



Biome-dependent responses of *Zea mays* yield and soil functionality to organic fertilization in Cambisols of Brazil

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Abstract

Monocropping systems of *Zea mays* L. in Brazilian biomes exert strong pressures on the functionality of Cambisols. This study aimed to assess the influence of organic fertilization on the chemical properties of Cambisols across four Brazilian biomes (Amazon, Atlantic Forest, Caatinga, and Cerrado), as well as on plant nutrient extraction patterns, the microbial community within the rhizosphere of *Z. mays*, and crop yield. Under greenhouse conditions over three cultivation cycles, soil pH, soil organic carbon (SOC), available P, total N, plant dry biomass, yield, macro- and micronutrient extraction, microbial gene abundance, and dsDNA content were evaluated in Cambisols from different Brazilian biomes under two treatments (organic fertilization × control). Higher values of SOC, available P, total N, shoot and root dry biomass, yield, extraction of N, P, Mg, S, B, Cu, Fe, and Zn, as well as bacterial and fungal gene abundance and dsDNA content, were observed in soils receiving organic fertilization. The findings suggest that organic fertilization enhances plant performance, soil fertility, nutrient dynamics, and rhizosphere functioning in Cambisols, contributing to improved maize yield. Organic inputs were associated with (i) increases in SOC, available P, and total N; (ii) greater abundance of bacterial and fungal genes and higher dsDNA content; (iii) enhanced extraction of macro- and micronutrients; and (iv) the potential to support the conservation of Cambisols while contributing to food security and sustainable agricultural practices.

Keywords Bacteria gene diversity · Cow manure · Fungi gene diversity · Maize · Soil chemical properties

1 Introduction

Maize (*Zea mays* L.) is a cornerstone of global agriculture due to its high productivity, wide adaptability, and multi-functional use as food, feed, and industrial raw material (Zapałowska and Jarecki 2024; Sikiru et al. 2024). In Brazil, maize plays a strategic role in national food security and agroindustrial systems, particularly in regions where soil conditions allow for high yield potential (Prudente Junior et al. 2024). Among these soils, Cambisols are of particular

relevance due to their widespread occurrence and agricultural suitability. These soils are generally characterized by relatively young profiles, good drainage, and moderate to high fertility; however, they may also exhibit considerable variability in physical and chemical properties depending on parent material and environmental conditions, which can influence crop performance and management responses (Nungula et al. 2024; Bolfe et al. 2024).

Cambisols are distributed across major Brazilian biomes, including the Amazon, Atlantic Forest, Caatinga, and Cerrado, where they support diverse agricultural systems (Bolfe et al. 2024). In the Cerrado, they contribute to large-scale grain production, while in the Atlantic Forest they are associated with forestry and agroforestry systems (Soares et al. 2024; Parron et al. 2024). In the Caatinga and Amazon regions, Cambisols are often used in smallholder and agroecological systems, where soil management plays a critical role in maintaining productivity and ecosystem services (González et al. 2024; Pegoraro et al. 2024). Despite their agricultural potential, these soils are susceptible to degradation processes such as nutrient depletion and erosion,

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particularly under intensive monocropping systems, which may compromise their long-term functionality.

Organic fertilization has been widely proposed as a strategy to improve soil quality and sustain crop productivity by enhancing soil organic matter, nutrient availability, and biological activity (Nath et al. 2024; Agegnehu et al. 2024). In addition to improving soil chemical properties, organic inputs play a fundamental role in regulating microbial communities, which are key drivers of nutrient cycling, organic matter turnover, and plant–soil interactions. Microbial responses to organic amendments may vary across biomes due to differences in climate, soil properties, and native microbial assemblages, potentially leading to distinct functional outcomes in agroecosystems. However, despite growing evidence of the benefits of organic fertilization, there remains limited understanding of how these responses are modulated by soil heterogeneity across different Brazilian biomes, particularly in Cambisols.

This gap is especially relevant when considering that the effectiveness of organic fertilization is not uniform and may depend on the interaction between soil properties, microbial communities, and plant physiological responses. A more integrative approach that simultaneously evaluates chemical, biological, and agronomic indicators is therefore needed to better understand the mechanisms underlying soil–plant–microbial interactions under organic management. In this context, a greenhouse experiment was conducted to assess how organic fertilization (cow manure) influences maize performance, Cambisol chemical properties, plant nutrient extraction patterns, and rhizosphere microbial communities across different Brazilian biomes (Amazon, Atlantic Forest, Caatinga, and Cerrado). It was hypothesized that: (1) organic fertilization alters soil fertility by increasing soil organic carbon, available P, and total N, with responses potentially varying among biomes (Liu et al. 2024); (2) improved soil conditions promote greater above- and belowground growth of *Z. mays* (Rehman et al. 2024); and (3) organic inputs enhance positive interactions within the rhizosphere microbial community (Anzuay et al. 2024). By integrating soil, plant, and microbial indicators

under controlled conditions, this study aims to advance the understanding of how organic fertilization influences the functional dynamics of Cambisols and to provide insights for sustainable agricultural management in tropical systems.

2 Materials and methods

2.1 Soils and treatments characterization

The top 20 cm layer of Cambisols was collected from eight natural ecosystems across Brazilian biomes: (i) Caatinga, (ii) Atlantic Forest, (iii) Amazon, and (iv) Cerrado (Table 1). All soils were collected in primary forest fragments (natural ecosystems), and they were classified as Cambisols (WRB 2022) (Fig. 1). The organic fertilization treatment consisted of well-rotted farmyard manure derived from cow manure. The characteristics of the organic fertilizer were: water content of 75%, C/N ratio of 21.13, N content of 20.84 g kg⁻¹, P content of 16.18 g kg⁻¹, K content of 31.18 g kg⁻¹, pH in water of 7.0, and electrical conductivity of 0.27 dS m⁻¹.

2.2 Experimental design

A greenhouse experiment was conducted from 2022 to 2024 using 6-L plastic pots, each filled with 5.0 kg of air-dried and sieved (<2 mm) soil samples. The experiment was replicated three times to guarantee quality assurance, quality control, and enhance the robustness and accuracy of our scientific research. Organic fertilizer was manually applied at a rate equivalent to 30 t ha⁻¹, which corresponded to a specific dose of 143 g per 6-L pot, maintaining consistency with the total application rate. The organic fertilization rate was calculated to meet crop nutrient demand according to established agronomic guidelines (de Souza et al. 2015; Nogueira et al. 2026). Additionally, we have a control treatment (unfertilized control) generating two treatments for each soil. Five replicates were prepared for each soil origin (4 biomes) × fertilization treatment (organic fertilization and control) using a completely randomized design (Fig. 2).

Table 1 Main description of Cambisol sites in the Brazilian biomes

Soil ID	Location	Geographic coordinates	Altitude (m.a.s.l)	Biome	Climate type (Köppen-Geiger classification)
#PB	Pombal, PB	6°47'34.01"S, 37°49'10.7"W	183	Caatinga	BSh
#RN	Caraúbas, RN	05°39'51"S, 37°47'56"W	767	Caatinga	BSh
#SC01	Curitibanos, SC	27°16'58"S, 50°35'04"W	987	Atlantic Forest	Cfb
#SC02	Campo Belo do Sul, SC	27°51'14"S, 50°49'21"W	1200	Atlantic Forest	Cfb
#AC01	Tarauacá, AC	8°09'51"S, 70°44'37"W	180	Amazon	Af
#AC02	Brasiléia, AC	11°02'20"S, 68°45'33"W	196	Amazon	Am
#DF	Brasília, DF	15°40'11"S, 48°01'07"W	1091	Cerrado	Aw
#GO	Goiânia, GO	16°43'22"S 49°15'16"W	832	Cerrado	Aw

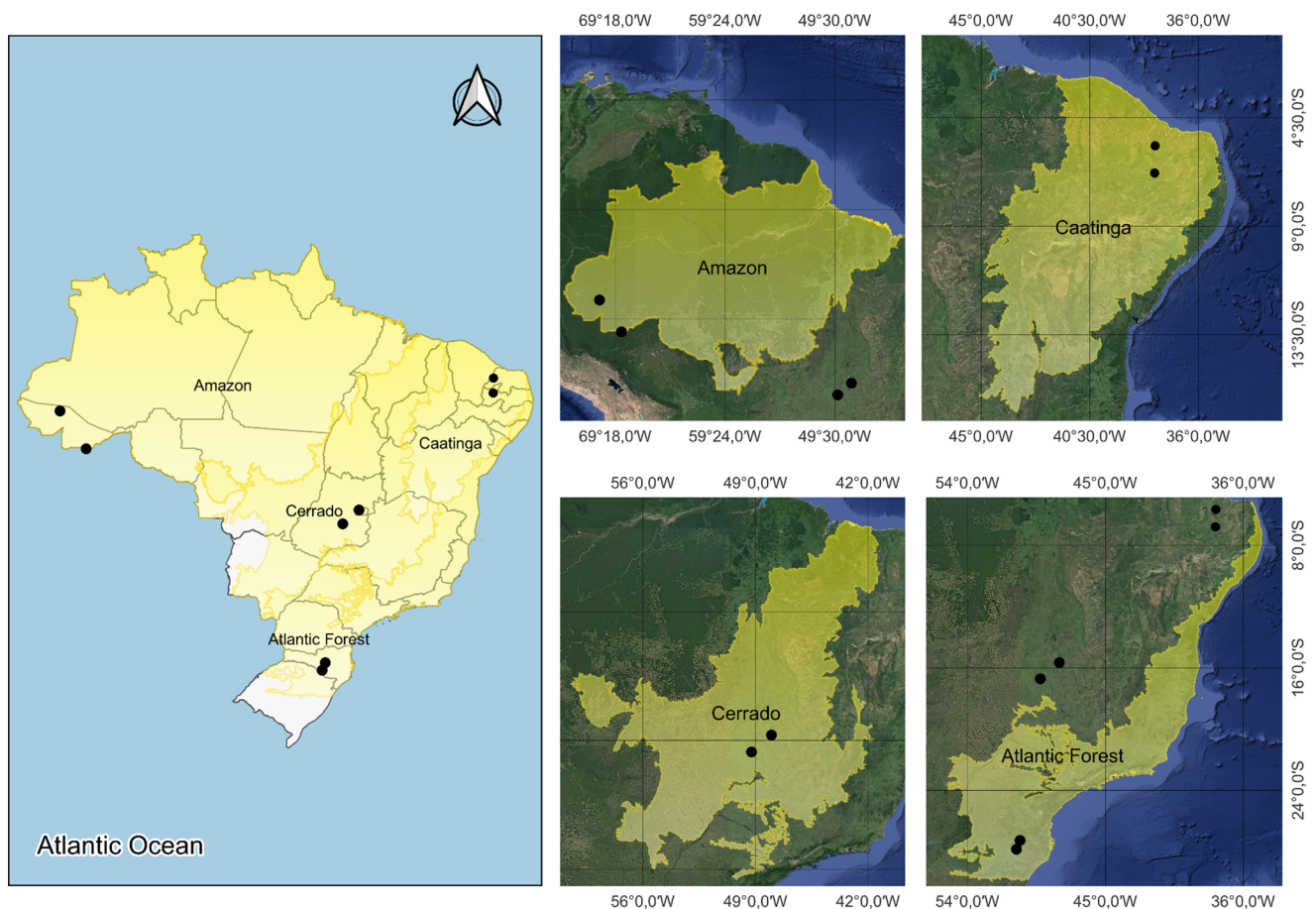


Fig. 1 Geographical distribution of sampled sites

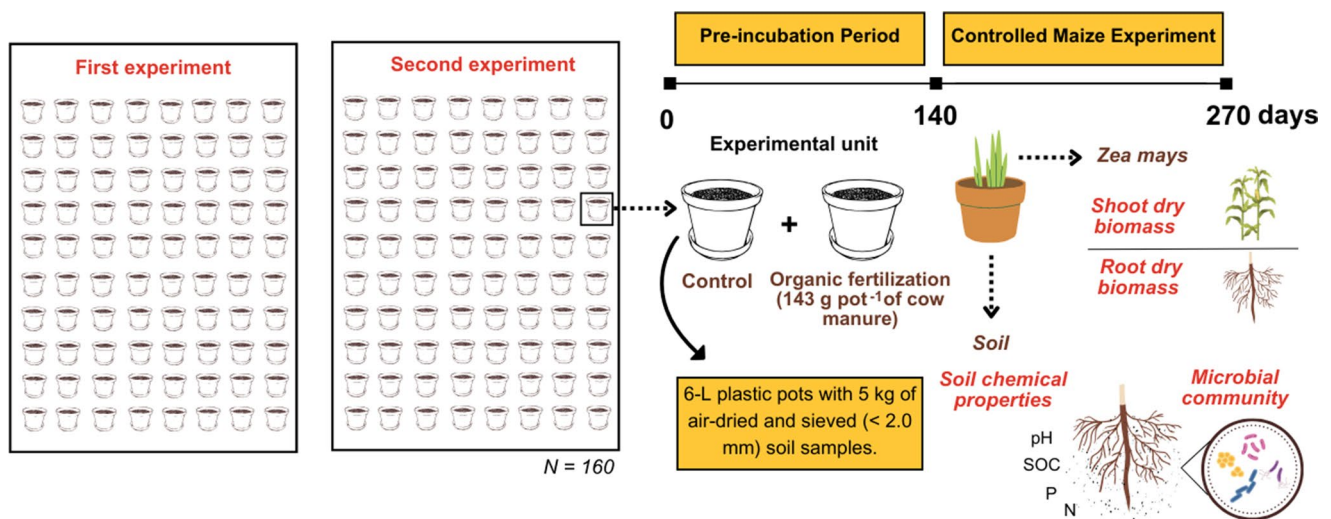


Fig. 2 Overview of the greenhouse experimental design (Pre-incubation period+Controlled maize experiment)

To mitigate potential issues associated with the incomplete decomposition of organic amendments, we implemented a pre-incubation treatment before initiating the experiment with *Z. mays*. A significant concern with the direct application of farmyard manure is that a substantial

portion may remain inadequately decomposed even after 120 days, potentially leading to inconsistencies in nutrient availability, microbial activity, and soil physicochemical properties. To address this, all pots, regardless of whether they received organic fertilization or not, were maintained

in a greenhouse at 80% of field capacity for 140 days prior to planting. This controlled pre-incubation period ensured the stabilization of organic matter decomposition, allowing microbial communities to process labile carbon sources and preventing transient spikes in soil nutrient availability that could confound experimental results. Consequently, this approach guaranteed that any substantial increase in soil parameters observed during the experiment could be attributed to genuine soil enhancement, rather than the mere presence of partially decomposed manure.

After the pre-incubation period, three seeds of maize cultivar “BRS-3042” were sown in each pot, and 5 days after emergence plant density was reduced to one per pot. For irrigation, we used distilled water during the experiment. The average temperature in the greenhouse was 28 °C, ranging from 20 °C to 35 °C, an irradiance of up to 70% of full sun, relative humidity ranging from 65 to 75%, and photoperiod of 16:8 h L: D. Maize was harvested 130 days after emergence, shoot and root biomass was harvested to determine dry biomass, seed weight was determined to estimate yield, and soil samples homogenized for chemical characterization and DNA extraction. Organic fertilized was homogenized and retrieved from packets. DNA was extracted from soil samples and organic fertilized. Both stored at -20 °C and analyzed within a 20 days of sample collection.

2.3 Shoot and root dry biomass, and yield of maize plants

Shoot and root dry biomass and yield were measured by considering each pot. Ears (including the husks, cobs, and kernels) were separated from leaves and stems (including internodes, sheaths, and tassels). Leaves and stems were dried in a forced draft oven for 24 h at 65 °C. For yield, kernels were dried, and the grain moisture content was standardized to 14% before yield estimation. We used data from leaves and stems to estimate shoot dry biomass, while data from kernels were used to estimate yield. For roots, we used the same procedure to estimate shoot dry biomass.

Table 2 Mean chemical properties ($n=10$) of the selected Cambisols before starting the greenhouse experiment

Soil type	Soil pH	SOC (g kg ⁻¹)	P (mg kg ⁻¹)	N (g kg ⁻¹)
#PB	6.51 (0.21)	7.51 (0.53)	3.60 (0.51)	0.61 (0.11)
#RN	6.97 (0.17)	4.41 (0.87)	2.42 (0.54)	0.57 (0.09)
#SC01	6.04 (0.14)	17.40 (0.96)	8.91 (0.15)	1.23 (0.08)
#SC02	5.30 (0.42)	33.93 (2.51)	10.90 (0.56)	1.58 (0.21)
#AC01	4.48 (0.10)	37.93 (0.50)	14.27 (0.43)	2.41 (0.28)
#AC02	4.78 (0.17)	30.98 (0.47)	17.43 (0.36)	4.21 (0.51)
#DF	3.90 (0.27)	15.32 (0.39)	8.08 (0.51)	0.99 (0.21)
#GO	3.78 (0.12)	16.11 (0.51)	7.49 (0.49)	0.91 (0.19)

Standard deviation in parenthesis. SOC=soil organic carbon; P=Soil available P extracted by Mehlich-I; and N=Total nitrogen

2.4 Relative chlorophyll contents and plant nutrition

Relative chlorophyll *a* and *b* contents in maize leaves were determined using a ClorofiLOG portable chlorophyll meter (Falker, Porto Alegre, Brazil). Measurements were carried out on all plants at 45 days after emergence, corresponding to the stage at which the fifth fully expanded photosynthetic leaf (counted from the apex) was present. After harvest, shoot biomass was oven-dried, weighed, and a representative subsample was finely ground for chemical analyses. Plant material was processed in a Wiley-type knife mill, and the concentrations of N, P, K, Ca, Mg, S, Na, Cu, Zn, Fe, Mn, and B were quantified following the analytical procedures described by Tedesco et al. (1995). Accordingly, nutrient extraction was estimated by multiplying nutrient concentrations by the plant dry biomass (shoot+root dry biomass), and the resulting values were expressed as kg ha⁻¹ for macronutrients and g ha⁻¹ for micronutrients and sodium.

2.5 Soil chemical characterization

To chemically characterize the soil samples, we analyzed several parameters: soil pH, soil organic carbon, available P, and total nitrogen. Soil pH was determined in a soil-water suspension with a 1:2.5 ratio. The soil organic carbon (SOC) content was measured by rapid oxidation with potassium dichromate as described by Okalebo et al. (1993). Available P was determined colorimetrically using a spectrophotometer at 882 nm after extraction with Mehlich-1, while total nitrogen was quantified after digesting soil samples with sulfuric acid and potassium sulphate, according to the Kjeldahl method (Black 1965). Additionally, soil properties were estimated before to start the experiment and they are presented in Table 2.

2.6 DNA extraction for microbial community composition

To characterize microbial community composition, we consider the abundance of Bacteria, and Fungi. Bacteria signify a diverse group of microorganisms essential for decomposing organic matter, fixing nitrogen, and promoting plant health. Fungi represent organisms that decompose complex organic materials, form symbiotic relationships with plants (mycorrhizae), and contribute to soil structure and fertility. We separated bulk from rhizospheric soil using a standardized protocol from Barillot et al. (2013). The dsDNA was extracted from frozen rhizosphere soil samples using the protocol described by Joergensen et al. (2024). The dsDNA was quantified with the QuantiFluor system using 485 nm

excitation and 520 nm emission in the FLUOstar Omega microplate reader. To account for DNA loss during extraction, dsDNA content and marker gene abundances were corrected by dividing the data by extraction efficiency, as described in Hemkemeyer et al. (2014). Bacteria, and Fungi were quantified via quantitative real-time PCR (qPCR), targeting ITS1 for fungi and the 16 S rRNA gene for Bacteria, using the LightCycler 480 SYBR Green I Master and Probes Master in the LightCycler 480 Instrument II. Primers used were: (i) NSI1 and 58A2R for Fungi (Martin and Rygielwicz 2005); and (ii) BAC338F and BAC805R with probe BAC516F for Bacteria (Yu et al. 2005). Reaction mixtures, cycling conditions, and cloning fragments for qPCR standards were used as proposed by Joergensen et al. (2024), and the standard preparation was performed as described by Rummel et al. (2021).

2.7 Statistical analysis

Prior to the statistical analyses, outliers were identified and removed from replicated data. Data normality and homogeneity of variances were assessed using the Shapiro–Wilk (“shapiro.test” function) and Bartlett (“bartlett” function) tests, respectively. When necessary, variables were transformed to meet normality assumptions and subsequently standardized using z-transformation (mean=0, standard deviation=1) to ensure comparability among variables. Differences among treatments were evaluated using two-way analysis of variance on ranks, followed by Tukey’s test at the 5% significance level ($p \leq 0.05$). Euclidean distance matrices were computed using the ‘vegan’ package. Principal component analysis (PCA) was performed as a dimensionality reduction technique to identify multivariate patterns and relationships among soil chemical properties, plant performance, and microbial community attributes across treatments (organic fertilization $\times$ control). To minimize multicollinearity, variables with variance inflation factor (VIF) values ≥ 4.0 were excluded from the analysis. The first two principal components explained 77.90% (PC1) and 9.85% (PC2) of the total variance, respectively. The interpretation of PCA results was based on the strength of correlation and variable contribution, with factor loadings ≥ 0.70 considered indicative of strong associations. The “*adonis*” function was used to determine the significance differences with PERMANOVA. Thus, variables with: (i) VIF higher than 4.0, and (ii) not significant p-values by PERMANOVA were not included in the PCA.

Structural equation modeling (SEM) was employed to disentangle the direct and indirect relationships among plant–soil functional processes and yield under fertilized and unfertilized conditions. Prior to analysis, all plant, soil, and microbial variables from each soil origin and fertilization

treatment were standardized using z-transformation to remove scale effects and homogenize variance across measurements, property groups, and sampling points. The standardized dataset was subsequently used in all multivariate analyses. Variables were grouped into three functional categories following Souza et al. (2016a, b; Rodrigues et al. (2016), and Souza et al. (2023): (i) plant performance (shoot dry biomass, chlorophyll *a* and *b* contents, and yield); (ii) plant nutrition (macro- and micronutrient extraction); and (iii) healthy rhizosphere (root dry biomass, bacterial and fungal gene copy numbers, and dsDNA content). These functional categories represent complementary dimensions of plant–soil functionality and were specified as latent variables in the SEM framework. Only indicators contributing more than 5% to the total explained variance were retained; variables below this threshold were excluded to ensure model parsimony and robustness.

The SEM approach followed a two-step procedure. First, a measurement model was constructed using confirmatory factor analysis (CFA) to validate the latent structure of the functional groups and their associated observed indicators, based on standardized factor loadings. Convergent validity was assessed by examining factor loadings (ranging between 0.70 and 0.90), average variance extracted ($AVE \geq 0.50$), and the statistical significance of indicator–construct relationships, ensuring that the observed variables adequately represented their respective latent constructs. Internal consistency was evaluated using composite reliability ($CR \geq 0.70$) and Cronbach’s alpha, confirming the reliability of each construct. Factorability of the dataset was additionally verified using the Kaiser–Meyer–Olkin (KMO) measure and Bartlett’s test of sphericity, together with the evaluation of eigenvalues, cumulative explained variance, and factor loadings. Second, a structural model was specified to assess the interactions among the latent variables and their effects on yield, thereby directly testing the hypothesized functional pathways regulating plant productivity. Separate SEMs were developed for fertilized and control (unfertilized) treatments to explicitly capture differences in system functioning under contrasting nutrient management scenarios. All models were implemented as single-level analyses integrating plant, soil, and microbial processes at the plot scale. Model estimation was performed using maximum likelihood procedures in R, employing the psych, lavaan, semTools, and MASS packages. Model adequacy was evaluated using multiple goodness-of-fit indices: the comparative fit index ($CFI > 0.95$), the standardized root mean square residual ($SRMR < 0.08$), and the root mean square error of approximation ($RMSEA < 0.06$). These criteria were used to ensure an adequate representation of the observed covariance structure and to identify the most plausible models explaining yield regulation through plant

performance, plant nutrition, and rhizosphere health under contrasting fertilization regimes. All statistical analyses were performed using R software v3.6.4.

3 Results

3.1 Plant dry biomass, chlorophyll content, and yield as influenced by the interaction among soil origins and fertilization treatments

Significant differences in shoot dry biomass ($p \leq 0.001$), root dry biomass ($p \leq 0.001$), chlorophyll *a* ($p \leq 0.01$), chlorophyll *b* ($p \leq 0.01$), and yield ($p \leq 0.001$) were observed due to the interaction among soil origin and fertilization treatments. In all soils, plants grown under organic fertilization showed markedly higher shoot biomass (11.51–19.34 g plant⁻¹) compared with the respective controls (1.97–8.29 g plant⁻¹), with the highest values observed in soils SC01, SC02, and AC02. A similar trend was observed for root dry biomass, which increased by two- to fourfold under organic fertilization, reaching maximum values in SC01, SC02, and AC01 soils. Chlorophyll *a* content was consistently enhanced by organic fertilization, particularly in DF and AC02 soils, indicating improved physiological status of the plants. For chlorophyll *b* content, no significant differences were observed among soil origins under organic fertilization; however, organic fertilization resulted in significantly higher chlorophyll *b* values compared with the control treatment across all soils. Grain yield responded strongly to organic fertilization in all soil origins, with increases ranging from approximately 50% to more than 200% relative to the

controls. The highest yields were obtained in SC01 and AC02 soils under organic fertilization (29.90 and 29.16 g plant⁻¹, respectively), whereas the lowest yields were recorded in the non-fertilized treatments, especially in PB, RN, and GO soils (Table 3).

3.2 Soil pH, soil organic carbon, available P, and total N as influenced by the interaction among soil origins and fertilization treatments

Organic fertilization with cow manure significantly altered the soil pH ($p \leq 0.05$), soil organic carbon ($p \leq 0.001$), available P ($p \leq 0.001$), and total N ($p \leq 0.01$) of Cambisols across all soil origins (Table 4). Soil pH showed limited variation among soil origins under organic fertilization, remaining within a moderately acidic range (5.8–6.2), whereas significant differences between fertilized and control treatments were observed in several soils, particularly AC01, AC02, DF, and GO, where organic fertilization increased soil pH relative to the controls. Soil organic carbon (SOC) was markedly enhanced by organic fertilization in all soil origins, with increases ranging from approximately two- to fivefold compared with the control treatments. The highest SOC contents were recorded in AC01 and AC02 soils under organic fertilization (41.00 and 39.48 g kg⁻¹, respectively), followed by SC02 and GO soils. Available phosphorus also responded positively to organic fertilization across all soils, with fertilized treatments consistently showing higher P concentrations than the controls, and maximum values observed in AC02 and AC01 soils. Total soil nitrogen exhibited a similar pattern, with organic fertilization significantly increasing N contents in all Cambisols, particularly in

Table 3 Shoot and root dry biomass, chlorophyll *a* and *b* contents, and yield of maize cv “BRS-3042” sown in Cambisols from different origins and influenced by organic fertilization (OF) with cow manure (30 t ha⁻¹)

Soil origin	Treatments	Shoot dry biomass (g plant ⁻¹)	Root dry biomass (g plant ⁻¹)	Chlorophyll <i>a</i> (FCI)	Chlorophyll <i>b</i> (FCI)	Yield (g plant ⁻¹)
#PB	OF	11.51 (1.57) cA	15.71 (1.17) bA	44.96 (0.27) cA	21.01 (0.21) aA	13.76 (0.61) dA
	Control	2.01 (0.59) cB	4.01 (0.98) cB	36.09 aB (0.31)	14.85 (0.19) aB	6.44 (0.59) cB
#RN	OF	13.43 (1.29) cA	13.01 (1.17) cA	45.94 (0.18) cA	22.03 (0.02) aA	14.57 (0.79) dA
	Control	1.97 (0.57) cB	3.79 (0.83) cB	34.33 (0.06) bB	12.98 (0.12) aB	6.41 (0.61) cB
#SC01	OF	19.34 (1.48) aA	25.64 (1.47) aA	47.59 (0.21) bA	23.93 (0.21) aA	29.90 (1.78) aA
	Control	8.01 (1.16) aB	11.56 (1.57) aB	32.02 (0.18) cB	12.09 (0.18) aB	8.57 (1.13) bB
#SC02	OF	18.22 (1.23) aA	26.11 (2.18) aA	48.98 (0.28) bA	22.84 (0.15) aA	21.84 (0.71) bA
	Control	7.99 (0.98) aB	12.17 (1.21) aB	34.59 (0.15) bB	10.11 (0.07) bB	11.22 (0.91) aB
#AC01	OF	17.33 (1.27) bA	25.91 (0.98) aA	43.94 (0.11) cA	21.84 (0.13) aA	21.81 (0.69) bA
	Control	8.29 (0.91) aB	10.13 (1.19) aB	31.01 (0.09) cB	13.48 (0.15) aB	9.67 (0.81) bB
#AC02	OF	18.12 (1.17) aA	18.19 (1.13) bA	49.93 (0.21) bA	22.92 (0.05) aA	29.16 (1.17) aA
	Control	8.02 (0.89) aB	9.17 (0.57) bB	35.54 (0.29) aB	14.56 (0.11) aB	8.79 (0.79) bB
#DF	OF	12.29 (0.71) cA	10.98 (1.34) dA	51.01 (0.16) aA	23.03 (0.09) aA	17.66 (2.01) cA
	Control	6.12 (0.59) bB	4.19 (0.81) cB	18.92 (0.15) dB	12.94 (0.17) aB	9.78 (1.15) bB
#GO	OF	11.69 (0.29) dA	9.63 (1.19) dA	45.69 (0.13) cA	21.99 (0.26) aA	18.13 (0.45) cA
	Control	1.99 (0.38) cB	4.12 (0.56) cB	33.93 (0.10) bB	14.56 (0.19) aB	10.17 (1.13) aB

OF=organic fertilization. Standard error in parenthesis. Lower case letters represent significant differences of soil origin, while capital letters represent significant differences of treatments by Tukey's test ($p \leq 0.05$)

Table 4 Mean values of soil pH, soil organic carbon, available P, and total N in Cambisols from different origins and influenced by organic fertilization (OF) with cow manure (30 t ha⁻¹)

Soil origin	Treatments	Soil pH	SOC (g kg ⁻¹)	P (mg kg ⁻¹)	N (g kg ⁻¹)
#PB	OF	5.9 (0.2) aA	10.01 (0.58) cA	8.01 (0.72) dA	1.13 (0.04) cA
	Control	6.5 (0.1) aA	3.45 (0.89) dB	2.41 (0.31) dB	0.17 (0.02) cB
#RN	OF	5.8 (0.1) aA	11.22 (0.58) cA	9.23 (0.79) dA	1.54 (0.11) cA
	Control	6.6 (0.1) aA	1.98 (0.57) dB	1.17 (0.17) dB	0.21 (0.03) cB
#SC01	OF	5.9 (0.1) aA	21.58 (1.49) bA	10.01 (0.13) cA	2.13 (0.98) bA
	Control	6.1 (0.2) aA	10.98 (1.32) bB	4.12 (0.21) cB	0.67 (0.04) cB
#SC02	OF	5.8 (0.2) aA	35.99 (3.29) aA	12.32 (1.12) cA	2.54 (0.83) bA
	Control	5.5 (0.1) bA	14.32 (2.81) aB	7.14 (0.98) bB	0.53 (0.02) cB
#AC01	OF	6.1 (0.2) aA	41.00 (2.74) aA	16.18 (2.01) bA	2.99 (0.33) bA
	Control	4.7 (0.1) cB	13.45 (1.58) aB	10.22 (1.83) aB	1.13 (0.23) bB
#AC02	OF	6.2 (0.1) aA	39.48 (2.46) aA	21.17 (0.19) aA	4.54 (0.57) aA
	Control	4.8 (0.2) cB	11.39 (0.98) bB	12.19 (0.21) aB	2.17 (0.89) aB
#DF	OF	6.2 (0.3) aA	21.09 (1.57) bA	10.13 (0.93) aA	2.13 (0.18) bA
	Control	4.1 (0.2) cB	8.32 (0.92) cB	6.17 (1.49) bB	0.38 (0.02) cB
#GO	OF	6.0 (0.2) aA	22.84 (2.81) bA	9.92 (1.38) dA	1.89 (0.54) cA
	Control	4.2 (0.1) cB	6.43 (0.59) cB	3.12 (0.32) cB	0.31 (0.04) cB

OF=organic fertilization. Standard error in parenthesis. SOC=Soil organic carbon, P=Soil available P extracted by Mehlich-1, and N=total nitrogen. Lower case letters represent significant differences of soil origin, while capital letters represent significant differences of treatments by Tukey's test ($p \leq 0.05$)

Table 5 Mean maize macronutrient extraction as influenced by soil origin and organic fertilization (OF) with cow manure (30 t ha⁻¹)

Soil origin	Treatments	N (kg ha ⁻¹)	P (kg ha ⁻¹)	K (kg ha ⁻¹)	Ca (kg ha ⁻¹)	Mg (kg ha ⁻¹)	S (kg ha ⁻¹)
#PB	OF	357.6 (0.2) bA	54.3 (0.4) bA	415.6 (2.3) aA	124.3 (0.7) aA	73.7 (0.4) aA	68.1 (0.3) aA
	Control	315.3 (0.9) aB	18.5 (0.2) bB	414.8 (1.4) aA	123.6 (0.5) aA	61.3 (0.4) aB	58.9 (0.9) aB
#RN	OF	362.8 (1.1) bA	52.0 (0.2) bA	404.9 (1.5) cA	121.3 (1.1) aA	75.9 (0.6) aA	67.4 (0.5) aA
	Control	310.2 (1.3) aB	17.5 (0.3) bB	408.3 (0.9) bA	124.6 (1.5) aA	60.5 (0.9) aB	54.3 (0.4) aB
#SC01	OF	364.2 (1.2) bA	55.6 (0.5) bA	410.7 (2.7) bA	123.7 (1.8) aA	76.5 (0.2) aA	69.6 (0.1) aA
	Control	307.3 (0.6) aB	21.0 (0.9) aB	407.4 (3.1) bA	122.9 (0.4) aA	59.4 (0.3) aB	51.1 (0.4) aB
#SC02	OF	391.6 (0.7) aA	61.2 (0.6) aA	410.3 (2.8) bA	123.5 (0.2) aA	75.7 (0.7) aA	67.9 (0.9) aA
	Control	305.4 (1.1) aB	19.6 (0.5) bB	406.3 (1.5) bA	121.8 (0.3) aA	68.6 (1.2) aB	50.5 (0.8) aB
#AC01	OF	351.1 (0.9) cA	63.9 (0.5) aA	411.2 (1.8) bA	124.8 (1.3) aA	77.7 (0.5) aA	69.8 (1.3) aA
	Control	300.0 (1.2) aB	22.5 (0.1) aB	401.0 (1.3) cA	121.0 (0.7) aA	61.9 (0.4) aB	51.3 (0.7) aB
#AC02	OF	355.3 (0.2) cA	65.9 (1.1) aA	404.4 (1.2) cA	120.5 (0.9) aA	79.4 (0.3) aA	68.7.4 (0.6) aA
	Control	314.2 (0.8) aB	18.6 (0.9) bB	406.5 (1.4) bA	119.3 (0.7) aA	58.9 (0.5) aB	55.4 (0.5) aB
#DF	OF	353.2 (1.1) cA	51.2 (1.3) bA	409.7 (1.6) bA	122.5 (0.6) aA	79.0 (0.6) aA	69.5 (1.1) aA
	Control	311.2 (1.5) aB	19.0 (0.8) bB	409.4 (1.4) bA	122.3 (0.7) aA	61.3 (0.7) aB	51.3 (0.2) aB
#GO	OF	361.3 (0.9) bA	51.2 (1.3) bA	405.4 (2.1) cA	128.5 (1.2) aA	75.7 (0.3) aA	69.0 (0.8) aA
	Control	308.4 (0.2) aB	17.5 (0.8) bB	408.3 (0.9) bA	128.9 (1.8) aA	59.5 (0.5) aB	50.2 (0.7) aB

OF=organic fertilization. Standard error in parenthesis. Lower case letters represent significant differences of soil origin, while capital letters represent significant differences of treatments by Tukey's test ($p \leq 0.05$)

AC02, AC01, and SC02 soils, where values exceeded 2.5 g kg⁻¹. In contrast, control treatments were characterized by low SOC, P, and N contents, especially in PB, RN, DF, and GO soils.

3.3 Maize macro- and micronutrients extraction as influenced by the interaction among soil origins and fertilization treatments

Organic fertilization with cow manure significantly increased macronutrient extraction by maize across all soil

origins (Table 5). Nitrogen and phosphorus extraction were consistently higher under organic fertilization than in the control treatments, with N extraction ranging from 351.1 to 391.6 kg ha⁻¹ and P from 51.2 to 65.9 kg ha⁻¹ in fertilized soils, whereas control treatments showed markedly lower values. The greatest N and P extraction occurred in SC02 and AC02 soils under organic fertilization, reflecting the combined effects of improved nutrient availability and higher biomass production. For potassium and calcium extraction, we did not find significant differences between fertilized and control treatments, and they did not differ

significantly among all soils. In contrast, magnesium and sulfur extraction were significantly enhanced by organic fertilization in all Cambisols, with the highest Mg extraction observed in AC02, DF, and AC01 soils, and the greatest S extraction recorded in SC01, AC01, DF, and GO soils (Table 5).

Organic fertilization with cow manure significantly affected micronutrient extraction by maize, whereas sodium extraction was largely unaffected by soil origin or fertilization (Table 6). Sodium extraction showed no significant differences between organic fertilization and control treatments across all Cambisols, indicating that Na uptake was not influenced by manure application. In contrast, boron extraction was consistently higher under organic fertilization in all soil origins, with fertilized treatments showing two- to threefold increases compared with the controls, particularly in SC01, SC02, AC01, and DF soils. Copper extraction was also significantly enhanced by organic fertilization in all soils, with the highest values observed in AC02, SC01, and AC01 soils, whereas control treatments exhibited substantially lower Cu removal. Iron extraction increased markedly with organic fertilization in most soil origins, with fertilized treatments reaching values above 4,500 g ha⁻¹, while control treatments showed significantly lower Fe extraction, especially in SC02, AC01, AC02, DF, and GO soils. Manganese extraction did not differ significantly between treatments in most soils, although fertilized treatments tended to show slightly higher values. Zinc extraction was significantly increased by organic fertilization in several soil origins, notably RN, SC02, and AC02, whereas in other soils, such as AC01 and GO, no significant differences between treatments were observed (Table 6).

3.4 Microbial gene copies and dsDNA content as influenced by the interaction among soil origins and fertilization treatments

Organic fertilization with cow manure significantly increased microbial abundance and dsDNA content in Cambisols from all soil origins (Table 7). Bacterial gene copy numbers were consistently higher under organic fertilization than in the control treatments, with values ranging from 65.29 to 81.23 × 10⁸ g⁻¹ soil in fertilized soils, compared with 27.22 to 37.22 × 10⁸ g⁻¹ soil in the controls. The highest bacterial abundance was observed in SC02, AC01, and AC02 soils under organic fertilization, whereas PB and RN soils exhibited the lowest values, indicating a clear influence of soil origin on bacterial populations. Fungal gene copy numbers also responded strongly to organic fertilization, increasing by approximately three- to sixfold relative to the controls across all soils. Fertilized treatments showed fungal abundances ranging from 1.23 to 2.51 × 10⁸ g⁻¹ soil, with the highest values recorded in AC02, AC01, and SC02 soils, while control treatments remained uniformly low and did not differ significantly among soil origins. Similarly, dsDNA content was significantly enhanced by organic fertilization in all Cambisols, with fertilized soils presenting values between 11.91 and 21.23 µg g⁻¹ soil, compared with 7.01 to 9.01 µg g⁻¹ soil in the control treatments. The greatest dsDNA contents were observed in AC02, SC02, and AC01 soils under organic fertilization, whereas PB, RN, and SC01 soils exhibited lower but still significantly increased values (Table 7).

Table 6 Mean maize micronutrient and sodium extraction as influenced by soil origin and organic fertilization (OF) with cow manure (30 t ha⁻¹)

Soil origin	Treatments	Na (g ha ⁻¹)	B (g ha ⁻¹)	Cu (g ha ⁻¹)	Fe (g ha ⁻¹)	Mn (g ha ⁻¹)	Zn (g ha ⁻¹)
#PB	OF	4243.4 (98.1) aA	0.50 (0.05) cA	366.6 (15.3) cA	4536.3 (103.9) aA	73.6 (5.1) aA	2501.2 bA
	Control	4346.8 (86.4) aA	0.36 (0.11) aB	289.9 (11.9) aB	3950.3 (98.4) aB	66.4 (3.3) aA	2270.5 bA
#RN	OF	4340.5 (89.2) aA	0.55 (0.09) bA	371.9 (12.4) bA	4695.4 (105.4) aA	75.6 (5.2) aA	2803.9 aA
	Control	4428.4 (81.1) aA	0.28 (0.03) bB	256.9 (13.2) bB	3892.4 (101.2) aB	61.9 (4.6) aA	2002.3 bB
#SC01	OF	4123.2 (91.4) aA	0.61 (0.02) aA	381.3 (9.2) bA	4659.3 (109.2) aA	74.5 (4.9) aA	2609.6 bA
	Control	4338.9 (78.2) aA	0.18 (0.05) cB	267.9 (12.4) bB	3794.3 (87.4) aB	62.3 (5.9) aA	2103.9 bB
#SC02	OF	4251.1 (67.2) aA	0.57 (0.11) aA	371.3 (8.7) bA	4785.5 (101.3) aA	72.9 (2.5) aA	2702.4 aA
	Control	4258.3 (89.1) aA	0.34 (0.02) aB	267.9 (13.4) bB	3505.0 (98.5) bB	61.0 (5.3) aA	2239.4 bA
#AC01	OF	4123.9 (90.1) aA	0.61 (0.04) aA	381.1 (16.4) bA	4506.9 (99.3) aA	74.5 (3.2) aA	2679.3 bA
	Control	4089.3 (83.2) aA	0.30 (0.03) bB	289.1 (11.9) aB	3209.4 (114.3) bB	62.9 (4.5) aA	2432.0 aA
#AC02	OF	4348.9 (91.2) aA	0.54 (0.06) bA	401.9 (8.5) aA	4609.5 (101.8) aA	75.6 (3.4) aA	2783.9 aA
	Control	4385.2 (82.4) aA	0.28 (0.02) bB	276.9 (9.3) bB	3509.6 (86.3) bB	64.5 (5.1) aA	2509.5 aA
#DF	OF	4371.1 aA (80.7)	0.58 (0.01) aA	371.3 (10.3) bA	4505.2 (91.2) aA	74.9 (4.9) aA	2498.4 cA
	Control	4248.3 aA (91.3)	0.23 (0.03) cB	281.2 (11.5) aB	3405.6 (102.9) bB	61.0 (4.3) aA	2109.2 bA
#GO	OF	4153.5 aA (81.4)	0.56 (0.04) bA	368.6 (14.8) cA	4609.0 (121.4) aA	77.7 (5.1) aA	2609.9 bA
	Control	4267.2 aA (94.3)	0.19 (0.03) cB	291.9 (13.2) aB	3207.9 (119.3) bB	60.1 (3.9) aA	2509.7 aA

OF=organic fertilization. Standard error in parenthesis. Lower case letters represent significant differences of soil origin, while capital letters represent significant differences of treatments by Tukey's test ($p \leq 0.05$)

Table 7 Mean number of gene copies for Bacteria, Fungi, and dsDNA content in Cambisols from different origins and influenced by organic fertilization (OF) with cow manure (30 t ha⁻¹)

Soil type	Treatments	Bacteria ($n \times 10^8 \text{ g}^{-1} \text{ soil}$)	Fungi ($n \times 10^8 \text{ g}^{-1} \text{ soil}$)	dsDNA ($\mu\text{g g}^{-1} \text{ soil}$)
#PB	OF	65.39 (2.39) cA	1.32 (0.21) cA	13.54 (0.31) cA
	Control	31.68 (1.39) bB	0.34 (0.10) aB	7.01 (0.21) aB
#RN	OF	65.29 (2.41) cA	1.23 (0.11) cA	12.79 (0.29) cA
	Control	27.22 (2.39) cB	0.41 (0.09) aB	7.21 (0.19) aB
#SC01	OF	71.31 (1.84) bA	1.40 (0.17) cA	11.91 (0.19) cA
	Control	33.49 (1.69) bB	0.49 (0.21) aB	8.01 (0.33) aB
#SC02	OF	81.23 (2.38) aA	2.01 (0.33) bA	20.91 (0.29) aA
	Control	36.11 (1.94) aB	0.41 (0.11) aB	8.43 (0.27) aB
#AC01	OF	80.17 (3.91) aA	2.33 (0.13) bA	19.29 (0.31) aA
	Control	37.22 (0.81) aB	0.39 (0.14) aB	8.59 (0.18) aB
#AC02	OF	81.09 (2.81) aA	2.51 (0.21) aA	21.23 (0.59) aA
	Control	36.48 (1.63) aB	0.44 (0.09) aB	9.01 (0.29) aB
#DF	OF	72.39 (3.28) aA	1.42 (0.18) cA	15.92 (1.19) bA
	Control	34.92 (2.10) bB	0.39 (0.13) aB	8.17 (0.29) aB
#GO	OF	74.59 (3.19) bA	1.51 (0.21) cA	16.79 (0.48) bA
	Control	36.17 (3.18) aB	0.44 (0.21) aB	7.49 (0.12) aB

OF=organic fertilization. Standard error in parenthesis. Lower case letters represent significant differences of soil origin, while capital letters represent significant differences of treatments by Tukey's test ($p \leq 0.05$)

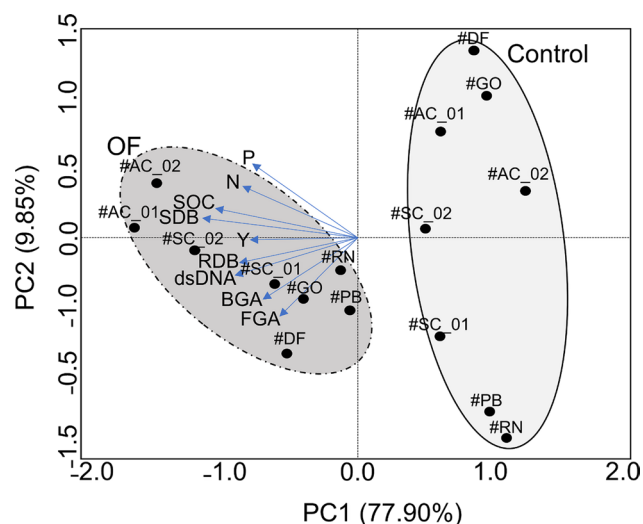


Fig. 3 PCA score plot of the soil chemical properties, plant dry biomass, yield, and microbial community composition data for the control and organic fertilization (OF) treatments. The lengths of the arrows indicate the strength of correlation of the studied variables for: soil chemical properties (SOC – soil organic carbon, P – available P, and N – total nitrogen); maize performance (SDB – shoot dry biomass, Y – yield, and RDB – root dry biomass); and microbial community composition (BGA – Bacteria gene abundance, FGA – Fungi gene abundance, and dsDNA content)

3.5 Plant–soil functional pathways controlling maize yield under organic fertilization and control conditions

Overall, 87.75% of the variation in the soil chemical properties, maize performance, and soil microbial community, respectively was explained by: (i) SOC, available P, and

total N for soil chemical properties; (ii) shoot dry biomass, root dry biomass, and yield for maize performance; and (iii) gene abundance of Bacteria, and Fungi, and dsDNA content for soil microbial community (Fig. 4). Soil organic carbon, available P, total N, shoot and root dry biomass, yield, gene abundance of Bacteria and Fungi, and dsDNA simultaneously explained the variation in the organic fertilization treatment (pots with a rate of 30 t ha⁻¹ of cow manure) (Fig. 3).

Structural equation modeling (SEM) was used to test the hypothesized causal relationships among soil fertility, rhizosphere microbial functioning, plant performance, and nutrient extraction, thereby directly addressing our central hypothesis that organic fertilization enhances the functional coupling between soil, microbiota, and plant systems. The SEM results revealed marked contrasts in the organization and strength of plant–soil functional pathways between organic fertilization and control conditions (Fig. 4). Under organic fertilization, the system was characterized by strong, predominantly positive interactions among functional domains, supporting our hypotheses that improvements in soil fertility and microbial activity promote plant growth. Healthy rhizosphere exerted a pronounced positive influence on soil fertility (path coefficient=12.87) and plant performance (7.81), while soil fertility strongly enhanced plant performance (31.07), confirming that increases in soil organic carbon, available P, and total N are key drivers of plant responses. Plant nutrient extraction was positively linked to soil fertility (17.39) and showed a weaker direct association with the rhizosphere (1.01). Plant performance emerged as the main proximal driver of yield, with a strong positive effect (9.60), indicating that organic fertilization promotes an integrated and synergistic plant–soil system that efficiently translates belowground processes into productivity. In contrast, under control conditions,

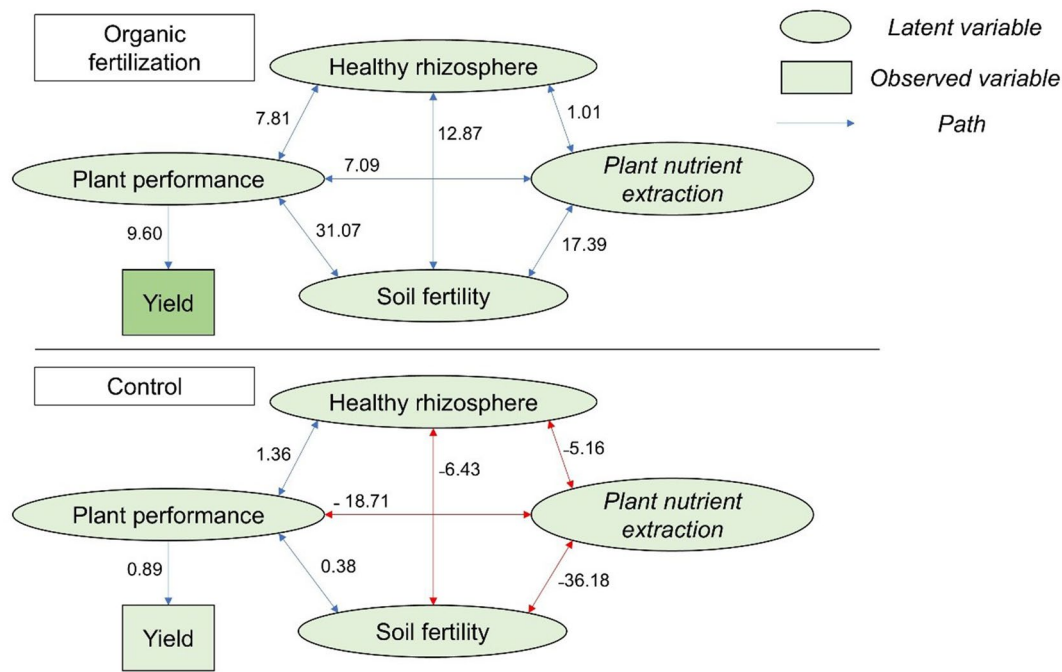


Fig. 4 Structural equation models describing plant–soil functional pathways regulating yield under organic fertilization and control conditions. Arrows represent significant effects at $p \leq 0.01$. Blue (positive) and red (negative) arrows represent estimated values that indicate the proportion of response variation explained by relationships with

other variables. Values associated with arrows indicate standardized path coefficient. For organic fertilization: $\chi^2 = 131.19$, $p \leq 0.01$, RMSEA = 0.027, and CFI = 0.98; for control: $\chi^2 = 128.11$, $p \leq 0.01$, RMSEA = 0.031, and CFI = 0.96

functional relationships were weaker and frequently negative, indicating a decoupling of plant–soil interactions and thus not supporting our initial hypotheses. Healthy rhizosphere showed a modest positive association with plant performance (1.36) but exerted negative effects on plant nutrient extraction (−5.16) and soil fertility (−6.43). Soil fertility was negatively related to plant nutrient extraction (−36.18), and plant performance exhibited a strong negative association with nutrient extraction (−18.71), suggesting physiological constraints and limited resource availability under unfertilized conditions. The effect of plant performance on yield was minimal (0.89), highlighting the reduced capacity of the system to convert plant functional performance into productivity in the absence of organic fertilization (Fig. 4).

4 Discussion

4.1 Overall findings indicate that organic fertilization positively influence the plant performance, soil fertility, plant nutrient extraction patterns, root dry biomass, bacterial and fungal gene abundance, and dsDNA content in Cambisols from different Brazilian biomes

Overall, our findings demonstrate that organic fertilization exerts a pervasive and coordinated influence on plant

performance, soil fertility, plant nutrient extraction patterns, and rhizosphere health across Cambisols from distinct Brazilian biomes (Souza et al. 2025). Organic fertilization consistently enhanced maize shoot and root biomass, chlorophyll *a* and *b* contents, and yield, while simultaneously improving key soil chemical properties, including soil organic carbon, available phosphorus, and total nitrogen (Souza et al. 2017). These improvements were accompanied by marked increases in the extraction of both macro- and micronutrients (notably N, P, Mg, S, B, Cu, Fe, and Zn), indicating that manure application not only increased nutrient availability but also strengthened the capacity of plants to acquire and utilize soil-derived resources (Melo et al. 2019). Concurrently, indicators of rhizosphere health—such as root biomass, bacterial and fungal gene abundance, and total dsDNA content—were consistently higher under organic fertilization, highlighting the role of manure inputs in stimulating microbial activity and reinforcing plant–microbe interactions (Benevenuto et al. 2025).

By integrating soils from eight locations spanning major Brazilian biomes and evaluating responses over three consecutive greenhouse cycles, this study provides robust evidence that organic fertilization restructures plant–soil interactions in a consistent and predictable manner, despite inherent soil heterogeneity. Cow manure was selected as the organic input because of its recognized capacity to improve

soil fertility and biological functioning through direct nutrient supply and the stimulation of microbial processes, a rationale supported by recent literature (Głąb et al. 2024; Priya et al. 2024). Our results corroborate and extend previous findings showing strong linkages between organic fertilization and plant growth, soil nutrient dynamics, and microbial community structure, reinforcing the view that organic amendments act as central drivers of integrated plant–soil functioning and rhizosphere health (Yu et al. 2024; Zhou et al. 2024).

4.2 Organic fertilization promoting plant performance (Dry biomass production, chlorophyll content, and yield)

Organic fertilization with cow manure consistently promoted maize performance across Cambisols from contrasting Brazilian biomes, indicating that organic inputs can override inherent soil differences by strengthening fundamental plant–soil processes. The pronounced increases in shoot and root dry biomass, chlorophyll *a* and *b* contents, and grain yield under organic fertilization reflect an integrated response driven by improved nutrient availability, enhanced physiological status, and greater carbon allocation to belowground organs (Priya et al. 2024). The strong biomass and yield responses, particularly in soils from Atlantic Forest (SC01 and SC02) and Amazon (AC02) biomes, suggest that these Cambisols were especially responsive to organic inputs, likely due to improved synchronization between nutrient release from manure and plant demand (da Silva et al. 2022). Enhanced chlorophyll *a* content under organic fertilization indicates increased photosynthetic capacity, while the uniform increase in chlorophyll *b* across soil origins suggests a generalized improvement in light-harvesting efficiency, independent of soil-specific constraints (Barbosa et al. 2021).

The observed gains in plant performance can be mechanistically attributed to the slow and sustained release of essential macro- and micronutrients from cow manure, particularly nitrogen and phosphorus, which are central to chlorophyll synthesis, carbon assimilation, and biomass accumulation (Singh et al. 2025). In addition to direct nutrient supply, manure application stimulates soil microbial activity and rhizosphere functioning, promoting nutrient mineralization and root–microbe interactions that enhance nutrient uptake efficiency (Jagadesh et al. 2024). These biological processes likely contributed to the two- to four-fold increases in root biomass, reinforcing positive feedbacks between root growth, nutrient acquisition, and shoot development (Priya et al. 2024). Collectively, the combined effects of improved soil fertility, enhanced microbial activity, and increased photosynthetic capacity explain the

substantial yield gains observed under organic fertilization, demonstrating that cow manure acts not only as a nutrient source but also as a regulator of plant physiological performance and productivity in tropical Cambisols (Głąb et al. 2024; Luo et al. 2024; Wen et al. 2024).

4.3 Changes in key soil fertility properties as influenced by the interaction between soil origins and organic fertilization

Organic fertilization with cow manure induced consistent and significant changes in key soil fertility properties across Cambisols from contrasting Brazilian biomes, highlighting a strong interaction between soil origin and fertilization management. The moderate increase and stabilization of soil pH under organic fertilization, particularly in soils from Amazon (AC01, AC02) and Cerrado (DF, GO) biomes, reflects the buffering capacity of cow manure, whose neutral to slightly alkaline nature mitigates soil acidity and reduces the intensity of acid-driven constraints typical of tropical Cambisols (Liu et al. 2024). Although pH values under organic fertilization converged toward a moderately acidic range across soils, the pronounced differences relative to the controls in inherently more acidic soils underscore the importance of organic amendments in chemically constrained systems (Dhaliwal et al. 2024; Jagadesh et al. 2024; Sagar et al. 2024).

The marked enrichment of soil organic carbon across all soil origins, with two- to fivefold increases relative to unfertilized treatments, demonstrates the central role of manure-derived organic inputs in rebuilding carbon pools and enhancing soil structural and functional integrity (Shao et al. 2024). Higher SOC contents in soils from Amazon (AC01 and AC02) biomes suggest a greater capacity for carbon stabilization, potentially linked to soil texture, mineralogy, and organo–mineral associations that favor organic matter protection (Shao et al. 2024). Increased SOC not only reflects carbon accumulation but also underpins improvements in nutrient retention and availability, particularly phosphorus (Dhaliwal et al. 2024). The consistent rise in available P under organic fertilization likely resulted from both direct P inputs and reduced P fixation, as organic ligands and increased exchange capacity associated with higher SOC can complex Fe and Al oxides, thereby enhancing P mobility in acidic environments (Carneiro et al. 2019). Similarly, the substantial increases in total soil nitrogen across all Cambisols indicate effective incorporation and gradual mineralization of manure-derived N, supporting sustained nutrient supply rather than short-term pulses (Chen et al. 2024).

Collectively, these fertilization-induced changes in pH, SOC, available P, and total N demonstrate that organic amendments do more than supplement nutrients; they

modify the chemical framework of the soil in ways that promote nutrient retention, reduce chemical limitations, and enhance overall soil fertility (Daunoras et al. 2024). The persistence of these improvements across diverse Cambisols emphasizes the capacity of organic fertilization to partially override inherent soil constraints, thereby creating a more favorable edaphic environment for plant growth and rhizosphere functioning across contrasting Brazilian biomes.

4.4 Plant nutrient extraction patterns: Evidence of increased N, P, Mg, S, B, Cu, Fe, and Zn extraction as influenced by soil origin and organic fertilization

Organic fertilization with cow manure substantially altered maize nutrient extraction patterns, indicating that manure-driven changes in soil nutrient availability and plant growth translated into enhanced nutrient uptake across contrasting Cambisols (Xu et al. 2026). The consistent increases in N and P extraction under organic fertilization reflect both the direct nutrient inputs supplied by manure and indirect effects mediated by increased biomass production and improved soil fertility, particularly soil organic carbon and available P (Liu et al. 2026). These responses were most pronounced in soils from Atlantic Forest and Amazon biomes, suggesting that soils with greater responsiveness to organic inputs more efficiently converted added nutrients into plant uptake, likely due to improved nutrient synchronization and enhanced rhizosphere activity. In contrast, the lack of significant fertilization effects on K and Ca extraction across soil origins indicates that these nutrients were not limiting for maize growth under the studied conditions, or that their availability was primarily controlled by inherent soil mineralogy rather than short-term organic amendments (Jiang et al. 2024). The marked increases in Mg and S extraction under organic fertilization highlight the role of manure as an important source of secondary nutrients and as a driver of improved cation exchange capacity and sulfate availability through organic matter mineralization (Gao et al. 2025).

Micronutrient extraction patterns further underscore the capacity of organic fertilization to enhance plant nutrient acquisition through combined chemical and biological mechanisms. The strong and consistent increases in B, Cu, and Fe extraction across soil origins suggest that manure application enhanced micronutrient availability via complexation with organic ligands, reduced fixation, and increased root–microbe interactions in the rhizosphere (Bazgar et al. 2025). The pronounced response of Fe extraction, in particular, is consistent with organic matter–mediated mobilization processes that increase Fe solubility and root accessibility (Carneiro et al. 2019). In contrast, the limited response of Mn and the absence of treatment effects on Na

extraction indicate that these elements were largely governed by soil-specific redox conditions or background concentrations rather than organic inputs (Hu et al. 2025). Variable Zn responses among soils further highlight the importance of soil origin in modulating micronutrient dynamics, reflecting differences in parent material, sorption capacity, and organic matter interactions (Qi et al. 2026). Collectively, these findings demonstrate that organic fertilization not only increases the magnitude of nutrient extraction but also reshapes the hierarchy of nutrient limitations across soils, reinforcing the role of manure in promoting integrated soil–plant functioning and improving the efficiency of nutrient use in tropical Cambisols (Priya et al. 2024).

4.5 Stimulation of Bacteria and Fungi gene abundance and dsDNA content and rhizosphere functioning by organic fertilization

Organic fertilization is an important driver to soil microbial communities into tropical ecosystems (Yan et al. 2024). Our results showed that organic fertilization can significantly enhance bacterial gene abundance, fungal gene abundance, and double-stranded DNA (dsDNA) content in Cambisols by providing a rich source of organic matter that stimulates microbial activity and diversity. The increase in bacterial and fungal gene abundance reflects not only the rise in microbial biomass but also the functional potential of the microbial community to degrade organic matter and cycle nutrients (Luo et al. 2024; Wen et al. 2024). In our study, we may consider that the cow manure introduced a variety of nutrients and organic compounds that serve as substrates for microbial growth (Wen et al. 2024). This organic input favored the proliferation of beneficial bacterial genera like *Pseudomonas*, *Bacillus*, and *Rhizobium*, which are associated with nitrogen fixation and organic matter decomposition (Sagar et al. 2024). Similarly, fungal genera such as *Trichoderma*, *Aspergillus*, and *Penicillium* contribute to phosphorus solubilization and disease suppression, leading to improved plant health (Vurukonda et al. 2024; Jagadesh et al. 2024). The increased microbial activity results in higher gene copy numbers for both bacteria and fungi, reflecting an enhanced microbial biomass and diversity. Additionally, the organic matter from organic fertilization contributes to higher dsDNA content in the soil, as the microbial communities expand and their cellular components accumulate in the soil matrix (Wei et al. 2024; Luo et al. 2024). This accumulation of dsDNA content is a marker of overall microbial biomass and functional potential, indicating a thriving microbial ecosystem that enhances nutrient cycling (Yu et al. 2024). This microbial enrichment improves nutrient cycling, soil health, and overall soil fertility in all studied Cambisols.

4.6 Multivariate integration and reorganization of plant–soil functional pathways under organic fertilization

In the context of a PCA of Cambisols subjected to organic fertilization with cow manure, it was found that 87.75% of the variation in soil chemical properties, maize performance, and soil microbial community was explained by specific factors. For soil chemical properties, soil organic carbon (SOC), available phosphorus (P), and total nitrogen (N) were the key explanatory variables. Maize performance was primarily influenced by shoot dry biomass, root dry biomass, and yield. The soil microbial community's variation was elucidated by the gene abundance of Bacteria and Fungi, as well as dsDNA content. These factors collectively explained the variation observed in the organic fertilization treatment, where pots received an application rate of 30 t ha⁻¹ of cow manure. The interaction between the enriched organic matter from cow manure and the soil resulted in enhanced nutrient availability and microbial activity, which in turn promoted better plant growth and productivity (Priya et al. 2024). This analysis underscores the significant role of plant–soil interactions in driving the observed improvements in soil health and maize performance under organic fertilization in Cambisols (Dhaliwal et al. 2024).

The structural equation modeling highlights a fundamental reorganization of plant–soil functional pathways induced by organic fertilization, shifting the system from a fragmented to a highly integrated mode of functioning. Under organic fertilization, the dominance of positive and reinforcing interactions among the rhizosphere, soil fertility, plant nutrient extraction, and plant performance indicates that manure inputs promoted a coherent coupling between belowground biological processes and aboveground productivity (Carneiro et al. 2019; Dhaliwal et al. 2024; Jagadesh et al. 2024; Sagar et al. 2024). The strong influence of the rhizosphere on soil fertility and plant performance suggests that enhanced microbial activity and root–microbe interactions improved nutrient mobilization and acquisition, thereby strengthening soil–plant feedbacks (Shao et al. 2024). In this context, soil fertility acted as a central integrator linking rhizosphere functioning to plant performance, which in turn emerged as the primary proximal driver of yield, demonstrating that organic fertilization increased the efficiency with which nutrient and biological processes were translated into biomass production and grain yield (Liu et al. 2026). In contrast, the control system exhibited weakened and frequently antagonistic relationships, reflecting a decoupling of biological activity, nutrient dynamics, and plant growth under unfertilized conditions. Negative associations between soil fertility, nutrient extraction, and plant performance suggest that limited nutrient availability imposed physiological

constraints and intensified competition between plant demand and soil supply, reducing the capacity of the system to sustain productive feedback loops (Hu et al. 2025). The minimal influence of plant performance on yield in the control further indicates that, in the absence of organic inputs, improvements in vegetative growth did not effectively translate into reproductive output (Gao et al. 2025). Collectively, these patterns demonstrate that organic fertilization not only increases nutrient availability but restructures the functional architecture of the plant–soil system, promoting synergistic interactions that enhance resource-use efficiency and yield formation in Cambisols.

5 Conclusion

This study evaluated how organic fertilization with cattle manure influenced soil fertility, microbial functioning, and maize performance in Cambisols from distinct Brazilian biomes. Overall, the results suggested that organic fertilization promotes a coordinated improvement in soil–plant functioning, consistent with our initial hypothesis that the addition of organic inputs enhances soil fertility and supports plant growth. Increases in soil organic carbon, available phosphorus, and total nitrogen were associated with improved plant biomass, nutrient extraction, and yield, indicating a tighter coupling between soil resources and plant performance under fertilized conditions. The integration of chemical, biological, and agronomic indicators represents a key contribution of this study, demonstrating that changes in soil fertility are accompanied by shifts in microbial activity and community attributes. Multivariate analyses further indicate that a large proportion of the variability in the system is explained by these interacting components, reinforcing the role of organic matter as a central driver of soil health and plant productivity. These findings contribute to advancing the understanding of how tropical Cambisols respond to organic amendments and highlight the relevance of biologically mediated processes in regulating agroecosystem functioning.

From a practical perspective, the results suggest that the use of cattle manure may represent a viable strategy to improve soil quality and crop performance, potentially reducing reliance on mineral fertilizers and supporting more sustainable agricultural systems. In this context, the study aligns with broader efforts to enhance food security and promote environmentally sound management practices in tropical regions. However, the findings should be interpreted considering some limitations. The study was conducted under controlled greenhouse conditions using a pot experiment, which may not fully capture the complexity and variability of field environments. In addition, the

evaluation was restricted to a specific soil type (Cambisols), which may limit the generalization of the results. Future research should therefore focus on validating these findings under field conditions across a wider range of soils, climates, and management systems. Long-term studies are particularly needed to assess the persistence of the observed effects and their implications for soil carbon dynamics and ecosystem sustainability. Expanding the scope to include different organic inputs, crop species, and microbial functional analyses would also provide a more comprehensive understanding of plant–soil–microbial interactions in tropical agroecosystems.

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Data availability Data sharing is applicable with a formal and justified request for the corresponding author.

Declarations

Competing interests The authors declare no competing interests.

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References

- Agegnehu G, Woldearegay BS, Desta G, Amede T, Mekonnen K, Legesse G, Gashaw T, van Rooyen A, Degefu T, Thorne P (2024) Variation in wheat yield and soil properties at different landscape positions, nutrient sources, and rates in the tropical cereal-based cropping systems of Ethiopia. *Soil Res* 62:e24036. <https://doi.org/10.1071/SR24036>
- Anzuay MS, Viso NP, Ludueña LM et al (2024) Biological inoculants and chemical fertilizers application produce differential effects on rhizobacterial community structure associated to peanut (*Arachis hypogaea* L.) and maize (*Zea mays* L.) plants. *Symbiosis* 92:75–90. <https://doi.org/10.1007/s13199-023-00959-z>
- Barbosa LS, de Souza TAF, Lucena EO et al (2021) Arbuscular mycorrhizal fungi diversity and transpiratory rate in long-term field cover crop systems from tropical ecosystem, northeastern Brazil. *Symbiosis* 85:207–216. <https://doi.org/10.1007/s13199-021-00805-0>
- Barillot CDC, Sarde C-O, Bert V, Tarnaud E, Cochet N (2013) A standardized method for the sampling of rhizosphere and rhizoplane soil bacteria associated to a herbaceous root system. *Ann Microbiol* 63:471–476. <https://doi.org/10.1007/s13213-012-0491-y>
- Barzgar Z, Towfighi H, Fathi-Gerdeldani A, Shahbazi K, Heidari A, Etesami H et al (2025) Molecular determinants of humic and fulvic acids in enhancing micronutrient availability in calcareous soils: a comparative study on Fe, Mn, Zn, and Cu dynamics. *Sci Rep* 15:e34142. <https://doi.org/10.1038/s41598-025-06678-3>
- Benevenuto PAN, Pereira FAC, Barbosa SM, da Silva RF, Silva MA, da Silva GF et al (2025) Deep Tillage improves the rhizosphere environment in rainfed coffee cultivation on dense Cambisols through plant-soil interaction. *Rhizosphere* 34:e101080. <https://doi.org/10.1016/j.rhisph.2025.101080>
- Black CA (1965) Methods of soil analysis, Part 2. In: Black CA (ed) *Agronomy monograph No 9*. American Society of Agronomy, Madison, WI 771–1572. 205
- Bolfe ÉL, Victoria DC, Sano EE, Bayma G, Massruhá SMFS, de Oliveira AF (2024) Potential for agricultural expansion in degraded pasture lands in Brazil based on geospatial databases. *Land* 13:e200. <https://doi.org/10.3390/land13020200>
- Carneiro KAA, Azevedo MC, Fraga VS, Dias BO, Souza TAF et al (2019) Perdas de fósforo por lixiviação em Neossolo Regolítico adubado com esterco bovino curtido em condições semiáridas. *Rev EducAmazônica* 23:261–285
- Chen Z, Zhang S, Li Y, Chi B, Huang W, Wu J (2024) Effects and mechanisms of kitchen waste organic fertilizers application on soil nitrogen transformation, plant pathogenic virulence genes, and metabolites. *Chem Engin J* 496:e154125. <https://doi.org/10.1016/j.cej.2024.154125>
- Da Silva LJR, Souza T, Laurindo LK, Nascimento GS, Lucena EO, Freitas H (2022) Aboveground biomass, carbon sequestration, and yield of *Pyrus pyrifolia* under the management of organic residues in the Subtropical ecosystem of Southern Brazil. *Agronomy* 12:231. <https://doi.org/10.3390/agronomy12020231>
- Daunoras J, Kačergius A, Gudiukaitė R (2024) Role of soil microbiota enzymes in soil health and activity changes depending on climate change and the type of soil ecosystem. *Biology* 13:e85. <https://doi.org/10.3390/biology13020085>
- de Souza TAF, Rodrigues AF, Marques LF (2016a) Long-term effects of alternative and conventional fertilization on macroarthropod community composition: a field study with wheat (*Triticum aestivum* L.) cultivated on a Ferralsol. *Org Agric* 6:323–330. <https://doi.org/10.1007/s13165-015-0138-y>
- Dhaliwal SS, Dubey SK, Kumar D et al (2024) Enhanced organic carbon triggers transformations of macronutrients, micronutrients, and secondary plant nutrients and their dynamics in the soil under different cropping systems-A Review. *J Soil Sci Plant Nutr*. <https://doi.org/10.1007/s42729-024-01907-6>
- Gao X, Zhang J, Mostofa KM, Zheng W, Liu CQ, Senesi N et al (2025) Sulfur-mediated transformation, export and mineral complexation of organic and inorganic C, N, P and Si in dryland soils. *Sci Rep* 15:1–21. <https://doi.org/10.1038/s41598-025-94920-3>

- Głąb T, Gondek K, Mierzwa-Hersztek M (2024) Impact of soil organic bioregeneration amendments on maize biomass and soil physical quality. *Agriculture* 14:e1020. <https://doi.org/10.3390/agriculture14071020>
- González OF, Baquero-Echeverri S, Caicedo-García JP, Loaiza-Usuga JC, Polanía J (2024) Soil quality: an indicator of recovery in a nature reserve in the Colombian Andes. *Agroforest Syst* 98:1153–1166. <https://doi.org/10.1007/s10457-023-00951-y>
- Hemkemeyer M, Pronk GJ, Heister K et al (2014) Artificial soil studies reveal domain-specific preferences of microorganisms for the colonisation of different soil minerals and particle size fractions. *FEMS Microbiol Ecol* 90:770–782. <https://doi.org/10.1111/1574-6941.12436>
- Hu H, Menhas S, Zhu S, Lin D (2025) A review on soil amendments for cadmium sequestration and methane emission reduction in paddy soils. *Crit Rev Environ Sci Technol* 55:1777–1801. <https://doi.org/10.1080/10643389.2025.2572301>
- Jagadeesh M, Dash M, Kumari A, Singh SK, Verma KK, Kumar P, Bhatt R, Sharma SK (2024) Revealing the hidden world of soil microbes: Metagenomic insights into plant, bacteria, and fungi interactions for sustainable agriculture and ecosystem restoration. *Microbiol Res* 285:e127764. <https://doi.org/10.1016/j.micres.2024.127764>
- Jiang M, Dong C, Bian W, Zhang W, Wang Y (2024) Effects of different fertilization practices on maize yield, soil nutrients, soil moisture, and water use efficiency in northern China based on a meta-analysis. *Sci Rep* 14:e6480. <https://doi.org/10.1038/s41598-024-57031-z>
- Joergensen RG, Hemkemeyer M, Beule L et al (2024) A hitchhiker's guide: estimates of microbial biomass and microbial gene abundance in soil. *Biol Fert Soils* 60:457–470. <https://doi.org/10.1007/s00374-024-01810-3>
- Li H, Song X, Wu D, Wei D, Li Y, Ju X (2024) Partial substitution of manure increases N₂O emissions in the alkaline soil but not acidic soils. *J Environ Manage* 359:e120993. <https://doi.org/10.1016/j.jenvman.2024.120993>
- Liu Y, Zhang L, Lou Y et al (2024) Soil organic carbon pools under long-term mineral and organic amendments: a multisite study. *Carbon Res* 3:e29. <https://doi.org/10.1007/s44246-024-00121-4>
- Liu Q, Zhao S, Li Y (2026) Optimized organic-inorganic fertilization enhances soil carbon sequestration and wheat productivity: Evidence from hierarchical carbon pool analysis. *Field Crops Res* 337:e110274. <https://doi.org/10.1016/j.fcr.2025.110274>
- Luo Y, Lopez JBG, van Veelen HPJ et al (2024) Effects of different soil organic amendments (OAs) on extracellular polymeric substances (EPS). *Eur J Soil Biol* 121:e103624. <https://doi.org/10.1016/j.ejsobi.2024.103624>
- Martin KJ, Rygielwicz PT (2005) Fungal-specific PCR primers developed for analysis of the ITS region of environmental DNA extracts. *BMC Microbiol* 5:e28. <https://doi.org/10.1186/1471-2180-5-28>
- Melo LN, Souza TAF, Santos D (2019) Transpiratory rate, biomass production and leaf macronutrient content of different plant species cultivated on a Regosol in the Brazilian semiarid. *Russ Agricult Sci* 45:147–153. <https://doi.org/10.3103/S1068367419020150>
- Nath D, Laik R, Das A, Pramanick B, Peromaiyan P, Singh SK, Kumari V, Jatav SS, Sattar A (2024) Index for refining soil health assessment through multivariate approach under diverse agro-climatic zones in the Indo-Gangetic basin of Bihar. *Sci Total Environ* 943:e173774. <https://doi.org/10.1016/j.scitotenv.2024.173774>
- Nogueira JC, Souza T, Dias TJ, Freire da Silva R, Pereira WE (2026) *Trichoderma asperelloides* enhances watermelon salinity tolerance via integrated morphophysiological and biochemical responses. *J Crop Health* 78:26. <https://doi.org/10.1007/s10343-026-01292-3>
- Nungula EZ, Mugwe J, Massawe BHI, Gitari HI (2024) Morphological, pedological and chemical characterization and classification of soils in Morogoro District, Tanzania. *Agric Res* 13:266–276. <https://doi.org/10.1007/s40003-023-00693-4>
- Okalebo JR, Gathua KW, Woomer PL (1993) Laboratory methods of plant and soil analysis: a working manual (Technical bulletin n. 1). Tropical Soil Biology and Fertility Programme, Nairobi
- Parron LM, Peixoto RTG, da Silva K, Brown GG (2024) Traditional yerba mate agroforestry systems in Araucaria Forest in southern Brazil improve the provisioning of soil ecosystem services. *Conservation* 4:115–138. <https://doi.org/10.3390/conservation4010009>
- Pegoraro RF, Cardoso GR, Sampaio RA, Martins AF, Maia VM, Soares VASF (2024) Pineapple and sorghum litter contribution for nutrient mineralization in a Cambisol. *Commun Soil Sci Plant Anal* 55:1564–1578. <https://doi.org/10.1080/00103624.2024.2321926>
- Priya E, Sarkar S, Maji PK (2024) A review on slow-release fertilizer: Nutrient release mechanism and agricultural sustainability. *J Environ Chem Eng* 12:e113211. <https://doi.org/10.1016/j.jece.2024.113211>
- Prudente Junior AC, Vianna MS, Williams K, Galdos MV, Marin FR (2024) Application of the JULES-crop model and agrometeorological indicators for forecasting off-season maize yield in Brazil. *Heliyon* 10:e29555. <https://doi.org/10.1016/j.heliyon.2024.e29555>
- Qi LI, Hengjie LIU, Linfeng LI, Anwen XIAO, Weifang HU, Fenghua ZHAI et al (2026) Typical mineral additions promote soil mineral-associated organic carbon sequestration: Interactions between Fe oxides and microbial-derived peptides. *Pedosphere*. <https://doi.org/10.1016/j.pedsph.2026.01.011>
- Rehman A, Hua J, Pinzon S, Mirabela FIM, Loredana C, Milin IA (2024) Fertilizer use and agricultural practices in the paradox of maize crop production and environmental sustainability. *Heliyon*. <https://doi.org/10.1016/j.heliyon.2024.e34743>
- Rodrigues AF, de Souza TAF, Marques LF et al (2016) Agricultural management practices: Effects on soil properties, root growth and sesame yield. *Russ Agricult Sci* 42:321–327. <https://doi.org/10.3103/S1068367416050165>
- Rummel PS, Beule L, Hemkemeyer M, Schwalb SA, Wichern F (2021) Black soldier fly diet impacts soil greenhouse gas emissions from frass applied as fertilizer. *Front Sustain Food Syst* 5:709993. <https://doi.org/10.3389/fsufs.2021.709993>
- Sagar S, Singh A, Bala J, Chauhan R, Kumar R, Bhatia RK, Walia A (2024) Insights into cow dung-based bioformulations for sustainable plant health and disease management in organic and natural farming system: a review. *J Soil Sci Plant Nut* 24:30–53. <https://doi.org/10.1007/s42729-023-01558-z>
- Shao G, Xu Y, Zhou J, Tian P, Ai J, Yang Y, Zamanian K, Zeng Z, Zang H (2024) Enhanced soil organic carbon stability in rhizosphere through manure application. *Soil Till Res* 244:e106223. <https://doi.org/10.1016/j.still.2024.106223>
- Sikiru S, Abioye KJ, Adedayo HB, Adebukola SY, Soleimani H, Anar M (2024) Technology projection in biofuel production using agricultural waste materials as a source of energy sustainability: A comprehensive review. *Renew Sustain Energy Rev* 200:e114535. <https://doi.org/10.1016/j.rser.2024.114535>
- Singh K, Singh R, Nwosu NJ, Omara P, Sharma L, Dunn BL, Singh H (2025) Optimizing nutrient delivery in agronomic crops: a review of enhanced efficiency fertilizers. *J Plant Nut Soil Sci* 4:570–584. <https://doi.org/10.1002/jpln.12010>
- Soares AKM, Crestana S, Ferreira RRM, Rodrigues VGS (2024) Assessment of the impact of conservation measures by modeling soil loss in Minas Gerais, Brazil. *Environ Monit Assess* 196:e358. <https://doi.org/10.1007/s10661-024-12509-1>

- Souza TAF, Rodrigues AF, Marques LF (2016b) Long-term effects of alternative and conventional fertilization II: Effects on *Triticum aestivum* L. development and soil properties from a Brazilian Ferralsols. *Russ Agric Sci* 42:11–16. <https://doi.org/10.3103/S1068367416010195>
- Souza TAF, Rodrigues AF, Marques LF (2017) The trend of soil chemical properties, and rapeseed productivity under different long-term fertilizations and stubble management in a Ferralsols of Northeastern Brazil. *Org Agr* 7:353–363. <https://doi.org/10.1007/s13165-016-0164-4>
- Souza T, Nascimento GDS, Batista DS, Silva AMO, Campos MCC (2025) The role of forest conversion and agroecological practices in enhancing ecosystem services in Tropical Oxisols of the Amazon basin. *Forests* 16:e740. <https://doi.org/10.3390/f16050740>
- Vurukonda SSKP, Fotopoulos V, Saeid A (2024) Production of a rich fertilizer base for plants from waste organic residues by microbial formulation technology. *Microorganisms* 12:e541. <https://doi.org/10.3390/microorganisms12030541>
- Wei X, Xie B, Wan C, Song R, Zhong W, Xin S, Song K (2024) Enhancing soil health and plant growth through microbial fertilizers: mechanisms, benefits, and sustainable agricultural practices. *Agronomy* 14:e609. <https://doi.org/10.3390/agronomy14030609>
- Wen X, Qin X, Long X-E, Li Q (2024) Microbial necromass facilitated the humification process through amino sugar reactions during the co-composting of cow manure plus sawdust. *Environ Sci Poll Res*. <https://doi.org/10.1007/s11356-024-34381-9>
- WRB - IUSS Working Group WRB (2022) World Reference Base for Soil Resources. International soil classification system for naming soils and creating legends for soil maps, 4th edition, International Union of Soil Sciences (IUSS), publishing company: Austria
- Xu K, Zhang QQ, Cai YY, Luo XJ, Zhai YQ, Liu WR, Ying GG (2026) Diagnosing spatial decoupling of manure and crop nutrients in China: drivers and multi-objective optimization for sustainable redistribution. *Sustainable Agric* 4:e11. <https://doi.org/10.1038/s44264-025-00120-x>
- Yan H, Wu Y, He G, Wen S, Yang L, Ji L (2024) Fertilization regime changes rhizosphere microbial community assembly and interaction in *Phoebe bournei* plantations. *Appl Microbiol Biotechnol* 108:e417. <https://doi.org/10.1007/s00253-024-13106-5>
- Yu Y, Lee C, Kim J, Hwang S (2005) Group-specific primer and probe sets to detect methanogenic communities using quantitative real-time polymerase chain reaction. *Biotechnol Bioengin* 89:670–679. <https://doi.org/10.1002/bit.20347>
- Yu Y, Zhang Q, Kang J, Xu N, Zhang Z, Deng Y, Gillings M, Lu T, Qian H (2024) Effects of organic fertilizers on plant growth and the rhizosphere microbiome. *Appl Environ Microbiol* 90:e01719–e01723. <https://doi.org/10.1128/aem.01719-23>
- Zapałowska A, Jarecki W (2024) The impact of using different types of compost on the growth and yield of corn. *sustainability* 16:e511. <https://doi.org/10.3390/su16020511>
- Zhou S, Chang T, Zhang Y, Shaghaleh H, Zhang J, Yang X, Qin H, Talpur MMA, Hamoud YA (2024) Organic fertilizer compost alters the microbial composition and network structure in strongly acidic soil. *Appl Soil Ecol* 195:e105263. <https://doi.org/10.1016/j.apsoil.2023.105263>

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