Review Article

Microbial Community Dynamics in the Rhizosphere of Sunflower and Comparative Oilseed Crops: Functional Roles and Strategies for Sustainable Agriculture

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Abstract : The rhizosphere represents a highly dynamic interface where plant roots interact with the surrounding soil matrix, fostering a diverse and functionally complex microbial community. These microbiota play essential roles in plant growth promotion, nutrient cycling, and resilience to biotic and abiotic stresses. In recent years, plant-associated microbial communities have garnered increasing attention for their potential to enhance agroecosystem sustainability. This review examines microbial community shifts in the rhizosphere and bulk soil of sunflower (*Helianthus annuus*), a key oilseed crop known for its adaptability to marginal soils and environmental stressors. The differences in microbial composition and functional potential between rhizosphere and bulk soil are analyzed, with emphasis on the roles of plant genotype, root exudation, and environmental variables such as salinity and climatic conditions. Particular focus is placed on beneficial bacterial genera including *Pseudomonas, Azotobacter*, and *Bacillus*, which contribute to nutrient acquisition and stress mitigation. Additionally, fungal taxa such as *Fusarium, Aspergillus*, and *Alternaria* are discussed in the context of decomposition, symbiosis, and plant–microbe interactions. Comparative insights from other oilseed crops—such as soybean, rapeseed, and peanut—are presented to contextualize microbiome patterns unique to sunflower. The functional attributes of rhizosphere microbes, including phytohormone production, pathogen suppression, and nutrient solubilization, are explored in detail. Furthermore, this review highlights microbiome engineering approaches, such as the application of biofertilizers and plant growth-promoting rhizobacteria (PGPR), aimed at improving crop productivity and resilience. The integration of high-throughput sequencing technologies and advanced bioinformatics has deepened our understanding of these complex microbial networks. Finally, the review identifies existing knowledge gaps and outlines future research directions to optimize rhizosphere microbiomes for enhanced agro-ecological performance in sunflower and related oilseed crops.

Keywords: Rhizosphere, Microbiome, Sunflower, Oilseed-crops, Soil.

Introduction

In recent decades, a paradigm shift has transformed our understanding of plant biology, redefining plants not as autonomous organisms but as hosts to complex, dynamic, and co-evolving microbial consortia. The term plant microbiota refers to a taxonomically diverse assemblage of bacteria, fungi, archaea, and protists that colonize distinct plant compartments, including the rhizosphere (root-associated soil), phyllosphere (leaf surfaces), and endosphere (internal tissues) [1–3]. These microbial communities form a

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functional continuum with their host, significantly influencing plant development, nutrient acquisition, stress tolerance, and immune responses. Throughout their life cycle, plants engage in continuous and reciprocal interactions with these microorganisms, which respond dynamically to plant exudates, environmental cues, and inter-microbial signaling networks. These interactions are not incidental but integral to plant fitness and productivity, particularly under fluctuating environmental conditions. The emerging holobiont concept, which views the plant and its associated microbiota as a single evolutionary and ecological unit, emphasizes the interdependence of host and microbiome [2,4]. This framework challenges traditional reductionist models that isolate host-pathogen or host-symbiont relationships, instead advocating for a systems-level understanding of the plant as a metaorganism.

A central question in holobiont ecology is whether the host plant or its microbial partners predominantly shape microbiome structure and function. While plant genotype, root architecture, and exudate composition are known to influence microbial recruitment, growing evidence indicates that microbial communities also actively modulate host physiology, metabolism, and immune signaling [2,5]. This bidirectional co-dependence has been conceptualized as the “symbiosis cascade effect,” wherein host and symbiont co-regulate each other’s traits to maintain homeostasis and functional integration within the holobiont [2]. Notably, microbiomes play a pivotal role in plant adaptation to environmental stresses by altering gene expression, root morphology, and metabolite production. The ability of plants to modulate their microbial consortia in response to biotic and abiotic stimuli represents a novel dimension of phenotypic plasticity and ecological resilience [3,6]. These insights carry important implications for crop breeding, particularly in the context of climate resilience and sustainable agricultural practices. From an ecological and evolutionary standpoint, identifying the core microbiota—microbial taxa that are consistently associated with specific hosts or habitats—is crucial. These core taxa are believed to perform essential functions such as nutrient solubilization, phytohormone biosynthesis, and pathogen suppression [3,7]. Elucidating the identity and function of these persistent microbial associates provides critical insights into plant-microbiome dependency and underscores the potential of incorporating microbial traits into plant selection and crop improvement programs.

The Rhizosphere as a Microbial Interface

The rhizosphere—the narrow zone of soil influenced by root exudates and microbial activity—is a hotspot of biological interactions between plants and a diverse array of microorganisms. Often referred to as the plant’s "second genome," the rhizosphere microbiome can comprise tens of thousands of microbial taxa, ranging in function from mutualists to pathogens [8]. This dynamic microbial community is integral to plant development, contributing to nutrient solubilization, growth promotion, pathogen suppression, and stress mitigation. Notably, plants grown in identical soil conditions can harbor distinct rhizosphere microbial communities, underscoring the plant’s active role in shaping its microbiome through root-secreted metabolites and immune signaling [8]. Despite increasing recognition of the rhizosphere microbiome’s ecological importance, the mechanisms governing microbial community assembly and host interaction remain only partially understood. Both biotic factors—such as plant genotype, microbial competition, and symbiosis—and abiotic factors—such as soil pH, moisture, and nutrient availability—contribute to the structure and function of the rhizosphere microbiome [9].Key microbial functions include enhancing disease resistance, modulating plant immune responses, and promoting stress tolerance, often via pathways mediated by plant-derived metabolites [10]. While many rhizosphere microorganisms confer benefits to the plant host, others include phytopathogens and even opportunistic human pathogens, rendering the rhizosphere a complex ecological battleground where microbial consortia can either reinforce or compromise plant health [11].

This complexity has spurred growing interest in microbiome-based approaches to restructure rhizosphere communities in favor of plant-beneficial taxa. Research on disease-suppressive soils has revealed that certain bacterial phyla—particularly Proteobacteria, Firmicutes, and Actinobacteria—are consistently associated with suppression of pathogens such as *Rhizoctonia solani*. Functional genomic analyses suggest that microbial genes encoding nonribosomal peptide synthetases and stress-induced secondary metabolites play key roles in mediating this suppression [12]. For instance, metatranscriptomic studies of Rhizoctonia-infected sugar beet rhizospheres reveal enhanced microbial stress-response activity and enrichment of antagonistic bacterial families, indicating a microbiome-mediated defense mechanism [13]. However, the domestication of crop plants has inadvertently contributed to reduced rhizosphere microbial diversity. Modern cultivars often lack the ability to recruit or maintain beneficial microbial partners to the same extent as their wild relatives [14]. Breeding-driven changes in root architecture, exudation profiles, and litter chemistry may disrupt historically co-evolved microbial partnerships. In response, a “back to the roots” approach has been proposed—emphasizing the study of native plant microbiomes and leveraging these natural microbial consortia in modern crop systems.

Plant genetics and environmental heterogeneity jointly shape rhizosphere microbial composition. For example, a study involving 27 maize inbred lines grown at five different field sites found significant variation in rhizobacterial diversity, with moderate heritability observed in community traits. This suggests that microbial recruitment is at least partially encoded in the plant genome and may be harnessed in future plant breeding programs [15]. As chemical-intensive agriculture increasingly threatens soil microbial diversity and ecosystem resilience, the rhizosphere emerges as a promising frontier for sustainable plant health management. Understanding how root exudates, agronomic practices, and pathogen invasion influence microbial recruitment is essential for designing microbiome-based strategies for crop resilience [16]. The concept of a "biased rhizosphere"—a zone shaped by selective plant-microbe interactions—has emerged as a theoretical framework for developing next-generation biofertilizers through targeted manipulation of microbial populations [6]. Despite centuries of co-evolution, the full potential of rhizospheric microbes remains underexploited. Harnessing this microbial reservoir—particularly through root exudate engineering, synthetic microbial consortia design, and microbiome-informed breeding—offers new avenues to enhance plant stress tolerance, nutrient use efficiency, and reduce dependency on agrochemicals.

Microbial Dynamics in Sunflower Rhizosphere vs Bulk Soil

The rhizosphere of sunflower (*Helianthus annuus*) constitutes a specialized ecological niche that differs markedly from the surrounding bulk soil in both taxonomic composition and functional potential. Extensive studies have shown that plant roots function as selective filters, actively enriching specific microbial taxa while suppressing others. This root-mediated selection gives rise to a distinct rhizosphere microbiome that is more metabolically active and functionally specialized than microbial communities in bulk soil [17]. In sunflower, this selection process consistently favors the enrichment of plant growth-promoting rhizobacteria (PGPR), including members of the genera *Bacillus, Pseudomonas, Azotobacter*, and *Rhizobium*. These taxa are known for their abilities to fix atmospheric nitrogen, solubilize phosphate, and synthesize phytohormones such as indole-3-acetic acid (IAA), thereby contributing to plant growth and resilience [18,19]. Additionally, fungal genera such as *Aspergillus, Penicillium*, and *Fusarium* are frequently detected in the rhizosphere. These fungi engage in both mutualistic and antagonistic interactions with the plant host, playing roles in nutrient cycling, root colonization, and pathogen suppression [20]. Functionally, rhizosphere microbes contribute to biocontrol via the production of antifungal metabolites, hydrogen cyanide, and siderophores, which sequester iron and inhibit pathogenic microbes [21].

A key factor influencing this microbial differentiation is the composition of sunflower root exudates, which are particularly rich in organic acids and phenolic compounds. These compounds act as chemoattractants and metabolic substrates for a wide range of beneficial microorganisms, including hydrocarbon-degrading and phytoremediation-associated bacteria [22]. For example, *Pseudomonas spp*. enriched in sunflower rhizospheres have been shown to degrade polycyclic aromatic hydrocarbons (PAHs), underscoring the ecological potential of sunflower-microbe partnerships in soil detoxification [23]. Metagenomic analyses have revealed that the sunflower rhizosphere harbors an increased abundance of genes involved in nitrogen metabolism, oxidative stress response, and microbial signaling pathways relative to bulk soil [18,24]. This functional enrichment suggests that sunflower roots foster a dynamic microbial community that is both responsive to environmental cues and actively involved in supporting plant health. Interestingly, while environmental factors such as soil type, moisture, and nutrient availability do influence microbial structure, the effect of root exudation appears to be more dominant in shaping rhizosphere composition and activity [19]. Typically, microbial diversity is higher in bulk soil; however, the rhizosphere microbiome is more functionally specialized and less taxonomically diverse [17]. Furthermore, the rhizosphere microbial community is not static—its composition changes throughout the plant's developmental stages (e.g., vegetative growth, flowering, seed set), correlating with shifts in root exudate profiles and nutrient demands [25].

Comparative studies with other oilseed crops—such as soybean (*Glycine max*), rapeseed (*Brassica napus*), and peanut (*Arachis hypogaea*) demonstrate that sunflower recruits a distinct microbial consortia. These communities often include taxa with enhanced capabilities for stress mitigation, hydrocarbon degradation, and other phytoremediation-related functions, reflecting sunflower's adaptability to marginal and contaminated soils [26].A comparative overview of the rhizosphere microbiomes of sunflower and selected oilseed crops, highlighting key taxonomic and functional differences is provided in Table1.

Table 1. Comparative Overview of Rhizosphere Microbiomes in Sunflower and Other Oilseed Crops

Crop	Dominant Microbial Taxa	Functional Traits	Sequencing/Study Approach
Sunflower	*Bacillus*, *Pseudomonas*, *Actinobacteria*, *Fusarium*, *Aspergillus*	Nutrient solubilization, PAH degradation, stress resistance, antifungal activity [17,18,20,22]	Shotgun metagenomics, 16S/ITS amplicon sequencing
Soybean	*Bradyrhizobium*, *Pseudomonas*, *Bacillus*, *Flavobacterium*	Nitrogen fixation, nodulation, disease suppression [19,26]	16S rRNA sequencing, culture-based
Peanut	*Pseudomonas_M indica*, *Bacillus*, *Sphingomicrobium*	Growth promotion, stress tolerance, microbial turnover [25]	16S rRNA + culture-based metagenomics
Rapeseed	*Streptomyces*, *Sphingomonas*, *Flavobacterium*	Phytohormone production, carbon cycling, pathogen resistance [26]	RNA-SIP + high-throughput sequencing

Factors Influencing Microbiome Shifts

The composition and dynamics of plant-associated microbiomes are highly plastic, governed by a complex interplay of plant genetics, environmental variables, and agricultural management practices. In sunflower (*Helianthus annuus*), these factors profoundly influence rhizosphere microbial structure, diversity, and function across different developmental stages and ecological contexts.

Plant Genotype is a primary determinant of rhizosphere microbiome assembly. Variations in root architecture, exudate chemistry, and physiological status among sunflower cultivars can lead to genotype-specific microbial recruitment [27]. Studies have demonstrated that even when grown under uniform environmental conditions, genetically distinct sunflower varieties host unique microbial communities. These genotype-dependent differences are particularly evident in so-called “microbial hubs” key taxa that exert strong influence on the overall microbiome structure and stability [18]. The domestication of crops has further altered plant-microbe interactions. Modern sunflower cultivars, shaped by selection for aboveground agronomic traits, often show reduced rhizosphere microbial diversity compared to their wild progenitors [14]. This is partly due to diminished root traits essential for microbial recruitment, leading to a loss of microbial partners critical for nutrient acquisition and stress tolerance.

Environmental stresses such as salinity, drought, and nutrient limitation significantly impact microbiome composition. Under saline conditions, sunflower rhizospheres are enriched with osmotic stress-tolerant taxa such as Bacteroidota and Actinobacteriota, which contribute to ion balance and stress mitigation [28]. Similarly, drought and high-temperature stress modify root exudate profiles, favoring microbial taxa capable of supporting root elongation, water retention, and reactive oxygen species (ROS) detoxification [29]. Soil properties including pH, texture, organic matter content, and mineral composition serve as the foundational filters for microbial community assembly. While plant genotype acts as a biological selector, the soil microbiome represents the initial species pool available for recruitment. Even with identical plant genotypes, microbial assemblages can vary dramatically across soil types due to differences in geochemistry and habitat structure [15]. Agricultural practices are another major driver of microbiome shifts. Intensive tillage, synthetic fertilizers, pesticide applications, and monoculture systems disrupt microbial niches and often reduce beneficial microbial diversity. Excessive nitrogen fertilization, for example, suppresses nitrogen-fixing bacteria, while fungicides can non-selectively reduce both pathogens and mutualistic fungi [30]. In contrast, integrated nutrient management, the application of biofertilizers, and minimal chemical inputs have been shown to enrich beneficial microbial taxa in the sunflower rhizosphere.

Temporal dynamics also shape microbiome composition. Rhizosphere microbial communities are synchronized with plant developmental phases, with distinct shifts occurring during vegetative growth, flowering, and senescence. In sunflower, bacterial richness often peaks during the flowering stage, coinciding with heightened root activity and increased exudation [25]. Climatic and geographic factors such as temperature, precipitation, and regional edaphic history further modulate microbial community structure. Arid and warm climates tend to favor stress-resilient, metabolically specialized microbial taxa. Additionally, biogeographic patterns influence microbial endemicity, leading to location-specific microbiome profiles even under cultivation of the same crop species [31].

Methodologies in Microbiome Research

The burgeoning interest in plant–microbe interactions has been catalyzed by significant advances in molecular biology, sequencing technologies, and bioinformatics. These methodological developments have enabled comprehensive exploration of both the composition and functional attributes of microbial communities, thereby uncovering their critical roles in plant health, productivity, and resilience to environmental stressors.

Amplicon Sequencing (16S rRNA and ITS)

Amplicon sequencing remains one of the most widely used approaches for profiling microbial communities. It targets conserved taxonomic marker genes—most commonly the 16S rRNA gene for bacteria and archaea, and the internal transcribed spacer (ITS) regions for fungi. This method offers a cost-effective and scalable overview of microbial diversity and relative abundance within a sample [32,33]. However, it has limitations in taxonomic resolution, particularly at the species or strain level, and does not provide functional information. Despite these constraints, amplicon sequencing remains a foundational tool in rhizosphere microbiome studies, including those focused on Helianthus annuus [17].

Shotgun Metagenomics

Shotgun metagenomic sequencing enables the untargeted sequencing of all DNA present in a sample, providing detailed insights into both microbial taxonomy and functional gene content. This method allows for strain-level identification and the detection of rare or unculturable taxa. Functional annotation of metagenomic datasets has revealed enrichment of genes related to nitrogen metabolism, siderophore production, and detoxification in the sunflower rhizosphere [24,34]. As such, shotgun metagenomics is particularly valuable for understanding functional ecology and guiding microbiome engineering efforts.

Metatranscriptomics and Metaproteomics

To investigate the active functions within microbial communities, researchers employ metatranscriptomics (RNA-based) and metaproteomics (protein-based) techniques. These approaches capture dynamic gene expression and protein synthesis profiles, offering real-time insights into microbial responses to biotic and abiotic stimuli [34]. For example, metatranscriptomic studies of disease-suppressive soils have identified upregulated microbial stress-response pathways following pathogen attack, elucidating mechanisms of microbiome-mediated plant defense [12].

Root Exudate and Metabolite Profiling

Root exudates play a pivotal role in shaping rhizosphere microbiomes by acting as selective chemoattractants. Profiling the chemical composition of exudates using techniques such as mass spectrometry (MS) and nuclear magnetic resonance (NMR) provides valuable insights into plant–microbe signaling. Key metabolites—including flavonoids, organic acids, and simple sugars—have been shown to selectively enrich plant-beneficial microbes in the sunflower rhizosphere [36].

Bioinformatics Tools and Statistical Analysis

The explosion of high-throughput sequencing data has necessitated the use of advanced computational tools for data analysis. Open-source platforms such as QIIME2, phyloseq, and MicrobiomeAnalyst are widely used for sequence processing, alpha and beta diversity analysis, functional prediction, and biomarker identification [37,38]. Despite their utility, challenges remain due to the complexity of environmental datasets, incomplete reference databases, and the need for improved statistical robustness.

Experimental Design and Multi-Omics Integration

Robust experimental design is essential for generating reproducible and interpretable microbiome data. This includes proper randomization, biological replication, inclusion of control samples, and temporal sampling to capture dynamic microbial shifts. Increasingly, microbiome studies are integrating multiple omics layers—genomics, transcriptomics, metabolomics—with plant phenotyping data. Such systems biology approaches are crucial for unraveling complex plant–microbe interactions and are increasingly applied in crop improvement programs [31].

Microbiome Engineering and Agro-Ecological Enhancement

As modern agriculture grapples with the dual imperatives of increasing food production and mitigating environmental degradation, microbiome engineering has emerged as a promising strategy to enhance plant productivity, sustainability, and resilience. Targeted manipulation of the plant-associated microbiome—particularly within the rhizosphere—offers the potential to improve nutrient uptake, suppress phytopathogens, and confer tolerance to abiotic stresses. A well-established approach in microbiome engineering is the application of plant growth-promoting rhizobacteria (PGPR) as inoculants. Key genera include *Bacillus, Pseudomonas, Azospirillum*, and *Rhizobium*, known for their roles in biological nitrogen fixation, phosphate solubilization, siderophore production, and synthesis of phytohormones such as indole-3-acetic acid (IAA) [39]. In sunflower, inoculation with strains like Pseudomonas aeruginosa and *Bacillus subtilis* has demonstrated improvements in seed quality, oil content, and phosphorus-use efficiency [21,40].

An emerging synergistic strategy combines PGPR with biochar a porous, carbon-rich soil amendment. The structured matrix of biochar enhances microbial habitat, promotes metabolite exchange, and increases inoculant persistence under field conditions. In sunflower cultivation on saline-alkaline soils, biochar co-applied with PGPR significantly reduced cadmium uptake and improved plant tolerance to salinity [41]. Recent advancements have led to the design of synthetic microbial consortia (SynComs) engineered communities composed of well-characterized microbial taxa with complementary functions. SynComs are typically constructed to enhance specific outcomes such as pathogen suppression, nutrient mobilization, or hormone regulation [42]. Compared to single-strain inoculants, SynComs offer improved functional stability and predictability, though challenges in field performance and ecological compatibility remain.

A novel and integrative strategy is rhizobiome-informed breeding, which leverages plant genetic variation to select genotypes with enhanced capabilities for recruiting beneficial microbiota. For example, specific quantitative trait loci (QTLs) associated with root exudate composition have been linked to increased colonization by beneficial microbes and greater disease resistance [40]. This approach holds promise for developing cultivars optimized for microbiome compatibility, thereby embedding microbial advantages into crop genetics. Climate-resilient microbial partnerships are gaining attention as global environmental variability intensifies. Certain microbial taxa produce stress-mitigating compounds such as ACC deaminase, trehalose, and other osmoprotectants that alleviate plant stress under drought and salinity conditions [23]. Engineering or selecting for microbiomes capable of producing these metabolites represents a powerful tool for climate adaptation in agriculture.

Table 2: Microbiome Manipulation Strategies for Agro-Ecological Enhancement

Strategy	Microbial Agent(s)	Target Benefit
PGPR inoculation	*Pseudomonas*, *Bacillus*, *Azotobacter*	Enhances growth, nutrient uptake, hormone production [44,45]
PGPR + Biochar	PGPR strains + biochar	Reduces metal toxicity, improves soil structure and resilience [46]
Synthetic microbial communities	Engineered *Pseudomonas*, *Bacillus*, *Rhizobium*	Biocontrol, enhanced root colon ization, predictability [47]
Rhizobiome-informed breeding	Host genotypes with QTLs for exudate profiles	Selective microbial recruitment, improved resistance [40]
Screening for stress-resilient microbes	ACC deaminase, osmoprotectant-producing strains	Drought and salinity mitigation, improved plant fitness [23]

Despite the promise of microbiome-based technologies, several barriers remain. Field performance of microbial inoculants often varies across agro-ecological zones due to differences in soil properties, climate, and native microbiota. Therefore, field validation, cost-effectiveness, and ecological compatibility are critical for scaling microbiome interventions. Furthermore, the development of regulatory frameworks and engagement with key stakeholders—including farmers, extension professionals, and policymakers—is essential for translating microbiome innovations from the laboratory to realworld agricultural systems [43]. The key microbiome manipulation strategies for agro-ecological enhancement in sunflower and related cropping systems are summarized in table 2.

Conclusion

This review underscores the critical ecological functions of rhizosphere microbial communities in sunflower (*Helianthus annuus*) and other oilseed crops. These microbiomes are highly dynamic, shaped by plant genotype, environmental conditions, and agricultural practices, reflecting the intricate and adaptive nature of plant–microbe interactions. Sunflower, due to its distinctive root exudation patterns and tolerance to marginal soils, emerges as a valuable model for studying microbiome assembly and functionality in the rhizosphere. The observed differences between rhizosphere and bulk soil microbial communities emphasize the selective recruitment capabilities of plants and the functional specialization of root-associated microbes. Beneficial microbial taxa such as PGPR and mycorrhizal fungi contribute to plant health through nutrient mobilization, pathogen suppression, and stress mitigation, offering opportunities for microbiome-based agricultural enhancement. Future research should focus on elucidating the mechanistic underpinnings of microbiome shifts across developmental stages and environmental gradients. Integrating microbiome data into plant breeding, soil management, and climate adaptation strategies represents a promising frontier for developing resilient, sustainable agro-ecosystems.

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