Evaluation of Antibiotic Resistance Patterns and Trends among Patients at Selected Secondary Healthcare Facilities in Taraba State, Nigeria (2019–2023)

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ABSTRACT

Background: Antimicrobial resistance is a growing global public health challenge, disproportionately affecting low- and middle-income countries such as Nigeria, where surveillance and antimicrobial stewardship systems remain limited, particularly at secondary healthcare levels.

Objective: This study evaluated antibiotic resistance patterns and temporal trends among bacterial isolates from patients attending selected secondary healthcare facilities in Taraba State, Nigeria, between 2019 and 2023.

Methods: A retrospective cross-sectional study was conducted using microbiology laboratory records from three secondary healthcare facilities between January 2019 and December 2023. Data on patient demographics, specimen types, bacterial isolates, and antibiotic susceptibility test results were extracted and analysed using descriptive statistics.

Results: A total of 2,057 patient samples were analysed, with females accounting for 55.1% and adults for 51.6% of cases. Urine (32.0%) and high vaginal swabs (21.6%) were the most common specimens. Overall antimicrobial resistance was 72.0%. High resistance rates were observed among coliforms (98.9%) and Proteus species (94.9%). Significant inter-facility variation was noted, with the highest resistance recorded at General Hospital Gembu (97.4%). Resistance peaked in 2019 and declined to 65.5% in 2023.

Conclusion: Antimicrobial resistance remains alarmingly high in secondary healthcare facilities in Taraba State, with notable temporal and facility-level variations. Strengthening antimicrobial stewardship, laboratory capacity, and routine surveillance is urgently required.

What this study adds: This study provides multi-year antimicrobial resistance data from secondary healthcare facilities in northeastern Nigeria, highlighting facility-specific patterns and temporal trends to inform targeted antimicrobial stewardship and infection prevention strategies.

Keywords: Antimicrobial resistance; Antibiotic susceptibility; Bacterial isolates; Secondary healthcare; Nigeria; Laboratory surveillance

INTRODUCTION

Antimicrobial resistance (AMR) has emerged as one of the most urgent global health challenges of the 21st century, with profound implications for morbidity, mortality, and healthcare costs.[1] The World Health Organization (WHO) has identified AMR as a top-ten global health threat, warning that without coordinated action, the world is heading toward a “post-antibiotic era” in which common infections and minor injuries could once again become fatal.[2] Recent estimates indicate that bacterial AMR was directly responsible for

approximately 1.27 million deaths and contributed to nearly 5 million deaths worldwide in 2019, with the greatest burden borne by low- and middle-income countries (LMICs).[3]

The impact of AMR is particularly devastating in sub-Saharan Africa, where weak health systems, high infectious disease prevalence, and limited diagnostic capacity increases the problem.[4] In LMICs such as Nigeria, AMR surveillance remains fragmented, and stewardship efforts are underdeveloped. Irrational prescribing, unregulated access to antibiotics, poor infection prevention and control (IPC) measures, and limited diagnostic capacity are major drivers of resistance.[5] Antibiotics are widely available over the counter, often used without prescription, and sometimes of substandard quality, further accelerating the spread of resistance.[6] In this context, reliable local data on antimicrobial resistance patterns are essential to guide empirical therapy, inform stewardship interventions, and support evidence-based health policy.

However, most published studies in Nigeria focused on tertiary hospitals and urban centers, leaving significant gaps in knowledge about resistance patterns in secondary healthcare facilities, which serve as the first point of referral for a large segment of the population.[7]

Evidence from other Nigerian settings illustrates the severity and variability of the AMR problem. High levels of multidrug resistance among clinical isolates—particularly to third-generation cephalosporins—have been reported in Lagos State.[7] Similarly, elevated resistance rates among Escherichia coli and Staphylococcus aureus have been documented in Kano.[8] A multicentre study further demonstrated substantial inter-facility variability in resistance patterns across hospitals in Lagos and the Federal Capital Territory, underscoring the context-specific nature of AMR.[9] These findings are consistent with global evidence indicating that resistance patterns are influenced by local prescribing behaviours, infection control practices, patient demographics, and environmental factors.[10,11]

Despite these insights, most AMR studies in Nigeria continue to focus on tertiary healthcare institutions, with limited attention to secondary-level facilities.[12] This represents a critical gap, as secondary healthcare facilities manage a large volume of patients and frequently rely on empirical treatment due to limited laboratory capacity. Inappropriate empirical antibiotic use in such settings can contribute to treatment failure, increased morbidity, and the further propagation of resistant pathogens, particularly in common infections such as urinary tract infections, bloodstream infections, and respiratory tract infections.

Taraba State, located in northeastern Nigeria, represents an important but understudied context in the fight against AMR. The state's healthcare system is largely dependent on secondary healthcare facilities that serve semi-urban and rural populations. These facilities often lack robust diagnostic infrastructure and formal antimicrobial stewardship programmes, conditions that may facilitate inappropriate antibiotic use and the emergence of resistance. Despite the state's strategic location and population dynamics, there has been no comprehensive assessment of AMR trends in its secondary healthcare system. Understanding the prevalence, patterns, and determinants of AMR in this setting is therefore essential for guiding local interventions and contributing to Nigeria's National Action Plan on AMR (2017–2022).[13]

This study evaluates antibiotic resistance patterns and temporal trends over a five-year period (2019–2023) in three secondary healthcare facilities in Taraba State, Nigeria. By analysing demographic, clinical, and facility-level factors, it provides context-specific evidence to inform antimicrobial stewardship interventions, strengthen laboratory and surveillance systems, and support policy efforts aimed at mitigating the spread of AMR in resource-limited settings.

METHODS

Ethical considerations

Ethical approval for this study was obtained from the Taraba State Ministry of Health Research Ethics Committee (Approval number: TRSHREC/2024/023). Permissions were also secured from the management of the participating healthcare facilities. Patient confidentiality was strictly maintained by anonymising all identifiers prior to data extraction and analysis. The study was conducted in accordance with the principles of

the Declaration of Helsinki.[14]

Study design and setting

This was a retrospective cross-sectional study based on laboratory and clinical records collected between January 2019 and December 2023. The study was conducted in three secondary healthcare facilities in Taraba State, Nigeria: First Referral Hospital, Mutum-Biyu; General Hospital Gembu, Sardauna; and General Hospital Takum, Takum. These facilities were selected due to their diagnostic capacity, geographic distribution, and representation of both rural and semi-urban populations within the state.

Study population and selection

The initial dataset comprised 2,249 patient records retrieved from the participating healthcare facilities. A systematic data cleaning and validation process was conducted to enhance accuracy and analysis reliability.

Records were excluded if they met any of the following criteria:

- Incomplete demographic information (n = 76)
- Unclear or missing antibiotic susceptibility test (AST) results (n = 54)
- Apparent data entry errors (n = 29)
- Duplicate entries from the same patient within a single episode of infection (n = 33)

After these exclusions, the final study population consisted of 2,057 patient records, which formed the basis for analysis.

Inclusion and exclusion criteria

Inclusion criteria were:

- All patient samples processed for microbiological culture and antibiotic susceptibility testing between 2019 and 2023
- Samples yielding identifiable bacterial isolates with complete AST results

Exclusion criteria were:

- Samples with no bacterial growth or growth of contaminants, mixed flora, or fungi
- Isolates with incomplete or missing susceptibility results
- Duplicate isolates from the same patient within a single episode of infection

Data collection and sources

Data were extracted using a structured data collection form from laboratory registers and medical records. Information collected included patient demographics (age and sex), specimen type (e.g., urine, stool, blood, wound swab), date of sample collection, bacterial isolates identified, and corresponding antibiotic susceptibility results.

The primary data source consisted of microbiology laboratory registers maintained by the participating healthcare facilities, which documented culture results and antimicrobial susceptibility profiles.

Laboratory procedures

Bacterial identification and antimicrobial susceptibility testing were performed by the respective hospital laboratories using standard microbiological procedures. Clinical specimens, including urine, blood, sputum, stool, and wound swabs, were cultured on appropriate media and examined for bacterial growth. Identification

of isolates was based on colony morphology, Gram staining, and conventional biochemical tests.

Antibiotic susceptibility testing was conducted using the Kirby–Bauer disk diffusion method on Mueller–Hinton agar, in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines. Results were interpreted and categorised as susceptible or resistant based on CLSI criteria.

Statistical Analysis

Data were entered into Microsoft Excel, cleaned, and exported for analysis using Jamovi version 2.3.28 (built on the R statistical platform). Descriptive statistics were used to summarise patient demographics, specimen distribution, and antimicrobial resistance patterns.

Associations between categorical variables (e.g., age, sex, specimen type, and facility) and antimicrobial resistance were assessed using chi-square tests. Temporal trends in resistance patterns were analysed across the study period (2019–2023). Statistical significance was set at $p < 0.05$.

RESULTS

A total of 2,057 clinical samples collected between 2019 and 2023 from three secondary healthcare facilities in Taraba State were analysed. Findings are presented according to demographic characteristics, microbiological profile, and antimicrobial resistance (AMR) patterns.

Demographic and Clinical Characteristics

The demographic characteristics of the study population are summarised in Table 1. Females accounted for 55.1% (n = 1,134) of the samples, while males represented 44.9% (n = 923). The majority of patients were aged 21–40 years (52.0%), followed by 0–20 years (19.3%), 41–60 years (17.9%), and ≥61 years (10.7%).

Most samples were obtained from outpatients (89.5%), with only 10.5% from inpatients. Regarding facility distribution, General Hospital Takum (GHT) contributed the largest proportion of samples (60.4%), followed by First Referral Hospital (FRH) (20.1%) and General Hospital Gembu (GHG) (19.5%).

The number of samples varied across the study period, peaking in 2020 (30.4%) and declining to 14.0% in 2023.

Table 1. General Description of the Study Population (2019-2023)

Characteristics	**Variables**	**n**	**%**
Sex	Male	923	44.9
	Female	1134	55.1
Age (Years)	0-20	398	19.3
	21-40	1070	52.0
	41-60	368	17.9
	61 and above	221	10.7
Healthcare Facility	FRH	414	20.1
	GHG	401	19.5
	GHT	1242	60.4

Hospital Unit	In-patient	216	10.5
	Out-patient	1841	89.5
Date (Year)	2019	256	12.4
	2020	626	30.4
	2021	520	25.3
	2022	366	17.8
	2023	289	14.0
Total Population		**2057**	**100.0**

Abbreviations: FRH: First Referral Hospital; GHG: General Hospital Gembu; GHT: General Hospital Takum.

Distribution of bacterial isolates

The distribution of bacterial isolates is presented in Table 2. Of the total samples analysed, 67.6% yielded bacterial growth, while 32.4% showed no growth.

Among isolates, Gram-negative organisms (35.6%) were slightly more prevalent than Gram-positive organisms (32.0%).

Among Gram-positive bacteria, Staphylococcus spp. were the most frequently isolated (29.1%), followed by Streptococcus spp. (2.6%) and Bacillus spp. (0.2%).

Among Gram-negative bacteria, Escherichia coli was the most common isolate (18.5%), followed by Salmonella spp. (10.3%), coliforms (4.3%), and smaller proportions of Proteus spp., Pseudomonas spp., and Klebsiella spp.

Table 2. Distribution of Pathogens (Bacterial Isolates)

Pathogen		n	**(%)**
Gram-Positive			
Bacillus spp		3	0.2
Staphylococcus spp		602	29.1
Streptococcus spp		54	2.6
Subtotal Gram-Positive		**659**	**32**
Gram-Negative			
Coliform		89	4.3
Escherichia coli		381	18.5
Klebsiella spp		3	0.2
Proteus spp		39	1.9

Pseudomonas spp		8	0.4
Salmonella spp		212	10.3
Subtotal Gram-Negative		**731**	**35.6**
No Bacteria Growth		**666**	**32.4**
Total		**2057**	**100**

Antimicrobial resistance patterns by demographic and clinical characteristics

Antimicrobial resistance analysis was conducted on 1,391 isolates with complete susceptibility results. The overall resistance rate was 72.0%, while susceptibility was 28.0% (Table 3).

Resistance was slightly higher among females (72.8%) compared to males (70.8%), although this difference was not statistically significant ($p = 0.362$).

Significant variation in resistance was observed across age groups ($p < 0.001$), with the highest resistance among patients aged ≥61 years (90.2%), followed by those aged 0–20 years (84.2%).

A significant temporal trend was observed ($p < 0.001$), with resistance highest in 2019 (80.7%) and progressively declining to 65.5% in 2023 (Figure 1).

Facility-level differences were also significant ($p < 0.001$). General Hospital Gembu (GHG) recorded the highest resistance rate (97.4%), compared to First Referral Hospital (FRH) (79.1%) and General Hospital Takum (GHT) (64.1%).

Inpatient samples showed significantly higher resistance (88.7%) compared to outpatient samples (70.2%) ($p < 0.001$).

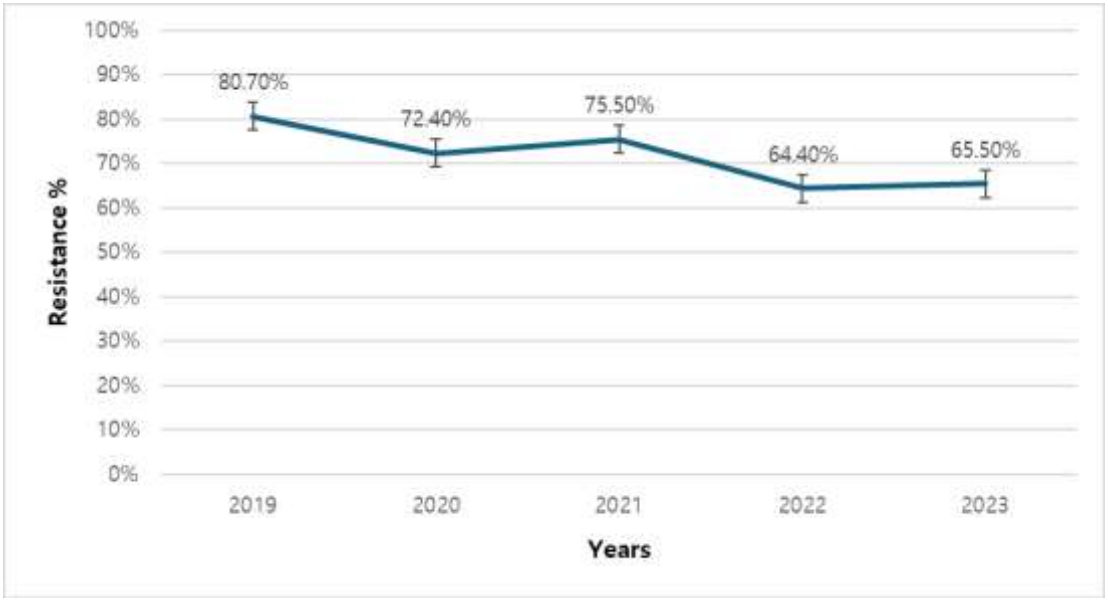
Table 3. Antimicrobial Resistance Patterns by Demographic and Clinical Characteristics

Variable	Resistance (n, %)	Susceptibility (n, %)	Total N (%)	P-value
Sex				0.362
Male (M)	412 (70.8)	171 (29.2)	583 (41.9)	
Female (F)	589 (72.8)	219 (27.2)	808 (58.1)	
Total	1001 (72.0)	390 (28.0)	1391 (100)	
Age				<0.001
0-20	283 (84.2)	77 (15.8)	360 (25.9)	
21-40	296 (79.6)	201 (20.4)	495 (35.5)	
41-60	255 (79.4)	79 (20.6)	334 (24.0)	
61+	169 (90.2)	33 (9.8)	202 (14.5)	
Total	1001 (72.0)	390 (28.0)	1391 (100)	
Year				<0.001

2019	138 (80.7)	33 (19.3)	171 (12.3)	
2020	305 (72.5)	116 (27.5)	421 (30.3)	
2021	283 (75.5)	92 (24.5)	375 (27.0)	
2022	163 (64.4)	90 (35.6)	253 (18.2)	
2023	112 (65.5)	59 (34.5)	171 (12.3)	
Total	1001 (72.0)	390 (28.0)	1391 (100)	
Hospital				<0.001
GHT	604 (64.1)	338 (35.9)	942 (67.7)	
FRH	174 (79.1)	46 (20.9)	220 (15.8)	
GHG	223 (97.4)	6 (2.6)	229 (16.5)	
Total	1001 (72.0)	390 (28.0)	1391 (100)	
Department				<0.001
Outpatient	883 (70.2)	375 (29.8)	1258 (90.4)	
Inpatient	118 (88.7)	15 (11.3)	133 (9.6)	
Total	**1001 (72.0)**	**390 (28.0)**	**1391(100)**	

Abbreviations: FRH: First Referral Hospital, GHG: General Hospital, Gembu GHT: General Hospital Takum

Figure 1. Antimicrobial resistance trends by year, 2019–2023.



This figure shows the proportion of resistant bacterial isolates by calendar year across three secondary healthcare facilities in Taraba State, Nigeria, illustrating the decline in resistance from 2019 to 2023.

Antimicrobial resistance patterns by pathogen

Resistance patterns across bacterial isolates are presented in Table 4. Overall, high resistance rates were observed across most pathogens ($p < 0.001$).

Among Gram-positive organisms, Bacillus spp. showed complete resistance (100%), followed by Streptococcus spp. (79.6%) and Staphylococcus spp. (69.3%).

Among Gram-negative organisms, coliforms (98.9%) and Proteus spp. (94.9%) exhibited the highest resistance rates. Other notable resistance levels were observed in Pseudomonas spp. (87.5%), Salmonella spp. (71.2%), and Escherichia coli (66.4%).

These findings highlight substantial variability in resistance patterns across bacterial species, with particularly high resistance among Gram-negative organisms.

Table 4. Antimicrobial Resistance Patterns of Pathogens

Pathogen	**Resistance (n, %)**	**Susceptibility (n, %)**	**Total (N, %)**	**P-value**
Gram-positive				<0.001
Bacillus spp.	3 (100)	0 (0.0)	3 (0.2)	
Staphylococcus spp.	417 (69.3)	185 (30.7)	602 (43.3)	
Streptococcus spp.	43 (79.6)	11 (20.4)	54 (3.9)	
Gram-negative				<0.001
Coliform	88 (98.9)	1 (1.1)	89 (6.4)	
E. coli	253 (66.4)	128 (33.6)	381 (27.4)	
Klebsiella spp.	2 (66.7)	1 (33.3)	3 (0.2)	
Proteus spp.	37 (94.9)	2 (5.1)	39 (2.8)	
Pseudomonas spp.	7 (87.5)	1 (12.5)	8 (0.6)	
Salmonella spp.	151 (71.2)	61 (28.8)	212 (15.2)	
Total	1001 (72.0)	390 (28.0)	1391 (100)	<0.001

DISCUSSION

This study provides important insights into antimicrobial resistance (AMR) patterns across demographic groups, time periods, and healthcare facilities in selected secondary healthcare settings in Taraba State, Nigeria. The findings reinforce the growing body of evidence that AMR remains a major public health challenge in low- and middle-income countries and demonstrate that resistance is not confined to tertiary institutions but is also widespread in secondary healthcare facilities, where a large proportion of the population seeks care.[16]

Temporal Trends in Antimicrobial Resistance

A key finding of this study is the observed decline in resistance from 80.7% in 2019 to 65.5% in 2023, although resistance remained consistently high (>60%) throughout the study period. This modest reduction may reflect the impact of national and global efforts, including the implementation of Nigeria's National Action Plan on AMR (2017–2022), which emphasised antimicrobial stewardship, surveillance, and public awareness.[17,18]

However, the persistently high resistance levels suggest that these interventions have not been sufficiently effective at the secondary healthcare level. Similar trends have been reported in other Nigerian studies, where

improvements are gradual but insufficient to significantly curb resistance.[19] This underscores the need for sustained and context-specific interventions, particularly in resource-limited settings.

Variation Across Healthcare Facilities

The study revealed substantial inter-facility variation in resistance patterns, with General Hospital Gembu (97.4%) exhibiting markedly higher resistance compared to First Referral Hospital (79.1%) and General Hospital Takum (64.1%). These differences likely reflect variations in prescribing practices, infection prevention and control (IPC) measures, laboratory capacity, and patient case mix.

Comparable facility-level disparities have been documented in studies from Lagos and the Federal Capital Territory, highlighting the localized nature of AMR patterns.[7,9] These findings emphasise that antimicrobial stewardship interventions must be tailored to individual facilities rather than adopting a uniform national approach.[20]

Pathogen-Specific Resistance Patterns

The overall resistance rate of 72.0% observed in this study is consistent with national and global reports of increasing AMR burden.[21] Gram-negative organisms were slightly more prevalent than Gram-positive organisms, aligning with global trends indicating a growing dominance of resistant Gram-negative pathogens.

High resistance rates were observed among key pathogens, including coliforms (98.9%), Proteus spp. (94.9%), and Escherichia coli (66.4%), all of which are commonly implicated in community and hospital-acquired infections. Among Gram-positive organisms, Streptococcus spp. (79.6%) and Staphylococcus spp. (69.3%) also demonstrated substantial resistance, consistent with previous Nigerian studies.[8,22]

The high resistance observed across multiple pathogen groups highlights the widespread nature of the problem and the urgent need for strengthened antimicrobial stewardship and infection control strategies.[12]

Comparison with Other Studies

The resistance patterns identified in this study are comparable to findings from tertiary healthcare institutions across Nigeria, where high resistance to commonly used antibiotics such as cephalosporins and fluoroquinolones has been reported.[12] This suggests that the drivers of AMR—such as irrational antibiotic use, inadequate diagnostic capacity, and weak stewardship systems—are pervasive across all levels of the healthcare system.

Beyond Nigeria, similar multidrug resistance patterns are widespread across West Africa. Recent systematic data from countries including Ghana and Senegal confirm a high prevalence of resistance, particularly among Gram-negative organisms such as Escherichia coli and Klebsiella pneumoniae.[23] Globally, these findings are consistent with surveillance data highlighting increasing resistance among Enterobacteriaceae to first-line antibiotics.[24]

Drivers of Antimicrobial Resistance

The high levels of resistance observed in this study are likely driven by multiple interacting factors. The widespread availability of antibiotics without prescription in Nigeria promotes self-medication, inappropriate use, and incomplete treatment courses, all of which contribute to resistance development.[25]

Within healthcare facilities, the absence of structured antimicrobial stewardship programmes often leads to empirical prescribing without microbiological confirmation.[5] In addition, inadequate infection prevention and control practices—such as poor hand hygiene, overcrowding, and suboptimal sterilisation—facilitate the transmission of resistant organisms.[5]

Contextual factors specific to Taraba State, including limited healthcare funding, weak laboratory infrastructure, and the absence of coordinated surveillance systems, further exacerbate the problem.[26] These local challenges are compounded by global factors such as population mobility and the transnational spread of resistant

pathogens.[27]

Implications for Practice and Policy

The high levels of resistance observed in this study carry critical implications for clinical practice and national health policy. Given the declining efficacy of traditional first-line treatments for typhoid complications in Lagos, clinicians in secondary healthcare facilities must shift away from indiscriminate empirical antibiotic use toward evidence-based prescribing.[28] Addressing this challenge requires expanding access to routine culture and susceptibility testing to guide therapy.[29] This clinical transition is now a core priority of the Nigeria National Action Plan for Antimicrobial Resistance 2.0 (2024–2028), which mandates a multisectoral "One Health" approach to strengthen surveillance, promote rational antimicrobial use, and improve diagnostic infrastructure nationwide.[30]

At the policy level, there is a need for stronger enforcement of prescription-only antibiotic policies and tighter regulation of drug distribution.[29] Integrating antimicrobial stewardship programmes into secondary healthcare facilities should be prioritised, alongside continuous training of healthcare workers on rational antibiotic use.[30] Public health interventions, including community education on the risks of self-medication, are also essential. Furthermore, linking healthcare facilities to national and global surveillance systems, such as the WHO Global AMR Surveillance System (GLASS), would enhance data sharing and support evidence-based decision-making.[31]

LIMITATIONS

This study has several limitations. First, its retrospective design relied on routinely collected laboratory data, which may be subject to incomplete or inconsistent documentation across facilities. Second, the use of conventional culture and disk diffusion methods limits the ability to detect specific resistance mechanisms, such as extended-spectrum beta-lactamases (ESBLs) and carbapenemase production, potentially underestimating the true burden of resistance.[32]

Additionally, variations in laboratory capacity, patient populations, and clinical practices across the three facilities may have influenced the observed resistance patterns, limiting the generalisability of the findings. Future studies incorporating molecular diagnostics and facility-specific analyses would provide more detailed insights.

CONCLUSION

This study demonstrates that antimicrobial resistance among bacterial isolates in secondary healthcare facilities in Taraba State is alarmingly high and consistent with national, regional, and global trends. The persistence of high resistance levels, despite some temporal decline, underscores the urgent need for strengthened antimicrobial stewardship, improved laboratory capacity, and enhanced surveillance systems.

Addressing the multifactorial drivers of AMR—including irrational antibiotic use, weak regulatory enforcement, and inadequate infection control—requires coordinated action at multiple levels. Targeted interventions at the facility level, supported by national policies and global partnerships, are essential to mitigate the spread of resistance and improve patient outcomes.

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Competing Interests

The authors declare that they have no financial or personal relationships that may have inappropriately influenced them in writing this article.

Authors' Contributions

Frank Ada Nwubuma - Conceptualised the study, Designed the methodology, Conducted data curation and Formal analysis, and Drafted the original manuscript.
Keumji Jung - Supervised the research, Contributed to methodology refinement, Validated the analysis, and Critically reviewed and Edited the manuscript.
Both authors read and approved the final version of the manuscript.

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Data Availability

The data that support the findings of this study are available from the corresponding author upon reasonable request. Access to the dataset is subject to institutional approval to ensure confidentiality and ethical compliance, as it involves hospital-based patient records.

Disclaimer

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Use of artificial intelligence (AI) tools

Artificial intelligence (AI) tools were used to support language editing and structuring of the manuscript. These tools did not contribute to data collection, analysis, or interpretation. All scientific content, results, and conclusions are the sole responsibility of the authors.

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