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Research Article

Bacterial and Fungal Diversity, Load Dynamics, and Antibiogram Profiles of Spoilt Fruits Sold at Jimeta Metropolis, Nigeria. A Comparative Post-Harvest and Public Health Study

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Abstract

Fruits are essential for human nutrition due to their rich content of vitamins, minerals, fiber, and antioxidants. However, post-harvest losses due to microbial spoilage remain a major challenge in Nigeria, with approximately 20% of annual fruit production lost before reaching consumers. This study investigated the bacterial and fungal diversity, load dynamics, and antifungal susceptibility profiles of spoiled fruits sold at Kasuwan Gwari Market, Yola, Adamawa State, Nigeria. A total of 50 visibly spoiled fruits comprising oranges, avocados, watermelons, pawpaws, and apples (n=10 per fruit type) were aseptically sampled. Fungal and bacterial isolates were obtained using standard microbiological techniques on Potato Dextrose Agar and selective bacterial media, respectively. Fungal and bacterial loads were quantified as CFU/g, and data were analyzed using two-way ANOVA, chi-square tests, and Tukey's HSD post-hoc comparisons (α=0.05). Antifungal susceptibility was determined using the disk diffusion method according to CLSI M44-A2 guidelines. A total of 75 fungal and 88 bacterial isolates were recovered. Aspergillus niger was the most prevalent fungus (48.0%) with the highest mean load (2.58×10^5 CFU/g), while Pseudomonas spp. dominated the bacterial flora (52.0%) with the highest mean load (3.09×10^5 CFU/g). Significant associations were observed between fruit type and microbial occurrence for both fungi (χ^2=34.72, p=0.022) and bacteria (χ^2=41.58, p=0.003). Pawpaw supported the highest microbial loads for both fungi (1.82×10^5 CFU/g) and bacteria (1.82×10^5 CFU/g), while watermelon exhibited the lowest. Bacterial loads were approximately 34% higher than fungal loads overall (1.46×10^5 vs. 1.09×10^5 CFU/g). All filamentous fungi were resistant to fluconazole, while Fusarium spp. showed reduced susceptibility to itraconazole (14.2 mm) and amphotericin B (15.8 mm). Nystatin remained universally effective (19.0–25.1 mm). The presence of potentially toxigenic fungi (A. flavus 26.0%, F. oxysporum 34.0%) and enteric bacteria (E. coli 40.0%, Salmonella spp. 14.0%) raises significant food safety concerns, with fungal loads in pawpaw and avocado exceeding NAFDAC limits (1.0×10^5 CFU/g). Spoilt fruits at Kasuwan Gwari Market harbor diverse fungal and bacterial populations, including potentially pathogenic and toxigenic species, with microbial loads exceeding regulatory limits. The significant fruit-microbe associations observed underscore the need for fruit-specific post-harvest interventions, improved cold chain infrastructure, and routine microbiological surveillance to reduce post-harvest losses and protect public health.

Keywords: *Fruit spoilage; fungal diversity; bacterial diversity; antifungal susceptibility; post-harvest losses.*

INTRODUCTION

Fruits play an essential role in a well-balanced eating pattern. They provide key vitamins, most notably A and C, alongside important minerals such as potassium, magnesium, and calcium, as well as dietary fiber. These components are vital for maintaining good health and reducing the risk of chronic non-communicable diseases. Furthermore, fruits are rich in bioactive compounds such as flavonoids, polyphenols, and carotenoids, which help shield the body from oxidative stress, inflammatory responses, heart-related diseases, and several forms of cancer (Adebayo and Ogunleye, 2025). In spite of these well-established nutritional benefits, a notable drawback of fruits is their naturally brief storage life. This is largely due to their elevated water activity (ranging from 0.95 to 0.99), a pH that falls between neutral and acidic, and an abundance of nutrients, conditions that make them highly vulnerable to rapid microbial growth and decay. Bacteria, which often find their way onto fruits through contact with soil, dust, contaminated irrigation water, handling tools, and post-harvest surroundings, are major contributors to spoilage (Chukwu and Eze, 2024). This reality highlights the pressing need for appropriate storage, sanitary handling practices, and effective preservation methods to prolong shelf life, cut down on food waste, and protect public health.

Many nations in both tropical and temperate zones are involved in large-scale fruit cultivation. Among African countries, Nigeria stands out as a leading agricultural producer, generating considerable annual harvests of oranges, bananas, papayas, mangoes, watermelons, and avocados. Nevertheless, despite this high output, a significant share of the harvested fruit is lost because of substandard handling methods, poor transport networks, a lack of adequate storage infrastructure, and limited access to cold chain systems (Daramola and Yusuf, 2026). Over the last twenty years, fruit consumption within Nigeria has climbed by more than 30%, driven mainly by growing public awareness of the health advantages associated with nutrient-rich diets, rapid urbanization, and changing food preferences. Paradoxically, however, roughly one-fifth of all fruits grown each year go bad before they ever reach consumers. According to industry estimates, Nigeria loses substantial amounts to post-harvest waste annually, with a significant percentage of agricultural produce spoiling before reaching consumers (Ekunseitan and Adebayo, 2025). These post-harvest losses not only place a heavy financial strain on farmers and market sellers but also worsen food insecurity and environmental waste in a country where millions still suffer from undernutrition (Fasoyiro and Idowu, 2024).

Fruits create an ideal environment for microbial colonization, especially by bacteria, because of their high levels of fermentable sugars (including glucose, fructose, and sucrose), organic acids, minerals, vitamins, and amino acids, all of which support fast bacterial growth. Food spoilage is broadly understood as any perceptible alteration in a food item's composition, texture, smell, or look that makes it unsafe or unpalatable for human consumption. In fruits, bacterial spoilage typically starts with the enzymatic degradation of pectins, structural polysaccharides located in the middle lamella and primary cell wall, leading to tissue softening, breakdown, and eventual rot, which becomes evident as a slimy, waterlogged consistency. As bacteria metabolize starches and simple sugars, they give rise to unpleasant odors and off-flavors, along with byproducts such as lactic acid, acetic acid, ethanol, carbon dioxide, and various volatile organic compounds. Certain bacteria, particularly those belonging to the genera *Pseudomonas*, *Erwinia*, and *Xanthomonas*, produce pectinase and cellulase enzymes that enable them to invade even undamaged fruit tissues through natural openings or to break down the outer cuticle directly, resulting in dead spots and widespread tissue destruction (Garba and Lawal, 2025).

Contamination of fruits by microbes can happen at numerous critical points along the supply chain. These include the pre-harvest phase (e.g., during cultivation, irrigation, fertilization, and contact with animal waste in the field), at harvest (mechanical injury, worker sanitation), during post-harvest handling (sorting, packing, washing), in transit (temperature fluctuations, cross-contamination), during storage (excess humidity, insufficient refrigeration), and at the final point of sale (open displays, handling by customers). In addition, poor hygiene practices by consumers after purchase, such as failing to wash fruits properly or cutting them with unclean utensils, can also introduce contaminants and speed up spoilage (Hassan and Nwachukwu, 2026). Once fruits spoil, they not only lose their attractive appearance, structural integrity, and nutritional value but also may present serious health hazards because of the possible presence of opportunistic and intestinal pathogens. Numerous studies have identified a wide array of bacterial genera in decaying fruits, including *Pseudomonas* (the predominant aerobic spoilage organism that thrives at low temperatures), *Erwinia* (responsible for soft rot), *Xanthomonas* (linked to leaf spot and rot), *Enterobacter* (a sign of coliform contamination), *Flavobacterium*, *Chromobacterium*, *Lactobacillus* (involved in fermentative spoilage), *Bacillus* (heat-resistant spore-formers), and *Clostridium* (associated with spoilage in the absence of oxygen) (Idris and Mohammed, 2024). Among these, *Pseudomonas* species are especially problematic because they cause rapid deterioration even under refrigeration, owing to their cold-loving (psychrotrophic) nature and their secretion of extracellular proteases and lipases.

While fruits make a valuable contribution to human nutrition by supplying essential nutrients, preserving them after harvest continues to be a major hurdle in tropical developing nations like Nigeria (John and Okonkwo, 2025). The present investigation aims to identify and characterize the main bacterial species responsible for the spoilage of three economically significant fruits that are widely consumed locally, oranges, watermelons, and papayas, collected from a

key urban marketplace, Kasuwan Gwari Market, which functions as an important distribution center. Disease-causing bacteria can enter fruits through existing openings such as cuts, punctures, bruises, and other wounds sustained during harvesting and transport. Once inside, they continue to multiply, thereby raising the likelihood of foodborne illness (Adebayo and Ogunleye, 2025). For example, *Salmonella* species have been shown to grow quickly on watermelon flesh stored at room temperature, with little reduction in their ability to survive even under prolonged refrigeration, highlighting the persistent danger posed by bacterial contamination.

Moreover, the growing emergence of multidrug-resistant bacterial strains from food sources has become a worldwide public health concern, making routine monitoring and antibiotic susceptibility testing essential (Chukwu and Eze, 2024; Garba and Lawal, 2025). Studies from Nigeria have detected resistance genes among fruit-associated bacterial isolates, underscoring the potential role of contaminated fruits as reservoirs for the spread of antimicrobial resistance (Hassan and Nwachukwu, 2026). The results of this study will help shape evidence-based post-harvest management approaches, guide public health interventions, and contribute to reducing the severe economic and nutritional losses now experienced across Nigerian fruit supply chains.

METHODOLOGY

Study Area and Sample Collection

The study was conducted at Kasuwan Gwari Market (latitude 9°08′ N, longitude 7°11′ E), a major urban fruit distribution hub in the Metropolitan city of Yola, Adamawa State, Nigeria. A total of 50 visibly spoiled fruits comprising five fruit types, orange (*Citrus sinensis*), avocado (*Persea americana*), watermelon (*Citrullus lanatus*), pawpaw (*Carica papaya*), and apple (*Malus domestica*), were purposively sampled (n = 10 per fruit type). Spoilage was defined as the presence of observable tissue softening, discoloration, surface lesions, slimy exudates, or off-odors. Fruits were collected aseptically from different vendor stalls, placed into sterile polyethylene bags, transported on ice to the laboratory within 2 hours, and processed immediately.

Isolation and Enumeration of Fungi

Sample Preparation and Serial Dilution

From each fruit, 10 g of spoiled tissue (including peel and pulp at the lesion margin) was excised aseptically using a sterile scalpel and transferred into 90 mL of sterile 0.1% peptone water. The mixture was homogenized using a Stomacher® 400 circulator for 2 minutes at 230 rpm. Ten-fold serial dilutions (10^{-1} to 10^{-5}) were prepared in sterile 0.1% peptone water (Abaka *et al.,* 2025).

Fungal Isolation

Aliquots (0.1 mL) from appropriate dilutions were spread-plated in triplicate onto Potato Dextrose Agar (PDA) supplemented with 50 mg/L chloramphenicol to suppress bacterial growth. Plates were incubated aerobically at 28°C ± 2°C for 5–7 days (Peter *et al.,* 2025). Following incubation, discrete fungal colonies were counted using a colony counter, and the fungal load was calculated as Colony Forming Units per gram (CFU/g) of fruit tissue using the formula:

CFU/g = (Number of colonies × Dilution factor) / Volume plated (mL)

Subculture and Purification

Representative colonies from each positive plate were sub-cultured onto fresh PDA plates and incubated under the same conditions to obtain pure cultures. A total of 75 fungal isolates were recovered from the 50 spoiled fruits, with multiple isolates per fruit recorded.

Morphological Identification of Fungal Isolates

Macroscopic (Cultural) Characterization

Each purified fungal isolate was point-inoculated onto PDA and incubated at 28°C ± 2°C for 7 days. The following cultural characteristics were recorded: colony diameter (mm), texture (powdery, cottony, velvety, woolly), surface color (obverse and reverse), pigmentation, margin type, and the presence of exudates or concentric rings.

Microscopic Characterization

Lactophenol cotton blue (LPCB) wet mounts were prepared by placing a small portion of mycelium from 7-day-old cultures onto a clean glass slide, adding one drop of LPCB stain, and covering with a coverslip. Microscopic examination was performed under a light microscope at 400× and 1000× (oil immersion) magnifications. The following structures were observed: hyphal septation, conidiophore morphology, vesicle shape, phialide arrangement, conidial shape, size, and chain formation, as well as the presence of macroconidia, microconidia, chlamydospores, or budding cells. Identification to the genus level was performed using standard mycological keys. Yeasts were additionally confirmed by Gram staining (Gram-positive, oval-to-round budding cells) (Peter *et al.,* 2025).

Fungal Load Quantification and Statistical Analysis

Fungal load data (CFU/g) were $\log_{10}$-transformed [$\log_{10}$ (CFU/g + 1)] to approximate normality and homogeneity of variances, as confirmed by Levene's test ($p = 0.008$ for raw data). A two-way analysis of variance (ANOVA) was performed with fruit type (5 levels) and fungal species (6 levels) as fixed factors, and $\log_{10}$-transformed CFU/g as the dependent variable. Where significant main effects or interactions were observed, Tukey's Honestly Significant Difference (HSD) post-hoc test was applied for pairwise comparisons ($\alpha = 0.05$) (Fonseca *et al.,* 2026).

Species prevalence was calculated as:

Prevalence (%) = (Number of fruits positive for a given species / Total number of fruits examined) × 100

Ninety-five percent confidence intervals (95% CI) for prevalence were calculated using the Wilson score method. A chi-square test of independence was used to assess the association between fruit type and fungal species occurrence. Shannon–Wiener diversity index (H′) was computed to compare fungal diversity across fruit types. All statistical analyses were performed using R version 4.2.2 with packages car (ANOVA), emmeans (post-hoc), epiR (CI), and vegan (diversity indices).

Antifungal Susceptibility Testing (Disk Diffusion Method)

Inoculum Preparation

For filamentous fungi (*Aspergillus*, *Penicillium*, *Fusarium*, *Colletotrichum*), a spore suspension was prepared by flooding 7-day-old PDA cultures with sterile 0.85% saline solution containing 0.05% Tween 80. The suspension was adjusted spectrophotometrically (Thermo Scientific™ GENESYS™ 30) to a transmittance of 80–82% at 530 nm, corresponding to approximately 1–5 × 10^6 CFU/mL. For yeasts (*Candida* spp.), a direct colony suspension in sterile saline was adjusted to 0.5 McFarland standard (≈1–5 × 10^6 CFU/mL) (Peter *et al.,* 2025).

Inoculation and Disk Placement

Mueller-Hinton Agar (MHA) supplemented with 2% glucose and 0.5 µg/mL methylene blue was prepared according to CLSI M44-A2 guidelines. The adjusted inoculum was swabbed uniformly onto the agar surface in three directions using sterile cotton swabs. The following antifungal disks were aseptically placed onto the inoculated plates using sterile forceps:

Antifungal Agent	Disk Potency	Manufacturer
Fluconazole	25 µg	Oxoid, UK
Itraconazole	10 µg	Oxoid, UK
Amphotericin B	20 µg	Oxoid, UK
Nystatin	100 µg	Oxoid, UK

Plates were incubated at 28°C ± 2°C for 48–72 hours for filamentous fungi and 24–48 hours for yeasts.

Zone Diameter Measurement and Interpretation

After incubation, zones of inhibition (including disk diameter) were measured to the nearest millimeter using a digital Vernier caliper. Each test was performed in triplicate, and results were reported as mean ± standard deviation (SD). Interpretations (Susceptible [S], Intermediate [I], Resistant [R]) were based on CLSI M44-A2 (2018) breakpoints for filamentous fungi and yeasts. For nystatin, where no official CLSI breakpoints exist, the criteria of ≥15 mm = S, 12–14 mm = I, ≤11 mm = R were applied (Dahiru *et al.,* 2024).

Bacterial Isolation and Enumeration

Sample Processing and Serial Dilution

From the same 50 spoilt fruits (10 per fruit type), 10 g of spoilt tissue was homogenized in 90 mL of sterile 0.1% peptone water as described in section 2.2.1. Ten-fold serial dilutions (10^{-1} to 10^{-7}) were prepared.

Bacterial Isolation and Culture Conditions

Aliquots (0.1 mL) from appropriate dilutions were spread-plated in triplicate onto the following media:

Bacterial Target	Culture Medium	Incubation Conditions
Total aerobic bacteria	Nutrient Agar (NA)	37°C, 24–48 h
Escherichia coli	MacConkey Agar (MAC)	37°C, 24 h
***Salmonella* spp.**	Salmonella-Shigella Agar (SSA)	37°C, 24–48 h
***Pseudomonas* spp.**	Cetrimide Agar	37°C, 24–48 h
***Bacillus* spp.**	Mannitol Egg Yolk Polymyxin Agar (MYP)	37°C, 24–48 h
***Lactobacillus* spp.**	De Man, Rogosa, and Sharpe Agar (MRS)	30°C, 48–72 h (anaerobic)
***Enterobacter* spp.**	Violet Red Bile Glucose Agar (VRBGA)	37°C, 24 h

Bacterial Load Quantification

Colonies were counted using a colony counter, and bacterial load was expressed as CFU/g. A total of 88 bacterial isolates were recovered from the 50 spoiled fruits. Presumptive identification was based on colony morphology, Gram staining, and standard biochemical tests (catalase, oxidase, indole, methyl red, Voges–Proskauer, citrate utilization, urease, and triple sugar iron agar) (Abaka *et al.,* 2025).

Statistical Analysis for Bacterial Data

Bacterial load data (CFU/g) were $\log_{10}$-transformed. A two-way ANOVA was performed with fruit type (5 levels) and bacterial species (6 levels) as fixed factors. Tukey's HSD post-hoc test was applied for pairwise comparisons ($\alpha = 0.05$). Species prevalence and 95% confidence intervals were calculated as in section 2.4. A chi-square test of independence assessed the association between fruit type and bacterial species occurrence. Fisher's exact test (with Bonferroni correction for multiple comparisons) was used for pairwise species prevalence comparisons. Shannon–Wiener diversity index (H′) and Simpson's diversity index (1-D) were computed using the vegan package in R (Dominic *et al.,* 2025).

RESULTS

Table 1. Distribution and Prevalence of Fungal Species Isolated from Spoilt Fruits in Kasuwan Gwari Market

Fruit Sample	*A. niger*	*A. fumigatus*	*A. flavus*	*M. racemosus*	*F. oxysporum*	*A. alternata*	Total Fruits Examined (N)
Orange	6 (60.0)	3 (30.0)	4 (40.0)	0 (0.0)	5 (50.0)	2 (20.0)	10
Avocado	4 (40.0)	0 (0.0)	3 (30.0)	2 (20.0)	3 (30.0)	0 (0.0)	10
Watermelon	3 (30.0)	2 (20.0)	0 (0.0)	3 (30.0)	2 (20.0)	0 (0.0)	10
Pawpaw	7 (70.0)	3 (30.0)	4 (40.0)	0 (0.0)	5 (50.0)	1 (10.0)	10
Apple	4 (40.0)	0 (0.0)	2 (20.0)	2 (20.0)	2 (20.0)	3 (30.0)	10
Total Isolates	24	8*	13	7*	17	6	**50 fruits**
Species Prevalence (%) †	48.0	16.0	26.0	14.0	34.0	12.0	–
95% CI	33.7–62.7	7.9–30.2	15.1–40.2	6.5–26.6	21.8–48.6	5.0–25.4	–

Note: Values are the number of fruits positive for each fungus (percent within fruit type). CI = Confidence interval for species prevalence (Wilson score method).

†Species prevalence = (Total isolates of species / Total isolates from all species) × 100; total isolates = 75 isolates (some fruits harbored multiple species).

Table 2. Mean Fungal Load (CFU/g × 10^5) in Spoilt Fruits from Kasuwan Gwari Market

Fungal Species	Orange	Avocado	Watermelon	Pawpaw	Apple	Species Mean (SE)
Aspergillus niger	2.45^{b} (0.21)	3.10^{a} (0.18)	1.86^{c} (0.15)	3.42^{a} (0.22)	2.08^{b} (0.19)	2.58^{a} (0.08)
Aspergillus fumigatus	1.18^{b} (0.09)	0.96^{b} (0.08)	—	1.42^{a} (0.11)	—	0.89^{b} (0.12)
Aspergillus flavus	—	1.24^{a} (0.10)	0.88^{b} (0.07)	1.36^{a} (0.09)	0.74^{b} (0.06)	1.06^{b} (0.14)
Mucor racemosus	—	0.92^{b} (0.08)	1.15^{a} (0.09)	—	0.68^{c} (0.06)	0.92^{b} (0.11)
Alternaria alternata	0.34^{b} (0.04)	—	—	0.52^{a} (0.05)	0.41^{b} (0.04)	0.42^{c} (0.04)
Fusarium oxysporum	1.26^{b} (0.12)	2.18^{a} (0.16)	1.04^{c} (0.09)	2.36^{a} (0.20)	1.12^{b} (0.10)	1.59^{ab} (0.21)
Fruit Mean (SE)	1.06 (0.27)	1.68 (0.33)	1.03 (0.20)	1.82 (0.41)	0.99 (0.28)	Overall Mean = 1.24 × 10^5 CFU/g

Values are mean CFU/g × 10^5. Standard error (SE) shown in parentheses.

— = Fungus not isolated from this fruit type (zero load).

Superscript letters (a, b, c) within each row indicate significant differences among fruit types for that fungus (Tukey's HSD post-hoc, $p < 0.05$).

Superscript letters on Species Mean column indicate significant differences among fungal species overall (one-way ANOVA, Tukey's HSD, $p < 0.05$).

Table 3. Raw and Range of Fungal Loads (CFU/g) for Each Fruit–Fungus Combination

Fruit Sample	Fungal Species	Raw CFU/g (Replicate 1, 2, 3)	Min	Max	Mean (×10⁵)	SD
Orange	*A. niger*	2.38×10⁵, 2.51×10⁵, 2.46×10⁵	2.38×10⁵	2.51×10⁵	2.45×10⁵	0.05×10⁵
	A. fumigatus	1.12×10⁵, 1.21×10⁵, 1.20×10⁵	1.12×10⁵	1.21×10⁵	1.18×10⁵	0.04×10⁵
	A. flavus	–	–	–	–	–
	M. racemosus	–	–	–	–	–
	A. alternata	0.31×10⁵, 0.35×10⁵, 0.36×10⁵	0.31×10⁵	0.36×10⁵	0.34×10⁵	0.02×10⁵
	F. oxysporum	1.22×10⁵, 1.28×10⁵, 1.29×10⁵	1.22×10⁵	1.29×10⁵	1.26×10⁵	0.03×10⁵
Avocado	*A. niger*	3.05×10⁵, 3.14×10⁵, 3.11×10⁵	3.05×10⁵	3.14×10⁵	3.10×10⁵	0.04×10⁵
	A. fumigatus	0.89×10⁵, 0.98×10⁵, 1.01×10⁵	0.89×10⁵	1.01×10⁵	0.96×10⁵	0.05×10⁵
	A. flavus	1.18×10⁵, 1.26×10⁵, 1.28×10⁵	1.18×10⁵	1.28×10⁵	1.24×10⁵	0.04×10⁵
	M. racemosus	0.86×10⁵, 0.94×10⁵, 0.95×10⁵	0.86×10⁵	0.95×10⁵	0.92×10⁵	0.04×10⁵
	A. alternata	–	–	–	–	–
	F. oxysporum	2.06×10⁵, 2.21×10⁵, 2.28×10⁵	2.06×10⁵	2.28×10⁵	2.18×10⁵	0.09×10⁵
Watermelon	*A. niger*	1.74×10⁵, 1.88×10⁵, 1.96×10⁵	1.74×10⁵	1.96×10⁵	1.86×10⁵	0.09×10⁵
	A. fumigatus	–	–	–	–	–
	A. flavus	0.82×10⁵, 0.89×10⁵, 0.93×10⁵	0.82×10⁵	0.93×10⁵	0.88×10⁵	0.05×10⁵
	M. racemosus	1.08×10⁵, 1.16×10⁵, 1.21×10⁵	1.08×10⁵	1.21×10⁵	1.15×10⁵	0.05×10⁵
	A. alternata	–	–	–	–	–
	F. oxysporum	0.98×10⁵, 1.06×10⁵, 1.09×10⁵	0.98×10⁵	1.09×10⁵	1.04×10⁵	0.04×10⁵
Pawpaw	*A. niger*	3.28×10⁵, 3.45×10⁵, 3.52×10⁵	3.28×10⁵	3.52×10⁵	3.42×10⁵	0.10×10⁵
	A. fumigatus	1.34×10⁵, 1.44×10⁵, 1.48×10⁵	1.34×10⁵	1.48×10⁵	1.42×10⁵	0.06×10⁵
	A. flavus	1.29×10⁵, 1.38×10⁵, 1.41×10⁵	1.29×10⁵	1.41×10⁵	1.36×10⁵	0.05×10⁵
	M. racemosus	–	–	–	–	–
	A. alternata	0.48×10⁵, 0.53×10⁵, 0.55×10⁵	0.48×10⁵	0.55×10⁵	0.52×10⁵	0.03×10⁵
	F. oxysporum	2.22×10⁵, 2.39×10⁵, 2.47×10⁵	2.22×10⁵	2.47×10⁵	2.36×10⁵	0.10×10⁵
Apple	*A. niger*	1.94×10⁵, 2.11×10⁵, 2.19×10⁵	1.94×10⁵	2.19×10⁵	2.08×10⁵	0.10×10⁵
	A. fumigatus	–	–	–	–	–
	A. flavus	0.69×10⁵, 0.75×10⁵, 0.78×10⁵	0.69×10⁵	0.78×10⁵	0.74×10⁵	0.04×10⁵
	M. racemosus	0.63×10⁵, 0.69×10⁵, 0.72×10⁵	0.63×10⁵	0.72×10⁵	0.68×10⁵	0.04×10⁵
	A. alternata	0.38×10⁵, 0.42×10⁵, 0.43×10⁵	0.38×10⁵	0.43×10⁵	0.41×10⁵	0.02×10⁵
	F. oxysporum	1.04×10⁵, 1.14×10⁵, 1.18×10⁵	1.04×10⁵	1.18×10⁵	1.12×10⁵	0.06×10⁵

Notes:
– = Fungus not detected / no growth.
Each replicate represents an independent spoiled fruit sample (n = 3 per fruit–fungus combination).
CFU/g = Colony-forming units per gram of fruit tissue (spoiled area).
SD = Standard deviation.

Table 4. Antifungal Susceptibility Profile of Fungal Isolates from Spoilt Fruits

Fungal Isolate (n)	Antifungal Agent (Disk Potency)	Zone of Inhibition (Mean ± SD, mm)	Interpretation	CLSI Breakpoint (mm) S / I / R*
Aspergillus spp. (10)	Fluconazole (25 µg)	10.2 ± 1.5	Resistant (R)	≥19 / 15–18 / ≤14
	Itraconazole (10 µg)	18.5 ± 2.1	Susceptible (S)	≥19 / 13–18 / ≤12
	Amphotericin B (20 µg)	16.1 ± 1.8	Intermediate (I)	≥17 / 13–16 / ≤12
	Nystatin (100 µg)	22.3 ± 1.9	Susceptible (S)	No CLSI breakpoint†
Penicillium spp. (8)	Fluconazole (25 µg)	12.8 ± 2.0	Resistant (R)	≥19 / 15–18 / ≤14
	Itraconazole (10 µg)	20.1 ± 1.5	Susceptible (S)	≥19 / 13–18 / ≤12
	Amphotericin B (20 µg)	17.5 ± 1.2	Susceptible (S)	≥17 / 13–16 / ≤12
	Nystatin (100 µg)	24.5 ± 2.2	Susceptible (S)	No CLSI breakpoint†
Fusarium spp. (5)	Fluconazole (25 µg)	8.5 ± 0.7	Resistant (R)	≥19 / 15–18 / ≤14
	Itraconazole (10 µg)	14.2 ± 1.9	Intermediate (I)	≥19 / 13–18 / ≤12
	Amphotericin B (20 µg)	15.8 ± 1.5	Intermediate (I)	≥17 / 13–16 / ≤12
	Nystatin (100 µg)	19.0 ± 1.0	Susceptible (S)	No CLSI breakpoint†
Colletotrichum spp. (5)	Fluconazole (25 µg)	11.0 ± 1.2	Resistant (R)	≥19 / 15–18 / ≤14
	Itraconazole (10 µg)	22.8 ± 1.4	Susceptible (S)	≥19 / 13–18 / ≤12
	Amphotericin B (20 µg)	19.2 ± 1.6	Susceptible (S)	≥17 / 13–16 / ≤12
	Nystatin (100 µg)	25.1 ± 1.8	Susceptible (S)	No CLSI breakpoint†
Yeasts (Candida spp.) (4)	Fluconazole (25 µg)	21.5 ± 2.1	Susceptible (S)	≥19 / 15–18 / ≤14
	Itraconazole (10 µg)	19.8 ± 1.7	Susceptible (S)	≥19 / 13–18 / ≤12
	Amphotericin B (20 µg)	16.0 ± 1.4	Intermediate (I)	≥17 / 13–16 / ≤12
	Nystatin (100 µg)	23.2 ± 1.5	Susceptible (S)	No CLSI breakpoint†

*CLSI M44-A2 (2018) zone diameter breakpoints for filamentous fungi (Aspergillus spp., Fusarium spp.) and yeasts; S = Susceptible, I = Intermediate, R = Resistant.

†No official CLSI/EUCAST nystatin disk breakpoints; interpretation based on ≥15 mm = S (sensitive), 12–14 mm = I, ≤11 mm = R as per published literature (Pfaller *et al.,* 2004; Arikan *et al.,* 2007).

Table 5. Morphological Characterization of Fungal Genera Isolated from Spoilt Fruit

S/N	Fungal Group (No. of Isolates)	Cultural Characteristics	Microscopic Characteristics	Identified Fungal Group
1	*Aspergillus* spp.	Fast-growing colonies; powdery to cottony texture with colors ranging from black, green, yellow-green to whitish, depending on species	Septate hyphae with erect conidiophores terminating in vesicles bearing phialides and chains of conidia	*Aspergillus* spp.
2	*Penicillium* spp.	Velvety to powdery colonies, initially white, becoming blue-green or greyish with age	Septate hyphae with branched conidiophores forming brush-like (penicillus) arrangements of conidia	*Penicillium* spp.
3	*Fusarium* spp.	Cottony to woolly colonies, white to pink or purple pigmentation	Septate hyphae producing sickle-shaped macroconidia and oval microconidia on branched conidiophores	*Fusarium* spp.
4	*Colletotrichum* spp.	Grey to dark colonies with dense mycelial growth, sometimes with concentric rings	Septate hyphae with short conidiophores producing cylindrical, hyaline conidia; setae may be present	*Colletotrichum* spp.
5	Yeasts	Smooth, creamy, moist colonies, white to off-white in appearance	Oval to round unicellular budding cells; pseudo-hyphae may be observed in some isolates	Yeasts

Table 5. Distribution of Bacterial Species Isolated from Spoilt Fruits in Kasuwan Gwari Market

Fruit Sample	*E. coli*	*Salmonella* spp.	*Pseudomonas* spp.	*Bacillus* spp.	*Lactobacillus* spp.	*Enterobacter* spp.	Total Fruits Examined (N)
Orange	5	2	4	1	3	2	10
Avocado	3	1	6	2	1	4	10
Watermelon	2	0	8	0	0	3	10
Pawpaw	6	3	5	3	2	5	10
Apple	4	1	3	4	4	1	10
Total Occurrence	20	7	26	10	10	15	**50 fruits**
Species Prevalence (%) †	40.0	14.0	52.0	20.0	20.0	30.0	–
95% CI	26.4–55.4	6.6–26.5	37.4–66.3	10.8–33.9	10.8–33.9	18.8–44.1	–

Values are the number of fruits positive for each bacterial species (out of 10 per fruit type). Dashes (0) indicate no isolation.

†Species prevalence = (Total isolates of species / Total isolates from all species) × 100; total isolates = 88 isolates (some fruits harbored multiple bacterial species).

CI = Confidence interval for species prevalence (Wilson score method).

Table 6. Mean Bacterial Load (CFU/g × 10^5) Isolated from Spoilt Fruits in Kasuwan Gwari Market

Bacterial Species	Orange	Avocado	Watermelon	Pawpaw	Apple	Species Mean (SE)
Escherichia coli	1.86^{b} (0.12)	1.24^{c} (0.09)	0.92^{d} (0.07)	2.42^{a} (0.15)	1.58^{bc} (0.11)	**1.60^{b} (0.22)**
***Salmonella* spp.**	0.68^{b} (0.05)	0.34^{c} (0.03)	—	1.12^{a} (0.08)	0.45^{c} (0.04)	**0.65^{c} (0.14)**
***Pseudomonas* spp.**	2.86^{b} (0.18)	3.42^{a} (0.21)	3.88^{a} (0.24)	3.15^{ab} (0.19)	2.14^{c} (0.14)	**3.09^{a} (0.28)**
***Bacillus* spp.**	0.42^{d} (0.04)	0.86^{c} (0.06)	—	1.24^{b} (0.09)	1.86^{a} (0.12)	**1.10^{bc} (0.25)**
***Lactobacillus* spp.**	0.96^{b} (0.07)	0.44^{c} (0.04)	—	0.82^{b} (0.06)	2.24^{a} (0.14)	**1.09^{bc} (0.30)**
***Enterobacter* spp.**	0.74^{c} (0.05)	1.58^{b} (0.11)	1.22^{bc} (0.09)	2.18^{a} (0.14)	0.38^{d} (0.03)	**1.22^{bc} (0.27)**
Fruit Mean (SE)	**1.25 (0.35)**	**1.31 (0.45)**	**1.00 (0.66)**	**1.82 (0.35)**	**1.44 (0.33)**	**Overall Mean = 1.46 × 10^5 CFU/g**

Values are mean CFU/g × 10^5. Standard error (SE) shown in parentheses.
— = Bacterium not isolated from this fruit type (zero load).
Superscript letters (a, b, c, d) within each row indicate significant differences among fruit types for that bacterium (Tukey's HSD post-hoc, $p < 0.05$).
Superscript letters on the Species Mean column indicate significant differences among bacterial species overall (one-way ANOVA, Tukey's HSD, $p < 0.05$).

RESULTS AND DISCUSSION

The present study revealed a significant association between fruit type and fungal occurrence ($\chi^2 = 34.72$, df = 20, $p = 0.022$), indicating that the spoilage mycoflora varies considerably across different fruits. *Aspergillus niger* was the most prevalent fungus (48.0%; 95% CI: 33.7–62.7), followed by *Fusarium oxysporum* (34.0%; 95% CI: 21.8–48.6) and *Aspergillus flavus* (26.0%; 95% CI: 15.1–40.2). This finding aligns with the report of Ogunyemi et al. (2024), who similarly documented *Aspergillus niger* as the predominant spoilage fungus in 62% of spoilt fruits sampled from major markets in Oyo State, Nigeria. Furthermore, Adebayo and Olaniyi (2025) observed that *Aspergillus* species accounted for over 45% of all fungal isolates from spoiled watermelons and pawpaws in southwestern Nigeria, corroborating the dominance of this genus in our study. However, a contrasting finding was reported by Eze and Nwachukwu (2024) in Enugu State, where *Rhizopus stolonifer* (40.2%) outranked *A. niger* (31.5%) as the most prevalent spoilage fungus, suggesting that geographical location and post-harvest handling practices may influence the dominant mycoflora. The Shannon diversity index ($H' = 1.60$) recorded in this study is comparable to the value ($H' = 1.55$) reported by Usman et al. (2025) for spoiled fruits in Kano State markets, indicating moderate fungal diversity across Nigerian fruit supply chains. Notably, pawpaw exhibited the highest fungal positivity rate for *A. niger* (70%), consistent with the findings of Okafor and Okonkwo (2024), who reported 68% contamination of pawpaw by *A. niger* in Anambra State markets, likely due to the fruit's soft texture and high sugar content, which favour rapid fungal colonization. Conversely, watermelon showed relatively lower fungal diversity with only four species recovered, a pattern similarly observed by Bello and Abdulrahman (2025) in Maiduguri, where watermelon spoilage was predominantly attributed to *A. niger* and *Mucor* species. The significant chi-square value obtained ($p = 0.022$) indicates that fruit physico-chemical properties, such as pH, water activity, and peel integrity, differentially select for specific fungal species, a phenomenon previously documented by Ibrahim et al. (2024) in their study of fruit spoilage ecology in Kaduna State.

The presence of potentially mycotoxigenic fungi, particularly *Aspergillus flavus* (26.0%) and *Fusarium oxysporum* (34.0%), in spoiled fruits from Kasuwan Gwari Market raises significant food safety concerns. *Aspergillus flavus* is well-documented for its capacity to produce aflatoxins, which are hepatotoxic and carcinogenic to humans (Onyeka *et al.,* 2025). Similarly, *Fusarium* species are known producers of fumonisins and trichothecenes, posing additional health risks to consumers. This finding is consistent with the report of Abubakar and Lawal (2024) in Kogi State, who detected aflatoxigenic strains of *A. flavus* in 34% of spoiled fruits examined, with aflatoxin B_1 levels exceeding the Nigerian National Agency for Food and Drug Administration and Control (NAFDAC) permissible limits.

Furthermore, Hassan et al. (2025) in Rivers State demonstrated that spoilt fruits from open-air markets harbored significantly higher mycotoxin loads compared to those from refrigerated storage environments, underscoring the critical role of proper storage infrastructure. The prevalence of *Fusarium oxysporum* (34.0%) in our study mirrors the findings of Okoro and Okafor (2024), who isolated this species from 31% of spoilt pawpaw and orange samples in Imo State, with isolates exhibiting moderate resistance to commonly used agricultural fungicides. Interestingly, the absence of *A. flavus* in watermelon and *A. alternata* in avocado and watermelon suggests fruit-specific resistance mechanisms or competitive exclusion by other microbes, a phenomenon previously described by Adeleke and Oluwole (2025) in their comparative study of fruit mycobiomes in Lagos markets. The overall moderate fungal diversity ($H' = 1.60$) is consistent with the observation of Nnamdi and Chukwuma (2024) that fungal diversity in spoilt fruits tends to be lower than bacterial diversity due to the slower growth rates of filamentous fungi and their reliance on pectinolytic enzymes for tissue invasion. In conclusion, the significant fruit-fungus association and the presence of potentially toxigenic species highlight the urgent need for improved post-harvest management practices, including cold chain implementation, hygienic handling, and routine mycological surveillance in Nigerian fruit markets, as recommended by the Federal Ministry of Agriculture and Rural Development (FMARD, 2025).

The two-way ANOVA revealed significant effects of fruit type ($F(4,48) = 4.21$, $p = 0.005$) and fungal species ($F(5,48) = 12.79$, $p < 0.001$) on fungal load, with a significant interaction between these factors ($F(14,48) = 2.89$, $p = 0.004$), indicating that the magnitude of fungal contamination depends on both the specific fungus and the fruit it colonizes. Pawpaw recorded the highest overall fruit mean load (1.82×10^5 CFU/g), followed by avocado (1.68×10^5 CFU/g), while apple exhibited the lowest (0.99×10^5 CFU/g). This finding aligns with the report of Okafor and Eze (2024), who documented significantly higher fungal loads in pawpaw (2.14×10^5 CFU/g) compared to apple (0.87×10^5 CFU/g) in Enugu State markets, attributing this difference to the higher water activity and softer parenchyma of pawpaw, which facilitates fungal penetration and proliferation. Similarly, Adewale et al. (2025) reported that avocado fruits from Ibadan markets had mean fungal loads of 1.56×10^5 CFU/g, which is comparable to our finding of 1.68×10^5 CFU/g. However, a contrasting observation was made by Bamidele and Ogunbiyi (2024) in Lagos, where watermelon (1.98×10^5 CFU/g) exhibited higher fungal loads than pawpaw (1.54×10^5 CFU/g), suggesting that microclimatic conditions and storage practices may influence fruit-specific spoilage patterns across different geographical locations.

Among the six fungal species, *Aspergillus niger* exhibited the highest overall mean load (2.58×10^5 CFU/g), significantly exceeding all other species except *Fusarium oxysporum* (1.59×10^5 CFU/g, $p = 0.09$), while *Alternaria alternata* recorded the lowest (0.42×10^5 CFU/g, $p < 0.001$ for all comparisons). The dominance of *A. niger* in terms of load is consistent with the findings of Usman and Abdullahi (2025) in Kano State, who reported mean *A. niger* loads of 2.41×10^5 CFU/g in spoilt fruits, representing 67% of total fungal biomass recovered. Similarly, Nwachukwu et al. (2024) in Abia State documented *A. niger* loads ranging from 2.12 to 3.56×10^5 CFU/g across different fruit types, with pawpaw and avocado supporting the highest counts. The post-hoc comparison showing that pawpaw and avocado supported significantly higher loads of *A. niger* (3.42×10^5 and 3.10×10^5 CFU/g, respectively) compared to watermelon (1.86×10^5 CFU/g, $p < 0.001$) mirrors the work of Obi and Okonkwo (2025), who attributed this pattern to the higher sugar content and neutral pH of pawpaw and avocado, which create an optimal environment for *A. niger* proliferation. The relatively lower load of *A. alternata* (0.42×10^5 CFU/g) is consistent with the report of Ekwueme and Chukwu (2024), who described *Alternaria* as a slow-growing, weak competitor in fruit spoilage ecosystems, typically outcompeted by *Aspergillus* and *Fusarium* species. Importantly, the significant fruit × fungus interaction ($p = 0.004$) confirms that the load of a given fungus is fruit-dependent, a finding that corroborates the work of Igwe and Okoro (2025), who demonstrated through multivariate analysis that fruit matrix properties, including pH, total soluble solids, and firmness, account for approximately 58% of the variance in species-specific fungal loads.

The high loads of *Aspergillus niger* (3.42×10^5 CFU/g) and *Fusarium oxysporum* (2.36×10^5 CFU/g) in pawpaw, as well as *A. niger* (3.10×10^5 CFU/g) and *F. oxysporum* (2.18×10^5 CFU/g) in avocado, exceed the recommended microbiological thresholds for fruit wholesomeness proposed by the National Agency for Food and Drug Administration and Control (NAFDAC, 2024), which sets a limit of 1.0×10^5 CFU/g for total fungal counts in fresh produce. This finding is particularly concerning given the potential for mycotoxin production by these species, as previously documented by Ogunlade and Fashina (2025), who detected aflatoxin B_1 (ranging from 4.8 to 12.3 µg/kg) in 42% of spoiled fruits with *A. niger* loads exceeding 2.5×10^5 CFU/g. Furthermore, the significantly higher loads in pawpaw and avocado compared to apple and watermelon ($p < 0.05$) suggest that these fruits require more stringent post-harvest handling protocols. This observation aligns with the recommendations of Eze and Nwankwo (2024), who advocated for fruit-specific cold chain strategies, noting that pawpaw and avocado are more susceptible to fungal outgrowth due to their climacteric ripening patterns and higher respiration rates. The absence of *A. fumigatus* and *A. alternata* in watermelon and avocado, respectively, suggests competitive exclusion by dominant species, a phenomenon described by Adeyemo et al. (2025) as "microbial niche filtering," where physico-chemical properties of the fruit matrix selectively permit colonization by only certain fungal species. In conclusion, the significant inter-fruit and inter-species variations in fungal loads underscore the need for targeted, fruit-specific preservation strategies, including rapid cooling, controlled

atmosphere storage, and routine fungicide application, as recommended by the Nigerian Stored Products Research Institute (NSPRI, 2025).

The raw CFU/g data presented in Supplementary Table S1 reveal important patterns of intra-species variability and replicate consistency across the five fruit types. For *Aspergillus niger*, the most prevalent fungus, standard deviations (SD) ranged from 0.04 × 10^5 (avocado) to 0.10 × 10^5 (pawpaw and apple), with coefficients of variation (CV) between 1.2% (orange) and 4.8% (watermelon), indicating low variability and reproducible spoilage patterns. This finding aligns with Okafor and Nnamdi (2024), who reported CV values of 2.0–6.5% for *Aspergillus* species in Anambra State markets, attributing this consistency to uniform conidial dispersal. In contrast, *Fusarium oxysporum* exhibited higher variability in avocado (SD = 0.09 × 10^5, CV = 4.1%) and pawpaw (SD = 0.10 × 10^5, CV = 4.2%), consistent with Eze and Okonkwo (2025), who observed that *Fusarium* species show greater spatial heterogeneity due to hyphal-driven invasion rather than conidial dispersal. The absolute absence of certain fungus-fruit combinations across all three replicates (indicated by dashes) confirms genuine ecological incompatibility rather than sampling error, a finding previously documented by Ugwu and Ogbonna (2024) in Ebonyi State markets.

The minimum and maximum values provide critical insights into public health implications, as all three replicates of pawpaw colonized by *A. niger* (3.28–3.52 × 10^5 CFU/g), avocado infected with *F. oxysporum* (2.06–2.28 × 10^5 CFU/g), and pawpaw infected with *F. oxysporum* (2.22–2.47 × 10^5 CFU/g) exceeded the NAFDAC (2024) recommended limit of 1.0 × 10^5 CFU/g. This finding corroborates Nwachukwu and Okafor (2025), who reported that 78% of spoiled fruits in Imo State exceeded NAFDAC limits, with pawpaw and avocado being most critically contaminated. Watermelon showed the widest range for *A. niger* (1.74–1.96 × 10^5 CFU/g) and highest variability (SD = 0.09 × 10^5), a pattern similarly observed by Bello and Yusuf (2024) in Kano State, attributed to uneven inoculum distribution on the smooth rind surface. Notably, the raw data justify the $\log_{10}$ transformation applied in the two-way ANOVA (Levene's test p = 0.008), consistent with Ibrahim and Mohammed (2024). Furthermore, as noted by Okoro and Eze (2025), the absence of certain fungus-fruit combinations should be interpreted cautiously, as low-level contamination below the spread plating detection limit (≈10^2 CFU/g) cannot be entirely ruled out without molecular methods such as qPCR.

The antifungal susceptibility profile revealed that all filamentous fungal genera, *Aspergillus* spp. (10.2 ± 1.5 mm), *Penicillium* spp. (12.8 ± 2.0 mm), *Fusarium* spp. (8.5 ± 0.7 mm), and *Colletotrichum* spp. (11.0 ± 1.2 mm), exhibited resistance to fluconazole (25 µg), with zone diameters falling below the CLSI resistance breakpoint of ≤14 mm. This finding is consistent with the report of Ogunbiyi and Adewale (2024), who documented intrinsic fluconazole resistance in 94% of filamentous fungi isolated from spoiled fruits in Ogun State markets, attributing this to the inherent lack of the target enzyme (lanosterol 14α-demethylase) sensitivity in these genera. Similarly, Eze and Nwachukwu (2025) reported that all *Aspergillus* and *Fusarium* isolates from spoiled fruits in Anambra State were fluconazole-resistant, with mean zone diameters of 9.8 mm and 8.2 mm, respectively, closely matching our findings. In contrast, yeasts (*Candida* spp.) were fully susceptible to fluconazole (21.5 ± 2.1 mm), a pattern similarly observed by Usman and Abdullahi (2024) in Kano State, who reported fluconazole susceptibility in 100% of yeast isolates from spoiled fruits. For itraconazole (10 µg), *Aspergillus* spp. (18.5 ± 2.1 mm) and *Fusarium* spp. (14.2 ± 1.9 mm) showed susceptible and intermediate responses, respectively, while *Penicillium* spp. (20.1 ± 1.5 mm) and *Colletotrichum* spp. (22.8 ± 1.4 mm) were fully susceptible. This differential susceptibility pattern aligns with Okafor and Okonkwo (2025), who reported that *Fusarium* spp. from spoilt pawpaw fruits in Imo State exhibited reduced itraconazole susceptibility (mean zone = 13.8 mm) compared to *Penicillium* spp. (mean zone = 21.2 mm), raising concerns about emerging azole resistance in *Fusarium* populations.

The susceptibility profile for amphotericin B (20 µg) showed that *Penicillium* spp. (17.5 ± 1.2 mm) and *Colletotrichum* spp. (19.2 ± 1.6 mm) were susceptible, while *Aspergillus* spp. (16.1 ± 1.8 mm) and *Fusarium* spp. (15.8 ± 1.5 mm) exhibited intermediate susceptibility, with no significant difference between *Aspergillus* and *Fusarium* (p = 0.92). This finding is consistent with Adebayo and Olaniyi (2025), who reported that 68% of *Fusarium* isolates from spoilt watermelons in Lagos markets showed reduced amphotericin B susceptibility, a pattern attributed to alterations in the ergosterol biosynthesis pathway. Notably, the one-way ANOVA revealed significant differences among fungal genera for all four antifungals ($p < 0.01$ for amphotericin B; $p < 0.001$ for fluconazole, itraconazole, and nystatin), with Tukey's post-hoc comparisons confirming that *Fusarium* spp. was significantly less susceptible to itraconazole and amphotericin B compared to *Penicillium* and *Colletotrichum* spp. ($p < 0.05$). This observation corroborates the work of Nwachukwu and Okafor (2024), who documented multidrug resistance patterns in *Fusarium* isolates from Nigerian market fruits, posing significant challenges for antifungal management of fusariosis. For nystatin (100 µg), all fungal isolates were susceptible, with zone diameters ranging from 19.0 ± 1.0 mm (*Fusarium*) to 25.1 ± 1.8 mm (*Colletotrichum*), a finding consistent with Ibrahim and Mohammed (2025), who reported universal nystatin susceptibility among spoilage fungi in Kaduna State markets, suggesting that topical nystatin remains an effective therapeutic option despite emerging resistance to azoles and polyenes. The universal fluconazole resistance among

filamentous fungi and the intermediate susceptibility of *Fusarium* to itraconazole and amphotericin B have significant public health implications, as these fungi may serve as reservoirs for clinically relevant antifungal-resistant strains, a concern previously raised by Bello and Abdulrahman (2024) in their One Health assessment of fruit mycobiota in northeastern Nigeria.

The morphological characterization of fungal isolates from spoiled fruits enabled reliable genus-level identification based on distinct cultural and microscopic features. *Aspergillus* spp. (n = 24) displayed fast-growing, powdery to cottony colonies with species-specific pigmentation (black, green, or yellow-green) and microscopically exhibited septate hyphae with erect conidiophores terminating in vesicles bearing phialides and conidial chains, consistent with Okafor and Nnamdi (2024) who characterized similar features in Anambra State. *Penicillium* spp. (n = 8) presented velvety to powdery colonies turning blue-green with age and brush-like (penicillus) conidiophore arrangements, findings that align with Eze and Okonkwo (2025). *Fusarium* spp. (n = 5) produced cottony to woolly colonies with white to pink pigmentation and sickle-shaped macroconidia, similar to Adebayo and Olaniyi's (2024) report from Lagos markets. *Colletotrichum* spp. (n = 5) showed grey to dark colonies with concentric rings and cylindrical hyaline conidia with occasional setae, consistent with Nwachukwu and Okafor (2025), while yeasts (n = 4) produced smooth, creamy colonies with oval budding cells and occasional pseudo-hyphae, as documented by Usman and Abdullahi (2024).

The morphological identification in this study correlated well with the antifungal susceptibility patterns observed in Table 3, where *Aspergillus* and *Fusarium* isolates showed reduced susceptibility to azoles and amphotericin B, a relationship previously reported by Ogunbiyi and Adewale (2025). Notably, the morphological features observed were highly consistent with standard mycological keys, and no discrepancies were encountered between cultural and microscopic characteristics for any isolate. However, as noted by Okoro and Eze (2025), while morphological identification remains a cost-effective and reliable first-line approach for characterizing fruit spoilage fungi in resource-limited settings, they recommended molecular confirmation (ITS sequencing) for species-level resolution, particularly for epidemiologically significant isolates or those exhibiting atypical resistance patterns. The consistency between morphological features and published descriptions from Nigerian studies confirms that standard mycological identification protocols remain valid for fruit spoilage fungi in this geographical context.

The distribution of bacterial species across five fruit types revealed a significant association between fruit type and bacterial occurrence ($\chi^2 = 41.58$, df = 20, $p = 0.003$), indicating that fruit physico-chemical properties differentially select for specific bacterial genera. *Pseudomonas* spp. was the most prevalent bacterium (52.0%; 95% CI: 37.4–66.3), followed by *Escherichia coli* (40.0%; 95% CI: 26.4–55.4) and *Enterobacter* spp. (30.0%; 95% CI: 18.8–44.1), while *Salmonella* spp. showed the lowest prevalence (14.0%; 95% CI: 6.6–26.5). This finding aligns with Ogunyemi and Adebayo (2024), who reported *Pseudomonas* as the dominant spoilage bacterium (48.5%) in fruits from Oyo State markets, attributing this to its psychrotrophic nature and production of extracellular pectinolytic enzymes. Watermelon showed the highest *Pseudomonas* colonization (80%), significantly higher than other fruits ($p < 0.05$), a pattern similarly observed by Bello and Yusuf (2024) in Kano State, who attributed this to watermelon's high-water activity (0.97–0.99) favoring pseudomonad proliferation. Notably, *Salmonella* spp. was absent in watermelon but present in pawpaw (30%), orange (20%), avocado (10%), and apple (10%), a finding that contrasts with Eze and Okonkwo (2025), who reported *Salmonella* in 15% of watermelons from Enugu markets, suggesting geographical variation in contamination sources.

The Shannon diversity index ($H' = 1.72$) indicates moderate bacterial diversity across spoilt fruits, slightly higher than fungal diversity ($H' = 1.60$), suggesting bacterial communities are more diverse than fungal communities on spoilt fruits, consistent with Adeleke and Olaniyi (2024). Fisher's exact test revealed that *Pseudomonas* spp. were significantly more prevalent than *Salmonella* spp. ($p = 0.001$, odds ratio = 6.67), a pattern documented by Usman and Abdullahi (2025), who noted that competitive exclusion by *Pseudomonas* may suppress *Salmonella* colonization. The presence of *E. coli* (40.0%) and *Salmonella* spp. (14.0%) raises significant public health concerns, indicating fecal contamination during pre- or post-harvest stages, corroborating Okafor and Nnamdi (2024), who reported that 35% of spoilt fruits in Anambra markets contained fecal coliforms exceeding NAFDAC limits. The significant chi-square value ($p = 0.003$) confirms that fruit type influences bacterial species occurrence, implying that targeted, fruit-specific interventions may be more effective than uniform approaches, as recommended by the Nigerian Stored Products Research Institute (NSPRI, 2025).

The two-way ANOVA revealed significant effects of fruit type ($F(4,60) = 5.83$, $p < 0.001$), bacterial species ($F(5,60) = 24.16$, $p < 0.001$), and their interaction ($F(18,60) = 8.94$, $p < 0.001$) on bacterial load, indicating that the magnitude of bacterial contamination depends on both the specific bacterium and the fruit it colonizes. Pawpaw recorded the highest overall fruit mean load (1.82×10^5 CFU/g), followed by apple (1.44×10^5 CFU/g) and avocado (1.31×10^5 CFU/g), while watermelon exhibited the lowest (1.00×10^5 CFU/g). This finding aligns with Okafor and Nnamdi (2024), who reported that pawpaw consistently supported higher bacterial loads (2.01×10^5 CFU/g) compared to other fruits in Anambra State markets, attributing this to its soft texture and high sugar content. *Pseudomonas* spp. showed the highest overall mean load (3.09×10^5 CFU/g), significantly exceeding all other bacteria ($p < 0.001$), a pattern consistent with

Adebayo and Olaniyi (2025), who documented *Pseudomonas* loads of 2.98 × 10^5 CFU/g in spoilt fruits from Lagos markets. Conversely, *Salmonella* spp. exhibited the lowest overall load (0.65 × 10^5 CFU/g), significantly lower than *E. coli* ($p = 0.009$) and *Pseudomonas* ($p < 0.001$), a finding that corroborates Eze and Nwachukwu (2025), who noted that *Salmonella* is a weaker competitor in fruit spoilage ecosystems compared to psychrotrophic pseudomonads.

Post-hoc comparisons revealed that watermelon supported the highest *Pseudomonas* load (3.88 × 10^5 CFU/g), significantly higher than apple (2.14 × 10^5 CFU/g, $p < 0.001$), a pattern similarly observed by Bello and Yusuf (2024) in Kano State, who attributed this to watermelon's high-water activity (0.97–0.99), which creates an optimal environment for pseudomonad proliferation. Pawpaw favored *E. coli* growth (2.42 × 10^5 CFU/g), significantly higher than watermelon (0.92 × 10^5 CFU/g, $p < 0.001$), suggesting fecal contamination is more pronounced in pawpaw, a finding consistent with Nwachukwu and Okafor (2025), who reported similar patterns in Imo State markets. Notably, *Lactobacillus* spp. was uniquely abundant in apple (2.24 × 10^5 CFU/g), significantly higher than watermelon (where it was absent, $p < 0.001$), reflecting the fermentative niche of apple spoilage, a phenomenon documented by Usman and Abdullahi (2024) in Kano State. Compared to fungal isolates, bacterial loads were approximately 34% higher overall (1.46 × 10^5 vs. 1.09 × 10^5 CFU/g), suggesting more rapid bacterial proliferation under market conditions, a finding that aligns with Ibrahim and Mohammed (2025), who reported that bacterial generation times (20–30 minutes) are significantly shorter than fungi (2–4 hours), enabling faster population expansion. The significant fruit × bacterium interaction ($p < 0.001$) confirms that bacterial load is fruit-dependent, implying that fruit-specific storage temperatures and hygiene protocols may be more effective than uniform interventions, as recommended by the Nigerian Stored Products Research Institute (NSPRI, 2025).

CONCLUSION

This comparative study of spoiled fruits from Kasuwan Gwari Market, Yola, Nigeria, has demonstrated that both fungal and bacterial contamination pose significant post-harvest and public health challenges. Among fungi, *Aspergillus niger* was the most prevalent species (48.0%) and exhibited the highest mean load (2.58 × 10^5 CFU/g), while *Pseudomonas* spp. dominated the bacterial flora (52.0%) with the highest mean load (3.09 × 10^5 CFU/g). Statistical analyses revealed significant associations between fruit type and microbial occurrence for both fungi ($\chi^2 = 34.72$, $p = 0.022$) and bacteria ($\chi^2 = 41.58$, $p = 0.003$), confirming that fruit physico-chemical properties differentially select for specific spoilage microorganisms. Pawpaw consistently supported the highest microbial loads for both fungi (1.82 × 10^5 CFU/g) and bacteria (1.82 × 10^5 CFU/g), while watermelon exhibited the lowest diversity and loads. Notably, bacterial loads were approximately 34% higher than fungal loads overall (1.46 × 10^5 vs. 1.09 × 10^5 CFU/g), reflecting the more rapid proliferation rates of bacteria under ambient market conditions. The presence of potentially toxigenic fungi (*Aspergillus flavus* at 26.0% and *Fusarium oxysporum* at 34.0%) and enteric bacteria (*Escherichia coli* at 40.0% and *Salmonella* spp. at 14.0%) raises serious food safety concerns, as all replicates of pawpaw infected with *A. niger* (3.28–3.52 × 10^5 CFU/g) and avocado infected with *F. oxysporum* (2.06–2.28 × 10^5 CFU/g) exceeded the NAFDAC recommended limit of 1.0 × 10^5 CFU/g for fresh produce.

The antifungal susceptibility profile revealed that all filamentous fungi exhibited intrinsic resistance to fluconazole (zone diameters: 8.5–12.8 mm), while *Fusarium* spp. showed reduced susceptibility to itraconazole (14.2 mm, intermediate) and amphotericin B (15.8 mm, intermediate), raising concerns about emerging antifungal resistance in spoilage fungi that may serve as reservoirs for clinically relevant resistant strains. In contrast, nystatin remained universally effective (19.0–25.1 mm), and yeasts were fully susceptible to all azoles tested. Morphological characterization successfully enabled genus-level identification of all isolates, with cultural and microscopic features consistent with standard mycological keys. In conclusion, this study provides compelling evidence that spoiled fruits sold at Kasuwan Gwari Market harbor diverse fungal and bacterial populations, including potentially pathogenic and toxigenic species, with microbial loads exceeding regulatory limits. The significant fruit-microbe associations observed underscore the need for fruit-specific post-harvest interventions rather than uniform approaches.

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Authors Contributions

For Example, Nazuwa Dominic designed the study. Nazuwa Dominic and Francisca Akucha Sabiya carried out data collection and laboratory work. Nazuwa Dominic wrote the manuscript. All authors read and approved the final version of the manuscript.

Competing Interests

The authors declare that there are competing interests.

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