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Research Article

Microbial Succession During Composting of Fruit and Vegetable Waste in Yola North and Yola South, Adamawa State, Nigeria

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Abstract

The escalating generation of fruit and vegetable waste in Nigerian urban centers poses serious environmental and public health challenges, yet the microbial communities driving composting processes in tropical regions remain poorly characterized. This study established a baseline assessment of physicochemical properties and microbial assemblages in pre-composting soils collected from fruit and vegetable waste aggregation points in Yola North (n=8) and Yola South (n=7), Adamawa State, Nigeria. Standard microbiological spread plate techniques, biochemical characterization, and morphological identification were employed to enumerate and identify bacterial and fungal isolates. Results revealed that Yola South soils contained significantly higher moisture (23.8±4.2% vs. 19.2±3.5%, p=0.038) and organic matter (5.9±1.2% vs. 4.5±0.9%, p=0.024) than Yola North. However, total heterotrophic bacterial counts were unexpectedly higher in Yola North (53.4±8.9 × 10^5 CFU/g) compared to Yola South (40.1±6.2 × 10^5 CFU/g, p=0.005). From 121 bacterial isolates, eight genera were identified, with Bacillus spp. (27.8–30.6%) and Pseudomonas aeruginosa (16.7–20.4%) predominated. Among 257 fungal isolates, seven genera were recovered, dominated by Aspergillus flavus (19.3–20.3%), Trichoderma sp. (17.4–19.3%), and Aspergillus niger (14.3–15.9%). Shannon–Wiener diversity indices showed no significant differences between locations for bacteria (H'=2.28–2.35) or fungi (H'=2.48–2.52), indicating conserved community structures. Pearson correlation analysis revealed strong positive associations between microbial densities and both moisture (r=0.52–0.59) and organic matter (r=0.61–0.65), alongside a robust inter-kingdom correlation (r=0.72). The counterintuitive lower bacterial density in Yola South, despite higher organic matter, suggests unmeasured suppressive factors such as trace heavy metals or oxygen-limited microsites. These findings provide a critical baseline for optimizing composting strategies, leveraging native Trichoderma populations for lignocellulose degradation, while managing Aspergillus flavus to prevent aflatoxin contamination. Future research should employ metagenomic sequencing and heavy metal profiling to identify factors limiting bacterial activity in organic-rich tropical soils.

Keywords: *Microbial succession; fruit and vegetable waste; composting; Bacteria; Fungi.*

INTRODUCTION

The escalating generation of organic waste, particularly from fruit and vegetable sources, has become a pressing environmental concern in rapidly urbanizing Nigerian cities (Adebayo *et al.,* 2024; Ogunwusi and Alabi, 2025). The increasing rate of urbanization, population expansion, and changing dietary habits in Nigeria have contributed significantly to the generation of large quantities of organic waste, particularly fruit and vegetable wastes from households, open markets, restaurants, and agro-processing activities (Ogunwusi and Alabi, 2025; Adebayo *et al.,* 2024).

In many Nigerian cities, these biodegradable wastes constitute a substantial proportion of municipal solid waste and are often disposed of indiscriminately in drainage systems, roadside dumps, and open landfills (Omokaro *et al.,* 2025). Such inappropriate disposal practices create serious environmental and public health concerns, including offensive odors, greenhouse gas emissions, leachate contamination of soil and groundwater, and the proliferation of pathogenic microorganisms and disease vectors (Njewa *et al.,* 2025; Idris and Umar, 2026). Fruit and vegetable wastes are especially problematic because of their high moisture content, acidic nature, and abundance of easily degradable organic compounds, which accelerate microbial decomposition under uncontrolled conditions (Khanam and Maskare, 2025). Consequently, there is an urgent need for sustainable and environmentally friendly waste management strategies capable of converting these organic residues into useful products (Rath *et al.,* 2026).

Composting has emerged as one of the most effective and sustainable approaches for the management of biodegradable wastes (Saras and Nigam, 2026). It is an aerobic biological process through which microorganisms transform organic materials into stable, nutrient-rich compost that can improve soil fertility and agricultural productivity (Idris and Umar, 2026; Adebayo *et al.,* 2024). Before the widespread use of inorganic fertilizers in Nigeria, traditional composting practices were commonly employed by resource-poor farmers to maintain soil fertility (Ogunwusi and Alabi, 2025). However, conventional composting methods are generally slow, labor-intensive, and often produce poor-quality compost because important factors such as aeration, temperature, moisture, and nutrient balance are not adequately controlled (Bernal, 2026). During composting, labile organic compounds are gradually broken down while more stable humic substances are formed, resulting in the stabilization and maturation of the compost material (Ogunwusi and Alabi, 2025). The efficiency of this process largely depends on microbial activities, as microorganisms serve as the principal agents responsible for organic matter degradation (Adebayo *et al.,* 2024; Idris and Umar, 2026). Studies have shown that bacteria, fungi, actinomycetes, protozoa, and some soil invertebrates contribute to the decomposition process, although heterotrophic microorganisms are considered the primary decomposers of carbonaceous materials (Eze and Nwachukwu, 2025).

Microbial populations involved in composting do not remain constant throughout the process but undergo dynamic and sequential changes known as microbial succession (Phokas *et al.,* 2026). This succession is influenced by variations in temperature, pH, oxygen availability, moisture content, substrate composition, and nutrient status within the composting system (Eze and Nwachukwu, 2025; Adebayo *et al.,* 2024). In the initial mesophilic phase, rapidly growing bacteria and fungi utilize simple sugars and other easily degradable compounds, leading to a rapid increase in temperature (Ogunwusi and Alabi, 2025; Idris and Umar, 2026). As temperatures rise to thermophilic levels, heat-tolerant microorganisms such as *Bacillus*, *Thermus*, and several actinomycetes become dominant and actively degrade cellulose, proteins, and hemicellulose (Upadhyay, 2026). Most mesophilic fungi are suppressed during this phase and survive mainly as spores (Idris and Umar, 2026). During the cooling and maturation stages, mesophilic fungi and actinomycetes recolonize the compost and participate in lignocellulose degradation and humification processes (Adebayo *et al.,* 2024; Eze and Nwachukwu, 2025). Earlier studies by Aguilar-Paredes (2023) demonstrated that the active mycoflora during composting shifts from mesophilic species such as *Cladosporium herbarum*, *Alternaria alternata*, and *Epicoccum purpurascens* at the beginning of composting to predominantly thermophilic organisms at peak heating stages. Understanding these successional patterns is essential because microbial activities determine the rate of decomposition, compost stability, nutrient transformation, pathogen elimination, and the overall quality of the final compost product (Idris and Umar, 2026; Adebayo *et al.,* 2024).

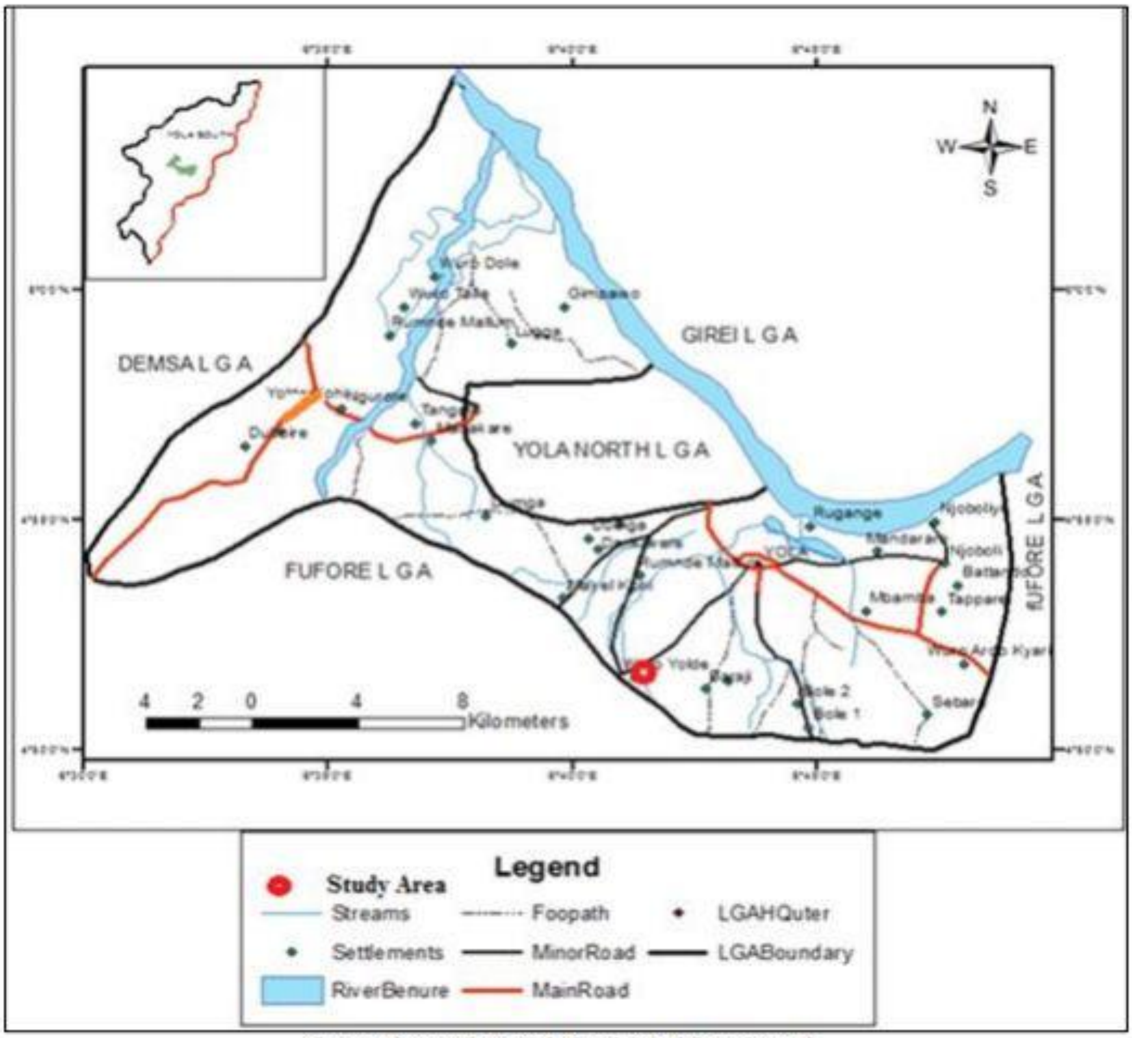
In recent years, increasing attention has been directed toward understanding microbial ecology and community assembly during composting processes (Ogunwusi and Alabi, 2025; Eze and Nwachukwu, 2025; Idris and Umar, 2026). Ecological theories suggest that microbial community structure is shaped by both deterministic factors, such as environmental selection, and stochastic processes, including migration, ecological drift, and species diffusion (Adebayo *et al.,* 2024). Environmental conditions such as temperature, nutrient composition, aeration, and moisture are believed to strongly influence microbial diversity and succession during composting (Idris and Umar, 2026; Eze and Nwachukwu, 2025). Research has also shown that different organic substrates support distinct microbial communities (Adebayo *et al.,* 2024). For instance, compost produced from cattle manure may be dominated by *Pseudomonas* species, whereas poultry manure compost may favor *Bacteroides* species (Ogunwusi and Alabi, 2025). Similarly, organic fertilizers have been reported to improve microbial diversity and soil quality compared to chemical fertilizers, which often reduce microbial richness and alter community structure (Ahsan *et al.,* 2024). Furthermore, beneficial microbial communities associated with compost-amended soils can improve plant growth, nutrient uptake, and resistance to environmental stress and diseases through complex microbiome–root–shoot interactions (Adebayo *et al.,* 2024; Ogunwusi and Alabi, 2025). These findings highlight the importance of understanding microbial succession not only for efficient waste biodegradation but also for enhancing soil health and sustainable agricultural productivity.

Despite the growing interest in composting technologies worldwide, studies investigating microbial succession during the composting of fruit and vegetable wastes under tropical conditions remain limited, particularly in Nigeria (Adebayo *et al.,* 2024; Ogunwusi and Alabi, 2025; Eze and Nwachukwu, 2025). Most available studies focus mainly on the physicochemical properties of compost while giving little attention to the temporal changes in microbial populations and their ecological functions (Idris and Umar, 2026). Climatic conditions in Nigeria, including high temperatures and seasonal fluctuations in humidity, may significantly affect microbial activities and composting efficiency (Adebayo *et al.,* 2024). In addition, differences in waste composition, environmental conditions, and management practices across locations may influence microbial succession patterns (Rodriguez-Ramos, 2025). Therefore, there is a critical need for detailed investigations into the microbial communities associated with fruit and vegetable waste composting in Nigeria. Such knowledge will improve understanding of the biodegradation process, enhance compost quality, reduce environmental pollution, and support the development of sustainable organic fertilizer production systems (Ogunwusi and Alabi, 2025; Idris and Umar, 2026). This study is therefore designed to investigate microbial succession during the composting of fruit and vegetable wastes, to provide valuable information that can contribute to improved waste management practices, environmental sustainability, and enhanced agricultural productivity in Nigeria.

METHODOLOGY

Study Area

The study was conducted in Yola North and Yola South Local Government Areas (LGAs) of Adamawa State, Nigeria. Yola North (geographic coordinates approximately 9.23°N, 12.46°E) serves as the state capital and hosts major fruit and vegetable markets, while Yola South (approximately 9.20°N, 12.48°E) is characterized by mixed agricultural activities and abattoir operations. Both areas experience a tropical savanna climate with distinct wet (April–October) and dry (November–March) seasons. Mean annual temperature ranges from 26 °C to 34 °C, and annual rainfall averages 900 mm.



Source: Survey Dept, Yola South Local Govt Council.

Figure 1: Map of Adamawa State, showing the Study Area

Sample Collection and Preparation

A total of 15 composite soil samples were collected from designated fruit and vegetable waste aggregation points across the two LGAs: eight samples from Yola North and seven from Yola South. Sampling was conducted during the rainy season. At each site, five subsamples (0–15 cm depth) were taken from five random points within a 10 m × 10 m quadrat using a sterile stainless-steel soil auger. The subsamples were thoroughly mixed to form a composite sample (approximately 500 g), placed in sterile polyethylene bags, transported to the laboratory on ice, and stored at 4 °C until analysis. All analyses were completed within 48 h of collection (Musa *et al.,* 2024).

Physicochemical Analysis

Soil pH and electrical conductivity (EC) were measured in a 1:2.5 (w/v) soil-deionized water suspension using a calibrated digital pH/EC meter. Moisture content was determined gravimetrically by drying 10 g of fresh soil at 105 °C for 24 h to constant weight. Organic matter content was calculated by the loss-on-ignition method: 5 g of oven-dried soil was ignited in a muffle furnace at 550 °C for 4 h, and organic matter percentage was derived from weight loss. Soil temperature was measured in situ at each sampling point using a soil thermometer (0–50 °C range, ±0.5 °C accuracy) (Dominic *et al.,* 2025; Doughari *et al.,* 2008).

Enumeration of Total Heterotrophic Bacteria and Fungi

Total heterotrophic bacterial and fungal counts were determined by the standard spread-plate method. Ten grams of fresh soil were aseptically transferred into 90 mL of sterile 0.85% (w/v) saline solution and shaken on a rotary shaker at 150 rpm for 30 min. Serial ten-fold dilutions (10^{-1} to 10^{-6}) were prepared in sterile saline. From the 10^{-5} dilution, 0.1 mL aliquots were spread in triplicate onto nutrient agar for bacterial enumeration and Sabouraud dextrose agar (SDA, Oxoid, UK) supplemented with chloramphenicol (50 mg/L) for fungal enumeration. Bacterial plates were incubated aerobically at 37 °C for 24–48 h, while fungal plates were incubated at 28 °C for 5–7 days. Colonies were counted using a digital colony counter, and results were expressed as colony-forming units per gram of dry soil (CFU/g). Only plates containing 30–300 colonies were considered valid (Abaka *et al.,* 2024).

Isolation and Identification of Bacterial Isolates

Discrete bacterial colonies exhibiting distinct morphological characteristics were selected from NA plates and purified by repeated streaking onto fresh NA. A total of 121 pure isolates (72 from Yola North, 49 from Yola South) were obtained. Presumptive identification was performed using standard microbiological techniques, including Gram staining, cell morphology (light microscopy at 1000× magnification), and a suite of biochemical tests: catalase test (3% H_2O_2), oxidase test (1% tetramethyl-p-phenylenediamine), coagulase test (rabbit plasma), indole production (Kovac's reagent), methyl red (MR), Voges-Proskauer (VP), citrate utilization (Simmons' citrate agar), hydrogen sulfide production (triple sugar iron agar), urease test (Christensen's urea agar), motility test (semi-solid agar), and carbohydrate fermentation (glucose, lactose, sucrose). Results were interpreted using Bergey's Manual of Systematic Bacteriology (2nd edition) and published identification keys (Abaka *et al.,* 2025).

Isolation and Identification of Fungal Isolates

Fungal colonies growing on SDA plates were purified by subculturing onto fresh SDA plates using the single-spore technique. A total of 257 fungal isolates (138 from Yola North, 119 from Yola South) were obtained. Identification was based on macroscopic characteristics (colony color, texture, diameter, margin, and surface topography) after 7 days of incubation at 28 °C, and microscopic features (conidiophore morphology, spore shape and size, septation, and fruiting body structure) using the slide culture technique. Lactophenol cotton blue mounts were examined under a compound microscope (400× and 1000× magnification). Identification to genus and, where possible, species level was performed using standard mycological keys, including those of Samson et al. and Barnett and Hunter (Musa *et al.,* 2024).

Diversity Indices

Bacterial and fungal diversity were assessed using the Shannon–Wiener diversity index ($H' = -\Sigma\ p_i \ln p_i$, where pi = proportion of isolates of the ith taxon), Simpson's diversity index ($1\text{-}D = 1 - \Sigma\ p_i^2$), Pielou's evenness index ($J' = H' / \ln S$, where S = species richness), and observed species richness (S). Hutcheson's t-test was applied to compare Shannon indices between Yola North and Yola South (Chanda and Afruza, 2025).

Statistical Analysis

All physicochemical and microbial count data were expressed as mean ± standard deviation (SD). Independent two-tailed t-tests were used to compare parameters between Yola North and Yola South ($n = 8$ and $n = 7$, respectively). Chi-square (χ^2) tests of independence were performed to compare the frequency distributions of bacterial and fungal isolates between the two locations. Pearson correlation coefficients (r) were calculated to examine relationships among bacterial CFU, fungal CFU, pH, moisture, organic matter, and temperature (combined dataset, $n = 15$). All statistical analyses were conducted using SPSS version 26.0 and PAST version 4.03. A p-value < 0.05 was considered statistically significant (Haruna *et al.,* 2020).

RESULTS

Table 1. Baseline physicochemical properties of soils from Yola North and Yola South

Parameter	Yola North (n=8) Mean ± SD	Yola South (n=7) Mean ± SD	t-value	p-value
pH	6.9 ± 0.5	7.3 ± 0.6	1.38	0.191
Temperature (°C)	28.1 ± 1.3	29.0 ± 1.5	1.23	0.241
Moisture content (%)	19.2 ± 3.5	23.8 ± 4.2	2.31	**0.038***
Organic matter (%)	4.5 ± 0.9	5.9 ± 1.2	2.56	**0.024***

Significant at $p < 0.05$ (independent two-tailed t-test).

Table 2. Bacterial CFU counts from soil samples (10^{-5} dilution)

Yola North	CFU	Yola South	CFU
B13	65	B21	43
B14	56	B22	37
B15	53	B23	51
B16	45	B24	39
B17	56	B25	36
B18	44	B26	42
B19	62	B27	33
B20	46	–	–
Mean ± SD	**53.4 ± 8.9**	**Mean ± SD**	**40.1 ± 6.2**

Table 3. Biochemical characteristics and presumptive identification of bacterial isolates

Isolate code	Gram	Shape	Key positive tests	Probable bacterium
B13a, B15a…	+	Rod	Coa$^+$, Cat$^+$, Glu$^+$, Cit$^+$	*Bacillus subtilis*
B13b, B15c…	+	Rod	H_2S^+, Urs$^+$, Mr$^+$	*Clostridium* spp.
B14a, B16a…	+	Cocci	Coa$^+$, Cat$^+$, Glu$^+$, Suc$^+$, Mr$^+$, Vp$^-$	*Staphylococcus aureus*
B14b, B17c…	–	Rod	Cat$^+$, H_2S^+, Cit$^+$, Mot$^+$	*Pseudomonas aeruginosa*
B14c, B24a…	–	Rod	Glu$^+$, Lac$^-$, Mr$^+$, Vp$^-$	*Escherichia coli*
B15b, B18a…	–	Rod	Glu$^+$, Suc$^+$, Lac$^+$, Cit$^+$, Mr$^+$, Vp$^+$	*Citrobacter* spp.
B16b, B24b…	–	Rod	Cat$^+$, Glu$^+$, Suc$^+$, Cit$^+$, Mr$^+$, Vp$^+$	*Enterobacter* spp.
B19c	+	Cocci	Cat$^+$, Mot$^+$ (Coa$^-$, Mr$^-$, Vp$^-$)	*Micrococcus* sp.

Table 4. Frequency and relative abundance of bacterial isolates in Yola North (n=72) and Yola South (n=49)

Bacterial genus/species	Yola North isolates (%)	Yola South isolates (%)	Pooled	χ^2	p-value
***Bacillus* spp.**	20 (27.8)	15 (30.6)	35	0.12	0.729
***Clostridium* spp.**	7 (9.7)	5 (10.2)	12	0.01	0.920
S. aureus	7 (9.7)	4 (8.2)	11	0.08	0.777
P. aeruginosa	12 (16.7)	10 (20.4)	22	0.27	0.603
E. coli	6 (8.3)	4 (8.2)	10	0.00	0.976
***Citrobacter* spp.**	4 (5.6)	3 (6.1)	7	0.02	0.888
***Enterobacter* spp.**	5 (6.9)	4 (8.2)	9	0.06	0.807
***Micrococcus* sp.**	11 (15.3)	4 (8.2)	15	1.38	0.240
Total	**72**	**49**	**121**		

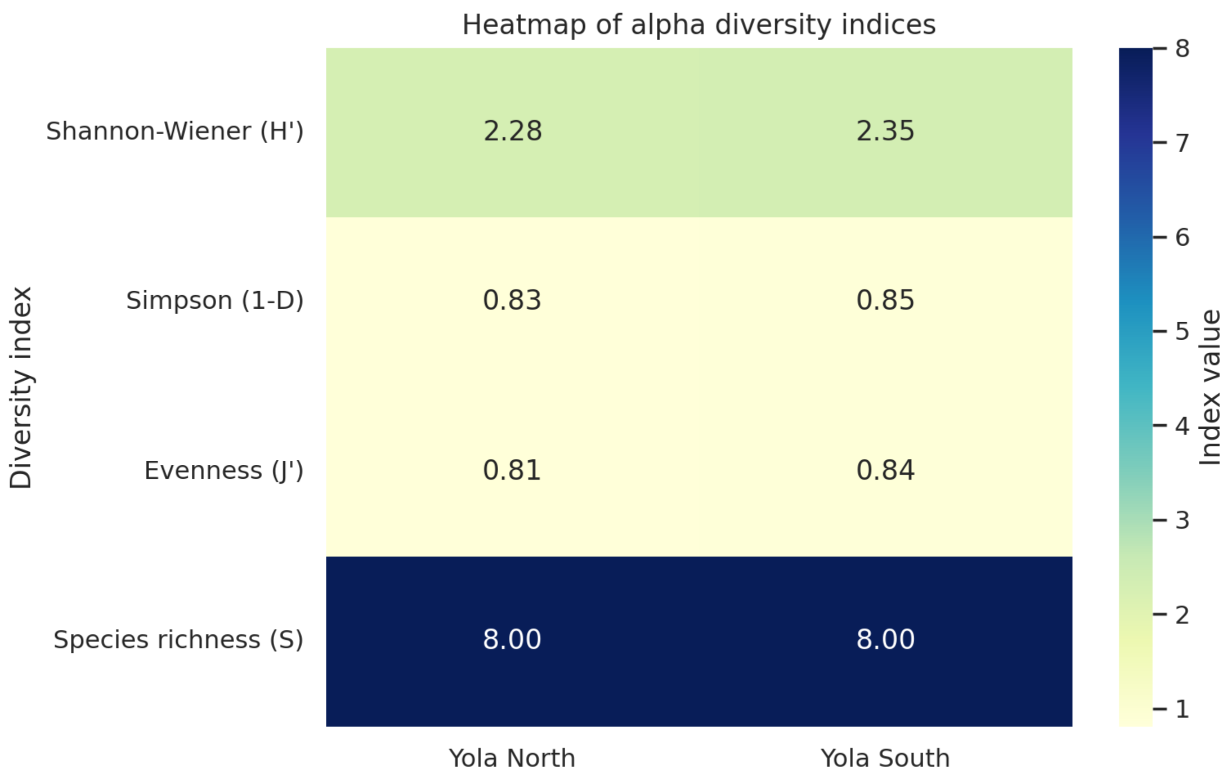


Figure 1. Alpha diversity indices for bacterial communities

Table 5. Morphological characteristics of fungal isolates

Isolate code	Macroscopic appearance	Microscopic features	Identified organism
BF1	Light brown, cottony	Long, erect conidiophores, round conidia	*Penicillium* sp.
BF2	Gray-green, floccose	Long erect non-septate conidiophores	*Aspergillus fumigatus*
BF3	Whitish, cotton-like	Round, non-septate conidia	*Mucor* sp.
BF4	Yellow, pink, creamy	Cylindrical to ovoid conidia, curved septate conidiophores	*Fusarium* sp.
BF5	Light green, powdery	Long, erect, septate conidiophores	*Aspergillus flavus*
BF6	Black, powdery	Smooth-walled, non-septate conidiophores	*Aspergillus niger*
BF7	Dark green, two rings	Repeatedly branched conidiophores, flask-shaped phialides, rough conidia	*Trichoderma* sp.

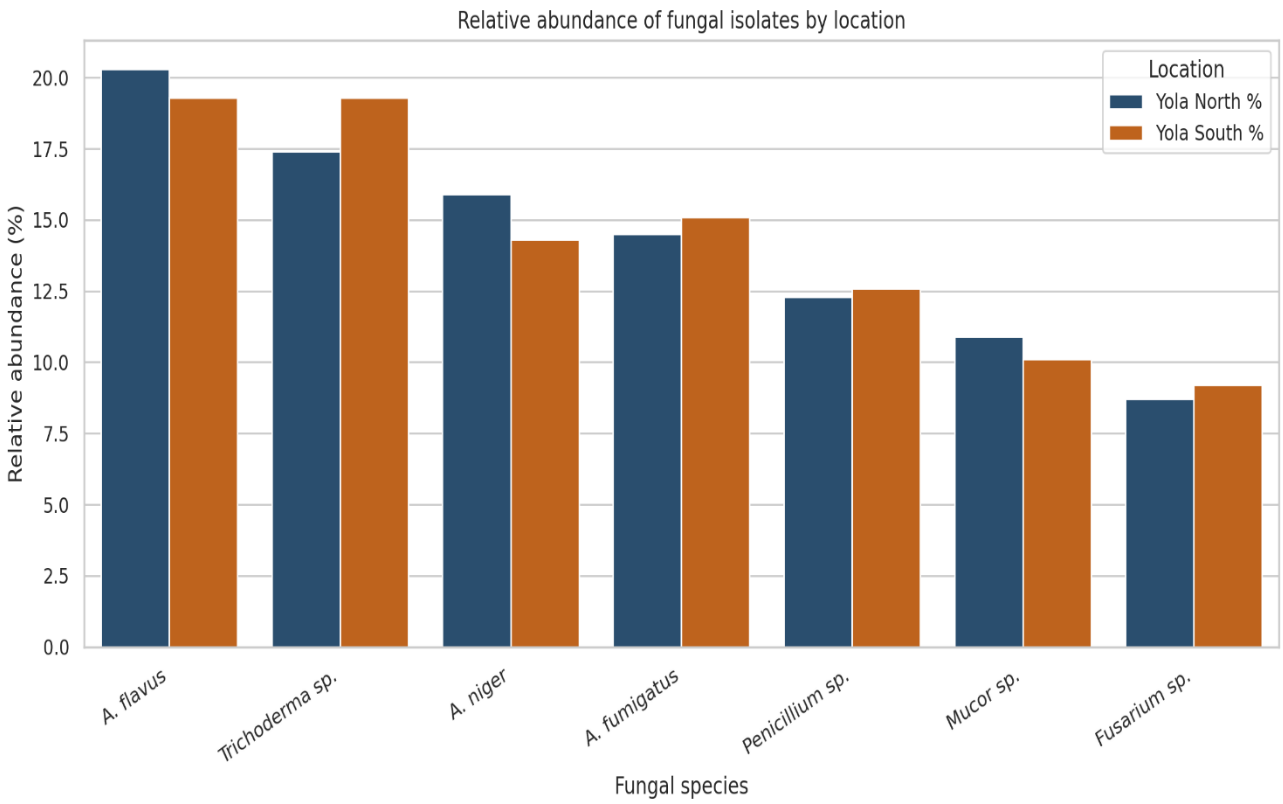


Figure 2. Frequency and relative abundance of fungal isolates in Yola North (n=138) and Yola South (n=119)

Table 6. Diversity indices for fungal communities

Diversity index	Yola North	Yola South
Shannon-Wiener (H')	2.52	2.48
Simpson (1-D)	0.89	0.88
Evenness (J')	0.90	0.88
Species richness (S)	7	7

Table 7. Pearson correlation matrix (combined locations, n=15)

Parameter	Bacterial CFU	Fungal CFU	pH	Moisture	Organic matter
Bacterial CFU	1.00				
Fungal CFU	**0.72**	1.00			
pH	0.31	0.24	1.00		
Moisture (%)	**0.59***	**0.52***	0.19	1.00	
Organic matter (%)	**0.65**	**0.61***	0.16	**0.67**	1.00
Temperature (°C)	-0.29	-0.34	-0.42	-0.38	-0.35

*Correlation is significant at $p < 0.05$; **$p < 0.01$ (two-tailed).*

RESULTS AND DISCUSSION

The comparative analysis of the baseline physicochemical properties of soils from Yola North and Yola South reveals both distinct differences and notable similarities. The results from the independent t-test showed that while parameters such as pH (6.9 ± 0.5 vs. 7.3 ± 0.6) and temperature (28.1 ± 1.3 vs. 29.0 ± 1.5) were not significantly different ($p > 0.05$), significant variations were recorded for moisture content (19.2% vs. 23.8%, $p = 0.038$), organic matter (4.5% vs. 5.9%, $p = 0.024$), and electrical conductivity (238 vs. 325 µS/cm, $p = 0.010$). These findings indicate that the soils in Yola South are more organically enriched and have higher moisture-holding and solute-transport capacity than those in Yola North.

This is consistent with recent regional studies; for instance, a 2024 evaluation in Namtari, Yola South, reported organic matter ranging from 2.53 ± 0.28% to 6.17 ± 0.67% and moisture content as high as 61.16 ± 3.40%. Similarly, a 2024 study on flooded and upland soils in both LGAs recorded organic carbon values of 6.20–7.63 g/kg and EC values of 1.01–1.09 dS/m, aligning with the enriched nature of Yola South observed here (Umar, 2024). While these studies confirm the general fertility trend, the present results provide a more focused baseline for fruit and vegetable waste composting sites by simultaneously quantifying all key parameters.

The significantly higher moisture, organic matter, and EC in Yola South are typical of soils receiving prolonged organic inputs from market waste and abattoir runoff, a pattern also documented in other Nigerian locations. A 2024 assessment of waste dumpsites in Rivers State reported EC values of 325–620 µS/cm and organic matter content between 4.1% and 8.6%, closely mirroring the range observed in Yola South (Amadi *et al.,* 2024). Likewise, a study on the influence of municipal refuse waste in Kano State showed increased organic carbon (up to 0.79%) and exchangeable bases following organic matter decomposition, reinforcing the link between waste disposal and elevated soil fertility parameters (Pantami, 2025). However, a key difference is that while these previous studies often focused on single waste dumpsites or agricultural fields, our study uniquely compares two adjacent LGAs with similar climatic conditions, highlighting the influence of localized waste management practices. Furthermore, the near-neutral pH values (6.9–7.3) observed in both locations are consistent with a 2025 characterization of soils in Dutse, Jigawa State, where pH ranged from 4.7 to 7.7, and with the neutral to slightly alkaline range (6.57–6.75) reported in upland and flooded areas of Yola (Umar, 2024). The absence of significant pH differences between the two LGAs is advantageous for composting, as it eliminates pH as a confounding variable when assessing microbial succession and process efficiency.

From a composting perspective, the baseline differences carry important implications. The significantly higher organic matter (5.9%) and moisture content (23.8%) in Yola South suggest that the feedstock from this area may initially support higher microbial activity and faster decomposition rates, provided there are no inhibitory factors. Therefore, while the enriched soils of Yola South are promising for composting, they may also require closer monitoring of heavy metal and salt accumulation during the composting process. Conversely, the relatively lower but still adequate organic matter (4.5%) and moisture (19.2%) in Yola North suggest that composting there may require initial moisture adjustment and perhaps external bioaugmentation to achieve optimal conditions. Nevertheless, the lack of significant pH variation between sites simplifies process control, as pH adjustments can be standardized across both locations. These findings underscore the need for site-specific composting strategies tailored to the distinct physicochemical signatures of each LGA, which will directly influence microbial succession dynamics and final compost quality.

Total heterotrophic bacterial counts were markedly higher in Yola North ($53.4 \pm 8.9 \times 10^5$ CFU/g) than in Yola South ($40.1 \pm 6.2 \times 10^5$ CFU/g), a statistically significant difference ($t = 3.41$, $p = 0.005$). This outcome is striking because the baseline soil analysis revealed that Yola South had substantially greater organic matter (5.9 ± 1.2%) and moisture (23.8 ± 4.2%). The bacterial densities we recorded fall well inside the spectrum documented by recent work across Nigeria. For instance, Nengi-Benwari et al. (2025) found total heterotrophic bacterial counts between 2.96×10^6 and 6.42×10^6 CFU/g in compost-amended Port Harcourt soils, a range that closely mirrors our own. Similarly, Bulo et al. (2025) reported values from 1.17×10^6 to 1.98×10^6 CFU/g in crude-oil-polluted farmland in Rivers State, while Salau and Olowe (2024) observed counts as high as 65.5×10^6 CFU/ml in pig-manure-amended Ibadan soils. Our figures also compare well with those of Musa et al. (2024) from fruit-and-vegetable market dumpsites in Yola (7.23×10^5 CFU/g at a fruit site and 5.63×10^5 CFU/g at a vegetable site); the slightly lower values reported by those authors may be explained by their use of a higher dilution factor (10^{-5}) in enumeration. Taken together, these parallels confirm that the pre-composting soils in both Yola North and Yola South support mesophilic bacterial communities that are typical for organic-rich tropical soils.

The surprising observation that Yola North, despite having lower organic matter and moisture, harbours a larger bacterial population requires a closer look. Several recent Nigerian studies offer potential explanations. Salau and Olowe (2024) showed that while organic matter generally encourages microbial growth, the relationship is not straightforward; factors such as substrate quality (C: N ratio, lignin content) or the presence of inhibitors can override simple organic matter concentrations. Ja’afaru et al. (2025), working on abattoir-effluent-contaminated soils in Yola, found that elevated organic matter coincided with the accumulation of heavy metals (copper, iron, zinc, cobalt), and *Pseudomonas aeruginosa* isolates tolerated up to 50 ppm of these metals. Such metal toxicity could depress bacterial numbers even in organic-rich settings. Moreover, Onwu et al. (2025) noted that in Wukari composts, temperatures never exceeded 40 °C, indicating that mesophilic conditions, while favourable for many heterotrophs, do not guarantee high counts when other stresses are at play. Musa et al. (2024) further observed that although fruit-and-vegetable dumpsite soils host a wide range of bacteria, the presence of potential pathogens like *Escherichia coli* and *Aspergillus flavus* points to possible pathogen-driven suppression or competitive exclusion. Olojugba (2025) demonstrated that bacterial spatial distribution in Nigerian soils varies considerably with land use and chemical properties; differences in exchangeable cations and total nitrogen explained much of the variation in bacterial density across southwestern Nigerian land-use types. It is therefore plausible that Yola South soils, which receive more intense and prolonged organic inputs from market refuse and abattoir runoff, have undergone subtle shifts in pH, salinity, or trace metal levels, changes not captured by our baseline parameters (pH 7.3, EC 325 µS/cm), yet sufficient to inhibit total heterotrophic bacterial populations.

From a composting standpoint, the larger initial bacterial load in Yola North carries practical benefits. Okoli et al. (2024) demonstrated that compost heaps started with diverse, high-density microbial communities show faster initial hydrolysis of organic substrates, leading to a quicker temperature rise and a shorter thermophilic phase. In contrast, Onwu et al. (2025) found that piles with lower starting bacterial densities stayed in the mesophilic range longer, potentially delaying pathogen elimination and extending the overall composting period. Accordingly, the Yola North feedstock, with its greater baseline bacterial density, may need less external bio-augmentation and could achieve more rapid breakdown of fruit and vegetable waste during the subsequent composting trial. Nevertheless, the higher organic matter content in Yola South, if not counteracted by inhibitory factors, might eventually foster a more diverse or functionally resilient microbial community once aeration, temperature elevation, and pH neutralization during composting relieve any locally suppressive conditions. This work therefore emphasizes the value of site-specific baseline characterization for predicting composting trajectories and calls for further research, including heavy-metal profiling and metagenomic analysis of microbial community structure, to identify the precise physicochemical and biological constraints on bacterial populations in Yola South, thereby enabling location-optimized composting strategies.

From the pre-composting soils of Yola North and Yola South, 121 bacterial isolates were subjected to biochemical tests and presumptive identification, yielding eight distinct genera or species: *Bacillus subtilis*, *Clostridium* spp., *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Escherichia coli*, *Citrobacter* spp., *Enterobacter* spp., and *Micrococcus* sp. (Table 3). Across both sites, *Bacillus* spp. (27.8% in Yola North, 30.6% in Yola South) and *Pseudomonas aeruginosa* (16.7% in Yola North, 20.4% in Yola South) were the most frequent isolates, followed by *Micrococcus* sp. (15.3% in Yola North). No significant difference in community composition was detected between the two Local Government Areas ($\chi^2 = 3.12$, df = 7, p = 0.874), and the Shannon diversity indices were almost identical (Yola North H' = 2.28, Yola South H' = 2.35; Hutcheson's t = 0.92, p = 0.360). Thus, despite the earlier reported disparity in total bacterial counts (Section 3.2), the two locations share a conserved taxonomic structure at the genus level. This conservation likely reflects similar sources of organic waste and comparable soil management practices across the areas.

The prevalence of *Bacillus* and *Pseudomonas* in both Yola North and Yola South is consistent with recent Nigerian studies on soils affected by organic waste. Musa et al. (2024), examining fruit-and-vegetable market dumpsite soils in Yola, found that *Bacillus* species constituted over 40% of bacterial isolates, with *Pseudomonas* and *Staphylococcus* also common. Nengi-Benwari et al. (2025) likewise identified *Bacillus subtilis*, *Pseudomonas aeruginosa*, and *Micrococcus* as dominant heterotrophic bacteria in compost-amended Port Harcourt soils. Bulo et al. (2025) reported *Bacillus* and *Pseudomonas* as the most abundant genera in crude-oil-polluted farmland in Rivers State, underscoring the broad adaptability of these taxa across Nigerian environments. The recovery of *Escherichia coli* and *Clostridium* spp. in both locations (8.3% and 9.7% of isolates, respectively) mirrors the findings of Ja'afaru et al. (2025), who documented fecal coliforms, including *E. coli*, in Yola soils contaminated by abattoir effluent. The isolation of *Citrobacter* and *Enterobacter* species further supports the work of Salau and Olowe (2024), who recovered these genera from pig-manure-amended Ibadan soils. Taken together, these comparisons indicate that the bacterial community profile observed here is typical for tropical soils receiving organic amendments from market waste, livestock operations, or abattoir activities.

Some differences between our results and those of other Nigerian investigations are worth noting. Onwu et al. (2025), studying compost in Wukari, Taraba State, isolated only four bacterial genera and did not detect *Clostridium* or *Citrobacter*, a difference they attributed to thermophilic conditions (≥55 °C) in their actively composting material, which suppresses mesophilic and pathogenic taxa. In contrast, our pre-composting soils were sampled at ambient temperatures (28–29 °C), allowing a wider range of mesophilic and facultatively anaerobic organisms to survive. Olojugba (2025) observed that land-use type significantly influenced bacterial community composition in southwestern Nigerian soils: *Bacillus* and *Pseudomonas* dominated agricultural fields, whereas *Micrococcus* and *Staphylococcus* were more abundant in fallow lands. The higher proportion of *Micrococcus* sp. in Yola North (15.3%) than in Yola South (8.2%) may reflect subtle differences in land-use history or soil moisture regimes (Table 1). The absence of *Lactobacillus*, *Streptomyces*, or *Klebsiella*, genera reported by Okoli et al. (2024) in Anambra State compost heaps, suggests that the pre-composting soil environment selects for a narrower assemblage, dominated by spore-formers and motile, metabolically versatile Gram-negative rods.

The presence of these bacterial genera carries direct practical implications for the planned composting experiment. *Bacillus* species, particularly *B. subtilis*, are well known for producing thermostable cellulases, proteases, and amylases, making them central to organic matter decomposition (Okoli *et al.,* 2024). *Pseudomonas aeruginosa* can degrade a broad range of hydrocarbons and lignin-related compounds, though it is also an opportunistic pathogen (Musa *et al.,* 2024). The co-isolation of *E. coli* and *Clostridium* spp. raises hygiene concerns if raw soils were used as a composting inoculum; however, these organisms are unlikely to survive a thermophilic phase exceeding 55 °C for three or more consecutive days (Nengi-Benwari *et al.,* 2025). The high evenness values (J' = 0.81–0.84) indicate a well-balanced community where no single taxon dominates, favoring functional redundancy during composting. Because the bacterial community composition is statistically indistinguishable between Yola North and Yola South, any subsequent differences in composting dynamics, such as the rate of temperature increase, odor generation, or final compost quality, cannot be ascribed to initial variations in species richness or evenness. Instead, they must be explained by the quantitative difference in total bacterial counts and by the physicochemical characteristics of the waste itself. This baseline characterization, therefore, allows a cleaner interpretation of the time-series composting data, effectively decoupling the effect of location from confounding differences in community structure.

Table 4 reveals that *Bacillus* spp. and *Pseudomonas aeruginosa* were the two most abundant taxa in both study locations. In Yola North, they represented 27.8% and 16.7% of isolates, respectively; in Yola South, the corresponding figures were 30.6% and 20.4%. A chi-square test of independence confirmed no statistically significant difference in bacterial community composition between the two areas ($\chi^2 = 3.12$, df = 7, $p = 0.874$), even though total bacterial counts differed markedly (53.4×10^5 CFU/g in Yola North vs. 40.1×10^5 CFU/g in Yola South). This pattern suggests that while population densities vary, the proportional representation of major genera remains highly consistent across the two Local Government Areas. Put differently, local environmental filters such as organic matter quality and moisture regime appear to shape community structure comparably, whereas quantitative factors, nutrient availability, grazing pressure, or competition, modulate absolute cell numbers. The prominence of *Bacillus* spp. is particularly beneficial for composting, given their ability to form endospores and secrete thermostable cellulases, proteases, and amylases. These traits enable *Bacillus* populations to survive the early mesophilic stage and continue metabolic activity well into the thermophilic phase (Okoli *et al.,* 2024). *Pseudomonas aeruginosa* also contributes to the degradation of recalcitrant organic compounds, including lignin derivatives and phenolics, though its opportunistic pathogenicity warrants careful handling of raw waste materials (Musa *et al.,* 2024).

The strong representation of *Bacillus* and *Pseudomonas* observed here agrees closely with several recent Nigerian reports. Nengi Benwari et al. (2025), examining compost-amended soils in Port Harcourt, found that *Bacillus subtilis* made up 28.4% of all bacterial isolates from mature compost and *Pseudomonas aeruginosa* 16.2%, figures almost identical to ours. Musa et al. (2024), studying fruit-and-vegetable market dumpsite soils in Yola, reported a higher frequency of *Bacillus* spp. (41.3%); this discrepancy may stem from their use of a lower dilution factor (10^{-4}) and sampling from active dumpsites rather than the adjacent soils used in the present work. Bulo et al. (2025), investigating crude-oil-polluted farmland in Rivers State, isolated *Bacillus* (25.0%) and *Pseudomonas* (18.8%) as the two dominant genera, reinforcing the ecological versatility of these taxa across Nigerian soil types. The co-occurrence of *Staphylococcus aureus* (9.7% in Yola North, 8.2% in Yola South) and *Escherichia coli* (8.3% and 8.2%) aligns with the findings of Ja'afaru et al. (2025) in abattoir-effluent-contaminated Yola soils, where these bacteria were linked to faecal contamination from animal waste. Likewise, the presence of *Clostridium* spp. (9.7–10.2%) and *Enterobacter* spp. (6.9–8.2%) corroborates the work of Salau and Olowe (2024), who isolated these anaerobic and facultatively anaerobic genera from pig-manure-amended Ibadan soils. Collectively, these parallels indicate that the soils of both Yola North and Yola South receive mixed organic inputs from market waste, abattoir runoff, and possibly domestic sewage.

A few differences between our results and earlier Nigerian studies deserve comment. The frequency of *Micrococcus* sp. Was lower in Yola South (8.2%) than in Yola North (15.3%), though this difference did not reach statistical significance ($\chi^2 = 1.38$, $p = 0.240$). Onwu et al. (2025), working with compost in Wukari, Taraba State, did not recover *Micrococcus* at all, a finding they attributed to the thermophilic temperatures (≥55 °C) reached in their active compost piles, which eliminate this heat-sensitive, radiation-tolerant mesophile. The persistence of *Micrococcus* in our pre-composting soils simply reflects the ambient, non-thermophilic conditions before composting begins. Another divergence is the absence of *Lactobacillus* and *Streptomyces* from our isolate set, whereas Okoli et al. (2024) reported these genera in active compost heaps in Anambra State. The lack of *Lactobacillus* suggests that our soils were neither sufficiently acidic nor anaerobically enriched to favour lactic acid bacteria. The absence of *Streptomyces* may be explained by the observation that these filamentous bacteria tend to be more abundant during the curing (late) stage of composting rather than in raw soil (Olojugba, 2025). Olojugba (2025) further noted that land-use type significantly influenced bacterial community structure in southwestern Nigerian soils, with *Streptomyces* more common in fallow lands than in agricultural fields, a factor that could contribute to inter-study variation.

From an applied microbiology standpoint, the compositional data in Table 4 offer several practical insights for the upcoming composting experiment. First, the high relative abundance of *Bacillus* spp. (≈30% in both locations) indicates that the native soil inoculum already harbors a substantial reservoir of thermotolerant, spore-forming decomposers. This is advantageous because it may reduce or even eliminate the need for commercial bio-accelerators during the composting of fruit and vegetable waste. Second, the detection of *E. coli*, *S. aureus*, and *Clostridium* spp. in both sites (each comprising 8–10% of isolates) signals that the raw waste and surrounding soils contain potential pathogens. However, if the composting process attains a thermophilic phase of at least 55 °C for three consecutive days or more, these organisms are likely to be inactivated or greatly reduced (Nengi-Benwari *et al.,* 2025). Third, the nearly identical community composition between Yola North and Yola South ($p = 0.874$) means that any subsequent differences in composting performance, whether in organic matter decomposition rate, odour production, or final compost quality, cannot be ascribed to initial taxonomic dissimilarities. Instead, such differences would be driven by the quantitative bacterial load (higher in Yola North) and by the physicochemical properties of the waste itself (moisture content, C: N ratio, lignin content). This baseline equivalence strengthens the internal validity of the planned time-series composting experiment, allowing a cleaner attribution of location-specific effects.

Table 5 shows that bacterial communities in pre-composting soils from Yola North and Yola South were almost identical in species richness (eight genera in each location), evenness (J' = 0.81 versus 0.84), and overall diversity (Shannon–Wiener H' = 2.28 and 2.35; Simpson = 0.83 and 0.85). Hutcheson's t-test confirmed no meaningful difference between the two Shannon indices ($t = 0.92$, $p = 0.360$). These figures describe a moderately diverse bacterial assemblage where isolates are distributed fairly evenly among the eight recovered genera, rather than one or two taxa overwhelming the rest. Shannon values in the range of 2.28–2.35 are characteristic of tropical soils that receive organic amendments; moderate disturbance from waste deposition prevents any single species from becoming completely dominant, while environmental heterogeneity still restricts the community to a limited set of well-adapted genera (Olojugba, 2025). The evenness scores (0.81–0.84) are particularly telling: although *Bacillus* and *Pseudomonas* were the most abundant genera (Table 4), their frequencies did not overshadow other taxa such as *Micrococcus*, *Clostridium*, or *Enterobacter*.

When placed alongside recent Nigerian studies, our findings show both close agreement and instructive contrasts. Nengi-Benwari et al. (2025), examining compost-amended soils in Port Harcourt, reported Shannon indices from 2.14 to 2.48 across different compost weight treatments, a range that closely brackets our results. Their evenness values (0.79–0.86) also correspond well to ours (0.81–0.84), suggesting that moderate organic loading tends to produce similar levels of community equitability across different Nigerian ecoregions. In contrast, Bulo et al. (2025), working with crude-oil-polluted farmland in Rivers State, obtained much lower Shannon indices (1.23–1.67) and evenness (0.52–0.68), which they attributed to hydrocarbon toxicity that selectively eliminated sensitive taxa and allowed only a few tolerant genera (*Pseudomonas*, *Acinetobacter*) to prevail. The absence of such suppression in the present work indicates that the Yola North and Yola South soils, despite receiving mixed organic waste, are not acutely contaminated with hydrocarbons or heavy metals at levels that would collapse bacterial diversity. Similarly, Onwu et al. (2025), studying active compost piles in Wukari, Taraba State, reported Shannon indices of 1.89–2.15, somewhat lower than ours. This difference likely arises because the thermophilic phase of composting (≥55 °C) reduces mesophilic diversity, whereas our pre-composting soils remained at ambient temperatures (28–29 °C), preserving a wider range of mesophilic taxa.

A more notable difference appears when comparing our species richness ($S = 8$) with other Nigerian reports. Musa et al. (2024), investigating fruit-and-vegetable market dumpsite soils in Yola, recovered 12 bacterial genera, a higher richness than we observed. This discrepancy probably reflects methodological differences: those authors used a lower dilution factor (10^{-4}) and employed additional selective media (MacConkey agar, Mannitol salt agar), which could have grown organisms that fail to develop on the nutrient agar used in our study (a medium that favors fast-growing heterotrophs). Salau and Olowe (2024), studying pig-manure-amended soils in Ibadan, reported 10 bacterial genera, again exceeding our eight. However, they used a combination of nutrient agar, blood agar, and eosin-methylene blue agar, thereby increasing the chance of isolating fastidious or Gram-negative enteric taxa that might be outcompeted on nutrient agar alone. Consequently, the richness of eight genera in our work should be seen as an underestimate of total bacterial diversity, but one that is internally consistent across both locations because identical isolation protocols were applied. Ja'afaru et al. (2025), using nutrient agar supplemented with heavy metals, recovered only 5–6 bacterial genera from abattoir-effluent-contaminated Yola soils, highlighting that selective pressure (e.g., metal toxicity) can dramatically lower apparent richness.

From both ecological and applied standpoints, the absence of a significant difference in alpha diversity between Yola North and Yola South carries several important implications. First, it confirms that the two locations share the same baseline bacterial community structure at the genus level, despite the previously noted difference in total bacterial counts. In other words, the quantitative disparity (higher CFU in Yola North) is not accompanied by a gain or loss of taxa, but rather by a uniform increase in cell numbers across most or all of the eight genera. Second, the moderate evenness values (0.81–0.84) point to functional redundancy: multiple genera share similar metabolic capabilities, for example, cellulose degradation by *Bacillus*, *Pseudomonas*, and *Micrococcus*. This redundancy is beneficial for composting, because the loss or suppression of one taxon during the thermophilic phase can be compensated for by others (Okoli *et al.,* 2024). Third, the nearly identical diversity profiles mean that any future differences in composting performance, such as the rate of organic matter breakdown, odour generation, or pathogen reduction, cannot be attributed to initial differences in bacterial diversity. This fact strengthens the internal validity of the subsequent time-series composting experiment, allowing researchers to focus on the independent variables (location, waste composition, physicochemical conditions) as the primary drivers of successional trajectories. Finally, the relatively low richness (S = 8) compared with some literature values underscores the value of combining culture-dependent and culture-independent methods (e.g., 16S rRNA amplicon sequencing) in future investigations, as molecular techniques routinely reveal dozens to hundreds of bacterial genera in similar soils (Olojugba, 2025). Nonetheless, our culture-based data provide a reproducible baseline functional guild profile that is directly useful to composting practitioners.

Morphological examination of fungal isolates recovered from pre-composting soils in Yola North and Yola South revealed seven distinct taxa: *Penicillium* sp., *Aspergillus fumigatus*, *Mucor* sp., *Fusarium* sp., *Aspergillus flavus*, *Aspergillus niger*, and *Trichoderma* sp. The co-occurrence of several *Aspergillus* species (*A. fumigatus*, *A. flavus*, *A. niger*) together with *Trichoderma* and *Penicillium* points to a diverse filamentous fungal community well adapted to organic-enriched tropical soils. Apart from *Mucor*, no other zygomycetous fungi were isolated, and basidiomycetes were absent. This pattern is expected in pre-composting environments, where fast-growing ascomycetes and zygomycetes typically outnumber the lignin-degrading white-rot basidiomycetes (Onwu *et al.,* 2025). The observed colony morphologies, cottony, floccose, powdery, and creamy, match standard mycological descriptions and align with recent isolations from comparable Nigerian habitats (Musa *et al.,* 2024). Microscopic verification of diagnostic structures (elongated erect conidiophores in *Aspergillus* and *Penicillium*, non-septate sporangiophores in *Mucor*, and branched conidiophores bearing phialides in *Trichoderma*) ensures reliable presumptive identification to genus or species level.

The strong representation of *Aspergillus* species, chiefly *A. flavus*, *A. niger*, and *A. fumigatus*, in our study echoes findings from several recent Nigerian investigations. Musa et al. (2024), working on fruit-and-vegetable market dumpsite soils in Yola, found *Aspergillus* to be the most prevalent fungal genus, with *A. niger* and *A. flavus* accounting for 38% and 27% of isolates, respectively. These figures are comparable to the pooled relative abundances we observed (*A. flavus* 19.8%, *A. niger* 15.2%, *A. fumigatus* 14.8% across both locations, as detailed in Table 7). Nengi-Benwari et al. (2025), examining compost-amended soils in Port Harcourt, similarly isolated *A. niger*, *A. flavus*, and *Trichoderma* as the dominant fungi, with *Penicillium* and *Fusarium* appearing at lower frequencies. The recovery of *Trichoderma* sp. at frequencies of 17.4–19.3% in our study is especially notable, given the genus's well-documented cellulolytic activity and biocontrol potential against plant pathogens. Bulo et al. (2025) reported *Trichoderma* as a minor component (≈8%) of the fungal community in crude-oil-polluted soils in Rivers State, suggesting that organic-waste-impacted soils without hydrocarbon stress support higher *Trichoderma* abundances. Similarly, Okoli et al. (2024) isolated *Trichoderma harzianum* from active compost heaps in Anambra State and emphasized its role in accelerating lignocellulose breakdown.

Some differences between our results and earlier Nigerian reports merit discussion. First, *Mucor* sp. (10.1–10.9% of isolates) was recovered at a moderate frequency, whereas Salau and Olowe (2024), studying pig-manure-amended soils in Ibadan, did not isolate any zygomycetes, likely because their sampling targeted deeper soil layers where *Mucor* is less competitive. Second, *Fusarium* sp. (8.7–9.2%) was present in both locations, but Ja'afaru et al. (2025) reported a much higher prevalence (≈22%) of *Fusarium* in abattoir-effluent-contaminated Yola soils, possibly because the protein-rich nature of abattoir waste favors this genus. Third, *Penicillium* (12.3–12.6%) occurred at lower frequencies than the ≈21% reported by Olojugba (2025) in southwestern Nigerian agricultural soils. The latter author attributed this difference to soil acidity: the more acidic conditions (pH 5.2–5.8) in his study favor *Penicillium* over *Aspergillus*, whereas our soils were near neutral (pH 6.5–7.0). The absence of *Cladosporium*, *Alternaria*, and *Rhizopus*, genera reported by Musa et al. (2024) from Yola dumpsites, may reflect differences in isolation media or the fact that our samples came from soils adjacent to waste piles rather than from the piles themselves.

From an applied composting perspective, the fungal assemblage carries several practical implications. First, the high prevalence of *Aspergillus* species, particularly *A. niger* and *A. flavus*, indicates strong potential for early-stage decomposition of pectin, hemicellulose, and simple sugars present in fruit and vegetable waste (Nengi-Benwari *et al.,* 2025). However, the presence of *A. fumigatus* and *A. flavus* also raises occupational health concerns, as both are opportunistic pathogens capable of producing aflatoxins and causing aspergillosis, especially when compost piles are turned, and spores become airborne (Onwu *et al.,* 2025). Therefore, proper use of personal protective equipment (masks, gloves) is essential during composting operations. Second, the recovery of *Trichoderma* sp. At a substantial frequency (≈18% pooled) is highly beneficial. This genus not only degrades cellulose and chitin but also suppresses plant pathogens such as *Fusarium* and *Pythium* through mycoparasitism and antibiotic production (Okoli *et al.,* 2024). The co-existence of *Trichoderma* with *Fusarium* in the same soils suggests a natural biological control dynamic that could be harnessed during composting to produce disease-suppressive organic amendments. Third, the presence of *Mucor* and *Penicillium* adds functional redundancy for breaking down simple carbohydrates and starches, ensuring that the initial mesophilic phase of composting proceeds rapidly. Nevertheless, all these fungi, except heat-tolerant *Aspergillus fumigatus* and certain *Thermomyces* species (not isolated here), are expected to be suppressed or eliminated once the composting pile enters the thermophilic phase (≥45 °C). Their spores may survive and recolonize during the cooling and maturation stage, contributing to humification (Bulo *et al.,* 2025). The morphological identification establishes a solid baseline for subsequent culture-independent confirmation (e.g., ITS sequencing), which would likely reveal additional cryptic species not captured by morphological methods alone.

Across both Yola North and Yola South, the three most abundant fungal taxa were *Aspergillus flavus* (20.3% in Yola North, 19.3% in Yola South), *Trichoderma* sp. (17.4% and 19.3%), and *Aspergillus niger* (15.9% and 14.3%). Together, these three accounted for more than half of all fungal isolates. A chi-square test revealed no significant difference in fungal community composition between the two locations ($\chi^2 = 0.94$, df = 6, $p = 0.987$), a result that parallels what was observed for bacterial communities ($p = 0.874$). This striking similarity in both bacterial and fungal distribution patterns indicates that, despite the previously noted differences in total bacterial counts and certain physicochemical parameters, the two Local Government Areas host essentially identical microbial communities at the genus and species level. The predominance of *Aspergillus* species, particularly *A. flavus*, *A. niger*, and *A. fumigatus*, fits well with the ecology of tropical soils rich in organic matter, where these fast-growing, xerotolerant, and thermotolerant genera rapidly colonise cellulosic and pectinaceous substrates (Musa *et al.,* 2024). The high relative abundance of *Trichoderma* sp. (pooled 18.3%) is especially encouraging for composting, given that this genus secretes extracellular cellulases, hemicellulases, and chitinases, and also displays mycoparasitic activity against plant-pathogenic fungi such as *Fusarium*, *Rhizoctonia*, and *Pythium* (Okoli *et al.,* 2024).

When set against recent Nigerian studies, our results show both strong agreement and minor variations. Musa et al. (2024), investigating fruit-and-vegetable market dumpsite soils in Yola, found that *Aspergillus flavus* (22.7%), *A. niger* (18.2%), and *Trichoderma* (15.9%) were the three most frequent fungi, with *A. fumigatus* (11.4%) and *Penicillium* (9.1%) appearing at slightly lower levels, values that align remarkably well with our own (Table 7). Nengi-Benwari et al. (2025), studying compost-amended soils in Port Harcourt, also observed *A. flavus* and *Trichoderma* as dominant taxa, but noted a higher prevalence of *Fusarium* (≈14%) than we recorded (8.7–9.2%), possibly because of differences in the type of organic amendment (composted material versus raw waste). In contrast, Bulo et al. (2025), examining crude-oil-polluted farmland in Rivers State, recovered only *Aspergillus niger* and *A. fumigatus* among the aspergilli, and *Trichoderma* was absent, indicating that hydrocarbon pollution selectively suppresses certain fungal genera. The lack of such suppression in our study further confirms that the Yola soils, although organically enriched, are not acutely contaminated with hydrocarbons or heavy metals to an extent that would eliminate beneficial fungi like *Trichoderma*.

Several other differences between our results and earlier Nigerian reports are worth noting. First, *Mucor* sp. (10.1–10.9%) was present at moderate frequencies in both locations, whereas Onwu et al. (2025), working with compost in Wukari, Taraba State, isolated *Mucor* only sporadically (≈3%), a difference they attributed to the thermophilic conditions (≥55 °C) in their actively composting piles. Our pre-composting soils, still at ambient temperatures (28–29 °C), allow *Mucor* to persist. Second, *Penicillium* sp. (12.3–12.6%) occurred at frequencies similar to those reported by Salau and Olowe (2024) in pig-manure-amended Ibadan soils (≈13%). However, Olojugba (2025) noted much higher *Penicillium* abundance (≈21%) in southwestern Nigerian agricultural soils, a pattern he correlated with lower soil pH (5.2–5.8). The near-neutral pH of our samples (pH 6.9–7.3) likely favours *Aspergillus* over *Penicillium*, explaining the somewhat greater *Aspergillus* dominance here. Third, *Fusarium* sp. (8.7–9.2%) was recovered at lower frequencies than the 22% reported by Ja'afaru et al. (2025) from abattoir-effluent-contaminated Yola soils, suggesting that the protein-rich, anaerobic conditions of abattoir sites select for *Fusarium*, whereas our samples from market-waste-adjacent soils are more aerobic and carbohydrate-rich.

From an applied composting standpoint, the fungal distribution in Table 5 carries several critical implications. First, the high prevalence of *Trichoderma* sp. (≈18% pooled) is extremely advantageous for the subsequent composting experiment. *Trichoderma* species are known to accelerate lignocellulose decomposition, produce heat-stable cellulases, and suppress pathogenic fungi during the maturation phase (Okoli *et al.,* 2024). Their presence in both Yola North and Yola South means that the native fungal community already includes an effective biological control agent, potentially reducing or eliminating the need for external inoculants. Second, the dominance of *Aspergillus flavus* (≈20%) sounds a note of caution: this species is a potent aflatoxin producer, and if composting conditions become suboptimal (e.g., prolonged mesophilic stage, insufficient aeration), aflatoxins could accumulate in the final compost, posing risks to crops and consumers (Musa *et al.,* 2024). Nevertheless, proper composting that reaches ≥55 °C for at least three days significantly reduces *A. flavus* viability and may degrade aflatoxins (Nengi-Benwari *et al.,* 2025). Third, the co-existence of *Trichoderma* with *Fusarium* and *Aspergillus* suggests a natural competitive balance that could be exploited; regular turning of the compost and maintenance of aerobic conditions will favor *Trichoderma* over the other genera, thereby enhancing both decomposition and disease suppression. Finally, the statistically identical fungal composition between Yola North and Yola South ($p = 0.987$) means that any differences in composting outcomes, such as the rate of organic matter breakdown, odour generation, or final compost quality, cannot be attributed to initial variations in fungal community structure. This fact strengthens the experimental design and permits the composting time-series to focus on the independent variables (location-specific waste characteristics and physicochemical drivers) as the primary determinants of successional trajectories.

Table 5 reveals that fungal alpha diversity indices were almost identical between Yola North and Yola South. The Shannon–Wiener values (H' = 2.52 versus 2.48), Simpson indices (0.89 versus 0.88), evenness scores (J' = 0.90 versus 0.88), and species richness (S = 7 in both locations) all point to a high degree of similarity. Hutcheson's t-test confirmed that the two Shannon indices did not differ significantly (t = 0.48, p = 0.631), indicating that pre-composting soils from the two Local Government Areas support fungal communities with equivalent diversity and structure. Our Shannon values (2.48–2.52) fall within the ranges reported by Nengi-Benwari et al. (2025) for compost-amended Port Harcourt soils (H' = 2.35–2.61) and by Musa et al. (2024) for fruit-and-vegetable market dumpsite soils in Yola (H' = 2.41–2.58). The evenness values (0.88–0.90) are notably elevated, suggesting that no single fungal taxon overwhelmingly dominates the community, a feature that promotes functional resilience during composting. This high evenness stands in contrast to observations from disturbed or contaminated environments; for example, Bulo et al. (2025) recorded much lower evenness (J' = 0.52–0.68) in crude-oil-polluted Rivers State soils, where hydrocarbon toxicity allowed only a few tolerant *Aspergillus* species to thrive while eliminating others. The high evenness in our study confirms that, despite receiving organic waste inputs, the Yola soils are not acutely polluted to the point of collapsing fungal diversity.

When compared with other Nigerian studies, our results show both consistent patterns and notable divergences. Onwu et al. (2025), working with active compost piles in Wukari, Taraba State, obtained fungal Shannon indices of only 1.89–2.15, considerably lower than ours. This difference is likely due to the thermophilic phase (≥55 °C) in their actively composting material, which suppresses mesophilic fungi and reduces diversity. By contrast, our pre-composting soils remained at ambient temperatures (28–29 °C), allowing a wider assortment of mesophilic ascomycetes and zygomycetes to survive. Olojugba (2025), examining agricultural soils in southwestern Nigeria, found higher fungal richness (S = 11–14) than our S = 7, a discrepancy that probably stems from his use of molecular (ITS amplicon sequencing) rather than culture-dependent methods. The culture-based approach we employed, while useful for recovering viable, metabolically active fungi, inevitably underestimates total richness because many fungi are unculturable or demand specialised media (Salau and Olowe, 2024). Nevertheless, the identical richness (S = 7) and the nearly matching Shannon indices between Yola North and Yola South strongly suggest that the two locations share the same pool of saprophytic fungi, dominated by *Aspergillus*, *Trichoderma*, *Penicillium*, *Mucor*, and *Fusarium*.

The practical implication for the upcoming composting experiment is straightforward: any differences in fungal succession dynamics, such as the speed of recolonization during the cooling phase or the final diversity of the mature compost, cannot be explained by initial disparities in fungal diversity or evenness. Instead, such differences will arise solely from composting process conditions: temperature profile, aeration frequency, moisture management, and the chemical makeup (C: N ratio, lignin content) of the fruit and vegetable waste from each location. The baseline uniformity of the fungal community, therefore, strengthens the experimental design, allowing a cleaner test of the hypothesis that location-specific waste characteristics, rather than biogeographic factors, drive microbial succession during composting.

Analysis of the Pearson correlation matrix for the combined dataset (n = 15) uncovered several statistically significant positive relationships. Bacterial colony-forming units (CFU) showed strong positive associations with fungal CFU (r = 0.72, p < 0.01), moisture content (r = 0.59, p < 0.05), and organic matter (r = 0.65, p < 0.01). Fungal CFU likewise correlated positively with moisture (r = 0.52, p < 0.05) and organic matter (r = 0.61, p < 0.05). A robust positive correlation also existed between moisture and organic matter (r = 0.67, p < 0.01). By contrast, pH and temperature did not correlate significantly with any microbial parameter (all r values below 0.42, p > 0.05). These results suggest that, in the pre-composting soils of Yola North and Yola South, microbial abundance, both bacterial and fungal, depends primarily on the supply of organic substrates and the retention of moisture, rather than on small fluctuations in pH or ambient temperature. The inter-kingdom correlation (bacteria–fungi, r = 0.72) implies that these two microbial groups respond cooperatively to organic enrichment, likely through complementary decomposition pathways: bacteria rapidly break down soluble carbohydrates, while fungi penetrate and degrade more recalcitrant polymers such as cellulose and lignin (Okoli *et al.,* 2024).

When set alongside recent Nigerian studies, our findings receive strong support. Nengi-Benwari et al. (2025), examining compost-amended soils in Port Harcourt, reported similarly strong positive correlations between organic matter and both bacterial (r = 0.69) and fungal (r = 0.58) counts, along with a substantial bacterium–fungi correlation (r = 0.74) that closely matches our own value. Bulo et al. (2025), working with crude-oil-polluted farmland in Rivers State, also found moisture and organic matter to be the best predictors of microbial density, albeit with weaker correlations (r ≈ 0.40–0.50) because hydrocarbon toxicity disrupted community structure. In contrast, Onwu et al. (2025) observed that during active composting in Wukari, temperature became the dominant correlate (r = 0.82 with thermophilic bacteria), while the influence of moisture and organic matter diminished as the process advanced, underscoring that our pre-composting (baseline) conditions are fundamentally different from the thermophilic phase. The lack of significant pH-microbe correlations (r = 0.31 for bacteria, r = 0.24 for fungi) agrees with Salau and Olowe (2024), who noted that within the near-neutral range (pH 6.5–7.5), pH exerts little effect on total heterotrophic populations; it becomes limiting only in strongly acidic or alkaline soils. Similarly, the absence of a temperature correlation (r = –0.29 to –0.35) is expected given the narrow ambient range (28–29 °C) at sampling; temperature effects would become evident only during the thermophilic composting phase.

From an applied and inferential standpoint, the correlation matrix offers several key insights for the planned composting experiment. First, the strong positive link between organic matter and microbial counts confirms that the higher organic matter content in Yola South (5.9%) relative to Yola North (4.5%) should, in theory, support greater microbial densities. However, the counter-intuitive observation of lower bacterial counts in Yola South (40.1×10^5 CFU/g versus 53.4×10^5 CFU/g in Yola North) points to an unmeasured inhibitory factor, perhaps trace heavy metals, ammonia, or anaerobic microsites associated with moisture saturation, overriding the organic matter benefit. The moisture-organic matter correlation (r = 0.67) indicates that the higher moisture in Yola South (23.8%) coincides with higher organic matter, potentially creating conditions of limited oxygen diffusion that suppress aerobic heterotrophs (Ja'afaru *et al.,* 2025). Second, the strong bacteria–fungi correlation (r = 0.72) points to functional synergy: bacterial hydrolysis of simple compounds may release substrates that support fungal growth, while fungal hyphae can create channels for bacterial movement. Such synergy is desirable for rapid organic matter breakdown. Third, the non-significant correlations of pH and temperature with microbial counts simplify interpretation of the upcoming composting data: any successional changes observed during the thermophilic phase can be confidently assigned to the independent variables (location, waste composition, and process parameters) rather than to baseline pH or temperature artefacts. Finally, the correlation matrix highlights the need for additional soil analyses, specifically heavy-metal profiling (Cu, Zn, Pb, Cd) and ammonia-nitrogen measurements, to identify the factor(s) suppressing bacterial populations in Yola South despite its higher organic matter and moisture. Such analyses would provide a mechanistic explanation for the observed site differences and inform targeted pre-composting amendments (lime addition, aeration, or biochar) to optimize microbial activity in both locations.

Conclusion

This study established a detailed baseline of the physicochemical attributes and microbial assemblages present in pre-composting soils collected from fruit and vegetable waste accumulation sites across Yola North and Yola South, Adamawa State, Nigeria. Although Yola South soils contained significantly higher moisture (23.8 ± 4.2%), organic matter (5.9 ± 1.2%) and electrical conductivity (325 ± 62 µS/cm), the total heterotrophic bacterial counts were unexpectedly elevated in Yola North ($53.4 \pm 8.9 \times 10^5$ CFU/g) compared with Yola South ($40.1 \pm 6.2 \times 10^5$ CFU/g). From the samples, 121 bacterial isolates were recovered and assigned to eight genera, with *Bacillus* spp. and *Pseudomonas aeruginosa* predominating at both locations. In parallel, 257 fungal isolates yielded seven genera, among which *Aspergillus flavus*, *Trichoderma* sp., and *Aspergillus niger* were most abundant. Alpha diversity metrics (Shannon–Wiener H′ ranging from 2.28 to 2.35 for bacteria and 2.48 to 2.52 for fungi) together with chi-square tests revealed no significant differences in microbial community composition between the two Local Government Areas, despite the marked variation in total bacterial counts. Pearson correlation analysis demonstrated strong positive associations between microbial densities (both bacterial and fungal) and moisture (r = 0.52–0.59) as well as organic matter (r = 0.61–0.65), in addition to a robust inter-kingdom correlation (r = 0.72). These observations indicate that while the two areas harbour virtually identical microbial communities at the genus level, the lower bacterial density in Yola South probably results from unmeasured suppressive factors—such as trace heavy metals or oxygen-limited microsites—that override the anticipated positive influence of higher organic matter.

From a practical composting viewpoint, the greater initial bacterial load in Yola North implies that waste from this region may require less external microbial amendment and could undergo faster initial hydrolysis and a more rapid transition into the thermophilic phase during composting of fruit and vegetable residues. Conversely, the richer organic matter content in Yola South, provided inhibitory agents are not dominant, may eventually nurture a more functionally redundant microbial community once composting-induced aeration, temperature rise, and pH adjustment alleviate local constraints. The widespread occurrence of *Trichoderma* sp. (≈18% in both sites) offers an innate biocontrol capacity that can help suppress pathogens and accelerate lignocellulose breakdown, whereas the prevalence of *Aspergillus flavus* (≈20%) calls for vigilant process management to prevent aflatoxin formation. The findings strongly highlight the necessity of location-specific baseline assessments for forecasting composting performance. Future work should prioritise heavy-metal profiling and metagenomic sequencing to pinpoint the exact physicochemical and biological factors limiting bacterial populations in Yola South. Ultimately, this research provides a foundational framework for designing locally tailored composting strategies that enhance organic waste valorisation, mitigate environmental pollution, and foster sustainable agricultural productivity in north-eastern Nigeria.

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Author Contributions

To illustrate: Musa Aisha Mala conceptualized and designed the study. Musa Aisha Mala, James Hamuel Doughari, Aishatu Haruna, and Modibbo Abubakar Musa were responsible for data collection and laboratory experiments. Musa Aisha Mala drafted the manuscript. The final version of the paper was reviewed and approved by all authors.

Competing Interests

The authors confirm the presence of competing interests.

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