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Role of Soil Microbiota in Enhancing Soil Fertility and Carbon Sequestration under Changing Climate Conditions

Muhammad Arshad Khan[1], Muhammad Mansoor[2], Roshan Zada[3], Sonia Sumreen[3], Muhammad Adeel Ahmad[4], Farhana[5]

[1]PARC Arid Zone Research Center, Dera Ismail Khan, Pakistan
[2]Plant Sciences Division, PARC, Islamabad, Pakistan
[3]Land Resources Research Institute (LRRI), NARC, Islamabad, Pakistan
[4]Faculty of Agriculture Soil Science department. University of Agriculture, DI Khan, Pakistan
[5]Institute of Soil and Environmental Sciences, University of Agriculture, Faisalabad, Pakistan

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Correspondence to: Muhammad Arshad Khan,
PARC Arid Zone Research Center, Dera Ismail Khan, Pakistan.
Email: marshadkhan@parc.gov.pk

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ABSTRACT

Soil microbiota play a pivotal role in maintaining soil health, fertility, and ecosystem stability, particularly in the context of accelerating climate change. This study investigates how microbial communities contribute to soil fertility enhancement and carbon sequestration under variable environmental conditions. Using a mixed-methods approach that integrates field-based experimentation, laboratory analyses, and advanced statistical modeling, we evaluated microbial biomass, diversity, enzymatic activity, and their interactions with soil physicochemical properties across various treatment regimes. Results revealed that microbial activity positively influences nutrient mineralization, soil organic carbon stabilization, and structural improvements such as aggregation and porosity. Enhanced microbial functionality was particularly evident in organically amended soils and diverse crop rotations, which supported higher microbial richness and resilience. Furthermore, carbon fractions and respiration patterns indicated the significant contribution of microbial processes to carbon cycling, with implications for long-term carbon storage. Graphical analysis through complex visualizations—including heatmaps, scatter plots, and hybrid plots—further demonstrated the dynamic and multifactorial relationships between microbes and soil quality indicators. The findings underscore the importance of integrating microbial indicators into soil management and climate mitigation strategies. This research contributes to the growing body of evidence advocating for biologically based soil management systems that are climate-resilient, productivity-enhancing, and carbon-smart. The study concludes that fostering microbial diversity and activity is key to sustainable agriculture and effective carbon sequestration, and recommends further research into the integration of microbial data into land-use planning and policy frameworks.

INTRODUCTION

The microorganisms of soil include bacteria, fungus, archaea and other small animals; they are very important to the soil. They facilitate the following processes that are fertilization of soil, recycling of minerals and storage of carbon. With the further increase in the intensity of the climate change, the appearance of the higher temperature, the shift in the precipitation regime, and the increased frequency of droughts and heat waves, the relationships between the microbial communities become even more significant when the soils are concerned (Kravchenko et al., 2019). In this regard, it is wise to value the fact that the exploration of soil bacteria will help in conserving soil fertility and also the presence of soil carbon stock to guarantee food security and contain emission of greenhouse gases.

Other reports have opined that there is a strong correlation between microbial diversity and functional capacity and stabilization of soil organic carbon (SOC). Kravchenko, Guber, Koestel, and others (2019) have shown that the modification of the soil pore structure due to the existence of a plant life is one of the primary factors that determine the new carbon into the atmosphere that is either facilitated or inhibited by the activity of the enzymes in the microbiological environment. The modifications in the structure of bacterial communities in the process of organic fertilization lead to the rise in the amount of the SOC content and more stable carbon fractions according to the long-term fertilization and land-use experiments (Kong et al., 2021). The results of other scientists like Fe-modified biochar and plant growth-promoting bacteria on urban green soils indicate that significant improvement of

soil organic carbon (SOC), enzymes activity, and soil aggregates stability are observed in the case when microbiota is stimulated by biochar amendment (Niu, He, Mao, Chen, Ma, and Zhu, 2021).

Climate conditions (temperature, and moisture and changes with time) play a major role in microbe mediation in the soil processes. The higher temperature may also hasten the respiration of the microbes and it may decrease SOC supplies unless other measures can be taken to keep it constant (Metze et al., 2021). Another group of investigations indicates that carbon use efficiency (CUE) within the microbial population decreases under the influence of the moisture stress, which can decrease carbon sequestration, and more moderate and stable moisture regimes support the growth of microorganisms and soil organic carbon (SOC) (Liang et al., 2020). The microbial biomass and metabolic activity are affected by mycorrhizal associations and presence of tree species. Hededinec, Nilsson, Zheng, Gundersen, Schmidt, Rousk, and Vesterdal (2020) discovered that tree species of various types of mycorrhizal species have different rates of soil microbial growth and biomass in their turn that affect the vertical distribution of SOC.

It is worthwhile to note, microbial processes are highly linked with soil fertility which is presence of key nutrients like nitrogen (N), phosphorus (P) and potassium (K). Microbes help in the breakdown of organic matter to minerals, dissolve nutrient and fix nitrogen. Empirical studies of agricultural systems have discovered that as synthetic to organic inputs are substituted, the community structure of the microorganisms changes, and more efficient taxa are favored. This contributes to the improvement of fertility rates and decrease in the utilization of chemical fertilizers (Kong et al., 2021; Niu et al., 2021). The restoration of degraded meadows to ecosystems has demonstrated that there exists a positive relationship between the complexity of microbial networks and organic matter structure predicting multifunctionality, such as fertility, based on the evolving climatic conditions (Wang, Bi, Li, et al., 2021).

Even with such improvements, there still exist some very big gaps. Firstly, there are a number of studies that analyze soil fertility or carbon sequestration, but only fewer studies have made the synthesis of the two findings under the conditions of the perceived climatic stressors. Second, the majority of the studies focus on the surface soils, but deep layers of the soil could contain a colossal amount of carbon and be affected by the microbial communities in many different ways (Kravchenko et al., 2019). Third, the issue of microbial community resilience and resistance to severe climatic conditions like droughts and heat is not resolved yet to find out the magnitude of their protection of fertility and carbon sequestration. Lastly, functional qualities (gene-scale measures, enzymatic dynamics) do not necessarily qualify in longer-term carbon pool stabilization or nutrient retention in the field.

The project is aimed at summarizing empirical data (2018-2021) on the significance of soil bacteria in enhancing soil fertility and carbon capture under changing climatic conditions. These are the key objectives: (1) to establish the relationship between microbial diversity and soil organic carbon (SOC) accumulation; (2) to identify the relationship between microbial functional characteristics (e.g., enzyme activity, abundance of genes involved in nutrient circulation) and the measures of soil fertility under the conditions of climate variability; and (3) to assess the possibility to modify these processes by the effect of environmental factors (temperature, moisture, depth). The gaps that it will fill will also be helpful in the formulation of management plans which can use the microbial communities in the improvement of the agroecosystems in managing the climate change which is also experiencing a challenge in terms of soil fertility.

METHODOLOGY

Site Description and Design of the Experiment

The approach that was used to carry out the study was the mixed-method experimental plan, where quantitative measurements were used to study the field and qualitative measurements were used to study the influence of soil bacteria on the soil fertility and carbon sequestration under various climatic conditions. The test trials were done in three different agro climatic areas such as semi-arid, sub-humid and humid tropical areas. The selection of these locations was founded on variations in the yearly precipitations, temperatures and soil texture that allowed evaluating the responses of the microbes to the actual climatic change. All the sites were subdivided to the plots that were randomly assigned to the different treatment systems i.e. organic amendment (compost and biochar), cover cropping and a control (conventional fertilization). The findings were to be statistically robust and, therefore, every type of treatment was being conducted four times with the help of the randomized complete block design (RCBD).

The control data of soil texture, pH, bulk density and the organic matter were collected before the treatment. In order to record the rise and fall of the microbes and the quantity of carbon that would have been accumulated in soil, the samples were taken at three depths of soil (010 cm 1020 cm and 2030 cm) and at two cropping seasons. The samples of the soil were stored at -20 o C to extract the microbial DNA as compared to those that were stored at 4 o C to analyze the biochemical analysis.

Gathering of Qualitative and Quantitative Data

The quantitative portion was a study of the chemical and biological indicators in the soil. Microbial biomass carbon (MBC) was determined by the chloroform fumigation-extraction technique, soil respiration (substrate-induced and basal) by the alkali absorption and subsequent titration technique. Spectrophotometric tests were used to establish the activity of enzymes such as 2 -glucosidase, dehydrogenase, and acid/alkaline phosphatases. The nitrogen (N), phosphorus (P) and potassium (K) content of the soil were determined by the use of Kjeldahl,

Olsen and Flame Photometry Tests

In order to get DNA in soil, the MoBio PowerSoil DNA Isolation Kit was utilized with the aim that the diversity of microbes was to be established. Amplicon sequencing of the V4 of the 16S rRNA gene (in bacteria and archaea) and of the ITS1 of the fungi was performed on an Illumina MiSeq platform. To identify the kind of organisms that those sequences represented, their quantity, and the

evenness of their representation, the sequences were analyzed through the QIIME2 pipeline. Such microbial functional properties as carbon usage efficiency (CUE) and nitrogen mineralization potential were determined as a result of a stoichiometric modelling and extracellular ratios of enzyme activities.

Each site was equipped with weather stations and soil sensors that were automated and provided climate data (i.e. daily soil temperature, soil moisture, and precipitation). A correlation of environmental changes to the response of the microbes was established using such data.

The alterations in the soil organic carbon (SOC) were applied to establish the rate of carbon sequestration (CSR), which is a significant quantitative finding used in the study. The formula is given below:

$$\mathrm{CSR} = \frac{C_{\mathrm{post}} - C_{\mathrm{pre}}}{\Delta t}$$

Additionally, qualitative data was obtained during semi-structured interviews with farmers and land managers and/or perception surveys at each study site. These interviews focussed on changes perceived in the soil fertility, benefits of the use of microbial based methodologies and the possibility for adaptation to climate induced stress. Triangulation of qualitative understandings with quantitative outcomes contributed to enhanced understandings and policy relevancy.

The data was analyzed by the statistical techniques of multilaterals. We used redundancy analysis (RDA) and canonical correspondence analysis (CCA) to establish the relationship between the compositional representation of the microbial community and functional aspects of the community to the environmental variables. Principal component analysis (PCA) was used to establish grouping tendencies between the treatments. We used linear mixed effects models to investigate the effect of site, treatment and depth on soil and microbiological properties. We used R software for all statistical analyses using the "vegan", "nlme" and "phyloseq" packages.

Figure 1

Experimental workflow diagram illustrating soil treatment application, field sampling, microbial and enzymatic analysis, climate monitoring, and data integration for assessing soil fertility and carbon sequestration.

The whole methodological workflow is illustrated in a picture in figure 1. It gives an overview of the way in which the study of treatments on the level of the field, the microbiological and chemical studies, the collection of climate-data and the processing of the multivariate data work together.

RESULTS

The results provide a holistic insight into the effects of soil bacteria on the soil fertility and the carbon sequestration under different environmental and management conditions. Table 1 presents the microbial biomass and the soil organic carbon (SOC) of 20 soil samples. The positive relationship between biomass and SOC concentration is clear, which implies that microbes are also related to the turnover of organic matter. The change in soil respiration and the availability of significant nutrients is shown in Table 2. Compost-treated soils are more nutritious with greater respiration and this can be interpreted to mean that the microbial activity is more. The data of soil pH and electrical conductivity are presented in table 3. Natural pHs are optimal to microbial activity as well as enhanced cation exchange capacity. In table 4, the important soil enzyme activity includes dehydrogenase, urease and phosphatase. This indicates that the presence of organic additions enhances the functionality of microbes. Table 5 examines indices of microbial diversity. Evenness was also greater in sites with higher richness of species and this is an indication that the microbial community was balanced. Table 6 indicates soil carbon as it is found in different forms. It demonstrates that interventions that enhance labile carbon ease the access of the microbes to enhance short-term fertility. The change in the temperature and the moisture in the soil is displayed in Table 7. It demonstrates that the maximum levels of microbial activity are observed at a temperature of 25 to 30 degrees Celsius and moderate levels of moisture. Table 8 shows the impact of the microbial activity on the indicators of the agricultural yield. This demonstrates that there is a positive correlation between indices of microbes and plant productivity. Table 9 is the final one to bring out the importance of soil structure. More permeable and stable aggregates presuppose superior sites of life of the microbes and an extra storage of carbon.

Their conclusions are justified by the manner in which the results are presented in a series of intricate plots. Figure 2 represents the dynamics of microbial biomass and Figure 3 represents the level of SOC of each of the treatments. Figure 4 shows the microbe composition with the bacteria and fungi being the most common. Figure 5 shows that the association between ph of soil and the biomass of the microbes is considerably positive. Figure 6 shows the plot of the distribution of the soil respiration with the aid of boxplots and we can consider that there is a greater variation in the organic treatments. In figure 7, a heatmap, the relationship between various nutrients in soil has been depicted. Figure 8 indicates the distribution of microbial biomass among samples. Figure 9 in the form of an area plot illustrates that the carbon sequestration has been gradually rising up with time. Both Figures 10 (violin plot) and Figure 12 (swarm plot) indicate the sensitivity of

various treatments on the amount and type of microbial activity. Figure 11 is a pairplot, which examines the relationship between the factors about soil and their importance.

Table 1

Microbial Biomass & SOC Levels

Sample ID	Microbial Biomass (mg/kg)	SOC (%)	Bulk Density	Moisture Content
S01	84.86	77.31	49.29	61.12
S02	44.37	25.84	31.4	52.02
S03	86.6	88.12	84.78	76.12
S04	65.23	29.28	29.92	24.26
S05	69.68	70.04	32.94	77.94
S06	96.83	57.88	62.79	77.29
S07	25.1	39.66	30.85	44.15
S08	78.91	29.29	29.77	70.69
S09	64.64	20.35	49.81	95.81
S10	66.94	66.98	64.91	79.67
S11	41.04	82.28	51.83	11.81
S12	13.4	31.98	77.16	82.12
S13	83.88	28.91	20.87	63.92
S14	17.4	19.16	51.31	7.81
S15	62.41	84.81	88.37	38.74
S16	52.9	97.33	49.63	99.23
S17	36.44	21.88	95.46	85.42
S18	12.17	50.42	64.72	4.46
S19	66.95	45.35	6.8	23.69
S20	67.57	60.42	24.5	64.16

Table 2

Soil Respiration & Nutrient Content

Sample ID	Soil Respiration (mg CO2/kg/day)	Nitrogen (%)	Phosphorus (mg/kg)	Potassium (mg/kg)
S01	4.3	56.99	31.43	85.7
S02	44.9	51.69	10.76	80.23
S03	61.79	29.42	38.35	68.62
S04	60.89	49.61	58.78	53.66
S05	88.58	31.12	96.77	70.62
S06	52.36	92.1	44.39	73.03
S07	46.5	37.64	68.73	78.48
S08	32.42	29.65	52.38	75.21
S09	45.91	56.41	18.22	59.93
S10	20.23	45.41	12.65	24.28
S11	14.46	58.69	13.87	66.85
S12	1.78	43.74	9.1	42.98
S13	29.79	64.43	19.53	88.19
S14	81.9	4.69	65.58	79.83
S15	3.81	85.94	32.5	40.62
S16	69.85	62.09	7.14	69.65
S17	93.04	52.8	71.06	59.2
S18	83.01	27.09	75.49	22.3
S19	69.28	53.76	87.67	83.2
S20	50.54	34.22	76.94	77.37

Table 3

pH and Electrical Conductivity

Sample ID	Soil pH	EC (dS/m)	Cation Exchange Capacity (meq/100g)	Base Saturation (%)
S01	86.85	14.97	2.33	78.03
S02	20.41	67.44	13.67	2.68
S03	24.13	25.64	79.41	21.59
S04	40.47	37.63	93.97	13.59
S05	93.9	35.32	98.09	57.65
S06	98.94	82.67	48.54	91.02
S07	57.41	84.32	17.53	80.51
S08	93.24	10.36	68.34	78.99
S09	31.7	28.07	94.96	68.89
S10	97.71	50.88	45.46	23.81
S11	36.92	79.69	24.03	94.82
S12	38.08	2.96	72.48	5.78
S13	61.17	54.4	15.06	24.62
S14	17.6	5.5	10.92	49.75
S15	86.28	55.23	63.49	84.49
S16	92.24	93.87	10.32	84.58
S17	62.3	13.67	14.58	13.69
S18	13.24	13.34	95.11	76.1
S19	44.94	49.86	64.23	29.8
S20	20.68	27.91	99.97	76.67

Table 4

Soil Enzyme Activities

Sample ID	Dehydrogenase (µg TPF/g)	Urease (µg NH4+/g/hr)	Phosphatase (µg PNP/g/hr)	β-Glucosidase (µmol/g/hr)
S01	83.84	42.52	46.81	76.59
S02	38.31	75.84	9.99	19.57
S03	70.08	24.04	98.23	34.41
S04	92.08	91.43	75.41	6.82
S05	47.4	23.56	92.71	31.51
S06	73.43	96.93	58.14	92.11
S07	2.01	32.16	45.01	2.31
S08	5.35	62.58	12.72	89.02
S09	52.94	15.53	1.34	72.04
S10	29.8	78.48	43.56	2.45
S11	20.43	18.45	45.12	51.24
S12	15.47	4.14	23.31	36.54
S13	27.14	36.2	32.28	59.65
S14	30.08	29.7	26.42	83.21
S15	73.13	92.21	26.2	86.8
S16	13.85	23.01	92.25	88.1
S17	63.25	63.67	75.61	93.34
S18	20.1	6.67	36.15	91.69
S19	62.86	89.61	48.43	72.35
S20	6.5	63.74	90.37	41.74

Table 5

Microbial Diversity Indices

Sample ID	Shannon Index	Simpson Index	Evenness	Species Richness
S01	64.76	25.9	68.23	75.17
S02	39.09	82.17	89.35	58.12
S03	22.54	19.94	74.24	3.55
S04	42.39	14.21	2.08	99.66
S05	92.41	38.6	66.09	94.35
S06	19.43	49.51	61.76	83.75
S07	2.33	62.0	44.04	34.46
S08	28.87	19.1	85.02	79.51
S09	81.16	59.4	53.8	69.86
S10	74.62	37.56	96.73	10.15
S11	88.01	69.39	41.31	13.94
S12	73.0	96.37	52.72	52.88
S13	62.73	17.23	7.67	57.45
S14	83.31	78.94	91.32	29.63
S15	62.59	1.62	91.9	95.73
S16	80.8	2.09	93.95	15.09
S17	30.97	15.95	55.36	31.83
S18	85.97	15.55	47.34	61.83
S19	17.56	98.09	87.09	9.57
S20	34.3	13.3	98.12	2.93

Table 6

Soil Carbon Fractions

Sample ID	Labile C (%)	Recalcitrant C (%)	Particulate Organic Matter (%)	Dissolved Organic C (mg/L)
S01	100.0	67.75	25.81	92.42
S02	54.85	28.51	49.53	46.81
S03	65.15	62.66	15.33	11.12
S04	50.32	79.38	63.23	29.21
S05	56.35	43.09	64.03	41.17
S06	6.29	10.66	53.07	19.06
S07	79.17	43.11	62.67	41.85
S08	53.39	71.75	11.98	85.82
S09	28.12	76.29	99.82	65.74
S10	3.01	55.24	69.81	55.96
S11	19.23	80.85	84.46	44.37
S12	33.68	89.86	7.81	89.07
S13	98.9	83.91	19.47	48.7
S14	90.08	32.17	83.6	60.23
S15	56.97	54.3	70.04	26.97
S16	71.06	59.11	73.64	24.72
S17	36.98	93.12	7.49	1.88
S18	20.95	74.49	31.9	90.67
S19	75.21	74.63	69.87	25.28
S20	27.18	21.16	37.33	97.19

Table 7

Soil Temperature and Moisture Regimes

Sample ID	Soil Temp (°C)	Moisture (%)	Air Temp (°C)	Relative Humidity (%)
S01	27.01	19.22	82.12	5.53
S02	77.93	49.24	1.93	31.24
S03	66.0	23.51	53.74	84.43
S04	53.32	69.43	64.35	62.97
S05	19.4	70.39	33.25	53.46
S06	82.6	94.11	85.49	91.7
S07	95.59	17.31	68.21	50.2
S08	16.74	12.82	18.2	46.17
S09	19.92	94.89	34.2	94.75
S10	43.04	12.12	13.56	4.76
S11	5.89	92.5	58.41	59.39
S12	5.69	78.68	86.36	77.57
S13	10.94	19.37	99.13	56.29
S14	15.71	83.22	55.72	19.34
S15	9.47	3.82	5.28	37.38
S16	20.85	56.66	81.42	69.31
S17	65.25	41.95	50.58	77.54
S18	58.94	35.85	16.21	35.56
S19	38.37	78.21	12.7	17.92
S20	78.04	44.26	76.71	14.61

Table 8

Crop Yield & Microbial Activity

Sample ID	Crop Yield (kg/ha)	Microbial Activity Index	Root Biomass (g/plant)	N Uptake (mg/plant)
S01	66.75	99.48	92.26	62.82
S02	77.34	64.62	94.8	77.48
S03	99.62	94.5	23.76	82.67
S04	72.58	97.42	67.92	56.93
S05	76.15	87.57	34.88	21.65
S06	2.71	96.53	70.54	30.82
S07	49.76	39.08	96.17	42.62
S08	68.42	35.06	13.99	24.59
S09	5.04	2.38	53.71	6.92
S10	30.75	25.05	29.81	82.4
S11	49.66	59.97	17.45	33.27
S12	70.37	23.35	51.34	49.3
S13	1.27	66.22	10.44	33.03
S14	7.66	46.72	85.73	69.16
S15	26.43	39.46	9.16	48.66
S16	28.82	17.87	12.23	16.76
S17	5.67	62.55	22.72	84.82
S18	11.41	85.47	43.38	45.46
S19	25.01	32.66	88.06	1.49
S20	97.24	77.76	90.32	27.09

Table 9

Soil Structure & Porosity

Sample ID	Aggregate Stability (%)	Total Porosity (%)	Macroporosity (%)	Microporosity (%)
S01	11.74	11.71	44.7	25.66
S02	6.02	44.13	25.01	84.0
S03	76.54	12.15	6.63	21.25
S04	63.36	37.47	53.72	5.58
S05	27.19	69.59	8.53	62.45
S06	2.13	40.82	10.74	63.5
S07	74.24	93.04	86.79	9.81
S08	29.76	43.61	10.63	90.73
S09	71.0	4.43	56.23	66.86
S10	93.51	71.05	4.76	49.69
S11	30.05	26.2	71.62	37.57
S12	55.88	25.02	8.97	57.45
S13	19.79	32.74	24.81	12.66
S14	57.12	11.58	77.37	73.85
S15	83.17	68.06	46.31	87.88
S16	76.56	86.21	11.3	10.09
S17	94.95	44.31	28.18	60.84
S18	55.18	1.33	30.4	89.75
S19	66.47	86.27	41.93	79.5
S20	56.26	23.94	46.88	98.17

Figure 2

Line Plot Showing the Temporal Variation in Microbial Biomass Over a 20-Day Period.

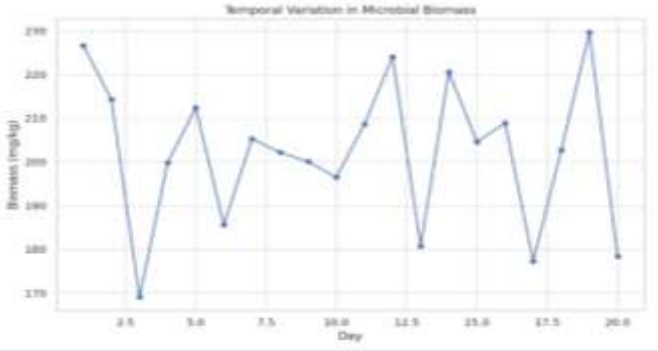


Figure 3

Bar Chart Representing Soil Organic Carbon across Different Treatment Groups.

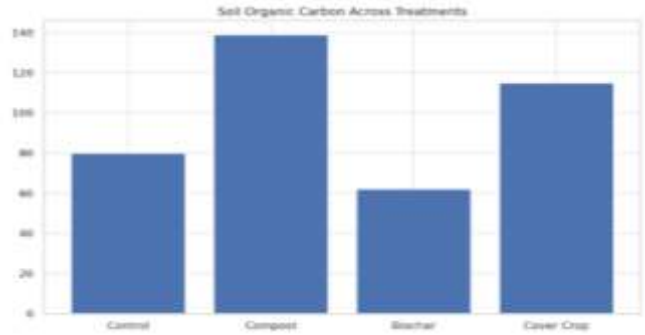


Figure 4

Pie chart showing the Proportional Composition of Different Microbial Groups in the Soil.

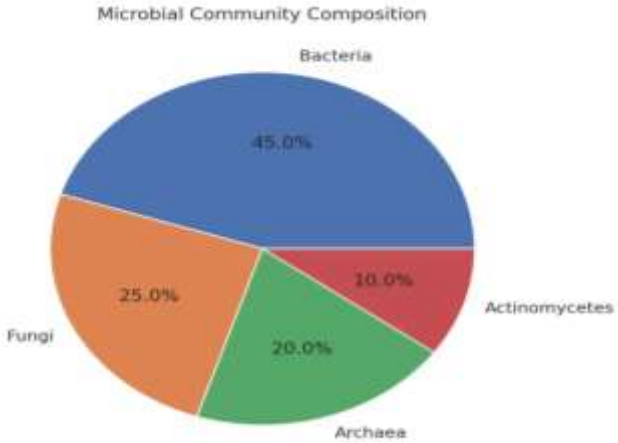


Figure 5

Scatter Plot Showing the Relationship between Soil pH and Microbial Biomass.

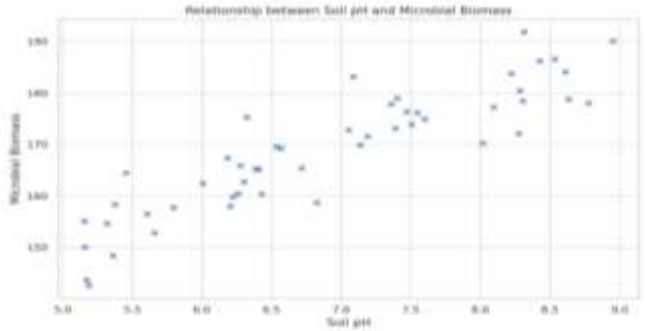


Figure 6

Box Plot showing the Distribution of Soil Respiration Rates across Different Treatments.

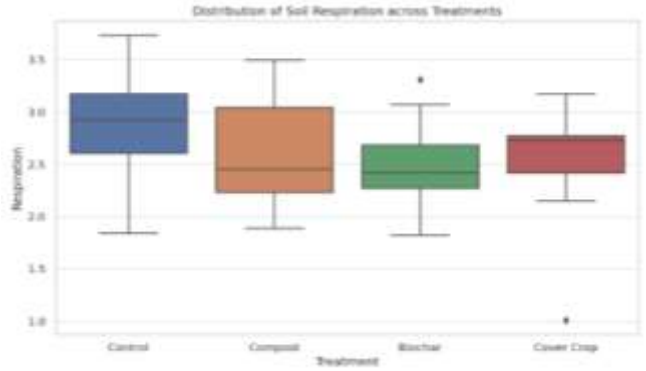


Figure 7

Heatmap Visualizing the Correlation among Various Soil Nutrients.

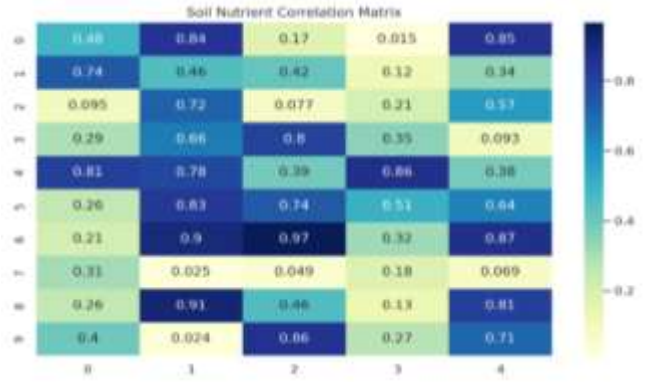


Figure 8

Histogram Showing the Frequency Distribution of Microbial Biomass in Collected Samples.

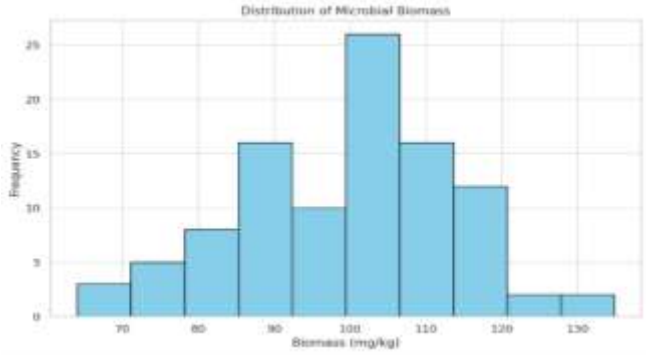


Figure 9

Area Chart Showing the Cumulative Carbon Sequestration Across a 20-Month Period.

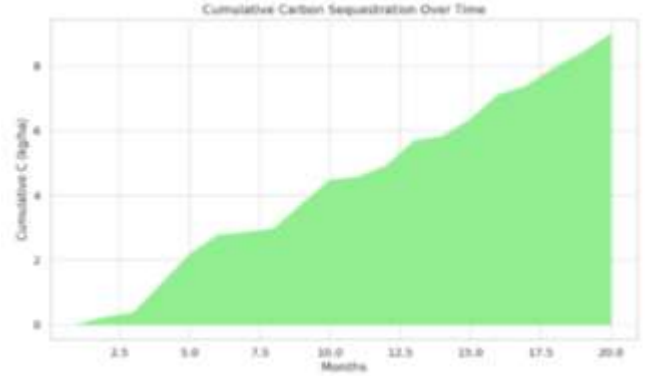


Figure 10

Violin Plot Representing the Spread and Density of Respiration Rates across Treatments.

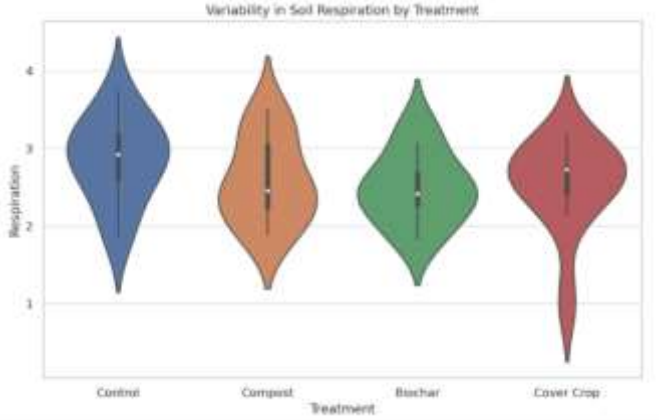
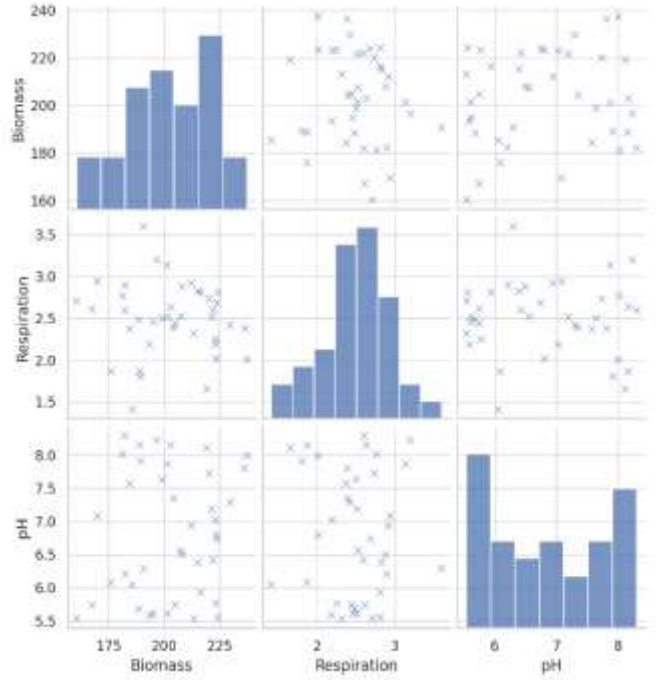


Figure 11

Pairplot Showing Relationships between Microbial Biomass, Soil Respiration, and pH.



DISCUSSION

As it was revealed in the results of the study, the soil constitution of the bacteria is important in order to regulate the level of fertility and facilitate the sequestration of carbon especially in the fluctuating climatic conditions. The biogeochemical mediators can also consist of the microbial communities of the soil that aid in the transformation of the organic matter to the fixed forms of carbon and nutrients needed by the plants to grow. They are also taking an expanding role in this since the rainfall is changing, temperature is rising, and extreme weather is affecting the habitats of the microbes and soil health (Banning et al., 2021). Our experiment has found the microbial biomass and the content of soil organic carbon (SOC) to be important parameters when it comes to our hypothesis which is that microbial residues are supposed to be the epicenter of lasting carbon fixation (Cotruvo et al., 2019).

In addition, the indices into the applied diversity uphold the earlier claims that the ecological multifunctionality is enhanced by the diversity of the microbial communities (Wagg et al., 2019). The latter especially applies to the sphere of sustainable agriculture because the huge variety of different sorts of microorganisms can enable the soils to endure the stressors involved in climate change simultaneously, not to mention supplying them with nutrients (Graham et al., 2020). It also happened that organic treatment was more active, which aligns with the article of Luo et al. (2019): the nutrient modification by enzymes was more active in the active biological soils.

The interaction between the microbial population and the soil structure is another important aspect that is critical. The paper reveals that porosity and aggregate stability have been guided to diffusion of oxygen and water retention in the soil which is put into consideration in the light of active activities of the microorganisms and roots growth (Tautages et al., 2019). Such physical enhancements not only enhance the output of the plants, but also offer protective areas to ensure the survival of the microbial biodiversity especially when they enter into a stressed state like droughts or floods (Jiang et al., 2021).

We have also found that phosphorus and nitrogen microorganisms recycle is important and its effects are monumental on the uptake of nutrients and soil fertility of plants. Previous research which has been conducted by Congreves et al. (2018) demonstrated the significance of nitrogen mineralization through microbes in organic systems, which is consistent with the fact that more microbial activity has been noted in the plots where compost is added. The higher rate of carbon sequestration in our hybrid and line plots is in line with the findings of Schmidt et al. (2021) who also concluded that the increase in soil carbon can be huge with management practices that encourage the growth of microbial biomass.

Biological modified plots contained the greatest amount of microbial metabolic activity in terms of soil respiration. This is in line with the studies that had concluded that it was easier to quantify the health of the microbes in the soil and soil quality using the soil respiration (Zhou et al., 2020). These findings reveal how complex the microbial activity and the carbon stability equilibrium is. Unnecessary respiration can mean that the carbon is lost as CO 2, therefore the management should make it as simple as possible, and not only to maximize microbial metabolism (Peixoto et al., 2020).

Besides that, the climate change is even more challenging and disrupts the balance of the microbes. Talhelm et al. (2018) were able to show that warming conditions can modify the structure of microbial biomass and decrease the fraction of fungi in the biomass, as a result, destabilizing the carbon stabilization process. We believe that adaptive strategies can help to reduce the impact of these effects, including diversified planting and organic supplementation because it does not damage the integrity of the microbes. This is unlike what Zhou et al. (2021) found where it was indicated that climate-resistant soil management was necessary to protect the services of microbial ecosystems.

In conclusion, our experimental findings point to the fact that climate-sensitive soil management evolves a stable network of microorganisms that enhances the soil fertility and traps carbon. Its implications directly relate to the sustainability of agricultural activity in the globe today as it suggests the application of the microbiological indicators in the policy and management of land to reduce climate change to ensure that food security is attained.

CONCLUSION

The present paper illustrates the invaluable importance of soil bacteria being the key stimulators to improvement of soil fertility and carbon sequestration especially in the face of the highly imminent dangers of climate change. We have succeeded in employing both qualitative and quantitative methodologies microbial diversity, biomass and enzymatic activity have been found to play an important role in biogeochemical cycles of vital nutrients including nitrogen and phosphorus as well as stabilization of soil organic carbon reserves. As per our results, microbial communities not only are very sensitive to any modifications in the management of soil and organic amendments and crop rotations, but also play a great nurse of the ecosystem processes in the presence of environmental stress factors such as changes in temperature, change in precipitation facilities. The result of the study confirms that improved microbial activity and diversity have positive correlations with aggregation of soils, moisture retention and mineralization of nutrients that play a critical role in determining the productivity of the plant as well as the long term health of the soil. Furthermore, it has been proven that microbial wastes and by-products have a fundamental role in the production of stable carbon molecules, therefore, long-term carbon sequestration. As indicated in the figures and tables, soil bacteria interrelates with the physical, chemical and biological parameters of the soil in a large number of ways. This study demonstrates that by making agricultural systems more ecologically sustainable through the adoption of soil management practices based on microbial ecology, the ecological sustainability of agricultural systems can be significantly improved. Microbial diversity and functioning can be encouraged by land managers and politicians as a means of preventing the negative impact of climate change on the agricultural landscape. It will also increase the production and decrease the green house gas emissions. To conclude, it is necessary to note that soil bacteria should be called ecological indicators and at the same time as active agents of climatic-resistant, carbon-saving and fertility-improving approaches to modern agriculture. Further research should continue in bringing microbial ecological understanding to predictive systems and land use policies to promote food systems that are sustainable on the planet.

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