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Multidrug-resistant *Escherichia coli* carriage and associated risk factors among healthy individuals in Rural Southwestern Nigeria

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ABSTRACT

Antimicrobial resistance (AMR), driven by multidrug-resistant (MDR) *Escherichia coli*, poses a significant public health threat, silently spreading through asymptomatic carriers. Limited data from rural areas highlight the need for focused studies to guide resistance control efforts. This study aimed to isolate faecal *Escherichia coli* (*E. coli)* from apparently healthy individuals in a rural community in Southwestern Nigeria, determine their antimicrobial resistance profiles, and evaluate risk factors associated with MDR *E. coli* carriage. A total of 347 stool samples were collected from healthy, consenting individuals. *E. coli* was isolated and identified using standard microbiological techniques. Antimicrobial resistance was assessed via the Kirby-Bauer disc diffusion method. Isolates were screened phenotypically for the extended spectrum beta-lactamase (ESBL) production and genotypically for ESBL genes (CTX-M, SHV, TEM). The data were analyzed using WINPEPI. *E. coli* was isolated from 269 participants (77.5%), yielding 555 isolates. High resistance rates were observed against sulphamethoxazole (94.0%), ampicillin (85.0%), and tetracycline (83.2%), while imipenem showed the lowest resistance (6.7%). Twenty-seven isolates (5%) were confirmed as ESBL producers. Among these, 17 (63%) carried at least one ESBL gene—TEM being the most common (44.4%). Additionally, 50.1% of the isolates were classified as MDR, with MDR *E. coli* carriage significantly associated with self-medication ($p = 0.05$). The widespread presence of MDR *E. coli* among healthy rural dwellers, coupled with its association with self-medication, highlights serious public health concerns and raises the urgent need for more evidence-based strategies to combat AMR.

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1. INTRODUCTION

Antimicrobial resistance (AMR) is one of the most pressing global health challenges of the 21st century. It is estimated to have directly caused 1.27 million deaths and contributed to nearly 5 million deaths globally in 2019 [1]. Without urgent intervention, AMR could lead to almost 10 million deaths annually by 2050, surpassing cancer as a leading cause of mortality. Most of these burdens would fall on lower-income regions, particularly sub-Saharan Africa [2].

Among the most concerning resistant pathogens is *Escherichia coli (E. coli)*, a versatile bacterium that exists as a harmless gut commensal and a potent pathogen responsible for urinary tract infections, bloodstream infections, and pneumonia. The emergence of multidrug-resistant (MDR) *E. coli*, particularly strains that produce extended-spectrum beta-lactamases (ESBLs), which are enzymes capable of hydrolyzing beta-lactam antibiotics, including third-generation cephalosporins, has rendered many first-line treatments ineffective. This resistance complicates clinical management and significantly increases healthcare costs.

While MDR *E. coli* has traditionally been associated with hospital-acquired infections, recent studies, such as the WHO Tricycle Surveillance Project, have shown that hospital-acquired infections often originate from community colonization, emphasising the need for a one health approach that integrates human, animal, and environmental health [3]. Also, a global meta-analysis published in 2025 found that the pooled prevalence of intestinal carriage of ESBL-producing *E. coli* was 25.4%, with 23.4% in healthy community members and 27.7% in hospitalised patients, indicating widespread asymptomatic colonisation [4]. The post-COVID-19 era has seen a surge in resistant gram-negative organisms, likely driven by increased and often inappropriate antibiotic prescriptions during the pandemic [5]. This silent spread of resistance genes through asymptomatic carriers complicates infection control and increases the risk of developing untreatable infections.

The acquisition of MDR *E. coli* by healthy community members is driven by various factors. Prior antibiotic use selects for resistant gut strains. Healthcare contact, even without active infection, increases risk due to contaminated environments. International travel to areas with high AMR prevalence also contributes to colonization. Within communities, poor food hygiene, such as the consumption of undercooked poultry or unwashed produce, and animal handling, serve as key transmission routes. Additionally, inadequate sanitation, including contaminated wastewater systems, facilitates faecal-oral spread, making MDR *E. coli* a silent and persistent threat [6], [7].

MDR *E. coli* is a major public health concern in Nigeria, where high rates have been consistently found in food, water, and human and animal populations. Previous research in urban and hospital settings across the country has highlighted significant resistance. For instance, studies in Lagos and Abuja found that almost all *E. coli* from beef cattle and their handlers were MDR [8], and similar high resistance levels have been noted in community and hospital settings in Ado-Ekiti [9], as well as in drinking water and healthy individuals in Osun and Oyo States [10], [11]. This body of work establishes the clear presence of MDR *E. coli* in Nigeria's urban and healthcare systems. Despite this evidence, there is a critical gap in understanding the carriage of MDR *E. coli* in healthy individuals within Nigeria's rural communities, where a large portion of the population resides. The unique interplay between humans, animals, and the environment in these areas creates a significant reservoir for resistant bacteria, which can easily spread from rural to urban centers and across international borders via the movement of people, animals, and agricultural products. To address this crucial gap, this study was conducted to investigate the carriage of MDR *E. coli* in healthy individuals in a rural setting, aiming to identify *E. coli* from faecal samples, determine their resistance profiles, and evaluate associated risk factors.

2. METHOD

2.1. Study location

This cross-sectional study was conducted at the Department of Medical Microbiology and Parasitology, Obafemi Awolowo University, Ile-Ife, Osun State, Nigeria. Samples were collected from a rural settlement in Ayedaade Local Government Area (7°37′0″N, 4°31′0″E), predominantly inhabited by Oyo-speaking people with a projected population of approximately 3,037 [12]. The community's water supply relies on two metallic tanks that distribute pipe-borne water and three strategically placed boreholes. Access to the community is often hindered by poor road conditions, especially during the rainy season, when flooding and overflowing rivers render the roads impassable. Healthcare services are limited to a single primary healthcare centre, staffed by professionals who commute from Ile-Ife, an ancient town located roughly ten kilometres away. Notably, this community lacks a dedicated drug dispensary. This community is typical of many rural communities in Nigeria and was thus selected for this study.

2.2. Sample and data collection

A total of 347 apparently healthy residents were recruited for this cross-sectional study using random sampling. Households that provided informed consent were included, while individuals who had taken antibiotics or had been ill within the previous 21 days were excluded. A validated, structured questionnaire was used to collect demographic data and information on the participants' water sources and waste disposal practices.

Stool samples were collected daily through house-to-house visits, primarily in the morning when participant availability was optimal. Each participant received a sterile container with a scoop, and detailed

pictorial instructions for aseptic collection were provided to prevent urine contamination. All samples were transported to the Medical Microbiology Laboratory at Obafemi Awolowo University within two hours of collection to ensure sample integrity for microbial analysis.

2.3. Bacterial isolation

Stool specimens were streaked onto eosin methylene blue (EMB) agar plates and incubated at 37 °C for 24 hours. Presumptive *E. coli* colonies were identified by their characteristic green metallic sheen or purple colouration. To obtain pure cultures, three to five morphologically distinct colonies exhibiting these traits were subcultured on sterile nutrient agar. This approach was intended to capture a broader diversity of strains with potentially varied resistance profiles. Pure isolates were further identified using standard biochemical tests, including indole production and citrate utilisation. *E. coli* ATCC 25922 was employed as a positive control [13]. Finally, the isolates were preserved in 16% glycerol broth and stored at 2–8 °C for future analysis.

2.4. Antimicrobial susceptibility testing

Antimicrobial susceptibility testing was conducted on the isolates using the Kirby-Bauer disc diffusion method on Mueller-Hinton Agar (MHA), following the Clinical and Laboratory Standard Institute (CLSI) guidelines [14]. A standardized bacterial inoculum (0.5 McFarland standard) was prepared for each isolate and spread onto MHA plates. A panel of ten antibiotic discs, including ceftazidime (30 µg), gentamicin (10 µg), nalidixic acid (30 µg), sulfamethoxazole (30 µg), chloramphenicol (30 µg), trimethoprim (5 µg), ciprofloxacin (5 µg), cefotaxime (30 µg), imipenem (10 µg), and ampicillin (10 µg), was then applied. Multidrug resistance (MDR) was defined as resistance to at least one antibiotic in three or more different classes.

2.6. Phenotypic determination of extended-spectrum beta-lactamase producers

ESBL producers were identified using cefotaxime (CTX 30 µg) and ceftazidime (CAZ 30 µg) discs, tested individually and in combination with clavulanic acid (10 µg) on Mueller-Hinton agar. A positive confirmatory test was defined as a ≥5 mm increase in the zone of inhibition for the combination disc compared to the single antibiotic disc [14]. *Klebsiella pneumoniae* ATCC 7006033 served as the positive control for ESBL production, while *Escherichia coli* ATCC 25922 was the negative control.

2.7. Genomic DNA extraction and genotypic detection of extended-spectrum beta-lactamse genes

Genomic DNA was extracted from the isolates using the boiling method, in which colonies were suspended in sterile water and heated at 95 °C for 20 min to lyse the cells before centrifugation at 12,000 rpm for 5 min. The DNA-rich supernatant was stored at −20 °C and used as a template for subsequent PCR amplification [15]. Positive isolates were screened for common ESBL-encoding genes (*bla*$_{TEM}$, *bla*$_{SHV}$, and *bla*$_{CTX-M}$) using specific primers as shown in Table 1. Each 25 µL PCR reaction contained 3 µL of template DNA, 12.5 µL of master mix (comprising 4µL dNTP mixture, 5µL 10X PCR buffer, 0.5µL Taq polymerase, and 0.5µL of each primer stock solution), and 6.5 µL of nuclease-free water, following a standard protocol with initial denaturation at 94 °C for 3 min, followed by 30 cycles of denaturation at 94 °C for 30 s, annealing at 60 °C for 30 s, and extension at 72°C for 1 min, with a final extension at 72 °C for 7 min. The PCR products were visualized by electrophoresis on a 1.5% agarose gel in TBE buffer at 100 V for 45 min. Gels were stained with ethidium bromide for 15 min, destained for 30 min, and then visualized under UV light using a UV transilluminator and documented with a camera [16]. The amplified products were not sequenced.

Table 1. PCR Primers for Specific ESBL Genes

Primer	Primer sequence 5 to 3'	Target gene	Amplicon size
TEMF	TTTCTGGTCGCCCTTATTCC	TEM	403
TEMR	ATCGTTGTCAGAAGTAAGTTGG		
SHVF	CGCCTGTGTATTATCTCCCT	SHV	293
SHV R	CGAGTAGTCCACCAGATCCT		
CTX-MF	CGCTGTTGTTAGGAAGTGTG	CTX-M	734
CTX-MR	GGCTGGGTGAAGTAAGTGAC		

2.8. Data analysis

Data were analyzed using Microsoft Excel (2021) [17] and WINPEPI (version 11.65) [18]. Univariate analysis was conducted to identify variables associated with MDR *E. coli* carriage, utilizing two-tailed Fisher's exact tests for categorical variables. All variables that were significant in the initial screening

were included in a multivariate logistic regression model. This final model was used to calculate the adjusted odds ratio (OR) and its corresponding 95% confidence interval (CI), assessing the relationship between MDR *E. coli* carriage and previously identified risk factors while controlling for confounding variables. Statistical significance was set at $p \leq 0.05$.

3. RESULTS AND DISCUSSION

3.1. Results

Stool samples from 269 participants (140 males and 129 females) yielded at least one morphologically distinct *E. coli* isolate per individual. Among them, 79 were children aged 0–14 years, and 73 were young adults, leading to a total recovery of 555 *E. coli* isolates. Regarding educational background, 41 participants reported no formal education, while only nine had an education level up to the Nigerian Certificate in Education. Of the 347 participants for whom family size data were available, 115 were from households with one to five members and 57 were from families with nine or more members.

High resistance rates were observed against sulfamethoxazole (94.0%), ampicillin (85.0%), and tetracycline (83.2%), whereas imipenem showed the lowest resistance (6.7%), as shown in Figure 1. A significant majority of the isolates (93.5%, 519) showed resistance to at least two antibiotics. Among these, 278 isolates (50.1%) were categorized as multidrug-resistant, meaning they were resistant to more than three classes of antibiotics. While a small fraction exhibited extreme resistance, with one isolate (0.2%) resistant to all 11 tested antibiotics and two isolates (0.4%) resistant to all antibiotic classes, a contrasting finding was that 10 isolates (1.8%) remained susceptible to all antibiotics tested, as shown in Table 2.

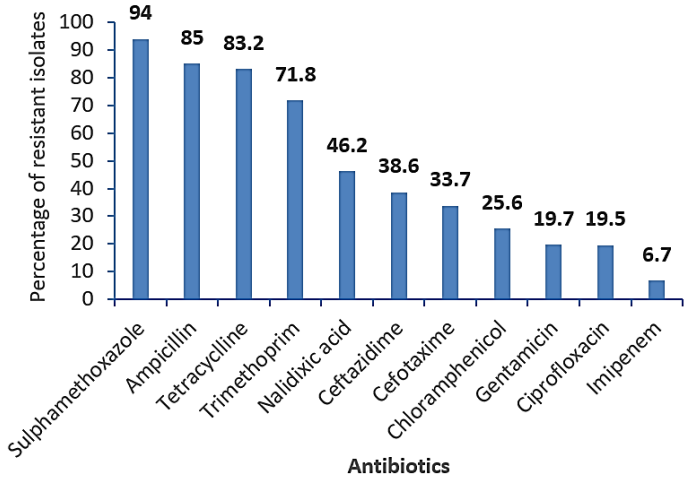

Figure 1. Antibiotic resistance profile

Table 2. Number of isolates resistant to different classes of antibiotics

Classes of antibiotics	Number of isolates	Percentage of isolates	Classes of antibiotics
0	10	1.8%	0
1	27	4.9%	1
2	97	17.5%	2
3	143	25.8%	3
4	139	25.1%	4
5	90	16.2%	5
6	34	6.1%	6
7	13	2.3%	7
8	2	0.4%	8
Total	555	100%	Total

Of the 27 ESBL-producing isolates screened for SHV, TEM, and CTX-M, two isolates (7.4%) harboured all three genes. Additionally, 11.1% of the isolates possessed at most two genes (TEM and CTX-M, SHV and TEM, or SHV and CTX-M), while 40.7% carried only one gene (TEM or SHV). TEM emerged as the predominant gene, present in 44.4% of the total isolates, as shown in Figure 2.

As shown in Table 3, there was no statistically significant association between multidrug resistance and gender or age (p>0.05). No significant associations were found for 'No formal education', 'Primary six', 'Secondary school' level of education, or 'Burying underground' and 'Bush waste disposal management' practices (p>0.05). However, there was a highly significant association between tertiary education and MDR *E. coli* carriage (p = 0.002). Multidrug resistance was observed in only 1.8% of individuals with tertiary education compared to 11.1% in those without it. Individuals who did not self-medicate had a lower percentage of multidrug resistance (57.6%) than those who self-medicated (42.4%). A significant association (p = 0.049) was observed between self-medication and the carriage of multidrug-resistant *E. coli.* Only 2.2% of individuals with multidrug resistance reported poor refuse management, compared with 8.9% in those without multidrug resistance. A significant association (p = 0.046) was found between poor refuse management and the carriage of MDR *E. coli* as shown in Table 3.

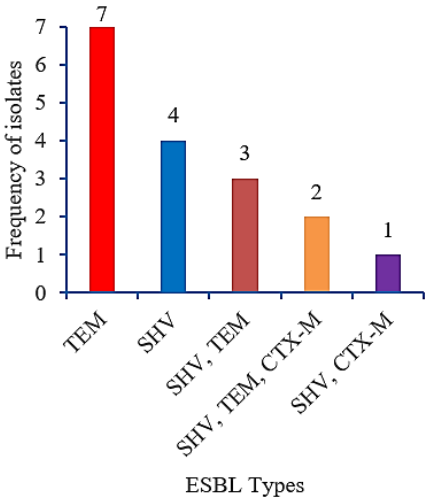

Figure 2. Distribution of ESBL genes

Table 3. Risk factors for carriage of multidrug-resistant *E. coli*

Characteristics	Multidrug resistance n = 224 (%)	Not multidrug resistant N = 45 (%)	Crude OR	95% CI	p-value†
Gender					
Female	102 (45.5)	27 (60.0)	0.56	0.27-1.12	0.101
Male	122 (54.5)	18 (40.0)			
Age					
Children	65 (29.0)	14 (31.1)	0.80	0.39-1.75	0.586
Young adult	65 (29.0)	8 (17.8)	1.89	0.81-4.95	0.143
Adult	94 (42.0)	23 (51.1)	0.69	0.35-1.39	0.323
Level of education					
No formal education	34 (15.2)	7 (15.6)	0.97	0.39-2.79	1.000
Primary six	71 (31.7)	15 (33.3)	0.93	0.45-1.98	0.862
Secondary school	115 (51.3)	18 (40.0)	1.58	0.79-3.23	0.192
Tertiary	4 (1.8)	5 (11.1)	0.15	0.03-0.72	0.008*
Drug use					
No self-medication	129 (57.6)	33 (73.3)	0.49	0.22-1.05	0.049*
Self-medication	95 (42.4)	12 (26.7)			
Waste disposal practices					
Burying underground	119 (53.1)	18 (40.0)	1.70	0.85-3.47	0.141
Bush waste disposal management	100 (44.6)	23 (51.1)	0.77	0.39-1.54	0.512
Poor refuse management	5 (2.2)	4 (8.9)	0.23	0.05-1.24	0.046*

†Fisher's exact test for dichotomous predictors; *statistically significant. OR; Odds ratio; CI, Confidence interval

The associated factors were further subjected to multivariate analysis using the binomial logistic regression model to determine the independent predictors of MDR *E. coli* carriage. Out of the variables that were tested, tertiary education (OR = 0.17; 95% CI = 0.04-0.77; p = 0.022), self-medication (OR = 2.03; 95%CI = 0.99-4.13; p = 0.05) and poor refuse management (OR = 0.19; 95%CI = 0.05-0.77; p = 0.02) were found to be independent predictors of MDR *E. coli* carriage in this study, as shown in Table 4.

Table 4. Independent predictors of carriage of multidrug-resistant *E. coli* in multivariate logistic regression model

Predictor	Adjusted OR	95%CI	p-value
Education (tertiary)	0.17	0.04-0.77	0.022*
Drug use (self medication)	2.03	0.99-4.13	0.05*
Waste disposal (poor refuse management)	0.19	0.05-0.77	0.020*

3.2. Discussion

3.2.1. Antibiotic resistance patterns

The observed high levels of antibiotic resistance to sulfamethoxazole (94.0%), ampicillin (85.0%), tetracycline (83.2%), and trimethoprim (71.8%) among apparently healthy community dwellers are deeply concerning and mirror findings from many studies in Nigeria and globally, reinforcing the understanding that AMR is a pervasive challenge extending beyond healthcare settings [19], [20]. These alarmingly high rates, particularly for broad-spectrum and commonly accessible antibiotics, are largely attributed to the widespread and often unregulated overuse and misuse of these drugs within the community, including self-medication and incomplete treatment courses, which facilitate selective pressure and the transfer of resistance genes. The comparatively low resistance to imipenem (6.7%) is likely a reflection of its higher cost and restricted clinical use, which limits bacterial exposure and consequently preserves its efficacy, making it a crucial last-resort option. The significant presence of resistant strains in healthy individuals underscores their role as silent reservoirs of AMR, contributing to the continued circulation and transmission of resistance within the community, thereby complicating effective infection control and treatment outcomes [21].

The finding that 50.1% of *E. coli* isolates from apparently healthy community dwellers exhibited MDR is highly consistent with recent and ongoing surveillance across Nigeria and other low- and middle-income countries, where *E. coli* frequently serves as an indicator of circulating antimicrobial resistance [22]. A recent study from Ethiopia found 43% MDR in human-origin *E. coli*, with very high resistance to almost all the tested drugs [23]. The prevalence in this study underscores the significant role that healthy individuals play as silent reservoirs and disseminators of AMR within the community, even without active infection [24]. Although some of the reasons for these observed high MDR rates have been previously mentioned, the extensive use of antimicrobials as growth promoters or for prophylaxis in livestock and aquaculture could also be a contributing factor [25]. Resistant strains can then spread through the food chain, contaminated water, and direct contact, further exacerbating the problem in community settings [26].

The finding that 27.4% of faecal *E. coli* isolates from healthy rural community dwellers demonstrated resistance to either ceftazidime or cefotaxime, or both, is a significant concern, with wider public health implications [20]. This level of third-generation cephalosporin resistance in commensal *E. coli* is consistent with previous studies from different parts of Nigeria that have reported varying but often high rates of ESBL producers in both clinical and environmental samples, as well as in the gut microbiota of healthy individuals [27], [28]. Other African studies have reported similar results [23].

3.2.2. Resistance genes prevalence

The analysis of 27 ESBL-producing isolates revealed that TEM was the most prevalent gene, either alone or in combination, with two isolates (7.4%) harbouring all three screened genes (SHV, TEM, and CTX-M). This multidrug resistance mechanism presents a significant challenge for antibiotic treatment, aligning with the documented trends of increasing co-occurrence of ESBL genes [29]. Furthermore, 11.1% of the isolates possessed combinations of two genes (TEM and CTX-M, SHV and TEM, or SHV and CTX-M), highlighting the diverse genetic profiles contributing to ESBL production, often driven by horizontal gene transfer and clonal expansion [30]. The largest group, accounting for 40.7% of the isolates, carried only a single gene (TEM or SHV), underscoring their individual contribution to the ESBL phenotype. The predominance of TEM, found in 44.4% of the isolates, is consistent with many previous studies that identified TEM and SHV as historically common ESBL types [31], although CTX-M types have become increasingly prevalent worldwide since the early 2000s [32]. Although this study focused on ESBL-producing isolates, the presence of these resistance genes has implications for healthy individuals. Asymptomatic carriers can harbour ESBL-producing bacteria in their gut flora, serving as reservoirs for community-acquired infections and facilitating the spread of resistance, a major public health concern [24]. Studies conducted in Osun State, Nigeria, that reported the prevalence of ESBL-producing bacteria often identified TEM and CTX-M as common genotypes in both clinical and community settings [26], further validating the findings of this study within the local context. This highlights the ongoing need for robust surveillance and evidence-based policies to guide infection control measures in the region [20].

3.2.3. Risk factors

Our data offer significant insights into the factors influencing the carriage of MDR *E. coli* within a community, presenting findings that largely resonate with the broader scientific understanding while also introducing an intriguing anomaly. The inverse relationship between tertiary education and MDR *E. coli* carriage is a striking revelation ($p = 0.022$), with only 1.8% of highly educated individuals carrying MDR strains compared to 11.1% in the non-MDR group. This finding suggests that higher educational attainment may act as a protective factor against MDR *E. coli* colonisation. This aligns with existing research indicating that health literacy improves with education, leading to better hygiene practices, greater awareness of antibiotic stewardship principles, and potentially different healthcare-seeking behaviours [33]. For instance, more educated individuals might be less prone to self-medication or more likely to adhere to prescribed antibiotic regimens, thereby reducing selective pressure for resistance. They might also have better access to clean water and sanitation facilities, further minimising exposure to environmentally resistant bacteria [34].

The significant association between self-medication and MDR *E. coli* carriage ($p = 0.05$) is a crucial finding that strongly corroborates global concerns regarding antibiotic resistance. Our data show that 42.4% of MDR *E. coli* carriers engaged in self-medication, a considerably higher proportion than the 26.7% in the non-MDR group. This direct link reinforces the established understanding that inappropriate use of antibiotics, common in self-medication scenarios involving incorrect dosages, durations, or selection of antibiotics for viral infections, creates a strong selective pressure. This pressure favours the survival and proliferation of resistant bacterial strains, ultimately contributing to the rise of MDR pathogens in the community [35]. Many studies worldwide have identified irrational antibiotic use as the primary catalyst for the escalating antimicrobial resistance crisis [20], [36]. This is particularly pertinent in regions such as Osun State, Nigeria, where access to prescription-only antibiotics may be less regulated, contributing to higher rates of self-medication and subsequent resistance development.

Perhaps the most perplexing finding was the inverse association between poor refuse management and MDR *E. coli* carriage ($p = 0.046$). Counter to intuitive expectations, only 2.2% of the MDR group reported poor refuse management, compared with 8.9% in the non-MDR group. Generally, poor sanitation and inadequate waste disposal are significant contributors to the environmental spread of pathogens, including antibiotic-resistant bacteria [37]. This unexpected result prompts several considerations. It is plausible that the definition or assessment of "poor refuse management" within this study might not fully capture the specific pathways through which resistant bacteria are transmitted, or it might relate to a perceived practice rather than an objective one. For example, the open dumping of waste, while seemingly "poor," might not lead to direct human exposure if it occurs in remote areas. Alternatively, there may be unmeasured confounding factors. For example, if individuals with better refuse management practices also have greater access to healthcare and thus higher exposure to antibiotics, it could obscure the expected positive correlation [38]. Furthermore, communities with overall lower population densities or different agricultural practices, which might incidentally correlate with certain refuse management styles, could influence the prevalence of resistant strains differently [39]. Further in-depth qualitative and quantitative research focusing on specific waste disposal behaviours, environmental sampling for resistant bacteria, and comprehensive socioeconomic factors is necessary to fully decipher this unexpected correlation.

The absence of a statistically significant association between MDR *E. coli* carriage and sex or age ($p>0.05$) suggests that, within this particular community, these demographic variables are not the primary drivers of resistance acquisition. This indicates that behavioural and socioeconomic factors, such as education and self-medication practices, may play a more dominant role in shaping the landscape of antimicrobial resistance in this specific context. This aligns with research suggesting that while age and gender can sometimes be factors, behavioural risk factors often hold more weight in community-level resistance [40]. The findings collectively emphasise the multifaceted nature of antimicrobial resistance, underscoring the critical need for context-specific interventions that go beyond general demographic considerations to target modifiable risk behaviours and improve public health infrastructure.

4. CONCLUSION

This study revealed the pressing issue of widespread antibiotic resistance in rural community settings in Nigeria, driven by socioeconomic and behavioural factors. The high prevalence of MDR *E. coli* and ESBL-producing strains among healthy individuals underscores their critical role as silent reservoirs, continually fuelling the spread of AMR. Although higher education seems to confer a protective effect, likely due to enhanced health literacy, the strong association between self-medication and MDR *E. coli* carriage remains a significant concern. Ultimately, combating this escalating public health threat necessitates comprehensive interventions, including robust surveillance, targeted public education campaigns, and stringent regulatory measures to promote judicious antibiotic use and limit the spread of resistance within the

community. A specific recommendation would be to organize community-wide forums to educate the population on what MDR is and how to guide against it. Wider studies examining MDR *E. coli* in different rural communities across Osun State and Nigeria are needed to better understand the present realities and guide public health policies regarding antibiotic resistance in Nigeria. A limitation of this study is that no environmental sampling was performed for comparative analysis. It must also be noted that there is a likelihood of reported bias in self-reported data captured by the questionnaire.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

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C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

INFORMED CONSENT

Informed consent was obtained from all individuals included in this study.

ETHICAL APPROVAL

Ethical approval for this study was obtained from the Research Ethics Committee of the Institute of Public Health, Obafemi Awolowo University, Ile-Ife, Nigeria. Before commencement, permission was also secured from the traditional ruler of the community, who oversees several neighbouring villages within the study area. All participants provided verbal informed consent prior to recruitment. To ensure confidentiality, no personally identifiable information, such as names or traceable codes, was recorded or used during data collection and analysis.

DATA AVAILABILITY

The data supporting the findings of this study are available upon request from the corresponding author [OB]. The data, which contain information that could compromise the privacy of research participants, are not publicly available due to certain restrictions.

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