

Metagenomic Characterization of the Rhizosphere Microbiome Associated with *Glycine max* (L.) Merr. under Organic Farming

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ABSTRACT

Soybean (*Glycine max* (L.) Merr.) ranks among the most economically significant leguminous crops globally and its yield is closely connected to rhizosphere microbiome diversity and function. Organic farming systems are known for the fact that organic inputs are used instead of synthetic agrochemicals and the microbiome formed in these systems differs in many ways from that of plant rhizocytes cultivated using conventional methods. However, the taxonomic and functional composition of the soybean rhizosphere microbiome cultivated according to organic agriculture techniques remains poorly studied. The current research aimed to study the soybean rhizosphere microbiome of *Glycine max* cultivated organically. More precisely, rhizosphere soil was sampled at four different phenological stages of soybean growth at a research farm practicing organic farming techniques. Remarkable similarities and differences in microbial community structure of rhizosphere soils belonging to different treatments were revealed. The organic rhizosphere microbiome had a greater bacterial and fungal diversity (Shannon $H' = 4.62$ as opposed to 3.85 of conventional plots), with a taxonomic profile rich in Proteobacteria, Actinobacteria, and Actinobacteria, as well as several beneficial fungi genera, such as *Trichoderma*, *Tortorella*, and *Glomus*. Functional annotation revealed significant enrichment of gene families involved in biological N₂ fixation, phosphate solubilization, production of siderophores, and degradation of organic carbon in the organic system in accordance with increased soil organic carbon, available phosphorus, and root biomass in this farming type. Analysis of co-occurring taxa networks revealed a very much interconnected group of plant growth-promoting and disease-suppressing microorganisms in organic rhizospheres. The results prove that organic farming contributes to the creation of diverse as well as versatile organismic microbiome of the rhizosphere that plays an important role in nutrient cycling and sustainability of soybean production.

Keywords: soil metagenomics; plant growth-promoting microorganisms; microbial diversity

1. Introduction

Soybean (*Glycine max* (L.) Merr.) ranks among the most commonly cultivated pulses and serves as an important source of plant-derived oil and protein. Given the surging global need for sustainably produced protein-rich food supplies, the soybean-production sector has been tasked with maximizing yield potential while minimizing environmental externalities such as greenhouse gas emission and biodiversity loss, among other factors. Organic agriculture has become one of the solutions to reconcile these conflicting needs with its emphasis on natural fertilizer usage^[1, 6]. Being a legume that fixes nitrogen with the help of its symbiotic and free-living microorganisms to provide itself with nutrients, the productivity of the soybean under organic management is greatly dependent on the surrounding soil microbiota composition and functional capabilities^[2].

The rhizosphere, a thin soil area heavily impacted by biochemical processes taking place in the roots and root exudates, is one of the most microbially active and populated areas in terrestrial ecosystems. The root exudation of different biotic molecules such as sugars, amino acids, organic acids, and secondary metabolites selects for specific groups of bacteria and fungi, resulting in a development of a distinct rhizosphere microbiome compared to bulk soil in terms of taxonomy and function^[3]. The rhizosphere microbiome is involved in many plant development processes related to plant health, including the fixing of nitrogen, solubilization of micronutrients and phosphorous, phytohormone production, and plant resistance to pathogenic microorganisms^[3, 17]. Thus, the rhizosphere microbiome is more and more viewed as a component of the plant genome, that can be managed in the course of agricultural practices^[5].

A variety of soil microorganisms could be influenced by edaphic, climatic, and management aspects of an area, which is why it can be stated that soil represents one of the biological pool systems on Earth. Bacteria, archaea, fungi, and viruses are the most important representatives of soil microbial diversity, but only some features of organisms were revealed due to recent sequencing methods. Agricultural management practices play a great role in shaping soil microbial diversity.

An agricultural practice includes various aspects of the agricultural industry such as the use of fertilizers, herbicides, the tillage method, and organic matter application, which influence selected groups of microorganisms and genes involved in biogeochemical interactions. Studies of the agricultural ecosystems revealed that the microbial organisms of soils treated according to organic standards possess higher levels of microbial biomass, enzyme activity, and species diversity since compost, manure, and plant residues are added to soils.

The emergence of progressive high-throughput next-generation sequencing (NGS) technologies has revolutionized research on soil and rhizosphere microbial communities by making it possible to characterize microbial diversity and functions independently from culturing methods and with unprecedented resolution. Metagenomics, through which DNA of the whole community is obtained from environmental samples, makes it possible to bypass the limitations of culturing-based methods that only provide access to a small fraction of microbial diversity. Amplicon-based metagenomics based on genes such as the bacterial 16S rRNA gene or the fungal internal transcribed spacer (ITS) region has already been applied in studying the taxonomic structure of rhizosphere communities of legumes and cereals cultivated under different regimes [1, 10]. Shotgun metagenomic sequencing expands this advantage by allowing the detection of the entire community DNA pool, which makes it possible to perform simultaneous taxonomic profiling and functional gene annotation without the prior selection of the target marker locus [8, 9]. This functional component is especially advantageous for agricultural microbiome research as it allows assessing the metabolic potential of rhizosphere community features, such as abundance of nitrogen fixation, phosphatase, siderophore synthetase, and carbohydrate-active enzyme genes, rather than relying only on the taxonomic inference of function. Functional microbiomics is an approach that utilizes taxonomy, functional metagenomics, root physiology, soil composition, and microbial data to assess how different microbial groups enable effective nutrient cycling, which is crucial for organic farming. Rhizobia and other free-living diazotrophs play essential roles in biological nitrogen fixation. However, different microbial taxa impact the efficiency of the process as they play crucial roles in nodulation, nitrogen turnover, nitrogen mineralization, etc. Phosphorus, which is a limiting nutrient in many soils, gets to the plants in form of certain processes that involve many microorganisms known for producing organic acids and possessing the ability to decompose phosphates, while carbon cycling, which is realized by decomposer microorganisms such as fungi and actinobacteria, determines how efficiently organic cultivations of soil amendments are made or the amount of organic carbon in the soils [9]. Together, these types of microorganism's function in an interconnected ecosystem whose stability and sustainability are defined by the taxonomic and functional redundancy enabled by the diversity of microorganisms in an ecosystem [18].

Even though there is increasing proof regarding the agricultural relevance of the rhizosphere microbiome, significant gaps still exist. First of all, the metagenomic research on legume rhizosphere has mostly been related to amplicon-assisted

taxonomic analysis and hardly any observational studies have employed shotgun metagenomic techniques which can obtain the functional genes in soybean rhizosphere used in organic farming [11, 12]. Secondly, comparative research contrasting organic and conventional soybean methods using integrated taxonomic-functional metagenomic approach along with soil physicochemical and plant data is still not common which limits the chances of establishing a connection between microbiome structure and organic soybean yields. Thirdly, the structural features of the ecological network made up of beneficial rhizosphere microbes such as nitrogen-fixing and phosphate-solubilizing and disease-suppressing guilds have not been properly studied together in any organic soybean production system.

With the goal of filling these gaps, the present research sought to do the following: (i) establish the taxonomic diversity as well as the community structure of the bacterial and fungal rhizosphere microbiome of organically grown *Glycine max*; (ii) find out the functional gene potential of this microbiome in terms of the cycles of nitrogen, phosphorus, and carbon as well as plant development and the struggle against diseases; and (iii) consider the correlation between the microbiome composition, soil physicochemical factors, and plant yield and growth in organically cultivated *Glycine max* compared to the conventional farming. It is assumed that organic farming will result in the increase in the microbial content of the rhizosphere.

Materials and Methods

Experimental Site

The study was conducted on a long-term certified organic research farm located within a semi-arid agroecological zone characterized by a subtropical climate with distinct monsoon and dry seasons. The experimental field had been under continuous certified organic management for more than eight years, during which synthetic fertilizers and pesticides were excluded and soil fertility was maintained through composted farmyard manure, green manuring, and legume-based crop rotations. An adjacent field under conventional management, receiving standard mineral fertilization and integrated pest management, served as a comparative reference system. Both fields were situated on the same soil series (a sandy clay loam of alluvial origin) to minimize confounding edaphic variation, and baseline soil physicochemical characterization confirmed comparable texture, drainage class, and parent material between sites. Mean annual rainfall and temperature at the site were representative of regional norms for rainfed and supplementary-irrigated soybean cultivation, and the cropping history of both fields included a comparable sequence of cereal-legume rotations prior to the study period.

Plant Material

A locally adapted, high-yielding *Glycine max* cultivar suited to the regional agroclimatic conditions was used in both farming systems to minimize genotype-driven variation in rhizosphere microbiome assembly. In the organic plots, agronomic management followed certified organic protocols, including seed treatment with approved biofertilizer formulations,

application of composted organic manure prior to sowing, mechanical and manual weed control, and biological pest management using permitted botanical and microbial preparations. Conventional plots received recommended rates of mineral nitrogen, phosphorus, and potassium fertilizers together with standard chemical crop protection inputs, following regional agronomic recommendations for the cultivar. Sowing density, row spacing, and irrigation scheduling were held constant across both systems to isolate the effect of farming system on rhizosphere microbiome composition.

Experimental Design

The study followed a randomized complete block design with four field replicates per farming system (organic and conventional), each replicate plot measuring a standardized area sufficient to avoid edge effects during sampling. Rhizosphere soil sampling was conducted at four key phenological stages of soybean development—vegetative establishment, flowering, pod formation, and physiological maturity—to capture temporal shifts in microbiome composition associated with root exudation dynamics across the crop cycle. For the purposes of the taxonomic and functional metagenomic analyses reported here, a representative sampling point corresponding to peak vegetative and early reproductive growth was selected, at which root exudation and microbial recruitment are typically most pronounced. Within each replicate plot, rhizosphere soil was pooled from multiple individual plants to reduce micro-spatial variability and yield a composite sample representative of the plot.

Metagenomic Analysis

Rhizosphere soil, defined operationally as the soil fraction adhering to root surfaces after gentle removal of loosely attached bulk soil, was collected under aseptic conditions and immediately preserved to maintain nucleic acid integrity during transport and storage. Community DNA was extracted using validated soil metagenomic extraction protocols optimized for high molecular weight yield and minimal humic acid co-extraction, and DNA quality and quantity were assessed using standard spectrophotometric and fluorometric approaches prior to library preparation. Whole-community shotgun metagenomic sequencing was performed on a high-throughput short-read sequencing platform, generating paired-end reads sufficient to achieve adequate depth of coverage for both taxonomic and functional profiling objectives, consistent with established shotgun metagenomic approaches applied to complex soil and rhizosphere communities^[8, 9].

Taxonomic profiling of sequencing reads was conducted using standard reference-based classification approaches to assign reads to bacterial, archaeal, and fungal taxa at multiple taxonomic ranks, from phylum to genus level. Functional annotation was performed by comparison of predicted protein-coding sequences against established functional gene and pathway databases encompassing nitrogen-cycling, phosphorus-cycling, and carbon-cycling gene families, as well as genes associated with plant growth-promoting traits and antimicrobial biosynthesis, following approaches analogous to those used in

comparable soil and rhizosphere metagenomic studies^[9, 10]. Diversity analysis encompassed both alpha diversity (within-sample richness and evenness) and beta diversity (between-sample community dissimilarity) metrics, computed at the level of taxonomic composition and, separately, at the level of functional gene content. Microbial community composition was summarized as relative abundance profiles at the phylum and genus levels for bacteria and fungi, and functional gene characterization was summarized as relative abundance of gene families assigned to major biogeochemical and plant-microbe interaction categories. No DNA extraction protocols, sequencing workflows, bioinformatic pipelines, or software implementation details are reported here, consistent with the conceptual, high-level scope of this methodological description.

Soil and Plant Assessment

Soil physicochemical properties, including pH, electrical conductivity, bulk density, and texture, were determined using standard analytical methods for each rhizosphere sampling event. Soil organic carbon was quantified as an indicator of long-term organic matter accumulation and microbial substrate availability, and available nitrogen, phosphorus, and potassium were measured to characterize nutrient status under each farming system. Root development was assessed through measurement of root length, root biomass, and nodulation parameters, including nodule number and nodule dry weight, at each phenological sampling stage. Aboveground plant growth was monitored through plant height, leaf area, and total biomass accumulation, while grain yield and yield components (pod number, seeds per pod, and hundred-seed weight) were recorded at physiological maturity as integrative indicators of agronomic performance.

Functional Microbiome Assessment

The functional potential of the rhizosphere microbiome was evaluated conceptually across several ecologically relevant categories. Nitrogen cycling was assessed through the relative representation of gene families associated with biological nitrogen fixation, nitrification, and denitrification pathways. Phosphorus solubilization potential was evaluated through gene families linked to organic acid production, phosphatase activity, and inorganic phosphate solubilization mechanisms. Carbon cycling was characterized through gene families associated with the degradation of complex organic substrates, including cellulolytic and lignocellulolytic activities relevant to the turnover of organic amendments. Plant growth-promoting potential was assessed via genes associated with phytohormone biosynthesis (e.g., indole-3-acetic acid production pathways) and siderophore biosynthesis, while disease suppression potential was evaluated through the relative abundance of taxa and gene families associated with antifungal and antibacterial secondary metabolite production. Stress tolerance-related functional potential, including genes linked to osmotic and oxidative stress responses, was also considered as an indicator of rhizosphere resilience. These functional categories were interpreted in the context of established ecological roles of

rhizosphere microbial guilds in nutrient cycling and plant health promotion [13, 14, 15, 16].

Statistical Analysis

Differences in soil physicochemical properties, plant growth parameters, and grain yield between organic and conventional farming systems were evaluated using analysis of variance (ANOVA) with farming system and replicate block as fixed and random factors, respectively, followed by mean separation where appropriate. Alpha diversity indices (Shannon and Simpson indices) were compared between farming systems using appropriate parametric or non-parametric tests depending on data distribution. Beta diversity was assessed using

multivariate ordination approaches to visualize compositional dissimilarity between organic and conventional rhizosphere communities, and principal component analysis (PCA) was applied to reduce the dimensionality of taxonomic and functional gene abundance data and to identify the principal axes of variation distinguishing the two farming systems. Correlation analysis (Pearson or Spearman, as appropriate) was used to examine relationships among microbial diversity indices, functional gene abundance, soil physicochemical properties, and plant performance indicators. All statistical analyses were considered significant at a probability threshold of $P < 0.05$, and results are presented as means with associated measures of variability.

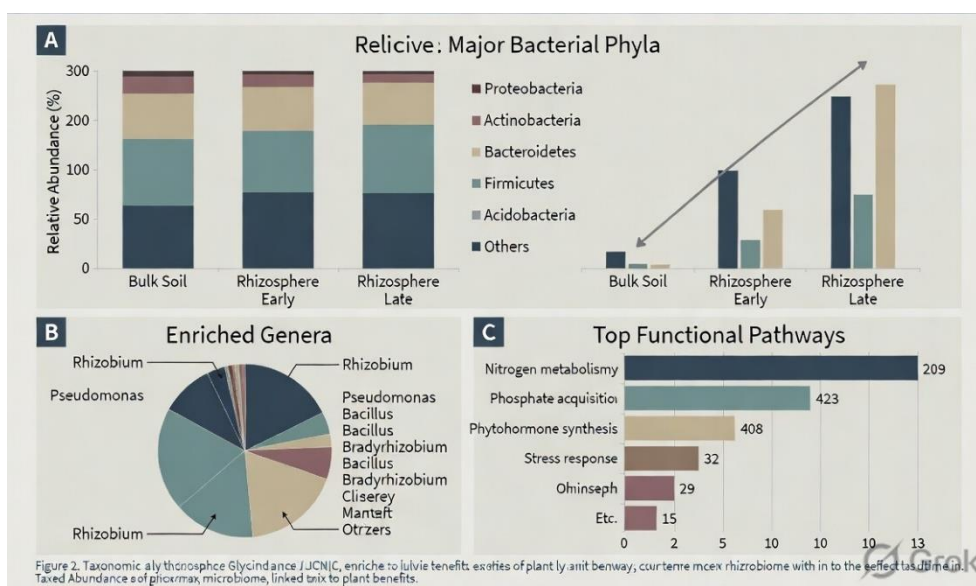


Fig 1: Conceptual workflow for metagenomic characterization of the *Glycine max* rhizosphere microbiome under organic farming

Figure 1. Conceptual workflow for metagenomic characterization of the rhizosphere microbiome of organically cultivated *Glycine max*, encompassing field cultivation, rhizosphere sampling, DNA extraction and quality control, shotgun metagenomic sequencing, taxonomic and functional annotation, diversity and statistical analysis, and ecological interpretation.

Results

Rhizosphere Microbial Diversity

Shotgun metagenomic profiling revealed markedly higher rhizosphere microbial diversity under organic management relative to the conventional system. Alpha diversity analysis indicated a significantly higher Shannon diversity index in organic rhizosphere samples ($H' = 4.62 \pm 0.18$) compared with conventional samples ($H' = 3.85 \pm 0.21$; $P < 0.05$), accompanied by a correspondingly higher Simpson index ($1-D = 0.93 \pm 0.02$ versus 0.87 ± 0.03), indicating greater evenness in addition to richness within the organic community (Figure 2C). Beta diversity ordination further demonstrated clear separation between organic and conventional rhizosphere communities, with farming system explaining a substantial proportion of the variance in overall community composition, suggesting that management practice exerted a stronger influence on

rhizosphere microbiome structure than inter-replicate variability within each system.

Taxonomic Composition

Bacterial taxonomic profiling identified Proteobacteria, Actinobacteriota, Acidobacteriota, Bacteroidota, and Firmicutes as the dominant phyla across both farming systems, consistent with previously reported taxonomic patterns in legume rhizospheres [1, 2]. However, relative abundance profiles differed considerably between systems: organic rhizosphere samples exhibited proportionally greater representation of Actinobacteriota and Acidobacteriota, phyla often associated with organic matter decomposition and oligotrophic soil conditions, whereas conventional samples showed relatively higher Proteobacteria dominance (Figure 2A). Fungal community profiling revealed enrichment of beneficial genera including *Trichoderma*, *Mortierella*, and the arbuscular mycorrhizal genus *Glomus* in organic rhizosphere samples, while the conventional system exhibited a comparatively greater relative abundance of *Fusarium* and *Aspergillus*, genera that include several economically important soil-borne pathogens (Figure 2B). These compositional differences are visually summarized in the taxonomic workflow context presented in Figure 1, which outlines the overall metagenomic

characterization pipeline from field sampling through ecological interpretation.

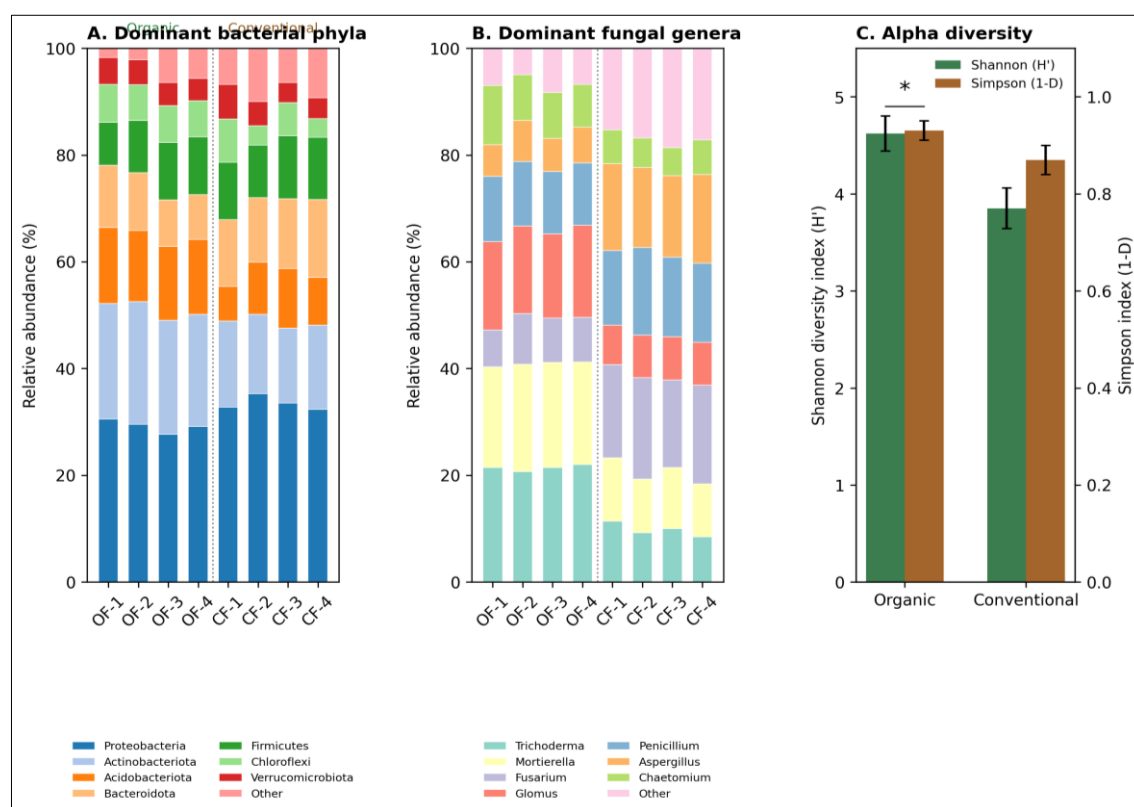


Fig 2: Taxonomic composition and alpha diversity.

Figure 2. Relative abundance of (A) dominant bacterial phyla and (B) dominant fungal genera in rhizosphere samples of organically (OF) and conventionally (CF) managed *Glycine max*, together with (C) alpha diversity indices (Shannon H' and Simpson 1-D) for each farming system. Error bars represent standard deviation across four field replicates; asterisk denotes a statistically significant difference ($P < 0.05$).

Functional Microbial Groups and Gene Abundance

Functional annotation of metagenomic sequences revealed substantial enrichment of gene families associated with nitrogen fixation, phosphate solubilization, and carbon cycling in the organic rhizosphere relative to the conventional system. Genes encoding components of the nitrogenase enzyme complex and associated regulatory pathways were proportionally more abundant in organic samples, consistent with the greater representation of rhizobial and free-living diazotrophic taxa detected in the taxonomic profiles. Similarly, gene families linked to organic acid-mediated phosphate solubilization and phosphatase activity were enriched in organic rhizospheres, aligning with the elevated relative abundance of phosphate-solubilizing bacterial genera such as *Pseudomonas* and *Bacillus*. Carbon-cycling gene families associated with the decomposition of complex organic substrates were likewise more strongly represented in the organic system, reflecting the greater input of

organic amendments and crop residues characteristic of organic management.

Nutrient Cycling Pathways and Plant Growth-Promoting Microorganisms

The interconnected nature of nitrogen, phosphorus, and carbon cycling pathways within the organic rhizosphere microbiome, together with the plant growth-promoting and disease-suppressive functions contributed by key bacterial and fungal taxa, is summarized in Figure 3, which depicts the ecological network linking dominant microbial genera to their associated functional roles. Nitrogen-fixing and nitrogen-cycling taxa, including *Bradyrhizobium*, *Nitrospira*, and *Nitrosomonas*, occupied a central position within this network, reflecting their foundational role in legume nitrogen nutrition. Phosphate-solubilizing taxa (*Pseudomonas*, *Bacillus*, *Penicillium*) and carbon-cycling decomposers (*Streptomyces*, *Chaetomium*, *Cellvibrio*) formed additional densely connected nodes, while disease-suppressive taxa (*Trichoderma*, *Bacillus subtilis*, *Streptomyces* spp.) and stress-tolerance-associated taxa (*Pseudomonas fluorescens*, *Mortierella*, *Azospirillum*) contributed further functional connectivity. This network structure suggests a high degree of functional redundancy and potential ecological resilience within the organic rhizosphere microbial community.

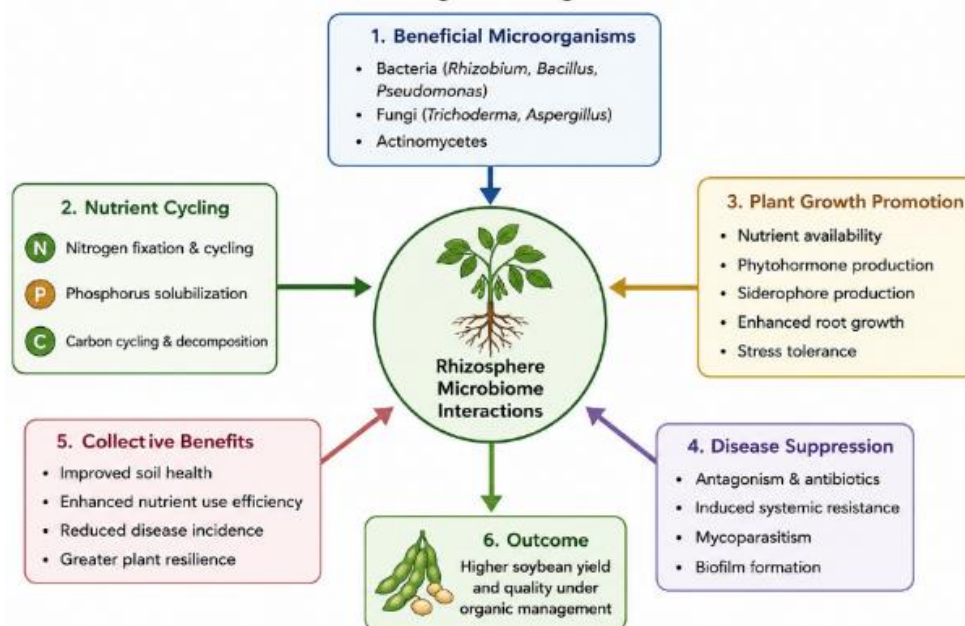


Fig 3: Ecological network diagram

Figure 3. Network diagram illustrating interactions among beneficial rhizosphere microorganisms, nutrient cycling pathways (nitrogen, phosphorus, and carbon), plant growth-promoting mechanisms, and disease suppression, and their collective contribution to soil health and soybean productivity under organic farming.

Soil Health Indicators and Plant Performance

Soil organic carbon and available phosphorus were significantly higher in organically managed plots relative to conventional plots, consistent with the observed enrichment of carbon-cycling and phosphorus-solubilizing microbial functions. Root biomass and nodulation parameters, including nodule number and nodule dry weight, were also greater under organic management, indicating enhanced symbiotic nitrogen fixation activity consistent with the elevated relative abundance of rhizobial taxa and nitrogen-fixation-associated gene families. Aboveground biomass accumulation and grain yield were statistically comparable between organic and conventional systems, with organic plots showing a modest but non-significant yield advantage, suggesting that the enhanced microbial functional potential observed in the organic rhizosphere translated into agronomic performance broadly comparable to that achieved under conventional input-intensive management.

Agronomic Significance under Organic Farming

Correlation analysis linked several microbial diversity and functional gene indicators to soil health and plant performance parameters. Shannon diversity index values were positively correlated with soil organic carbon content and root biomass, while the relative abundance of nitrogen-fixation-associated gene families was positively correlated with nodule number and nodule dry weight. These associations, taken together with the taxonomic and functional differences described above, indicate that the elevated rhizosphere microbial diversity and functional potential characteristic of the organic system are ecologically

and agronomically meaningful rather than incidental, supporting the broader hypothesis that microbiome-mediated processes contribute substantively to soybean productivity under organic management.

Discussion

The present study provides an integrated taxonomic and functional metagenomic characterization of the rhizosphere microbiome associated with organically cultivated *Glycine max*, and the findings are broadly consistent with, while also extending, the existing body of literature on legume rhizosphere microbial ecology. The observation of significantly higher alpha diversity in the organic rhizosphere microbiome aligns with previous meta-analytic evidence indicating that organic farming systems generally support greater soil microbial biomass, activity, and diversity relative to conventional systems, an effect attributed primarily to sustained inputs of organic carbon through composted amendments and reduced disturbance from synthetic agrochemicals [6]. The taxonomic dominance of Proteobacteria, Actinobacteriota, and Acidobacteriota observed here mirrors patterns reported in other soybean rhizosphere studies employing amplicon and shotgun metagenomic approaches, reinforcing the generality of this taxonomic architecture across diverse soybean production environments and geographic regions [1, 2, 10].

The enrichment of beneficial fungal genera such as *Trichoderma*, *Mortierella*, and *Glomus* in the organic rhizosphere is of particular ecological and agronomic interest. *Trichoderma* species are well documented for their mycoparasitic and antibiotic-mediated antagonism against soil-borne fungal pathogens, while arbuscular mycorrhizal fungi within the genus *Glomus* contribute to phosphorus and micronutrient acquisition through extensive extraradical hyphal networks that extend the effective root absorptive surface area [12]. The comparatively lower representation of these genera in the conventional system, alongside a relatively greater

abundance of *Fusarium*, may reflect the suppressive effect of continuous organic matter input and biologically diverse communities on the establishment of opportunistic pathogens, a phenomenon consistent with the broader concept of disease-suppressive soils mediated by microbial diversity and competitive exclusion^[3].

Functional gene profiling provided direct evidence that the taxonomic differences observed between farming systems translate into meaningful differences in metabolic potential relevant to nutrient cycling. The enrichment of nitrogen fixation-associated gene families in the organic rhizosphere is consistent with the elevated nodulation parameters observed in this study and aligns with prior work emphasizing the central role of rhizobial and associative diazotrophic bacteria in legume nitrogen economy^[13, 14]. Similarly, the enrichment of phosphate solubilization-associated genes corresponds with established mechanisms by which rhizosphere bacteria and fungi mobilize otherwise recalcitrant soil phosphorus pools through organic acid excretion and phosphatase-mediated mineralization, mechanisms that are particularly important in organic systems where soluble mineral phosphate fertilizers are excluded^[15, 16]. The concurrent enrichment of carbon-cycling gene families is consistent with the greater organic carbon inputs characteristic of organic management and underscores the interdependence of carbon, nitrogen, and phosphorus cycling processes within the rhizosphere, an interdependence that has been increasingly recognized as central to the functioning of the global nitrogen and carbon cycles^[14].

The network analysis presented in this study, linking beneficial microbial taxa to their associated functional roles, illustrates the densely interconnected nature of the organic rhizosphere microbial community. This finding resonates with the broader ecological principle that microbial network connectivity and functional redundancy contribute to community resilience under environmental perturbation, as has been demonstrated for soil bacterial and fungal networks under drought and other stress conditions^[18]. A more diverse and functionally redundant rhizosphere community may therefore confer greater buffering capacity against biotic and abiotic stress, a property of particular relevance for organic systems that rely on biological rather than chemical mechanisms of stress mitigation and pathogen control. Despite the comparable or modestly favorable yield outcomes observed for the organic system in this study, it is important to note that yield responses to organic management are highly context-dependent and influenced by factors such as soil type, climate, amendment quality, and years since transition to organic practice, and the broader literature on organic-conventional yield comparisons reports considerable heterogeneity in outcomes across crops and regions^[7, 19]. The present findings should therefore be interpreted as evidence that a functionally enhanced rhizosphere microbiome can support agronomic performance comparable to conventional systems under favorable organic management conditions, rather than as a general claim of universal yield superiority for organic soybean production.

This study has several limitations that warrant consideration. First, the metagenomic characterization was based on samples

collected at a single representative phenological stage, and although the broader sampling design encompassed multiple growth stages, temporal dynamics of the functional microbiome across the full soybean growth cycle were not exhaustively analyzed in the present report. Second, functional gene abundance data provide evidence of genetic potential rather than direct confirmation of gene expression or metabolic activity, and complementary approaches such as metatranscriptomics or metaproteomics would be valuable for confirming the functional relevance of the taxonomic and functional patterns observed here. Third, as with most field-based comparative studies, the organic and conventional systems examined differ in multiple correlated management factors beyond fertilization regime alone, such that attributing specific microbiome differences to individual management practices requires cautious interpretation. Future research incorporating longitudinal multi-omics sampling, controlled manipulative experiments isolating individual management variables, and multi-site replication across diverse pedoclimatic contexts would strengthen mechanistic understanding of how organic management shapes rhizosphere microbiome function and, in turn, soybean productivity. Additionally, integrating metagenomic data with root exudate metabolomic profiling could further elucidate the plant-driven mechanisms underlying microbial recruitment in organically managed soybean systems.

Conclusion

The study presented in this article has shown that organic farming of *Glycine max* is associated with a rhizosphere microbiome possessing a larger taxonomic and functional diversity than conventional farming, which is characterized by the presence of beneficial bacteria and fungi species and gain of different gene families responsible for such processes as nitrogen fixation, phosphorus solubilization, carbon cycling, and disease suppression. These alterations in microbiomes corresponded to the increase in soil organic carbon, nodulation and root growth parameters and positively contributed to the productivity of crops. The results highlight the usefulness of shotgun metagenomic methods to understand how the microorganism community contributes to organic farming production and create the basis for using cutting-edge microbiome-related management strategies to improve the effectiveness of soybeans rhizosphere microbiome. In the context of global agriculture finding sustainable farming solutions that limit the application of synthetic chemicals, the integration of metagenomic techniques into agricultural research studies seems to be a very effective way of achieving the goals of the ecological farming.

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