**Metagenomics of Sugarcane Rhizosphere for Sustainable Productivity in the Changing Environment: A Review**

**Abstract**

Sugarcane (*Saccharum officinarum L*.) is one of the most valuable cash crops globally. However, continuous monoculture practices, excessive fertilizer application, and soil disruption due to various economic activities have led to the degradation of soil quality, ultimately impacting crop productivity. The rhizosphere is the area where plant roots and soil connect and this zone consist of many different microbes that boost crop productivity by making nutrients accessible, synthesizing growth regulating hormones, and preventing growth of pathogenic microbes. Generally, culturable microbes get well characterized and documented while non culturable micobes get neglected in different studies. Hence in the present review article an emphasis is given to explain the roles played by uncultured microbial populations, particularly in rhizosphere. The functions of *Bradyrhizobium*, *Pseudomonas*, *Streptomyces*, and *Burkholderia* in pathogen control, phosphate solubilization, nitrogen fixation, and phytohormone synthesis, have been highlighted. The advances in metagenomics such as 16S rRNA gene sequencing and analysing function genes, have greatly increased our ability to understand microbial diversity and their role in crop productivity. Further, metagenomic studies of rhizospheric microbiomes have a great potential in increasing the efficiency of sugarcane productivity without detriment to natural resources, by developing bioinoculants and biocontrol agents.

**Keywords:** Bioinformatics, Microbial Diversity, Metagenomics, Rhizosphere, Sustainable Agriculture, Sugarcane (*Saccharum officinarum*).

1. **Introduction**

In tropical and subtropical nations, sugarcane (*Saccharum officinarum L*.) is a major cash crop that provides raw materials for sugar mills and other related industries. Over 26 million hectares area under for sugarcane farming globally. The leading countries in sugarcane cultivation are Brazil, India, Thailand, and China (Anna Herforth et al., 2020). Brazil has utilized sugarcane to generate ethanol as a sustainable energy resource (Vandenberghe *et al.,* 2022). Sugarcane cultivation considerably contribute to the income of millions of farming households and finally the Indian economy (Vinayaka & Prasad, 2024). The sugar business is a major agro-based sector in the country, employing over a million individuals and significantly contributing to rural economies (Solomon, 2016). Nonetheless, sugarcane farming has numerous challenges, including a reduction in soil nutrients, limited water availability, and infestations by various pests and pathogens (Srivastava, 2012).

A dynamic mix of biotic and abiotic variables influences sugarcane's overall production and performance. Among the biotic factors are pests, pathogens, and competing plant species. Insect pests, including borers, aphids, and root grubs, inflict direct physical harm to plant tissues, diminishing photosynthetic efficiency and compromising overall plant vitality (Kumar *et al.,* 2024). A diverse array of pathogens, encompassing fungus, bacteria, and viruses, are accountable for significant diseases such as red rot, smut, wilt, leaf scald, and mosaic, all of which impair plant health and restrict cane quality and output (Kumar *et al.,* 2024). These pathogens disrupt physiological processes, damage vascular tissues, and affect sugar accumulation. The presence of nematodes around the root area hinders the roots’ ability to absorb water and nutrients which causes the plant to grow poorly and be more at risk of secondary infections. Major diseases in sugarcane such as red rot, smut, wilt, leaf scald and mosaic, are mainly caused by pathogens such as fungi, bacteria and viruses and all of these can destroy sugarcane health and limit its production (Kumar *et al.,* 2024). Because of these pathogens, normal physiology get disturbed, vascular supply is damaged and the buildup of sugar happens. Weed competition in the early growth stages significantly hinders access to vital resources such as nutrients, light, and moisture, while also acting as alternative hosts for pests and diseases. The aggregate effect of these biotic pressures can result in significant reductions in cane yield and quality if not managed properly

Abiotic stresses are equally influential in determining sugarcane productivity. Temperature fluctuations, particularly prolonged heat or cold spells, adversely affect sugarcane metabolism and developmental stages, disrupting photosynthesis, tillering, and weakening the plan overall resilience and growth (Kumar *et al.,* 2024). In addition to the weather conditions, the soil health and condition of the play a major and much less recognized role in sugarcane’s growth and development. Rhizosphere, the regions close to plant roots play a crucial role in defining how well plants withstand temperature, water scarcity and weather extremes (Abru *et al.,* 2021).

The rhizosphere is located where a plant’s roots reach the soil and supports the plant’s good bacteria for nutrients, immune system and growth. Most of the connections here ensure the nutrient cycling, roots growths and defence against disease. The healthy growth and proper nutrition of sugarcane depend on nitrogen-fixing, phosphate-solubilizing and PGPR bacteria (Abbaszadeh-Dahaji *et al.,* 2017). The enzymes, hormones and antibiotics made by soil microbes help the roots become sturdy and safe from disease (Lamizadeh *et al.,* 2016). Maintaining the rhizosphere helps retains soil structure, allows for better access to water and optimizes where organic materials are found. If microbial diversity is reduced in the soil, the roots of plants may not grow properly and the crops productivity will be reduced (Lamizadeh *et al.,* 2016). The role of agricultural practises and increasing urbanization and infrastructure growth on physiochemical properties of the soil, impact on rizosphere and long-term crop productivity is summarized.

1. **Soil Properties and Their Impact on Sugarcane Growth**
	1. **Soil Physical Factors**

Soil properties greatly influence how nutrients, microbes, and vitality are involved in sugarcane production. (Khoiri *et al.,* 2021). The solubility of nutrients in soil is primarily influenced by soil pH, which subsequently affects essential elements such as nitrogen, phosphorus, and potassium. Tropical plants need the pH of their nutrient solution to be between 6.5 and 7.5 (Kingston, n.d.) Another helpful property is organic carbon which aids the microbial community in fixing nitrogen and solubilizing phosphorus. (Pantelides *et al.,* 2023). Because sugarcane has a long development phase, the water-holding capacity guarantees a constant and gradual flow of water to the roots, especially under drought conditions (Augustine *et al.,* 2015). Chemical fertilizers diminish organic matter content, negatively impact microbial activity, and lead to nutrient depletion, thereby compromising soil health.

* 1. **Soil Dynamics**
		1. **Impact of Industrial growth on Topsoil Demand**

India's fast urbanization and industrialization have raised demand for topsoil, a resource necessary for brick production, building, and land reclamation. Large-scale government projects like Smart Cities, industrial corridors, and roads have sped up the building of infrastructure and frequently require topsoil from rural areas. Farmers, particularly in places with low economic status, perceive the selling of topsoil as an immediate financial remedy, particularly during adverse crop seasons or economic hardship. The allure of immediate harvest may entice some; however, the loss of topsoil ultimately poses significant challenges to the land's sustainability.



**FIG 1: The Impact of Industrial Expansion on Topsoil Demand and how Bioeconomy supports in Providing Sustainable Solutions for Farmers**

* + 1. **Indiscriminate Use of Fertilizers**

The widespread and unregulated practice of using chemical fertilizers in vast fields has disrupted the natural soil microbiome, particularly in an intense sugarcane cultivation. Not only can excess nitrogen and phosphorus inputs cause leaching and nutrient imbalances, but they are also preventing essential native microbial communities important for nutrient cycling. Beneficial bacteria such as *Rhizobium*, *Azospirillum*, and *Pseudomonas*, they play important roles such as nitrogen fixation and phosphorus solubilization among others are usually overshadowed or suppressed in chemically enriched environments. This imbalance leaves the soil weakens the soil’s self-renewing capacity and increases the dependence on external inputs. It degrades soil health over time and lowers the long-term productivity. The metagenomic proof demonstrates the decline in the levels of functional genes such as nifH and phoD in over fertilized soils; this points out to the ecological cost of chemical overdependence (Liu *et al.,* 2021).

* + 1. **Continuous Irrigation**

Continuous irrigation systems through surface flooding or uncontrolled drip systems result in waterlogging and consequent reduced oxygen availability in the soil. An anaerobic environment significantly impacts aerobic microbial populations and alters the nature of the rhizosphere microbiome. Excessive irrigation leads to salinization, particularly in dry and semi-arid regions where salts concentrate in the root zones.

Elevated soil salinity, as seen by increased electrical conductivity (EC), adversely impacts microbial enzyme performance and diminishes nutrient uptake efficiency in plants. Functional metagenomic profiling reveals profile shows that genes associated with the synthesis of siderophores and stress tolerance are less expressed in continuously irrigated fields, thus indicating that functionality levels of the microbial environment is impaired under hydrological stress (Pang *et al.,* 2021).

* + 1. **Ratoon Cropping**

Ratoon cropping results in microbial exhaustion and progressive soil fatigue, despite its economic benefits of lower planting costs and faster crop turnover. Beneficial soil organisms decline as a result of repeated regrowth cycles that do not adequately replenish organic matter and microbial diversity (Pang *et al.,* 2021). This approach weakens the rhizosphere's resistance and gives opportunistic and occasionally harmful bacteria the upper hand. Ratooning, according to research, causes a reduction in genes (like those for nitrogen, phosphates and fungi) that benefit the roots.

* + 1. **Monoculture**

Cultivating only sugarcane for several years can reduce the range of microbial species, particularly the population of the *Streptomyces* and *mycorrhizal* fungi become less common. When the soil is too uniform in microbial diversity and microbes involved in nutrient cycles, disease defence and enduring stress tolerance declines., it is difficult to stop pests, diseases and stress caused by environmental factors (Liu et al.,2021). since Maintaining diversity by using intercropping, cover crops and crop rotation helps keep microbes in balance and ensures the farm is productive over time (Gao *et al.,* 2019).

* + 1. **Global Environmental Changes**

With the climate moving towards warmer environments, new patterns of rainfall, more CO₂, more droughts or floods are getting observed. These environmental changes have also changed the composition and actions of rhizosphere microbes. These environmental changes also change the root exudates production and the way beneficial microbes stick to the roots (Naylor *et al.,* 2020). Also, changes in environmental conditions can turn off microbial genes responsible for getting nutrients, dealing with stresses and preventing infection by pathogens. Further, when things become very hot and dry, microbes need to build osmolytes such as trehalose and proline, but production of all these osmolarities depends on microbial community composition and how much active the microbes are. Both metagenomics and meta-transcriptomics help spot changes in microbial groups and allow agriculture scientists to deal with these uncertainties (Q. Liu *et al.,* 2021).

1. **Sugarcane Rhizosphere Metagenomic for microbial Diversity and Dynamics**

**Rhizosphere**

It is the area of soil near plant roots that is affected by root exudates and is crucial to the link between plants and soil (Niu *et al.,* 2021). It includes a range of microbes, for example bacteria, fungi, actinomycetes and archaebacteria. Some bacterial species *Burkholderia, Pseudomonas* and *Rhizobium* found in the rhizosphere help plants by converting nitrogen, providing access to phosphate and a speed up growth of both the roots and shoots by producing phytohormones (S. R. Singh *et al.,* 2021).. There are certain fungi, like *Trichoderma* and *mycorrhizal* species which cling to the roots of plants and help them uptake more phosphorus and guard against diseases (Devi *et al.,* 2020). Among Several plant growth-promoting traits of *Streptomyces* provide to plants, one is production of antibiotics that manage or minimize the numbers of harmful microorganisms in the soil, therefore increasing the likelihood of plant survival (Yadav *et al.,* 2021).

Since microbes reduce the need for chemicals, rhizosphere microorganisms ought to be considered natural biofertilizers (Kumar *et al.,* 2024). Nitrogen-fixing bacteria increase the amount of nitrogen available to plants and improve their efficiency in using it (Singh *et al.,* 2023). Many times, phosphorus is found as insoluble phosphate rock, but certain microorganisms that solubilize phosphorus allow plants to absorb that phosphorus, so fewer synthetic fertilizers are needed (Rizvi *et al.,* 2021). These microbial communities improve the way plants absorb nutrients, especially iron which promotes healthy plant growth (S. R. Singh *et al.,* 2021).

Better soil, microbial, and root health help sugarcane farmers achieve higher and sustainable production (Yin *et al.,* 2019). Using metagenomics helps find out how soil bacteria around plant roots are affected by chemicals and understand the roles they have in the rhizosphere (Ameen *et al.,* 2024). Because of metagenomics, researchers today can observe the variety and activity of microorganisms in the rhizosphere of sugarcane. Many culture-based techniques are limited, because it’s sometimes impossible to grow a diverse range of microbe groups. Most microbes, whether they are cultured or not, can have their genetic material accessed by metagenomics This conclusion was discussed by Khoiri et al. in 2021 (Khoiri *et al.,* 2021). It involves finding DNA from microbes at random in environmental samples and having technology that can process a huge amount of sequence data. (Khoiri *et al.,* 2021). Studies based on metagenomics reveal the details of soil structure and the important microbes for plant health and sugarcane production.

Deep understanding of the fundamental structural, species, and functional characteristics of the microbial ecosystem for plant health and productivity has been made possible by the application of metagenomics to sugarcane rhizosphere research. Metagenomics involves the sequencing of genetic targets that are conserved within a microbial community, such as the universally conserved 16S rRNA gene, which is utilized for bacterial identification (Wani *et al.,* 2024). According to Moneda et al. (2022), the microbial taxa that culture-based methods were unable to identify were discovered because the targeting of this particular marker allows classification down to the genus and species level. Additional significant functional gene markers include genes linked to siderophore synthesis, phoD for phosphorus metabolism, and nifH for nitrogen fixation (Wani *et al.,* 2024). These have been used to pinpoint the metabolic roles of a variety of microorganisms in the sugarcane plant's rhizosphere (Li *et al.,* 2017). Gene markers provide useful information on the advantageous effects of bacteria on plants and their general health, as well as the ability to evaluate the metabolic capacity of the microbial assemblages involved (Klindworth *et al.,* 2013).


**FIG 2: The Role of Metagenomics in Exploring Unculturable Microbes (The figure displays why metagenomics lets us find microbes and their traits that culture-based tools cannot detect. The process points out important steps in analysis: gathering DNA, sequencing it, annotating results and examining their functions.)**

 The use of metagenomics shows that microbial taxa that help and are required for sugarcane growth are most abundant in the rhizosphere. These bacteria generally participate in the nitrogen cycle (Monenda *et al.,* 2022). Because of the strong reactivity of these species, sequencing soil samples from the sugarcane rhizosphere has shown the presence of nifH gene sequences (Moneda *et al.,* 2022). Metagenomics studies have shown that *Bacillus* and *Pseudomonas* are some of the bacteria that help neutralize (solubilize) phosphates. Li et al. (2020) point out that these bacteria use organic acids to release phosphorus into plant roots, so the plant can more easily absorb them. Looking at the activities of the phoD gene in sugarcane rhizosphere, it was clear that high-productivity soils had more active phosphorus pathways, suggesting the bacteria made phosphorus more accessible.

The other main group in the sugarcane microbial community are the actinomycetes and Streptomyces is the main genus of actinomycetes. Because they can produce antibiotics that help defend plants from diseases, they play an important role in agriculture (Li *et al.,* 2020). Through metagenomic studies Abdellatif and colleagues found that actinobacteria in sugarcane soil produce high numbers of genes that produce antimicrobials. (Abdellatif *et al.,* 2024). Similarly Ansari et al. (2024), has found that high-productive soils contain more genes associated with antibiotic formation, proving that actinomycetes help in maintaining disease resistant soil (Ansari *et al.,* 2024). It has also been noticed by scientists that specific strategies employed by microbes can change the productivity levels of various soil types. The number of microbes and genes in soil tends to be higher in highly productive soils than in others (Ansari *et al.,* 2024). Genes from plants with Mycorrhizal Symbiosis can tolerate stress and nutrition loss better (Pang *et al.,* 2021). Lower soil productivity and sugarcane yield are features of low-productivity soils, mainly because they have less active and diverse microbes (Ansari *et al.,* 2024).

The current understanding of sugarcane rhizosphere microbial prospecting has been improved by metagenomics, which expands on microbial taxa, functional genes, and metabolic pathways. Particularly important for agricultural sustainability are the discovery and identification of non-culturable microbes as well as the clarification of their roles in nitrogen fixation, phosphate solubilization, antibiotic synthesis, and siderophore synthesis. Some of its benefits have also been challenged for suggesting that producing biofertilizers and microbial inoculants might boost sugarcane yield significantly while reducing the need for fertilizers made of chemicals. Future efforts to enable the dynamic display of these microbial entities surrounding changing environmental relations and gene expression must continue to prioritize metatranscriptomics and metaproteomics (Ameen *et al.,* 2024).

* 1. **The Challenges of Uncultured Microbes**

Among the plethora of microorganisms present in rhizosphere, many remain uncultured under current laboratory conditions and the culture media available. However, these microbes may be crucial for plant development, disease prevention, and nutrient cycling, are found in soil ecosystems. In the sugarcane rhizosphere also, where plant roots interact with microbial communities, these uncultured bacteria are particularly significant. Finding and analyzing microbes without culturing them, revealing their presence even without being directly observed and learning about their roles in converting nitrogen and breaking down organic matter has all been made possible by metagenomics studies. Through metagenomics we can monitor change in number as well as type of both culturable as non-culturable microbes, in the changing soil conditions due to efferent environmental factors and economic activities (Streit & Schmitz, 2004). Further, studying gene expression of soil microbe’s, meta-transcriptomics allows us to measure changes in the different biochemical pathways leading to survival and multiplication of microbial communities and their impact on sugarcane production. Hence, metagenomics and meta-transcriptomics methods can be used to develop biofertilizers to promote sustainable farming and deal with problems such as soil deterioration and deficiency of nutrients in the different type of soil and environmental conditions (Mendes *et al.,* 2017).

* 1. **Rhizosphere Dynamics and Microbial Diversity**

Root exudates with substances like sugars and organic acids entice special bacteria to nearby soil and influence their actions there (Niu *et al.,* 2021). Carrying out studies using metagenomic data, scientists have found out that in the rhizosphere bacteria, fungi, actinomycetes and archaea team up to support the sugarcane plant by boosting uptake of nutrients, managing stress and suppressing harmful microbes (Mokrani *et al.,* 2020).

* + 1. **Bacterial Contributions:** In the rhizosphere of sugarcane, the frequent bacterial species are *Burkholderia*, *Azospirillum*, *Bradyrhizobium* and *Pseudomonas* and they are very important for both plant growth and nutrient usage (Gupta *et al.,* 2022). Because of their shape, *Burkholderia* and *Azospirillum* are able to contribute in nitrogen fixation and show more effective versions of nitrogenase and *nifH* genes (P. Singh *et al.,* 2023). Organic acids made by *Pseudomonas* meet the needs of the soil phosphates, as they are used by plants (Pan *et al.,* 2023). Further. they make chemicals called siderophores that gather Fe³⁺ ions which means they take the iron away from pathogens (P. Singh *et al.,* 2023).

* + 1. **Fungal Roles in Plant Growth and Defense:** *Glomus* and *Trichoderma* species which are mycorrhizae, help plants by occupying the area near plant roots and boosting the of essential nutrient and water (Mokrani *et al.,* 2020). Mycorrhizal Glomus species help plants take up phosphorus when soil nutrients are low. *Trichoderma* uses hydrolytic enzymes and antifungal compounds to stop Fusarium and Pythium. When stress hits, gibberellin-producing fungi work to build the biomass of sugarcane by turning on ways to deal with drought, so these fungi matter in managing biotic stress (Niu *et al.,* 2021).

* + 1. **Actinomycetes and Pathogen Suppression:** Facultative bacteria, for example Streptomyces, can suppress pathogens such as Rhizoctonia and Verticillium by producing antibiotic and chemical compounds (Yadav *et al.,* 2021). Further, Such bacteria digest various complex molecules found in the soil, improving availability in the soil (Pantelides *et al.,* 2023). Indicating the importance of bacteria in keeping up the health of rhizospheres by cycling nutrients and preventing infections (Pantelides *et al.,* 2023).

* + 1. **Archaea and Specialized Functions:** Even though archaea are rarer than bacteria in the rizosphere, they are important in handling nitrogen and producing methane in the absence of oxygen (Pang *et al.,* 2021). Because of their ability to break down nitrogen and control greenhouse gas emissions, *Methanosarcina* and *Nitrosopumilus* are valuable for maintaining productive soils (Chen *et al.,* 2024).

* + 1. **Phytohormone Production:** Indole-3-acetic acid (IAA) and other types of auxins, gibberellins and cytokinins, are made by some species of bacteria, helping plants to develop more effectively. Boosted root development and increased nutrient absorption have been noticed thanks to IAA in *Azospirillum* and *Burkholderia* (Nong *et al.,* 2022). Increasing cytokinin levels supports shoot growth and tillering which in turn produces a larger harvest. It has also been observed that water stress encourages *Trichoderma* and similar fungi to release gibberellin which helps plants manage the stress from low water (Pang *et al.,* 2021).

* + 1. **Stress Tolerance and Abiotic Interactions:** Many stresses such as salinity, drought and high metal concentrations, can be coped with by rhizosphere microorganisms by using different adaptation strategies. For better water use efficiency in dry conditions, *Bacillus* releases Osmo-protectants called proline and trehalose (Gupta *et al.,* 2020). Further, some bacterial species help sugarcane growth by reducing salt absorption in roots and keeping the internal salt levels well balanced under high salinity conditions. Moreover, Certain bacteria reduce heavy metal concentrations in the soil, enabling effective sugarcane cultivation on suboptimal soils (Niu *et al.,* 2021).
		2. **Siderophore Production:** The micronutrient iron is generally lacking in soils, mainly due to how poorly it dissolves and becomes available. Plant-usable iron is made available through the use of siderophores which are produced by Streptomyces and Pseudomonas. According to Pang et al. (2021) and Singh et al. (2021), along with helping plants absorb nutrients, genes involved in siderophores play a critical role in maintaining sugarcane health and shielding it against harmful fungi and bacteria in soil.

* + 1. **Metabolic Synergy and Microbial Interactions:** Many different microbial species in the rhizosphere symbiotic complex boost how soil and plants are used. Treating nutritional availability with both NFB and PSB is shown by Gupta et al. (2020) to do better than treating with either alone. Glomus interacting with Pseudomonas in the soil makes the rhizosphere stable, increases its nutrient levels and improves its productivity (Pradhan *et al.,* 2023). Examining productive soils through metagenomics shows that lots of diversity exists in microbial genes of nitrogenase, phosphate-solubilizing and siderophore which implies that having various metabolic activities is important for the health of sugarcane fields (Nong *et al.,* 2022).

* 1. **Abundance of Uncharacterized Microbes Identified**

Metagenomic analysis enables the observation of all microbial taxa, including uncultured and unidentified species, a feat unattainable by only culture-dependent approaches (Nong *et al.,* 2022). Certain unidentified bacteria can execute distinctive actions and contain specific enzymes that facilitate nutrient cycling and safeguard plants within the sugarcane root ecosystem (Table 1; Fig 2). Metagenomic analyses of sugarcane rhizospheres comprise many unidentified Proteobacteria. These bacteria are crucial to nitrogen fixation, phosphate solubilisation, and siderophore synthesis, among other functions (Pradhan *et al.,* 2023). Further, unidentified Ascomycota represent additional uncharacterized species within the fungal communities of sugarcane rhizospheres. Metagenomic data can be used to identify gene clusters associated with the generation of secondary metabolites (Abdellatif *et al.,* 2024; Barka *et al.,* 2016). Antibacterial properties of novel actinomycetes have the capacity to protect soil and plant health from these diseases.

**Table 1 : Abundance and Dominant and Uncharacterized Microbial Taxa in Sugarcane Rhizosphere**

|  |  |  |  |
| --- | --- | --- | --- |
| **Microbial Group** | **Dominant Taxa** | **Uncharacterized Taxa** | **Functional Role** |
| Bacteria | *Burkholderia,Azospirillum* | Unclassified Pr)oteobacteria | Phosphate Solubilization, Nitrogen Fixation(Bergmark *et al.,* 2012) |
| Fungi | *Trichoderma, Glomus* | Unknown Ascomycota | BiocontrolPhosphorus Uptake(Devi *et al.,* 2020 |
| Actinomycetes | *Streptomyces* | UnidentifiedActinomycetes | Pathogen Suppression,Antibiotic Production(Li *et al.,* 2020) |
| Archaea | *Methanosarcina, Nitrosopumilus* | Novel Euryarchaeota | Nitrogen Cycling, Methane Metabolism,(Offre *et al.,* 2013) |



**FIG 3: Functional Diversity of Sugarcane Rhizosphere Microbiota (The rhizosphere's sugarcane microbial populations' functional diversity is illustrated in this figure, with focus given to functions such siderophore production, phosphate solubilization, nitrogen fixation, and stress tolerance.)**

* 1. **Rhizosphere Microbiota Sugarcane and Other Crop**

In particular, the rhizosphere microbiota of sugarcane differs greatly from that of short-term crops, rice, wheat and maize (Fig 3). Sugarcane which is often cultivated a perennial crop, releases a major amount of root exudates while it is growing. Among the components of exudates are sugars, amino acids, organic acids and various secondary metabolites which attract given species of microorganisms (Pahalvi *et al.,* 2021). These exudates' nature and amount are very different from those of short-term crops, which enhances the nutrient-rich environment that supports a diverse microbial community in terms of both structure and function.

Comparative metagenomic analysis of cereals showed notable differences in bacterial and fungal composition, including differences in gene richness and unique functional traits (Pantelides *et al.,* 2023). They found that the sugarcane rhizosphere had higher levels of nitrogen-fixing bacteria, specifically *Burkholderia* and *Azospirillum*, but not in the rice and wheat rhizospheres. These bacteria rely on the nifH gene to help atmospheric nitrogen become usable ammonia (a form that plants use) (Pantelides *et al.,* 2023; Gupta *et al.,* 2022). However, in the rhizospheres of cereals, nitrogen-fixing organisms are scarce, and natural nitrogen is not abundant; chemical sources are most important. In sugarcane soil, both Pseudomonas and Streptomyces bacteria which make siderophores, have become more common. By releasing iron in the area around plant roots, siderophores also do away with pathogenic bacteria by outcompeting them (Cornelis *et al.,* 2011; Scavino *et al.,* 2013). They found a significant drop in siderophore genes in the metagenomics of both rice and wheat rhizospheres which may weaken iron absorption and disease defence in the crops.

Sugarcane being perennial helps build solid and dependable groups of microbes within the soil. Abundant root exudation makes many microbes redundant and sugarcane rhizobacteria show good resistance to drought, salt and pathogen attack. (Bardgett & Van Der Putten, 2014). Conversely, short-cycle crops like rice and wheat demonstrate less microbial stability due to their shorter growth duration and smaller root radii compared to cereals (Bardgett & Wardle, 2003). Notable differences in archaeal communities exist within sugarcane rhizospheres, with a more significant syntrophic connection observed among the methanogenic archaeal species Methanosarcina in saturated soils. Since well-drained cereal crop soils do not significantly enhance anaerobic settings, it is linked to methane metabolism and nitrogen cycling in anaerobic circumstances, which are relatively limited (Coyotzi Alcaraz, 2014).



**FIG 4: Comparative Analysis of Microbial Composition in Sugarcane vs. Other Crops (This figure shows the differences in the microbial abundance, composition, and key functional genes found in the rhizospheres of wheat, rice, maize, and sugarcane. It highlights how abundant siderophore-producing and nitrogen-fixingsiderophore-producing bacteria found in sugarcane.)**

* 1. **Sugarcane Rhizosphere of High vs. Low Productivity Soils**

The microbiota of the sugarcane rhizosphere differs from that of other plant rhizosphere investigations. Among the cereal and annual crops are maize, wheat, and rice. The physico-chemical state of the soil's nutrient status, as well as the actions taken during soil management, all have an impact on the composition, diversity, and functional potential of high and low-productivity soil. (S. R. Singh *et al.,* 2021; Solomon, 2016; Verma *et al.,* 2022). High microbial divaricate density is typically linked to soil with high productive capacity, which enhances plant growth, nutrient cycling rate, and foundation stress resistance. Conversely, the low soil productivity is linked to the microbial population's lower heterogeneity, which in turn affects the fields' output. (Ahmed *et al.,* 2024).

Highest productivity through the use of PGPR such as *Burkholderia, Azospirillum* and *Rhizobium*, calls for a carbon-rich environment and as little phosphorus as possible. The bacteria make it possible for nitrogen gas to turn into materials plants can use (Bergmark *et al.,* 2012). Phosphate-solubilizing bacteria such as Bacillus and *Pseudomonas* help make insoluble phosphate more easily available to plants which is crucial in agriculture since it mitigates a major nutrient deficiency (Gupta *et al.,* 2020). Because of the unique extra layers, the soil provides a place for mycorrhizal fungi to thrive which provides additional phosphate, results in more water access and improves how soil holds together (Pradhan *et al.,* 2023). Soil structure affects how well soil suppresses diseases because of *Streptomyces* and *actinomycetes*’ activities in releasing antibiotics and enzymes (Niu *et al.,* 2021). This is just one way these bacteria share work to help nutrients, roots and soil remain healthy for good plant growth.
 In contrast, soils with poor productivity led to a decrease in the population of these beneficial bacteria. The principal reasons contributing to microbiological fascism in these soils are ongoing sugarcane cultivation and excessive reliance on synthetic fertilisers. Various studies have qualified that this task leads to an increase in stress-resistant and opportunistic bacteria that bring little benefit to the plant. One example is (Krishan K. Verma *et al.,* 2025) which stated that continually planting the same crop leads to fewer nitrogen-fixing bacteria, while dangerous microorganisms increase. Such changes reduce how nutrients are recycled in soil which makes it less fertile and crops more prone to disease and unusual stress.

Use of metagenomic approaches has discovered differences in the way microbes function in high-yield and low-yield soil environments. The high-productivity soils contained many genes that contribute to useful functions such as the genes that allow nitrogen fixation (nifH), metabolize phosphate (phoD) and make siderophore. Because of these genes, nutrients recirculate and are used more effectively, increasing sugarcane production immediately (Ahmed *et al.,* 2024). Because low-productivity soils have fewer working genes, fewer nutrients are available and plant growth is not supported (Yadav *et al.,* 2021). The activity of microbial communities in soil and their enzyme production are increased in very productive soils. According to the authors, microorganisms in soil are helpful for the plant’s health and the expansion of the soil’s fertility (H. B. Li *et al.,* 2017).

Because of different environmental conditions and management approaches, soil types differ. Mainly, soils contain a pH nearly neutral, good suitable moisture and a healthy amount of organic carbon for microorganisms to thrive (kumar et al 2024). When soils are not very productive, they often have a wrong pH balance, less organic carbon and cannot hold water very well; this results in fewer and less active microbes (Pantelides *et al.,* 2023).

According to Liu and his co-researchers (2017), adding organics to low-yielding soils makes the soil microbes with beneficial genes more abundant. Kumar et al. (2024) explain that choosing different crops to grow in a rotation of farm fields results in better and more balanced health of the soil’s microorganisms. Intensive agriculture can be controlled with these approaches and water waste in sugarcane fields can be reduced (Kumar *et al.,* 2024). Likewise, challenges with weak soil productivity can be addressed with special measures, among them are adding microbes, applying biofertilizers and increasing organic matter. Examining soil metagenomics may help identifiaction of useful microbes that work better and improve soil fertility (Kumar *et al.,* 2024).

1. **Applications in Sustainable Agriculture**

Rhizosphere microbiomes could act as a large source for boosting sustainable sugarcane farming. Some microbes like *Rhizobium* and *Azospirillum* help plants by changing inaccessible atmospheric nitrogen into a type they can use (Gupta *et al.,* 2020). *Bacillus* and *Pseudomonas* species too help make phosphorus available for plants by solubilising solid phosphates. Pantelides *et al.,* 2023 have stated that PSB helps sugarcane roots uptake more phosphorus, thereby reducing the need for a lot of chemical phosphate fertilisers. Rhizosphere bacteria also generate biocontrol substances, that increases plant defences by making and releasing antifungal and antibacterial agents.. Moneda et al. (2022) study showed *Trichoderma*-based biopesticides helped to reduce sugarcane root rot by 40%. These bio-fertilizer highly environment friendly and help crop plants against different stresses (Pradhan *et al.,* 2023). Mokrani et al (2020), reported positive impact of application of bacterial cultures in sugarcane cultivation under drought conditions. Developments in metagenomics-based fertilisers and inoculants customized to for target soil and crop combination can benefit sustainable farming. The fertilisers can be created with a special mix to match both the soil and the crops grown in each region. Scavino et al. (2013) and Gupta et al. (2022) clearly point out that performing metagenomic analysis can help identify microorganisms with specific features that increase the performance of biofertilizers and biopesticides in sugarcane agriculture. For microbial ecologists and those working in biotechnology, the diversity among rhizosphere microbes provides a major opportunity to increase crop productivity and develop sustainable farming.

Exploring the rhizosphere microbiome will help India’s sugarcane sector benefit in many areas. Microbial technology helps solve important problems in farming such as a lack of soil nutrients and pest infestations, without harming the environment when sugarcane is grown (Jiang *et al.,* 2012). Still, microbial inoculants and biofertilizers are available, but the use of these strategies is limited by a lack of awareness and access for farmers (Niu *et al.,* 2021). This would be the first case of using such technology for sugarcane management and it could greatly revolutionize the way crops are grown economically and with new ideas.

1. **Challenges and Knowledge Gaps**

Promoting the utilization of rhizosphere microbial abundance for agricultural sustainability is subject to several limitations. The primary concern is that the proof-of-concept shown in laboratory settings has substantial limitations regarding its applicability to real-world scenarios, as managing and addressing soil heterogeneity and its response to external conditions and indigenous microbial communities is necessary for the effectiveness of microbial inoculants in crops (Chen *et al.,* 2024). It is generally observed that microorganisms that work well in controlled environments are susceptible to competition and experience reduced efficiency in a variety of field conditions (Gupta *et al.,* 2022), and that nitrogen-fixing and phosphate-solubilizing bacteria are unable to develop strong growth under variable environmental conditions. Presently. no globally accepted techniques exist for the development and usage of microbial inoculants. According to (Moneda *et al.,* 2022), this has led to inconsistency in the efficacy of microbial products due to changes in formulation and storage, so farmers have lost trust in their performance. Morover, metagenomic assessment cannot be performed on a broad scale, particularly in developing nations, due to the substantial expenses linked to sophisticated DNA sequencing methodologies (R. Li *et al.,* 2020). Further, it remains insufficient to assign an accurate functional annotation for increasingly complex species, including a comprehensive microbiological reference database.

It is noticeable that presently we lack information on how microbes sense and respond to environmental challenges. According to Niu et al. (2021), there is little information available about how microbes respond to drought, salinity and conditions that break the link between plants and their microbes. This calls for standardized processes, technology that is easy to use and research efforts linking metagenomic experiments with functional research, to tackle the lack of knowledge (Moneda *et al.,* 2022).

1. **Conclusion**

The sugarcane rhizosphere represents a diverse and transient microbial habitat crucial for augmenting yield, quality, and overall soil health in the context of sustainable agriculture. Different studies have provided extensive insights into phosphate-mobilizing, nitrogen-fixing, siderophore-producing, and phytohormone-synthesizing microorganisms. These bacteria are highly beneficial for nutrient cycling, stress tolerance, and disease suppression, serving as the essential basis for innovative eco-friendly technologies, including, biopesticides, biofertilizers, and microbial consortia.

Translating laboratory experiment results to field applications remains a difficulty due to variability in soil properties, chemical reactions, environmental conditions, and inadequate understanding of microbial responses. These challenges indicate the necessity for innovative and high-throughput technologies, including standardised techniques for meticulous experimental design, ongoing cost reduction of sequencing technologies, and the development of integrative multi-omics approaches. Enhanced longitudinal studies in the field and targeted microbiological interventions can further bridge the divide between theory and practice.
 Incorporating the complexity of the microbial population in the rhizosphere into agricultural systems might reduce pesticide usage, improve crop yields, and address the emerging challenge of sustainable food supply for the increasing global population. Integrative methodologies, coordinated research projects, and the shift to a philotectonic perspective will explain the abilities of microbial diversity in order to improve sugarcane output, simultaneously defining the post-industrial future as an ideal basis for sustainable agriculture.

1. **Future Directions**

It is important to use advanced and interdisciplinary techniques to analyse microbial communities in the sugarcane rhizosphere, as this can meet present needs and improve agricultural production efficiency. There is potential in using techniques like metagenomics, metatranscriptomics, proteomics and metabolomics. This integrative approach is used to study how microbes are useful, behave and change their ways in different changing environment. Niu et al. (2021) point out that metatranscriptomics can help study how microbes respond to drought and salinity stress which is important for growing stress-resistant microbial populations.

Hence, one must carry out field-based testing of microbial inoculants in several types of farming environments. Due to variations in the physical and microbial habitats of the soil, field recovery of microbiological counts is typically lower than laboratory measurements (Chen *et al.,* 2024). Long-term research that accounts for these characteristics will facilitate a deeper knowledge of how to improve microbial application and its stability. Recent metagenomic analyses have introduced the notion of precision agriculture, which necessitates the provision of site-specific and crop-specific molecular and genotypic inoculants, as well as individualised bio-amendments (Chen *et al.,* 2024). Access to microbial genomics and the availability of genomic information, coupled with standardised annotation tools and pipelines, will enhance functional profiles (Pan & Cai, 2023).
 Synthetic biology research holds promise for creating microbial communities with improved functional characteristics. To solve agricultural issues like nutrient-deficient soils or pest infestations or improve crop stability and soil fertility, these designer consortia could be precisely created for particular agricultural issues such as pest problems or nutrient-deficient soils (Mokrani *et al.,* 2020). It highlightes the importance of how microbial traits might work together depending on environmental conditions.

Disclaimer (Artificial intelligence)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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