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SOIL–PLANT–MICROBE INTERACTIONS IN LEGUME CROPS (CHICKPEA AND LENTIL): A REVIEW OF RHIZOSPHERE DYNAMICS AND NUTRIENT USE EFFICIENCY

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Abstract

Legume crops such as chickpea (Cicer arietinum L.) and lentil (Lens culinaris Medik.) play a pivotal role in global food and nutritional security, providing high-quality plant protein, essential micronutrients (Fe, Zn, folate), and performing biological nitrogen fixation (BNF) that reduces synthetic fertilizer dependency and enhances soil health. This review synthesizes the complex soil–plant–microbe interactions in the rhizosphere of these pulses, emphasizing the tripartite symbiosis among legumes, rhizobia (Mesorhizobium spp. for chickpea; Rhizobium leguminosarum bv. viciae for lentil), and plant growth-promoting rhizobacteria (PGPR) such as Pseudomonas, Bacillus, and Azospirillum. Key mechanisms include enhanced nutrient acquisition (N, P, Fe via siderophores and organic acids), induced systemic resistance against biotic stresses (Fusarium wilt, Ascochyta blight), and improved abiotic stress tolerance (drought, salinity) through ACC deaminase activity, antioxidant enzyme induction, and osmolyte accumulation. The review highlights how root exudates shape microbial community assembly, the vertical transmission of core microbiota from seed to seed, and the contribution of these interactions to nutrient use efficiency (NUE), water use efficiency (WUE), and yield stability in low-input systems. Integrated strategies combining elite rhizobial inoculants, PGPR consortia, and legume-cereal rotations offer sustainable pathways to boost productivity by 20–50%, mitigate climate vulnerabilities, and combat hidden hunger in semi-arid regions of South Asia, Africa, and the Middle East.

1. INTRODUCTION

The global agricultural landscape is currently facing a convergence of challenges characterized by a burgeoning human population, which is expected to reach nearly 10 billion by the middle of the twenty-first century, and the intensifying pressures of climate change (Just Agriculture, 2022). In this context, leguminous crops, specifically chickpea (Cicer arietinum L.) and lentil (Lens culinaris Medik.), emerge as pivotal instruments for ensuring food security and ecological stability (Mahto et al., 2025). These pulses are not merely sources of affordable, high-quality protein for over 30% of the global population; they are biological engines capable of atmospheric nitrogen fixation, a process that restores soil fertility and reduces the anthropogenic reliance on synthetic nitrogenous fertilizers (Mabrouk et al., 2023). The cultivation of these pulses contributes to a reduction in greenhouse gas emissions and a mitigation of the environmental degradation associated with modern intensive farming (Gashu et al., 2025).

Chickpea, ranking third in global pulse production, is recognized for its significant dietary value and its resilience in low-input farming systems. Lentils, similarly, are distinguished by their versatility and genetic diversity, allowing them to thrive in varied agro-ecological conditions where other crops might fail (Crop Trust, 2024). Beyond their role as a "poor man's meat," these crops provide essential micronutrients such as iron (Fe), zinc (Zn), and folate, addressing the widespread issue of "hidden hunger" in developing regions (HarvestPlus, 2020). The integration of legumes into cropping systems has been shown to enhance soil physical properties, reducing bulk density and improving water infiltration through "bio-ploughing" by deep-rooted varieties (Akchaya et al., 2025). These system-level benefits translate into yield increases of 30–35% in terms of main crop equivalents and improvements in water use efficiency of up to 25% (Codon Publications, 2025).

Table 1: Nutritional and Environmental Significance of Chickpea and Lentil

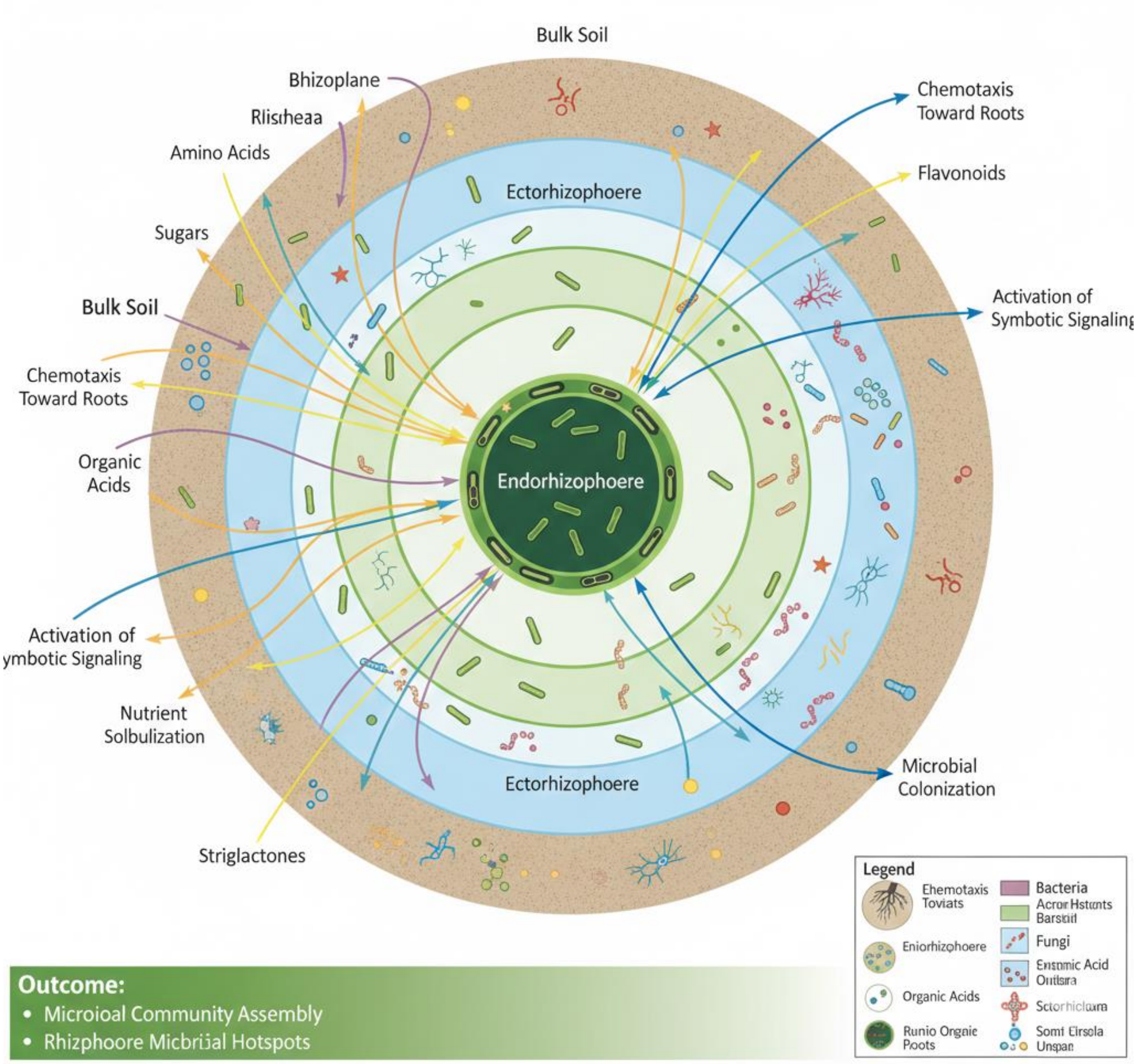
Nutrient/Trait	Chickpea (Cicer arietinum)	Lentil (Lens culinaris)	Global Significance
Protein Content	~20% - 22%	~21% - 25%	Essential for plant-based diets (Codon Publications, 2025)
Biological N2 Fixation	~125 kg N/ha/season	Variable (High)	Reduces urea/synthetic N use (Gashu et al., 2025)
Iron (Fe) Concentration	4.6 - 9.8 mg/100g	7.8 - 9.0 mg/100g	Combats global anemia (Codon Publications, 2025; HarvestPlus, 2020)
Key Amino Acids	Leucine, Phenylalanine	Leucine, Lysine	Balanced human nutrition (Codon Publications, 2025)
Major Growing Regions	Semi-arid Asia and Africa	Global (High adaptability)	Climate resilience (Varshney et al., 2024)

2. Fundamental Principles of Rhizosphere Dynamics

The rhizosphere represents the most biologically active interface between the plant and the terrestrial environment, defined as the thin layer of soil directly influenced by root secretions and microbial activity (Hartmann et al., 2022. This zone is characterized by a "rhizosphere effect," where the concentration of microorganisms is several orders of magnitude higher than in the surrounding bulk soil (Wu et al., 2023). This microbial proliferation is fueled by the release of photosynthetically fixed carbon in the form of root exudates, which include sugars, amino acids, organic acids, and complex secondary metabolites (Koprivova & Kopriva, 2022). The rhizosphere is not a homogenous zone but is stratified into the endorhizosphere (internal root tissues), the rhizoplane (root surface), and the ectorhizosphere (adjacent soil) (Ahlawat, 2007).

Within this micro-environment, plants and microbes engage in a sophisticated "cross-talk" that determines the health and productivity of the crop. The composition of the rhizosphere soil differs fundamentally from bulk soil, exhibiting higher levels of enzyme activity and faster nutrient cycling (Mukherjee, 2019). Roots act as biological engineers, modifying soil pH through the release of protons or organic anions and altering soil porosity to enhance water retention and aeration (Malviya et al., 2021). This selective environment acts as a filter, recruiting beneficial taxa such as plant growth-promoting rhizobacteria (PGPR) and arbuscular mycorrhizal fungi (AMF) while simultaneously attempting to suppress soil-borne pathogens (Balti et al., 2024). The assembly of this microbiome is driven by a complex interplay of host genotype, soil type, and environmental variables, with modern research shifting toward "rhizosphere engineering" to optimize these interactions for sustainable production (Joshi et al., 2025). The rhizosphere represents a highly dynamic microenvironment where root exudates regulate microbial recruitment and activity. The spatial organization of this zone and the role of root exudates in shaping microbial communities are summarized in figure 1.

Figure 1 Rhizphosore Zonation and Root Exudate-Medated Microbial Recruitment



2.1 Root Exudation as a Driver of Microbial Recruitment

Root exudates serve as the primary currency of the rhizosphere, acting as both metabolic substrates and specific signaling molecules. These compounds comprise primary metabolites, such as glucose and glutamate, which provide energy for microbial growth, and secondary metabolites like flavonoids and strigolactones, which mediate highly specific symbioses (Wang et al., 2025). The chemical signature of these exudates is highly dynamic, varying across plant developmental stages from seedlings to reproductive phases and in response to environmental stressors such as nutrient deficiency or drought (Root Exudate Reviewers, 2024).

In chickpea and lentil, the recruitment of beneficial microbes is a non-random process. For instance, phosphorus deficiency triggers the activation of specialized transporters, such as ALMT and MATE, leading to the secretion of malate and citrate (Aravindakshan et al., 2021). These organic acids not only solubilize mineral phosphorus but also act as chemoattractants for phosphate-solubilizing bacteria (PSB) (Fe-Biofortification Team, 2025). Furthermore, the synthesis of these metabolites is tightly regulated by phytohormones such as auxin and jasmonic acid, ensuring that the plant's metabolic output is coordinated with its physiological needs (Nguyen et al., 2022). This metabolic synchronization allows legumes to cultivate a "personalized" microbiome that facilitates nutrient uptake and provides a first line of defense against abiotic and biotic stresses (Lv et al., 2021).

Table 2: Categories and Ecological Functions of Root Exudates in Legumes

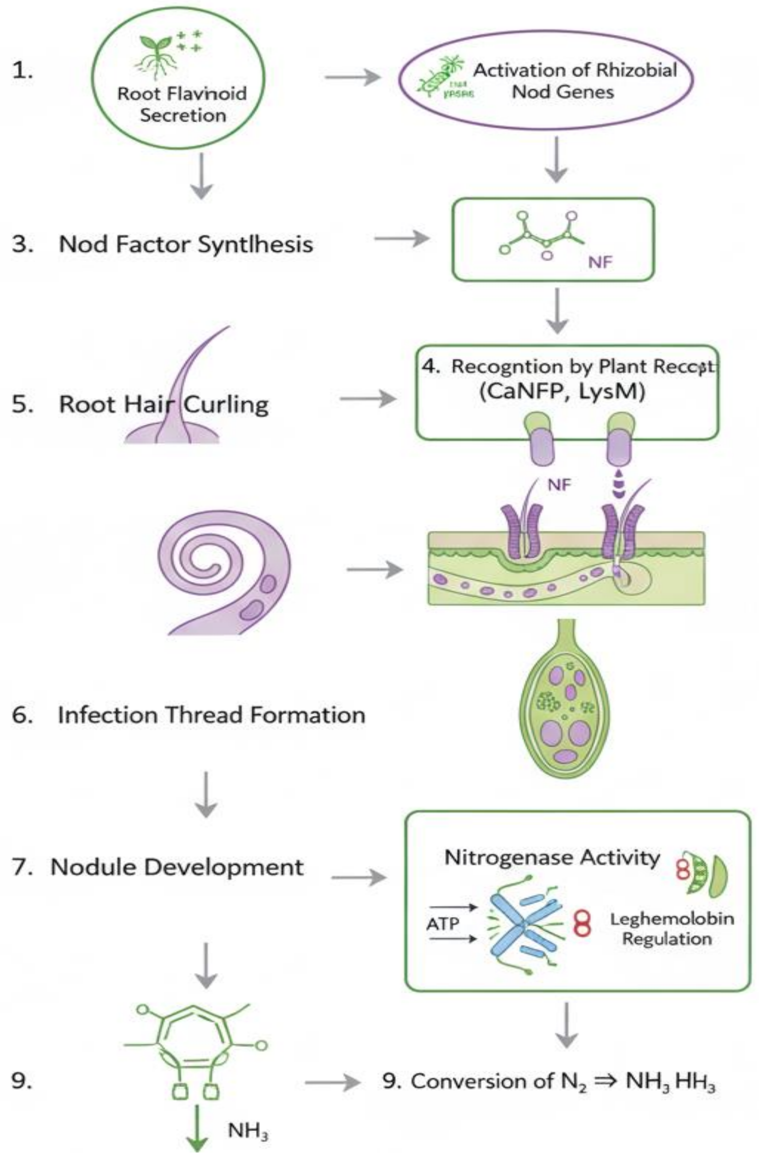
Exudate Category	Specific Compounds	Biological/Ecological Function
Primary Metabolites	Glucose, Fructose, Amino Acids	Universal carbon and nitrogen sources for microbes (Root Exudate Reviewers, 2024)
Organic Acids	Citric, Malic, Oxalic, Lactic	Nutrient mobilization (P, Fe, Zn), pH reduction (Yadav et al., 2024; Fe-Biofortification Team, 2025)
Flavonoids	Luteolin, Genistein, Naringenin	Rhizobial attraction, nod gene activation (Mahto et al., 2025)
Strigolactones	5-deoxystrigol, Sorgolactone	AMF hyphal branching and signaling (Akiyama et al., 2005)
Enzymes	Acid Phosphatases, Phytases	Mineralization of organic phosphorus (Hartmann et al., 2022)
Antimicrobials	Phenolics, Alkaloids	Suppression of soil-borne pathogens (Balti et al., 2024)

3. Molecular Orchestration of Symbiotic Nitrogen Fixation

The hallmark of leguminous crops is their capacity for biological nitrogen fixation (BNF), a tripartite interaction involving the host plant, specialized rhizobia, and the soil environment (Tavasolee et al., 2011). In chickpea, this symbiosis is primarily established with Mesorhizobium species, such as Mesorhizobium ciceri and M. mediterraneum, which possess the unique ability to inhabit root nodules and convert atmospheric N_2 into plant-available ammonia (NH_3) (Zhang et al., 2024). The process is initiated by a complex molecular dialogue; chickpea roots secrete specific flavonoids that serve as signals for the rhizobia. In response, the bacteria activate their nod genes, synthesizing lipo-chitooligosaccharides known as Nod factors. These signaling molecules are perceived by the plant through LysM and LRR-type receptors, such as CaNFP, triggering root hair curling and the formation of an infection thread (Ben Gaied et al., 2024).

Inside the developing nodule, the rhizobia differentiate into bacteroids, where the nitrogenase enzyme complex facilitates the reduction of N_2. This reaction is highly energy-intensive and oxygen-sensitive, requiring a delicate balance maintained by the plant-produced protein leghemoglobin, which buffers oxygen levels to protect the enzyme while allowing for cellular respiration (Roy et al., 2020). Genetic studies have identified several key regulatory genes, including GST and Nodulin6 that are essential for successful nodulation and fixation efficiency (Jeong et al., 2024). Furthermore, the availability of nitrogen in the soil acts as a regulatory feedback mechanism; high nitrate levels can suppress nodule formation, whereas nitrogen-deficient soils stimulate the release of flavonoids and the recruitment of symbiotic partners (Amiri, 2021). The establishment of symbiotic nitrogen fixation involves a highly coordinated molecular signaling cascade between legumes and rhizobia. The major steps involved in this signaling pathway are presented in figure 2.

Figure 2: Molecular Signaling Pathway of Symbotic Nitrogen Fixation in Chickpea



3.1 Enhancing Fixation Efficiency through Biotechnology

Current research in chickpea and lentil improvement focuses on maximizing the efficiency of BNF through both microbial selection and genetic engineering. Inoculation with superior strains of Mesorhizobium has been shown to significantly increase nodule dry weight, nitrogen uptake, and final grain yield (Huang, 2024). For instance, the use of the CP-M41 strain in conjunction with blended NPSB fertilizers in Ethiopia resulted in grain yields of over 3,000 kg/ha, representing a nearly 38% increase over control treatments (Kiros & Atsede, 2024).

At the genomic level, the advent of CRISPR/Cas9-mediated genome editing provides opportunities to target genes such as CaNFP to enhance nodule formation in low-nodulating genotypes. Additionally, the use of microbial consortia combining Mesorhizobium with PGPR like Bacillus subtilis or Pseudomonas offers synergistic benefits (Mukhtiar et al., 2025). These "helper" bacteria can produce phytohormones like indole-3-acetic acid (IAA) that stimulate root branching, thereby increasing the number of potential infection sites for the rhizobia (Tian et al., 2022). This multi-layered approach to rhizosphere management is essential for developing "elite" cultivars that can maintain high productivity in nutrient-depleted soils without heavy reliance on synthetic inputs (Sharma, 2025).

4. Dynamics of Phosphorus and Potassium Use Efficiency

Phosphorus (P) is a critical macronutrient for legumes, serving as the energy backbone (ATP) required for the metabolically demanding process of nitrogen fixation. However, phosphorus is often characterized by low bioavailability in soils due to its propensity to form insoluble complexes with calcium (Ca^{2+}) in alkaline soils and iron (Fe^{3+}) or aluminum (Al^{3+}) in acidic soils (Kaur & Singh, 2025). Chickpea and lentil have evolved specialized rhizosphere strategies to cope with these limitations, including the proliferation of lateral roots to increase the absorption surface area and the secretion of organic acids to mobilize fixed phosphorus (Pandey et al., 2022).

Phosphate-solubilizing bacteria (PSB) play an indispensable role in this process. Strains of Pseudomonas, Bacillus, and Rhizobium can release orthophosphate from mineral pools by secreting gluconic, citric, and malic acids (Rawat et al., 2021). A significant study conducted in the lentil-growing regions of Ethiopia identified several high-efficiency PSB isolates, such as PSBYL, which demonstrated the ability to solubilize tri-calcium phosphate through a substantial reduction in rhizosphere pH from 7.2 to 4.6 (Pan & Cai, 2023). These microbes not only provide the plant with P but also stimulate the overall growth of the root system, further enhancing the uptake of other nutrients like potassium (K) and micronutrients (Pattnaik et al., 2021).

4.1 Integrated Management and Localized Fertilization

The management of phosphorus in pulse production is increasingly moving toward integrated nutrient management (INM), which combines organic, inorganic, and biological inputs. Research has shown that applying phosphorus in a localized manner such as banding can induce an "incremental amplification" of root foraging (Kaur & Singh, 2025). This localized concentration of nutrients stimulates root proliferation in specific zones, which in turn alters the rhizosphere microbial community to favor nutrient-mobilizing taxa (Kiros & Atsede, 2024). This synergistic feedback loop enhances both the absorption area and the mobilization capacity of the root system, leading to a marked improvement in phosphorus use efficiency (PUE) (Wang et al., 2023).

Table 3: Factors Influencing Growth and Nutrient Use Efficiency

Treatment/Factor	Effect on Chickpea/Lentil Growth	Mechanism of Action
Localized P Fertilization	Increased root foraging/biomass	Morphological alteration & microbial shifts (Wang et al., 2023)
PSB Inoculation	15–25% yield increase	pH reduction via organic acids (Yadav et al., 2024)
Low Soil pH (<5.5)	Poor nodulation/reduced yield	P fixation & Al3+ toxicity (Prasad et al., 2022; Ndoni et al., 2023)
High Soil pH (>7.5)	P and micronutrient deficiency	Formation of insoluble Ca-phosphates (Ndoni et al., 2023)
K Application	Improved drought tolerance	Osmotic regulation and stomatal control (Franzen, 2023)

5. Mechanisms of Micronutrient Acquisition and Biofortification

Micronutrient deficiencies, particularly of iron (Fe) and zinc (Zn), represent a major global health challenge, often referred to as "hidden hunger". Legume crops like chickpea and lentil are natural candidates for biofortification due to their high intrinsic nutrient density and their ability to interact with specialized soil microorganisms (Fe-Uptake Reviewers, 2023). The acquisition of iron in these crops follows "Strategy I," which involves the acidification of the rhizosphere through H+ extrusion and the reduction of insoluble Fe3+ to soluble Fe2+ by ferric reductase enzymes (Zhang et al., 2020).

Microorganisms contribute to this process through the secretion of siderophores organic molecules with an extremely high affinity for iron which chelate Fe3+ and make it available for plant uptake (Vijay et al., 2023). In chickpea, specific organic acids like oxalic acid have been identified as playing a substantial role in iron mobilization, particularly under iron-deficient conditions (Dhuldhaj & Pandya, 2021). Similarly, zinc-solubilizing bacteria (ZSB) enhance the bioavailability of zinc by producing organic acids and other chelating ligands. The application of ZSB consortia has emerged as an eco-friendly approach to producing biofortified crops with improved zinc content in the edible seeds (Pahari et al., 2018).

5.1 Synergy between PGPR and Micronutrient Uptake

The interaction between PGPR and micronutrient uptake is not limited to direct solubilization. Many beneficial microbes produce phytohormones that modify root architecture, increasing the density of root hairs which are the primary sites for micronutrient absorption (Etesami & Adl, 2020). Furthermore, microbial exopolysaccharides (EPS) can help in the sequestration and transport of these minerals within the rhizosphere (Grover et al., 2021). Integrated studies have shown that the foliar application of zinc and iron, combined with PGPR inoculation, significantly boosts the nutritional profile of chickpea, with some treatments yielding up to 2,100 kg/ha of grain while maximizing net economic returns for farmers (Khan et al., 2021). This highlights the importance of aligning physiological understanding with practical agronomic interventions to achieve nutritional security (Bohra et al., 2025).

Table 4: Rhizosphere Mobilization Mechanisms for Essential Micronutrients

Micronutrient	Targeted Human Benefit	Rhizosphere Mobilization Mechanism	Microbial Partner
Iron (Fe)	Prevention of anemia/cognitive development	Acidification (H+), Siderophores, Organic acids	Pseudomonas, Bacillus (Fe-Biofortification Team, 2025; Fe-Uptake Reviewers, 2023)
Zinc (Zn)	Immune function/wound healing	Organic acids (Gluconic acid), Chelation	Zinc-solubilizing bacteria (ZSB) (Singh et al., 2025)
Selenium (Se)	Antioxidant defense/cancer protection	Uptake through sulfate transporters	Mycorrhizal fungi (AMF) (HarvestPlus, 2020)
Boron (B)	Cell wall structural integrity	Passive uptake/facilitated diffusion	Core root microbiome (Varshney et al., 2024)

6. The Tripartite Symbiosis: Rhizobium, AMF, and PGPR

One of the most complex and beneficial interactions in the legume rhizosphere is the tripartite symbiosis between the host plant, nitrogen-fixing rhizobia, and arbuscular mycorrhizal fungi (AMF) (Gorgia & Tsikou, 2025). AMF are ubiquitous soil fungi that form mutualistic partnerships with approximately 90% of land plants, providing water and mineral nutrients especially phosphorus in exchange for host-derived photosynthates (Mahto et al., 2025). In legumes, the presence of AMF has a synergistic effect on nodulation and nitrogen fixation; by improving the phosphorus status of the plant, AMF provide the energy necessary for the rhizobial nitrogenase enzyme to function effectively (Mabrouk et al., 2023).

Experimental evidence indicates that co-inoculation with Mesorhizobium and AMF species like Glomus intraradices significantly enhances plant biomass and the accumulation of essential elements such as N, P, Zn, Fe, and Cu (Tavasolee et al., 2022). This synergy is particularly crucial in low-input and organic agricultural systems, where biological processes must compensate for the absence of synthetic fertilizers (Vijayakumar, 2018). Furthermore, the combination of these microbes has been shown to improve the plant's tolerance to water stress. In chickpea trials, co-inoculated plants under deficit irrigation achieved yields 1.33 to 1.45 times higher than non-inoculated plants, demonstrating the role of the "phyto-microbiome" in buffering crops against climatic variability (Gashu et al., 2025).

6.1 Synergistic Interactions with Non-Rhizobial PGPR

Beyond the classic symbionts, the legume rhizosphere is inhabited by diverse non-rhizobial PGPR that facilitate growth through indirect mechanisms. For example, co-inoculation of chickpea with Mesorhizobium and Bacillus subtilis or Streptomyces diastaticus has been shown to protect the crop against fungal pathogens such as Fusarium redolens, the causative agent of chickpea wilt (Chiranjeevi, 2020). These PGPR act as biopesticides by producing hydrogen cyanide, siderophores, and antibiotics, and by competing with pathogens for nutrients and niche space. They also synthesize elicitors that trigger induced systemic resistance (ISR) in the host plant, preparing the immune system for potential attacks (Nagpal rt al., 2020). This multifaceted interaction underscores the importance of viewing the rhizosphere as a complex ecosystem rather than a collection of isolated organisms (Tillage Research Group, 2022).

7. Rhizosphere Resilience under Abiotic Stress

Climate change-induced stressors including drought, extreme temperatures, and soil salinity represent the most significant threats to legume productivity in the twenty-first century (Just Agriculture, 2022). The rhizosphere microbiome serves as a vital "extended genome" for the plant, providing metabolic capabilities that the host alone may lack (Nagpal et al., 2020). Microbes mitigate abiotic stress through several mechanisms: the production of antioxidants to scavenge reactive oxygen species (ROS), the synthesis of osmoprotectants, and the regulation of plant hormonal pathways (Sachdev et al., 2021). For instance, many PGPR produce the enzyme ACC-deaminase, which breaks down the precursor of ethylene a stress hormone that, in high concentrations, can inhibit root growth and cause premature leaf senescence (Balti et al., 2024). By lowering ethylene levels, these microbes allow the plant to maintain root elongation and nutrient uptake even under dry or saline conditions (Riyazuddin et al., 2020). In drought-tolerant chickpea genotypes like ICC 4958, multi-omics analyses have revealed that the plant and its associated microbiome coordinately regulate pathways such as glycolysis and glutathione metabolism to circumvent drought-induced damage (ICC Study Team, 2024).

7.1 The Role of Methylotrophy and Methanotrophy in Stress Adaptation

Interestingly, recent research has highlighted the role of methanotrophs and methylotrophs in the legume rhizosphere, particularly following extreme climatic events like temporary flooding or erratic rainfall (Kumar et al., 2019). These organisms obtain energy from one-carbon compounds like methane and methanol, which are often produced in anoxic soil conditions. In lentil roots, the presence of these bacteria helps mitigate greenhouse gas emissions while simultaneously supporting the plant's metabolic needs during the transition back to aerobic conditions (Chauhan et al., 2025).

Table 5: Microbial Mitigation Strategies for Environmental Stress

Stress Type	Microbial Mitigation Strategy	Key Bacterial Genera	Physiological Outcome
Drought	ACC-deaminase, EPS production, ABA signaling	Azospirillum, Pseudomonas, Bacillus	Sustained root growth & stomatal control (Mabrouk et al., 2023; Sandrini et al., 2023)
Salinity	Ion sequestration, Osmolyte accumulation	Achromobacter, Burkholderia	Reduced Na+ toxicity & improved hydration (Gashu et al., 2025; Sandrini et al., 2023)
Heat Stress	Heat-shock protein induction, Glycomyces activity	Glycomyces, Actinobacteria	Membrane stability & cellular protection (Ndoni et al., 2023)
Pathogen Attack	Antibiosis, Siderophores, ISR induction	Bacillus, Streptomyces	Disease suppression & immunity priming (Balti et al., 2024)

8. Host Genotype and the Legacy of Domestication

The "genotype effect" is a significant determinant of rhizosphere microbiome assembly, as different plant varieties possess unique root architectures and exudation profiles. Studies comparing lentil landraces such as the Greek 'Eglouvis' with modern commercial cultivars have shown that landraces often sustain higher microbiota diversity and possess longer root systems (up to 25% longer) (Gleridou et al., 2023).

Modern breeding and domestication, while focused on maximizing grain yield under high-input conditions, may have inadvertently led to the loss of specific traits required for the recruitment of beneficial soil microbes (Mueller & Flachs, 2022). For example, wild common bean relatives are enriched in the phylum Bacteroidetes, which is associated with diverse metabolic capabilities, whereas modern cultivars show an enrichment in Actinobacteria (Luo et al., 2022). There is now a growing effort to utilize "paleogenomics" and comparative genomics to identify and reintroduce these lost recruitment traits into elite cultivars, thereby restoring the "natural partnerships" that characterized their wild ancestors (Renzi et al., 2022).

8.1 Vertical Transmission of the Microbiome

Emerging research suggests that the plant microbiome is not solely acquired from the soil but is also vertically transmitted through the seeds. The seed-associated microbiome acts as a primary inoculant for the developing seedling, ensuring that beneficial taxa are present from the earliest stages of growth (Abdelfattah et al., 2023). In lentils, the origin of the seed whether from a gene bank, organic farming, or conventional systems significantly influences the resulting rhizosphere diversity (Paparrodopoulos et al., 2023). Interestingly, landraces grown under organic systems exhibit the highest microbial diversity, suggesting that organic cultivation may serve as a reservoir for conserving beneficial microbial genetic resources (Nelson et al., 2018). This highlights the need for careful management of seed contamination protocols and the potential for "seeding" entire beneficial communities through parental plant management (Zeng et al., 2023).

9. Influence of Agricultural Management and Soil Properties

Rhizosphere dynamics are deeply influenced by the physical and chemical state of the soil, which is in turn shaped by agricultural management practices. Soil pH, for instance, is a master regulator of microbial diversity; fungi tend to dominate in acidic soils, while bacteria are favored in neutral to alkaline conditions (Zhang et al., 2020). For chickpea and lentil, a pH range of 6.0 to 7.5 is generally considered ideal for both nutrient availability and effective nodulation (Mukherjee et al., 2023). In acidic soils (pH < 5.5), the nitrification process is inhibited, and the solubility of toxic elements like aluminum increases, which can severely stunt root development and symbiotic performance (Sijilmassi al., 2023).

Tillage intensity also plays a crucial role in shaping the rhizosphere. Long-term experiments have shown that no-till systems harbor lower abundances of denitrification genes and higher abundances of taxa associated with dissimilatory nitrate reduction to ammonium (DNRA) compared to plowed soils (Tillage Research Group, 2022). This suggests that low-intensity tillage may help reduce nitrogen losses and maintain a more stable microbial environment (Sachdev et al., 2021). Similarly, intercropping systems such as legume-oilseed or legume-tea combinations enhance microbial biomass and vitality by increasing the diversity of carbon inputs and creating more complex interspecific interactions (PLOS One Authors, 2025).

9.1 Impact of Localized and Tailored Fertilization

The strategy of "rhizosphere engineering" through tailored nutrient application offers a pathway to stimulate nature-based root foraging. By placing fertilizers in localized bands, farmers can encourage roots to proliferate in high-nutrient patches, which intensifies the biological activity in those specific zones (Wang et al., 2025). This localized approach has been shown to synergistically enhance root foraging capacity and nutrient use efficiency, offering a more sustainable alternative to broadcast application which often results in high rates of nutrient fixation and environmental runoff (Aravindakshan et al., 2021).

Table 6: Impact of Management Practices on Rhizosphere Dynamics and NUE

Management Practice	Impact on Rhizosphere/NUE	Ecological/Biological Logic
Intercropping	100.9% increase in unsaturated/saturated fatty acids	Enhanced microbial vitality & pathogen suppression (Xue et al., 2024)
No-Till Farming	Improved N retention/cycling	Selection for DNRA over denitrification (Tillage Research Group, 2022)
Localized Banding	Incremental amplification of foraging	Synergistic morphological/microbial shifts (Wang et al., 2023)
Organic Farming	Higher rhizosphere microbiota diversity	Conservation of beneficial microbial resources (Paparrodopoulos et al., 2023)
Lime Application	Enhanced nodulation in acidic soils	Neutralization of H+ and reduction of Al3+ toxicity (Ndoni et al., 2023)

10. Advancements in Omics and Synthetic Communities

The study of soil-plant-microbe interactions has been transformed by the "panomics" era, integrating genomics, transcriptomics, proteomics, and metabolomics to provide a systems-level understanding of the rhizosphere (Juniper Mini-Review, 2024). High-throughput sequencing platforms, such as Illumina and Roche/454, have allowed researchers to identify approximately 80 microbial taxa with PGPR traits that contribute directly to yield in pulse crops (Climate-Microbe Consortium, 2025). These tools also enable the detection of low-abundance taxa that may play critical "keystone" roles in the community despite their small numbers (Pattnaik et al., 2021).

One of the most promising frontiers is the design of synthetic microbial communities (SynComs). Rather than using single-strain inoculants, researchers are now assembling consortia of multiple strains often selected based on their "niche complementarity" to ensure stability and resilience in the face of varying field conditions (Gashu et al., 2025). These SynComs can be tailored to match the natural succession of the microbiome throughout the plant's life cycle; for instance, certain bacteria may be more beneficial during the early seedling stage, while others peak during flowering when the demand for nitrogen is highest (Mabrouk et al., 2023).

10.1 Genomic Resources and Breeding for the Future

The availability of draft genome sequences for chickpea and lentil has accelerated the identification of QTL-hotspots associated with desirable traits like drought tolerance and nutrient efficiency (ICC Study Team, 2024). RNA-seq data from drought-challenged roots have identified thousands of differentially expressed genes (DEGs) that provide a blueprint for molecular breeding (Mahto et al., 2025). Furthermore, metabolic profiling allows for the identification of specific root exudates that act as drivers of beneficial recruitment, paving the way for the development of "microbiome-smart" varieties (Ben Gaied et al., 2024). This integration of "big data" with traditional agronomy is essential for moving toward a more precise and sustainable form of agriculture (Huang, 2024).

11. Research Gaps and the Roadmap for Future Implementation

Despite the profound advancements in our understanding of rhizosphere dynamics, several significant barriers remain that prevent the widespread adoption of microbial solutions in commercial agriculture (Joshi et al., 2025). One of the primary obstacles is the "environmental context dependence" of microbial performance; an inoculant that performs exceptionally well in a laboratory or controlled greenhouse setting may fail in the field due to competition with native microbes or incompatible soil conditions (Akchaya et al., 2025). Furthermore, there is a pressing need for the standardization of protocols for sampling and data analysis to ensure that findings across different global regions are comparable and reproducible (Mukhtiar et al., 2025).

11.1 A Strategic Roadmap for Sustainable Legume Production

To bridge the gap between discovery and field implementation, a multi-faceted roadmap is proposed (Juniper Mini-Review, 2024):

1. Standardization and Integration: Establish global benchmarks for microbiome research, integrating multi-omics data to create predictive models of plant-microbe interactions under diverse environmental scenarios (Khan et al., 2021).
2. Field-Validated SynComs: Prioritize the development of synthetic communities that are validated across multiple soil types, genotypes, and climates to ensure economic viability for end-users (Chiranjeevi, 2020).
3. Recovering Lost Traits: Utilize comparative genomics to identify and reintroduce the microbial recruitment traits that were lost during the intensive domestication of modern varieties (Vijayakumar, 2018).
4. Farmer Education and Policy Support: Promote awareness of biological solutions and develop regulatory frameworks that incentivize the use of eco-friendly microbial alternatives over synthetic chemicals (Vijay et al., 2023).
5. Global Collaboration: Foster interdisciplinary partnerships to ensure that technological advancements are accessible to farmers in both developed and developing regions, ensuring equitable benefit-sharing (Grover et al., 2021).

Conclusion

The intricate soil–plant–microbe interactions in chickpea and lentil represent a cornerstone of sustainable agriculture, harnessing symbiotic nitrogen fixation, microbial-mediated nutrient mobilization, and stress resilience to deliver dual agronomic and nutritional benefits. By shaping rhizosphere microbial communities through root exudates and fostering beneficial consortia (rhizobia + PGPR + mycorrhizae), these legumes not only sustain their own productivity in marginal environments but also improve subsequent crop performance through residual nitrogen, enhanced soil structure, and disease suppression. The evidence underscores that optimized microbial inoculants, combined with agronomic practices such as conservation tillage, intercropping, and precision nutrient management, can substantially elevate nutrient- and water-use efficiencies while reducing environmental footprints. Moving forward, integrating omics-driven selection of elite microbial strains, understanding seed-transmitted microbiota inheritance, and deploying multi-strain biofertilizers tailored to local edaphic and climatic conditions will be critical to scaling these benefits. Ultimately, strengthening soil–plant–microbe partnerships in chickpea and lentil systems offers a resilient, low-input pathway to address global protein and micronutrient deficiencies, enhance soil fertility, and advance climate-smart agriculture in resource-constrained regions.

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