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ORIGINAL RESEARCH ARTICLE

High burden of extended-spectrum β-lactamase-producing and multidrug-resistant *Proteus* species and Enterobacteriaceae from market ecosystems in Oye-Ekiti, Nigeria

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ABSTRACT

Market ecosystems can act as reservoirs of antimicrobial-resistant bacteria. Local data on antibiotic-resistant bacteria from market environments in Oye-Ekiti remain limited. This study isolated environmental Gram-negative bacteria from market samples, determined their antimicrobial susceptibility profiles, calculated multiple antibiotic resistance (MAR) indices, and screened for extended-spectrum β-lactamase (ESBL) production. A total of 114 Gram-negative isolates were recovered from sewage (n = 21), market table surfaces (n = 82), and soil (n = 11) using standard cultural and biochemical methods. Susceptibility was tested by the Kirby–Bauer disc diffusion method. MAR indices were calculated and ESBL production was screened by the double-disc synergy test. *Proteus vulgaris* predominated (62; 54.4 %), followed by *P. mirabilis* (16; 14.0 %) and *Escherichia coli* (15; 13.1 %). High resistance was observed to meropenem (113/114; 99 %), ceftriaxone (104/114; 91 %), amikacin (103/114; 90 %), and gentamicin (99/114; 81 %). Among isolates tested against the respective agents, resistance reached 102/102 (100 %) for nitrofurantoin and 101/102 (99 %) for cefepime. Notably, *Proteus* species possess well-documented intrinsic resistance to nitrofurantoin (and several other agents); therefore, the observed 100 % resistance to nitrofurantoin among the predominantly *Proteus*-dominated isolate set is consistent with both intrinsic mechanisms and possible acquired resistance. MAR indices ranged from 0.33 to 1.00; the great majority exceeded the 0.20 threshold indicative of high selective pressure. Eighteen isolates (15.8 %) were phenotypically ESBL-positive, mainly *P. vulgaris* recovered from table surfaces. The sampled markets harbour multidrug-resistant Gram-negative bacteria, including ESBL producers. Improved sanitation of food-contact surfaces, routine environmental surveillance, and antimicrobial stewardship are recommended. Identification was phenotypic only; molecular confirmation is required in future work.

Keywords: Gram-negative bacteria, antimicrobial resistance, ESBL, multiple antibiotic resistance, market ecosystem, One Health, *Proteus*, intrinsic resistance.

Introduction

Antibiotic resistance is a major public health challenge affecting humans, animals, foods, and environmental health. It is now recognized as a major One Health issue because antibiotic-resistant bacteria and antibiotic resistance genes circulate among humans,

animals, food products, water, soil, wastewater, market environments and ecosystems (Abukhattab *et al.,* 2023; Hiruy *et al*., 2022; Rahman et al., 2021). Environmental settings are also important reservoirs of antibiotic-resistant bacteria, particularly where wastewater, animal wastes, poor sanitation, and food-handling activities favour bacterial survival and transmission (Amin *et al.,* 2021; Hiruy *et al.,* 2022; Mao *et al.,* 2021). The Gram-negative bacteria such as *Escherichia coli, Klebsiella pneumoniae*, *Salmonella* spp., and *Proteus* spp. are of particular concern because they cause foodborne and opportunistic infections. Furthermore, they readily acquire antibiotic resistance determinants, including extended-spectrum β-lactamases (ESBLs) genes (Ababneh *et al.,* 2022; Amin *et al.,* 2024; Ding *et al.,* 2021; Islam *et al.,* 2024; Nath *et al.,* 2023). Some of these bacteria carry virulence properties and their presence in foods and adjoining market environments increase the risk of transmission of gastrointestinal diseases (Parvin *et al.,* 2022; Rahman *et al.,* 2021).

Among environmental Enterobacteriaceae, *Proteus* species occupy a distinctive niche. *Proteus mirabilis* and *P. vulgaris* are common inhabitants of soil, water and the gastrointestinal tracts of humans and animals; they are frequently recovered from food-contact surfaces and wastewater in open-market settings. Clinically, they are important opportunistic pathogens responsible for urinary-tract infections, wound infections and, less commonly, bacteremia, especially in immunocompromised hosts. Of direct relevance to susceptibility testing, *Proteus* spp. possesses well-characterized intrinsic resistance mechanisms: they are naturally resistant to nitrofurantoin, tetracyclines, colistin and, in many strains, to polymyxins. These intrinsic traits must be distinguished from acquired resistance (for example, ESBL- or carbapenemase-mediated resistance to third-generation cephalosporins and carbapenems) when interpreting antimicrobial susceptibility data. Failure to recognize intrinsic resistance can lead to over-estimation of the acquired-resistance burden and to inappropriate clinical or public-health conclusions. Consequently, any environmental survey that recovers a high proportion of *Proteus* isolates must explicitly account for these baseline intrinsic resistances before attributing elevated resistance rates solely to selective pressure or gene transfer.

The market ecosystem creates a unique combination of environmental conditions and factors that select for pathogenic and non-pathogenic bacteria that can harbour different types of antibiotic resistance genes (ARGs) (Dong *et al.,* 2025; Parvin *et al.,* 2022; Xiao *et al.,* 2024). Also, market ecosystems aggregate fresh produce, meat, fish, wastewater, soil, food-contact surfaces, and human traffic, creating conditions that are favourable for contamination and dissemination of antibiotic-resistant bacteria from market environment to humans (Dong *et al.,* 2025; Parvin *et al.,* 2022; Xiao *et al.,* 2024). Antibiotic-resistant Gram-negative bacteria have been recovered from retail fish, poultry, leafy vegetables, and different market surfaces in several countries. A study by Habib *et al.* (2023), reported that *Escherichia coli* in fresh salad vegetables was recovered from retailers in Dubai and the genomic analysis revealed that several antimicrobial resistance determinants were present in the samples (Alhabib & Elhadi, 2024; Elsafi *et al.,* 2024; Habib *et al.,* 2023; Sajeev *et al.,* 2023). Similar studies in Nigeria show that fresh retail leafy and salad vegetables in Okada, Edo State, harboured antibiotic-resistant Gram-negative bacteria. Jesumirhewe *et al.* (2022), isolated and genomically characterized antibiotic-resistant Gram-negative bacteria, such as *Proteus mirabilis, Acinetobacter baumannii,* and *Klebsiella quasipneumoniae,* from different fresh

retail leafy and salad vegetables. Several resistance determinants, including qnrD1, were also found. Igbinosa *et al.* (2023), determined a significant increase of resistance to different antibiotic classes and the presence of beta-lactamase genes in multidrug-resistant extended-spectrum β-lactamase (ESBL)-producing *E. coli* from vegetables and ready-to-eat salads bought from open markets in Edo State. Additionally, a significant frequency of multidrug-resistant *E. coli* (56.3 %) with exceptionally high resistance to ceftazidime and imipenem was reported by Adebowale *et al.* (2022) in live bird markets in Abeokuta, Ogun State.

Surveillance of antibiotic-resistant bacteria in different environments has been identified as crucial towards providing real-time and current data on antibiotic resistance in respective environments. However, most surveillance efforts for antibiotic resistance focus excessively on humans and clinical environments and community settings (Collineau *et al.,* 2023; Diallo *et al.,* 2020). In addition, substantial surveillance gaps exist in extra-clinical environments and market ecosystems. This supports the importance of the present study to determine the extent of antibiotic-resistant bacteria in typical rural market ecosystems.

In Nigeria, the presence of multidrug-resistant and ESBL-producing *E. coli* in meats, food samples and generally within agricultural environments has been reported (Al-Mustapha *et al.*, 2022; Igbinosa *et al.,* 2023). Comparable data from market ecosystems in Oye and Ilupeju Ekiti are lacking. Therefore, this study was carried out to isolate and identify environmental Gram-negative bacteria from different market environments in Oye-Ekiti and determine their antimicrobial susceptibility to different commonly used antibiotics. It also determined the multiple antibiotic resistance characteristics and presumptively identified those Gram-negative bacteria that can produce extended-spectrum β-lactamases (ESBL).

Materials and methods

Study locations

The study was conducted in selected markets in Oye (7°48'N, 5°19'E), Ekiti State, Southwest Nigeria. The markets serve as localized commercial hubs for indigenous trade and commerce. Several people come to the markets on selected days when higher commercial activities are present. Several food items are sold in the markets, including fruits and vegetables, meats and associated products. The local environment of the market is characterized by drainage channels, stalls and stables, and local meat-processing facilities.

Sample collection

Environmental samples were collected aseptically from three sources in the markets: sewage/wastewater, market table surfaces and soil. The sewage was collected in sterile bottles and immediately taken to the laboratory for processing. Table stalls and surfaces were sampled using sterile swab sticks moistened with sterile normal saline. Soil samples in the immediate market environments were dug out to 3 cm depth using a sterile spatula into sterile containers.

Isolation and identification of Gram-negative bacteria

Gram-negative bacteria were isolated using standard methods. One hundred millilitres of sewage samples were filtered through a 0.45 µm Millipore membrane filtration system and placed on MacConkey and EMB agar plates. Soil suspensions were prepared by combining a measured quantity of soil with sterile diluent in a 1:10 weight-to-volume ratio, followed by thorough homogenization. Tenfold serial dilutions of these suspensions were made instantly in sterile diluent. Measured aliquots from the chosen dilutions were then inoculated onto suitable agar media using the spread-plate technique. After incubation under appropriate conditions, colonies were enumerated and reported as colony-forming units (CFU) per gram of soil.

The surface swabs were streaked directly. Plates were incubated at 35 °C for 24 h. Pure isolates were identified by initial colonial morphologies, Gram staining, and conventional biochemical tests (Islam *et al.,* 2024; Sajeev *et al.*, 2023).

Antimicrobial susceptibility testing

Susceptibility to antibiotics was determined using the Kirby–Bauer disc diffusion method on Mueller–Hinton agar (Igbinosa *et al.,* 2023; Parvin *et al.,* 2022). The discs included ciprofloxacin (5 µg), gentamicin (10 µg), ceftriaxone (30 µg), meropenem (10 µg), cotrimoxazole (25 µg), amikacin (30 µg), aztreonam (30 µg), amoxicillin–clavulanate (30 µg), cefepime (30 µg), nitrofurantoin (300 µg) and others. Zones were interpreted according to standard guidelines. Isolates were classified as susceptible, intermediate, or resistant. The multiple antibiotic resistance (MAR) index was calculated as the number of antibiotics to which an isolate was resistant divided by the total number of antibiotics tested against that isolate. An MAR index > 0.20 was taken to indicate origin from an environment with high antibiotic selective pressure (Ayandele *et al.,* 2020; Pan *et al.,* 2024).

Detection of ESBL production

All Gram-negative bacteria isolated were screened for ESBL production using the double-disc synergy test (DDST). Third-generation cephalosporin discs, cefotaxime (30 µg) and ceftriaxone (30 µg), were placed approximately 20 mm equidistant from an amoxicillin–clavulanic acid disc (30 µg). Observation of an enhanced zone of inhibition was used to indicate ESBL production (Habib *et al.*, 2023; Igbinosa *et al.,* 2023; Sajeev *et al.,* 2023). The bacteria were subsequently designated as ESBL and non-ESBL producers.

Results

Frequency and distribution of isolates

One hundred and fourteen Gram-negative isolates belonging to 12 species were recovered (Table 1). *Proteus vulgaris* was the most predominant bacterium (62; 54.4 %), followed by *P. mirabilis* (16; 14.0 %) and *E. coli* (15; 13.1 %). Table surfaces yielded the largest number of Gram-negative bacterial isolates (82; 71.9 %), followed by sewage (21; 18.4 %) and soil (11; 9.6 %) (Table 2). Table surfaces carried the highest burden of bacteria, with *Proteus* spp. as the most commonly recovered organisms (Table 3).

High resistance rates were recorded for the majority of the bacteria (Table 4). Antibiotic resistance rates exceeded 80 % for meropenem (113/114; 99 %), ceftriaxone (104/114; 91 %), amikacin (103/114; 90 %), and gentamicin (99/114; 81 %). Resistance to ciprofloxacin and cotrimoxazole was also substantial (77/114; 68 % and 74/114; 65 %, respectively). Lower resistance was observed to amoxicillin–clavulanate (36/114; 35 %) and aztreonam (50/114; 49 %). Some agents (nitrofurantoin, cefepime, cefuroxime, tetracycline, cefotaxime, cefoperazone) were tested against a subset of isolates; among those tested, resistance reached 102/102 (100 %) for nitrofurantoin and 101/102 (99 %) for cefepime. Resistance patterns by individual bacterial species are shown in Table 5.

MAR indices ranged from 0.33 to 1.00 (Table 6). All isolates were resistant to at least four antibiotics. The most frequent index was 0.83 (27 isolates; 23.7 %), followed by 0.75 (23; 20.1 %) and 1.00 (12; 10.5 %). The elevated indices observed here indicate substantial antimicrobial selective pressure in the sampled markets. Detailed resistance phenotype patterns are presented in Table 7.

Eighteen of the 114 isolates (15.8 %) were phenotypically positive for ESBL production by the double-disc synergy test (Table 8). *Proteus vulgaris* accounted for the majority (12 isolates), followed by *E. coli* (2). Most ESBL-positive isolates were recovered from table surfaces (Table 9).

Table 1. Frequency of Gram-negative bacterial isolates recovered from environmental samples (n = 114)

S/N	Suggested Organism	Number (%)
1	*Proteus vulgaris*	62 (54.4)
2	*Proteus mirabilis*	16 (14.0)
3	*Escherichia coli*	15 (13.1)
4	*Enterobacter aerogenes*	4 (3.5)
5	*Salmonella enterica typhi*	3 (2.6)
6	*Yersinia enterocolitica*	3 (2.6)
7	*Edwardsiella tarda*	3 (2.6)
8	*Klebsiella oxytoca*	2 (1.8)
9	*Citrobacter koseri*	2 (1.8)
10	*Proteus hauseri*	2 (1.8)
11	*Klebsiella pneumoniae*	1 (0.9)
12	*Serratia marcescens*	1 (0.9)
	Total	**114**

Table 2. Distribution of isolates by environmental sample source

Sample Source	Number of Isolates (%)
Sewage	21 (18.4)
Table surface	82 (71.9)
Soil	11 (9.6)
Total	**114**

Table 3. Distribution of isolates by environmental sample source and species

Sample	P. vulg.	P. mir.	E. coli	E. aer.	S. Typhi	K. pneu.	K. oxy.	C. kos.	P. haus.	Y. ent.	S. marc.	E. tarda
Sewage	11	4	2	-	2	-	-	1	-	-	-	1
Table surface	46	12	12	3	1	1	1	1	-	2	1	2
Soil	5	-	1	1	-	-	1	-	2	1	-	-
Total	**62**	**16**	**15**	**4**	**3**	**1**	**2**	**2**	**2**	**3**	**1**	**3**

Abbreviations: P. vulg. = Proteus vulgaris; P. mir. = Proteus mirabilis; E. aer. = Enterobacter aerogenes; S. Typhi = Salmonella enterica Typhi; K. pneu. = Klebsiella pneumoniae; K. oxy. = Klebsiella oxytoca; C. kos. = Citrobacter koseri; P. haus. = Proteus hauseri; Y. ent. = Yersinia enterocolitica; S. marc. = Serratia marcescens; E. tarda = Edwardsiella tarda.

Table 4: Frequency and percentage of antibiotic resistance among Gram-negative isolates

S/N	Antibiotic	Resistant (n/N; %)
1	Meropenem (MEM)	113/114 (99.0)
2	Ceftriaxone (CTR)	104/114 (91.0)
3	Amikacin (AMK)	103/114 (90.0)
4	Gentamicin (GEN)	99/114 (81)
5	Ciprofloxacin (CIP)	77/114 (68)
6	Cotrimoxazole (COT)	74/114 (65)
7	Aztreonam (AT)	50/114 (49)
8	Amoxicillin–clavulanate (AUG)	36/114 (35)
9	Nitrofurantoin (NIT)*	102/102 (100)
10	Cefepime (CPM)*	101/102 (99)

*Tested against a subset of isolates; denominators are therefore lower than 114. Note that *Proteus spp.* is intrinsically resistant to nitrofurantoin.

Table 5: Distribution of antibiotic resistance counts by bacterial species

Antibiotic	*P. vulg.*	*P. mir.*	*E. coli*	*E. aer.*	*S. typhi*	*K. pneu.*	*K. oxy.*	*C. kos.*	*P. haus.*	*Y. ent.*	*S. marc.*	*E. tarda*
AUG	16	5	6	3	2	-	1	1	-	1	-	3
AT	18	4	8	3	1	1	1	1	-	2	-	1
MEM	43	12	14	4	3	1	2	2	2	3	1	3
NIT	44	12	14	4	3	1	1	2	2	2	-	3
COT	31	7	10	3	2	1	2	1	2	3	1	3
GEN	39	10	13	3	3	1	2	2	2	2	1	1
CTR	42	9	13	4	3	1	2	2	2	3	1	3
CPM	44	12	14	4	3	1	1	2	2	2	-	3
AMK	31	7	10	4	3	1	2	2	2	3	1	3
CIP	39	10	12	4	2	1	2	1	2	1	1	3

Values are absolute counts of resistant isolates for each species–antibiotic combination. Abbreviations as in Table 3. AUG = amoxicillin–clavulanate; AT = aztreonam; MEM = meropenem; NIT = nitrofurantoin; COT = cotrimoxazole; GEN = gentamicin; CTR = ceftriaxone; CPM = cefepime; AMK = amikacin; CIP = ciprofloxacin.

Table 6: Distribution of multiple antibiotic resistance (MAR) index among isolates (N = 114)

MAR Index	Frequency (%)
0.33	4 (3.5)
0.41	3 (2.6)
0.50	11 (9.7)
0.58	10 (8.8)
0.66	14 (12.3)
0.75	23 (20.1)
0.83	27 (23.7)
0.91	10 (8.8)
1.00	12 (10.5)
Total	**114 (100)**

Table 7: Resistance phenotype patterns among isolates

No. of antibiotics	Resistance pattern	Frequency
4	MEM-NIT-CPM-CIP	1
4	MEM-NIT-CPM-AMK	1
4	NIT-CTR-CPM-CIP	1
4	MEM-NIT-CTR-CPM	1

No. of antibiotics	Resistance pattern	Frequency
5	AT-MEM-NIT-GEN-CPM	1
5	MEM-NIT-GEN-AMK-CIP	1
5	MEM-NIT-CTR-CPM-AMK	1
6	AT-MEM-NIT-CTR-CPM-AMK	2
6	MEM-NIT-GEN-CTR-CPM-AMK	7
6	MEM-NIT-COT-GEN-CPM-AMK	2
7	MEM-NIT-GEN-CTR-CPM-AMK-CIP	3
7	VAN-MEM-NIT-GEN-CTR-CPM-AMK	4
7	VAN-MEM-NIT-COT-GEN-CPM-AMK	2
8	VAN-MEM-NIT-COT-GEN-CPM-AMK-CIP	1
8	AT-VAN-MEM-NIT-GEN-CTR-CPM-CIP	1
8	VAN-MEM-NIT-COT-GEN-CTR-CPM-AMK	3
9	AT-VAN-MEM-NIT-COT-CTR-CPM-AMK-CIP	3
9	VAN-MEM-NIT-COT-GEN-CTR-CPM-AMK-CIP	7
9	AT-VAN-MEM-NIT-GEN-CTR-CPM-AMK-CIP	2
9	AUG-AT-VAN-MEM-NIT-GEN-CTR-CPM-AMK	2
10	AT-VAN-MEM-NIT-COT-GEN-CTR-CPM-AMK-CIP	6
10	AUG-VAN-MEM-NIT-COT-GEN-CTR-CPM-AMK-CIP	6
10	AUG-AT-VAN-MEM-NIT-COT-GEN-CTR-CPM-AMK	3
11	AUG-AT-VAN-MEM-NIT-COT-GEN-CTR-CPM-AMK-CIP	8
12	VAN-MEM-COT-GEN-CTR-AMK-CIP-CHL-CRX-TET-CPZ-CTX	8
12	AUG-AT-VAN-LBC-MEM-NIT-COT-GEN-CTR-CPM-AMK-CIP	4

Only the most frequent or representative patterns are listed for brevity; the full set of patterns appears in the original data tables. VAN = vancomycin; LBC = levofloxacin; CHL = chloramphenicol; CRX = cefuroxime; TET = tetracycline; CPZ = cefoperazone; CTX = cefotaxime.

Table 8: Distribution of ESBL-producing Gram-negative isolates by species

S/N	Organism	ESBL-positive (%)
1	*Proteus vulgaris*	12 (10.5)
2	*Escherichia coli*	2 (1.8)
3	*Enterobacter aerogenes*	1 (0.9)
4	*Yersinia enterocolitica*	1 (0.9)
5	*Proteus hauseri*	1 (0.9)
6	*Proteus mirabilis*	1 (0.9)
	Total	**18 (15.8)**

Table 9. Distribution of ESBL-producing isolates by sample source

Sample Source	ESBL-positive (n)
Sewage	1
Table surface	15
Soil	2
Total	**18**

Discussion

This study determined the frequencies of multidrug-resistant bacteria among environmental Gram-negative isolates recovered from a typical open-market ecosystem in Oye-Ekiti, Nigeria. Overall, the findings reveal a high occurrence of multidrug resistance. *Proteus* spp. constituted the most commonly isolated group, followed by *E. coli*. Other recovered genera

included *Enterobacter*, *Klebsiella* and related Enterobacteriaceae. These organisms form part of the intestinal flora of humans and animals; their presence in a market ecosystem is therefore indicative of environments heavily impacted by faecal contamination (Igbinosa *et al.,* 2023). Comparable studies in Nigeria and elsewhere have likewise documented antibiotic-resistant Gram-negative bacteria in market and agricultural settings (Al-Mustapha et al., 2022; Igbinosa *et al.*, 2023; Parvin *et al.,* 2022; Xiao *et al.*, 2024).

A critical distinction must be drawn between intrinsic and acquired resistance, especially given the predominance of *Proteus* species. *Proteus* spp. is intrinsically resistant to nitrofurantoin, tetracyclines and colistin. Consequently, the 100 % resistance to nitrofurantoin observed among the isolates tested against this agent is expected on biological grounds and should not be interpreted solely as evidence of recent selective pressure or horizontal gene transfer. In contrast, resistance to carbapenems (meropenem 99 %), third- and fourth-generation cephalosporins (ceftriaxone 91 %, cefepime 99 % of those tested), and aminoglycosides (amikacin 90 %, gentamicin 81 %) cannot be explained by intrinsic mechanisms alone. These phenotypes indicate acquired resistance, most likely mediated by ESBLs, carbapenemases or other transferable determinants. The phenotypic detection of ESBL production in 15.8 % of isolates (predominantly *P. vulgaris* from table surfaces) further supports the presence of acquired β-lactamase-mediated resistance within the market environment.

From a market-biosecurity perspective, the high rates of acquired resistance to carbapenems and third-generation cephalosporins are of particular public-health concern. Food-contact surfaces (table tops used for display and cutting of meat and produce) yielded the majority of isolates and the majority of ESBL producers. Inadequate cleaning of these surfaces creates persistent reservoirs that can continuously contaminate fresh foods and expose vendors and consumers to multidrug-resistant organisms. Once introduced into the food chain, such bacteria may colonize the human gut or cause opportunistic infections that are difficult to treat with first-line β-lactams. The elevated MAR indices (most > 0.20 and many approaching 1.00) reinforce the conclusion that the sampled markets experience substantial antimicrobial selective pressure, whether from direct antibiotic use, contamination of wastewater, or both. Strengthening daily sanitation of food-contact surfaces, segregating raw-meat handling areas, and instituting routine environmental monitoring would therefore constitute immediate, practical biosecurity interventions.

The table surfaces appear to have the highest carriage of Gram-negative bacteria, followed by the sewage samples. The tables are used for the display of various food items and for cutting meat by vendors who sell directly to consumers. Heavy bacterial carriage implies low levels of hygiene and intermittent biosecurity risk. Surfaces and equipment that are not properly cleaned can become hotspots for the emergence and persistence of multidrug-resistant Gram-negative bacteria (Parvin *et al.*, 2022; Xiao *et al.,* 2024; Amin *et al.,* 2024; Dong *et al.,* 2025).

Several studies have reported increasing resistance to conventional antibiotics among bacteria from open-market settings. High resistance to β-lactams among *E. coli* isolates in Nigerian environments has been documented by Igbinosa *et al.* (2023). Al-Mustapha *et al.* (2022), recorded resistance rates exceeding 80 % for β-lactams and aminoglycosides. Abdel-

Hameed *et al*. (2025), observed widespread resistance to carbapenems and cephalosporins among environmental Gram-negative pathogens. Habib *et al*. (2023), recorded high co-resistance to β-lactams, fluoroquinolones and aminoglycosides in market-derived Enterobacteriaceae. The present data are therefore consistent with regional and international trends, while adding local evidence from a previously under-sampled rural market ecosystem in Ekiti State.

Conclusion

Environmental samples from markets in Oye-Ekiti yielded a diverse set of Gram-negative bacteria dominated by *Proteus vulgaris*. High rates of resistance to carbapenems, cephalosporins and aminoglycosides, elevated multiple-antibiotic-resistance indices, and the presence of ESBL-producing isolates indicate that these market environments harbour multidrug-resistant organisms. While the near-universal resistance to nitrofurantoin is partly attributable to the intrinsic resistance of *Proteus* spp., the high prevalence of resistance to carbapenems and third-generation cephalosporins reflects acquired mechanisms of clear public-health significance.

Specific policy and practice changes are warranted. Local market authorities should institute mandatory daily sanitation protocols for all food-contact surfaces, with particular attention to meat-cutting tables. Regular environmental microbiological surveillance targeting both total Gram-negative load and phenotypic ESBL/carbapenem resistance should be incorporated into existing public-health inspection programmes. Antimicrobial stewardship messages directed at livestock producers and market vendors should emphasize the one health consequences of antibiotic misuse. Finally, future studies must incorporate molecular identification and resistance-gene detection to confirm phenotypic findings and to map the precise genetic determinants circulating in these ecosystems.

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