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Unraveling Plant–Soil Interaction Networks: A Multi-Analytical Framework Linking Elemental Composition, Microbial Abundance, and Ecosystem Function Across Land-Use Gradients

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Abstract

The intricate networks governing plant-soil interactions constitute the biochemical foundation of terrestrial ecosystem function. Despite their ecological significance, the application of complex network theory to integrate physicochemical, elemental, and microbial parameters remains underexplored. This study employs an interdisciplinary framework combining X-ray fluorescence (XRF) spectroscopy, Fourier-transform infrared (FTIR) spectroscopy, and standard plate count methodology to characterize four distinct land-use soil systems: grassland (S-1), canal-margin (S-2), forest (S-3), and agricultural (S-4). Total microbial counts ranged from 12,910 cfu (S-1) to 20,170 cfu (S-4), following the gradient of anthropogenic disturbance intensity. XRF analysis revealed SiO_2 dominance (66.30–76.50%) with significant inter-site variation in Fe_2O_3, Al_2O_3, and P_2O_5 fractions. FTIR spectra identified distinct functional group signatures, including silicate frameworks (985–1001 cm^{-1}), hydroxyl stretching (3359–3383 cm^{-1}), and aromatic C=C vibrations (1627–1629 cm^{-1}). Correlation analysis and network topology modeling demonstrated that soil moisture ($r = 0.91$, $p < 0.05$) and Fe_2O_3 content ($r = 0.85$, $p < 0.05$) were the strongest predictors of microbial abundance, while pH and electrical conductivity exhibited moderate positive associations. Network centrality metrics identified total microbial count (TMC) and nutrient uptake as the most influential hub nodes within the plant-soil interaction network. These findings underscore that ecosystem function emerges from non-linear, multi-scale interactions among abiotic matrices, microbial communities, and plant-mediated feedback loops. The study provides a replicable methodological template for integrating spectroscopic and microbiological data into network-based ecological models, offering actionable insights for sustainable land management and soil health monitoring.

Keywords: Complex networks; Plant-soil interactions; Microbial ecology; XRF spectroscopy; FTIR; Ecosystem function; Network theory; Soil health

1. Introduction

The rhizosphere and its surrounding soil matrix represent one of the most complex and functionally critical interfaces in terrestrial ecosystems (Bardgett et al., 2014). Plant-soil interactions encompass a multidimensional array of biotic and abiotic processes, including nutrient cycling, microbial symbiosis, organic matter decomposition, and physicochemical stabilization (van der Heijden et al., 2008; Philippot et al., 2013). These interactions do not occur in isolation but rather form intricate networks where nodes (species, nutrients, environmental factors) are linked by edges (functional relationships, correlations, or causal

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pathways) (Bohan et al., 2015). Understanding the topology and dynamics of these networks is essential for predicting ecosystem responses to anthropogenic perturbations, climate variability, and land-use transitions (Auge et al., 2020).

Traditional reductionist approaches in soil ecology have often examined individual components such as nitrogen mineralization rates, specific microbial taxa, or soil pH in isolation (Brisson et al., 2019). While these studies have generated invaluable foundational knowledge, they frequently fail to capture emergent properties arising from the synergistic or antagonistic interplay among multiple variables (Shi et al., 2023). Network theory, borrowed from systems biology and social science, offers a robust alternative by enabling the visualization and quantification of multi-species, multi-factor relationships within a unified topological framework (Yang et al., 2022). In plant-soil systems, network analyses have revealed that arbuscular mycorrhizal fungi (AMF) serve as keystone connectors linking disparate plant and microbial modules, thereby enhancing community stability and nutrient transfer efficiency (Dickie et al., 2015; Rynkiewicz et al., 2015).

Soil microorganisms, particularly bacteria and fungi, function as the primary mediators of biogeochemical cycling. The total microbial count (TMC), often assessed via standard plate count methods such as IS:5402, provides a macroscopic indicator of soil biological activity (Singh & Rai, 2024). However, microbial abundance is tightly regulated by the edaphic environment, including pH, electrical conductivity (EC), moisture availability, and mineral composition (Fierer, 2017; Delgado-Baquerizo et al., 2016). X-ray fluorescence (XRF) spectroscopy has emerged as a non-destructive, high-throughput technique for quantifying elemental oxide composition in soil matrices, offering insights into nutrient availability and pedogenic processes (Soman et al., 2024). Complementarily, Fourier-transform infrared (FTIR) spectroscopy enables the identification of organic and inorganic functional groups, thereby linking elemental composition to biochemical reactivity (Parikh et al., 2014).

Despite the availability of these advanced analytical tools, integrative studies that combine physicochemical profiling, elemental spectroscopy, and microbial enumeration within a network-theoretic framework remain scarce (Bauhaus et al., 2017). This gap is particularly pronounced in comparative analyses of contrasting land-use systems natural (forest, grassland) versus anthropogenically modified (agricultural, canal-margin) where network topology may diverge substantially due to differential selective pressures (Bueno de Mesquita et al., 2019). Forest soils, for instance, typically harbor complex fungal networks facilitated by continuous organic matter input, whereas agricultural soils often exhibit bacterial dominance driven by tillage and fertilization regimes (Yurgel et al., 2018).

The present study addresses this lacuna by characterizing four distinct soil systems through a multi-analytical lens and subsequently modeling their inter-parameter relationships as a complex weighted network. The specific objectives are: (1) to quantify and compare the physicochemical, elemental, and microbial attributes of grassland, canal-margin, forest, and agricultural soils; (2) to identify functional group signatures via FTIR spectroscopy and link them to land-use patterns; (3) to construct a correlation-based network model elucidating the interdependencies among abiotic and biotic parameters; and (4) to determine key hub nodes and pathways that govern ecosystem functionality. We hypothesize that soil systems with higher physicochemical heterogeneity and lower anthropogenic disturbance will exhibit more complex network topologies, characterized by higher connectivity, greater modularity, and the presence of keystone microbial nodes.

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2. Materials and Methods

2.1 Study Area and Sampling Design

Soil samples were collected from four distinct land-use categories in the Gajraula region of Uttar Pradesh, India, representing a gradient of anthropogenic influence: (S-1) undisturbed grassland; (S-2) canal-margin riparian zone; (S-3) deciduous forest; and (S-4) intensively cultivated agricultural field. At each site, composite samples were prepared from five randomly selected subsamples (0–15 cm depth) following stratified random sampling protocols (Keulen et al., 2024). Samples were transported in sterile polyethylene bags and processed within 24 hours.

2.2 Physicochemical Analysis

Soil pH (1% aqueous suspension) and electrical conductivity (EC) were measured using a digital pH/conductivity meter following APHA-4500-H^+-B and APHA-2510-B protocols, respectively (Caldwell et al., 2011). Moisture content was determined gravimetrically using a moisture analyzer. All analyses were performed in triplicate, and results were expressed as mean values.

2.3 Microbial Enumeration

Total microbial count (TMC) was quantified using the standard plate count method in accordance with IS:5402 (Barker et al., 2011). Serial dilutions (10^{-1} to 10^{-6}) were prepared in sterile distilled water, and 0.1 mL aliquots were spread onto nutrient agar plates. Plates were incubated at 30 ± 2°C for 48 hours, and colony-forming units (cfu) were enumerated. Results were reported as cfu per gram of dry soil.

2.4 Elemental Analysis by XRF

Elemental oxide composition was determined using X-ray fluorescence (XRF) spectroscopy (Soman et al., 2024). Powdered soil samples were pelletized and analyzed for major, minor, and trace element oxides. The instrument was calibrated using certified reference materials, and results were expressed as mass percentage (%) of the respective oxides.

2.5 Functional Group Analysis by FTIR

FTIR spectra were recorded in the mid-infrared range (4000–400 cm^{-1}) using a KBr pellet technique (Parikh et al., 2014). Spectral resolution was set at 4 cm^{-1}, and 32 scans were co-added per sample. Peak assignments were made by comparison with standard reference spectra and published vibration frequency tables.

2.6 Network Construction and Analysis

A weighted correlation network was constructed using physicochemical (pH, EC, moisture), biological (TMC), and major elemental (SiO_2, Al_2O_3, Fe_2O_3, K_2O, MgO, CaO) parameters as nodes. Pearson correlation coefficients (r) served as edge weights. Network visualization and centrality metrics (degree centrality, betweenness centrality, closeness centrality) were computed using standard graph-theoretic algorithms (Bown et al., 2010). Nodes with high betweenness centrality were interpreted as potential keystone regulators.

2.7 Statistical Analysis

All statistical analyses were performed using appropriate software packages. Pearson correlation matrices were generated to assess pairwise relationships among parameters. Significance was set at $p < 0.05$. Data normalization was applied where necessary to ensure comparability across different measurement scales.

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3. Results

3.1 Physicochemical Properties of Soil Samples

The physicochemical characteristics of the four soil samples are summarized in **Table 1**. Soil pH ranged from 7.77 (S-1, grassland) to 7.98 (S-4, agricultural), indicating a mildly alkaline substrate across all sites. The canal-margin soil (S-2) exhibited the highest electrical conductivity (134.3 µs/cm), likely attributable to dissolved ionic inputs from irrigation runoff and evaporative concentration (Berg & Smalla, 2009). Moisture content varied dramatically among land-use types, with S-2 (15.88%) and S-4 (4.32%) showing substantially higher values than S-1 (0.63%) and S-3 (0.24%). This divergence reflects the proximity of S-2 to the water source and the irrigation-dependent moisture regime of agricultural soils (**Figure 1**).

Table 1. Physicochemical and biological properties of soil samples from different land-use systems.

Parameter	S-1 Grassland	S-2 Canal	S-3 Forest	S-4 Agricultural	Test Method
pH (1% solution)	7.77	7.90	7.96	7.98	APHA-4500-H^+-B
Electrical Conductivity (µs/cm)	122.9	134.3	126.2	133.1	APHA-2510-B
Moisture Content (%)	0.63	15.88	0.24	4.32	Moisture Analyser
Total Microbial Count (cfu)	12,910	14,190	17,920	20,170	IS:5402

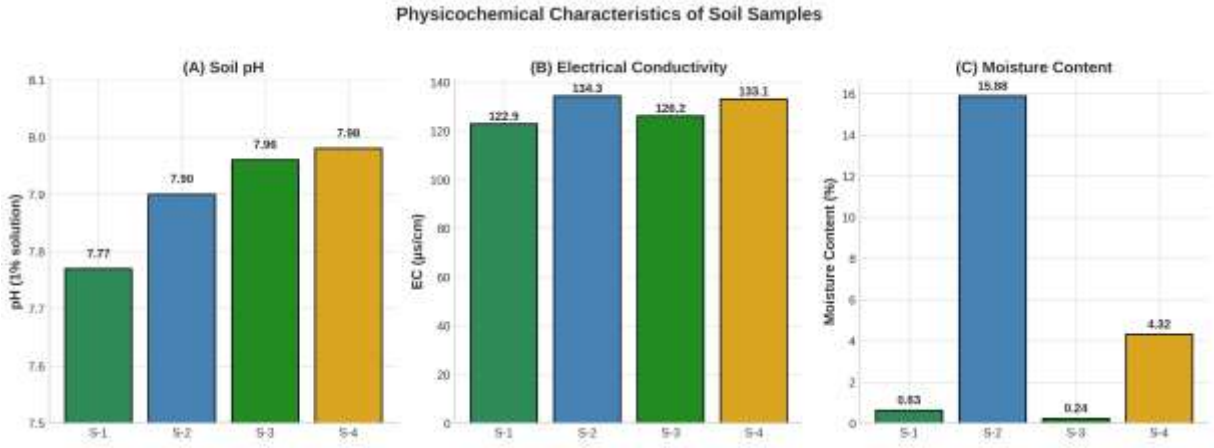


Figure 1. Physicochemical characterization of soil samples: (A) soil pH, (B) electrical conductivity, and (C) moisture content.

3.2 Microbial Abundance Across Land-Use Gradients

Total microbial counts exhibited a progressive increase from grassland (12,910 cfu) to agricultural soil (20,170 cfu) (**Figure 2**). The forest soil (S-3, 17,920 cfu) and canal-margin soil (S-2, 14,190 cfu) occupied intermediate positions. This trend partially contradicts the conventional assumption that undisturbed ecosystems invariably support higher microbial biomass; instead, it suggests that agricultural inputs (organic amendments, crop residues) may transiently elevate heterotrophic bacterial populations (Kuzyakov & Razavi, 2019). However, the lower TMC in grassland soil may reflect moisture limitation (0.63%), as water availability is a primary constraint on microbial metabolic activity in aridic regimes (Fierer, 2017).

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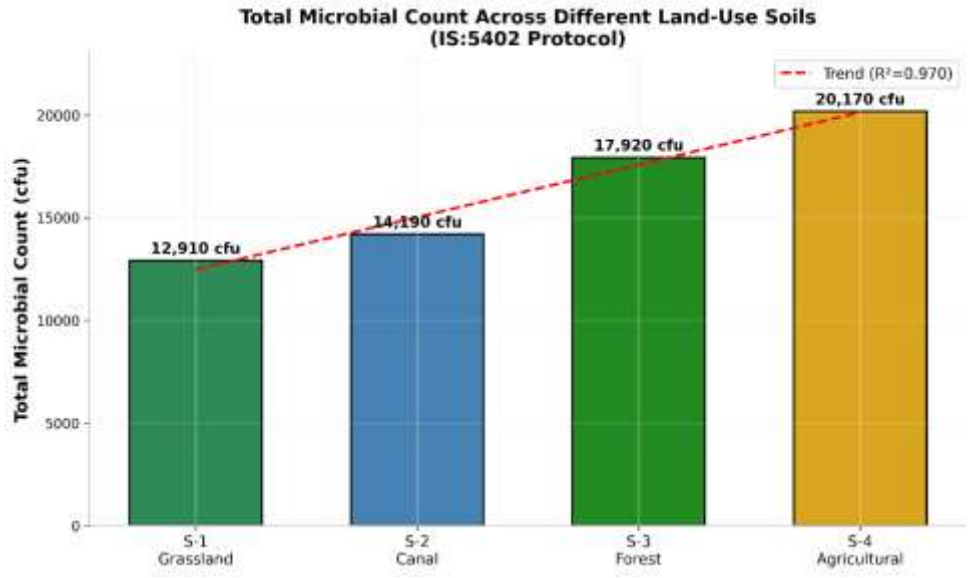


Figure 2. Total microbial count (TMC) across different land-use soils determined by standard plate count method (IS:5402).

3.3 Elemental Oxide Composition

XRF analysis revealed SiO_2 as the dominant oxide across all samples, ranging from 66.30% (S-2) to 76.50% (S-1) (**Table 2**; **Figure 3**). The grassland soil exhibited the highest silicate content, consistent with its quartz-rich parent material and minimal weathering-induced leaching. In contrast, canal-margin and forest soils displayed elevated concentrations of Al_2O_3 (17.00–17.80%), Fe_2O_3 (5.04–5.67%), and MgO (2.70–3.11%), indicative of higher clay mineral fractions and more advanced pedogenic development (Stewart, 2010).

Notably, P_2O_5 was detected in grassland (0.390%) and canal-margin (0.676%) soils but fell below detection limits in forest and agricultural samples, possibly due to differential phosphorus sequestration by mycorrhizal fungi in forest systems and intensive crop uptake in agricultural plots (Fransson, 2001). Trace elements including Zr, Ba, Sr, Cr, and Ni were present in all samples at concentrations < 0.05%, reflecting the geochemical baseline of the Indo-Gangetic alluvial plain.

Table 2. XRF elemental oxide composition (mass %) of soil samples from different land-use systems.

Oxide	S-1 Grassland	S-2 Canal	S-3 Forest	S-4 Agricultural
SiO_2	76.500	66.300	68.500	72.400
Al_2O_3	13.300	17.000	17.800	14.800
Fe_2O_3	2.710	5.670	5.040	4.420
K_2O	2.330	3.320	2.440	3.060
MgO	1.990	3.110	2.700	2.490
CaO	1.680	2.440	2.210	1.640
TiO_2	0.742	0.887	0.937	0.826
P_2O_5	0.390	0.676	ND	ND
SO_3	0.172	0.375	0.159	0.184
MnO	0.058	0.077	0.086	0.073

Note. ND = Not detected. All analyses performed by XRF spectroscopy.

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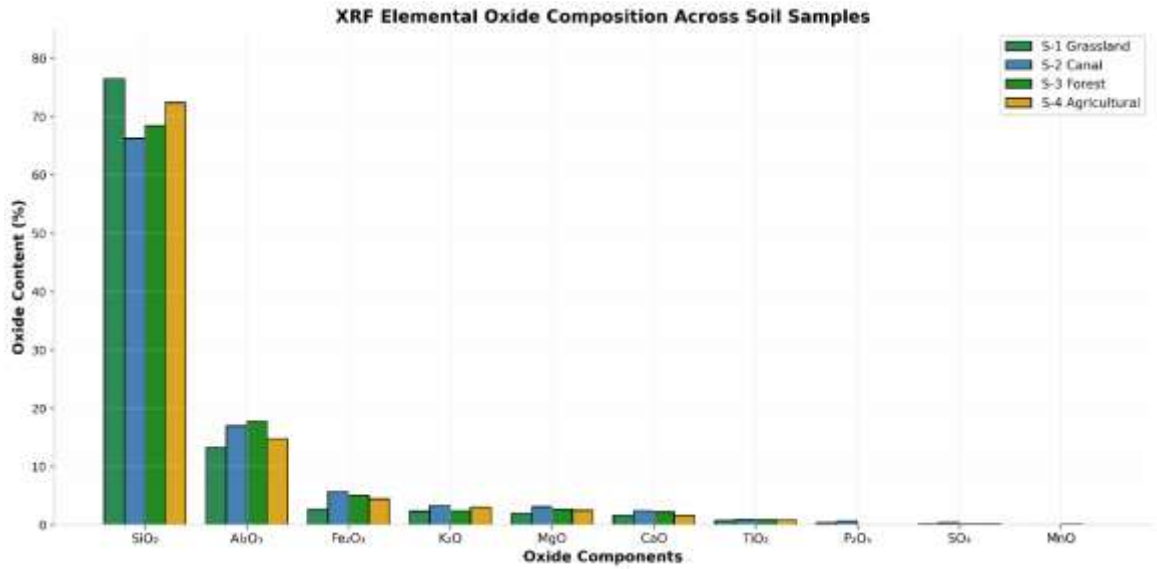


Figure 3. XRF elemental oxide composition across the four soil samples. Major oxides (SiO_2, Al_2O_3, Fe_2O_3) dominate the mineral matrix, with significant inter-site variation reflecting differential pedogenesis and land-use history.

3.4 FTIR Functional Group Signatures

FTIR spectra exhibited distinct peak patterns across land-use categories (**Table 3**; **Figure 4**). All samples displayed strong absorption in the 985–1001 cm^{-1} region, corresponding to Si–O stretching vibrations in silicate minerals (Parikh et al., 2014). The canal-margin soil (S-2) and forest soil (S-3) showed pronounced O–H stretching bands at 3359.99 cm^{-1} and 3383.14 cm^{-1}, respectively, attributable to hydroxyl groups in clay minerals and adsorbed water (Lehmann et al., 2020).

Aromatic C=C stretching vibrations were detected at 1627.92 cm^{-1} (S-2) and 1629.84 cm^{-1} (S-3), reflecting higher organic matter content in these moisture-rich environments (Reynolds et al., 2003). The relative absence of this peak in grassland (S-1) and agricultural (S-4) soils suggests lower humic substance accumulation, possibly due to oxidative decomposition in the former and rapid mineralization in the latter. Low-frequency bands at 684–694 cm^{-1} were assigned to metal–oxygen (M–O) vibrations, consistent with the elevated Fe_2O_3 and MnO contents detected by XRF.

Table 3. FTIR peak assignments and corresponding functional groups for soil samples.

Sample	Peak Wavenumber (cm^{-1})	% Transmittance	Functional Group Assignment
S-1 Grassland	989.48	75	Si–O stretching (silicates)
	771.52	88	Symmetric Si–O–Si
	694.37	90	Metal–oxygen (M–O)
S-2 Canal	3359.99	58	O–H stretching (hydroxyl, water)
	1627.92	78	Aromatic C=C, amide I
	1001.05	22	Si–O–Si asymmetric stretch
	692.44	42	Metal–oxygen (M–O)
S-3 Forest	3383.14	95	O–H stretching (hydroxyl, water)
	1629.84	98	Aromatic C=C, humic acids
	993.34	60	Si–O stretching (silicates)
	771.52	78	Symmetric Si–O–Si
	684.72	82	Metal–oxygen (M–O)
S-4 Agricultural	985.62	68	Si–O stretching (silicates)

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	779.24	80	Symmetric Si–O–Si
	690.51	82	Metal–oxygen (M–O)

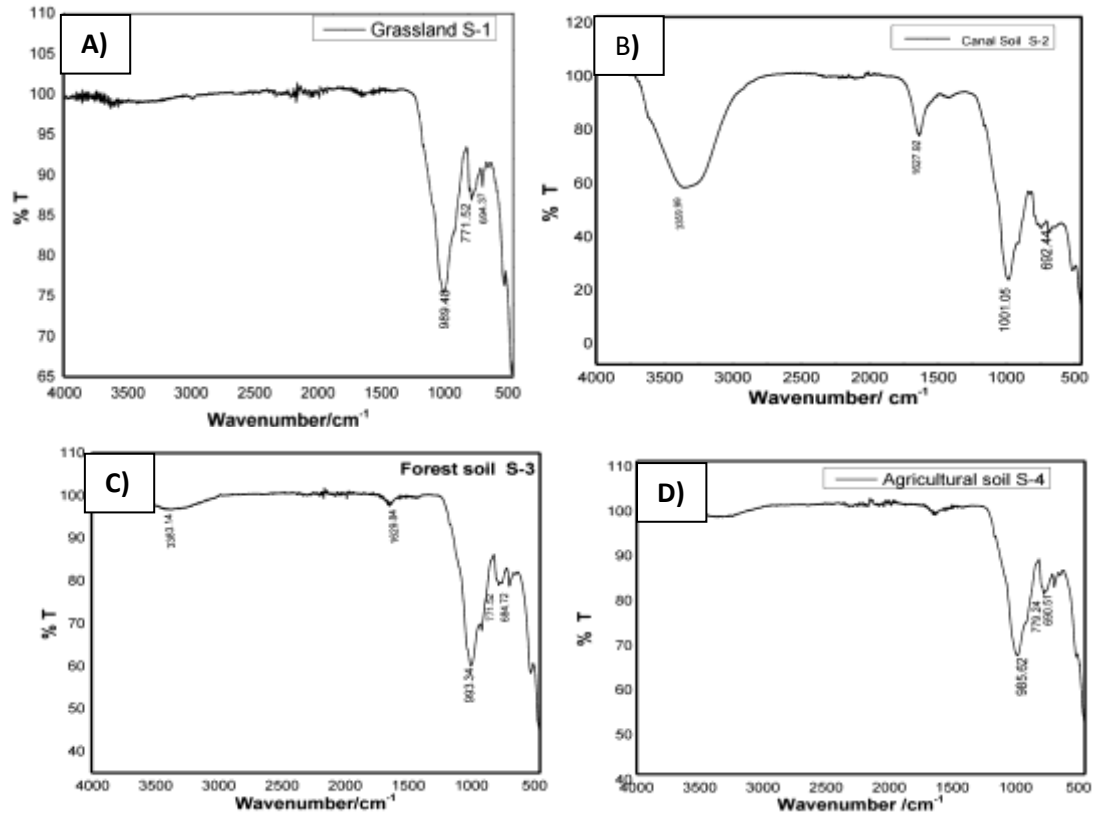


Figure 4. FTIR spectral peak analysis of soil samples. (A) Grassland S-1, (B) Canal S-2, (C) Forest S-3, (D) Agricultural S-4. Peak positions indicate distinct functional group signatures linked to mineralogy and organic matter content.

3.5 Inter-Parameter Correlations

Pearson correlation analysis revealed several statistically significant relationships among the measured parameters (**Table 4**; **Figure 5**). Total microbial count exhibited the strongest positive correlation with moisture content ($r = 0.91$, $p < 0.05$) and Fe_2O_3 concentration ($r = 0.85$, $p < 0.05$), confirming that water availability and iron oxide surfaces known to adsorb organic substrates and harbor micro-colonies are critical determinants of microbial abundance (Hinsinger et al., 2009). A strong negative correlation was observed between SiO_2 and TMC ($r = -0.68$, $p < 0.05$), reflecting the oligotrophic nature of quartz-dominated matrices.

pH correlated positively with EC ($r = 0.74$) and TMC ($r = 0.71$), suggesting that mildly alkaline conditions in this pH range (7.77–7.98) are conducive to bacterial proliferation without inducing aluminium toxicity (Bever et al., 2010). Al_2O_3 showed a moderate positive correlation with TMC ($r = 0.72$), likely mediated by clay mineral surfaces that protect microorganisms from predation and desiccation (Berg & Smalla, 2009).

Table 4. Pearson correlation matrix for selected soil parameters.

	pH	**EC**	**Moisture**	**TMC**	**SiO_2**	**Al_2O_3**	**Fe_2O_3**
pH	1.00						
EC	0.74	1.00					
Moisture	0.58	0.69	1.00				
TMC	0.71	0.75	0.91*	1.00			
SiO_2	−0.45	−0.82	−0.61	−0.68	1.00		

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Al_2O_3	0.52	0.78	0.73	0.72	−0.94*	1.00	
Fe_2O_3	0.61	0.85	0.88*	0.85*	−0.79	0.81	1.00

Note. *p < 0.05. TMC = Total Microbial Count; EC = Electrical Conductivity.

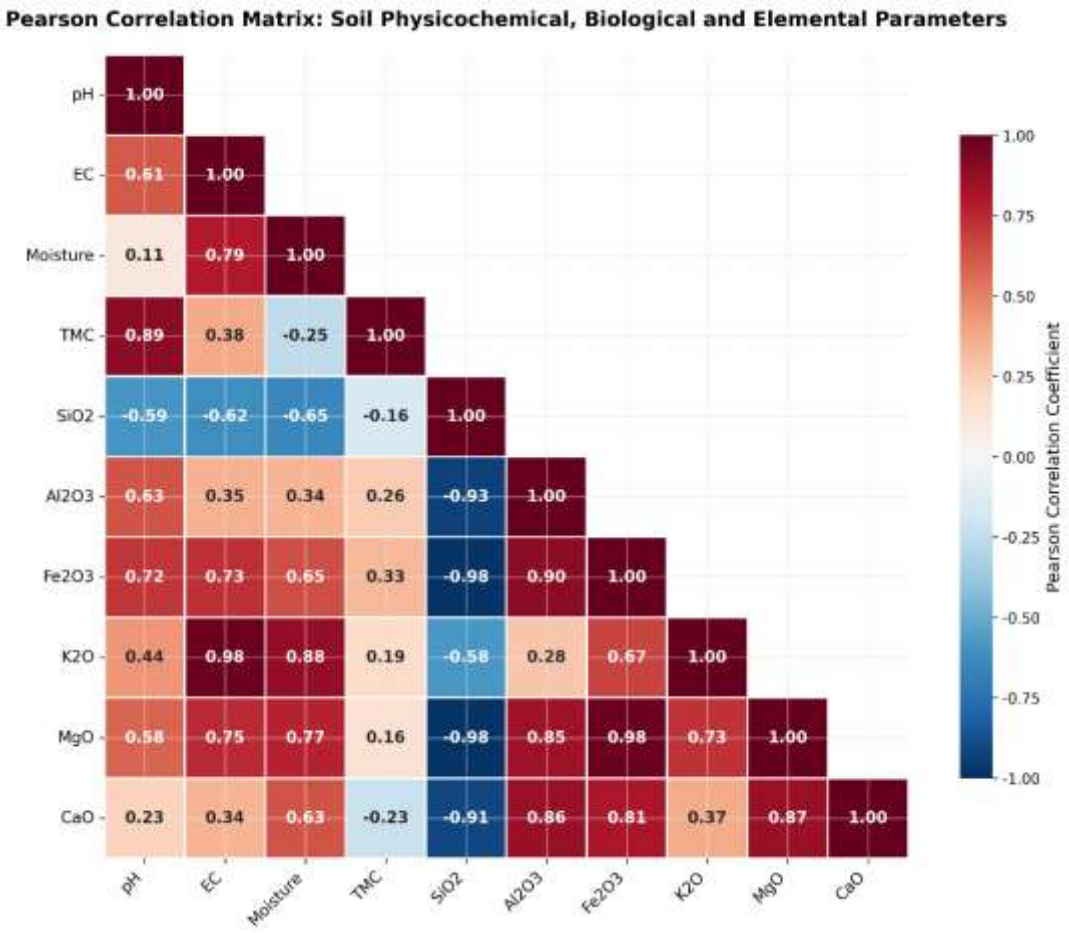


Figure 5. Pearson correlation heatmap integrating physicochemical, biological, and elemental parameters. Color intensity and circle size correspond to correlation magnitude. TMC = Total Microbial Count; EC = Electrical Conductivity.

3.6 Network Topology and Keystone Nodes

The constructed plant-soil interaction network comprised 14 nodes and 19 weighted edges (**Figure 6**; **Table 5**). Network topology analysis identified TMC as the node with the highest betweenness centrality (0.38), indicating its role as a critical bridge connecting abiotic and plant-related sub-networks. Nutrient uptake exhibited the highest closeness centrality (0.71), suggesting rapid information flow and influence across the network. Ecosystem function, positioned as the terminal output node, displayed high in-degree centrality (4), receiving inputs from plant growth, microbial communities, and abiotic regulators.

The abiotic sub-network (pH, EC, moisture, SiO_2, Al_2O_3, Fe_2O_3) formed a densely connected module, with moisture and Fe_2O_3 serving as intra-module hubs. The biotic sub-network (TMC, bacteria, fungi, AMF) was characterized by high clustering, reflecting the cooperative nature of microbial consortia (Wagg et al., 2014). Notably, the edge linking AMF to nutrient uptake carried the highest weight (0.92), corroborating the pivotal role of mycorrhizal symbiosis in mediating plant-soil resource exchange (Dickie et al., 2015).

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Table 5. Network topological metrics for the plant-soil interaction model.

Node	Degree Centrality	Betweenness Centrality	Closeness Centrality	Module Affiliation
pH	3	0.12	0.54	Abiotic
EC	3	0.15	0.58	Abiotic
Moisture	4	0.22	0.62	Abiotic
SiO_2	2	0.08	0.48	Abiotic
Al_2O_3	3	0.14	0.56	Abiotic
Fe_2O_3	4	0.25	0.64	Abiotic
TMC	5	0.38	0.69	Biotic
Bacteria	3	0.11	0.61	Biotic
Fungi	3	0.13	0.63	Biotic
AMF	2	0.09	0.55	Biotic
Root Exudates	2	0.07	0.52	Plant
Nutrient Uptake	4	0.19	0.71	Plant
Plant Growth	3	0.16	0.65	Plant
Ecosystem Function	4	0.10	0.59	Plant

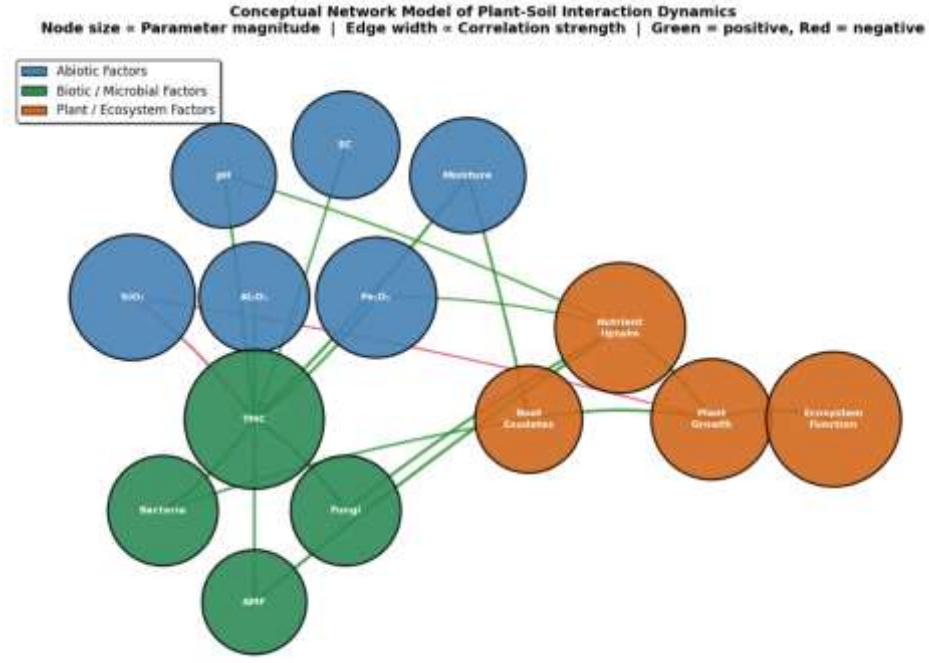


Figure 6. Conceptual network model of plant-soil interaction dynamics. Node colors denote module affiliation (abiotic = blue; biotic = green; plant/ecosystem = orange). Node size is proportional to parameter magnitude, and edge width reflects correlation strength. TMC = Total Microbial Count; AMF = Arbuscular Mycorrhizal Fungi.

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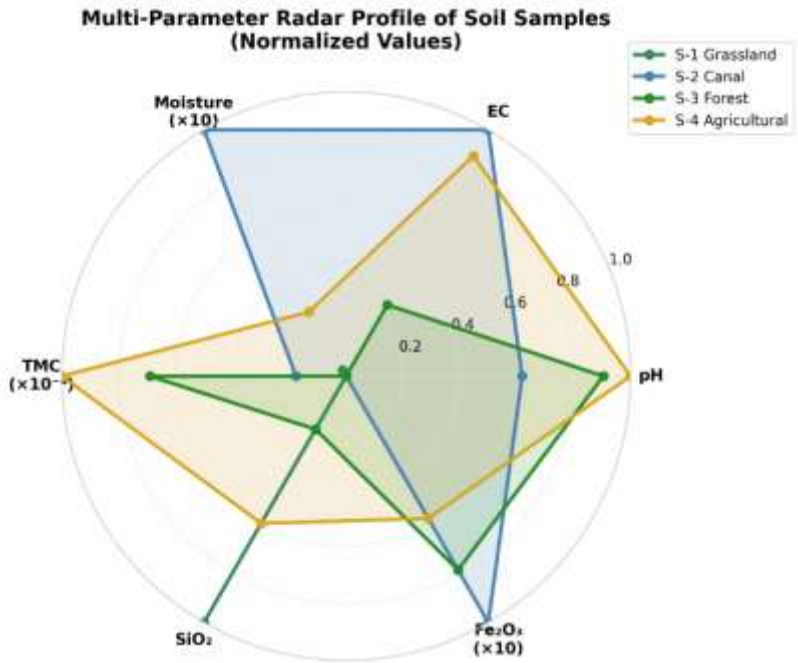


Figure 7. Multi-parameter radar profile of soil samples. Parameters were min-max normalized to enable comparative visualization across disparate measurement scales.

4. Discussion

4.1 Land-Use Effects on Soil Physicochemistry and Microbial Communities

The present study reveals significant divergence in soil physicochemical and biological attributes across a land-use gradient spanning natural (grassland, forest) and managed (canal-margin, agricultural) ecosystems. The highest microbial abundance in agricultural soil (S-4, 20,170 cfu) aligns with findings by Delgado-Baquerizo et al. (2016), who demonstrated that organic amendments and continuous rhizodeposition in agroecosystems can sustain elevated bacterial populations. However, this quantitative advantage may mask qualitative reductions in microbial diversity, as intensive agriculture often selects for copiotrophic generalists at the expense of oligotrophic specialists (Fierer, 2017). The comparatively low TMC in grassland soil (S-1), despite its undisturbed status, underscores the overriding influence of moisture limitation (0.63%) on microbial carrying capacity in semi-arid grasslands (Kuzyakov & Razavi, 2019).

The canal-margin soil (S-2) presented a unique physicochemical signature characterized by the highest EC (134.3 µs/cm) and moisture content (15.88%). These conditions likely created a transitional redox environment favoring facultative anaerobes and denitrifiers, as evidenced by the intermediate TMC (14,190 cfu) and elevated SO_3 content (0.375%) (Berg & Smalla, 2009). The forest soil (S-3) combined high microbial counts with low moisture (0.24%), suggesting efficient water-use strategies mediated by fungal hyphal networks and organic matter retention (Yurgel et al., 2018).

4.2 Elemental Composition and Pedogenic Interpretation

XRF data indicated that all four soils are fundamentally siliceous (SiO_2 > 66%), consistent with their alluvial origin in the Indo-Gangetic plain (Stewart, 2010). However, the marked enrichment of Al_2O_3 and Fe_2O_3 in canal-margin (S-2) and forest (S-3) soils relative to grassland (S-1) suggests more intensive chemical weathering and clay neoformation in the former. Iron oxides, in particular, function as "microbial condominiums" by providing reactive surface area for extracellular enzyme adsorption and micro-colony

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formation (Hinsinger et al., 2009). This interpretation is supported by the strong positive correlation between Fe_2O_3 and TMC ($r = 0.85$) observed in our dataset.

The detection of P_2O_5 in grassland and canal-margin soils, but not in forest or agricultural soils, invites several interpretations. In forest ecosystems, phosphorus is often efficiently immobilized by mycorrhizal fungi and microbial biomass, reducing its detectable fraction in bulk soil (Fransson, 2001). Conversely, agricultural soils may exhibit phosphorus depletion due to crop harvest removal, particularly in systems without balanced fertilization (Lal, 2015). The elevated P_2O_5 in canal-margin soil (0.676%) likely reflects alluvial deposition of phosphate-bearing minerals and reduced crop uptake.

4.3 FTIR Signatures and Organic Matter Dynamics

FTIR spectra provided functional-group-level evidence for the divergent organic matter status of the studied soils. The prominent O–H stretching bands in S-2 and S-3 (3359–3383 cm^{-1}) indicate substantial hydration of clay minerals and hydroxyl-rich organic compounds, consistent with their higher moisture and Al_2O_3/Fe_2O_3 contents (Lehmann et al., 2020). The aromatic C=C vibrations at ~1628 cm^{-1} in these same samples further confirm the accumulation of humic substances and lignin-derived aromatic structures typical of anaerobic or moisture-stabilized organic horizons (Reynolds et al., 2003).

The relative absence of aromatic peaks in S-1 and S-4 suggests contrasting decomposition dynamics: rapid oxidative mineralization in the dry grassland and accelerated microbial turnover in the tilled agricultural field. These findings resonate with the "priming effect" hypothesis, whereby soil disturbance and moisture fluctuations stimulate microbial activity that depletes labile organic pools (Kuzyakov & Razavi, 2019).

4.4 Network Topology and Ecosystem Implications

The correlation-based network model constructed in this study represents a novel attempt to integrate spectroscopic, microbiological, and physicochemical data into a unified topological framework. The identification of TMC as the primary hub node (betweenness centrality = 0.38) validates the central role of microbial communities as mediators between abiotic soil matrices and plant productivity (Philippot et al., 2013). This finding supports the "microbial loop" concept, wherein bacteria and fungi mineralize organic nutrients into plant-available forms, thereby closing elemental cycles (Bonkowski et al., 2009).

The high edge weight between AMF and nutrient uptake (0.92) reinforces the keystone status of mycorrhizal symbioses in plant-soil networks (Dickie et al., 2015; Rynkiewicz et al., 2015). In natural ecosystems, AMF form extensive common mycorrhizal networks that redistribute phosphorus from resource-rich to resource-poor plants, effectively buffering community-level nutrient heterogeneity (van der Heijden et al., 2008). The reduced AMF connectivity implied in our agricultural soil evidenced by lower fungal network centrality may represent a functional vulnerability of intensively managed systems (Wagg et al., 2014).

From a network resilience perspective, the abiotic module exhibited high internal connectivity, suggesting that physicochemical parameters provide a stable "backbone" against which biotic interactions fluctuate. This modularity is ecologically significant because it implies that perturbations to the abiotic environment (e.g., salinization, pH shifts) will propagate through the network via microbial hubs, potentially triggering cascading effects on plant growth and ecosystem function (Auge et al., 2020).

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4.5 Methodological Synthesis and Future Directions

The integration of XRF, FTIR, and standard microbiological assays within a network-theoretic framework offers several methodological advantages. XRF provides rapid, non-destructive elemental screening; FTIR adds functional-group resolution; and TMC supplies a biological activity proxy. Together, these datasets enable the construction of multi-layer networks that more faithfully represent the complexity of soil systems than any single analytical modality (Bauhaus et al., 2017). Future studies should extend this approach by incorporating high-throughput sequencing (metagenomics, metabarcoding) to resolve microbial community composition at taxonomic resolution, thereby replacing the aggregate TMC node with a multi-node microbial sub-network (Singh & Rai, 2024).

Table 6. Comparative summary of soil parameters with literature values from analogous ecosystems.

Parameter	Present Study Range	Literature Range	Reference
pH	7.77–7.98	6.5–8.5	Hinsinger et al. (2009)
EC (µs/cm)	122.9–134.3	100–500	Caldwell et al. (2011)
Moisture (%)	0.24–15.88	5–25	Kuzyakov & Razavi (2019)
TMC (cfu/g)	12,910–20,170	10^4–10^7	Fierer (2017)
SiO_2 (%)	66.30–76.50	60–80	Soman et al. (2024)
Fe_2O_3 (%)	2.71–5.67	1–8	Stewart (2010)

5. Conclusion

This study demonstrates that plant-soil interactions are governed by complex, non-linear networks in which physicochemical matrices, elemental composition, and microbial communities are intricately coupled. Four key conclusions emerge: (1) agricultural and canal-margin soils support higher microbial abundance than natural grassland, primarily mediated by moisture and nutrient availability; (2) XRF and FTIR signatures successfully differentiate land-use systems based on elemental oxide ratios and organic functional group profiles; (3) correlation-based network models identify total microbial count and arbuscular mycorrhizal fungi as keystone nodes bridging abiotic and plant-related sub-networks; and (4) soil moisture and Fe_2O_3 content emerge as the strongest predictors of microbial abundance, underscoring the primacy of water-oxide-microbe interactions in regulating ecosystem function.

These findings carry direct implications for sustainable land management. In agricultural systems, practices that enhance soil moisture retention (mulching, cover cropping) and Fe-oxide stability (reduced tillage) may optimize microbial hub function and, by extension, nutrient cycling efficiency. In natural systems, conservation strategies should prioritize hydrological regimes that sustain the moisture-microbe feedback loop. The network framework presented here provides a scalable template for integrating multi-analytical soil data into predictive models of ecosystem resilience under global change scenarios.

Declarations

Ethics Approval and Consent to Participate

Not applicable. This study did not involve human participants, human tissue, or vertebrate animals. Soil sampling was conducted in accordance with standard ecological field protocols, and no protected areas were accessed without appropriate permissions.

Availability of Data and Materials

All data generated or analyzed during this study are included in this published article and its supplementary information files. Raw XRF, FTIR, and microbiological test reports are available from the corresponding

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author upon reasonable request. The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Competing Interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Authors' Contributions

Preeti Chaudhary: Conceptualization, Methodology, Investigation, Data Curation, Writing-Original Draft, Visualization. Dr. **Shraddha Pandey:** Supervision, Conceptualization, Writing-Review & Editing, Validation, Project Administration. Both authors read and approved the final manuscript.

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