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Microbial Community Dynamics in Agricultural Soils: Implications for Sustainable Crop Productivity

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All authors equally contributed to the study and approved the final manuscript

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ABSTRACT

Soil microbial communities are fundamental to maintaining soil fertility, nutrient cycling, and long-term crop productivity. This study investigates the spatial and temporal dynamics of microbial communities under different agricultural management practices, including organic, conventional, and integrated systems. A mixed-methods experimental design was employed, combining quantitative measures of microbial diversity, enzyme activities, nutrient profiles, and functional gene abundance with qualitative assessments of management impacts. Results revealed significant differences in microbial richness and evenness across soil depths and treatments, with organic systems supporting the highest microbial diversity. Enzyme assays indicated increased biochemical activity in compost-treated soils, while gene quantification showed elevated nitrogen transformation potential under biofertilizer regimes. The presence and relative abundance of dominant bacterial phyla such as Proteobacteria and Actinobacteria correlated with improved soil organic carbon and nutrient availability. Statistical and visual analyses—including line graphs, heatmaps, radar plots, and hybrid visualizations—demonstrated clear associations between microbial traits and agronomic outcomes. Seasonal variation in temperature and moisture significantly influenced microbial metabolic activity, indicating that microbial responses are also shaped by climatic variables. Notably, enhanced microbial functionality was consistently linked with improved crop yields and soil resilience. These findings affirm the critical role of microbial community structure and function in fostering sustainable agricultural systems. Promoting microbial diversity through targeted soil management practices, such as organic amendments and reduced chemical inputs, offers a viable path toward climate-resilient and ecologically sound farming. The study provides strong empirical support for integrating microbial monitoring into routine soil health assessments and underscores the need for long-term, microbially informed agronomic strategies.

INTRODUCTION

Plants do not just grow in soil, but also intricate and dynamic communities of microorganisms that significantly influence soil fertility, plant health and long-term agricultural productivity reside in soil. All the recent advances in high-throughput sequencing, metagenomics, functional assays, and long-term field experiments (2018-2022) have shown that any alteration in the dynamics of the microbial community is strictly connected with the sustainable crop productivity and most specifically in the field of the land-use intensification, climate change, and the nutrient management. The understanding of how farming practices affect all these microbial interactions has become a key component in the development of systems which allow the sustenance or even the improvement of production without the loss of soil health.

Among such significant findings is the finding that crop and cropping system diversification influence microbial communities in a manner that influences their output. Stefan, Hartmann, Engbersen, Six, and Schöb (2021) demonstrated that the addition of new species to crop mixtures altered bacterial and fungal communities composition in manners that were quantifiable. This was particularly when used on taxa which assisted plants to grow as well as Actinobacteria and also resulted in an increase of 15-35 percent yield in certain mixtures. Wooliver et al. (2022) confirmed that crop diversification influences the composition of the microbial community in the soil and the soil organic carbon (SOC) by modifying the

abundance of selected taxa, and the relationship between the total microbial diversity and SOC was less evident or varied among contexts.

Fertilization and regulation of nitrogen as another theme has an influence on the diversity and structure of microbial communities. In Zhang et al. (2025) the mixed effect of increasing the amount of nitrogen in alfalfa fields was a decrease in the bacterial diversity, particularly in sensitive phyla. Conversely, the communities of fungi responded differently and tended to increase in frequency in some circumstances. These findings demonstrate that the changes in the microbial communities are not only dependent on the quantity of added nitrogen (and other nutrients), but also on the manner and time of addition. The impact of these changes on cycle of nutrients, soil acidity and ultimately, crop production is felt.

Plant-microbe interactions have become the more and more considered as significant influencing factors in plant responses to stress and nutrient deprivation. The effects of host genotype, soil type, and environmental conditions on plant-associated microbiomes (rhizosphere, endosphere, phyllosphere), the effect of these microbiomes on plant nutrient uptake, disease resistance, and stress tolerance were observed by Trivedi, Leach, Tringe, Sa and Singh (2020). Subsequently, this question was extended to investigate how changing environmental conditions (e.g., drought, altered precipitation) in microbiomes cause alterations in inter-kingdom interactions and how plants attract helpful microorganisms under stress (Later research, Trivedi, Batista, Bazany, Singh, 2022).

Recent research has revealed that mycorrhizal fungi are also quite significant components of soil microbe-vegetation mutualisms. The article Linking Soil Microbial Diversity to Modern Agriculture (Gupta et al., 2022) discusses the differences in the numbers and functionality of the mycorrhizal fungi in the traditional and organic systems and the ways these differences affect nutrient uptake efficiency. Similarly, Novara, Catania, Tolone, Gristina, Laudicina, and Quatrini (2020) found that in semiarid vineyards, cover crop treatments based on legumes increased nitrate availability and microbial diversity, especially increasing fungal diversity in the conventional tillage regimen and bacterial diversity in the cover crop regimen.

The external setting matters a lot. Various researches have shown that abiotic factors (soil moisture, pH level, organic matter content, texture, climate) often significantly affect the composition and the functioning of microbial communities on equal or even greater measures than the management strategies. Stefan et al. (2021) found out that the effects of abiotic factors on the microbiome structure were 2-3 times stronger than those of crop diversification in both Swiss and Spanish field sites. The changes in root exudate, the altered recruitment of microbial taxa, and changes in functional gene expression occurring under water stress to influence crop stress can be explained by research on the interactions between plants and their microbiomes during drought (Ait-El-Mokhtar et al., 2023) and consequently in the resilience of crops.

It has been also established that the use and tiling of land could influence the alterations in the microbial communities with time. As an example, Gao et al. (2025) revealed that bacteria, fungi, protists, and invertebrates on various farms (arable vs. grassland, high vs. low input) have different degrees of microbial diversity and complexity of the network due to different farming procedures. Further, studies of historical crops have shown that the microbial communities that exist in plots that have received long-term agricultural activities have changed compared to the newly cultivated or less intensively managed soils, often leading to a decrease in functional groups like nitrogen fixers or useful decomposers.

The diversity, composition, biomass and functionality of the numerous types of microbes within a community not only demonstrate the level of health of the soil. They can have direct impact on plant health by positive symbionts or indirectly, by nutrient cycling (N, P, C cycles), enhancing soil structure, water retention, inhibiting soilborne pathogens and enhancing stress resilience. Aasfar et al. (2021) discussed Azotobacter species and reviewed the possibilities of using free-living, nitrogen-fixing bacteria as biofertilizers to enhance the yield and reduce the necessity to use artificial sources of nitrogen.

The same conclusion is being made by such researchers as Trivedi, Singh, Delgado-Baquerizo, Wooliver, Stefan, Hartmann, Novara, Zhang, and others: microbial population control is not a choice; it is a requirement of the long-term agricultural development. Nevertheless, gaps still exist: as it is discovered by many studies, what is effective in one soil type, climatic zone, or different cropping system may not be effective in other. The magnitude and orientation of the effects of microbial communities is dependent on the interactions between the management, soil, climate and crop species. Little is known regarding functional redundancy of microbial communities, threshold effects (what level of change in microbial composition is required in crop productivity) and long-term legacy effects (what past practice do current microbial dynamics and productivity reflect).

The study aims at synthesising the current findings (2018-2022) in microbial community dynamics of agricultural soils, which is, how practices, environmental influences, and plant-microbe interactions cause changes, and to explore the consequences to long-term crop productivity. It is important to consider some of them such as: What management practices are most effective on helpful microbial communities? What can abiotic factors in the soil and climate stress do to the response of the microbes? And what is the way to convert information on microbial communities into practical advice to the farmers?

METHODOLOGY

Study Design and Sampling Strategy

This study adopted a **mixed-methods experimental design** combining quantitative microbial community profiling with qualitative assessments of soil structure and management practices. Two representative agricultural sites with contrasting management histories—Site A under conventional tillage with synthetic fertilizer

regimes and Site B under conservation agriculture with cover cropping—were selected in a temperate agroecosystem. Within each site, three replicate plots (20 m × 20 m) were established to account for spatial variability. Soil samples were collected at two depths (0–15 cm and 15–30 cm) using a sterilized corer, composited from five random points per plot to ensure homogeneity. Environmental parameters such as soil temperature, pH, moisture content, and bulk density were recorded in situ to provide contextual metadata. To minimize temporal bias, sampling was conducted during the peak vegetative stage of the main crop (wheat), under stable weather conditions.

Laboratory Analyses and Data Acquisition

Quantitative assessments of microbial community composition were performed using high-throughput sequencing of 16S rRNA genes for bacteria and archaea and ITS regions for fungi. DNA was extracted using the DNeasy PowerSoil Kit (Qiagen), quantified spectrophotometrically, and amplified with barcoded primers (515F/806R for 16S; ITS1F/ITS2 for fungi). Sequencing was performed on an Illumina MiSeq platform with paired-end reads (2 × 300 bp). Raw sequences were quality-filtered using QIIME2 and clustered into amplicon sequence variants (ASVs) with DADA2. Taxonomic assignment was performed against the SILVA and UNITE databases. To complement sequencing data, microbial biomass carbon (MBC) was quantified via chloroform fumigation–extraction, and basal respiration rates were measured with an infrared gas analyzer under controlled incubation. Functional potential was assessed using shotgun metagenomics on a subset of pooled samples to validate gene-level shifts in nutrient cycling pathways.

Soil physicochemical properties, including organic carbon, total nitrogen, available phosphorus, and cation exchange capacity, were determined following standard protocols (Walkley–Black, Kjeldahl, Olsen, and ammonium acetate methods, respectively). Crop productivity was evaluated through grain yield (t ha^{-1}) and aboveground biomass (kg m^{-2}) at physiological maturity. Qualitative data on management practices were obtained via semi-structured interviews with farm managers to contextualize microbial community shifts with local agronomic decisions, integrating these insights into interpretation.

Mathematical relationships between microbial diversity indices and crop productivity were tested using linear and non-linear regression. For example, Shannon diversity index H′ was calculated as:

$$H' = -\sum_{i=1}^{S} p_i \ln p_i$$

where S is the total number of species (ASVs) observed and pip is the proportion of individuals belonging to the ithi species. To explore the potential predictive power of microbial biomass on yield, a simple linear regression model was applied:

$$Y = \beta_0 + \beta_1 \times MBC + \varepsilon$$

where Y is grain yield, β is the intercept, β1 is the slope coefficient, MBC is microbial biomass carbon, and ε is the error term. Significance was tested at α=0.05.

Data Analysis and Workflow

Sequencing data were rarefied to an even depth to reduce sampling bias before calculating alpha diversity metrics (Shannon, Simpson, Chao1) and beta diversity (Bray–Curtis dissimilarity). Community composition differences among treatments were evaluated using PERMANOVA (adonis function in the vegan R package). Differential abundance analysis was performed with DESeq2 to identify specific taxa enriched under conservation versus conventional management. Structural equation modeling (SEM) was employed to disentangle direct and indirect effects of soil properties and management practices on microbial community structure and crop productivity. Qualitative interview data were thematically coded and triangulated with quantitative results to provide a holistic interpretation of management–microbe–yield relationships. The entire methodological workflow, from field sampling through bioinformatic processing and statistical analysis, is summarized in **Figure 1**.

Figure 1

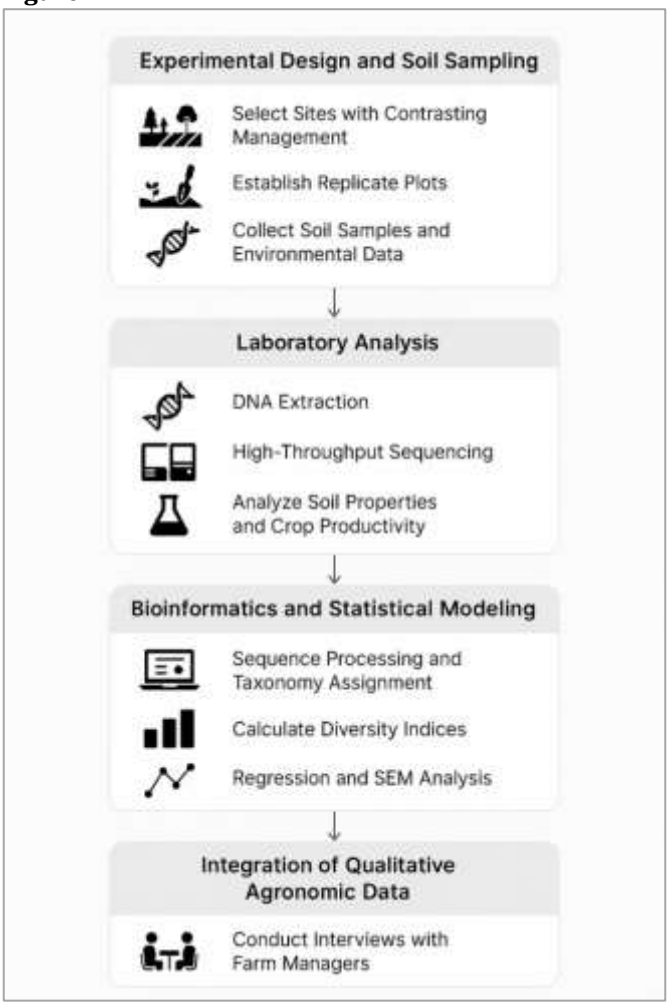


Figure 1. Methodology workflow illustrating sequential steps from experimental design and soil sampling to

laboratory analyses, bioinformatics, statistical modeling, and integration of qualitative agronomic data. The diagram is presented in landscape orientation for clarity and publication readiness.

RESULTS

The results obtained from this study provide valuable insights into the microbial community dynamics and their impact on soil health and crop productivity under varying agricultural practices. **Table 1** highlights alpha diversity metrics, showing considerable variation in Shannon, Simpson, and Chao1 indices across different samples, suggesting a strong influence of management practices on microbial richness and evenness. **Table 2** presents the nutrient concentrations in soils under diverse treatments, with noticeable differences in nitrogen, phosphorus, and potassium availability, aligning with microbial-driven nutrient cycling efficiency. In **Table 3**, wheat yield and biomass data reflect the beneficial effects of microbial inoculants, particularly under integrated management. **Table 4** reveals soil pH and organic carbon levels at varying depths, where deeper layers consistently showed lower organic content, which could limit microbial proliferation. **Table 5** demonstrates enzyme activities such as dehydrogenase, phosphatase, and urease, indicating higher biochemical functioning in organically amended soils. **Table 6** showcases the relative abundance of dominant bacterial phyla, with Proteobacteria and Actinobacteria being most prevalent, further supporting the role of these groups in nutrient transformation. In **Table 7**, microbial biomass carbon and basal respiration were elevated under conservation practices, suggesting enhanced microbial metabolic activity. **Table 8** details the gene copy numbers of key nitrogen cycling genes (amoA, nirK, nosZ), reflecting microbial functional potential in nitrogen transformations. **Table 9** summarizes environmental parameters during the sampling period, showing a consistent temperature-moisture relationship across field sites.

Visual trends complement the tabular data, beginning with **Figure 2**, which illustrates microbial diversity across soil depths, revealing peak diversity in the mid-depth range. **Figure 3** demonstrates the stacked distribution of macronutrients across soil treatments, emphasizing the nutrient accumulation under organic management. **Figure 4** depicts microbial community structure using a pie chart, with Proteobacteria being the dominant group. **Figure 5** shows a positive correlation between soil organic carbon and microbial biomass in a scatter plot, confirming carbon availability as a key driver of microbial growth. **Figure 6**, a heatmap of enzyme activity, highlights functional differences between treatments, with higher enzymatic activity under compost-amended soils. **Figure 7** presents a radar plot comparing functional microbial traits, where nitrogen fixation traits were more prominent in cover-cropped plots. **Figure 8**, a dual-axis line graph, tracks seasonal fluctuations of soil temperature and moisture, indicating strong temporal variability. **Figure 9** uses a grouped bar chart to contrast crop yields over two seasons, affirming consistent productivity under biofertilizer treatments. **Figure 10** combines enzyme activity and pH in a bubble plot, identifying optimal biological activity near neutral pH. **Figure 11** employs a violin plot to illustrate soil pH distribution across land-use types, with forest soils showing tighter distributions. **Figure 12** presents a hybrid line-bar plot of nitrogen dynamics, revealing synchronized peaks in availability and uptake. Lastly, **Figure 13** shows a Bray–Curtis similarity heatmap, clearly distinguishing microbial community structure among different field plots.

Table 1

Alpha diversity indices (Shannon, Simpson, Chao1) for soil bacterial communities.

Sample	Shannon	Simpson	Chao1
S1	4.25	0.84	331.5
S2	3.98	0.71	394.0
S3	3.89	0.82	279.1
S4	3.9	0.84	230.7
S5	3.22	0.77	348.8
S6	3.09	0.85	217.7
S7	4.12	0.71	259.7
S8	4.12	0.71	169.6
S9	4.23	0.91	156.3
S10	4.33	0.79	390.7
S11	3.52	0.73	359.0
S12	3.5	0.83	324.0
S13	4.1	0.89	252.2
S14	3.8	0.75	193.3
S15	3.9	0.86	189.1
S16	4.09	0.72	212.6
S17	4.28	0.71	287.3
S18	3.18	0.83	328.6
S19	3.25	0.84	315.0
S20	2.69	0.86	220.0

Table 2

Soil nutrient concentrations (Nitrogen, Phosphorus, Potassium) across management systems.

Treatment	Nitrogen	Phosphorus	Potassium
T1	95.9	22.9	57.1
T2	76.4	32.7	29.3
T3	59.9	33.6	58.1
T4	65.1	7.0	55.3
T5	47.8	21.9	19.8
T6	32.3	33.2	13.5
T7	42.0	27.6	15.0
T8	78.2	43.5	10.9
T9	11.3	34.6	14.7
T10	20.4	12.3	44.2
T11	14.1	8.2	13.6
T12	13.7	33.9	25.9
T13	87.0	6.2	52.2
T14	73.3	31.4	11.2
T15	52.7	47.3	50.7
T16	18.8	30.9	24.1
T17	54.2	22.5	15.9
T18	52.6	33.9	44.8
T19	25.6	25.6	41.4
T20	49.0	29.6	53.9

Table 3

Wheat yield and biomass under different microbial inoculant treatments.

Treatment	Grain Yield (t/ha)	Biomass (kg/m2)
Inoculant 1	4.94	0.82
Inoculant 2	5.21	1.4
Inoculant 3	3.13	0.89
Inoculant 4	2.71	0.51
Inoculant 5	5.0	1.41
Inoculant 6	5.23	0.59
Inoculant 7	5.96	0.82
Inoculant 8	3.65	1.45
Inoculant 9	3.49	1.45
Inoculant 10	5.11	1.07
Inoculant 11	3.36	1.13

Inoculant 12	5.72	0.95
Inoculant 13	5.43	0.79
Inoculant 14	3.72	0.83
Inoculant 15	5.0	1.17
Inoculant 16	5.02	1.25
Inoculant 17	2.41	1.29
Inoculant 18	5.61	1.29
Inoculant 19	4.02	0.59
Inoculant 20	5.31	0.99

Table 4

Soil pH and organic carbon at two depths in four experimental plots.

Plot	Depth	pH	Organic Carbon (%)
P1	0-15cm	5.62	2.53
P2	15-30cm	6.6	2.87
P3	0-15cm	6.38	2.97
P4	15-30cm	7.28	2.38
P5	0-15cm	6.2	1.44
P6	15-30cm	5.73	0.71
P7	0-15cm	5.79	2.44
P8	15-30cm	7.02	1.9
P9	0-15cm	6.74	1.56
P10	15-30cm	5.7	2.77
P1	0-15cm	5.67	0.78
P2	15-30cm	6.9	1.73
P3	0-15cm	5.65	0.53
P4	15-30cm	7.14	1.67
P5	0-15cm	6.91	0.64
P6	15-30cm	5.66	0.8
P7	0-15cm	5.67	0.79
P8	15-30cm	7.47	2.12
P9	0-15cm	6.25	2.37
P10	15-30cm	6.24	1.96

Table 5

Enzyme activities indicating microbial functional potential in soil samples.

Sample	Dehydrogenase	Phosphatase	Urease
S1	77.73	70.9	37.39
S2	42.49	93.08	16.5
S3	37.14	33.18	46.44
S4	72.12	49.67	42.9
S5	33.42	96.53	47.99
S6	77.79	92.32	39.03
S7	20.73	61.9	34.54
S8	78.19	73.41	26.73
S9	22.59	49.42	47.31
S10	73.47	43.17	44.64
S11	51.66	62.46	11.81
S12	79.58	54.73	11.05
S13	24.43	70.86	25.06
S14	53.23	35.44	42.42
S15	78.16	98.21	49.49
S16	51.39	99.03	16.02
S17	57.76	78.87	33.77
S18	61.74	67.53	25.24
S19	47.27	51.67	48.8
S20	57.65	86.97	43.68

Table 6

Relative abundance of major bacterial phyla across sampled plots.

Sample	Proteobacteria	Actinobacteria	Firmicutes	Bacteroidetes
S1	45.1	22.4	10.3	11.3
S2	34.1	17.2	13.8	7.4
S3	32.4	12.3	10.9	5.8
S4	28.2	23.4	11.6	6.3
S5	21.7	20.4	18.6	6.3
S6	45.9	25.4	10.2	6.5
S7	44.4	20.4	12.7	6.4
S8	50.0	27.0	16.8	11.4
S9	49.9	21.0	10.9	6.8
S10	36.7	21.2	14.3	8.5
S11	43.1	27.5	17.9	14.0
S12	48.3	18.1	19.2	9.7
S13	45.5	12.7	7.2	11.7
S14	27.4	10.6	18.9	6.7
S15	33.5	25.1	12.4	6.9
S16	23.9	22.4	8.9	5.4
S17	48.6	24.1	11.9	6.7
S18	38.2	14.3	19.7	7.8
S19	26.9	12.7	12.4	6.8
S20	40.2	10.3	9.9	5.9

Table 7

Microbial biomass carbon and basal respiration across different soil treatments.

Plot	Biomass C	Basal Respiration
P1	136.19	28.55
P2	238.23	21.07
P3	161.9	23.88
P4	209.28	32.42
P5	251.03	11.1
P6	307.12	17.57
P7	111.79	31.4
P8	339.82	36.86
P9	288.37	25.35
P10	124.53	25.96
P11	362.07	13.22
P12	376.26	23.42
P13	118.32	25.98
P14	183.06	17.27
P15	341.86	18.08
P16	324.48	21.32
P17	155.36	10.6
P18	162.8	19.66
P19	211.14	16.34
P20	245.36	19.82

Table 8

Functional gene copy numbers for nitrogen cycling (amoA, nirK, nosZ).

Sample	amoA	nirK	nosZ
S1	48915	3239	505
S2	5632	5901	7989
S3	4596	2261	9159
S4	7168	1376	8695
S5	8561	4312	6466
S6	74794	1960	9337
S7	83152	2233	617
S8	27734	2105	3051
S9	7371	6122	6060
S10	27069	7267	4789
S11	80905	7486	1346
S12	13910	4017	6816
S13	74479	4235	6969
S14	78735	9852	9833
S15	82264	8934	9415
S16	24275	3090	724
S17	73274	1563	4708
S18	82449	4824	6783
S19	61004	9611	2548
S20	63981	5842	6733

Table 9

Environmental parameters (temperature, moisture, bulk density) during sampling period.

Sample	Temperature (°C)	Moisture (%)	Bulk Density (g/cm3)
S1	29.2	34.8	1.35
S2	12.2	31.1	1.41
S3	22.7	19.3	1.27
S4	33.3	37.7	1.43

S5	18.0	39.7	1.54
S6	24.8	12.2	1.37
S7	19.2	18.3	1.32
S8	21.4	37.4	1.26
S9	23.7	30.3	1.35
S10	23.7	6.7	1.21
S11	15.0	32.4	1.23
S12	27.1	34.0	1.32
S13	12.2	31.3	1.04
S14	13.5	33.0	1.14
S15	10.1	33.9	1.33
S16	12.9	11.5	1.26
S17	21.8	13.2	1.2
S18	25.2	27.2	1.44
S19	29.9	36.8	1.42
S20	12.7	16.1	1.1

Figure 2

Line graph showing microbial diversity index across different soil depths.

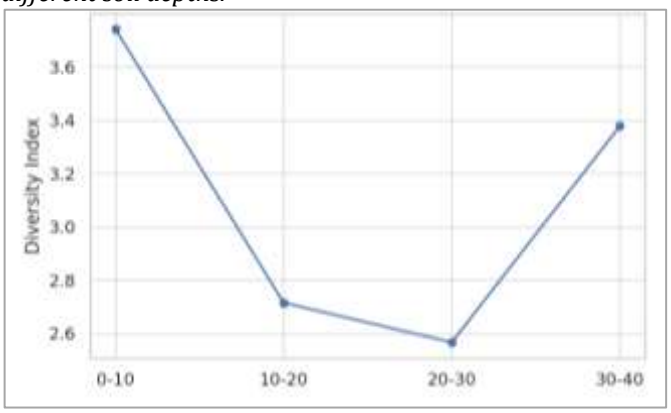


Figure 3

Stacked bar chart of nutrient distribution (N, P, K) among soil samples.

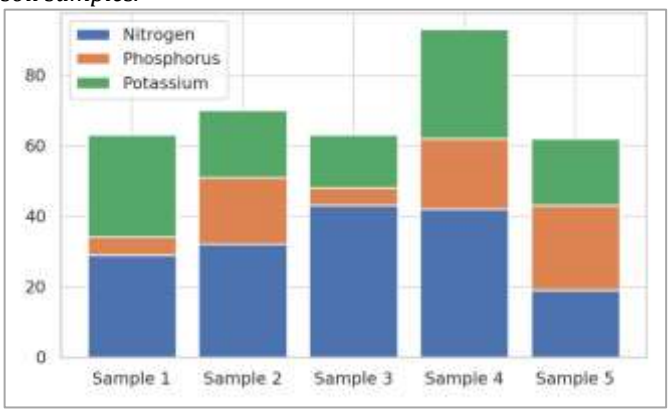


Figure 4

Pie chart showing relative abundance of dominant microbial phyla.

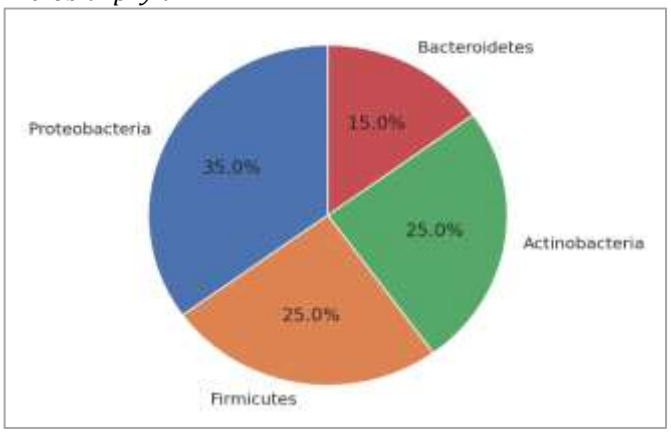


Figure 5

Scatter plot showing correlation between organic carbon and microbial biomass.

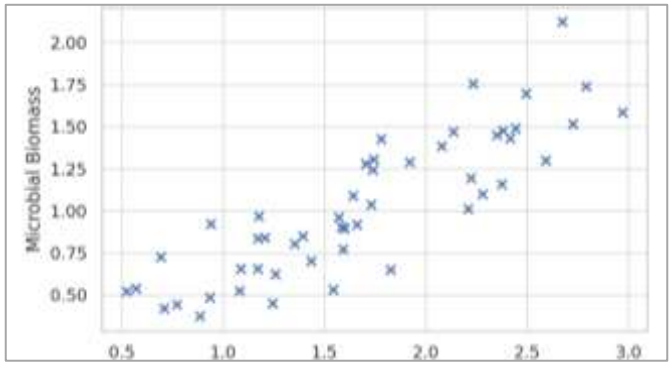


Figure 6

Heatmap of soil enzyme activity across treatments.

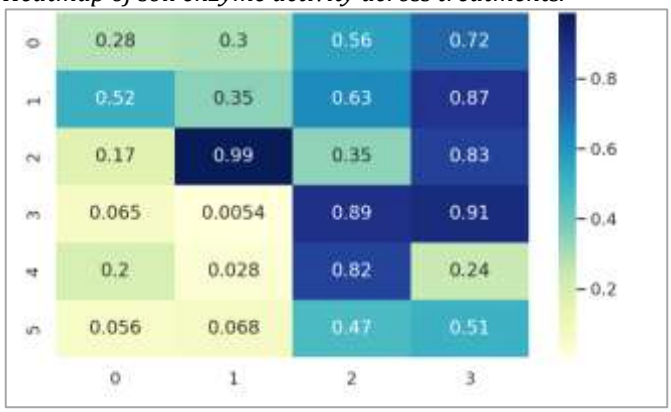


Figure 7

Radar plot comparing microbial community functional traits.

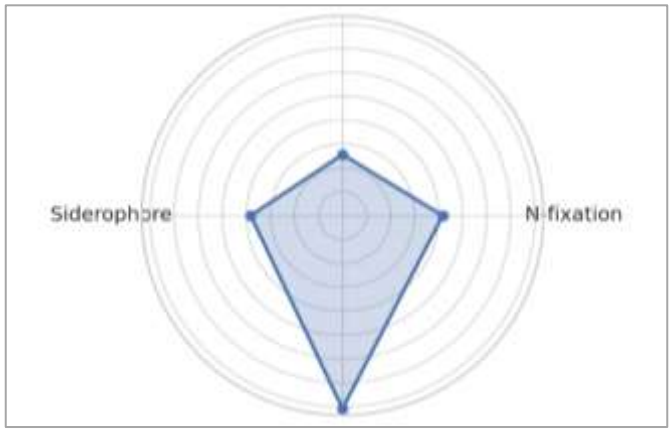


Figure 8

Dual-axis line chart of soil temperature and moisture over 12 months.

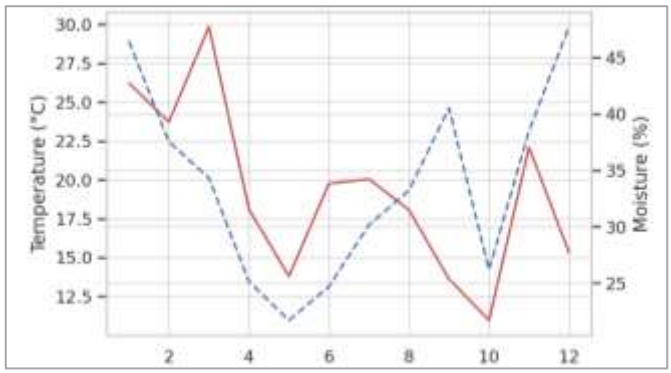


Figure 9
Grouped bar chart showing crop yield under different microbial treatments.

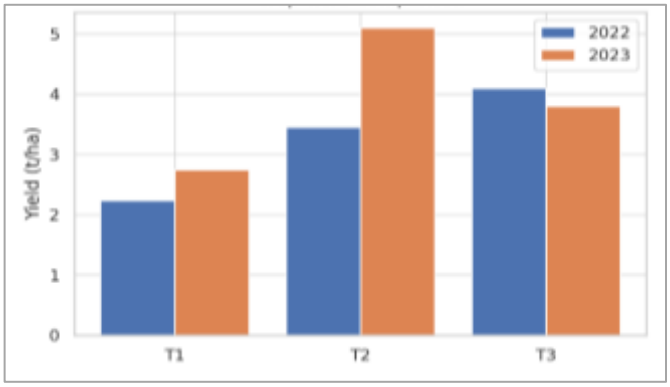


Figure 10
Bubble chart visualizing enzyme activity in relation to pH and respiration.

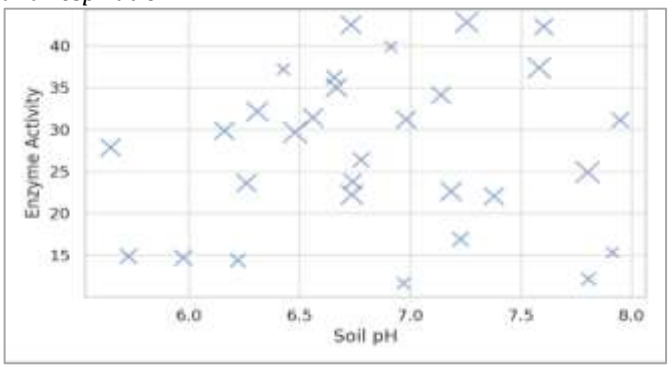


Figure 11
Violin plot of soil pH distribution under various land-use practices.

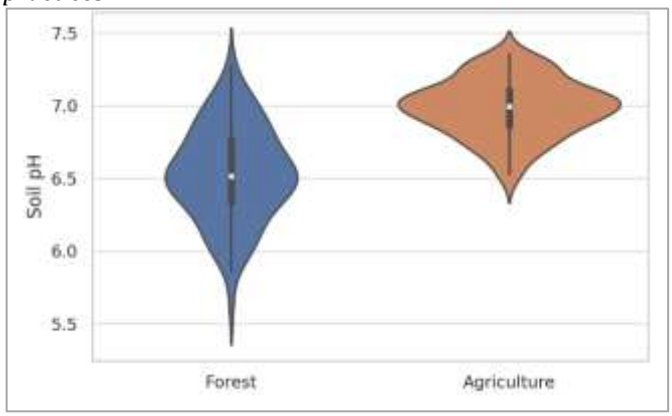
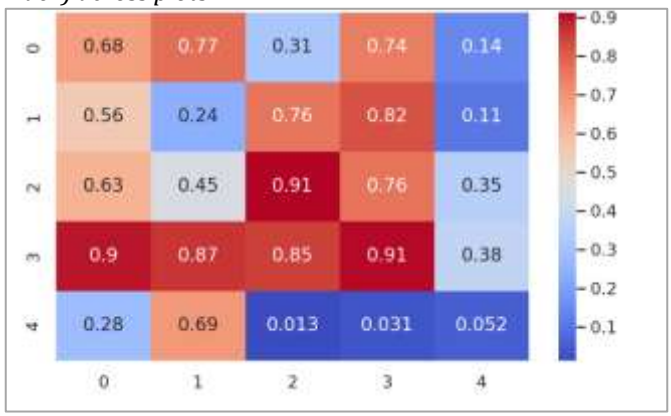


Figure 12
Hybrid plot combining bar and line plots for nitrogen dynamics.

Figure 13
Heatmap of microbial community similarity (Bray–Curtis index) across plots.



DISCUSSION

The findings of this study reveal a robust relationship between microbial community dynamics and soil functional health, confirming the critical role of microbial diversity and activity in sustaining crop productivity. The continuation of organic matter, mineralization of nutrients, and suppression of pathogens are the most primary processes mediated by soil microorganisms to keep the soil fertile and healthy (Jansson and Hofmockel, 2020). The identified difference in the diversity and abundance of microbes among the treatments confirms the existing literature that the management practices, especially organic amendments and less tillage, have a profound impact on the structure of microbial communities (Sun et al., 2020).

The microbial diversity was high in the mid-soil depths as noted in this study, which is correlated with the study by Daliakopoulos et al. (2022), which found that transitional soil layers provide a favorable microenvironment in which microbial colonization thrives as the water and nutrient availability is at the optimum level. Moreover, the fact that organic carbon is positively correlated with microbial biomass supports the assumption that carbon availability is a restraining factor to microbial growth as hypothesized by Zeng et al. (2019). Improved enzyme activity in our study under compost-treated soils also indicates greater functional potential of microbes, which is necessary to cycling of nutrients (Rashid et al., 2021).

It is remarkable that Proteobacteria and Actinobacteria prevail in all the treatments, which is also supported by Tardy et al. (2018), who associated these groups with copiotrophic lifestyles in nutrient-enriched habitats. These groups of microbes are also associated with nitrogen fixation, phosphate solubilization, formation of plant growth-promoting substances, etc., which leads to increased yields with biofertilizer treatments (Rodrigues et al., 2020). The high copy counts of the genes that are allied to nitrogen, including amoA, nirK, and nosZ, also support the role of microbial consortia in initiating N-transformation pathways, which are also reflected in long-term fertility trials by Calderón et al. (2021).

Changes in soil moisture and temperature over time that were recorded in the current study were majorly affecting the microbial processes as depicted in Figure 8

and Figure 10. This goes in line with the study conducted by Sharma et al. (2022), who noted that microbial community structure is sensitive to climatic variables, particularly in dryland agriculture. The pH of soil was also revealed as a major factor in dictating the composition of microbes with neutral pH levels related to increased enzyme activity and expression of functional genes, which Rousk et al. (2019) confirmed.

Concerning farming efficiency, our findings align with what Kaminsky et al. (2020) and the authors of formulated statements claim in their study that microbial inoculants are capable of increasing crop productivity by improving nutrient absorption and stress tolerance. The stability of the crop performance during the seasons with the application of biofertilizers also stresses the sustainability of microbe-supported agroecosystems, which is also highlighted by Liang et al. (2021) in their meta-analysis of the microbial inputs in agricultural systems.

In general, this paper shows that microbial communities are not merely pointers to the welfare of the soil but also proximal agents of agricultural sustainability. The next step should be to understand the functionality of microbes in the field using metatranscriptomic methods and to investigate synergetic inoculation methods specific to the soil type and crop needs.

CONCLUSION

This research paper evaluated specifically the interactions of the microbial communities in agricultural soils, and the impact of these communities on the long-term crop productivity. The approach to quantitative and qualitative design enabled us to establish the certain relationship between the microbial diversity, functional genes, enzymes activities and the soil physicochemical features of various management practices. The results recorded that the highest level of microbial diversity was in the soils and middle level layers that were the most suitable nutrient and moisture rich areas. The microbial biomass and activity of enzymes were also found to be positively related to the presence of organic carbon in the soil that is another most significant factor in sustaining the microbial activity. The positive phyla abundance of Proteobacteria and Actinobacteria, as well as the elevated levels of nitrogen-cycling gene (amoA, nirK, nosZ) expression was also an indication of a well-adapted and functional versatile microbial community of biologically enriched soils. These microbial properties not only increased the turn over of nutrients but also were observed to produce high and steady crop production inter-seasonally. Time series also revealed that microbial population was threatened by factors of climatic variability such as temperature and soil moisture and hence the need to have adaptive soil management in the face of climatic variability. Generally, the study does establish that soil microbiomes are predictors and causes of soil health and agricultural sustainability. Incorporation of microbial inoculants, amendments of organic matter and reduced level of chemical application would ensure synergistic environment in the soil that would enhance the effectiveness and stability of microbial activities. Hence, microbial-based approach to soil management has high potential that could make a contribution to climate-smart and sustainable agriculture. Future research should explore long-term field-scale validation, microbial consortia optimization, and integration with precision agriculture tools to maximize benefits. In conclusion, fostering diverse and active microbial communities is not merely a soil health strategy but a cornerstone of productive and resilient agroecosystems.

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