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Management Practices on Soil Biochemical Parameters and Rhizosphere Microbial Communities of Turmeric (*Curcuma longa* L.): An Overview

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ABSTRACT

Turmeric (*Curcuma longa* L.) a commercially important and nutrient-intensive crop, is extensively cultivated across various regions of India. The increasing population and intensification of agricultural practices have led to a decline in soil fertility and contributed to global climate change. This situation presents a formidable challenge to current turmeric cultivation methods, as the demand for food continues to rise. Therefore, it is imperative to optimize sustainable agricultural practices and mitigate the ecological impacts of food production to support a growing population. The review reveals that organic and integrated nutrient regimes generally enhance microbial diversity and support beneficial soil microorganisms, which contribute to improved soil health and potentially higher growth and yield in turmeric. In contrast, conventional practices are often associated with reduced microbial diversity and depletion of soil health. The review emphasizes the importance of sustainable agricultural practices in maintaining soil biodiversity and health, which are crucial for the long-term productivity and sustainability of turmeric farming. Additionally, advancements in rhizosphere research are highlighted, providing deeper insights into optimizing soil management practices for turmeric cultivation.

Key words: Organic, Plant-microbe interactions, Sustainable agriculture, Syncom, Turmeric.

Turmeric (*Curcuma longa* L.) which belongs to the family Zingiberaceae is a plant with historical connotations and a cultural reputation, widely used as a dye, condiment and medicine. Turmeric is believed to have originated in southeast Asian countries such as India, China and Vietnam, but is now cultivated globally in the tropics and subtropics (Fuloria *et al.,* 2022). The plant grows extensively throughout the country, mainly in states including Telangana Andhra Pradesh, Odisha, Tamil Nadu, West Bengal, Assam, Maharashtra, Bihar, Karnataka and Kerala (Mirjanaik *et al.,* 2020). One of the most expensive plants on the world market is the Curcuma plant which plays a major role in India's spice export and economy (Nair, 2019), India is the global leader in turmeric production, accounting for approximately 80% of the annual global output. Additionally, India excels in the export of turmeric and value-added turmeric products (Srinivasan *et al.,* 2016; Nair, 2013).

Turmeric output and land have increased during the last ten years as demand in international markets has risen (Aarthi *et al.,* 2020; Srinivasan *et al.,* 2016). As a result, individuals are employing various management approaches to boost production, including the use of chemical fertilizers (conventional nutrient management), which may compromise the soil's long-term viability. The quality of turmeric grown with chemical and inorganic fertilizers is currently compromised for export value and organic turmeric is gaining popularity in international markets with premium prices. Soil fertility influences both the quality and productivity of turmeric, which can be increased by effective agronomic management measures (Nandhini *et al.,* 2023).

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Bacteria, fungi, archaea and other microorganisms in the rhizosphere play crucial parts in nutrient cycling, organic matter breakdown, disease prevention and plant growth promotion (Kumar *et al.,* 2022). These interactions have a major effect on turmeric growth and yield. Different management approaches in turmeric production have emerged as a key aspect of long-term agricultural operations. Effective fertilizer management not only ensures optimum crop yields but also has an enormous effect on the diversity and function of the microbial community in the turmeric rhizosphere (Nandhini *et al.,* 2023). The impact of agricultural activities on soil quality has received international attention and it is vital to highlight the importance of measuring changes in soil quality as a result of these operations. A soil amendment treatment's performance is determined by its ability to directly supply

and encourage the synthesis of metabolites that are advantageous to the host plant, consequently improving nutrient absorption, disease resistance and yield (Berihu *et al.,* 2023). Different management regimes such as crop rotation, fertilization, irrigation and pest control profoundly impact the microbial properties of the rhizosphere and overall soil health and agricultural productivity. Within the field of soil quality, biochemical metrics representing microbial processes such as microbial biomass carbon and soil enzyme activities occupy center stage due to their sensitivity and importance, because biologically mediated processes in soils are vital to their ecological roles (Dick, 1992). This review focuses on understanding how different management approaches affect soil biology and microbial diversity in turmeric, which are key components towards a sustainable agricultural future.

Effect of management practices and their impacts on plant growth and soil health parameters

Turmeric thrives on a wide range of soils; nevertheless, because it is a nutrient-intensive crop, it requires appropriate organic manures and fertilizers to produce optimal outcomes. Maximum absorption of nutrients occurs during the active development phase (fourth and fifth months after planting), emphasizing the importance of timely delivery of nutrients such as nitrogen (N), phosphorus (P) and potassium (Srinivasan *et al.,* 2016). India has seen a significant shift towards organic farming practices in recent decades. This shift has led to a growing interest in understanding the impact of different management practices on soil biological processes and microbial diversity in turmeric cultivation. Though India leads in turmeric production, average productivity is exceedingly low due to an unequal and improper addition of chemical fertilizers and organic manures (Kandiannan and Chandaragiri, 2008).

Organic agricultural practices rely on renewable resources and assure long-term environmental sustainability. Organic farming affects the soil's physical, chemical and biological traits, improving its fertility. In comparison to chemical fertilizers, it is less expensive, less polluting and a sustainable practice. Kumar *et al.* (2018) study on turmeric indicated that applying farmyard manure, vermicompost and neem cake was the most effective nutrient management approach. Plant growth metrics including plant height, leaf area, tiller count and stem girth have all increased with the use of organic fertilizer. The use of organic amendments was shown to be effective in terms of yield, which might be attributed to the nutrient's ease of access and improved plant growth parameters. A comparable study conducted by Chamroy *et al.* (2015) demonstrated that a combination of 50% N (urea) + 50% N (poultry manure) organic fertilizer was more suitable in terms of turmeric growth, yield and quality when compared to the application of chemical fertilizers (60: 50: 120 kg NPK/ha). Kale *et al.* (1992) discovered that the application of vermicompost boosted the activity of beneficial microorganisms such as N_2 fixers and mycorrhizal fungi colonization; they play a major part in N_2 fixation and Phosphate mobilization, resulting in better nutrient uptake by the turmeric plant, which in turn leads to higher yield. Nandhini *et al.* (2023) conducted a study on a 28-year-long organic nutrient management field and found that there is a 48% increase in turmeric yield and a 62% rise in profitability in terms of net return. Furthermore, the study revealed considerable increases in soil biological characteristics, including higher soil enzyme activities and increased soil microbial biomass, linked to the long-term application of sustainable organic nutrient management strategies. Similar results were reported by Sahu *et al.* (2024).

The use of biofertilizers such as *Rhizobium* sp., *Azotobacter* sp. and *Azospirillum* sp. (Mącik *et al.,* 2020) or changes in nutrient profiles has a considerable impact on soil microbes in the turmeric rhizosphere (Virk *et al.,* 2024). For example, using biofertilizers can introduce beneficial bacteria into the soil, increasing nutrient availability and stimulating plant development. This can cause a shift in the makeup of soil microbiota, favoring beneficial microbes that improve the general health and productivity of turmeric plants. Furthermore, fertilizing strategies might modify the nutrient requirements and preferences of soil microbial communities, affecting their quantity and activity in the turmeric rhizosphere. Roy and Hore (2011) found that the use of *Azospirillum* aids in improved plant development due to their nitrogen fixing abilities and they were able to produce plant growth-enhancing hormones such as Indole Acetic Acid and Gibberellic Acid (Satyanarayana *et al.,* 2013). Tariq *et al.* (2024) reported that plant defense molecules such as polyphenols and phenols were higher in bioinoculant-treated plants, especially in *Pseudomonas putida* treated plants.

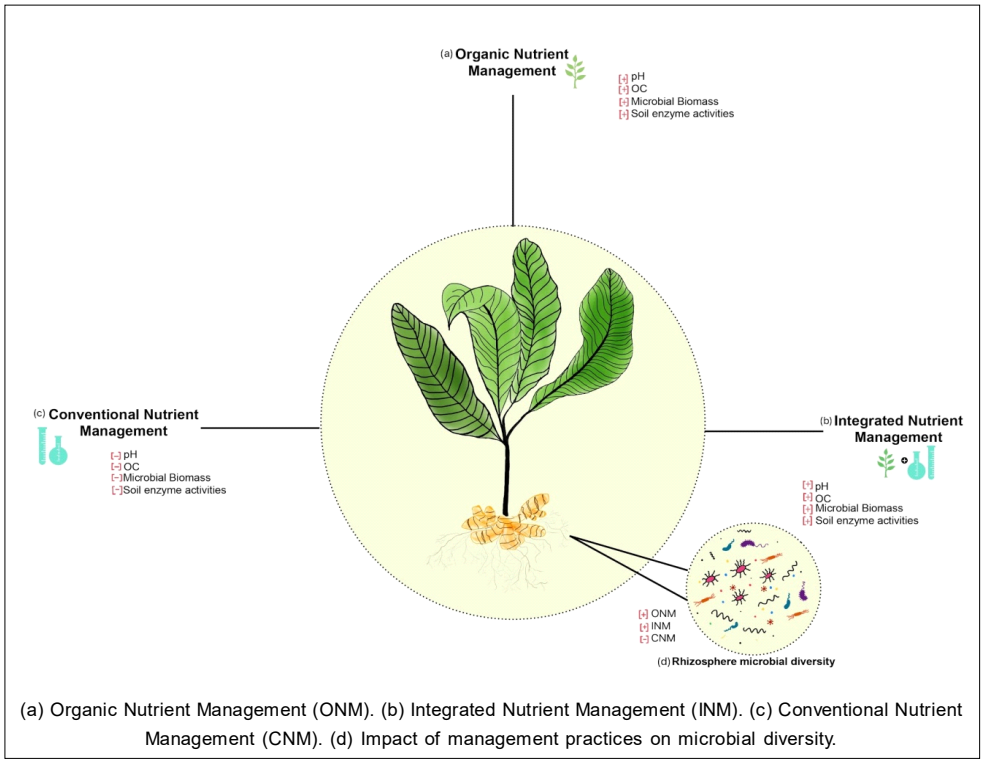
Integrated nutrient management (INM) involves a combination of organic manures, bio-fertilizers and chemical fertilizers to improve crop yield and quality while preserving soil health. INM strives to provide balanced nutrient availability, encourage sustainable farming and reduce environmental impact. To minimize losses due to leaching and volatilization, Integrated Nutrient Management (INM) strategically integrates nutrient sources to guarantee that nutrients are accessible in optimal proportions at the right times (Paramesh *et al.,* 2023). This approach enhances nutrient use efficiency and mitigates environmental pollution. Reduced reliance on chemical fertilizers decreases the risk of groundwater contamination and lowers greenhouse gas emissions associated with fertilizer production and application (Brodt *et al.,* 2011). While the initial setup costs for composting units or bio-fertilizers may be high, the long-term benefits and reduced dependence on expensive chemical fertilizers can ultimately lower overall production costs (Ahmed *et al.,* 2023; Nongbet *et al.,* 2022; Nandhini *et al.,* 2023; Hajam *et al.,* 2023; Kantwa *et al.,* 2023). The recommended dose of fertilizer supplies only two or three major nutrients, whereas the combined use of organic manure and fertilizer

can provide an adequate amount of all essential nutrients (Tripathi *et al.,* 2021). This encourages healthy plant growth and has a direct impact on crop productivity. Dinesh *et al.* (2010) demonstrated that the administration of organic manures (such as farmyard manure, vermicompost, neem cake and ash) and biofertilizers, in conjunction with chemical fertilizers, positively impacted microbial biomass, carbon content, nitrogen mineralization, soil respiration and enzyme activities. Srinivasan *et al*. (2016) reported that integrated nutrient management enables a reduction of up to 50% in the application of inorganic nitrogen fertilizers, significantly mitigating the adverse environmental effects of high-analysis chemical fertilizers.

Conventional nutrient management (CNM) or modern farming practices rely heavily on chemical fertilizers to improve plant growth and yield and applying various doses of N,P and K has been shown to significantly boost growth traits and total dry matter output (Prasath *et al.,* 2019). However, it is crucial to understand that this comes at a cost, such as detrimental effects on the environment and possible risks to human health (Thakur *et al.,* 2020). According to Wang *et al.* (2012) and Nandini *et al.* (2023), conventional farming methods are linked to a number of environmental problems, such as nitrate leaching, soil erosion, pollution and a decrease in soil organic matter, all of which eventually compromise soil quality. Ammonium fertilizers have the potential to lower soil pH because they increase the release of protons, which is a byproduct of improved nitrification processes and ammonium uptake by plants. This soil acidification can lead to nutrient deficiencies, reduced crop yields and deterioration of soil fertility (Barak *et al.,* 1997) in addition to which acidification of the soil can suppress the viability and activities of the rhizosphere bacterial community (Kunito *et al.,* 2024; Rousk *et al.,* 2010). A study on nutrient management systems in turmeric by Srinivasan *et al.* (2016) found that CNM registered lower levels of soil organic carbon, which in turn decreased soil microbial biomass carbon (Długosz and Piotrowska-Długosz, 2023) and activities of enzymes such as acid phosphatase, β-glucosidase and dehydrogenase. Rahman *et al.* (2021) and Prasath *et al.* (2019) reported that soils exclusively treated with inorganic fertilizers exhibited a limited microbial community due to the reduced availability of organic substrates. The impact of different management practices on soil biology and rhizosphere microbial community of turmeric (*Curcuma longa* L.) is shown in Fig 1.

The role of soil microorganisms in turmeric cultivation

The microbial colonization in plant organs is influenced by a range of biotic and abiotic stresses. Significant effects are played by variables such as root exudates, moisture content, pH, salinity, type of soil, texture, structure, organic matter, (Kumawat *et al.,* 2022; Saeed *et al.,* 2021;Yadav *et al.,* 2018; Jacoby *et al.,* 2017; Zilber-Rosenberg and Rosenberg, 2008) and factors such as altered nutrient



(a) Organic Nutrient Management (ONM). (b) Integrated Nutrient Management (INM). (c) Conventional Nutrient Management (CNM). (d) Impact of management practices on microbial diversity.

Fig 1: Impact of different management practices on soil biology and rhizosphere microbial community of turmeric (*Curcuma longa* L.).

composition which include soil carbon, soil available N, P, K, C : N ratio (Kumawat *et al.,* 2022; Bulgarelli *et al.,* 2013, Peiffer *et al.,* 2013), presence of Phyto-pathogens and environmental conditions. Donn *et al.* (2015) reported that microbial communities in the rhizosphere and rhizoplane are influenced by factors such as plant age, plant species and environmental conditions,undergoing dynamic modifications over time. In contrast, microbial communities in bulk soil remain relatively stable (Kong *et al.,* 2024). This finding highlights that microbial communities surrounding the plant root system are influenced by plant-released metabolites, allowing the plant to preferentially support beneficial organisms. Studies on sugarcane, potato and model plants such as Arabidopsis (Kumawat *et al.,* 2022) have demonstrated genotype-dependent variability in the rhizosphere's microbial population. Vinayarani and Prakash (2018) isolated *Bacillus cereus* from the rhizosphere of *Curcuma longa*. This isolate exhibited several beneficial properties, including the production of indole-3-acetic acid (IAA) and hydrogen cyanide (HCN) (Rana *et al.,* 2023), phosphorus solubilization, siderophore production and both cellulase and protease activity. Furthermore, *Bacillus cereus* promoted greater plant height while reducing rhizome rot caused by *Pythium aphanidermatum* and leaf blight caused by *Rhizoctonia solani*. Kumar *et al.* (2019) found nine bacterial strains in the *Curcuma longa* rhizosphere to investigate their role in plant growth and health. All isolates exhibited plant growth-promoting characteristics such as phosphate solubilization, indole-3-acetic acid (IAA) synthesis and ammonia production. Furthermore, practically all strains demonstrated antifungal activity against *Aspergillus niger* and *Alternaria alternata*.

The rhizosphere is the most intricate out of several niches due to its significant influence on plant growth and nutrition (Bandyopadhyay *et al.,* 2017; Lakshmanan *et al.,* 2014). It is the zone of soil surrounding plant roots, hosts a diverse community of microorganisms, including bacteria, fungi and archaea. This zone is characterized by complex interactions and a diverse community structure (Kumawat *et al.,* 2022; Saeed *et al.,* 2021). Turmeric rhizomes interact with numerous microbial species in the rhizosphere, some of which enter plant tissue as endophytes. Rhizospheric and endophytic species play a direct or indirect role in plant development and disease control and regulate factors such as morphology of growth, secondary metabolite production, curcumin concentration and antioxidant capabilities, *etc*. (Tripathi *et al.,* 2022; Kumar *et al.,* 2017).Three groups of PGPR mainly, α, β and γ-Proteobacteria were found to be prevalent in the turmeric rhizosphere. Dominant species include *Pseudomonas*, *Klebsiella*, *Agrobacterium*, *Azotobacter* and *Burkholderia*, representing nearly two-thirds of the Proteobacteria isolates (Kumar *et al.,* 2017). Additionally, bacterial endophytes like *Penibacillus*, *Klebsiella*, *Bacillus* and *Pseudomonas* (Vinayarani and Prakash, 2018) are significant inhabitants of the turmeric rhizome (Khan *et al.,* 2023). Beneficial microbes enhance plant growth by improving nutrient uptake through the solubilization of essential minerals such as phosphorus (P), potassium (K) and zinc (Zn) and by nitrogen fixation. They also produce plant growth promoting hormones such as auxin [(indole-3-acetic acid (IAA)], cytokinins and gibberellic acids (Khan *et al.,* 2023; Hakim *et al.,* 2021; Suman *et al.,* 2022). PGPRs contribute to the biocontrol of phytopathogens by producing antibacterial, antibiotic and antifungal compounds. Kumar *et al.* (2018) reported that bacterial strains, including *B. subtilis* CL1, *Bacillus* sp. CL3, *Klebsiella* sp. CL6, *B. cereus* CL7, *P. putida* CL9 and *P. fluorescens* CL12, exhibit significant antibacterial and antifungal properties, they produce bioactive compounds such as Ecomycins, Munumbicins, Pseudomycins and Kakadumycins that inhibit pathogenic bacteria and fungi (Christina *et al.,* 2013). These isolates formed zones of inhibition against fungi like *A. niger*, *A. alternata* and *B. fulva* and inhibited *E. coli*, except for *A. tumefaciens* CL5 and *A. chroococcum* CL13. Additionally, the isolated PGPRs produced iron-chelating siderophores, stimulated systemic resistance and alleviate biotic and abiotic stresses, enhancing the accumulation of secondary metabolites like curcuminoids in turmeric rhizomes. By understanding and leveraging these microbial interactions, it is possible to optimize turmeric cultivation practices for better yield and plant health (Khan *et al.,* 2023).

Apart from conventional methods, molecular techniques such as the multi-omics approach have provided new opportunities to study the rhizosphere microbiota mostly the unculturable population and investigate its impact on plant growth and health (Hellal *et al.,* 2023; Sharma *et al.,* 2020). Metagenomic sequencing methods highlight the dynamics of microbial community modifications, allowing exploration of their functional impacts (Berihu *et al.,* 2023). These techniques allow researchers to identify and quantify microbial populations, measure processes in the rhizosphere and simulate natural conditions in the laboratory (Azubuike *et al.,* 2016). By merging molecular approaches with traditional methodologies, we can acquire a better knowledge of the biotic and abiotic variables that shape the rhizosphere microbiota, as well as the complicated mechanisms that govern its impact on plant development, yield and disease resistance (Fadiji *et al.,* 2023). Understanding the soil microbiota is critical since it is a key component in attaining sustainable agriculture. This information enables us to limit the usage of artificial fertilizers and pesticides, improving soil quality for future generations. By understanding the natural interactions within the soil microbiome, we can promote healthier, more robust agricultural systems that are less reliant on synthetic inputs and more environmentally sustainable (Saeed *et al.,* 2021).

Understanding soil microbiota in turmeric rhizosphere

The rhizosphere has long been a source of great scientific interest, as it plays an important role in plant health, nutrient cycling and ecosystem functioning. Recent advances in the study have provided new light on the intricate dynamics

of this critical microhabitat. One key area of advancement is the understanding of root exudates and their impact on the rhizosphere microbiome (Ansari *et al.,* 2023; Afridi *et al.,* 2023). Root exudates, a diverse array of organic compounds or metabolites released by plant roots, have been shown to play a pivotal role in shaping the microbial communities that thrive in the rhizosphere (Sharma *et al.,* 2023; Olanrewaju *et al.,* 2019). These exudates serve as a source of energy and nutrients for the microbiome, while also acting as signaling molecules that can influence the composition and activity of the microbial community (Pantigoso *et al.,* 2022; Sun *et al.,* 2021). Understanding the dynamic metabolic fluxes in root exudates can be exploited to create a plant prebiotic in which substrates or precursors of biosynthetic pathways are added to boost the growth of specific microbial species or augment microbial activities that benefit the plant host (Song *et al.,* 2021a). Most environmental microbes (>95%) are uncul-turable (Singh *et al.,* 2009), indicating that only a small fraction of potentially beneficial microorganisms can be cultivated and engineered for agricultural applications. By utilizing metagenomic sequencing techniques, it is possible to reveal the workings of microbial community transitions and investigate their functional consequences about modifications in management regimes. Additionally, this will make it possible to apply the strategy to different agricultural systems and regions (Berihu *et al.,* 2023). Understanding the metabolite-driven successional trajectories within the soil microbial communities would allow for more targeted manipulation of the native soil microbiome to improve plant health. Therefore, leveraging the inherent capabilities of the extensive indigenous plant microbiome allows for the identification and utilization of novel and enhanced microbial functions (Qiu *et al.,* 2019).

Salas-Gonzɑlez *et al.* (2021) demonstrated that root diffusion barriers in the endodermis of Arabidopsis regulate microbiota assembly and homeostasis, while also being influenced by plant-associated microorganisms. The plant endodermis comprises Casparian strips and suberin, which restrict the diffusion of microbe-associated molecular patterns, essential for establishing the root microbiome and nutrient uptake. Suberin deposition varies with the plant's nutritional status and is regulated by hormones such as ethylene and abscisic acid (Barberon *et al.,* 2016). Microbes can interact with abscisic acid signals to modify root diffusion barriers, thereby enhancing plant stress tolerance. Pacheco-Moreno *et al.* (2024) discovered that the plant genotype influenced the recruitment of microbial populations into the rhizosphere of barley cultivars, resulting in varied microbiome composition and *Pseudomonas* abundance driven by root exudate secretion. Later a small number of loci in barley were found to be associated with the differential recruitment of taxonomically varied rhizosphere bacteria, with an NLR-like gene serving as one of the primary drivers of this phenomenon (Escudero-Martinez *et al.,* 2022). Another recent study demonstrated how FERONIA, a previously acknowledged receptor kinase (Guo *et al.,* 2018; Duan *et al.,* 2010 Stegmann *et al.,* 2017), regulates basal levels of reactive oxygen species to adversely affect *P. fluorescens* colonization in *Arabidopsis thaliana* (Song *et al.,* 2021b). According to Wang *et al.* (2021), it is observed that certain microorganisms and a given host's genetic makeup have an interrelationship.

Advancements in rhizosphere biological research

The rhizosphere microbiome is a complex network and strategically engineering microbial populations to enhance or optimize specific functions remains a substantial problem due to its lack of predictability (Afridi *et al.,* 2022; Thakur *et al.,* 2023; Kaur *et al.,* 2022). However, advancements in technologies such as genomics and metagenomics are rapidly advancing our understanding of microbial community structure and dynamics (Satam *et al.,* 2023). By integrating these technologies with metabolic modeling approaches, we can systematically elucidate the architecture of ecosystems (Berihu *et al.,* 2023). Through this enhanced understanding, beneficial microbial communities can be encouraged to colonize the rhizosphere. Additionally, plant genetic makeup can be manipulated, particularly the genes involved in attracting beneficial microbes, to promote the aggregation of beneficial species in the rhizosphere, thereby improving plant growth and productivity (Backer *et al.,* 2018).Genomic-based algorithms can help to develop testable hypotheses for strategically manipulating the rhizosphere microbiome. By finding specific substances that may operate as selective modulators of microbial communities, these algorithms can help design ecologically sound techniques to re-establish functional microbiomes in agricultural and other settings (Berihu *et al.,* 2023).

Nanofertilizers, composed of nanoparticles carrying macro- and micronutrients, offer a promising alternative to chemical fertilizers. These engineered materials facilitate targeted nutrient delivery and controlled release within the plant rhizosphere thereby minimizing nutrient loss through leaching and runoff and reducing degradation and volatility. Encapsulation within nanomaterials enables slow nutrient diffusion into the soil, thereby enhancing soil fertility and crop productivity over time (Nongbet *et al.,* 2022). Due to their high surface area-to-volume ratio and superior penetration ability, nanofertilizers improve crop productivity by promoting seed germination, nitrogen metabolism, photosynthesis, protein and carbohydrate synthesis and stress tolerance (Rautela *et al.,* 2021).

Rhizosphere engineering is a novel approach to encouraging beneficial microbe establishment and restoration of agro-ecosystems. Considerable evidence shows that plant growth, productivity and health are strongly influenced by plant-microbe inter-relationship (Hakim *et al.,* 2021; Masood *et al.,* 2020; Htwe *et al.,* 2019; Adesemoye and Egamberdieva, 2013) enhancing these relationships by engineering the rhizosphere can improve plant health and productivity, while also protecting against both biotic and abiotic stresses. This represents an eco-friendly and sustainable approach to agricultural production (Hakim

et al., 2021). In terms of rhizosphere engineering, Song *et al.* (2021a) examined numerous ways to create a habitat for beneficial microbiomes. A significant advancement in this field is the development of versatile and scalable synthetic microbial community (Syn Com) systems. Synthetic microbial communities (Syn Coms) are made up of three or more well-defined and trackable microbial strains designed to tackle specific research objectives. These consortia are critical for validating hypotheses and providing a practical insight into the interactions among various microbes, plants and environmental factors and helping to close existing knowledge gaps (Marín *et al.,* 2021). These systems involve the assembly of defined and controlled microbial communities from a broad collection of microbes, facilitating the study of microbial interactions within various natural and artificial microbiomes, including those of hosts (Berg *et al.,* 2020; McCarty *et al.,* 2019). The goal is to simplify microbial community complexity by monitoring and tracking changes in microbial inoculants in the environment.

This strategy seeks to achieve reproducibility in field applications, boosting robustness in colonization, crop yield and resilience against biotic and abiotic challenges in agriculture (Chen *et al.,* 2022; Mishra *et al.,* 2022). Recruitment of microbiota varies with plant variety. Zhang *et al.* (2019) discovered differences in nitrogen-use efficiency between two rice varieties, *Indica* and *Japonica*. Through microbiome profiling and genetic analysis, they identified the nitrogen transporter *NRT1.1B* as key to recruiting *indica*-enriched bacteria. Based on this, they designed SynComs with operational taxonomic units enriched in either *indica* or *japonica* (Marín *et al.,* 2021). The *indica*-enriched SynCom significantly enhanced rice growth. Furthermore, research has shown that multistrain microbial inoculants, such as SynComs, boost plant growth more consistently and effectively. For instance, SynComs provided longer-lasting plant protection compared to individual strains (Lee *et al.,* 2021).

CONCLUSION

Sustainable cultivation of turmeric presents significant challenges in contemporary agriculture. As synthetic fertilizers and pesticides are frequently employed to enhance production rate of turmeric and raise the concentration of compounds such as curcuminoids and sesquiterpenoids for the pharmaceutical industry, these techniques negatively influence the soil microbiota and alter plant-soil interactions. As there is a growing demand for safe organic food and sustainable agriculture, it is crucial to meticulously evaluate nutrient management practices to develop standardized agronomic methods that can sustain turmeric yield while reducing cultivation costs. Considering the significant role of the plant microbiome in enhancing host fitness, investigating and harnessing these microorganisms is vital for addressing agricultural challenges and sustainably augmenting productivity. There is a significant need in understanding how the plant genome shapes the microbiome in its rhizosphere and, in turn, how microbial populations interact with the plant under nutrient deprived conditions, plant pathogen invasion and during alterations in nutrient composition. By gaining this understanding and by using advanced techniques we can manipulate both the rhizosphere microbiome and the plant genome to improve yield and promote sustainable agriculture.

Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

Conflict of interest

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