, need to determine the bacterial pathogens

associated with wounds and the antibiotic susceptibility profile before treatment, in order to ascertain the extent of bacteria resistance to antibiotics, which will guide effective therapeutic plan for combating proliferation of antibiotic resistant bacteria. This research is aimed to determine the antibiotic resistant patterns of bacteria from patients with wounds in a tertiary hospital in southeastern, Nigeria.

Methods

Study Area:

The study was conducted in Alex Ekwueme University Teaching Hospital, Abakiliki (AEFUTHA). AEFUTHA is a public tertiary health institution that provides multi-specialist services in different areas of medicine. It is located along FMC Road in Abakiliki, the capital of Ebonyi state, situated at 6.32^{o} North latitude, 8.12^{o} East longitude and 117 meters elevation above the sea level. The population of the metro area was estimated to be 662,000 in the year 2023. It has an area of 532.2 Km^2 and is the center of the densely populated Igbo heartland in South East, Nigeria. Abakiliki has a humid tropical climate with the environment characterized by high, consistent temperatures (26^{o}C – 30^{o}C), high relative humidity (45% - 65%) during the long wet season and significant environmental pollution which enhances the proliferation of bacteria (Njoku *et al*., 2015).

Study design

The design was a cross-sectional study, carried out among patients with wound, attending Alex Ekwueme University Teaching Hospital, Abakiliki, Southeast Nigeria, between December, 2024 to February, 2025. In the study, wound swabs were collected and bacteria isolated from them. Antibiotics susceptibility test was then conducted with the bacteria isolates and the antibiotics resistance pattern determined from the results.

Study Population:

This study targeted patients with wounds attending Alex Ekwueme University Teaching Hospital, Abakiliki. Specifically the patients sampled were those with diabetic foot ulcers, surgical wounds, burns, sharp cuts, traumatic wounds and cancer wounds. Both inpatients and outpatients were considered.

Sample Size Determination

The minimum sample size for the study was determined using the Cochran (1977) formula:

$$\frac{n=Z^2 \rho (1 - p)}{e^2}$$

where, n= Sample size, Z = Z-value, ρ = population size, e = margin of error, with 95% confidence interval (i.e. $Z_{0.95}$=1.96), 31% proportion (Althubaiti, 2022). This was calculated to give a total of 102 participants who were selected using systematic random sampling.

Inclusion and Exclusion Criteria

All patients with wounds undertaking antibiotics for treatment who gave verbal consent to participate in the study were included. Patients without wounds, patients who have not started using antibiotics for treatment or those who declined consent were excluded.

Ethical Approval and Consent

Ethical approval with reference number NHREC/16/05/22/313 was obtained from Alex Ekwueme University Teaching Hospital Research and Ethical Committee (REC). Verbal consent to participate in the study was obtained from each patient selected.

Demographic Data Collection

Structured questionnaire was administered to the study participants to obtain

information on their age, gender, marital status and employment status.

Wound Swab Collection

One hundred and two (102) wound samples were collected from different sites of the 95 participants' body. The edges of the wounds were cleaned using sterile cotton wool soaked with sterile normal saline and the surface exudates removed. The wound was thereafter cleaned again with sterile normal saline solution and the area gently dabbed with sterile gauze to dry the surface (Shimekaw *et al*., 2022). Samples were aseptically obtained from the wounds by rotating a sterile cotton swab under adequate pressure without touching the nearby skin. They were properly labeled and transported to Alex Ekwueme Teaching Hospital Laboratory in an ice pack and processed within 2 hours of collection.

Culture of the Wound Swab Specimens for Bacteria Isolation

The swab samples were streaked onto the surface of sterile plates of Nutrient agar, Mannitol salt agar (MSA), Blood agar (BA) and MacConkey agar and the plates incubated for 24 hours at 37^{o}C. Distinct colonies were sub-cultured and pure isolates stored on Nutrient agar slants at 4^{o}C for further use (Cheesbrough, 2016).

Identification of Bacteria Isolates

Isolates were identified based on colony morphology, Gram's reaction, biochemical reactions and sugar fermentation test results, following the standards of Cheesbrough (2016).

Antibiotic Susceptibility Test

Antibiotic susceptibility testing of the isolates was determined using the Kirby Bauer disc diffusion method, and the results interpreted in line with the National Committee for Clinical Laboratory Standards guidelines (2015). Twenty-four-hour bacterial isolate suspension was standardized to 0.5 McFarlan turbidity and a loopful of the suspension was uniformly streaked on sterile Mueller Hinton Agar plates and allowed to stand for 3 minutes to dry. Commercially available antibiotic discs (BioTek, India) impregnated with Ampicillin (30µg), Ceporex (10µg), Gentamicin (10µg), Ciprofloxacin (10µg), Augmentin (30µg), Pefloxacin (10µg), Ofloxacin (10µg), Nalidixic acid (30µg), Septrin (30µg) and streptomycin (30µg) for Gram-negative bacteria and Norfloxacin (10µg), Gentamicin (10µg), Erythromycin (30µg), Ciprofloxacin (10µg), Amoxicillin (20µg), Ampiclox (20µg), Streptomycin (30µg), Levofloxacin .(20µg), Rifampicin (20µg) and Chloramphenicol (30µg) for Gram-positive bacteria were aseptically placed on the inoculated plates using a sterile forceps. These antibiotics belong to different classes of antibiotics; Penicillin, Cephalosporin, Aminoglycosides, Flouroquinolone, Macrolide, Suphonamide, Rifamycin and Amphenicol. The plates were incubated at 37^{o}C for 24 hours. The zone of inhibition was measured in millimeter and compared with the established interpretive breakpoints according to the guideline by CLSI (2015) and categorized as susceptible (S), intermediate (I) or resistant (R). The level of resistance (antibiotic resistance rate) were thereafter recorded as: >50% = high resistant, 20% – 50% = moderate resistant and <20% = low resistance (CLSI, 2015).

Data analysis

The data obtained from the study were statistically analyzed using IBM-SPSS (ver. 25.0; IBM Corp., Amonk, NY USA). The chi square test was employed to determine the association between the variables. Results were considered statistically significance at $p < 0.05$, with 95% confidence interval (Cl) used to describe the precision.

Results

Out of 102 wound samples collected for the study as presented in Table 1, 12 (11.8%) were from diabetic ulcers, 54(52.9%) post-surgical wounds, 18(17.6 %) burns, 7(6.9%) sharp cuts, 9(8.8 %) traumatic wound and 2(2.0 %) from cancer wounds.

Based on the colony morphology, microscopy, biochemical characteristics and sugar fermentation tests results presented in Table 2, a total of 93 isolates comprising of four Gram negative bacteria: 30 (32.3%) *Klebsiella* spp*.,* 10 (10.7%) *Pseudomonas aeruginosa,* 10 (10.7%) *Proteus mirabilis,* 5 (5.4%) *Escherichia coli*, and two Gram positive bacteria: 36 (38.7%) *Staphylococcus aureus* and 2 (2.2%) *Streptococcus pyogenes* were isolated. There were significant differences in the number of isolates of the bacteria species identified ($p < .0001$), with *Klebsiella* spp. (32.3%) as the most prevalent Gram negative bacteria, and *Staphylococcus aureus* (38.7%) was the most prevalent Gram positive bacteria.

As presented in Table 3, 59 (63.44%) of the isolates were from mono-bacterial infections while 34 (36.56%) were from 17 poly-bacterial infections. The difference in frequency of occurrence of mono- and poly bacterial infections is statistically significant ($p < .0001$). As shown in Table 3, *Staphylococcus aureus* and *Klebsiella* spp. were mainly observed in mono-bacterial infection while a combination of *Staphylococcus aureus* and *Klebsiella* spp. were the major isolates in poly-microbial infections.

Table 4 shows the prevalence of bacterial infections distributed according to the socio-demographic data. Bacterial infection was more prevalent among 31-40 year age group (74.2%), males (68.4%), widows (100%) and the retired (70%), with no significant association between each variables and occurrence of bacterial infection in wounds.

Table 1: Types of wound samples obtained

Types of wounds	Number of samples	Relative frequency (%)
Post-surgical	54	52.9
Burns	18	17.6
Diabetic	12	11.8
Traumatic	9	8.8
Sharp cuts	7	6.9
Cancer	2	2
Total	102	100

Table 2: Morphology/microscopy, biochemical characteristics and sugar fermentation of isolates

Macroscopic features	Gram stain reaction	Biochemical Tests									Fermentation Tests						Probable Organism (% occurrence)
		Cat	Ox	Cit	Co	Ur	Mot	Ind	MR	VP	Glu	Mal	Suc	Gal	Fru	Lac	
Deep golden yellow smooth, raised glistening colonies	+ve cocci	+	-	+	+	+	-	-	+	+	+	+	+	+	+	+	*Staphylococcus aureus* (38.7%)
Large gray-white mucoid colonies	-ve rods	+	-	+	-	+	-	-	-	+	+	+	+	+	+	+	*Klebsiella* spp. (32.3%)
Large flat and irregular edged circular green colonies	-ve rods	+	+	+	-	-	+	-	-	-	-	-	-	-	-	-	*Pseudomonas aeruginosa* (10.7%)
Fishy odour and bulls-eye colonies	-ve rods	+	-	+	-	+	+	-	+	-	+	-	-	-	-	-	*Proteus mirabilis* (10.7%)
1-4 mm diameter yellow colonies	-ve rods	+	-	-	-	-	+	+	+	-	+	-	-	+	-	+	*Escherichia. coli* (5.4%)
Beta haemolytic colonies	+ve cocci	-	-	-	-	-	-	-	-	-	+	+	+	+	+	+	*Streptococcus pyogenes* (2.2%)

Key: -ve= Negative, +ve = Positive, Cat =catalase, Ox =oxidase, Cit= citrate, Co= coagulase, Ur = urease, Mot = motility, Ind = indole, Mr= methyl –red, Vp= Voges-Proskauer, Glu= glucose, Mal= maltose, Suc-sucrose, Gal= galactose, Fru= fructose, Lac= lactose.

Table 3: Distribution of mono and poly-bacteria isolates from infected wounds

Variable	**Category (Bacterial Isolates)**	**No of occurrence of mono or poly bacterial isolates**	**Relative frequency (%)**
Mono- bacterial isolates	*Staphylococcus aureus*	21	27.63
	Streptococcus pyogenes	2	2.63
	Klebsiella spp.	17	22.37
	Pseudomonas aeruginosa.	8	10.53
	Proteus mirabilis	6	7.89
	Escherichia coli	5	6.58
	Sub-total	59	77.63
Poly-bacterial isolates	*Staphylococcus aureus* + *Klebsiella* spp.	13	17.11
	Proteus mirabilis + *Pseudomonas aeruginosa*	2	2.63
	Proteus mirabilis + *Staphylococcus aureus*	2	2.63
	Sub-total	17	22.37
	Total	76	100

The antimicrobial susceptibility pattern of Gram-negative bacteria isolates is represented in Table 5. From the results obtained, *Klebsiella* spp. was highly resistant (56.7% - 93.3%) to Amoxicillin, Cefixime, Erythromycin, Gentamycin, Cefotaxime, Ceftriaxone, Imipenem, and Ciprofloxacin but moderately resistant (33.3% - 40%) to Levofloxacin, Cefuroxime, Ofloxacin, and Azithromycin. *P. aeruginosa* recorded high (60% – 80%) resistance to all the antibiotics tested, with the exception of Ofloxacin, Gentamycin and Azithromycin. *Proteus mirabilis* exhibited moderate (20% – 50%) resistance to majority of the tested antibiotics except to Cefotaxime, Cefixime, Levofloxacin, Cefuroxime and Erythromycin. However, *E. coli* isolates as shown in Table 5, demonstrated high (60%) resistant to Augmentin, Cefotaxime, Cefixime, Imipenem, Erythromycin, Gentamycin and Ciprofloxacin.

Among Gram-positive bacteria isolates (Table 6), *Staphylococcus aureus* showed high (63.9% - 83.3%) resistance to Amoxicillin, Cefotaxime, Cefixime, Imipenem, Cefuroxime, Erythromycin, and Gentamycin. *Streptococcus* spp. was moderately (50%) resistant to 4 antibiotics: Cefotaxime, Cefixime, Levofloxacin, and Gentamycin.

Table 4: Prevalence of bacterial infections distributed according to demographic data

Variables	Category	No tested	No positive (%)	χ^2	95% CI	$p-value$
Age group (years)	<20	5	2(40)	4.077	0.118-0.769	0.538
	21-30	9	5(55.5)		0.267-0.811	
	31-40	35	26(74.2)		0.579-0.858	
	41-50	23	13(56.5)		0.368-0.746	
	51-60	19	12(63.2)		0.410-0.809	
	>60	11	8(72.7)		0.434-0.903	
Gender	Female	64	40(62.5)	0.242	0.503-0.733	0.623
	Male	38	26(68.4)		0.525-0.809	
Marital status	Widow	4	4(100)	0.077	0.510-100	0.782
	Married	77	50(64.9)		0.538-0.747	
	Single	21	12(57.1)		0.366-0.755	
Employment status	Civil servant	10	6(60)	0.075	0.313-0.832	0.784
	Business	70	47(67.1)		0.555-0.770	
	Unemployed	6	3(50)		0.188-0.812	
	Retired	10	7(70)		0.397-0.892	
	Student	6	3(50)		0.188-0.812	

χ^2 = chi square, 95% CI= 95% Confidence Interval, $p-value$ = level of significance (0.05)

Table 5: Antimicrobial Susceptibility Pattern of Gram-Negative Bacteria Isolates

Bacteria /No of isolates	Sensitivity pattern	Antibiotics (% of bacteria sensitivity, intermediate & resistance)											
		AUG	CTX	CRO	CEM	LBC	IMP	CXM	OFX	ERY	GEN	AZN	CIP
Klebsiella spp (n=30)	S	3(10)	5(16.7)	11(36.7)	2(6.7)	10(33.3)	10(33.3)	4(13.3)	17(56.7)	0(0)	8(26.7)	17(56.7)	7(23.3)
	I	1(3.3)	1(3.3)	2(6.7)	1(3.3)	8(26.7)	3(10)	11(36.7)	3(10)	2(6.7)	3(10)	1(3.3)	3(10.0)
	R	26(86.7)	24(80)	17(56.7)	27(90)	12(40)	17(56.7)	15(50)	10(33.3)	28(93.3)	28(93.3)	12(40)	20(66.7)
Pseudomonas aeruginosa (n=10)	S	0(0)	0(0)	1(10)	0(0)	1(10)	2(20)	0(0)	3(30)	1(10)	3(30)	5(50)	3(30)
	I	2(20)	2(20)	2(20)	2(20)	2(20)	2(20)	2(20)	2(20)	2(20)	2(20)	2(20)	2(20)
	R	8(80)	8(80)	7(70)	8(80)	7(70)	6(60)	8(80)	5(50)	7(70)	5(50)	3(30)	5(50)
Proteus mirabilis (n=10)	S	1(10)	1(10)	4(40)	1(10)	2(20)	3(30)	1(10)	3(30)	1(10)	3(30)	5(50)	4(40)
	I	7(70)	2(20)	2(20)	2(20)	2(20)	2(20)	2(20)	2(20)	2(20)	2(20)	2(20)	2(20)
	R	2(20)	7(70)	4(40)	7(70)	6(60)	5(50)	7(70)	5(50)	7(70)	5(50)	3(30)	4(40)
Escherichia coli (n=5)	S	0(0)	0(0)	1(20)	0(0)	2(40)	0(0)	2(40)	2(40)	0(0)	1(20)	1(20)	1(20)
	I	2(40)	2(40)	2(40)	2(40)	1(20)	2(40)	3(60)	1(20)	2(40)	1(20)	3(60)	1(20)
	R	3(60)	3(60)	2(40)	3(60)	2(40)	3(60)	0(0)	2(40)	3(60)	3(60)	1(20)	3(60)
Total (55)	S	4(7.3)	6(10.9)	18(32.7)	3(5.5)	15(27.3)	15(27.3)	8(14.5)	25(45.5)	2(3.6)	15(27.3)	28(50.9)	15(27.3)
	I	12(21.8)	7(12.7)	7(12.7)	7(12.7)	13(23.6)	9(16.4)	17(30.9)	8(14.5)	8(14.5)	8(14.5)	8(14.5)	6(10.9)
	R	39(70.9)	42(76.4)	30(54.5)	45(81.8)	27(49.1)	31(56.4)	30(54.5)	19(34.5)	45(81.8)	32(58.2)	19(34.5)	32(58.2)

Key: n- number, %- percentage, S- Sensitive (mm), I- Intermediate(mm), R – Resistant (mm) AUG: Amoxicillin (20µg); CTX: Cefotaxime (30µg); CRO: Ceftriaxone (30µg); CEM: Cefixime (30µg): LBC: Levofloxacin (20µg); IMP: Imipenem (30µg); CXM: Cefuroxime (30µg); OFX: Ofloxacin (10µg); ERY: Erythromycin (30µg); GEN: Gentamycin (10µg); AZN: Azithromycin (10µg); CIP: Ciprofloxacin (10µg)

Table 6: Antimicrobial Susceptibility Pattern of Gram-Positive Bacteria Isolates

Bacteria (no of isolates)	Sensitivity pattern	Antibiotics (% of bacteria sensitivity, intermediate & resistance)											
		AUG	CTX	CRO	CEM	LBC	IMP	CXM	OFX	ERY	GEN	AZN	CIP
Staphylococcus aureus (n=36)	S	8(22.2)	7(19.4)	18(50)	5(13.9)	17(47.2)	10(27.8)	7(19.4)	24(66.7)	11(30.6)	12(33.3)	19(52.8)	20(55.6)
	I	1(2.8)	1(2.8)	1(2.8)	1(2.8)	1(2.8)	1(2.8)	1(2.8)	1(2.8)	1(2.8)	1(2.8)	1(2.8)	1(2.8)
	R	27(75)	28(77.8)	17(47.2)	30(83.3)	18(50)	25(69.4)	28(77.8)	11(30.6)	24(66.7)	23(63.9)	16(44.4)	15(41.7)
Streptococcus pyogenes (n=2)	S	1(50)	0(0)	1(50)	0(0)	0(0)	1(50)	1(50)	1(50)	1(50)	0(0)	1(50)	1(50)
	I	1(50)	1(50)	1(50)	1(50)	1(50)	1(50)	1(50)	1(50)	1(50)	1(50)	1(50)	1(50)
	R	0(0)	1(50)	0(0)	1(50)	1(50)	0(0)	0(0)	0(0)	0(0)	1(50)	0(0)	0(0)
Total	S	9(23.7)	7(18.4)	19(50)	5(13.2)	17(44.7)	11(28.9)	8(21.1)	25(65.8)	12(31.6)	12(31.6)	20(52.6)	21(55.3)
	I	2(5.3)	2(5.3)	2(5.3)	2(5.3)	2(5.3)	2(5.3)	2(5.3)	2(5.3)	2(5.3)	2(5.3)	2(5.3)	2(5.3)
	R	27(71.1)	29(76.3)	17(44.7)	31(81.6)	19(50)	25(65.8)	28(73.7)	11(28.9)	24(63.2)	24(63.2)	16(42.1)	15(39.5)

Key: n- number, %- percentage, S- Sensitive (mm), I- Intermediate (mm),R – Resistant (mm) AUG: Amoxicillin (20µg); CTX: Cefotaxime (30µg); CRO: Ceftriaxone (30µg); CEM: Cefixime (30µg): LBC: Levofloxacin (20µg); IMP: Imipenem (30µg); CXM: Cefuroxime (30µg); OFX: Ofloxacin (10µg); ERY: Erythromycin (30µg); GEN: Gentamycin (10µg); AZN : Azithromycin (10µg);CIP: Ciprofloxacin (10µg)

Discussion

Out of the one hundred and two swab specimens collected from patients with different types of wounds at different regions of the body, post-surgical wounds (52.9%) were the most common. This is consistent with the report of Mohammed *et al*. (2017), who in their work obtained more of postoperative (28%) wounds among inpatients and outpatients attending University of Gondar Referral hospital, Ethiopia. The high number of samples from post-operative wound infections may be linked with prolonged patient hospitalization, inadequate preoperative hygiene, delayed healing and increase in the risk of complication (Zabaglo *et al*. 2024).

Klebsiella spp., *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Escherichia coli*, *Staphylococcus aureus* and *Streptococcus pyogenes* isolated in this study corroborate with the reports of other researchers (Wang *et al*., 2024; Hussein *et al*., 2025; Yucens *et al*., 2025), who among other bacteria isolated these organisms from wound infections. These bacteria have also been observed to be predominant among hospitalized patients, and are generally reported as most important hospital-acquired pathogens (Mohammed *et al*., 2017). Other organisms such as *Bacillus cereus* (James *et al*., 2023), *Acinetobacter baumannil, Enterobacter cloacae and Enterococcus faecalis* (Yucens *et al*., 2025), *Citrobacter freundii* (Hussein *et al*., 2025), isolated from patients with wound infection were not obtained in this research and may be ascribed to the site of wound or composition of medium used in isolation.

This study revealed that *Staphylococcus aureus* (38.7%) was the most occurring pathogen in wound infection, which agrees with the findings of many other researchers (Mulu *et al*., 2017; Tom *et al*., 2019; Nobel *et al*., 2022) who reported *Staphylococcus aureus* as the most frequently isolated bacterium in wound infection. The high prevalence of *Staphylococcus aureus* in wound infection has been related to the commensal nature of the bacterium on the skin which gives it easy access into the wound (Nobel *et al*., 2022), but Oladeinde *et al*. (2013) linked it to the fact that *Staphylococcus aureus* produces lethal virulence factors like coagulase, catalase, clumping-factor A and leucocidines which maintain infection and prolong healing in wounds. In this study, *Klebsiella* spp. (32.3%) was the most prevalent Gram negative bacterium and the second most frequently isolated. This observation is in line with the work of Mohammed *et al*. (2017) who reported *Klebsiella spp*. (12.5%) as the second most frequently isolated bacterium from wound infection among outpatients attending a Referral Hospital in Northwest Ethiopia. However, this report differs from that of Hussein *et al*. (2025), Yucens *et al*. (2025) who noted *Escherichia coli* as the most prevalent Gram-negative organism. They also reported *Pseudomonas aeruginosa* as the second most isolated organism. The percentage isolation of *Proteus mirabilis* (10.75%) in this study contradicts the work of Onsando *et al*. (2025). They recorded a low percentage (0.85%) of the organism from Kiss teaching and referral hospital in Kenya. Among the Gram positive organisms, *Streptococcus pyogenes* (2.2%) isolated supports the work of Yucens *et al*. (2025), who recorded a 3.1% *Streptococcus* spp. in their study. The diversity of bacteria in different studies of wound infections could be attributed to the number of participants, types of wounds, method of sampling, environmental factors, accessibility to health care services and individual health care conditions (Oladeinde *et al*., 2013).

The higher frequency of mono-bacterial species (77.63%) than poly-bacterial species in this study, supports the findings of other researchers in different parts of Africa. They reported a higher prevalence of mono-bacterial over poly-bacterial species from infected wounds (Asres, *et al*., 2017, Tom *et al*., 2019). The higher prevalence of mono-bacterial infection obtained in this study could be linked with the higher number of specimens (54) collected from post-surgical wounds. Mono-bacterial infections have been reported to be common with surgical acquired wounds which are predominantly dominated by *Staphylococcus aureus* that are fast in colonizing newly damaged skin (Hassan *et al*., 2022).

Poly-microbial infections obtained had combinations of two species of bacteria; *Staphylococcus aureus* + *Klebsiella* spp (17.11%), as the most prevalent, *Proteus mirabilis* + *Pseudomonas aeruginosa* (2.63%) and *Proteus mirabilis* + *Staphylococcus aureus* (2.63%). The observation of poly-microbial infection with two bacteria genera is in line with the work of Asres, *et al*. (2017), but differs in the species involved. They noted a common association between *Staphylococcus aureus* and *Pseudomonas aeruginosa*. Although *Staphylococcus aureus* was observed as the most frequently isolated bacterium in poly-microbial infection, it however, disagrees with the result of Tom *et al*. (2019) who reported *Escherichia coli* as the most frequently isolated organism in poly-microbial infections. The presence of mono-microbial or poly-microbial communities of bacteria has been relate to complex nature of wound infections that may include the wound state, microbial density, prior treatment of the wound, dermal moisture and nutrient availability (Hassan *et al*., 2022). It has also been reported that the interplay between bacteria in poly-microbial infections leads to bacterial synergy that enhances survival and hinder elimination of infection (Oladeinde *et al*., 2013), thereby, promoting antibiotic resistance.

The sociodemographic data on the prevalence of bacterial infection among the participants showed that infection though statistically not significant, was highest in age range of 31- 40 (74.2%) and least in <20 (40%). Contrary to our findings, Tom *et al*. (2019) reported a higher prevalence of infection amongst age groups 21 - 30 (24.5%). In this study, infection was more in males (68.4%) than in females (62.5%), though not statistically significant; it agrees with the reports of Bessa *et al*. (2013) where higher prevalence of infection was recorded in male participants. Additionally, Mulu *et al*. (2017) also noted that age and sex did not affect the prevalence of bacterial infections in wounds. Though not significant, the widowed population (100%) showed a greater prevalence of bacterial infections than the married (64.9%) and single (57.1%) population which is contrary to the results of Lilian *et al*. (2024) who reported 94.6% prevalence among married population. The most prevalent population of wound infected cases according to employment status was observed in retired population (70%), while the least population was the unemployed (50%) and students (50%). This research recorded no significant association between the variables and bacterial infection in wound.

Out of the twelve different antibiotics used, Amoxicillin, Cefotaxime, Cefixime and Erythromycin were the most highly resisted antimicrobials by Gram-negative isolates. The resistance of *Klebsiella* spp to Amoxicillin (86.7%), Cefotaxime (80%), Cefixime (90%), Erythromycin (93.3%) and Gentamicin (93.3%) observed in this study is similar to the report of Arvind *et al.* (2024), who noted 100% resistance of *Klebsiella* spp. to Cefixime, Cefotaxime and

Ceftazidime. *Pseudomonas aeruginosa* recorded over 70% resistance against the Cephalosporin antibiotics. This observation supports the works of Sharma *et al*. (2024), who also reported a similar effect on the antibiotics studied. While *Proteus mirabilis* recorded 70% resistance to Cephalosporin and Macrolide antibiotics groups, *Escherichia coli* showed 60% resistance to various classes of antibiotics tested. Among the Gram-positive bacteria, *Streptococcus pyogene*s was observed to be more susceptible to the antibiotics tested than the *Staphylococcus aureus*.

All Gram negative and Gram-positive bacteria isolated in this study resisted at least one antibiotic from the different classes of antibiotics tested. This observation is similar to the reports of Asres *et al*. (2017). Elevated rate of antibiotic-resistant bacteria in wound infections has been attributed to the high level of antibiotic abuse among patients (Asres *et al*., 2017). Other factors, such as, empiric treatment, over-prescription of antibiotics, lack of antibiotic use regulations and poor infection control in healthcare settings, have also been correlated with increased rise in antibiotic resistance (Bessa *et al*., 2013; Colson *et al*., 2021).

In conclusion, this study showed high occurrence of bacterial species from wound infection with *Staphylococcus aureus and Klebsiella spp* as the most frequently isolated Gram positive and Gram-negative bacteria respectively. Generally, high and moderate rates of antibiotic resistance were observed except for *Streptococcus pyogenes*. This highlights the urgent need for better infection control in healthcare settings, effective antimicrobial campaign program and targeted interventions in Southeast Nigeria.

Acknowledgement

Authors are grateful to the Management of Alex Ekwueme University Teaching Hospital, Abakiliki for permitting the collection of the samples used for this work.

Conflict of interest

Authors declare no conflict of interest.

Funding

Authors received no funding for the work

References

Althubaiti, A. (2022)**.** Sample size determination: A practical guide for health researchers**.** *Journal of General Family Medicine*, *14;24(2)*:72-78.

Arvind, P., Singh, T. B., Shilpa, K., Pranjal, K. P. and Vikash S. P. (2024). Association of sociodemographic with epidemiological profile of chronic wound patients attending a tertiary care hospital. *Indian Journal of Preventive and Social Medicine*, *55 (3)*: 196-204.

Asres, G., Legese, M. and Woldearegay, G. (2017). Prevalence of multidrug resistant bacteria in postoperative infections at Tikur Anbess specialized hospital, Addis, Ababa, Ethiopia. *Archives of Medicine*, *9(4)*:12

Bessa, L., Fazii, P., Giulio, M. and Cellini, L. (2013). Bacterial isolates from infected wounds and their antibiotic susceptibility pattern: some remarks about wound infection. *International Wound Journal*, *12(1)*:47-52

Breijyeh, Z., Jubeh, B. and Karaman, R. (2020). Resistance of Gram-negative bacteria to current antibacterial

agents and approaches to resolve it. *Molecules*, *16;25(6)*:1340.

Cheesbrough M. (2016). District laboratory practice in tropical countries. Cambridge University Press, UK.

Clinical and Laboratory Standards Institute (CLSI) (2015). Performance Standards for Antimicrobial Susceptibility Testing. Twenty fifth informational supplement, Clinical and Laboratory Standards Institute, Wayne, PA.

Cochran, W. G. (1977). Sampling techniques. 3rd edn. John Wiley & Sons, New York.

Colson, A. R., Morton, A., Årdal, C., Chalkidou, K., Davies, S. C., Garrison L. P., Jit M., Laxminarayan, R., Megiddo, I., Morel, C. and Nonvignon, J. (2021). Antimicrobial resistance: is health technology assessment part of the solution or part of the problem? *Value Health*, *24(12)*:1828–1834.

Cox, G. and Wright, G. D. (2013). Intrinsic antibiotic resistance: mechanisms, origins, challenges and solutions. *International Journal of Medical Microbiology*, *303*:287–292.

Diop, M., Bassoum, O., Ndong, A., Wone, F., Tamouh, A. G., Ndoye, T. Y., Daffe, R. O. *et al*. (2025). Prevalence of multidrug resistant bacteria in healthcare and community settings in West Africa: Systematic review and meta-analysis. *BMC Infectious Disease*, *25*:292

Hassan, M. A., El-Aziz, S. A., Elbadry, H. M, El-Aassar, S. A. and Tamer, T. M. (2022). Prevalence, antimicrobial resistance profile, and characterization of multi-drug-resistant bacteria from various infected wounds in North Egypt. *Saudi Journal of Biological Sciences*, *29(4)*:2978–2988

Hussein, K. S., Abdulmughni, G. T., Othaman, A. M., Al-Shami, H. Z., Al-Haidary, N. M., Assayaghi, R. M and Jahzar, K. H. (2025). Antimicrobial susceptibility patterns of bacteria isolated from wound infections in Al-Bayda Governorate Yamen. *BMC Infectious Diseases*, *25*:868

Ilyas, F., James, A., Khan, S., Haider, S., Ullah, S., Darwish, G., Taqvi S. A. H. R., Ali, R., Younas, Q. and Rheman, A. (2024). Multidrug-resistant pathogens in wound infections: A Systematic Review. *Cureus 16(4)*:e58760

Isomah, C., Ogbonna, S., Robinson, V. and Ogbuleka, N. (2023). Antibiogram of Wound Isolates of Patients Attending University of Port Harcourt Teaching Hospital, Nigeria. *South Asian Journal of Research in Microbiology,17(3)*: 36-43.

James, G. J., Douglas, S. I., Aleruchi, O. and Odu, N. N. (2023). Antibiogram and molecular characterization of bacteria isolated from wound specimens from a teaching hospital in Nigeria. *International Journal of Microbiology and Applied Sciences*, *2(2)*: 133-141

Kadam, S. and Shahane, K. (2019). Recent advances in non-conventional antimicrobial approaches for chronic wounds biofilms: have we found the clinic in the armor? *Biomedicine*, 7*(2)*, 35.

Lilian, N. C., Nneka, R. A., Ifeoma B. E., Chidozie V.U., Eucharia A. D and Ifeoma S. E. (2024). Microbial population of wound isolates and socio demographic characteristics in patients attending clinic in national orthopedic hospital, Enugu, Nigeria. *World Journal of Advanced Research Review*, *21(02)*, 1652–1659.

Mohammed, A., Seid, M., Gebrecherkos, T., Tiruneh, M. and Moges, F. (2017). Bacterial isolates and their antimicrobial susceptibility patterns of wound infections among inpatients and outpatients attending the University of Gondar referral hospital, Northwest Ethiopia. *International Journal of Microbiology*, 8953829

Mulu, W., Abera, B., Hailu, T., Ayele, H. and Abate, D. (2017). Bacterial agents and antibiotic resistance profiles of infections from different sites that occurred among patients at Debre Markos referral hospital, Ethiopia: a cross-sectional study. *Journal of Infectious Diseases*, *10(1)*:254.

Njoku, C., Okoro, C. G., Igwe, T. S., Ngene, P. N. and Ajana, A. J. (2015). Evaluation of water sources in Abakiliki southeastern Nigeria for domestic uses. *Journal of Agricultural and Ecological Research*, *2(1)*:87-91.

Nobel, F. A., Islam, S., Babu, G., Akter, S., Jebin, R., Sarker, T., Islam, A. and Johirul, M. (2022). Isolation of multidrug resistance bacteria from the patients with wound infection and their antibiotics susceptibility patterns: A cross-sectional study. *Annals of Medicine and Surgery*, *14*:84:104895.

Oladeinde, B. H., Omoregie, R., Olley, M., Arurube, J. A. and Onifade, A. A. (2013). A 5-year surveillance of wound infections at a rural tertiary hospital in Nigeria. *African Health Science*, *13(2)*:12-22

Onsando, S., Masanta, W., Nyerere, A., Njire, M. and Moriasi, G. (2025). Diversity and antibiotic susceptibility profiles at the surgical unit of Kisii teaching and referral hospital, Kenya. *PLoS One*, *20(6)*: e0326048

Sharma, S., Chauhan, A., Ranjan, A., Mathkor, D. M., Haque, S., Ramniwas, S., Tuli, H. S., Jindal, T. and Yadav, V. (2024). Emerging challenges in antimicrobial resistance: implications for pathogenic microorganisms, novel antibiotics and their impact on sustainability. *Frontiers in Microbiology*, *15*:1403168

Shimekaw, M., Tigabu, A. and Tessema, B. (2022). Bacterial profile, antimicrobial susceptibility pattern and associated risk factors among patients with wound infections at Debre Markos referral hospital, Northwest, Ethiopia. *International Journal of Low Extreme Wounds*, *21(2)*:182-192.

Tom, I. M., Ibrahim, M. M., Umoru, A. M., Umar, J. B. Bukar, M. A, Haruna, A. B. and Aliyu. A. (2019). Infection of wounds by potential bacterial pathogens and their resistogram.

Open Access Library Journal, *6(7)*: 1-3

Wang, C., Niu, X., Bao, S., Shen, W. and Jiang, C. (2024). Distribution patterns and antibiotic resistance profiles of bacterial pathogens among patients with wound infections in the Jiaxing region from 2021 to 2023. *Infectious Drug Resistant*, *9(17)*:2883-2896.

Wise, J. (2025). One in six bacterial infections worldwide are now resistant to antibiotics, WHO warns. *The British Medical Journal*, *391*: r2165

World Health Organization (2025). Global antibiotic resistance surveillance report. https://www.who.int.

Yucens, M., Sari, T., Aydemir, N., Ozturk, S. S., Akman, A., Inal, O. and Demirkan, F. (2025). Evaluation of pathogens isolated from wound infections and their antibiotic susceptibility profiles in wound care unit. *Journal of Infections in Developing Countries*, *19(9)*: 1351 – 1358

Zabaglo, M., Leslie, S. W. and Sharma, T. (2024). Postoperative wound infections. National Library of Medicine, Bookshelf ID: NBK560533 PMID 32809368

Zhao, C. and Zhao, W. (2020). NLRP3 Inflammasome – A key player in antiviral responses. *Frontiers in Immunology*, *11*:211.