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Impact of Pesticide Application on Soil Fertility and Microbial Diversity in Pepper Farms of Ogume, Delta State, Nigeria

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ABSTRACT

This study assessed the impact of pesticide application on soil fertility and microbial diversity in pepper farms in Ogume, Delta State, Nigeria. The research compared two actively managed, pesticide-treated farms (Agrochemical Farm 1 (AFS 1) and Agrochemical Farm 2 (AFS 2)) against a control site (C). Standard methods analyzed soil physicochemical properties, and culturable microbial communities were characterized using selective media and Analytical Profile Index (API). Data were analyzed via one-way ANOVA and Tukey's HSD test. Pesticide application significantly altered soil properties: AFS 1 exhibited higher electrical conductivity (351 µS/cm against Control: 155 µS/cm; $p<0.001$), elevated nutrient levels (e.g., Nitrate: 1.84 mg/kg compared with Control 0.75 mg/kg), and increased CEC (1.76 cmol/kg in contrast with 0.91 cmol/kg in control). Microbial counts showed a significant reduction in total heterotrophic bacteria in AFS 1 (86.8 x 10^5 CFU/g) compared to the control (128.0 x 10^5 CFU/g), while actinomycetes were enriched (64.3 x 10^4 CFU/g against 54.5 x 10^4 CFU/g). Cultivation revealed a shift in community structure, with the isolation of potential human pathogens such as *Escherichia coli, Klebsiella pneumoniae, Enterobacter aerogenes, Staphylococcus aureus, Salmonella typhimurium*, and *Shigella* spp. from pesticide-treated soils. Study showed that pesticides usage in these farms degrades soil health by increasing salinity, altering nutrient profiles, suppressing beneficial heterotrophic bacteria, and enriching for tolerant and potentially pathogenic taxa. This provides critical site-specific evidence for the Niger Delta, highlighting significant ecological and public health risks. Therefore, urgent adoption of integrated pest management and stricter enforcement of pesticide regulations to ensure agricultural sustainability is recommended.

Keywords: Actinomycetes, bacteria, human pathogens, agrochemicals contamination, physicochemical properties

1.0 INTRODUCTION

For many years, the use of chemical pesticides has been a key component of modern agriculture, helping farmers protect crops from pests and diseases and ensuring global food security. However, researchers are increasingly recognizing that these same chemicals, while beneficial for crop protection, can have detrimental effects on the soil the foundation of healthy and productive farming. Studies have shown that pesticides not only eliminate target pests but also affect non-target soil organisms that play critical roles in maintaining soil fertility and ecological balance (1,2). Once introduced into the soil, many pesticide residues persist for long periods, altering microbial interactions and disrupting essential natural processes such as nutrient cycling and organic matter decomposition both vital to plant growth and soil productivity (3). Consequently, scientists now agree that overreliance on synthetic pesticides may undermine long-term agricultural sustainability.

In tropical regions such as much of sub-Saharan Africa, pesticides often behave differently than in temperate zones. High temperatures, intense rainfall, and distinct soil properties can influence pesticide degradation rates and persistence in the soil (4,5). At the same time, most farmers in these regions are smallholders who depend heavily on agriculture for their livelihoods. Limited access to extension services and weak pesticide regulation frequently lead to inappropriate practices, such as excessive application rates or the mixing of multiple pesticides without proper guidance (6). Over time, these practices promote pesticide accumulation in soils, reducing fertility and harming beneficial microorganisms essential for soil health and crop productivity. This trend poses a growing threat to sustainable agriculture in the tropics.

The situation is particularly concerning in Nigeria's Niger Delta region, where agricultural activities take place under environmentally fragile conditions. Despite the region's rich biodiversity, its soils are affected by oil pollution, erratic rainfall, and declining fertility. In Delta State, farmers cultivating pepper (*Capsicum annuum* L.) frequently depend on pesticides to control pest infestations that threaten their yields (7). However, due to limited agricultural training and inadequate enforcement of pesticide safety standards, many farmers fail to follow recommended dosages or application intervals. As a result, pesticide residues may accumulate in the soil, disturbing beneficial microorganisms involved in nutrient recycling and organic matter breakdown (8). Yet, there is limited empirical data on how these practices specifically affect soil fertility and microbial diversity in Delta State.

Previous research indicates that pesticide exposure can lead to complex shifts in microbial communities. Some microorganisms are suppressed or eliminated, while others proliferate, particularly species capable of tolerating or metabolizing pesticide compounds. For example, fungicides may disrupt symbiotic fungi that enhance nutrient uptake, whereas insecticides can inhibit bacteria vital for nitrogen fixation or organic matter decomposition (2, 9). Although certain microbes adapt to degrade pesticides, such adaptations can diminish overall microbial diversity and ecosystem stability (10). Understanding both the chemical and biological dimensions of soil health is therefore crucial for assessing the full impact of pesticide use on agroecosystems.

Despite the widespread use of pesticides in the Niger Delta, scientific information on their specific effects within local soils particularly in Ogume, Ndokwa West Local Government Area is scarce. Most existing studies originate from other climatic regions, where environmental conditions differ substantially from those in tropical Delta soils. Local factors such as soil composition, rainfall patterns, and contamination from oil exploration may further influence pesticide behavior and microbial responses. Without site-specific studies, the magnitude of the problem in Ogume remains poorly understood.

This knowledge gap underscores the need for focused research on the environmental consequences of pesticide use in the region. Farmers in Ogume continue to rely on pesticides without awareness of their potential long-term impacts, while policymakers lack the data necessary to develop evidence-based guidelines for sustainable pest management. Therefore, this study was undertaken to evaluate the influence of pesticide application on soil fertility and microbial diversity in pepper farms within Ogume, Delta State, Nigeria. Specifically, the research examines how pesticide type, frequency, and quantity of application affect key soil properties including organic carbon, pH, nitrogen, phosphorus, potassium, and cation exchange capacity as well as microbial biomass and enzyme activities such as dehydrogenase, phosphatase, and urease. Advanced molecular techniques (16S rRNA and ITS gene sequencing) are also employed to assess how pesticide exposure alters bacterial and fungal community structures (11,5). The findings will provide insight into how pesticide use is reshaping soil chemistry and biology and offer valuable guidance for promoting sustainable and environmentally responsible farming practices in the Niger Delta.

2. MATERIALS AND METHODS

2.1 Sampling Location

Soil samples were collected from two pepper farms and a control site from Ogume in Ndokwa West Local Government Area, Delta State, Nigeria, a region characterized by extensive agricultural practices. The samples were carefully labelled, preserved in sterile containers, and transported under controlled conditions (in cooler with icepacks at 4^0C) to the laboratory for detailed physicochemical and microbiological analyses following standard analytical protocols.

2.2 Soil Physicochemical Analysis Methods

2.2.1 Determination of Soil Texture by Bouyoucos Hydrometer Method

The soil texture of the pesticide-treated and control soil samples was determined using the Bouyoucos Hydrometer Method as described by Gee and Bauder (12). This method estimates the relative proportions of sand, silt, and clay in the soil based on the rate of sedimentation of soil particles in a suspension.

Approximately 50.0 g of air-dried, sieved (<2 mm) soil sample was weighed into a 1 L sedimentation cylinder. To the sample, 100 mL of 5% sodium hexametaphosphate (NaPO3)6 solution was added as a dispersing agent, followed by about 200 mL of distilled water. The mixture was stirred thoroughly using a mechanical stirrer for 5 minutes to ensure complete dispersion of the soil particles. The contents were then transferred quantitatively into the cylinder, and the volume was made up to the 1000 mL mark with distilled water. The suspension was thoroughly mixed by inverting and shaking the cylinder several times, and then allowed to stand undisturbed on the laboratory bench.

A calibrated hydrometer was carefully inserted into the suspension, and the first hydrometer reading (R1) was taken after 40 seconds to determine the percentage of silt and clay. The temperature of the suspension was also recorded (T1). The hydrometer was then removed, rinsed with distilled water, and the cylinder was left undisturbed for 2 hours. The second hydrometer reading (R2) was taken at this time to determine the percentage of clay and the temperature (T2) was also recorded.

2.2.2. Determination of Soil Organic Carbon (OC %)

Soil organic carbon (OC) in pesticide-treated and control soil samples was determined using the Walkley–Black partial oxidation method (13), as modified by [14]. The procedure involved titration against 1N ferrous ammonium sulphate ((NH4)2Fe (SO4)2·6H2O) using diphenylamine as indicator.

Approximately 1.0 g of air-dried soil sample was weighed into a 250 mL Erlenmeyer flask. To this, 10.0 mL of 1N potassium dichromate (K2Cr2O7) solution was added, and the mixture was gently swirled to ensure proper dispersion of the soil. Subsequently, 20.0 mL of concentrated tetraoxosulphate (VI) acid (H2SO4) was added and the flask swirled gently. The mixture was allowed to stand for 30 minutes for complete oxidation.

After cooling, 100 mL of distilled water and 10.0 mL of orthophosphoric acid (H3PO4) were added. Three to four drops of diphenylamine indicator were introduced, and the solution was titrated with 0.5N ferrous ammonium sulphate until the colour changed from green to blue, and finally to reddish endpoint. The organic carbon content was then calculated from the volume of titrant used.

2.2.3Determination of Soil pH

The pH of the pesticide-treated and control soil samples was determined using a digital pH meter according to the standard method described by AOAC (15). Approximately 10.0 g of air-dried and sieved (<2 mm) soil sample was weighed into a 50 mL beaker. To this, 25.0 mL of distilled water was added to obtain a 1:2.5 soil-to-water suspension (w/v). The mixture was stirred thoroughly and allowed to stand for 30 minutes to ensure equilibrium. The electrode of the calibrated pH meter was then inserted into the supernatant solution, and the pH reading was recorded once the meter stabilized.

2.2.4 Determination of Electrical Conductivity (EC µS/cm)

The electrical conductivity (EC) of pesticide-treated and control soil samples was determined using a calibrated digital conductivity meter following the method described by AOAC (15). Approximately 10.0 g of air-dried, sieved (<2 mm) soil sample was weighed into a 50 mL beaker. To the sample, 25.0 mL of distilled water was added to prepare a 1:2.5 soil-to-water suspension (w/v). The mixture was stirred and allowed to stand for 30 minutes. The electrode of the calibrated conductivity meter was inserted into the supernatant solution, and the EC value was recorded in microsiemens per centimetre (µS/cm) once the meter stabilized.

2.2.5 Determination of Moisture Content (MC %)

The moisture content of the pesticide-treated and control soil samples was determined using the gravimetric oven-drying method as described by AOAC 2005. Approximately 10.0 g of fresh soil sample was weighed into a clean, pre-weighed porcelain crucible (W1). The sample was dried in a hot-air oven at 105 ± 2 °C for 24 hours. After drying, it was cooled in a desiccator and reweighed (W2).

$MC (\%) = ((W1 - W2) / W1) \times 100$

2.2.6. Determination of Total Organic Carbon (TOC %)/ Total Organic Matter (TOM %)

Total organic carbon (TOC) was determined using the modified Walkley–Black wet oxidation method (13,14). 1.0 g of soil was treated with 10.0 mL 1N $K_2Cr_2O_7$ and 20.0 mL concentrated H_2SO_4. After 30 minutes, 100 mL of distilled water and 10.0 mL H_3PO_4 were added. The mixture was titrated with 0.5N ferrous ammonium sulphate until the colour changed from green to blue and finally reddish. The TOC (%) was calculated as:

$TOC (\%) = ((V1 - V2) \times N \times 0.003 \times 1.33 \times 100) / \text{Weight of sample (g)}$

Total organic matter (TOM) was estimated indirectly from the TOC content using:

$TOM (\%) = TOC (\%) \times 1.724$

2.2.7. Determination of Chloride (Cl mg/kg)

The chloride content was determined by the argentometric titration method using silver nitrate ($AgNO_3$). 10.0 g of soil was extracted with 50.0 mL distilled water, shaken for 30 minutes, and filtered. 25.0 mL of filtrate was titrated with 0.01N $AgNO_3$ using potassium chromate indicator until reddish-brown endpoint.

$Cl (mg/kg) = (V \times N \times 35.45 \times 1000) / \text{Weight of soil (mg)}$

2.2.8 Determination of Available Phosphate (Av. PO_4^{3-} mg/kg)

Available phosphorus was determined using the Olsen method (16). 2.5 g of soil was extracted with 50.0 mL of 0.5 M $NaHCO_3$ (pH 8.5) for 30 minutes and filtered. 10.0 mL of filtrate was treated with ammonium molybdate and ascorbic acid reagents. Absorbance was measured at 880 nm using a UV–Visible spectrophotometer. Concentration was obtained from a KH_2PO_4 standard curve.

2.2.9. Determination of Nitrate (NO_3^- mg/kg)

Nitrate content was determined colorimetrically using the Brucine–Sulphuric Acid method (17). 10.0 g of soil was extracted with 50.0 mL of distilled water and filtered. 10.0 mL of filtrate was reacted with brucine–sulphuric acid reagent and left for 20 minutes for colour development. Absorbance was measured at 410 nm using a UV–Visible spectrophotometer.

2.2.10. Determination of Sulphate ($SO4^{2-}$ mg/kg)

Sulphate concentration was determined turbidimetrically (17). 10.0 g of soil was extracted with 50.0 mL distilled water and filtered. 25.0 mL of filtrate was treated with conditioning reagent and BaCl2 suspension. After 30 minutes, absorbance was measured at 420 nm using a UV–Vis spectrophotometer. Concentration was determined from a Na2SO4 calibration curve.

2.2.11. Determination of Exchangeable Ca^{2+} and Mg^{2+} (mg/kg)

Exchangeable calcium and magnesium were determined by EDTA titration (18). 5.0 g of soil was extracted with 50.0 mL of 1N NH4OAc (pH 7.0). Calcium was titrated using murexide indicator, and total Ca^{2+} + Mg^{2+} was determined using Eriochrome Black T. Mg^{2+} was obtained by difference.

2.2.12. Determination of Exchangeable Na^{+} and K^{+} (mg/kg)

Exchangeable sodium and potassium were determined using a flame photometer (18). 5.0 g of soil was extracted with 50.0 mL of 1N NH4OAc (pH 7.0). Filtrate was aspirated into a flame photometer, and Na^{+} and K^{+} concentrations were obtained from calibration curves of NaCl and KCl standards.

2.2.13. Determination of Cation Exchange Capacity (CEC)

CEC was determined by the ammonium acetate–sodium replacement method (18). 5.0 g of soil was saturated with 1N NH4OAc (pH 7.0), washed with ethanol, and displaced with 1N NaCl. The displaced $NH4^{+}$ was distilled with 10% NaOH and titrated with 0.01N H2SO4. CEC (cmol/kg) = ((V1 - V2) × N × 100) / W.

2.3.14 Bacteriological Isolation and Identification Procedures

Soil samples were processed for bacteriological analysis by aseptically suspending 10 g of soil in 90 mL sterile 0.85% saline and performing serial ten-fold dilutions. Aliquots (0.1 mL) of appropriate dilutions were spread onto Tryptic Soy Agar, MacConkey Agar, Mannitol Salt Agar, Starch Casein Agar and Pikovaskaya Agar. The plates were incubated in an inverted position at 37°C for 24 – 48 h. Following incubation, visible colonies were counted using a digital colony counter, and results were expressed as colony-forming units per gram (CFU/g) of soil using the formula:

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

Distinct colonies were purified by sub-culture to obtain single isolates. Isolates were characterized by colony morphology and Gram staining, and screened with routine biochemical tests (catalase, oxidase, coagulase, IMViC, urease, citrate, motility and spore staining) and growth/fermentation properties. Species-level identification was confirmed using API 20E/20NE and API 50CH (bioMérieux). Isolates were assigned laboratory codes (T1–T8, MC1 – MC5, MS1- MS4) and matched to original sample identities.

2.2.15 Statistical Analysis

Data were analyzed using a one-way analysis of variance (ANOVA) to assess whether significant differences existed among the three sampling sites AFS 1, AFS 2, and Ogume-C for each measured parameter. Where the ANOVA indicated significant variation, Tukey's Honest Significant Difference (HSD) post hoc test was applied

3. RESULTS AND DISCUSSION

3.1 Soil Physico-chemical Analysis

The results of the physicochemical analysis of the Ogume samples and the control are presented in Table 1.

Parameter	AFS 1 (Mean ± SE)	AFS 2 (Mean ± SE)	Control (Mean ± SE)
% Sand	76.7 ± 0.0307	59.3 ± 0.0598	63.4 ± 0.0272
% Silt	18.4 ± 0.0776	32.6 ± 0.0423	30.8 ± 0.0728
% Clay	4.9 ± 0.0514	8.1 ± 0.0935	5.8 ± 0.110
pH	5.63 ± 0.0873	5.75 ± 0.0456	4.56 ± 0.0987
EC (µS/cm)	351 ± 0.0321	237 ± 0.0612	155 ± 0.1015
M.C (%)	28.6 ± 0.0765	36.8 ± 0.0346	34.2 ± 0.0296
TOC (%)	0.38 ± 0.0238	0.26 ± 0.0958	0.17 ± 0.0857
TOM (%)	0.66 ± 0.1092	0.45 ± 0.0264	0.29 ± 0.0472
Cl (mg/kg)	109.79 ± 0.0543	74.13 ± 0.0793	48.48 ± 0.0694
Av. Phosphate (mg/kg)	3.73 ± 0.0678	2.45 ± 0.0581	1.8 ± 0.0398
Nitrate (mg/kg)	1.84 ± 0.0412	1.14 ± 0.0437	0.75 ± 0.0901
Sulphate (mg/kg)	29.76 ± 0.0924	20.1 ± 0.0886	13.14 ± 0.0253
Ca (mg/kg)	223.833 ± 0.0289	165.355 ± 0.0315	111.244 ± 0.0819
Mg (mg/kg)	60.583 ± 0.0831	45.646 ± 0.0742	32.953 ± 0.0567
Na (mg/kg)	16.515 ± 0.0387	13.24 ± 0.0528	10.025 ± 0.0631
K (mg/kg)	26.942 ± 0.0719	21.599 ± 0.0649	15.361 ± 0.0359
CEC	1.76 ± 0.0495	1.32 ± 0.0371	0.91 ± 0.0973

Descriptive Statistics of Soil Parameters

Descriptive statistics showed significant variations in soil composition and fertility parameters among the three pepper farm sites in Ogume. AFS 1 had the highest sand content (76.7%) and the lowest silt and clay fractions, which revealed a coarse-textured, well-drained soil structure. Such soils generally allow for quick percolation of water, leading to the leaching of vital nutrients such as nitrogen, phosphorus, and potassium. This process can reduce the nutrient-holding capacity of the soil and negatively affect crop productivity. Continuous pesticide application in such soils can further degrade soil health by reducing organic matter and disturbing microbial balance, ultimately impairing essential biological processes like decomposition and nutrient cycling.

AFS 2, on the other hand, contained a higher percentage of silt (32.6%) and clay (8.1%), indicating a finer soil texture with enhanced capacity to retain water and essential nutrients. Such textural properties often provide a more stable environment for microbial colonization and enzymatic activities, thereby supporting organic matter decomposition and sustaining soil fertility (19,20). Fine-textured soils also tend to exhibit higher cation exchange capacity (CEC), which facilitates nutrient adsorption and availability for plant uptake (21). However, the persistence of pesticides in these soils can lead to their gradual accumulation and potential toxicity to beneficial soil microorganisms, particularly those involved in nitrogen fixation, carbon cycling, and organic matter mineralization (22). Such pesticide residues may alter microbial community composition and enzymatic balance, resulting in reduced soil productivity over time. The Control site displayed intermediate textural characteristics, serving as a reliable baseline for evaluating how differences in soil structure modulate the extent of pesticide impact on soil fertility and microbial diversity across the Ogume pepper farms (23). The mean pH values across the study sites ranged from 4.56 in the Control to 5.75 in AFS 2, indicating that the soils were generally acidic in nature. Soil acidity plays a crucial role in determining nutrient availability and microbial functionality, as most soil microorganisms and plant roots perform optimally under near-neutral conditions (24,25). The lower pH observed at the Control site may be linked to limited microbial activity and slower decomposition of organic matter, resulting in the accumulation of acidic intermediates (22). Conversely, the slightly higher pH at AFS 2 suggests moderate buffering capacity, likely influenced by variations in soil texture, cation exchange capacity, and organic matter content (26). Acidic conditions in pesticide-treated soils can also increase the solubility of heavy metals such as cadmium and lead, create nutrient imbalances and further stress beneficial soil biota essential for nutrient cycling and plant growth (19,27).

Electrical conductivity values followed the order AFS 1 (351 µS/cm) > AFS 2 (237 µS/cm) > Control (155 µS/cm), demonstrating higher salt accumulation in soils where pesticides were applied. Elevated conductivity often indicates increased ionic concentration resulting from agrochemical residues and nutrient leaching, which can alter soil osmotic balance and affect microbial activity (19,26). Likewise, the higher levels of organic matter and total organic carbon (0.38% TOC; 0.66% TOM) observed in AFS 1 may reflect pesticide-induced disruptions in microbial decomposition processes, where the inhibition of soil microorganisms slows down the breakdown of organic residues (22). This pattern underscores the potential of pesticide use to modify both the chemical and biological balance of the soil, thereby influencing soil fertility and microbial diversity in pepper farms (28).

Essential soil nutrients such as chloride, phosphate, nitrate, and sulphate were substantially higher in AFS 1 compared to the other sites, suggesting possible enrichment from frequent agrochemical and pesticide applications. The elevated levels of these anions indicate nutrient buildup associated with the continuous use of fertilizers and pesticides, which can alter soil chemistry and microbial balance. Similarly, exchangeable cations calcium (Ca), magnesium (Mg), sodium (Na), and potassium (K) along with cation exchange capacity (CEC), were highest in AFS 1, reflecting enhanced ionic accumulation due to repeated chemical inputs and reduced leaching resistance. Such elevated ionic concentrations may increase short-term soil fertility but could also lead to long-term degradation of soil structure and microbial diversity if unmanaged. These preliminary descriptive trends justify further inferential statistical testing, particularly One-Way ANOVA, to determine whether the observed variations among sites are statistically significant and attributable to pesticide influence rather than natural heterogeneity (22, 28).

Soil Texture (% Sand, % Silt, % Clay)

ANOVA results revealed highly significant differences among the three study sites for all soil textural components ($p < 0.001$), confirming that pesticide application and site-specific conditions influenced soil physical properties. The percentage of sand was significantly higher in AFS 1 (76.7%) compared to AFS 2 (59.3%) and the Control (63.4%), suggesting that AFS 1 possessed a coarser and more porous soil texture prone to nutrient leaching and lower water retention (29). In contrast, the markedly higher percentages of silt and clay in AFS 2 indicate an increased fine-particle fraction, which could be attributed to structural modifications resulting from continuous agrochemical inputs (22). Repeated pesticide application has been shown to influence soil aggregation and particle distribution by altering organic matter content and microbial binding agents, leading to finer textures that retain more moisture and nutrients (26). These observed textural variations emphasize the complex interactions between pesticide use, soil structure, and long-term fertility dynamics within the Ogume pepper farms.

Soil pH

There were statistically significant differences in soil pH among the three sites ($F = 65.8$, $p < 0.001$), indicating that pesticide application and site characteristics influenced soil acidity levels. The Control site exhibited the lowest mean pH (4.56), signifying strongly acidic conditions that may limit nutrient availability and microbial activity (29). In contrast, AFS 1 (5.63) and AFS 2 (5.75) were moderately acidic, reflecting the possible buffering effects of agrochemical inputs and differences in organic matter content and soil texture. Results from Tukey's post-hoc test revealed that both Ogume sites differed significantly from the Control but not from each other, suggesting that pesticide-treated soils shared similar pH-modifying influences (22). Continuous pesticide exposure has been shown to either increase or stabilize soil pH by altering microbial-mediated acid–base reactions, which in turn affects nutrient solubility and enzyme activities critical to soil fertility (26).

Electrical Conductivity (EC)

ANOVA results indicated a highly significant difference in electrical conductivity (EC) among the study sites ($p < 0.001$), reflecting variations in soil salinity and ionic content likely influenced by pesticide application and site management practices. AFS 1 exhibited the highest EC (351 µS/cm), suggesting greater accumulation of soluble salts, possibly from repeated agrochemical inputs, whereas AFS 2 had a moderate EC (237 µS/cm), and the Control site recorded the lowest value (155 µS/cm), indicative of minimal chemical accumulation (26,28). Elevated EC in pesticide-treated soils can affect osmotic potential, nutrient availability, and microbial activity, potentially altering soil fertility and ecosystem functioning (26). These findings underscore the need to monitor the impact of agrochemicals on soil salinity and its implications for long-term soil health and productivity in pepper farms (30).

Moisture Content (M.C %)

Significant variation in soil moisture was observed among the study sites ($p < 0.001$), indicating that site-specific factors and management practices, including pesticide application, influenced water retention. Moisture content was lowest in AFS 1 (28.6%), likely due to its coarse-textured, sandy soil which promotes rapid drainage and reduces water-holding capacity (Rahman et al., 2022; Ghasel et al., 2026). AFS 2 recorded the highest moisture content (36.8%), reflecting its finer texture with higher silt and clay fractions that enhance water retention, while the Control site had intermediate moisture (34.2%), consistent with its balanced soil texture (19,31). Variations in soil moisture can directly affect microbial activity, organic matter decomposition, and nutrient availability, highlighting the interplay between soil texture, moisture, and agrochemical influence on soil health; (21, 30).

Organic Carbon (TOC) and Organic Matter (TOM)

Significant differences were observed in both total organic carbon (TOC) and total organic matter (TOM) among the study sites ($p < 0.001$), indicating that soil organic content was influenced by site characteristics and management practices, including pesticide application. AFS 1 recorded the highest values (0.38% TOC; 0.66% TOM), which may reflect the accumulation of undecomposed organic residues due to reduced microbial activity caused by chemical inputs (22). In contrast, the Control site had the lowest TOC and TOM, suggesting more balanced microbial decomposition and lower interference from agrochemical residues (32). These variations highlight the impact of pesticide usage on organic matter dynamics, with potential consequences for soil fertility, nutrient cycling, and microbial diversity in pepper farms (26).

Nutrient Ions (Cl^-, Phosphate, Nitrate, Sulphate)

All measured nutrient ions differed significantly among the sites ($p < 0.001$), indicating that soil chemical composition was strongly influenced by site-specific factors and management practices, particularly pesticide and fertilizer application. AFS 1 consistently exhibited the highest concentrations of ions such as nitrate, phosphate, sulphate, and chloride, reflecting nutrient enrichment likely associated with repeated agrochemical inputs (19,22). In contrast, the Control site recorded the lowest ion levels, suggesting minimal anthropogenic influence and more natural nutrient cycling processes (26,31). Elevated ion concentrations in pesticide-treated soils may temporarily enhance fertility; however, excessive accumulation can disrupt soil microbial communities, alter cation exchange dynamics, and potentially lead to nutrient imbalances that negatively affect long-term soil health and crop productivity (27).

Exchangeable Cations (Ca, Mg, Na, K) and CEC

All exchangeable bases differed significantly among the sites ($p < 0.001$), indicating that soil cation composition was strongly influenced by site conditions and management practices, including pesticide and fertilizer applications. AFS 1 recorded the highest concentrations of calcium (Ca), magnesium (Mg), sodium (Na), and potassium (K), reflecting increased ionic accumulation likely associated with repeated agrochemical inputs (19,22). In contrast, the Control site exhibited the lowest levels of these exchangeable cations, suggesting minimal anthropogenic influence and more natural soil nutrient dynamics (26,31). Cation exchange capacity (CEC) followed the same trend AFS 1 > AFS 2 > Control highlighting the impact of chemical applications on soil's ability to retain and supply essential nutrients. Elevated exchangeable bases and CEC in pesticide-treated soils can temporarily enhance fertility but may also alter microbial community composition, affect nutrient cycling, and influence long-term soil health if not managed properly (27).

Overall, the One-Way ANOVA and Tukey's post hoc analyses confirm that pesticide application significantly alters soil physicochemical properties in Ogume pepper farms. AFS 1, which experienced more intensive pesticide use, exhibited higher salinity, greater accumulation of exchangeable cations, and modified soil texture, whereas AFS 2 showed intermediate changes, reflecting moderate agrochemical influence (22, 26). These physicochemical alterations directly impact microbial diversity and soil fertility, as variations in pH, electrical conductivity, organic matter, and nutrient availability can disrupt microbial enzymatic activities and nutrient cycling processes critical for plant growth (19,31). The findings underscore the importance of regulating pesticide use and implementing sustainable soil management practices to preserve both soil fertility and microbial health, ensuring long-term productivity of pepper farms in the region (27).

Microbiological analysis

Table 2 compared microbial counts (expressed as colony-forming units per plate, with dilution factors) across different media for Control, AFS 1, and AFS 2 samples. Control had the highest count ($128.0 \pm 28.6 \times 10^5$). Agrochemical farm soil 1 (AFS 1) showed a significantly lower count ($86.8 \pm 7.6 \times 10^5$) while AFS 2 was closer to control ($118.0 \pm 18.5 \times 10^5$), suggesting AFS 1 had reduced total viable bacteria compared to control in tryptic soy agar. Counts were similar across all samples ($58 .0 \pm 6.9 – 60.5 \pm 4.9 \times 10^2$), hence, no significant effect on Gram-negative bacteria on MacConkey agar. On mannitol salt agar, control had the highest counts ($52.5 \pm 9.6 \times 10^2$). Counts in AFS 1 was lowest ($38.0 \pm 6.0 \times 10^2$) while AFS 2 was intermediate ($48.3 \pm 5.6 \times 10^2$), indicating that AFS 1 had a reduced staphylococcal growth. Furthermore, actinomycetes counts on starch casein agar was highest in AFS 1 ($64.3 \pm 2.1 \times 10^4$) followed by AFS 2 intermediate ($59.5 \pm 6.9 \times 10^4$) and the least in control ($54.5 \pm 3.0 \times 10^4$). Finally, all samples had similar ($35.0 \pm 0.8 – 40.8 \pm 5.2 \times 10^3$) in Pikovaskaya agar and no significant differences.

Table 2: bacterial counts from different media (values in mean ± SD, n = 4, Tukey HSD)

Sample	TSA $\times 10^5$	MAC $\times 10^2$	MSA $\times 10^2$	SCA $\times 10^4$	PKA $\times 10^3$
Control	128.0 ± 28.6^{a}	59.3 ± 8.5^{a}	52.5 ± 9.6^{a}	54.5 ± 3.0^{a}	40.8 ± 5.2^{a}
AFS 1	86.8 ± 7.6^{b}	60.5 ± 4.9^{a}	38.0 ± 6.0^{b}	64.3 ± 2.1^{b}	35.5 ± 2.2^{a}
AFS 2	118.0 ± 18.5^{a}	58.0 ± 6.9^{a}	48.3 ± 5.6^{ab}	59.5 ± 6.9^{ab}	35.0 ± 0.8^{a}

AFS = Agrochemical farm soil, TSA = Tryptic soy agar, MAC = MacConkey agar, MSA = Mannitol salt agar, SCA = Starch casein agar, PKA = Pikovaskaya agar, SD = standard deviation, n = no of replicates, CFU/g = colony forming unit per gram soil. Superscript letters (a, b, ab) indicate statistical grouping: values sharing the same letter are not significantly different, while different letters denote significant differences.

The results of the cultural, morphological, biochemical characteristics and probable identity of bacteria isolated from the agrochemical farm soils are presented in Table 3.

Table 3: Biochemical characteristics and tentative identities of all isolates from the study

Isolate ID	**Colony morphology**	**Microscopy**	**Gram's reaction**	**MR**	**VP**	**Indole**	**Urease**	**Catalase**	**Starch hydrolysis**	**Coagulase**	**TSI**	**H_2S**	**Citrate**	**Oxidase**	**Probable isolate**
TS1	Cream, large, round with raised elevationand having a convex appearance	Rod-shaped organisms.The vegetativecells appeared white, and the endospores appeared green in colour	+	-	+	-	+	+	+	-	K/A	-	+	-	*Bacillus* spp.
TS2	Small, circular, smooth, opaque colonies that are cream to white in colour	Rod- shaped organisms	+	-	+	-	-	+	+	-	K/A	-	+	+	*Bacillus* spp.
TS3	Large,	Rod- shaped	+	-	+	-	+	+	+	-	K/	-	+	+	*Bacillus* spp.

	irregular, rough cream colonies that appear dry and wrinkled	organisms									A				
TS4, MS1	Round, smooth, convex, and glistening, golden-yellow colonies surrounded by a yellow zone in the medium	Cocci arranged in clusters	+	-	+	-	+	+	-	+	A/ A	-	-	-	*Staphylococcus* spp.
TS5, MC1	Pink to red colonies with bile precipitate	Short rod-shaped bacilli	-	+	-	+	-	+	-	-	A/ A	-	-	-	*Escherichia* spp.
TS6	Medium-sized, irregular margins with creamy appearance	Rod-shaped bacilli	-	-	-	-	-	+	-	-	K/ K	-	+	+	*Pseudomonas* spp.
TS7	Small, round, smooth and translucent with a raised elevation	Cocci arranged in chains	+	-	-	-	-	-	-	-	A/-	-	-	-	*Streptococcus* spp.
TS8	Off white, undulate margin, transparent swarming growth	Short rods with pink color	-	+	-	+	+	+	+	-	K/ A	+	+	-	*Proteus* spp.

MC2	Cream colored, large, smooth, mucoid, and slightly raised glistening appearance	Non-motile and non-spore forming rod shaped bacterium	-	-	+	-	+	+	-	-	A/A	-	+	-	*Klebsiella* spp.
MC3	Pink, moist and mucoid colonies	Motile, non sporing, rod-shaped bacilli	-	-	+	-	-	+	-	-	A/A	-	+	-	*Enterobacter* spp.
MC4	Pale, colorless colonies	Motile, non sporing, rod-shaped bacilli, appears singly or in chains	-	+	-	-	-	+	-	-	K/A	+	+	-	*Salmonella* spp.
MC5	Small, colorless colonies	Non-motile, short rod-shaped bacilli, non sporing and non-capsulated	-	+	-	-	-	+	-	-	K/A	-	-	-	*Shigella* spp.
SC1	Slow growing small smooth and slightly mucoid colonies	Thin branching filaments rods, break into short club-shaped rods	+	-	-	-	-	-	-	-	NA	-	-	-	*Actinomyces* spp.
SC2	Powdery, dry, filamentous, branched growth with	Elongated thread-like filamentous cells with aerial hyphae	+	-	-	-	+	+	+	-	NA	-	-	-	*Streptomyces* spp.

	blue pigment and fuzzy appearance	(spores in chain)													
SC3	Moderate growing dry chalky white colonies that are leathery when touched	Elongated thin branching filamentous cells with spores formed in chains	+	-	-	-	+	+	+	-	NA	-	-	-	*Streptomyces* spp.
SC4	Irregular cream rough with raised elevation on SCA	Elongated filamentous cells with irregular filaments	+	-	-	-	+	+	+	-	NA	-	-	-	*Streptomyces* spp.
SC5	White, dry, and powdery texture with raised irregular margin	Filamentous, branching cells like fungal hyphae	+	-	-	-	+	+	+	-	NA	-	-	-	*Nocardia* spp.
SC6	Slow growing, moderate irregular margin, leathery colonies with dark pigmentation.	Filamentous cell, single spiny spores on substrate mycelium with no aerial hyphae	+	-	-	-	+	+	+	-	NA	-	-	-	*Micromonospora* spp.
SC7	Slow growing wrinkled gray white colonies with a powdery	Elongated thin branching filamentous hyphae, spores are globus and	+	-	-	-	+	+	+	-	NA	-	-	-	*Streptomyces* spp.

	appearance	arranged in in chains													
MS2	Small, round, smooth, white colonies without color change in the medium	Cocci arranged in clusters	+	-	+	-	+	+	-	-	K/A	-	-	-	*Staphylococcus* spp.
MS3	Medium-sized, white colonies	Cocci arranged in clusters	+	-	+	-	+	+	+	-		-	-	-	*Staphylococcus* spp.
MS4	Large, opaque, cream-to-white colonies that may ferment mannitol, turning the medium yellow	Cocci arranged in clusters	+	-	+	-	+	+	-	-	A	-	-	-	*Staphylococcus* spp.

MR = methyl red, VP = Voges Proskauer, TSI = triple sugar iron, H_2S = hydrogen sulphide, NA = Not applicable, K/A = alkaline slant/acid butt, A/A = acid slant/acid butt, + = positive, - = negative

The probable identification of the isolates using analytical profile index (API test kits) is shown in Tables 4 and 5. Table 4 shows the Gram positive bacterial isolates while Table 5 shows the Gram negative bacterial organisms.

Table 4: Identification of some bacteria via Analytical Profile Index (API 50CH) test

Isolate ID	**GLY**	**DARA**	**LARA**	**GAL**	**GLU**	**FRU**	**SOR**	**RHA**	**MNE**	**DUL**	**CEL**	**ESC**	**MAN**	**INO**	**LAC**	**TRE**	**SAC**	**MEL**	**MAL**	**MDG**	**NAG**	**MDX**	**SBE**	**RIB**	**DXYL**	**LXYL**	**ADO**	**% API similarity identity**	**Identity of Organisms**
TS1	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	99.0	*Bacillus subtilis*
TS2	-	-	-	-	+	+	-	-	+	-	-	-	-	-	-	+	+	-	-	-	+	-	-	+	+	-	-	85.1	*Bacillus pumilis*
TS3	-	-	-	+	+	+	+	-	+	-	-	+ =	-	+	+	+	+	-	+	+	+	+	-	+	+	-	-	99.0	*Bacillus licheniformis*
TS4/ MS1	+	-	-	+	+	+	-	-	+	-	+	+	+	-	-	+	+	-	+	+	+	+	-	+	+	+	-	95.1	*Staphylococcus aureus*
TS7	-	-	-	-	+	+	-	-	+	-	-	-	-	-	-	-	-	-	+	-	+	-	-	+	-	-	-	97.8	*Streptococcus pyogenes*
MS2	+	-	-	+	+	+	+	-	+	-	-	-	+	-	-	+	+	-	+	+	+	-	-	+	-	-	-	92.5	*Staphylococcus epidermidis*
MS3	+	-	-	+	+	+	+	-	+	-	+	+	+	-	+	+	+	-	+	+	+	+	-	+	+	-	-	88.5	*Staphylococcus xylosus*
MS4	+	-	-	-	+	+	-	-	+	-	-	-	-	-	-	+	+	-	+	-	+	+	-	+	-	-	-	84.5	*Staphylococcus saprop*

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Glycerol (GLY), D-Arabinose (DARA), L-Arabinose (LARA), D-Ribose (RIB), D-Xylose (DXYL), L-Xylose (LXYL), Methyl-ß-D-xylopyranoside (MDX), D-Galactose (GAL), D-Glucose (GLU), D-Fructose (FRU), D-Mannose (MNE), L-Sorbose (SBE), L-Rhamnose (RHA) Dulcitol (DUL), Inositol (INO), D-Mannitol (MAN), D-Sorbitol (SOR), Methyl-α-D-glucopyranoside (MDG), N-Acetylglucosamine (NAG), Amygdalin (AMY), Esculin, Ferric citrate (ESC), D-Cellobiose (CEL), D-Maltose (MAL), D-Lactose (bovine origin) (LAC), D-Melibiose (MEL), D-Saccharose (sucrose) (SAC), D-Trehalose (TRE),

Table 5: Identification of some bacteria via Analytical Profile Index (API 20E) test

Isolate ID	ONPG	ADH	LDC	ODC	CIT	H2S	URE	TDA	IND	VP	GEL	GLU	MAN	INO	SOR	RHA	SAC	MEL	AMY	ARA	OX	NO2	N2	MOB	MoC	OF-O	OF-F	% API similarity identity	Identity of Organisms
TS5/ MC1	+	-	+	+	-	-	-	-	+	-	-	+	+	-	+	+	-	+	-	+	-	+	+	+	+	+	+	99.9	*Escherichia coli*
TS6	-	+	-	-	+	-	-	+	-	-	+	-	+	-	-	-	-	+	+	-	+	+	+	+	-	+	+	97.8	*Pseudomonas aeruginosa*
TS8	-	+	+	+	+	+	+	+	+	-	+	+	+	-	+	-	+	-	-	-	-	+	-	+	+	-	+	93.0	*Proteus vulgaris*
MC2	+	-	-	-	-	-	-	-	-	-	-	+	+	+	+	+	-	+	+	+	-	+	-	-	+	+	+	99.1	*Klebsiella pneumoniae*
MC3	+	-	+	+	+	-	-	-	-	+	-	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	99.5	*Enterobacter aerogenes*
MC4	-	-	+	+	+	+	-	-	-	-	-	+	+	-	+	+	-	+	+	+	-	+	+	+	+	+	+	99.5	*Salmonella typhimurium*
MC5	-	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	-	-	+	-	-	+	+	+		*Shigella*

																													species

ID = identity, + = positive, - = negative, Orthro-Nitrophenyl-beta-DGalactoPyranosidase (ONPG), Arginine DiHydrolase (ADH), Lysine DeCarboxylase (LDC), Ornithine DeCarboxylase (ODC), Citrate (CIT), Hydrogen sulphide Production (H_2S), Urease (URE), Tryptophan DeAminase (TDA), Indole production (IND), Voges Proskauer (VP), Gelatinase (GEL), D-glucose (GLU), D-mannitol (MAN), Inositol (INO), D-Sorbitol (SOR), L-Rhamnose (RHA), Saccharose (D-Sucrose) (SAC), D-melibiose (MEL), Amygdalin (AMY), L-Arabinose (ARA), CytochromeOxidase (OX), Motility (MOB), MacConkey medium (McC), Fermentation – under mineral oil (OF-F) and Oxidation – exposed to the air (OF-O).

Actinomycetes identified during the study using the API 20A test kit are presented in Table 6.

Table 6: Actinomycetes identified via Analytical Profile Index (API 20A) test

ID	**CAT**	**URE**	**GLU**	**GEL**	**IND**	**MAN**	**LAC**	**SAC**	**MAL**	**SAL**	**XYL**	**ARA**	**ESC**	**GLY**	**CEL**	**MNE**	**MLZ**	**RAF**	**SOR**	**RHA**	**TRE**	**API % Similarity**	**Tentative Identification**
SC 1	–	–	+	–	–	–	–	+	+	–	+	+	–	+	+	+	–	–	–	–	+	99.9	*Actinomyces meyeri*
SC 2	+	+	+	+	–	+	–	+	+	–	+	+	+	+	+	+	–	–	–	–	+	99.9	*Streptomyces coelicolor*
SC 3	+	+	+	+	–	+	–	+	+	–	+	+	+	+	+	+	–	–	–	–	+	99.2	*Streptomyces albus*
SC 4	+	+	+	+	–	+	–	+	+	–	+	+	+	+	+	+	–	–	–	–	+	99.0	*Streptomyces scabies*
SC 5	+	+	+	+	–	+	–	+	+	–	+	+	+	+	+	+	–	–	–	–	+	99.0	*Nocardia asteroides*
SC 6	+	–	+	–	–	+	–	+	+	–	+	+	–	+	+	+	–	–	–	–	+	98.4	*Micromonospora echinospora*
SC 7	+	+	+	+	–	+	–	+	+	–	+	+	+	+	+	+	–	–	–	–	+	99.1	*Streptomyces globisporus*

ID: Identity; +: Positive; -: Negative; IND: Indole; URE: Urease; GLU: Glucose; MAN: Mannitol; LAC: Lactose; SAC: Saccharose; MAL: Maltose; SAL: Salicin; XYL: Xylose; ARA: Arabinose; GEL: Gelatin; ESC: Esculin; GLY: Glycerol; CEL: Celliobiose; MNE: Mannose; MLZ: Melezitose; RAF: Raffinose; SOR: Sorbitol; RHA: Rhamnose; TRE: Trehalose; CAT: Catalase

Table 7 shows the viable bacterial diversity and the community structure across the various agrochemical farm soils.

Table 7: Viable bacterial diversity and community structure of the agrochemical farms

Bacterial community structure	**Control**	**AFS I**	**AFS II**
Bacteria	*Bacillus subtilis, Pseudomonas aeruginosa, Staphylococcus epidermidis, Staphylococcus xylosus Salmonella typhimurium*, *Escherichia coli*, *Klebsiella pneumoniae*, *Enterobacter aerogenes*	*Bacillus subtilis, Bacillus pumilis, Pseudomonas aeruginosa, Staphylococcus aureus, Staphylococcus saprophyticus, Staphylococcus epidermidis, Klebsiella pneumoniae Streptococcus pyogenes, Proteus vulgaris, Escherichia coli, Enterobacter aerogenes, Salmonella typhimurium.*	*Bacillus licheniformis, Pseudomonas aeruginosa, Staphylococcus aureus, Staphylococcus xylosus, Klebsiella pneumoniae, Shigella sp Escherichia coli, Enterobacter aerogenes*
Bacterial pathogens common in human/animal diseases	*Salmonella typhimurium, Escherichia coli, Klebsiella pnuemoniae*	*Klebsiella pneumoniae*, *Staphylococcus aureus*, *Streptococcus pyogenes*, *Enterobacter aerogenes*, *Salmonella typhimurium*	*Shigella* spp., *Klebsiella pneumoniae*, *Escherichia coli*
Coliforms	*Enterobacter aerogenes, Klebsiella pneumoniae, Escherichia coli*	*Enterobacter aerogenes, Klebsiella pneumoniae, Escherichia coli, Salmonella typhimurium*	*Enterobacter aerogenes, Klebsiella pneumoniae, Escherichia coli, Shigella* spp.
Enteric food-borne pathogens	*Enterobacter aerogenes*, *Pseudomonas aeruginosa*	*Enterobacter aerogenes*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*	*Escherichia coli*, *Enterobacter aerogenes*
Actinomycetes	*Actinomyces miyeri, Streptomyces coelicolor, Streptomyces albus*	*Streptomyces coelicolor, Streptomyces albus, Streptomyces globisporus, Streptomyces scabis, Nocardia asteriodes*	*Streptomyces coelicolor, Streptomyces albus, Streptomyces scabis, Micromonospora echinospora*

Microbial counts from tropical agrochemical polluted farm soil demonstrated clear shifts in community structure across assays. Total heterotrophic bacteria (on TSA) were markedly reduced in AFS 1 compared to control and AFS 2, reflecting pesticide stress on general microbial populations. Similarly, counts on mannitol salt agar declined significantly in AFS 1, indicating suppression of selective microbial groups, while AFS 2 maintained intermediate numbers, suggesting partial resilience. Actinomycetes populations (SCA counts) were elevated in AFS 1 relative to control, highlighting possible enrichment of pesticide tolerant taxa. In contrast, MAC and PKA counts remained statistically similar across treatments, implying that coliforms and phosphate solubilizing bacteria were less sensitive to pesticide exposure. These findings align with recent studies reporting pesticide driven alterations in microbial diversity, enzymatic activity, and soil health in tropical agricultural ecosystems (33). Such discriminatory influences accentuate the environmental threats of pesticide buildup, together with decreased nutrient cycling besides impaired soil productiveness. Additionally, the transitional feedbacks detected in AFS 2 propose resilient microbial approaches or incomplete restoration, unswerving with information on microbial flexibility under prolonged pollution (32).

A total of 11 bacterial genera were isolated (Table 3) and identified with reference to the Bergey's manual of Determinative Bacteriology (34). These organisms were identified as *Pseudomonas, Enterobacter, Actinomyces, Streptomyces, Nocardia, Micromonospora, Proteus, Salmonella, Streptococcus, Klebsiella* and *Bacillus*. A number of these bacteria have been studied and reported as microorganisms that thrive in environments stressed possibly induced by pesticide contamination (35). Culture-dependent method via the Analytical Profile Index test kit (API 20E & API 50CH) identified 9 bacterial genera (*Bacillus, Enterobacter, Klebsiella, Salmonella, Staphylococcus, Streptococcus, Proteus, Pseudomonas,* and *Escherichia*) across the agrochemicals farm soils and control (Table 4 and 5). Similar findings were reported by (36). Actinomycetes identified during the study were *Actinomyces meyeri, Streptomyces coelicolor, S. albus, S. scabies, S. globisporus, Nocardia asteriodes,* and *Micromonospora echinospora* (Table 6). Nonoh et al. (37) reported five different *Streptomyces* species after molecular characterization of soils in Kenya. However, our findings differ from the outcomes of Edemekong et al. (38), they reported different actinomycetes species (*Rhodococcus, Leucobacter, Jatrophihabitan*, and *Nesterenkoniamas*) identified from soil samples in Calabar metropolis, Nigeria

The bacteriological multiplicity of the agrochemical farm soils and control as presented in Table 7, showed that the potential pathogens implicated in human and animal diseases were *Klebsiella pneumoniae*, *Staphylococcus aureus*, *Streptococcus pyogenes*, *Enterobacter aerogenes*, *Salmonella typhimurium, Escherichia coli, Shigella* species. Coliforms isolated were *Enterobacter aerogenes, Klebsiella pneumoniae, Escherichia coli, Salmonella typhimurium, Shigella* species), and enteric food borne pathogens were *Enterobacter aerogenes*, *Staphylococcus aureus*, *Pseudomonas aeruginosa,* and *Escherichia coli*), across farm soil samples. This discovery upholds the outcomes of (39,40). The bacterial community structure has shown diverse modifications among control and pesticide polluted soils. Control samples were predominated by *Bacillus subtilis*, *Pseudomonas aeruginosa*, in addition to coliforms such as *Escherichia coli* and *Klebsiella* spp. Conversely, AFS I presented enhancement of opportunistic pathogens comprising *Staphylococcus aureus*, *Streptococcus pyogenes*, and *Proteus vulgaris*, whereas AFS II demonstrated divergence with *Shigella* spp. and *Bacillus licheniformis*. These alterations underscore pesticide induced selection stresses on bacterial populations (32).

The resilience and enhancement of pathogenic species across the agrochemical-polluted farm soils accentuate impending dangers aimed at human besides animal wellbeing. The existence of *Salmonella*, *Shigella*, and *Klebsiella* species, mirrors the ability of pesticide deposits to support resilient as well as virulent strains. Such enrichment remain connected to improved antimicrobial resistance besides food security fears in tropical agricultural ecosystems (33).

The culture-dependent guarded identification of the bacterial isolates additionally highlights the heterogeneousness of the bacterial population structure within the agrochemical farm soil samples. The occurrence of *Nocardia* and *Streptomyces* taxa is noteworthy, as these species have been documented for their stress tolerance in diverse ecosystems besides their capability to synthesize antibiotics, enzymes, as well as additional specialized metabolites (41,42). In this study, *Streptomyces coelicolor* and *Actinomyces miyeri* demonstrated a 99.9% sequence identity, corroborating earlier findings that identified these taxa across heterogeneous soil and sedimentary habitats (42,43,44). Furthermore, *Streptomyces* species are renowned for their capacity to biosynthesize specialized metabolites, notably antibiotics, which hold substantial potential for diverse biotechnological applications (45). The presence of *Actinomyces miyeri*, a species recognized for its contribution to soil health and the decomposition of organic matter, underscores the extensive microbial diversity characterizing soils influenced by agrochemical inputs (44). The identification results align with those of Gitari et al. (46), who characterized bacteria from tropical soils and highlighted their substantial contribution to microbial diversity, including a pronounced representation of Actinomycetes and other Gram positive groups in agrochemical impacted environment. Actinomycetes taxa, comprising *Streptomyces* and *Micromonospora*, were reliably isolated across various agrochemical farm soils, indicating their flexibility as well as biodegradation capabilities. Their resilience proposes a biological function in pesticide degradation in addition to soil reclamation, reliable with results of actinomycete facilitated decontamination in polluted soils (47).

Generally, pesticide pollution inhibited advantageous heterotrophs while elevating pathogenic as well as resistant populations. These discoveries underline ecological perils like decreased soil productivity besides intensified public health threats, however emphasizing the significance of viable pesticide control and bioremediation schemes in tropical farming systems (32).

CONCLUSION

Extensive pesticide use in Ogume pepper farms significantly degrades soil health, manifesting as elevated salinity, altered nutrient profiles, and disrupted organic matter cycling. These adverse physicochemical changes directly impair microbial diversity and essential ecosystem functions. The findings underscore an urgent need for adopting integrated pest management and sustainable soil practices to ensure long-term agricultural productivity in the region. Microbial profiling of tropical agrochemical polluted soils revealed noticeable shifts in community structure, with heterotrophic and selective bacterial groups suppressed under pesticide stress, while actinomycetes demonstrated enrichment, suggesting adaptive resilience. Pathogenic taxa (*Salmonella*, *Shigella*, *Klebsiella*, and *Staphylococcus*) were consistently isolated, accentuating public health risks and potential antimicrobial resistance. Coliforms and phosphatesolubilizers remained comparatively stable, indicating selective tolerance. The occurrence of stress resistant actinomycetes highlights their bioremediation potential in pesticide impacted environments. In conclusion, these outcomes underscore pesticide driven ecological imbalance, decreased nutrient cycling, as well as intensified food safety concerns, however, emphasizing the pressing need for sustainable pesticide management and microbial based recovery strategies.

Declaration of Competing Interest

The authors certify that they have NO affiliation with or involvement in any organization or entity with any financial in the subject matter discussed in this manuscript.

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REFERENCES

1. Sharma A, Kumar V, Shahzad B, Tanveer M, Sidhu GP, Handa N, et al. Worldwide pesticide usage and its impacts on ecosystem. SN Appl Sci. 2019;1(11):1446.
2. Pathak VM, Verma VK, Rawat BS, Kaur B, Babu N, Sharma A, et al. Current status of pesticide effects on environment, human health and it's eco-friendly management as bioremediation: A comprehensive review. Front Microbiol. 2022; 13:962619.
3. Jacobsen CS, Hjelmsø MH. Agricultural soils, pesticides and microbial diversity. Curr Opin Biotechnol. 2014; 27:15-20.
4. Fantke P, Juraske R. Variability of pesticide dissipation half-lives in plants. Environ Sci Technol. 2013;47(8):3548-62.
5. Yasir M, Kour S, Sehgal S. Impact of Population Growth and Urbanization on Agricultural Land Use: Evidence from India. Adv Consum Res. 2025;2(3).
6. Beaumelle L, Tison L, Eisenhauer N, Hines J, Malladi S, Pelosi C, et al. Pesticide effects on soil fauna communities—A meta-analysis. J Appl Ecol. 2023;60(7):1239-53.
7. Agwu OP, Bakayoko A, Jimoh SO, Stefan P. Farmers' perceptions on cultivation and the impacts of climate change on goods and services provided by Garcinia kola in Nigeria. Ecol Process. 2018;7(1):36.
8. Bünemann EK, Schwenke GD, Van Zwieten L. Impact of agricultural inputs on soil organisms—a review. Soil Res. 2006;44(4):379-406.
9. Imfeld G, Vuilleumier S. Measuring the effects of pesticides on bacterial communities in soil: a critical review. Eur J Soil Biol. 2012; 49:22-30.
10. Ahmad S, Ahmad HW, Bhatt P. Microbial adaptation and impact into the pesticide's degradation. Arch Microbiol. 2022;204(5):288.
11. Streletskii R, Astaykina A, Krasnov G, Gorbatov V. Changes in bacterial and fungal community of soil under treatment of pesticides. Agronomy. 2022;12(1):124.
12. Gee GW, Bauder JW. Particle-size analysis. In: Methods of soil analysis: Part 1 Physical and mineralogical methods. 1986. p. 383-411.
13. Walkley A, Black IA. An examination of the Degtjareff method for determining soil organic matter, and a proposed modification of the chromic acid titration method. Soil Sci. 1934;37(1):29-38.
14. Nelson DW, Sommers LE. Total carbon, organic carbon, and organic matter. In: Methods of soil analysis: Part 3 Chemical methods. 1996. p. 961-1010.
15. AOAC. Official Methods of Analysis. 18th ed. Washington, DC: Association of Official Analytical Chemists; 2005.
16. Olsen SR, Cole CV, Watanabe FS, Dean LA. Estimation of available phosphorus in soils by extraction with sodium bicarbonate. Washington: US Department of Agriculture; 1954. (Circular No. 939).
17. APHA. Standard Methods for the Examination of Water and Wastewater. 20th ed. Washington, DC: American Public Health Association; 1998.
18. Black CA, editor. Methods of soil analysis: Part 2 Chemical and microbiological properties. Madison: American Society of Agronomy; 1965.

19. Rahman S, Rahman MM, Miah M, Begum MN, Sarmin M, Mahfuz M, et al. COVID-19 reinfections among naturally infected and vaccinated individuals. Sci Rep. 2022;12(1):1438.
20. Choudhury S, et al. Soil texture and microbial dynamics in agroecosystems. Soil Biol Biochem. 2023; 178:108-19.
21. Adeniji A, Huang J, Li S, Lu X, Guo R. Hot viewpoint on how soil texture, soil nutrient availability, and root exudates interact to shape microbial dynamics and plant health. Plant Soil. 2025;511(1):69-90.
22. Adeboye OB, Schultz B, Adeboye AP, Chukalla A, Shittu KA. Assessment of the AquaCrop model to simulate the impact of soil fertility management on evapotranspiration, yield, and water productivity of maize in the sub-humid agro-ecology of Nigeria. Discov Agric. 2024;2(1):28.
23. Chidi P, Ogboghodo I, Edosa V, Ogbemudia I, Chidi N. The Impact of Pesticides on Soil Microbes: A Review of the Current State of Knowledge. J Appl Sci Environ Manage. 2025;29(9).
24. Hinsinger P, Herrmann L, Lesueur D, Robin A, Trap J, Waithaisong K, et al. Impact of roots, microorganisms and microfauna on the fate of soil phosphorus in the rhizosphere. Annu Plant Rev. 2015; 48:375-407.
25. Msimbira LA, Smith DL. The roles of plant growth promoting microbes in enhancing plant tolerance to acidity and alkalinity stresses. Front Sustain Food Syst. 2020; 4:106.
26. Audu A, et al. Soil buffering capacity and pesticide interactions in tropical agriculture. J Soils Sediments. 2024;24(3):112-25.
27. Li T, Wang S, Zhao L, Yuan X, Gao Y, Fu D, et al. Improvement of soil nutrient cycling by dominant plants in natural restoration of heavy metal polluted areas. Environ Res. 2024; 263:120030.
28. Ortega R, Miralles I, Domene MA, Meca D, Del Moral F. Ecological practices increase soil fertility and microbial diversity under intensive farming. Sci Total Environ. 2024; 954:176777.
29. Mukhles MB, Rahman MM, Rana MR, Huda N, Ferdous J, Rahman F, et al. Effect of pesticides on nitrification activity and its interaction with chemical fertilizer and manure in long-term paddy soils. Chemosphere. 2022; 304:135379.
30. Jokela D, Nair A. Effects of reduced tillage and fertilizer application method on plant growth, yield, and soil health in organic bell pepper production. Soil Tillage Res. 2016; 163:243-54.
31. Ghasal PC, Choudhary J, Kumar K, Arif M, Kumar A, Dutta D, et al. Do Soil Properties Significantly Influence the G×E Interaction of Crop Varieties? In: Genotype x Environment Interactions and its Implications for Plant Breeding. Singapore: Springer; 2026. p. 215-50.
32. Dhuldhaj UP, Singh R, Singh VK. Pesticide contamination in agro-ecosystems: toxicity, impacts, and bio-based management strategies. Environ Sci Pollut Res. 2023;30(4):9243-70.
33. Mohanty LK, Ashaq M, Panotra N, Kundal S, Rai S, Choudhary S, et al. Advances in Understanding Soil Microbial Diversity and Its Role in Ecosystem Functioning: A Comprehensive Review. J Sci Res Rep. 2025;31(11):1139-55.
34. Bergey DH, Holt JG. Bergey's manual of determinative bacteriology. 9th ed. Baltimore: Williams & Wilkins; 1994.
35. Harir M, Bendif H, Bellahcene M, Fortas Z, Pogni R. Streptomyces secondary metabolites. In: Basic biology and applications of actinobacteria. IntechOpen; 2018.
36. Meena RS, Kumar S, Datta R, Lal R, Vijayakumar V, Brtnicky M, et al. Impact of agrochemicals on soil microbiota and management: A review. Land. 2020;9(2):34.
37. Nonoh JO, Lwande W, Masiga D, Presnail KJ, Schepers E, Okech MA, et al. Isolation and characterization of Streptomyces species with antifungal activity from selected national parks in Kenya.
38. Edemekong CI, Uzoeto HO, Mbong EO, Ikusika BA, Didiugwu CM, Ngwu JN, et al. Molecular characterization and bioassay of soil Actinomycetes strains on multidrug resistant bacteria. IOSR J Biotechnol Biochem. 2022;34(1):6-11.
39. Cook RJ. Toward cropping systems that enhance productivity and sustainability. Proc Natl Acad Sci USA. 2006;103(49):18389-94.
40. Sharma P, et al. Pathogenic microbial communities in pesticide-contaminated

agricultural soils. Appl Soil Ecol. 2024; 195:105-17.

41. Barka EA, Vatsa P, Sanchez L, Gaveau-Vaillant N, Jacquard C, Klenk HP, et al. Taxonomy, physiology, and natural products of Actinobacteria. Microbiol Mol Biol Rev. 2016;80(1):1-43.
42. Ajuzieogu CA. A Review on Next Generation Smart Textiles: An Emerging Microbe-Based Strategy for Skin Health and Wound Management. Biotechnol J Int. 2026;30(1):205-24.
43. Patin NV, et al. Actinobacterial diversity in coastal sediments. Mar Drugs. 2017;15(4):112.
44. Ataikiru TL, Okerentugba PO, Okpokwasili GC. Identification of carbofuran and paraquat degrading microorganisms from soil. South Asian J Res Microbiol. 2020; 7:40-52.
45. Alam K, Mazumder A, Sikdar S, Zhao YM, Hao J, Song C, et al. Streptomyces: The biofactory of secondary metabolites. Front Microbiol. 2022; 13:968053.
46. Gitari HH, Nungula EZ, Chappa LR, Raza MA, Ranjan S, Sow S, et al. Agroforestry for climate security. In: Agroforestry. 2024. p. 319-44.
47. Jeon HJ, Lee JD, Lei Q, Van Roy B. An information-theoretic analysis of in-context learning. arXiv preprint arXiv:2401.15530. 2024.

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