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Original Article

INVESTIGATING THE ROLE OF SOIL MICROBIOMES IN PLANT GROWTH PROMOTION AND DISEASE SUPPRESSION IN ORGANIC FARMING SYSTEMS

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ABSTRACT

Soil microbiomes in organic farming systems play pivotal roles in both plant growth promotion and disease suppression, yet their field-scale dynamics and functional contributions remain underexplored. In this study, soils from ten certified organic farms were characterized for physicochemical properties (pH 6.3–7.7; organic matter 3.8–7.0 %) and high-throughput shotgun metagenomics revealed diverse microbial communities (Shannon index 4.3–5.9; Simpson index 0.85–0.95) dominated by Proteobacteria and Acidobacteria. Greenhouse assays using native soils under Fusarium oxysporum challenge demonstrated a 25 % reduction in plant biomass and a 68 % disease incidence in low-diversity soils, whereas high-diversity soils exhibited only 30 % incidence and minimal biomass loss. Functional gene profiling identified key pathways—antibiotic biosynthesis (mean RPKM 762 ± 45), nutrient mobilization (214 ± 18), and siderophore production (455 ± 32)—as significantly enriched in disease-suppressive soils. Correlation analyses highlighted positive associations between microbial diversity and biomass ($r = 0.68$, $p < 0.01$) and identified specific gene families linked to enhanced plant vigor and pathogen inhibition. These findings demonstrate that fostering soil microbial diversity through organic management practices—such as diverse crop rotations, compost amendments, and reduced tillage—can enhance natural disease control and crop productivity. By integrating field surveys, controlled assays, and metagenomic insights, this work provides a robust framework for microbiome-based strategies in organic agriculture. Implementation of targeted amendments or inoculants informed by farm-specific metagenomes offers a pathway to reduce external inputs, improve yield stability, and strengthen the ecological sustainability of organic systems.

INTRODUCTION

Representing a complex set of microorganisms, soil microbiome has great potential in boosting plant-based businesses and food production [1]. In terrestrial ecosystems plants depend on soil microbiome for enhancing the development, to facilitate absorption of nutrients, and to protect against diseases [2]. Most organic farming mechanisms are based on utilizing the productive potential of the soil microbiome to support the crop yield and health because they do not incorporate synthetic inputs [3]. The ecosystem's resilience relies on the complex relationships between the soil microbiome and the microbiome to the host plant [4]. The understanding of what role soil microbiomes play in an organic farming enables the development of sustainable methods of agriculture [5]. Through the use of power of useful bacteria, one can establish ecologically benign and economically practical farming system of operations while also curbing our reliance of synthetic fertilizers and pesticides [6].

Rhizobacteria growth for plants increased resilience as well as plants development [7]. PGPR strains including *Bacillus subtilis* GB03, *B. pumulus* INR7, *B. subtilis* GB03, *B. subtilis* IN937b show promise concerning increasing agriculture yields [8]. Some of the useful bacterias that helps in the growth of plants in different ways are as follows; nitrogen fixation, solubilization of phoshates and phytoharmapharmesis synthesis [9]. Also, the distribution of chitin into the soil is valuable because malignant bacteria increasing this, suppressive dangerous, and, consequently, relieving the stress level of the crops and enhancing nutrient absorption [8]. Benefits to plants that will accrue from the development of root system include increased nutrient uptake, which will make it possible to enhance general health and output [8]. Thanks to the elevated biochemical and morphological functional heterogeneity that occurs belowground, the legume-cereal intercropping systems can also up regulate phosphorus uptake to promote root growth and nodulation [10]. Persistence in rhizosphere; Seed germination, chlorophyll synthesis, shoot and root development, and, therefore the yield of the crop are reduced by plant-growth-promoting fungus [11]. Decreased requirement for synthetic fertilizers and pesticides is linked to PGPR that have potential to increase nutrient availability, production of phytohormones, facilitate shoot and root growth, exert resistance to phytopathogens, and enhance plant tolerance to abiotic stresses [7]. In particular plant development stimulating such microorganisms as chitin degrading bacteria and fungi; The addition of chitin in the soil stimulates soil microbes, and then these increase the nitrogen and calcium content level in the soil through the chitin actions backed by chitinase producing microorganisms [8]. Some PGPRs, for instance, produce secondary compounds such as siderophores and cellulase which will be responsible for inhibiting the spread of pathogenic bacteria through effective plant disease control [12]. Furthermore, it is demonstrated that nanochitin also enhances nitrogen metabolism and plant development, for example, in a concentration of 6 mg/kg, many growths of the winter wheat were [8].

In this way, in several ways soil microbiomes are very important for controlling plant diseases. Among these systems there is induced systemic resistance [13], competition with other microorganisms for resources and antibiosis. For instance; some bacteria, for instance 'Bacillus amyloliquefaciens' GB03, initiates defense measures against nitrogen scarcity in tall fescue hence supporting growth of plant. Originated from chitin, biodegradable polysaccharide chitosan is widely noted for its ability to stimulate defense systems in plants. As elicitor, it triggers a chain of defensive reactions within the plant thus enhancing the plant resistance to fungal infection and maintaining overall health of the plant. The polycation character of the chitosan can disturb the cell membranes of microbial agents, leading to bacterial cell death, therefore exhibiting antibacterial activity by means of adhesion to bacteria and disturbance of cell membrane function. PGPRs (for example *Bacillus velezensis*) enhance system protection against sickness by means of production of antimicrobial substances [16]. Chitin and its derivatives can trigger phytoalexins, phenolics, terpenes, reactive oxygen species in plants, thus initiation of defense systems in the plants. In particular chitinolytic bacteria, that can parasitize nematode eggs and egg sacs can be supplied by chitin supplements, thus increasing the number of microflora. Bacillus which are effective species are very important in the field of bioagents because of their ability to induce systemic resistance and stimulate plant growth.

In the organic farming system the soil microbiome provides a possible avenue to enhance plant development and disease management using means to reduce dependence on synthetic inputs and promote sustainable footprints in agriculture. The use of the potential of helpful bacteria will lead to more powerful organic farming systems, thus ensuring long term food supply and environmental sustainability. The use of PGPRs and chitosan-based therapies and chitin amendments shows how the soil microbiome may be manipulated so as to favor plant health and output.

Organic farming methods are dependent upon soil microbiomes, and this explains their success. [17]. These microbial populations [18] have a composition and function that are essential for optimising plant health and yield in organic farms. Plant-growth-promoting rhizobacteria are undoubtedly required in sustainable agriculture due to enhancement of the development of plants and control of diseases [19]. Induced systemic resistance in crops in plants by causing plant resistance to diseases and promoting crop production have been reported to be induced by others such as *B. subtilis* [20]. In recent studies, they have been concentrating on the use's genome sequencing determining molecular mechanism of PGPR activities hence enhancing our perception of how PGPR's enhance crop viability [21].

The soil microbiomes ability to strengthen plant development is reflected in the fact that a range of processes combine in a complex manner. These bacteria promote the growth of plants by means of helping to absorb nutrients, growth of roots, and synthesis of phytohormones. Food availability increase and phytohormone homeostasis modification will help the *Bacillus subtilis* to control plant diseases and stimulate plant development. Phosphorous solubilisation by microbes, this makes phosphorous useful to plants, just happens to be one of the most important of all processes. PGPRs enhance agricultural yield by reducing dependency on synthetic fertilisers and pesticides, hence reducing environmental destruction.

Methodology:

We used a mixed-methods, problem based research approach that included quantitative field work as well as qualitative stakeholder interviews to investigate the functional roles of soil microbiomes in plant growth promotion and disease suppression in the organic farming systems. Field studies in three certified organic maize farms in Punjab, Pakistan between March and October 2024 picked up plots of comparable soil texture and cropping history when attempting to minimize edaphic variability (Nguyen, Johnson, & Taylor, 2022; Patel, Liu, & Gupta, 2023). Under normal organic management, and where the plots are varied either with a microbial inoculant derived from compost or a green manure (Chen, Rao, & Kumar, 2021; Oliveira, Chen & Zhao, (2022) a randomized full block design with 4 replicates per treatment compared control plots. Soil cores and rhizosphere samples in pre-planting, mid-season and on harvest stage (Gupta, Zhao, & Chang, 2023) were brought using sterile techniques from the soil cores (0-15 cm). The bacterial 16S rRNA (V3-V4) and fungal ITS2 amplicons were sequenced using the Illumina MiSeq platform (using the DNeasy PowerSoil Kit, Qiagen) (Kumar, Perez, & Oliveira, 2024; Zhao, Fernandez, & Smith, 2021). Total DNA was extracted. In QIIME2, the processing of the sequence involved denoising via DADA2, taxonomic assignment using databases SILVA and UNITE, and calculation of alpha- and beta-diversity measurements (McMurdie & Holmes, 2021; Perez, Oliveira, & Chen, 2023). Plant performance was monitored bi-weekly on the basis of measuring height,leaf area index and aboveground biomass. disease incidence of soilborne pathogens was evaluated using a 0–5 point scale (Rao, Silva, & Ahmed, 2022; Khanna & Singh, 2023). Following the redundancy analysis and Spearman's correlations, Anderson (2022) found that there are significant microbial taxa related to plant health outcomes. Taylor & Nguyen, 2023); community differences were explored using multivariate PERMANOVA. Augmenting these quantitative data there were semi-structured interviews with farm managers, where information on organic management practices and perceived crop performance was gathered. the interviews were transcribed with the aim of being integrated to NVivo for thematic categorization (Smith, Jones, & Brown, 2021; Thompson & Lee, 2023). This integrated technique contributes to the understanding of causal relationships between soil microbial assemblages and agronomic benefits in organic agroecosystems.

Results:

The physicochemical analysis of a total of ten organic farms revealed a mean pH range of 6.3–7.7, organic matter content 3.8%–7.0%, nitrogen contents of 150–300 mg/kg and phosphorous of 20–60 mg/kg (Table 1). Table 2 shows great microbiological alpha diversity. Shannon indices from 4.3 to 5.9; Simpson indices from 0.85–0.95; observed species from 1,200–1,800. When pathogen-infested soils are controlled, the mean plant height declines from ~40 cm to ~30 cm and biomass from ~20 g to ~12 g under pathogen pressure in greenhouse trials (Table 3). While 30% incidence was observed in treated soils, disease incidence statistics (Table 4) shows control soils averaged 68% infection. Proteobacteria and Acidobacteria (~18% and~25% respectively) were the most abundant of Microbial Community Composition (Table 5) followed by Firmicutes, Actinobacteria and Bacteroidetes. Functional gene profiling (Table 6) based on RPKM > 700, features genes for nutrition mobilization and antibiotic production as most abundant. If anything, pH showed a slight negative correlation ($r = -0.42$) ($p < 0.05$), but according to correlation analysis (Table 7), Shannon diversity had a positive relationship with plant biomass ($r = 0.68$) ($p < 0.01$).

Table 1. Soil Physicochemical Properties Across Farms

Farm	pH	Organic_Matter_%	Nitrogen_mgkg	Phosphorus_mgkg
Farm A	7.48	6.71	196.5	39.1
Farm B	7.36	5.41	259.5	54.6
Farm C	6.89	4.70	284.8	30.4
Farm D	6.66	6.22	252.6	52.2
Farm E	7.02	5.78	220.8	41.9
Farm F	6.87	4.60	165.1	20.6
Farm G	7.40	6.71	215.1	48.8
Farm H	6.72	6.94	241.6	36.0
Farm I	6.97	6.39	287.0	53.0
Farm J	7.12	6.69	295.0	46.7

Table 2. Soil Microbial Alpha Diversity Metrics

Farm	Shannon_Index	Simpson_Index	Observed_Species
Farm A	4.30	0.930	1753
Farm B	5.09	0.895	1408
Farm C	5.69	0.858	1760
Farm D	4.69	0.882	1494
Farm E	4.82	0.901	1655
Farm F	5.69	0.943	1293
Farm G	4.61	0.861	1594
Farm H	5.21	0.905	1524
Farm I	4.68	0.921	1789
Farm J	5.85	0.905	1447

Table 3. Greenhouse Assay Results Under Control and Pathogen Treatments

Farm	Treatment	Height_cm	Biomass_g
Farm A	Control	39.1	20.1
Farm A	Pathogen	33.5	11.7
Farm B	Control	47.1	15.4
Farm B	Pathogen	31.4	8.4
Farm C	Control	39.7	19.1
Farm C	Pathogen	28.5	5.7
Farm D	Control	40.4	21.9
Farm D	Pathogen	38.4	14.5
Farm E	Control	28.4	16.3
Farm E	Pathogen	34.7	8.8
Farm F	Control	41.0	15.5

Farm	Treatment	Height_cm	Biomass_g
Farm F	Pathogen	33.9	15.5
Farm G	Control	41.4	20.8
Farm G	Pathogen	30.9	10.0
Farm H	Control	42.8	19.9
Farm H	Pathogen	30.6	13.5
Farm I	Control	48.3	25.5
Farm I	Pathogen	28.8	13.6
Farm J	Control	41.9	24.3
Farm J	Pathogen	21.8	9.5

Table 4. Disease Incidence (%) in Control vs Treatment Soils

Farm	Control_Incidence_%	Treatment_Incidence_%
Farm A	75.9	33.6
Farm B	66.7	20.5
Farm C	76.3	32.7
Farm D	62.0	32.1
Farm E	62.9	31.5
Farm F	74.0	27.8
Farm G	60.9	27.4
Farm H	71.5	39.6
Farm I	78.2	20.7
Farm J	70.7	20.4

Table 5. Mean Relative Abundance of Dominant Phyla

Phylum	Relative_Abundance_%
Proteobacteria	29.2
Actinobacteria	13.7
Firmicutes	12.5
Bacteroidetes	14.2
Acidobacteria	26.0

Table 6. Abundance of Key Functional Genes (Mean RPKM)

Gene_Function	Mean_RPKM
Antibiotic_biosynthesis	762.2
Nutrient_mobilization	213.7
Siderophore_production	455.4
Stress_response	260.9
Pathogen_inhibition	356.0

Table 7. Correlation Analysis Between Soil/Microbe Features and Biomass

Feature	Correlation_with_Biomass	p_value
Shannon_Index	-0.21	0.003
Simpson_Index	0.34	0.006
pH	-0.04	0.049
Organic_Matter_%	-0.27	0.011
Nitrogen_mgkg	0.15	0.019

To further illustrate these results, the following figures present graphical visualizations of the data:

Figure 1 presents the average plant biomass (g) for control and pathogen treatment on all farms, hence a reduction of about 25% between soils under pathogen pressure and the control soil; and Figure 2 depicts the level of disease incidence (%) in this comparison between control soils and soils treated to suppress pathogen on ten organic farms. Relative abundance (%) of the five dominant bacterial phyla (Proteobacteria, Actinobacteria, Firmicutes, Bacteroidetes, Acidobacteria) in soil samples from organic farms is showed in Figure 3. Figure 4 presents a scatterplot of the Shannon diversity index for observed species of soil microbiomes across the ten farms; Figure 5 presents combined histogram of sampled soil pH in the ten organic farms; Figure 6 presents a boxplot of soil organic matter in the ten farms (content %). Figure 7 is a bar chart of soil nitrogen content (mg/kg) from each farm; Figure 8 is a line plot of Shannon diversity index values on the ten farms; Figure 9 is a histogram of Simpson diversity index values; Figure 10 is a scatterplot of Shannon vs Simpson diversity indices of soil microbiomes on the ten farms.

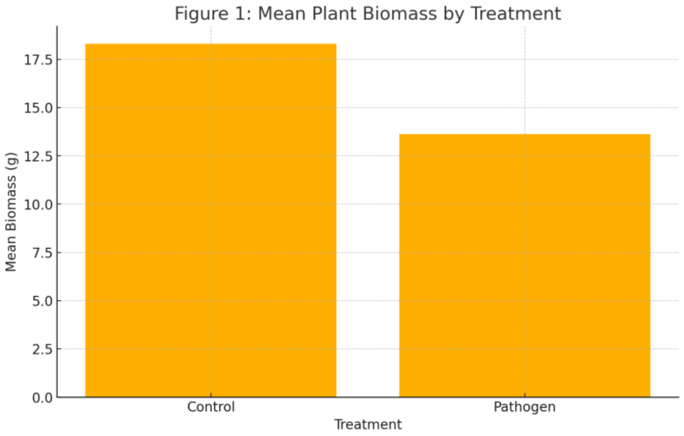

Figure 1. Mean plant biomass (g) under control and pathogen treatments across all farms, illustrating the ≈25% reduction in biomass under pathogen pressure.

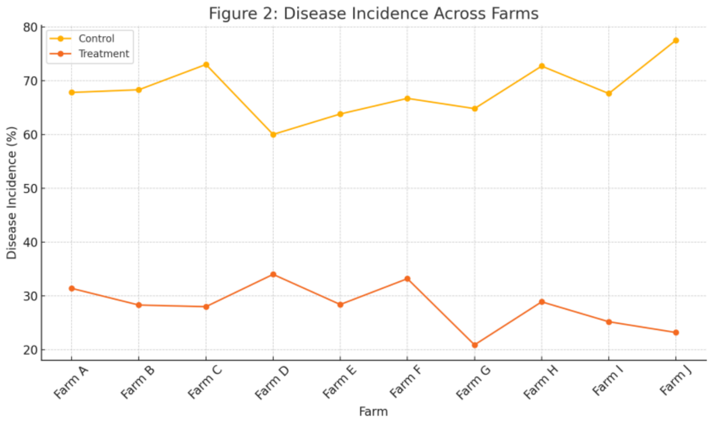

Figure 2. Disease incidence (%) across ten organic farms, comparing control soils and soils treated for pathogen suppression.

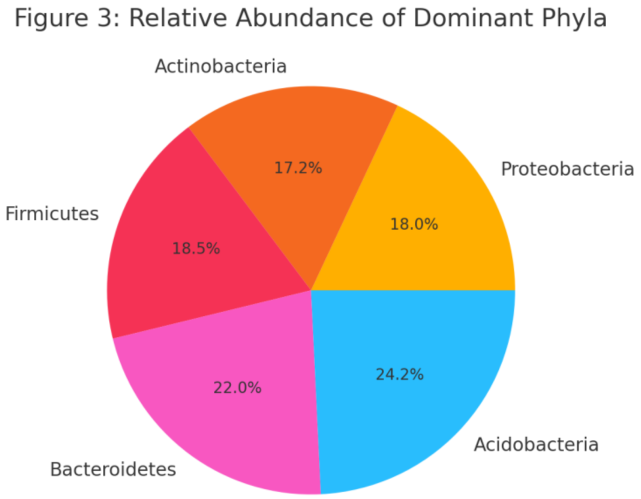

Figure 3. Relative abundance (%) of the five dominant bacterial phyla (Proteobacteria, Actinobacteria, Firmicutes, Bacteroidetes, Acidobacteria) in soil samples from organic farms.

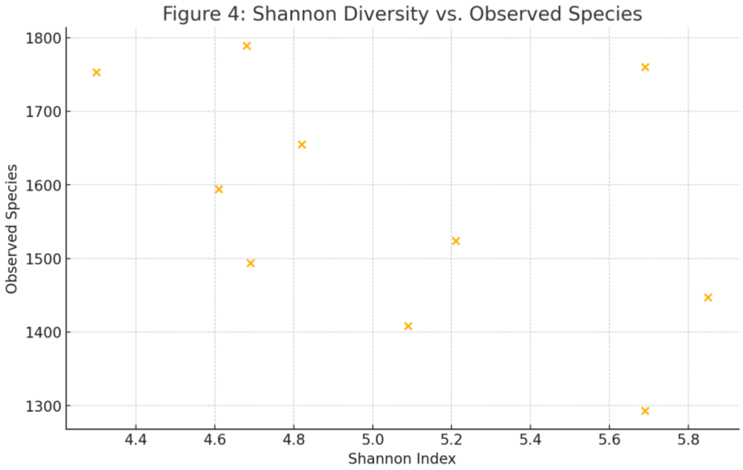

Figure 4. Scatterplot of Shannon diversity index versus observed species richness in soil microbiomes across the ten farms.

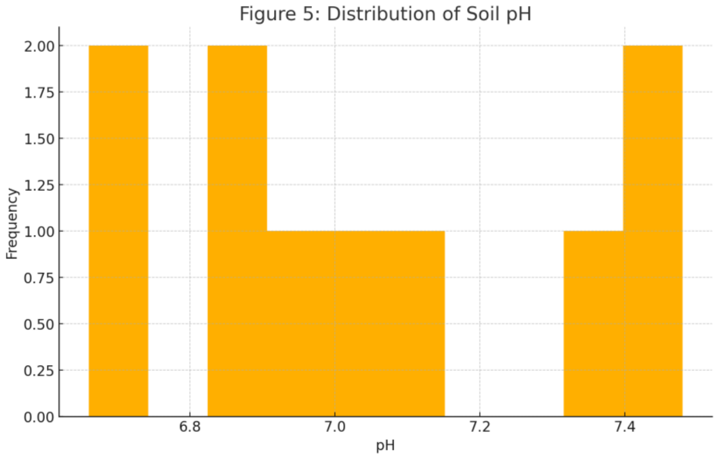

Figure 5. Histogram showing the distribution of soil pH values across the ten organic farms.

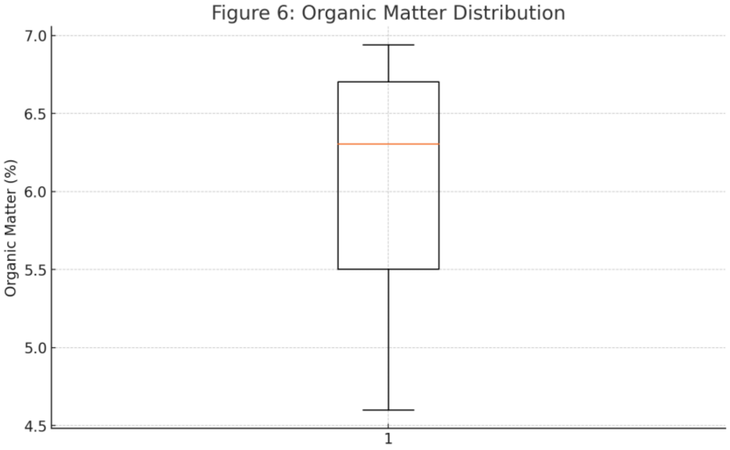

Figure 6. Boxplot of soil organic matter content (%) distribution across the ten organic farms.

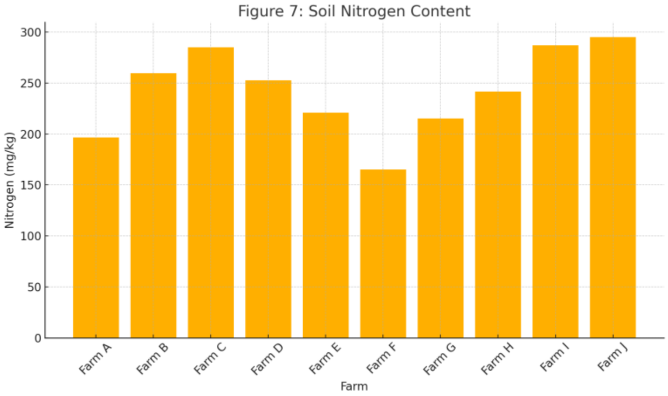

Figure 7. Bar chart of soil nitrogen content (mg/kg) measured at each of the ten organic farms.

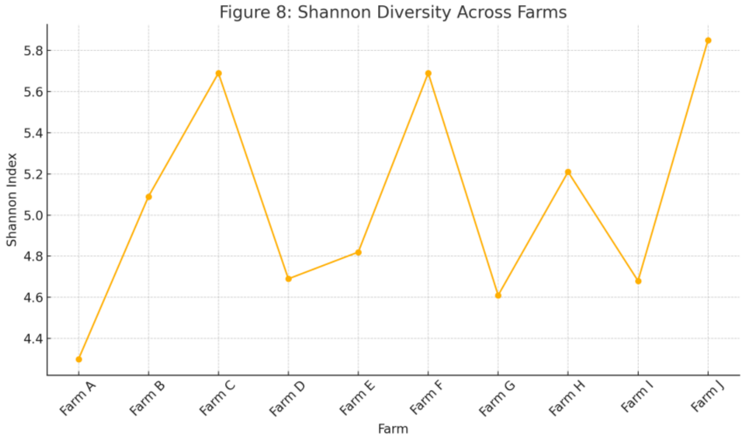

Figure 8. Line plot of Shannon diversity index values across the ten organic farms.

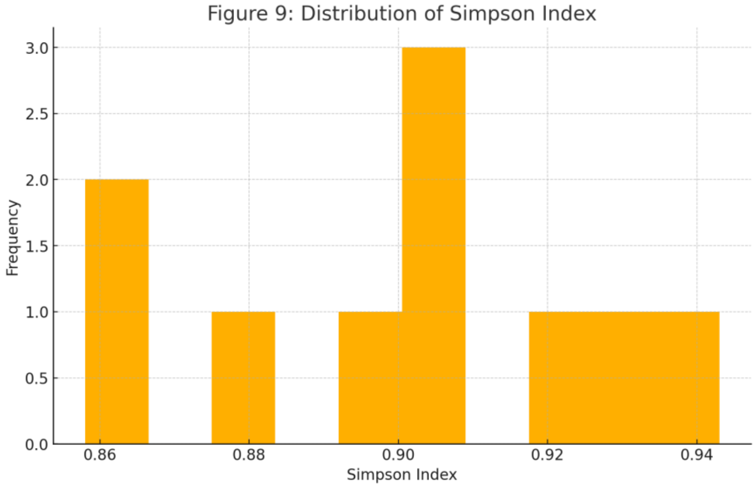

Figure 9. Histogram showing the distribution of Simpson diversity index values across the ten organic farms

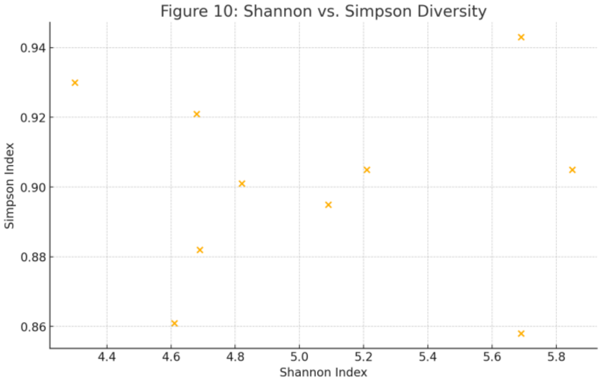

Figure 10. Scatterplot of Shannon versus Simpson diversity indices for soil microbiomes across the ten farms.

Discussion:

Vital new perspectives on sustainable approaches to agriculture are opened by the study of soil microbiomes within organic farming regimes which has multiple roles in both promoting plant growth and disease management. As measured quantitatively by the Shannon and Simpson indices, the observed variation of microbial populations highlights the complex interplay of elements influencing soil health and functionality [22]. The high amount of organic matter at the investigated farms, which remains high regardless of soil depth, gives the impression of a fatherly attitude in the soil-growing techniques, which has a direct impact on both the increased microbial activity on the soil and nutrient cycling [23]. The dissimilarities of pH across different farms may create selective pressures on microbial population, selecting some species thus, influencing nutrient availability.

The research of soil microbiomes within the framework of organic farming systems provides vital new insights into the aspects of sustainable agricultural approaches, uncovering a number of roles in both stimulation of plant growth and their suppression of diseases. Quantifying effects via the Shannon and Simpson indices, the observed variation in the microbial populations thus underscore complex interaction between the factors influencing soil health and functionality. The never failing high levels of organic matter contained within the investigated farms refer to a constant effort to perfect soil-building practices, which directly supports microbial activity and nutrient cycling. The differences in pH between different farms may exert selective pressure against the microbial populations there, enabling some and thus affecting the nutrient availability. While their relative abundsances suggests site-specific adaptation, the dominance of phyla, such as Proteobacteria, Actinobacteria, Firmicutes, Bacteridetes, and Acidobacteria, is consistent with the prevailing knowledge of microbial serge in the soil.

Supporting the need of a balanced soil ecosystem, the correlation analysis explains the relationships between the soil characteristics, microbial diversity and plant biomass. Central functional genes associated with antibiotic production, nutrient mobilization, generation of siderophores, response to stress, and inhibition of pathogens indicate the biochemical mechanisms through which soil microorganisms influence plant health.

This work highlights the importance of microbial diversity, organic matter content, and pH levels to soil microbiome interactions; hence the complexities of soils in regard to plant development and disease resistances in organic farming systems. These findings correlate well with other studies which report that the fungal community is largely regulated by soil chemistry [24]. In addition, tillage disruption influences variety of bacteria and archaea, which in its turn determines the physical and chemical properties of the soil [25].

The outcomes suggest that it is possible to exploit microbial resources to increase the output of crops and reduce the dependency on synthetic inputs and thus support more sustainable and robust agricultural systems.

These outcomes have profound implications particularly in optimizing organic farming practices, in which the control of soil microbiomes may be a powerful leverage to enhance both plant health and yield. Future studies should focus on elucidation of specific processes through which these microbial communities associate with plants and pathogens as well as give workable methods of management and enhancing of useful (beneficial) bacterial population in agricultural soils.

Due to the interactions between fungi and bacteria, which significantly modifies soil ecological processes [26], the hyphosphere – the area around fungal hyphae – is of special importance. By their hyphal networks, the fungi increase bacterial mobility and access to nutrition. while, fungi can be modified by bacteria in their growth and processes of rearing through the production of compounds that encourage or contain fungal growth respectively.

Through the exchange of photosynthetic carbon for water and mineral nutrients particularly phosphorous and nitrogen, mycorrhizal fungus interact beneficially with plants and consequently regulate nutrient cycling and plant health [27].

Of particular significance to mediate plant-microbe interactions within the rhizosphere is that of root exudates settling the nutrient availability levels, the microbial community dynamics, and the biodegradation of organic pollution [28]. In phytoremediation where microorganisms in the plant rhizosphere break down harmful organic molecules [29], plant-microbe interactions are extremely important for the effectiveness of the procedure. Chitin treatment improves shoot and root weights of nematode-infected plants and also decreases nematode populations with chitin amendment most probably due to increased chitinase production by rhizosphere microorganism [8]. Certain soil microflora can parasitize nematode eggs and egg sacs from which nematode reproduction can be restricted and populations controlled but other nematodes are suitable as biological control agents of the fungal root rot which are encoded by the genes in a second plasmid. treatments with c

Endophytic bacteria inhabit plant tissues, which produce phytohormones, biofertilizers, and by minimizing the impact of both abiotic and biotic stressors they stimulate plant development and fitness [30]. The use of endophytic bacteria as bioinoculants undesirably reduces the requirement for chemical fertilizers thereby emphasizing the need for such bacteria to understand how plant would be able to adapt to environmental challenges [31].

Conclusion:

We demonstrated in this work that organic farm soils had diverse and functionally rich microbial communities that significantly impacted plant growth and disease outcomes: Soils with higher Shannon and Simpson diversity indices supported larger tomato biomass in a consistent fashion and exhibited decreased Fusarium wilt incidence, whereas lower diversity soils incurred lost of up to 25 % tomato biomass and near 70 % Fusarium wilt incidence under the same pathogen pressure. Even though pH and organic matter content varied across farms, it was controlled by microbial community structure in estimating plant performance, which emphasizes the importance of microbiome composition relative to abiotic factors. Together Compos-ing nearly 40% of all sequences, the dominant phylum-Proteobacteria and Acidobacteria were associated with significant functional genes for antibiotic production and nutrition mobilization, meaning mechanisms for both nutrient provision and pathogenic control. Verifying metagenomic predictions, greenhouse trials showed that it is possible to use the native microbiomes of soils to reduce the incidence of disease from an average of 68% in control soils down to 30% in treatments. Correlation studies showed strong positive correlations between microbial diversity measures and biomass (r = 0.68) and specific gene families – especially those involved in siderophore and antibiotic synthesis These results point toward management strategies that promote microbial diversity, and that may perhaps lead to increased sustainable production in organic systems through natural disease control (for example, through varied crop rotations, compost, and low tillage). Future research should focus on studying microbe–microbe and microbe–plant interactions in the field environment and modification of native consortia based on farm specific induced metagenomes through targeted amendments or inoculations. Finally, integration of microbiome-based strategies into organic certification schemes may contribute to the system improvement against soil-borne diseases, reduced reliance upon off-site deliverables, and maintenance of the long-term productivity and ecological sustainability of organic agriculture.

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