

SOIL MICROBIAL PROCESSES FACILITATING NUTRIENT AVAILABILITY FOR CHICKPEA (*CICER ARIETINUM*) PRODUCTION

¹J.Yunusov

²B.Abdusattorov

¹Student of International agriculture university

²Professor of International agriculture university

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Abstract

Soil microorganisms play a central role in determining nutrient availability for chickpea (*Cicer arietinum*) production. The interactions between root-associated microbes and soil minerals influence the mobilization, transformation, and uptake of essential nutrients such as nitrogen, phosphorus, and micronutrients. This paper examines key microbial processes—including biological nitrogen fixation by *Mesorhizobium* species, phosphorus solubilization by plant growth-promoting rhizobacteria (PGPR), siderophore-mediated iron mobilization, and microbial decomposition of organic matter—that contribute to improved nutrient bioavailability in chickpea cultivation systems. Understanding these mechanisms is crucial for enhancing crop productivity, reducing dependence on synthetic fertilizers, and promoting sustainable agricultural management practices.

Keywords: *Soil microbes; nutrient availability; nitrogen fixation; phosphorus solubilization; chickpea (Cicer arietinum); rhizosphere microbiome; plant-microbe interactions; sustainable agriculture*

Introduction

Chickpea (*Cicer arietinum*) is an important legume widely cultivated in semi arid and subtropical regions due to its nutritional value and adaptability to low input farming systems (Varshney et al., 2013). In nutrient poor and drought prone soils, chickpea relies heavily on soil microorganisms for nutrient acquisition and growth (Jha et al., 2021). These microbes regulate nutrient cycling, organic matter decomposition, and the conversion of unavailable nutrients into plant accessible forms (Richardson & Simpson, 2011).

Biological nitrogen fixation is one of the most important microbial processes in chickpea cultivation. Symbiotic *Mesorhizobium* species convert atmospheric nitrogen into ammonia, supplying much of the crop's nitrogen needs while improving soil fertility (Rao et al., 2022; Zahran, 1999). Other beneficial microbes, such as *Pseudomonas* and *Bacillus*, solubilize phosphorus through organic acid and enzyme production, enhancing nutrient uptake (Khan et al., 2007). Arbuscular mycorrhizal fungi (AMF) further improve phosphorus acquisition, water use efficiency, and tolerance to drought and salinity (Smith & Read, 2008). In addition, soil microbes support micronutrient availability, including iron and zinc, through siderophore production and redox reactions (Verma et al., 2019).

With increasing emphasis on sustainable agriculture, improving the activity of beneficial soil microorganisms offers a practical approach to enhancing chickpea productivity, reducing dependence on chemical fertilizers, and maintaining long term soil health (Singh et al., 2020). This paper examines the major microbial processes involved in nutrient availability and their role in sustainable chickpea production.

Soil microorganisms regulate the bioavailability of essential nutrients through a range of biochemical processes that support chickpea growth and productivity. These processes include

biological nitrogen fixation, phosphorus solubilization, micronutrient mobilization, and organic matter decomposition. Together, they determine the nutrient supply capacity of the soil and directly influence chickpea nutritional status (Richardson & Simpson, 2011).

Biological Nitrogen Fixation

Nitrogen is one of the most limiting nutrients in chickpea production, particularly in semi-arid soils where mineral nitrogen is scarce (Rao et al., 2022). Chickpea forms a symbiotic relationship with *Mesorhizobium* species, which infect root hairs and initiate nodule formation. Within these nodules, nitrogenase enzymes convert atmospheric nitrogen (N₂) into ammonia (NH₃), supplying the plant with biologically available nitrogen (Zahran, 1999). Studies indicate that effective Rhizobium–legume symbiosis can provide 50–80% of the total nitrogen requirement for chickpea in low-input systems (Jha et al., 2021). The efficiency of this process depends on: the presence of compatible *Mesorhizobium* strains, adequate levels of micronutrients such as molybdenum and iron required for nitrogenase activity, and soil pH and moisture conditions (Rao et al., 2022).

Phosphorus Solubilization

Phosphorus (P) is the second-most limiting nutrient after nitrogen in chickpea systems, largely because most soil phosphorus exists in insoluble mineral complexes that plants cannot readily absorb (Khan et al., 2007).

Phosphate-solubilizing microorganisms (PSMs), including *Pseudomonas*, *Bacillus*, and *Aspergillus* species, release organic acids—such as gluconic, oxalic, and citric acids—that dissolve soil-bound phosphates. These microbes also produce phosphatase enzymes that mineralize organic phosphorus compounds, increasing P availability in the rhizosphere (Sharma et al., 2013).

Micronutrient Mobilization (Fe, Zn, Mn)

Micronutrients such as iron (Fe), zinc (Zn), and manganese (Mn) are essential for enzymatic reactions, chlorophyll production, and symbiotic nitrogen fixation. However, these nutrients often occur in oxidized or mineral-bound forms that are unavailable to plants (Kabir et al., 2021). Soil microbes enhance micronutrient availability through: siderophore production, which chelates Fe³⁺ and increases iron uptake, redox transformations that convert micronutrients to plant-available forms, and organic acid secretion that dissolves metal oxides (Verma et al., 2019).

Root Exudates and Microbial Recruitment

Chickpea roots secrete a mixture of sugars, amino acids, phenolics, flavonoids, and organic acids that influence microbial colonization in the rhizosphere. These exudates serve as energy sources and signaling molecules, attracting beneficial bacteria such as *Mesorhizobium*, *Pseudomonas*, and *Bacillus* species (Philippot et al., 2013). Flavonoids, in particular, play a key role in initiating communication with rhizobial bacteria by activating nodulation (nod) genes, which leads to nodule formation and nitrogen fixation (Rao et al., 2022).

Microbial Interactions and Functional Networks

The chickpea rhizosphere functions as a complex ecological network composed of bacteria, fungi, archaea, and protists interacting in cooperative and competitive relationships. Beneficial microbes such as plant-growth-promoting rhizobacteria (PGPR) enhance nutrient availability by fixing nitrogen, solubilizing phosphorus, and producing siderophores, while suppressing pathogens through antibiotic production and niche competition (Khan et al., 2007). Interactions between different microbial groups also produce synergistic effects. For example: Phosphate-solubilizing bacteria increase phosphorus availability, which in turn enhances nodulation and nitrogen fixation

by *Mesorhizobium* (Sharma et al., 2013). Siderophore-producing microbes improve iron uptake, supporting nitrogenase enzyme function in rhizobial symbiosis (Verma et al., 2019). PGPR enhance root growth, increasing the surface area available for microbial colonization (Niu et al., 2017).

Role of Arbuscular Mycorrhizal Fungi (AMF)

Arbuscular mycorrhizal fungi (AMF) form mutualistic associations with chickpea roots, extending hyphal networks into the soil that significantly enhance the plant's nutrient absorption capacity. AMF are particularly important for phosphorus uptake, as their hyphae access soil micropores and mineral surfaces beyond the reach of root hairs (Smith & Read, 2008). In chickpea systems, AMF improve: phosphorus acquisition, water-use efficiency, resistance to drought and salinity stress, and overall plant biomass and grain yield (Garg & Pandey, 2016). AMF also influence microbial community assembly by modifying root exudation patterns and creating microhabitats that support beneficial bacteria (Singh et al., 2020). When present alongside effective rhizobial strains, AMF further enhance nitrogen fixation by improving phosphorus supply, illustrating the multi-layered benefits of microbial symbioses (Smith & Read, 2008).



Picture 1. Mycorrhizal Fungi (AMF)

Retrieved from:

<https://share.google/BN5wvj2U3Kby9Lgvw>

Recent Advancements and Future Prospects

Recent work has moved from single-strain inoculants toward complex biofertilizers and microbial consortia that directly improve soil fertility and plant nutrition. Experimental studies show that applications of microbial fertilizers can significantly increase soil microbial richness, improve physicochemical properties, and promote plant growth, confirming that microbial products can function as tools to stabilize soil microecology and enhance nutrient availability (Zhang et al., 2024).

In chickpea, biofertilizers containing plant growth-promoting rhizobacteria (PGPR) have been tested under arid conditions. A recent study conducted by Nabati & Nezami, (2025) reported that a consortium containing sulfur-oxidizing, nitrogen-fixing, phosphate-solubilizing, and potassium-solubilizing bacteria substantially improved nutrient uptake, biomass, and grain yield of chickpea in an arid environment, highlighting the potential of PGPR-based fertilizers to compensate for poor soil fertility and water limitation.

A review by Singh, Singh, and Saravaiya (2018) concluded that *Mesorhizobium* inoculation consistently improves growth traits, nodulation, yield components, and nutrient uptake in chickpea, confirming biofertilizers as a viable strategy to reduce mineral nitrogen inputs. A related review by Eduru, Upadhyay, and Kamboj (n.d.) similarly documents that rhizobial inoculation increases yield components and growth parameters and can be effectively harnessed to enhance biological nitrogen fixation and soil nitrogen fertility in chickpea (Eduru et al., n.d.).

More recent work has progressed to multi-strain consortia. An experiment using combined inoculation of *Mesorhizobium* with two PGPR strains (*Streptomyces diastaticus* subsp. *diastaticus* and *Bacillus subtilis*) showed that the consortium simultaneously improved chickpea growth and

protected plants against *Fusarium redolens*, compared with plants exposed only to the pathogen (Nourinejhad Zarghani et al., 2025).

Rhizosphere Microbiome Characterization

Soil-type effects on microbial communities have been specifically studied in chickpea. A study on “Soil type influence nutrient availability, microbial metabolic diversity, eubacterial and diazotroph abundance in chickpea rhizosphere” reported that different soil types markedly influenced eubacterial and diazotrophic gene abundance, microbial metabolic potential, and nutrient availability in the rhizosphere of two chickpea cultivars (Kumar et al., 2021). This supports the idea that microbiome engineering in chickpea must be soil-context specific, as the same inoculant may behave differently in different soil environments.

Genome Editing and Bioengineering of Chickpea

In parallel with microbiome-based strategies, there has been rapid progress in genome editing of chickpea, particularly using CRISPR/Cas systems. A preprint by Gupta et al. (2022) established a stable transformation and CRISPR/Cas9-based genome-editing system for chickpea and demonstrated its applicability by knocking out the *CaPDS* (phytoene desaturase) gene as a visible proof of concept. This work shows that chickpea is technically amenable to precise gene editing, opening the door to targeting genes related to nutrient uptake, root architecture, and nodule development.

Specifically for chickpea, Mahto et al. (2025) discussed symbiotic nitrogen fixation and prospects for genome editing under changing climatic conditions. They proposed targeting host genes such as *CaNFP* and other nodulation and signaling components to enhance nitrogen fixation efficiency and reduce dependence on synthetic nitrogen fertilizers, particularly when combined with effective microbial inoculants (Mahto et al., 2025). This strategy directly couples host genome engineering with rhizobial symbiosis to optimize nutrient acquisition.

Conclusion

Soil microbial communities are fundamental to nutrient availability and productivity in chickpea cultivation. Through processes such as biological nitrogen fixation, phosphorus solubilization, micronutrient mobilization, and organic matter decomposition, rhizosphere microbes enhance nutrient cycling, plant growth, and long term soil fertility. Advances in microbiome profiling and molecular tools have improved understanding of chickpea–microbe interactions, showing that targeted inoculation and soil specific biofertilizer strategies can significantly improve crop performance and nutrient efficiency.

At the same time, CRISPR/Cas based genome editing offers new possibilities to enhance nutrient use efficiency and strengthen chickpea–microbe symbioses by modifying genes involved in nodulation, nutrient transport, and stress tolerance. Together, microbiome engineering, biofertilizer development, and genome editing are creating opportunities for integrated, sustainable nutrient management systems.

Future research should focus on combining multi omics technologies with field scale agronomy, improving host–microbe compatibility, and establishing safe regulatory frameworks for engineered microbes. These innovations can reduce dependence on chemical fertilizers, improve resilience to climate stress, and support sustainable chickpea production and global food security.

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