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Fertilizer changes soil bacteria community and soil quality on coffee agroforestry in the tropic

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ABSTRACT

Soil microbial communities are essential to ecosystem function, particularly in tropical agroforestry systems where land-use changes and fertilizer inputs can significantly alter soil health. Despite the increasing adoption of coffee agroforestry as a sustainable land management strategy, the specific impacts of different fertilizer types on soil bacterial diversity and quality remain insufficiently explored. This study aimed to assess how organic, inorganic, and mixed fertilizer treatments affect soil bacterial community structure and soil quality in a coffee agroforestry system in UB Forest, Indonesia, compared to an undisturbed protected area. Soil samples were collected three months post-fertilization and analyzed using next-generation sequencing to determine bacterial community structure and diversity indices. Soil chemical parameters were also assessed. Results showed that mixed fertilizer (MF) treatments enhanced soil total nitrogen, microbial population, and overall diversity, while organic fertilizer (OF) promoted higher bacterial richness and evenness. Inorganic fertilizer (IF) increased nutrient-specific bacterial populations but reduced overall diversity. Protected areas (PA) had high organic content but comparatively lower microbial diversity, possibly due to limited nutrient input and recalcitrant organic compounds. Principal Component Analysis revealed strong positive correlations between MF treatment and microbial and soil health indicators. This study demonstrates that combining organic and inorganic fertilizers optimizes microbial diversity and soil function, supporting more resilient and productive agroecosystems. Conversely, exclusive reliance on inorganic fertilizers may compromise microbial balance and long-term soil health.

Keywords: coffee agroforestry, next-generation sequencing, inorganic fertilizer, organic fertilizer, soil bacterial diversity, soil quality.

INTRODUCTION

In tropical agroecosystems, particularly those under agroforestry practices, soil microbial communities play a pivotal role in maintaining soil fertility, nutrient cycling, and overall ecosystem resilience. FAO (2019) defines soil quality as the capacity of soil to function in ecological systems and support the sustainability of plant, animal, and human life. Recent research trends have increasingly focused on the biotic and abiotic impacts of fertilization strategies, recognizing that fertilizer type can markedly influence soil microbial diversity and functionality (Amadou et al., 2020; Zandybay et al., 2024). However, while the individual effects of organic or inorganic fertilizers on soil chemistry are relatively well-documented, studies integrating these effects with microbial community responses, especially under agroforestry contexts remain limited.

Current findings indicate that fertilizer application may lead to nutrient imbalances, changes in microbial abundance, and alterations in soil biochemical processes (Siahaan et al., 2025;

Nurcholis et al., 2024). For example, mixed fertilizers have been shown to enhance soil respiration (Nugroho et al., 2023), but the underlying cause of whether microbial activation or increased organic matter decomposition has not been conclusively explained. Furthermore, earlier studies such as by Yusuf et al. (2021), have characterized the taxonomic composition of bacterial phyla in coffee plantations, but did not sufficiently investigate the ecological functions or shifts in diversity and richness due to different fertilization regimes. This study addresses these knowledge gaps by examining how different fertilizer types organic, inorganic, and mixed affect both the structure and diversity of soil bacterial communities as well as soil quality indicators in a tropical coffee agroforestry system. Unlike prior studies that focus solely on either soil chemistry or microbial taxonomy, we employ a combined metagenomic and edaphic approach using next-generation sequencing and soil quality metrics to evaluate fertilizer impacts across biotic and abiotic dimensions.

The novelty of this research lies in its comprehensive approach that not only compares protected forest areas and fertilized agroforestry plots, but also elucidates the interactions between soil bacterial diversity and chemical soil health parameters. This study contributes valuable insights into the development of integrated, sustainable fertilization strategies that support long-term productivity and ecological balance in tropical agroforestry systems.

MATERIAL AND METHOD

Study site

The research was conducted in the KHDTK (special purpose forest area) – UB forest located in Sumbersari Hamlet, Donowarih Village, Karangploso District, Malang Regency, East Java (Figure 1). The research location was at 7°49’25“ N latitude and 112°34’51” E latitude. The research site had a rainfall of 181.22 mm/month and an air temperature of 23.7 °C. The research design used was a randomized block design with 3 plots as replication based on different types of fertilizers (e.g., organic, inorganic, and mixed of organic and inorganic) and control treatment as a comparison from the protected area (Table 1). The organic fertilizer applied in this study was poultry manure, which

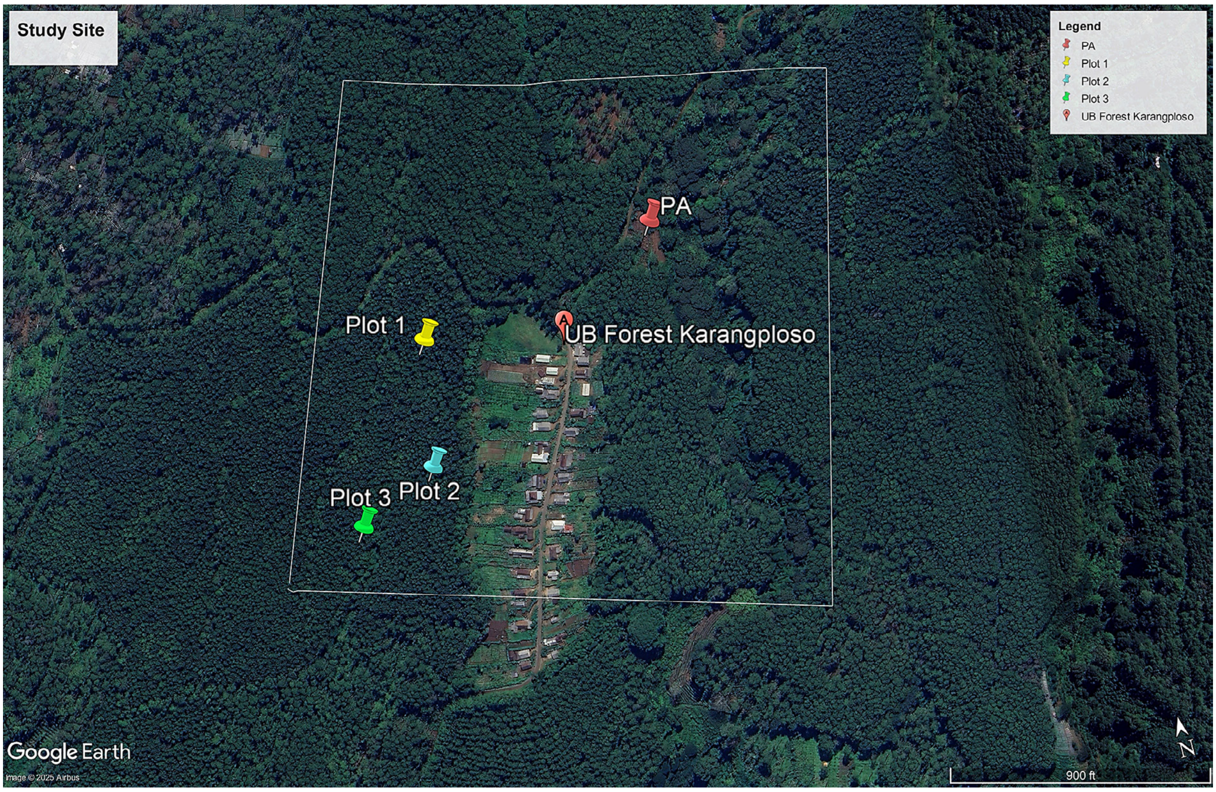


Figure 1. The location of the experimental plots; PA = protected area, and pine and coffee agroforestry system (Plots 1, 2, 3) that had an equal age of 10 years

Table 1. Fertilizer treatment combination

Combination of fertilizer types and doses		Fertilization doses (g/plant)			
		Poultry manure	Urea	SP-36	KCl
Organic fertilizer (OF)	1 (Fertilizer dosage that farmers currently use)	4846	-	-	-
	2 (Fertilizer dosage recommended by the International Coffee and Cacao Research Institute)	9261	-	-	-
	3 (Fertilizer dosage based on nutrient export turnover through harvest)	4322	-	-	-
Inorganic fertilizer (IF)	1 (Fertilizer dosage that farmers currently use)	-	157	59	42
	2 (Fertilizer dosage recommended by the International Coffee and Cacao Research Institute)	-	300	160	200
	3 (Fertilizer dosage based on nutrient export turnover through harvest)	-	140	72	157
Mixed fertilizer (MF)	1 (Fertilizer dosage that farmers currently use)	2423	78.5	29.5	21
	2 (Fertilizer dosage recommended by the International Coffee and Cacao Research Institute)	4630	150	80	100
	3 (Fertilizer dosage based on nutrient export turnover through harvest)	2161	70	36	78.5

typically contains 1.65% nitrogen, 0.06% phosphorus (P_2O_5), and 7.94% potassium (K_2O). The inorganic fertilizers consisted of urea, SP-36, and KCl. Urea containing 46% N, SP-36 is a phosphate fertilizer with 36% P_2O_5 content, and KCl (potassium chloride) contains 60% K_2O.

Sample collection

Soil sampling was conducted using a soil auger at 50 cm away from the coffee trunk (the area of fertilizer application). Soil samples for soil bacterial communities were taken compositely at a depth of 0–20 cm (Figure 2) from each plot, specifically organic, inorganic, mixed, and a protected area as a control with 3 replications. The homogenized samples were placed in pre-sterilized urine containers to avoid cross-contamination from sampling tools or the environment. Furthermore, all samples were immediately stored in a cooling box to preserve microbial DNA integrity prior to laboratory processing. While, soil sample for analyzing soil physicochemical properties were collected compositely from 4 sampling point at 0–20 cm from each plot then air-dried for a week and crushed to pass a 2 mm sieve. All soil samples were taken 3 months after fertilizer application. In addition, litter sample were collected in a 50 × 50 cm litter frame within the coffee trunk.

Analysis of soil characteristics

Soil characteristics were measured for soil pH (electrometric method), total N (Kjeldahl), moisture content (gravimetric method), total soil organic C (Walkey and Black), and soil bacteria population (total plate count). Soil samples (5 g) were suspended in 45 mL of 0.9% (v/v) sodium chloride solution. Subsequently, serial ten-fold

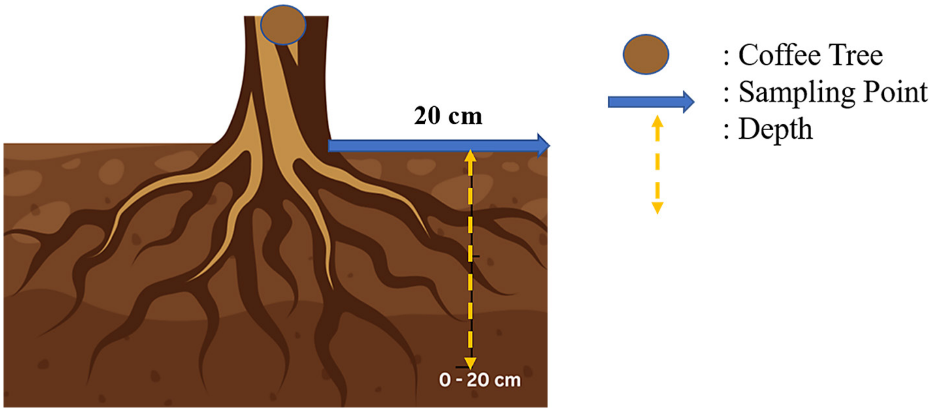


Figure 2. Sampling points

dilutions were prepared by transferring 1 mL of the sample suspension to 9 mL of sterile 0.9% NaCl solution, with dilutions extended to 10^{-7}. Aliquots of 0.1 mL from selected dilutions (10^{-6} and 10^{-7}) were plated onto nutrient agar medium containing 15 g/L agar, 5 g/L NaCl, 5 g/L peptone, 2 g/L yeast extract, and 1 g/L beef extract.

Analysis of litter quality

Lignin content was determined through the Van Soest Georing method, starting with the addition of acid detergent solution and antifoam to plant samples, followed by heating, filtration, drying, treatment with 72% H_2SO_4, and the contents were burned at 500 °C to obtain residual lignin. The lignin content was calculated based on the difference in weight before and after the freezing process. Meanwhile, total polyphenol analysis was carried out using a spectrophotometric method based on the reaction with Folin-Denis reagent, with a standard curve using tannic acid. Plant samples were extracted with 50% methanol, heated in a water bath, then filtered and diluted before being analyzed at a wavelength of 760 nm. The absorbance results were compared with the standard curve to calculate the % total extract polyphenols (TEP).

Analysis of bacterial community structure

Determination of soil bacterial community structure was carried out using a molecular-based metagenomic approach with next-generation sequencing (NGS) technology (Yusuf et al., 2021). DNA extraction was conducted using the Quick-DNA™ Fungal/Bacterial Miniprep Kit (USA), following the manufacturer's protocol. The 16S rRNA gene of the isolated bacterial DNA was amplified and sequenced using a thermal cycler with universal primers 27f (5′-GAG AGT TTG CTG GCT ATC CAG-3′) and 1492r (5′-CTA CGG CTA TGT CCT TAC GA-3′), which target the V1 and V9 regions of the gene (Wiryawan et al., 2022). The PCR amplification was carried out over 35 cycles, with the following conditions: initial denaturation at 95 °C for 5 minutes, denaturation at 95 °C for 30 seconds, annealing at 52 °C for 45 seconds, elongation at 72 °C for 90 seconds, and a final extension at 72 °C for 5 minutes. The PCR products were then visualized by agarose gel electrophoresis to confirm the presence and expected size of the amplified 16S rRNA gene fragments (Ustiatik et al., 2022). PCR product purification and library construction was prepared using NEBNext® Ultra™ DNA Library Prep Kit. Sequencing was performed on the Illumina platform. Following sequencing, the metagenomic data were processed as follows: (1) quality filtering of raw reads, (2) sequence assembly or binning, (3) taxonomic and functional annotation, and (4) visualization of the results. During the quality filtering stage, reads with low quality scores were removed. The high-quality reads were subsequently assembled into contigs or mapped to reference genome (SILVA database). QIIME software was used for OTU clustering ($\geq$ 97.5% similarity), taxonomic classification, and diversity analysis.

Data analysis

The relationship between soil chemical parameters and bacterial groups was analyzed using Principal Component Analysis (PCA) with R-studio. The PCA was performed using the 'ggplot2', 'corrplot', and 'factoextra' packages. Soil bacterial diversity was analyzed using the Total Taxa Number Estimator (Chao1), the Shannon-Wiener Index and the Simpson Index, with Indicator species analysis (IndVal) conducted using the 'labdsv' package in R-studio.

RESULT AND DISCUSSION

Soil characteristics and nutrient content

The study showed that land use form significantly affects soil biochemical characteristics (Table 2). Land management differences showed an increase in soil N-total and C-organic contents compared to the protected area (PA). Combined application of fertilizer (MF) resulted in the highest N-total content, followed by organic fertilizer (OF) and inorganic fertilizer (IF), all significantly higher than PA, due to increased N availability from organic matter and plant biomass, and in the case of IF, direct provision of N, despite with potential losses through leaching or volatilization (Siahaan et al., 2025). In contrast, PA had the lowest N-total due to the lack of additional inputs. Soil moisture was highest in PA, highlighting the role of forest ecosystems in retaining water, while IF and MF had lower levels which may be due to intensive tillage and reduced organic matter

Table 2. Soil quality on different land use

Sample	pH	Soil total N (%)	Soil organic C (%)	Soil moisture content (%)	Polyphenols (%)	Lignin (%)	Total plate count (CFU/g)
PA	6.80	0.40	6.97	10.30	1.77	4	2 × 10^7
OF	6.46	0.80	8.10	1.54	1.76	6.7	2.3 × 10^7
IF	6.42	0.78	8.33	1.12	0.40	8.7	2.1 × 10^7
MF	6.45	0.81	8.41	1.06	0.42	4	2.8 × 10^7

Note: PA (protected area), OF (organic fertilizer), IF (inorganic fertilizer),
MF (mixed fertilizer – combination of organic and inorganic fertilizer)

(Aladwan et al., 2024). The leaf litter in the PA and OF showed the highest polyphenol content, indicating the presence of beneficial bioactive compounds from decomposing organic matter (Sharma et al., 2025), which was drastically reduced in IF and MF. The high polyphenol result indicates a greater availability of complex substrates and antimicrobial compounds, which selectively influence microbial composition and richness (Makarewicz et al., 2021). The highest lignin content in IF was probably from undecomposed crop residues due to low microbial activity (Wang et al., 2023). Microbial activity indicated by total plate count (TPC), was highest in MF, followed by OF, IF, and lowest in PA, indicating that the combination of organic and inorganic fertilizers created a balanced environment for microorganisms (Nugroho et al., 2023).

Soil bacteria diversity

The analysis of soil bacterial diversity revealed that the OF treatment supported the highest number of observed taxa, indicating a greater variety of bacterial species present in the soil. This trend was also reflected in the Chao1 estimator (Table 3), which showed that OF had the highest potential total taxa count, including undetected or rare species. These findings align with the study by Fitria et al. (2021), which reported that organic fertilizer application enhances bacterial diversity by supplying nutrients and creating favorable conditions for microbial growth. Interestingly, although the MF treatment resulted in the highest total microbial population (TPC), it did not lead to the highest species richness or evenness. This suggests that MF enhances microbial abundance due to the combined nutrient inputs, while OF supports microbial diversity and ecological stability through the provision of complex organic substrates. The high diversity values in MF were accompanied by low evenness, as the microbial community was dominated by a few species. In contrast, the OF treatment displayed lower dominance values, indicating a more balanced distribution of bacterial species. These findings are supported by the diversity observed in the PA, where a relatively high Shannon index was recorded, suggesting substantial bacterial diversity. This could be attributed to the abundant organic matter and stable nutrient conditions that support a wide range of bacterial groups, as also reported by Wiryawan et al. (2022).

Additionally, the low Simpson index in the PA indicates minimal dominance by any single taxon, implying a more even and ecologically stable bacterial community, consistent with findings by Yusuf et al. (2021). While the IF treatment has also been shown to influence soil bacterial communities, they tend to promote the proliferation of certain taxa while reducing overall diversity due to altered soil chemical properties (Zhang et al., 2019).

Soil bacteria community

The soil bacterial community plays an important role in biochemical cycles, organic matter decomposition, and nutrient availability (Kiprotich et al., 2025). In this study, the treatments applied had a significant effect on the structure of the soil bacterial community, which showed significant compositional changes compared to the protected forest. It could be seen that the composition and dominance of bacteria were strongly influenced by land management (Figure 3a, b, c). At the phylum level (Figure 3a), PA, OF, IF, and MF showed differences. In the PA area, which represented an undisturbed natural ecosystem, the Bacillota phylum (previously known as Firmicutes) dominated the soil bacterial community, accounting for 85.12% of the total population. This suggests that high organic matter and stable moisture in forest soils support the proliferation of Bacillota, consistent

Table 3. Community structure and diversity of soil bacteria in UB forest

Plots	Observed species	Chao1	Shannon-Wiener	Simpson
PA	2922	4,764.5	3.56	0.895
OF	4495	6,447.7	4.37	0.829
IF	2732	4,082.5	4.92	0.933
MF	4212	5,811.0	5.86	0.988

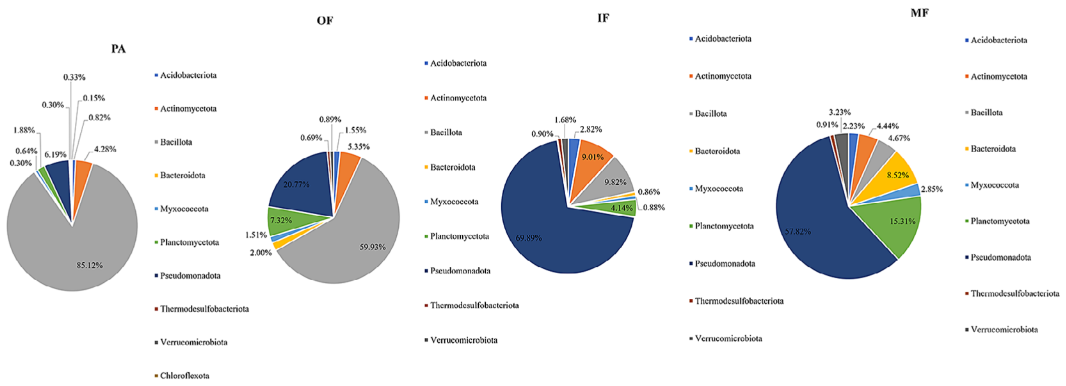
Note: PA (protected area), OF (organic fertilizer), IF (inorganic fertilizer),
MF (mixed fertilizer – combination of organic and inorganic fertilizer)

with their role in nutrient cycling and fermentation under organic-rich conditions (Yu et al., 2024). In contrast, Pseudomonadota was much less abundant in PA, representing only 2.00%. Meanwhile, in the areas treated with OF, Bacillota remained dominant at 59.93%, reflecting its adaptive capability, mainly through the spore-forming mechanism that allowed them to survive fluctuations in environmental conditions (Yan et al., 2023). However, a marked increase in Pseudomonadota was observed (30.77%), suggesting that organic inputs enhanced the abundance of metabolically active bacteria involved in nitrogen fixation and litter decomposition (Aladwan et al., 2024). Other phyla such as Actinomycetota (5.35%) and Bacteroidota (7.32%) were also more prominent under OF compared to PA. Conversely, inorganic fertilizer (IF) treatment shifted microbial dominance toward Pseudomonadota (69.89%), indicating that synthetic fertilizers promote bacteria well-adapted to mineral-rich environments (Song et al., 2024), potentially reducing overall microbial diversity. Bacillota declined sharply to 9.82% under IF. Notably, Chloroflexota (0.30% in PA, 0.89% in OF) and Verrucomicrobiota (0.64% in PA, 1.55% in OF) were not detected under IF, indicating that the inorganic nutrient-rich and carbon-poor environment may be unfavorable for these taxa (Wu et al., 2024). In the MF treatment, which was treated with a combination of organic and inorganic fertilizers, Pseudomonadota remained dominant (57.82%) but was accompanied by significant increases in Planctomycetota (15.31%), Bacteroidota (10.78%), and Chloroflexota (3.22%). The significant increase of Planctomycetota and Bacteroidota in MF was related to the soil conditions having the highest N-total, C-organic and bacterial populations (Table 2), indicate a more complex and dynamic soil environment resulting from nutrient mixture inputs. Bacteroidota, for instance, is known for degrading complex organic compounds (Hwang et al., 2024). Bacillota declined significantly in MF to just 4.67%, suggesting a community shift away from traditional saprophytic bacteria towards more metabolically specialized groups (Yu et al., 2024). Acidobacteriota was relatively stable in both PA (1.88%) and MF (2.23%), consistent with its physiological adaptability to pH variability (Peng et al., 2024). Actinomycetota increased under IF (9.01%) and MF (4.44%), in line with its role in breaking down complex organics and tolerating environmental fluctuations (Yan et al., 2023).

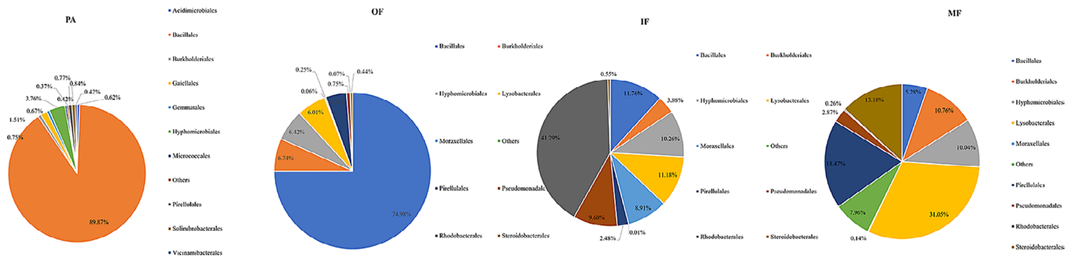
At the order level (Figure 3b), land management had a pronounced impact on community structure. PA and OF were dominated by Bacillales, accounting for 89.87% and 74.38%, respectively. This dominance is supported by the availability of organic substrates and stable soil conditions (Table 2), aligning with Bacillales' role in organic matter decomposition and nitrogen fixation (Setyaningsih et al., 2019). The dominant presence of Bacillales in PA and OF was supported by the availability of organic substrates and relatively stable soil conditions, in accordance with the findings of (Yan et al., 2023), which stated that Bacillales played an important role in organic matter decomposition and nitrogen fixation. In contrast, under IF management, the microbial community was dominated by the Rhodobacterales order.

This order was generally found in environments with high nitrogen levels and lower pH denitrification, which were common characteristics of soils treated with inorganic fertilizers. This dominance indicated that Rhodobacterales were able to adapt and thrive in soil chemical conditions altered by synthetic fertilizer inputs. However, Setyaningsih et al. (2019) indicated that such dominance might signal reduced soil microbial diversity due to chemical stress. Bacillales dropped to 3.88% under IF. Interestingly, Pirellulales (0.75% in PA, 0.07% in OF) and Micromonadales (0.42% in PA, 0.25% in OF) were not detected in IF, underscoring the unfavorable conditions for these taxa. In MF, the bacterial

a) Phylum



b) Order



c) Species

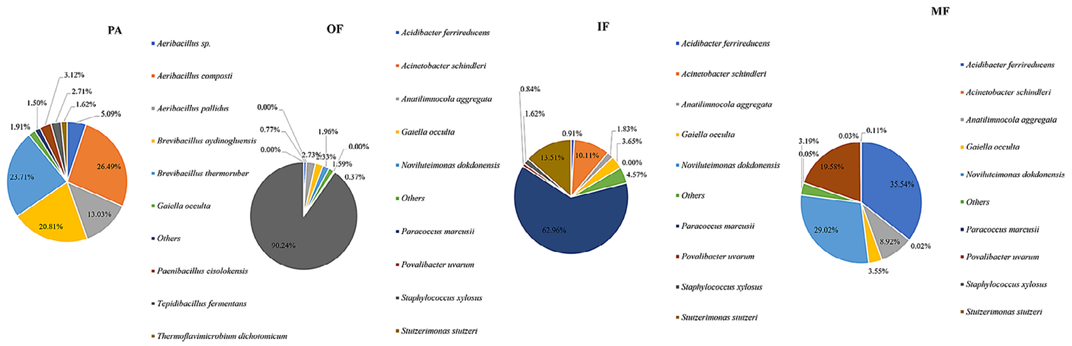


Figure 3. a) Abundance of the top 10 taxa at Phylum level; Note: PA: protected area as a control treatment; OF: organic fertilizer; IF: inorganic fertilizer; MF: mixed fertilizer; b) abundance of the top 10 taxa at order level; Note: PA: Protected area as a control treatment; OF: organic fertilizer; IF: inorganic fertilizer; MF: mixed fertilizer; c) abundance of the top 10 taxa at species level; Note: PA: protected Area as a control treatment; OF: organic fertilizer; IF: inorganic fertilizer; MF: mixed fertilizer

community was more diverse, with Lysobacterales (31.05%) and Pirellulales (18.47%) being most dominant. Lysobacterales are known for biocontrol potential and environmental tolerance (Bansal et al., 2023), while Pirellulales played a role in nitrogen cycling and was known to live in environments with balanced levels of soil organic C and soil N-total. Their increase in MF highlights the synergistic interaction of organic and inorganic inputs in supporting microbial functional diversity. Bacillales also declined significantly in MF (5.28%) compared to PA and OF, likely due to chemical-induced stress altering soil pH, salinity, and microbial equilibrium.

At the species level (Figure 3c), distinct patterns emerged. In PA, although no single species was overwhelmingly dominant (others: 23.71%), *Brevibacillus thermoruber* (20.81%) and *Bacillus cereus* (13.03%) were notably abundant. This reflects a more even microbial community in a stable, minimally disturbed environment (Setyaningsih et al., 2019). The OF treatment was dominated by *Staphylococcus xylosus* (90.28%), known for utilizing diverse carbon sources from organic matter (Li et al., 2024), and pH tolerance (Singh and Kumaria, 2023). This dominance suggests a positive response of *S. xylosus* to organic inputs. Notably, *Paracoccus marcusii* (dominant in IF) and *Acidibacter ferrireducens* (dominant in MF) were not detected under OF, indicating unsuitable conditions or competitive exclusion. The IF treatment was dominated by the species *Paracoccus marcusii* (62.08%), a Proteobacteria species known for thriving in nutrient-rich, low-organic environments (Trianto et al., 2019), and exhibiting diverse nitrogen metabolic pathways including denitrification (Kiprotich et al., 2025). This is in line with the soil condition in the IF treatment which has high total N content. In contrast, *S. xylosus* dropped to just 1.62% under IF, suggesting an uncompetitive environment for this species amid high mineral nutrient levels (Wiryawan et al., 2022). In the OF treatment, which tended to contain more humus and complex compounds, the condition is less suitable for *Paracoccus* sp. when compared to the availability of inorganic nitrogen directly in the IF treatment, resulted in competition with other decomposer bacteria. In the MF treatment, the dominating species are *Acidibacter ferrireducens* (35.54%), which is an acidophilic bacterium capable of reducing Fe(III) (Chen et al., 2020), and *Noviluteimonas dokdonensis* (29.62%). Soils with fertilizer combinations might experience slightly acidic pH changes due to decomposition of organic fertilizers and side effects of inorganic fertilizers (e.g., nitrification which release H^+ ion). These bacteria also took advantage of microaerophilic conditions and certain metal levels (such as Fe) that could be more available in MF treatment (Meiyerani et al., 2024). *Noviluteimonas dokdonensis* is a bacterium capable of living in nutrient-rich soils with little mineral salts (Wang et al., 2023). In OF treatment, the pH tended to be more neutral and there were a lot of competitions from decomposer bacteria (e.g. *Staphylococcus xylosus*). Similarly, *P. marcusii* dropped to 8.02% in MF, indicating that combined fertilization creates conditions less favorable for this species compared to IF treatment.

Interaction between fertilizer types and microbial communities

The principal component analysis (PCA) plot depicted the interaction between species and showed that different fertilizer treatments had a significant impact on the composition of soil bacterial communities. Figure 4 illustrates a multivariate distribution that explained 79% of the total data variation, with PC1 accounting for 45.6% and PC2 for 33.4%. Based on the direction and length of the vectors, the MF treatment closest to microbial diversity vectors, such as soil C-organic, soil N-total, total bacterial population, and Shannon diversity index, had a medium-strong correlation (0.25–0.75). This can be seen from the green vector color with lines that were very close and parallel to these parameters. Large microbial populations tended to be more diverse. This indicates that fertilizer combinations improved soil quality by providing nutrients and increasing soil organic matter, thus encouraging an increase in microorganism populations and soil microbial diversity, which is influenced by soil carbon and nitrogen content (Šimanský et al., 2021).

Simpson's diversity index parameter had a moderate correlation (0.25) as seen from the green color. There was a positive correlation to dominance (Simpson), which indicates that there are microbes that dominate in the IF treatment. The use of inorganic fertilizers could increase microbial diversity, but not significantly for species richness (Chao1). This is thought to be due to an increase in the availability of macro elements without an increase in organic matter (Chen et al., 2020).

The parameters polyphenols, lignin, and Chao 1 index had a medium-strong correlation (0.25–0.75) as seen from the blue-green vector color. There was a positive correlation to diversity (Chao1), indicating higher species richness in OF treatment, supported by the availability of complex substrates for microbes. Organic matter such as lignin and polyphenols supported complex microbial communities. Polyphenols and lignin showed strong associations with OF treatments. This content can come from crop residues and manure, which increase the complexity of substrates for soil microorganisms (Song et al., 2024).

The PA area appeared on the left side of the plot, aligned with the air temperature vector, suggesting that although it represents a natural condition, environmental factors such as higher temperature and extreme rainfall do not significantly support microbial biodiversity at this site. Soil pH and temperature parameters also had a moderate correlation (0.25–0.5) as seen from the green vector color pointing to the left. Soil pH and temperature were negatively associated with soil c-organic, soil N-total, total bacterial population, and microbial diversity (Shannon, Chao1, Simpson). This condition might be attributed to the presence of recalcitrant organic matter, such as lignin and

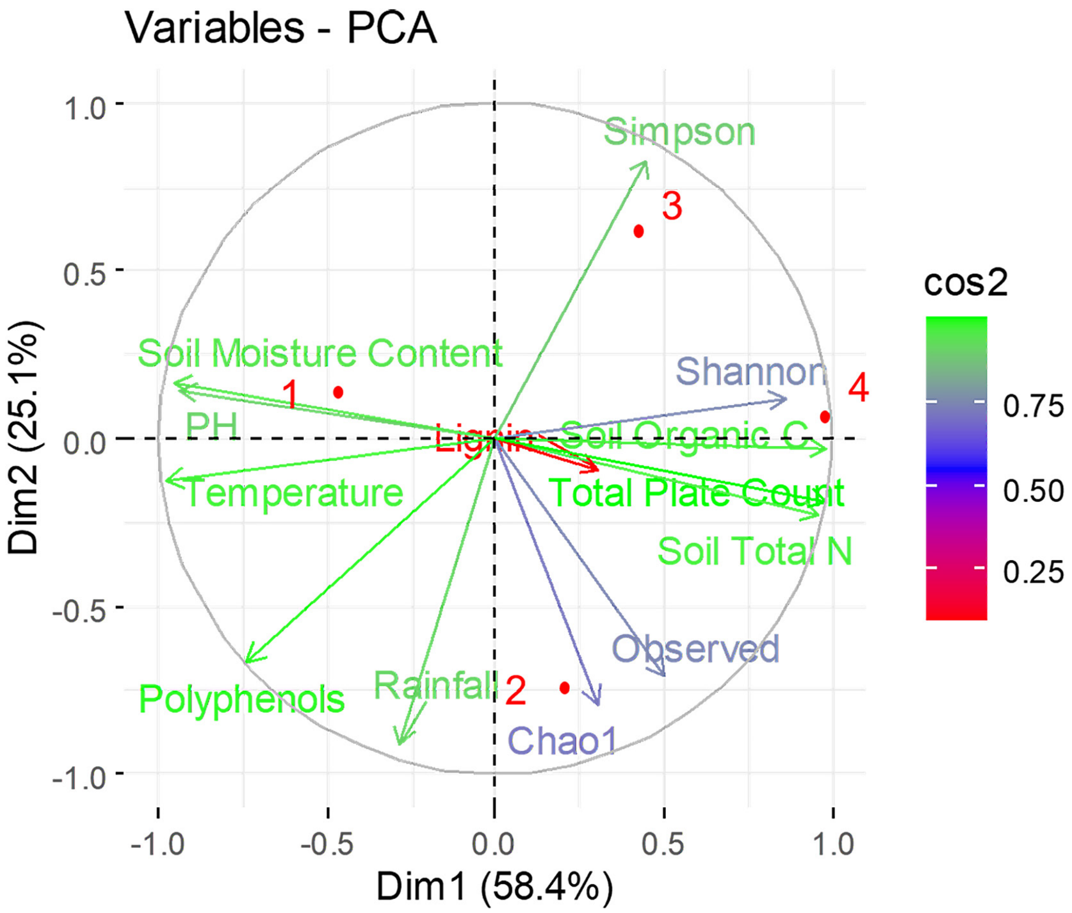


Figure 4. Interaction of fertilizer type and soil bacterial communities; Note: 1: protected area as a control treatment; 2: organic fertilizer; 3: inorganic fertilizer; 4: mixed fertilizer

polyphenols, which were shown to have a negative correlation with microbial diversity vectors. This indicates that natural protected forests with no human intervention had more stable temperature and pH, but relatively lower microbial diversity compared to fertilizer-treated management. The vector line was also in the opposite direction of the diversity indicator, triggering extreme conditions that could suppress microbial communities. Natural ecosystems supported stability, but diversity was not always higher than in disturbed ecosystems (Singh and Kumaria, 2023).

These findings underscore the critical role of fertilizer type in shaping soil bacterial communities and influencing soil quality in tropical coffee agroforestry systems. The combination of organic and inorganic fertilizers not only enhanced nutrient availability but also supported a more diverse and functionally balanced microbial community, reflecting improved ecosystem resilience and productivity. In contrast, sole application of inorganic fertilizers may lead to microbial imbalance and long-term soil degradation. The organic fertilizer treatment promoted microbial richness and even distribution, suggesting its potential for sustainable soil health management. Importantly, this study highlights that strategic fertilizer management in agroforestry systems can bridge the gap between agricultural productivity and ecological sustainability. These insights provide a scientific foundation for developing integrated nutrient management practices that sustain microbial biodiversity and optimize soil function, which is essential for long-term agricultural sustainability in tropical regions.

CONCLUSIONS

This study demonstrates that different fertilizer types significantly influence soil physicochemical properties and bacterial community dynamics in a tropical coffee agroforestry system. The mixed fertilizer treatment produced the highest total nitrogen, microbial population, and overall taxonomic diversity, suggesting a synergistic benefit of combining organic and inorganic inputs. The organic fertilizer treatment, however, resulted in the highest species richness and evenness, indicating its value in supporting a balanced and diverse microbial community through complex organic substrates. In contrast, the inorganic fertilizer increased specific nutrient-responsive taxa but reduced overall diversity and community evenness. At the taxonomic level, shifts in dominant phyla and species such as the prevalence of Bacillota in PA, *Staphylococcus xylosus* in OF, *Paracoccus marcusii* in IF, and *Acidibacter ferrireducens* in MF reflect how microbial structures are shaped by nutrient sources. Principal component analysis further confirmed strong associations between fertilizer types, soil chemical parameters, and microbial diversity patterns. While MF supports the highest microbial abundance and compositional complexity, OF is more beneficial for sustaining microbial richness and ecological stability. These findings emphasize that integrated fertilization strategies must be tailored to balance soil productivity with long-term microbial and soil health.

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