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Synanthropic Insects as Potential Mechanical Vectors of Enteric and Antibiotic-Resistant Bacteria on Fresh Vegetables Sold in Open Markets in Ibadan Metropolis, Nigeria

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Abstract: This study investigated the role of synanthropic insects as mechanical vectors of enteric and antibiotic-resistant bacteria in two major vegetable markets (Oje and Bodija) in Ibadan, Nigeria. Fresh vegetables, often consumed raw, are highly susceptible to microbial contamination in open-market environments where sanitation infrastructure is limited. Using a cross-sectional design, 1,117 insects, comprising houseflies, cockroaches, ants, and beetles, were collected alongside vegetable samples. Bodija Market accounted for the majority of insect collections (60.52%), though both markets exhibited high ecological diversity across the four taxa. Bacterial isolates were identified using conventional microbiological techniques, including Gram staining and biochemical profiling. Results confirmed the presence of several pathogens, including Escherichia coli, Klebsiella pneumoniae, Enterobacter cloacae, Salmonella enterica, Salmonella typhi, and Shigella dysenteriae, with total viable count loads reaching 1.9×10^{10} CFU/ml. Antibiotic susceptibility testing, conducted per CLSI (2023) guidelines, revealed near-universal resistance to cephalosporins, cotrimoxazole, and tetracycline. Notably, multidrug-resistant (MDR) phenotypes were documented across multiple species. The study found that insect-derived isolates exhibited higher species diversity and resistance prevalence than those from vegetables, confirming their role as reservoirs and transporters of antibiotic resistance. These findings provide a critical evidence base for the necessity of targeted integrated pest management, improved market sanitation, and enhanced food safety policies to reduce insect-mediated contamination and protect public health in urban settings.

Keywords: Antibiotic resistance, Enteric bacteria, Mechanical vectors, Synanthropic insects, Vegetable markets.

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Introduction

Food safety remains one of the most pressing global public health challenges of the twenty-first century. The World Health Organization (WHO) estimates that approximately 600 million people fall ill annually following consumption of contaminated food, resulting in 420,000 deaths and the loss of 33 million disability-adjusted life years (DALYs) (WHO, 2015). Fresh vegetables occupy a particularly critical position within this landscape, as they are frequently consumed raw, bypassing thermal processing that would otherwise inactivate pathogenic microorganisms. Globally, produce-associated outbreaks have been attributed to Salmonella spp., Escherichia coli O157:H7, Listeria monocytogenes, and Campylobacter spp. (Callejón et al., 2015; Painter et al., 2013). While contamination may originate from irrigation water, soil amendments, or post-harvest handling, emerging evidence underscores the role of synanthropic insects as significant yet underappreciated vectors in farm-to-fork transmission pathways (Nayduch & Joyner, 2013).

Synanthropic insects species that have evolved to exploit human-modified environments include the housefly (*Musca domestica*), blowfly (*Calliphora* spp.), German cockroach (*Blattella germanica*), and various ant species (Formicidae). These organisms thrive in close association with human settlements, waste sites, and food production facilities, positioning them as ideal bridge vectors between reservoirs of contamination and human food supplies (Graczyk et al., 2005; Schurmann et al., 2004). Critically, they function as mechanical vectors transporting microorganisms externally on body surfaces, appendages, and mouthparts, or internally through the digestive tract, without biological amplification of the pathogen (Greenberg, 1973; Levine & Levine, 1991).

Musca domestica alone has been shown to harbour more than 100 pathogenic microbial species, facilitated by regurgitation of salivary secretions and deposition of faecal droplets onto food substrates (Förster et al., 2007; Khamesipour et al., 2018). The external surface of a single housefly can carry in excess of one million bacteria, while gut flora may harbour an equally diverse and virulent microbial community (Mramba et al., 2007). Studies demonstrate that flies visiting contaminated substrates can transfer viable enteric pathogens, including *Salmonella* Typhimurium and *E. coli* O157:H7, to clean surfaces within seconds of contact, with pathogen viability maintained for several hours under ambient conditions (Alam & Zurek, 2004; Holt et al., 2007).

Of particular contemporary concern is the role of synanthropic insects in the environmental dissemination of antibiotic-resistant bacteria (ARB) and antibiotic resistance genes (ARGs). Insects inhabiting environments rich in antibiotic residues including agricultural settings where prophylactic use is prevalent may acquire and redistribute resistant strains through normal foraging activities (Zurek & Ghosh, 2014). Extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae, methicillin-resistant Staphylococcus aureus (MRSA), and carbapenem-resistant organisms have been isolated from field-caught houseflies and cockroaches (Blaak et al., 2014; Bonnedahl et al., 2017; Onwugamba et al., 2018). The capacity of these insects to bridge agricultural, peri-urban, and domestic environments means that resistance determinants may be transferred across ecological niches in which antibiotic selective pressure would otherwise be absent (Bawin et al., 2021).

Within the Nigerian context, research on food safety in open markets has largely emphasised bacteriological enumeration with minimal integration of entomological analysis. There is a notable scarcity of studies concurrently investigating insect vectors, bacterial contamination, and antibiotic resistance patterns within the same market environment (Odewale et al., 2025; Olanbiwoninu & Olanrewaju, 2024). The present study was therefore undertaken to: (i) collect and identify insect species associated with fresh vegetable displays in selected markets; (ii) isolate and characterise enteric bacteria from insect vectors and vegetable samples; (iii) determine antibiotic susceptibility profiles of recovered isolates; and (iv) evaluate the potential role of insects as mechanical carriers of antibiotic-resistant enteric bacteria in urban vegetable market environments in Ibadan metropolis, Nigeria.

Materials and Methods

Study Area and Design

This study was conducted in Ibadan metropolis, capital of Oyo State, southwestern Nigeria (latitude 7°20′–7°40′ N; longitude 3°50′–4°10′ E). A cross-sectional design with purposive sampling was adopted. Two major markets Oje and Bodija were selected based on size, volume of vegetable trade, and observable insect pressure. Both markets operate under conditions of limited waste management, inadequate drainage, and unrestricted insect access. Ibadan's tropical wet-and-dry climate (mean temperature 22–34°C; annual rainfall 1,200–1,500 mm) sustains continuous insect activity throughout the year, making it an ecologically suitable setting for investigating insect-mediated contamination.

Insect Collection and Identification

Sampling was conducted during peak market hours to maximise insect activity. Flying insects (principally Diptera) were collected using sweep nets and sticky traps positioned near vegetable stalls. Crawling insects cockroaches, ants, and beetles were collected by hand-picking with sterile forceps and adhesive traps placed adjacent to vegetable displays. Collected specimens were transferred into sterile labelled containers, transported to the laboratory, and immobilised by refrigeration to preserve external microbial flora. Each specimen was identified to the lowest feasible taxonomic level using standard entomological keys, based on body segmentation, wing structure, mouthparts, antennae, and leg morphology.

Vegetable Sample Collection

Fresh vegetable samples were collected aseptically from the same stalls where insect sampling was conducted, using sterile gloves and forceps directly from display surfaces. Each sample was sealed in a sterile labelled polyethylene bag and transported to the laboratory in insulated containers for processing within 24 hours. Outer leaves were removed; 10 g ofeach sample was homogenised with a mortar and pestle in peptone water and serially diluted in ten-fold steps.

Bacterial Isolation and Biochemical Characterisation

For insect samples, individual specimens were placed in sterile physiological saline (0.85% NaCl) and agitated for 2–3 minutes; aliquots of serial dilutions were plated onto selective media by spread plate technique. For vegetable samples, 10 g was homogenised in 225 mL sterile buffered peptone water; aliquots (0.1 mL) of dilutions 10^{-1}, 10^{-4}, 10^{-6}, and 10^{-8} were plated by pour plate method. Media employed included: Nutrient Agar (NA; total viable count), MacConkey Agar (MAC; Enterobacteriaceae), Salmonella-Shigella Agar (SSA; Salmonella/Shigella spp.), and Mannitol Salt Agar (MSA; Staphylococcus spp.). All plates were incubated at 37°C for 18–24 hours; distinct colonies were subcultured to purity and stored on NA slants at 4°C.

Isolate characterisation was based on colonial morphology, Gram staining, and a battery of biochemical tests: catalase (3% H_2O_2), oxidase (Kovács reagent), KOH string test (3% KOH), citrate utilisation (Simmons citrate agar), methyl red, Voges-Proskauer (α-naphthol/10% NaOH), starch hydrolysis (starch agar + Gram's iodine), and fermentation of 12 sugars (mannitol, sorbitol, dextrose, fructose, sucrose, lactose, sorbose, inositol, arabinose, trehalose, maltose, galactose).

Antibiotic Susceptibility Testing

Antibiotic susceptibility was assessed by disc diffusion on Mueller-Hinton Agar following CLSI (2023) guidelines. Overnight cultures adjusted to 0.5 McFarland turbidity were used to inoculate plates pre-incubated at 37°C for 20 minutes. Discs were applied equidistantly; plates were pre-cooled at 4°C for 30 minutes to allow antibiotic diffusion before incubation at 37°C for 18 hours. Antibiotics tested for Gram-negative organisms were: ceftriaxone (CTR, 30 µg), cefotaxime (CTX, 30 µg), cefoperazone (CPR, 30 µg), cefuroxime (CRX, 30 µg), tetracycline (TET, 30 µg), cotrimoxazole (COT, 10 µg), gentamicin (GEN, 10 µg), chloramphenicol(CHL, 30 µg), meropenem (MEM, 10 µg), ciprofloxacin (CIP, 5 µg), amikacin (AMK, 30 µg), and vancomycin (VAN, 30 µg). Zone diameters were interpreted according to CLSI (2023) breakpoints: susceptible ≥17 mm, intermediate 14–16 mm, resistant ≤13 mm. Multidrug resistance (MDR) was defined as resistance to agents in three or more antibiotic classes (Magiorakos et al., 2012).

Data Analysis

Entomological data were summarised using descriptive statistics (mean, median, standard deviation, minimum, maximum). The Shannon-Wiener diversity index (H') was computed to quantify species richness and evenness within insect assemblages. Bacterial prevalence was expressed as frequencies and percentages. Antibiotic resistance patterns were evaluated based on the proportion of isolates resistant to individual agents and the occurrence of MDR phenotypes.

Results and Discussion

Distribution, Abundance, and Diversity of Synanthropic Insect Vectors

A total of 1,117 synanthropic insects were collected across Oje (n = 441; 39.48%) and Bodija (n = 676; 60.52%) markets, comprising four taxonomic groups: houseflies, cockroaches, ants, and beetles (Table 1). The Bodija-to-Oje insect burden ratio of 1.53:1 is consistent with patterns reported in comparable sub-Saharan African urban markets, where larger, higher-throughput produce markets sustain greater synanthropic insect densities owing to increased organic waste accumulation and the volume of perishable commodities on open display (Abebe et al., 2020; Echeta et al., 2019).

Table 1: Distribution and relative frequency of synanthropic insect vectors across Oje and Bodija markets, Ibadan, Nigeria (N = 1,117).

Insect Group	Oje (n=441)	Bodija (n=676)	Total (N=1,117)	% of Total
Houseflies (*Musca domestica*)	120 (27.21%)	202 (29.88%)	322	28.83%
Cockroaches (*Blattella germanica / P. americana*)	112 (25.40%)	199 (29.44%)	311	27.84%
Ants (Formicidae)	107 (24.26%)	156 (23.08%)	263	23.55%
Beetles (Coleoptera)	102 (23.13%)	119 (17.60%)	221	19.79%
Total	**441**	**676**	**1,117**	**100%**

Note: Values in parentheses indicate within-market relative frequencies. Totals expressed as proportions of the overall sample (N = 1,117).

Descriptive statistics (Table 2) further illuminate this disparity. The mean insect count per species at Bodija (169.00; SD = 39.40) was 53% higher than at Oje (110.25; SD = 7.68). The narrow standard deviation at Oje (range: 102–120; span of 18 specimens) indicates a remarkably uniform inter-taxon distribution, contrasted with Bodija's wider intrasite range of 83 specimens (119 beetles to 202 houseflies). This differential likely reflects Bodija's larger spatial footprint and greater diversity of organic substrates available as breeding and foraging resources.

Table 2: Descriptive statistics for insect counts per species across both market sites.

Market	n	Mean	Median	SD	Min	Max
Oje Market	441	110.25	109.50	7.68	102	120
Bodija Market	676	169.00	177.50	39.40	119	202
Combined	**1,117**	**279.25**	**287.00**	**46.52**	**221**	**322**

Note: Descriptive statistics are calculated across the four insect taxa for each market site. SD = standard deviation.

Shannon-Wiener diversity indices (Table 3) of H’ = 1.3845 (Oje) and H’ = 1.3651 (Bodija) were near-maximal relative to the theoretical maximum for four equally distributed species of H’max = ln(4) = 1.3863. Such near-perfect evenness implies that entomological contamination risk at these markets is not attributable to a single dominant vector but constitutes a compound, multi-taxon hazard distributed evenly across the insect community a considerably more challenging scenario from a food safety management perspective than one characterised by a single dominant pest species.

Table 3: Shannon-Wiener diversity index (H') for insect assemblages at each market site and combined.

Market Site	**Shannon Index (H')**	**Interpretation**
Oje Market	1.3845	High diversity / near-maximum evenness
Bodija Market	1.3651	High diversity / near-maximum evenness
Combined	**1.3757**	**High diversity**

Note: H' values approaching ln(4) = 1.3863 indicate near-maximum evenness across a four-species assemblage.

Houseflies as Dominant and High-Risk Vectors

Musca domestica was the most abundant taxon (n = 322; 28.83%), with a higher absolute count at Bodija (n = 202) than at Oje (n = 120). This dominance reflects the species' prolific breeding in organic waste and manure, its indiscriminate feeding behaviour, and its high mobility features that allow it to bridge contamination reservoirs and food surfaces with great efficiency (Greenberg, 1973; Levine & Levine, 1991). Of particular relevance to AMR, field-caught houseflies from livestock-adjacent environments have been shown to carry ESBL-producing Enterobacteriaceae, carbapenem-resistant organisms, and colistin resistance genes on mobile genetic elements (Onwugamba et al., 2018; Zurek & Ghosh, 2014). The co-location of food animals, raw meat, and fresh produce at both Oje and Bodija creates precisely the mixed-use environment in which such cross-contamination pathways are most likely to be operational.

Cockroaches: Nocturnal Persistence and AMR Carriage

Cockroaches were the second most abundant group (n = 311; 27.84%), with near co-dominant representation alongside houseflies at Bodija Market (29.44% vs. 29.88% of site totals, respectively). This parity is epidemiologically consequential: while houseflies are predominantly diurnal, cockroaches are nocturnal foragers that continue traversing food storage areas and vegetable displays after trading hours, extending insect-mediated contamination risk throughout overnight storage periods during which active surveillance is absent (Pai et al., 2003; Tatfeng et al., 2005). The documented capacity of cockroaches to carry Klebsiella pneumoniae, MRSA, Pseudomonas aeruginosa, and MDR E. coli from gut contents and external surfaces in food market environments (Schurmann et al., 2004; Tatfeng et al., 2005) renders the high counts at both sites a substantive and previously undercharacterised risk factor for antibiotic-resistant bacterial contamination of fresh produce in this setting.

Ants and Beetles: Underappreciated Vectors

Ants (Formicidae; n = 263; 23.55%) exhibited consistent proportional representation across both markets (Oje: 24.26%; Bodija: 23.08%), suggesting that ant colonisation may be governed by structural microhabitat factors crevice availability, drain margins, and produce stacking areas that are broadly comparable across market types (Graczyk et al., 2005). Their tendency to access internal vegetable surfaces and penetrate packaging renders them effective vectors for depositing bacteria onto edible portions of produce in a manner not neutralised by surface washing alone (Moreira et al., 2005). Beetles (Coleoptera; n = 221; 19.79%) showed a marked between-site disparity (Oje: 23.13%; Bodija: 17.60%), which may reflect competitive exclusion by expanding housefly and cockroach populations at Bodija. Despite their lesser abundance, beetle mandibular activity can physically breach the outer cuticle of root vegetables and leafy greens, facilitating internalisation of surface bacteria into tissues inaccessible to post-harvest decontamination (Brandl, 2006; Olaimat & Holley, 2012).

Microbial Load of Vegetable Samples

Quantitative microbiological analysis revealed substantially high microbial burdens across all three selective culture media (Table 4). The Total Viable Count of 1.9×10^{10} CFU/ml far exceeds the internationally accepted safety limit of 10^5–10^6 CFU/g for fresh vegetables recommended by the International Commission on Microbiological Specifications for Foods (ICMSF, 2018) and the European Commission Regulation EC No.

2073/2005 for ready-to-eat produce. These values are consistent with comparable investigations in Nigerian and West African market settings; Oranusi et al. (2013) similarly reported TVC values of 10^8–10^{10} CFU/g in vegetables from Ota markets, attributing contamination to untreated irrigation water and poor post-harvest handling.

Table 4: Microbial load of vegetable samples from selected markets in Ibadan metropolis.

Culture Medium	Total Plate Count	Colony Forming Units (CFU/ml)
Total Viable Count (TVC)	194	1.9×10^{10}
Enterobacteriaceae Count	95	9.5×10^{10}
Salmonella-Shigella Count	74	7.4×10^{9}

TVC = Total Viable Count; CFU/ml = Colony Forming Units per millilitre.

The ambient temperature range of 34–37°C falls within the optimal growth range for mesophilic pathogens (optimum: 35–37°C), facilitating exponential bacterial proliferation during open-air display. Combined with near-neutral pH (6.80–6.89) broadly permissive for Enterobacteriaceae growth the physicochemical environment of these marketplaces effectively promotes pathogen survival and multiplication in the absence of cold chain infrastructure, a well-documented deficiency across informal food markets in low- and middle-income countries. The Enterobacteriaceae count of 9.5×10^{10} CFU/ml is particularly alarming, as this family encompasses primary causative agents of foodborne gastroenteritis, urinary tract infections, neonatal meningitis, and healthcare-associated infections. The Salmonella-Shigella count of 7.4×10^{9} CFU/ml confirms the presence of specific faecal-route pathogens, most plausibly introduced through untreated wastewater irrigation or direct insect-mediated transfer.

Bacterial Species Distribution and Characterisation

A total of 18 characterised isolates were recovered from vegetable samples, representing seven species: Escherichia coli (n = 5; 27.8%), Klebsiella pneumoniae (n = 5; 27.8%), Enterobacter cloacae (n = 3; 16.7%), Salmonella spp. (n = 3; 16.7%), and Shigella dysenteriae (n = 2; 11.1%). All isolates were Gram-negative, rod-shaped, catalase-positive, and KOH-positive profiles consistent with the family Enterobacteriaceae. Colonial morphology on SSA revealed small, raised, smooth, mucoid colonies with pale to black colouration (hydrogen sulphide precipitation a hallmark of Salmonella spp.); MAC isolates displayed the characteristic bimodal pattern of pink-to-red lactose-fermenting colonies (E. coli, Klebsiella, Enterobacter) and colourless non-lactose fermenters (Salmonella, Shigella).

Biochemical differentiation was achieved through IMViC profiling and ancillary tests. Shigella dysenteriae isolates were methyl red-positive, VP-negative, citrate-positive, oxidase-negative, and non-motile consistent with the genus's fermentative, non-motile profile and its classification in Bergey's Manual. Klebsiella pneumoniae exhibited VP-positive, methyl red-negative, citrate-positive, and non-motile profiles reflecting the butanediol fermentation pathway. Enterobacter cloacae was distinguished from Klebsiella by positive motility. E. coli isolates conformed to the classic IMViC pattern (+/+/−/−). Salmonella typhi and S. enterica were differentiated by variable motility and serovar-specific biochemical reactions.

Sugar fermentation profiling provided additional discriminatory resolution. Universal fermentation of mannitol, dextrose, fructose, sucrose, and trehalose was observed. The absence of gas production in Shigella dysenteriae isolates (SSAA001 and SSAA002) is diagnostically definitive, reflecting the absence of formate hydrogen lyase in this species. Lactose negativity in Salmonella and Shigella spp. is consistent with their non-lactose-fermenting status, a feature exploited by differential media for presumptive identification. The sorbitol-negative phenotype of most E. coli isolates warrants further molecular investigation: sorbitol-negative E. coli is associated with the O157:H7 serotype (EHEC), a major cause of haemorrhagic colitis and haemolytic uraemic syndrome (HUS), and its presence on market vegetables would carry significant public health implications.

Antibiotic Susceptibility and Multidrug Resistance

Antibiotic susceptibility testing revealed a predominantly resistant profile. Near-universal resistance was recorded against ceftriaxone (CTR), cefotaxime (CTX), cefoperazone (CPR), cefuroxime (CRX), tetracycline (TET), and cotrimoxazole (COT) across the majority of isolates. This pattern strongly suggests the production of extended-spectrum beta-lactamases (ESBLs), a major acquired resistance mechanism in Enterobacteriaceae capable of hydrolysing third-generation cephalosporins and aztreonam (Basset et al., 2022; Blaak et al., 2014). Co-resistance to cotrimoxazole and tetracycline further narrows empirical treatment options, as these agents constitute first-line therapies in

Nigerian primary healthcare settings where more expensive fluoroquinolones or aminoglycosides are often unavailable.

Ciprofloxacin (CIP) and amikacin (AMK) demonstrated the greatest residual activity. Ciprofloxacin inhibits DNA gyrase (topoisomerase II) and topoisomerase IV mechanisms distinct from beta-lactamases and therefore not cross-affected by ESBL production. Amikacin's structural modifications render it less susceptible to many aminoglycoside-modifying enzymes. However, resistance to ciprofloxacin was detected in several K. pneumoniae and E. coli isolates, reflecting the emergence of plasmid-mediated quinolone resistance (PMQR; qnr determinants) and chromosomal mutations in DNA gyrase/topoisomerase IV. Vancomycin exhibited no measurable activity against any isolate, as expected given its impermeable outer-membrane barrier against Gram-negative organisms; its inclusion served as a methodological negative control, confirming procedural integrity.

The MDR phenotypes documented defined as resistance to three or more antibiotic classes (Magiorakos et al., 2012) align with the global trajectory of increasing AMR in agricultural and food chain environments. Insect-derived isolates exhibited higher species diversity and resistance prevalence than vegetable-derived isolates, consistent with insects functioning as reservoirs of ARB acquired from waste-rich environments and as inter-environment shuttles for clinically significant resistance determinants (Bawin et al., 2021; Fotedar et al., 2020; Onwugamba et al., 2020). The concurrent presence of high-density insect populations in environments where fresh vegetables, raw meat, sewage effluent, and antibiotic-containing agricultural waste coexist creates a highly permissive setting for ARG acquisition and dissemination via both direct mechanical transfer and horizontal gene transfer (HGT) within insect gut communities (Zurek & Ghosh, 2014).

Mechanisms of Insect-Mediated Contamination and AMR Dissemination

Three principal mechanisms by which synanthropic insects at these markets could facilitate transfer of ARB to fresh vegetables are proposed. First, direct mechanical transfer via leg setae, tarsal pads, and proboscis contact during insect visitation to vegetable surfaces represents the most immediate route; multiple studies confirm the viability of transferred organisms for several hours post-deposition under tropical ambient temperatures (Alam & Zurek, 2004; Holt et al., 2007). Second, deposition of faecal droplets and regurgitated material characteristic feeding behaviours of houseflies and cockroaches introduces gut-associated ARB directly onto produce surfaces in quantities sufficient to initiate bacterial colonisation and biofilm formation on stomata, trichomes, and cut surfaces (Berger et al., 2010; Brandl, 2006). Third, HGT between resistant and susceptible bacteria within the high-density insect gut may amplify the local pool of ARGs implying that insects not merely redistribute pre-existing resistance determinants but actively generate novel resistance landscapes within the food environment (Zurek & Ghosh, 2014).

Public Health Policy Implications

The findings of this study carry direct policy implications for Nigeria and analogous LMIC settings. Fresh vegetables sold at Oje and Bodija are widely consumed raw, and their microbial safety is not safeguarded by mandatory processing or cold chain requirements. The demonstrated high insect burden, polymicrobial contamination, and widespread MDR provide an entomological and microbiological evidence base for the following targeted interventions: (i) implementation of integrated pest management (IPM) strategies encompassing sealed waste receptacles, scheduled refuse collection, and physical barriers (screens, covered display cabinets, protective netting) to limit insect access to open vegetable displays; (ii) investment in cold chain infrastructure to interrupt the temperature-dependent microbial growth cycle; (iii) enforcement of robust antimicrobial stewardship programmes and Nigeria's National Antimicrobial Resistance Action Plan (NARAP) to stem AMR gene dissemination through the food supply chain; and (iv) establishment of routine microbiological surveillance of market insects and vegetables, guided by a One Health framework integrating health authorities, environmental agencies, market associations, and local governments (Van Boeckel et al., 2014; WHO, 2019).

CONCLUSION

This study demonstrates that synanthropic insects principally houseflies, cockroaches, ants, and beetles are present at high abundance and near-maximum ecological evenness in two major fresh produce markets in Ibadan metropolis, Nigeria. Concurrently, vegetable samples were found to harbour dangerously high loads of enteric bacteria, including E. coli, K. pneumoniae, S. typhi, S. dysenteriae, and Enterobacter cloacae, at Total Viable Counts orders of magnitude above international safety thresholds. Near-universal resistance to cephalosporins, cotrimoxazole, and tetracycline, coupled with multidrug-resistant phenotypes, underscores the potential for these market environments to serve as hotspots for the acquisition and dissemination of antibiotic resistance via the food chain. Insect-derived isolates exhibited higher species diversity and resistance prevalence than vegetable-derived isolates, consistent with insects functioning as active reservoirs and inter-environment vectors of clinically significant ARB. These findings make a compelling case for urgently integrated pest management, cold chain investment, antimicrobial stewardship, and evidence-based food safety policy aligned with the One Health paradigm across urban informal food markets in Nigeria and comparable settings.

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