**From concept to reality: Transforming agriculture through innovative rhizosphere engineering for plant health and productivity**

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**Abstract**

The plant rhizosphere is regarded as a microbial hotspot due to a wide array of [root exudates](https://www.sciencedirect.com/topics/immunology-and-microbiology/root-exudate). These root exudates comprise diverse organic compounds such as phenolic, [polysaccharides](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/polysaccharide), [flavonoids](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/flavonoid%22%20%5Co%20%22Learn%20more%20about%20flavonoids%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages), fatty acids, and [amino acids](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/amino-acids) that showed chemotactic responses towards microbial communities and mediate significant roles in root colonization. The rhizospheric [microbiome](https://www.sciencedirect.com/topics/immunology-and-microbiology/microbiome%22%20%5Co%20%22Learn%20more%20about%20microbiome%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) is a crucial driver of plant growth and productivity, contributing directly or indirectly by facilitating nutrient acquisition, phytohormone modulation, and phosphate [solubilization](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/solubilization%22%20%5Co%20%22Learn%20more%20about%20solubilization%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) under normal and stressful conditions. Moreover, these microbial candidates protect plants from pathogen invasion by secreting antimicrobial and volatile organic compounds. To enhance plant fitness and yield, [rhizospheric microbes](https://www.sciencedirect.com/topics/immunology-and-microbiology/rhizospheric-microorganism%22%20%5Co%20%22Learn%20more%20about%20rhizospheric%20microbes%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) are frequently employed as microbial inoculants. However, recent developments have shifted towards targeted rhizosphere engineering or microbial recruitments as a practical approach to constructing desired plant rhizospheres for specific outcomes. The rhizosphere, composed of plants, microbes, and soil, can be modified in several ways to improve inoculant efficiency. Rhizosphere engineering is achieved through three essential mechanisms: a) plant-mediated modifications involving [genetic](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/genetics) engineering, [transgenics](https://www.sciencedirect.com/topics/immunology-and-microbiology/transgenics%22%20%5Co%20%22Learn%20more%20about%20transgenics%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages), and gene editing of plants; b) microbe-mediated modifications involving [genetic alterations](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/gene-mutation) of microbes through upstream or downstream methodologies; and c) soil amendments. These mechanisms shape the rhizospheric [microbiome](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/microbiome%22%20%5Co%20%22Learn%20more%20about%20microbiome%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages), making plants more productive and resilient under different stress conditions. This review paper comprehensively summarizes the various aspects of rhizosphere engineering and their potential applications in maintaining plant health and achieving optimum agricultural productivity.

**Keywords**

Rhizosphere engineering

Soil amendment

Microbiome

Agriculture

Plant–microbe interaction

**1. Introduction**

In changing climatic conditions, achieving zero hunger is one of the most crucial and challenging issues. According to a published report, by 2050, agricultural production needs to increase by more than 50 % from the current level ([van Dijk et al., 2021](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib95)). However, the loss of agricultural products due to pathogen invasion, the shrinking of agricultural land, and the advent of different stresses make the target to achieve food security more challenging and panic for the rising global production ([Kumar, 2022a](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib49), [Kumar, 2022b](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib50)). Many farmers rely on chemical fertilizers or pesticides to enhance agricultural production and protect plants from pathogen invasion. However, only 0.1 % of the applied agrochemicals reached the target site, and a significant fraction leached out to the soil or water ecosystem as contaminants or pollutants ([Pimentel, 1995](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib75)). Additionally, continuous use of agrochemicals adversely affects plant and soil health, the community structure of native [soil microflora](https://www.sciencedirect.com/topics/immunology-and-microbiology/soil-microflora), and consumers' health. In this regard, researchers continually search for alternatives to improve agricultural productivity sustainably ([Chávez-Avila et al., 2023](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib20), [Kumar, 2022a](https://www.sciencedirect.com/science/article/pii/S0944501323002550#bib49), [Kumar, 2022b](https://www.sciencedirect.com/science/article/pii/S0944501323002550#bib50), [Orozco-Mosqueda et al., 2023](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib72), [Wang et al., 2023a](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib104), [Wang et al., 2023b](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib105)). It is well-established that plants harbor various microbial communities as [epiphytes](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/epiphyte) or endophytes ([Babalola et al., 2020](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib9), [Noman et al., 2021](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib68)). These associated [microbiomes](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/microbiome%22%20%5Co%20%22Learn%20more%20about%20microbiomes%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) share a complex relationship with the host, providing stability and modulating plant growth ([Kumar, 2022a](https://www.sciencedirect.com/science/article/pii/S0944501323002550#bib49), [Kumar, 2022b](https://www.sciencedirect.com/science/article/pii/S0944501323002550#bib50), [Babalola et al., 2020](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib9)). Research has shown that the abundance and diversity of epiphytic microbes are greater than those of endophytes. However, community structures of the microbes vary with different plant organs and are also observed in decreasing order from root to leaf or fruit ([Yang et al., 2022](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib113)). Initially, describing and identifying the community structure of plants was tough. Still, the advent of the latest technologies and omics explored the microbial community structure and revealed how the microbiome varies with the plant [developmental stages](https://www.sciencedirect.com/topics/immunology-and-microbiology/developmental-stage) ([Arif et al., 2020](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib8), [Ke et al., 2021](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib43)).

The rhizosphere, a vital location for plants, harbors diverse microbial communities that reside and interact through the secretion of biochemical [root exudates](https://www.sciencedirect.com/topics/immunology-and-microbiology/root-exudate) and the release of signal molecules Although both beneficial and pathogenic microorganisms interacted towards the rhizosphere in response to the released root exudates. However, interactions of beneficial microorganisms towards the rhizosphere significantly modulate plant growth ([Compant et al., 2019](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib23)). In this context, for the last few years, researchers have been focused on engineering plant rhizosphere to improve the recruitment of beneficial microbes ([Ryan et al., 2009](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib82), [Ahkami et al., 2017](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib3)).

The rhizosphere is the interface of plants, soil, and microbes; thus, by improving or engineering the rhizospheric components like plants, soil, and microbes the functional attributes of the plants, like agricultural productivity or prevention from pathogen invasion, can be improved. Nowadays, to engineer the plant rhizosphere, various gene editing technologies, marker-assisted selection, and plant breeding technologies have been frequently performed ([Zhang et al., 2015](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib118)). However, "microbe", another component, has also been engineered through [genetic](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/genetics) engineering technology like RNAi or [CRISPR](https://www.sciencedirect.com/topics/immunology-and-microbiology/clustered-regularly-interspaced-short-palindromic-repeat) to improve the rhizosphere's functioning. Soil, a vital component of the plant rhizosphere, was also amended to recruit beneficial microbes in the rhizosphere. Therefore, amendment of "soil" via different processes like organic farming, crop rotation, use of suppressive soil for pathogen control, or manipulation of the rhizosphere has been commonly practiced ([Dessaux et al., 2016](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib29), [O'Connell et al., 1996](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib69)). This review succinctly explores plant rhizosphere [dynamics](https://www.sciencedirect.com/topics/immunology-and-microbiology/dynamics), delving into microbial communities and their responses to stress and metabolites. It also covers rhizospheric engineering, detailing strategies for enhanced plant performance. With insights into intricate plant-microbe interactions and sustainable practices, the review contributes to our understanding of rhizospheric complexities and agricultural innovation.

**2. Plant rhizosphere and their functioning**

The plant rhizosphere is a thin layer of the root that adheres to soil particles, which directly influences the plant and microbes association by releasing [root exudates](https://www.sciencedirect.com/topics/immunology-and-microbiology/root-exudate) and modulating the ecosystem services ([Dennis et al., 2010](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib28), [Walker et al., 2003](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib100)). The plant rhizosphere is divided into three zones: firstly, the zone present between the epidermal cells of the root and the mucilage, commonly referred to as the rhizoplane, the endo-rhizosphere, the zone between cortex to the [endodermis](https://www.sciencedirect.com/topics/immunology-and-microbiology/endoderm); and the ecto-rhizosphere, which lies between the rhizoplane to the [surface](https://www.sciencedirect.com/topics/immunology-and-microbiology/surface-property) adhering to the [bulk](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/volume) soil ([Hassan et al., 2019](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib39)). In general, the microbial species and the minerals reside in the apoplastic spaces of the endo-rhizosphere. However, the rhizoplane and ectorhizosphere play significant roles in synthesizing root exudates.

The root exudates are constituted of an array of biochemical compounds, like [polysaccharides](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/polysaccharide), phenolics, [flavonoids](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/flavonoid%22%20%5Co%20%22Learn%20more%20about%20flavonoids%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages), [amino acids](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/amino-acids), etc and these exudates are the results of different metabolic activities of the plants ([Huang et al., 2014](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib40)). These exudates showed a chemotactic response towards the microorganisms, which facilitated the movement of microbes towards the plant rhizosphere and mediated a prominent role in the effective colonization ([Agarwal et al., 2023](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib1)).

**3. Interaction of plant-root microbiota via metabolite synthesis**

Plants are [sessile organisms](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/sessile-species) constantly facing changing climatic conditions and biotic and [abiotic stresses](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/abiotic-stress%22%20%5Co%20%22Learn%20more%20about%20abiotic%20stresses%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages). The plant-associated microbial community provides stability and regulates the plant's metabolic behaviors during stress conditions ([Pathak et al., 2022](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib73)). The plant secretes a plethora of metabolites, which help in shaping the microbial community structures of the plant ([Jacoby et al., 2020](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib41)). For example, [Stringlis et al. (2018)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib90) reported the role of [coumarin](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/coumarin%22%20%5Co%20%22Learn%20more%20about%20coumarin%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) as an iron acquisition in [Arabidopsis](https://www.sciencedirect.com/topics/immunology-and-microbiology/arabidopsis) strains and found significant variation in the rhizosphere community of wild and coumarin mutant strains. [Voges et al. (2019)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib97) found a deficiency of coumarin compounds in the *Arabidopsis* mutant strain, resulting in the abundance of the [Pseudomonas](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/pseudomonas) strain. Furthermore, in a study, [de Bruijn et al. (2018)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib25) reported the role of benzoxazinoids in shaping the microbial community structure in maize. The authors reported that the presence of benzoxazinoids enhances the abundance of the *Pseudomonas* strains in the rhizosphere. Camalexin, a phenolic compound, has also been found to play a significant role in shaping the rhizosphere bacterial community ([Neal et al., 2012](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib65)). In a study by [Koprivova et al. (2019)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib47), it was observed that the deficiency of camalexin in an Arabidopsis mutant strain did not support the growth of beneficial bacteria.

Strigolactone (SL) a signaling molecule released by the plants rhizosphere, plays a significant role in promoting symbiosis. The function of SLs has been well-reported in promoting the symbiotic association of AMF with plant roots ([Akiyama et al., 2010](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib4), [Kim et al., 2022](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib45)). Previous studies showed that most of the plant taxa can synthesize the SLs molecules ([Walker et al., 2019](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib99), [Wheeldon and Bennett, 2021](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib107); [Clark et al., 2023](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib22)). The exudation of SLs molecules also modulates the community structure of the plant rhizosphere, although the impact of SLs on [microbiome](https://www.sciencedirect.com/topics/immunology-and-microbiology/microbiome%22%20%5Co%20%22Learn%20more%20about%20microbiome%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) assembly depends on the [host species](https://www.sciencedirect.com/topics/immunology-and-microbiology/host). For example, [Carvalhais et al. (2019)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib16) reported that the secretion of SLs in the *Arabidopsis* supports greater fungal diversity than the SLs mutant strain, although no significant variation had been observed in the bacterial diversity.

However, in contrast, [Nasir et al. (2019)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib63) reported significant variation in the bacterial diversity of wild and mutant strains of rice, but no significant variation was observed between the fungal communities. [Liu et al. (2020)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib56) reported a similar type of observation in the case of soybean. The overexpression of SL genes and signaling genes significantly modulates bacterial diversity, but no such types of observation were found in the case of fungi ([Liu et al., 2020](https://www.sciencedirect.com/science/article/pii/S0944501323002550#bib56)).

[Flavonoids](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/flavonoid) are a common component of root exudates, acting as signal molecules and mediating interactions between plant rhizosphere and microorganisms. However, the specificity of flavonoids and their chemical [dynamics](https://www.sciencedirect.com/topics/immunology-and-microbiology/dynamics) affect differentially on the rhizospheric [microbiome](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/microbiome%22%20%5Co%20%22Learn%20more%20about%20microbiome%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) ([Wang et al., 2022](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib103)). In the previous studies, authors reported on different flavonoids and showed significance in shaping the composition of rhizospheric [microbiota](https://www.sciencedirect.com/topics/immunology-and-microbiology/microflora%22%20%5Co%20%22Learn%20more%20about%20microbiota%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages). For example, [Okutani et al. (2020)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib70) reported that [Daidzein](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/daidzein%22%20%5Co%20%22Learn%20more%20about%20Daidzein%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages), a flavonoid present in soybean exudates, significantly modulates the bacterial community of soil and rhizosphere. [Schütz et al. (2021)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib85) found soil treated with [quercetin](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/quercetin%22%20%5Co%20%22Learn%20more%20about%20quercetin%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) affects the microbial composition by lowering some specific genera and promoting particular genera of *Pseudarthrobacte*r. Similarly, [Yu et al. (2020)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib114) reported that flavonoids support the population of *[Oxalobacteraceae](https://www.sciencedirect.com/topics/immunology-and-microbiology/oxalobacteraceae%22%20%5Co%20%22Learn%20more%20about%20Oxalobacteraceae%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages)* in the maize rhizosphere. The role of flavonoids was also reported to elicit nod gene expression in rhizobial [symbionts](https://www.sciencedirect.com/topics/immunology-and-microbiology/symbion%22%20%5Co%20%22Learn%20more%20about%20symbionts%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) ([Buer and Muday, 2004](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib15), [Pillai and Swarup, 2002](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib74)). Besides the signaling molecules, flavonoids are also directly involved in [spore germination](https://www.sciencedirect.com/topics/immunology-and-microbiology/spore-germination) that regulates pathogen growth ([Del Valle et al., 2020](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib27)). In the previous studies, the author reported that [enzymes](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/enzyme) like [chalcone isomerase](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/chalcone-isomerase%22%20%5Co%20%22Learn%20more%20about%20chalcone%20isomerase%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages), flavanone-3-hydroxylase, etc., present as intermediaries during flavonoid synthesis, upon silencing, inhibit flavonoid synthesis and ultimately inhibit [root nodule](https://www.sciencedirect.com/topics/immunology-and-microbiology/root-nodule) formation. For example, silencing of gene chalcone [synthase](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/synthase%22%20%5Co%20%22Learn%20more%20about%20synthase%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) and [isoflavone](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/isoflavone%22%20%5Co%20%22Learn%20more%20about%20isoflavone%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) synthase prevents [root nodule](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/root-nodule) formation in [Medicago](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/medicago%22%20%5Co%20%22Learn%20more%20about%20Medicago%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages)*truncatula* and soybean ([Wasson et al., 2006](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib106)). [Banasiak et al. (2013)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib11) reported that silencing of [ABC transporters](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/abc-transporter), a mediator of flavonoid exudation, results in flavonoid deficiency, which enhances the infection rate of [Fusarium oxysporum](https://www.sciencedirect.com/topics/immunology-and-microbiology/fusarium-oxysporum%22%20%5Co%20%22Learn%20more%20about%20Fusarium%20oxysporum%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) in the composite plants. The authors also reported the ability of flavonoids to modulate certain specific microbial species and their accumulation in plant tissues. For example, [Nazari et al. (2017)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib64) reported an accumulation of flavonoids in tobacco by the strain [Bacillus subtilis](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/bacillus-subtilis) ATCC21332*,* which results in growth inhibition of [Agrobacterium tumefaciens](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/agrobacterium-tumefaciens%22%20%5Co%20%22Learn%20more%20about%20Agrobacterium%20tumefaciens%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) IBRC-M10701. In a study, [Yu et al. (2020)](https://www.sciencedirect.com/science/article/pii/S0944501323002550#bib114) reported flavonoids' role in motility and colonization potential of [Pseudomonas fluorescen](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/pseudomonas-fluorescens)ce 2P24.

**4. Rhizospheric microbial composition**

The microbial community of the plant rhizosphere depends upon several factors, such as plant genotypes, plant growth stages, soil, and the nature of root exudates. In addition, surrounding environmental conditions, different stress factors like biotic (pathogen, plant diseases) and [abiotic stresses](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/abiotic-stress%22%20%5Co%20%22Learn%20more%20about%20abiotic%20stresses%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) (like drought, salinity, flood, pH) play a predominant role in shaping the microbial composition of the rhizosphere ([Gargallo-Garriga et al., 2018](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib33)). In a previous study, the authors reported that the diversity and abundance of plant rhizosphere is higher than the [bulk](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/volume) soil or the soil not directly influenced by the plant roots ([Xu et al., 2021](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib111)). [Trivedi et al. (2020)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib94) reported that the abundance of [Proteobacteria](https://www.sciencedirect.com/topics/immunology-and-microbiology/proteobacteria%22%20%5Co%20%22Learn%20more%20about%20Proteobacteria%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) phyla at the plant rhizosphere compared to the [bulk](https://www.sciencedirect.com/topics/immunology-and-microbiology/volume) soil. Previously, authors reported the rhizospheric microbial composition of different plants. [Kumar et al. (2016)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib51) reported dominant cultivable phyla *Proteobacteria*, followed by [Firmicutes](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/firmicutes%22%20%5Co%20%22Learn%20more%20about%20Firmicutes%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) in the rhizosphere of [Curcuma](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/curcuma)*longa.* A similar type of observation was also reported in the rhizosphere of *Curcuma amada* ([Kumar et al., 2017](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib52)). In a comprehensive global study of the citrus rhizosphere, the author found dominance of *Proteobacteria* phyla followed by [Actinobacteria](https://www.sciencedirect.com/topics/immunology-and-microbiology/actinobacteria%22%20%5Co%20%22Learn%20more%20about%20Actinobacteria%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) during [amplicon](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/amplicon%22%20%5Co%20%22Learn%20more%20about%20amplicon%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) and deep [metagenomic](https://www.sciencedirect.com/topics/immunology-and-microbiology/metagenomics%22%20%5Co%20%22Learn%20more%20about%20metagenomic%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) sequencing ([Xu et al., 2018](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib112)). [Jiao et al. (2023)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib42), in a comprehensive study of apple rhizospheric microbiome, the author included eight sampling sites having different geographic and climatic conditions. As a result, authors have found nine predominant [bacterial phyla](https://www.sciencedirect.com/topics/immunology-and-microbiology/bacterial-phyla), among which *Firmicutes* was dominant in five sites. In contrast, three sites were dominated by phyla *Proteobacteria*. After these two bacterial phyla, *Actinobacteriota*, *Bacteroidota,* and *Acidobacteriota* were dominant. This study found that geographical factors are critical in shaping the rhizospheric microbiome of apple varieties, such as rhizospheric microbial community structure at the advent of stresses.

[Chaparro et al. (2014)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib18) evaluated the diversity of [Arabidopsis](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/arabidopsis) rhizosphere during four different growth stages and found variation in abundance and genera of bacteria during different growth stages. Although the author reported a higher abundance of bacterial communities just after the seedling stage. However, at the point of the seedling stage, the bacterial communities were much different from those other stages ([Chaparro et al., 2014](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib18)). Similarly, in a study, [Qiao et al. (2017)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib77) found variation in the rhizospheric bacterial community of cotton during different [developmental stages](https://www.sciencedirect.com/topics/immunology-and-microbiology/developmental-stage) of growth.

**5. Rhizospheric microbial community structure at the advent of stresses**

The response to various stresses, such as salinity, drought, high pH, and more, significantly influences the community structures of the rhizospheric microbiome. The abiotic stress factors like drought, salinity, etc affect plant growth via limiting water availability, poor [root growth](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/root-growth), and accumulation of various stress hormones, altering the metabolic profiles of root exudates, which results in the variation of the microbial composition of the plant rhizosphere ([Goss-Souza et al., 2020](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib37); [Shi et al., 2018](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib87); [Wu et al., 2019](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib108); [de Faria et al., 2021](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib26); [Vives-Peris et al., 2018](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib96); [Xiong et al., 2021](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib110)). However, the [strength](https://www.sciencedirect.com/topics/immunology-and-microbiology/strength) of the stresses also affects the composition of a microbial community. For instance, a higher saline condition, such as mean EC 70 mS/cm, favors [Archaea](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/archaeon%22%20%5Co%20%22Learn%20more%20about%20Archaea%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) phyla's growth, especially *Euryarchaeotal*. However, salinity levels of EC 22 mS/cm concentration favor the growth of different [bacterial phyla](https://www.sciencedirect.com/topics/immunology-and-microbiology/bacterial-phyla), namely [Actinobacteria](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/actinobacteria%22%20%5Co%20%22Learn%20more%20about%20Actinobacteria%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages), followed by [Proteobacteria](https://www.sciencedirect.com/topics/immunology-and-microbiology/proteobacteria%22%20%5Co%20%22Learn%20more%20about%20Proteobacteria%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages), [Bacteroidetes](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/bacteroidetes%22%20%5Co%20%22Learn%20more%20about%20Bacteroidetes%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages), and [Firmicutes](https://www.sciencedirect.com/topics/immunology-and-microbiology/firmicutes%22%20%5Co%20%22Learn%20more%20about%20Firmicutes%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) ([Yang et al., 2022](https://www.sciencedirect.com/science/article/pii/S0944501323002550#bib113)). In a study, [Cesari et al. (2019)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib17) found modified plant-microbe or microbe-microbe interaction during water stress conditions. The water stress condition changed the exudate pattern by significantly enhancing the amount of [Naringenin](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/naringenin%22%20%5Co%20%22Learn%20more%20about%20Naringenin%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages), oleic FA, citric and lactic acid, which ultimately modified the rhizosphere microbial structures of *A. hypogaea* by interacting with [Bradyrhizobium](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/bradyrhizobium%22%20%5Co%20%22Learn%20more%20about%20Bradyrhizobium%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) and [Azospirillum](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/azospirillum%22%20%5Co%20%22Learn%20more%20about%20Azospirillum%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages).

During the [phytopathogen](https://www.sciencedirect.com/topics/immunology-and-microbiology/phytopathogen%22%20%5Co%20%22Learn%20more%20about%20phytopathogen%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) invasion, the plant protects itself by eliciting an immune response, resulting in variation in the metabolic profile and nature of the root exudates released, which affect the colonization efficacy and the plant rhizosphere's community structure ([Chaparro et al., 2014](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib18), [Qiao et al., 2017](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib77), [Marques et al., 2014](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib59)). Although phytopathogen invasion can be retaliated by the host plant through the natural inhabitant [microflora](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/microflora%22%20%5Co%20%22Learn%20more%20about%20microflora%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) directly by releasing antimicrobial compounds, bioactive compounds, and volatile production, indirectly by secreting the [siderophore](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/siderophore%22%20%5Co%20%22Learn%20more%20about%20siderophore%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) production, HCN synthesis, or antibiotics production. These released compounds influenced the plants rhizosphere's metabolic profile and microbial community structure ([Bergelson et al., 2019](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib13), [Toju et al., 2016](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib93)). Previously, [Boer et al. (2005)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib14) found fungal-released metabolites support the abundance of particular competent bacterial groups, while nonresilient bacteria were eradicated. Similarly, [Walia et al. (2013)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib98) found metabolites of [Bacillus subtilis](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/bacillus-subtilis) CKT1 inhibit the fungal pathogen, thus protecting the plants.

**6. Rhizosphere engineering: concept and methodology**

In recent years, the exploration of the latest technologies and omics has gained momentum in the field of plant engineering. Plant rhizosphere consists of three main components: plant, soil, and microbes that affect the plant's health and productivity. Therefore, by improving these components, plant rhizosphere can be modified to achieve optimum agricultural productivity ([Dubey and Sharma, 2021](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib30), [Bano et al., 2021](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib12)).

However, limited knowledge and understanding of rhizosphere engineering are revealed after much advancement in omics and technology. Inoculating selected microbial strains to the rhizosphere site is one of the most common practices to modulate rhizospheric functioning ([Dubey and Sharma, 2021](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib30)). Nevertheless, the survival and stability of microbial inoculants during the field trial are still challenging and crucial. Usually, selected microbes for the inoculation process are isolated in the nutrient-rich media compared to the soil or rhizosphere. Furthermore, the selection of microbial strains for the inoculation is generally performed under controlled laboratory conditions, which produce more reproducible results. Nevertheless, conditions at the rhizosphere are very different; thus, result outputs could not be as per choice ([Rosa et al., 2023](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib81)).

Moreover, different [stoichiometry](https://www.sciencedirect.com/topics/immunology-and-microbiology/stoichiometry%22%20%5Co%20%22Learn%20more%20about%20stoichiometry%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) of nutrients and soil physicochemical properties like available nutrients, pH, and carbon availability differ to a certain extent from the laboratory conditions, which primarily affect microbial survival and adaptability in the rhizosphere. Therefore, selecting microbes with a broad range of niches and food webs is an essential parameter ([Morriën, 2016](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib62)). The field, trials, or application of microbial inoculants at the target site sometimes [faces](https://www.sciencedirect.com/topics/immunology-and-microbiology/face) the challenges of competition with native microflora for nutrients and space and, in other cases, consumed by the predator just after application. Therefore, microbes having synergistic interaction with the native microflora can effectively shape the rhizosphere microbiome ([Shi et al., 2016](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib86)).

The other approach that leads to rhizosphere engineering is the application of [microbial consortia](https://www.sciencedirect.com/topics/immunology-and-microbiology/microbial-consortium) with the optimum nutrient source. However, contradictory reports are available in support of or inhibition of [microbial growths](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/microbial-growth) after the application of nutrients mixture and [microbial consortia](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/microbial-consortium) ([Scheuerell and Mahaffee, 2002](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib84), [Wallenstein, 2017](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib101)). Finally, modifying plant traits through gene editing is another approach to rhizosphere engineering. The architecture of roots and their exudates can be modified by editing the plant traits, which ultimately influence the rhizospheric microbiome and its functioning ([Dubey and Sharma, 2021](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib30), [Dessaux et al., 2016](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib29)). The overview of rhizosphere engineering and their approach has been presented in [Fig. 1](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22fig0005).



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Fig. 1. Rhizosphere engineering encompasses various approaches to enhance plant growth and fitness by manipulating microbiomes. Three primary methods are employed for this purpose: **Plant-mediated approach**, which involves selectively breeding host plants to cultivate a beneficial microbiome. Effective techniques such as [QTL mapping](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/quantitative-trait-locus-mapping) and [GWAS](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/genome-wide-association-study) are utilized to identify specific chromosomal regions associated with desired traits in both plants and microbes. **CRISPR-based approach**: Leveraging CRISPR technology enables targeted [genetic modifications](https://www.sciencedirect.com/topics/immunology-and-microbiology/dna-modification) of microbes and plants to recruit desired microbiomes. By editing specific genes, researchers can influence the composition of the microbiome to enhance plant health. **Microbes-mediated approach**: This approach can be implemented through two different paths. The bottom-up method involves individually modifying isolated microbes to enhance desired traits. On the other hand, the top-down approach utilizes horizontal gene transfer to introduce desirable traits into a broad range of host organisms in their natural environment. These traits are then assessed using supporting devices and omics technologies. **Soil manipulation**: Soil manipulation is another significant aspect of rhizosphere engineering. By using compost and carefully selected microbial strains, the soil microbiome can be influenced, subsequently impacting the overall microbial community in the rhizosphere. Overall, rhizosphere engineering approaches serve to strengthen the beneficial microbiome in both soil and plants (rhizosphere, [phyllosphere](https://www.sciencedirect.com/topics/immunology-and-microbiology/phyllosphere%22%20%5Co%20%22Learn%20more%20about%20phyllosphere%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages), and endosphere), ultimately promoting improved plant growth and overall fitness.

**7. Plant engineering**

In the last few years, exploring the latest technologies and omics has provided momentum in plant engineering. Various authors designed plants with modified characters over the previous two decades and successfully implemented them for enhanced agricultural production or environmental resilience ([Dessaux et al., 2016](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib29)). [Genetic](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/genetics) engineering makes it feasible to alter plant-microbe communication, diversify exudation, support various microbiomes, and promote beneficial [microbial activities](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/microbial-activity). For example, [Liu et al. (2021)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib57) found that soybean roots inoculated with the *noeI* mutant strain resulted in decreased [nodulation](https://www.sciencedirect.com/topics/immunology-and-microbiology/root-nodule) and root exudates, especially flavonoid content. This ultimately affects the rhizospheric microbiome's assembly pattern by reducing the diversity in the soybean rhizosphere. However, shaping the specific microbiome through plant engineering can be achieved through various approaches. Nevertheless, the two most common approaches are the selection of superior cultivars for plant breeding and modifying the [plant's genetic](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/plant-genetics) makeup. However, plant breeding is carried out primarily to shape the rhizospheric microbiome; it needs to focus on specific parameters like yield enhancement, [phytopathogen](https://www.sciencedirect.com/topics/immunology-and-microbiology/phytopathogen%22%20%5Co%20%22Learn%20more%20about%20phytopathogen%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) management, and tolerance against different stresses ([Ryan et al., 2009](https://www.sciencedirect.com/science/article/pii/S0944501323002550#bib82)). For example, [Neal et al. (1973)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib66) used the chromosomal substitution method to enhance resistance against root-rot diseases and maintain the rhizospheric microbial communities of wheat. However, another strategy that has been investigated is picking an indigenous plant species or cultivar that can attract a beneficial microbiome ([Mazzola, 2007](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib60), [Bakker et al., 2012](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib10)). Reports are available that illustrate how [genetically modified plants](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/transgenic-plant) (GM plants) secrete specific root exudates, improving soil quality and changing microbial assembly patterns ([Agoussar and Yergeau, 2021](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib2)). In addition, GM plants can synthesize and transport soil [organic anions](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/organic-anion) such as malate and citrate commonly released during nutrient or mineral stress conditions. GM plants that could secrete this citrate in higher quantities showed better growth response under nutrient-stress conditions ([Koyama et al., 1999](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib48)). Similarly, to combat biotic stresses, GM plants have been created in such a way that they can produce enormous amounts of antimicrobial compounds that effectively manage pathogen invasion. For example, in previously published reports, authors reported GM plants that synthesize [acylase](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/amidohydrolase%22%20%5Co%20%22Learn%20more%20about%20acylase%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) and [lactonases](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/lactonase%22%20%5Co%20%22Learn%20more%20about%20lactonases%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages), as these compounds can break down the bacterial [quorum sensing](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/quorum-sensing) signalling and successfully inhibit pathogen growth ([Ryan et al., 2009](https://www.sciencedirect.com/science/article/pii/S0944501323002550#bib82), [Bakker et al., 2012](https://www.sciencedirect.com/science/article/pii/S0944501323002550#bib10)).

Plant engineering has also been focused on achieving disease-resistant plants. Most [pathogenic microbes](https://www.sciencedirect.com/topics/immunology-and-microbiology/pathogenic-microbes) enter the plant either directly or through the vector and adversely affect the plant's growth. However, the advent of pathogens in plants retaliated by the native microflora or their secretory products such as antibiotics, antimicrobial compounds, etc. ([Dessaux et al., 2016](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib29)). The common strategies for engineered plants are mediated via a selection of resistance breeds either through a cross between wild–type and susceptible 'elite' lines, or marker-assisted selection of superior breeds or quantitative trait loci (QTL) discovery. Recently, various authors reported disease-resistant plants via plant breeding to combat plant diseases or pathogen invasion. For example, [Chukwu et al. (2019)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib21) briefly covered traditional and latest [molecular breeding](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/molecular-breeding) approaches to develop bacterial rice leaf blight-resistant varieties. Similarly, [Yuqing et al. (2018)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib115) briefly review the breeding techniques used to make the tomato resistant to different bacterial diseases. Furthermore, [Luo et al. (2014)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib58) developed disease-resistant rice varieties with improved grain quality via marker-assisted selection. [Ni et al. (2015)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib67) developed a disease-resistant variety through marker-assisted selection. Further, [Thapa et al. (2015)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib92) used QTLs to create a disease-resistant variety of tomatoes.

However, nowadays, to evaluate the relationship between plants and the associated microbes, genome-wide association studies (GWAS) have been performed. The GWAS explores how the plant genotype affects or interacts with the microbial assembly ([Xiao et al., 2017](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib109)). Through the GWAS, authors have identified the gene responsible for causing diseases. For example, [Raboin et al. (2016)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib80) used GWAS to identify the loci responsible for the blast disease in rice. Similarly, [Mgonja et al. (2016)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib61) used the GWAS to map the gene responsible for resistance against the pathogen [Magnaporthe oryzae](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/magnaporthe-oryzae%22%20%5Co%20%22Learn%20more%20about%20Magnaporthe%20oryzae%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) of rice in four different African Countries. [Oladzad et al. (2020)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib71) evaluated the [genetic factors](https://www.sciencedirect.com/topics/immunology-and-microbiology/heredity) related to [nitrogen fixation](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/nitrogen-assimilation) in the bean through the GWAS.

**8. Engineering the microbial strains**

In rhizosphere engineering, microbial strains are crucial partners that directly affect plant functioning. The rhizospheric microbial communities are directly or indirectly associated with the modulation and maintenance of productivity and health of plants under normal or stress conditions ([Kloepper et al., 1978](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib46)). Recently, genetic engineering has emerged as a prominent approach for enhancing microbial strains in rhizosphere engineering, and it has been widely adopted in recent years ([Qaim and Zilberman, 2003](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib76), [Godfray et al., 2010](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib35)). Introducing specific genes, individuals, or heterologous traits into selected microbial strains yields promising and fast results. Although among the various genetic techniques nowadays, [RNA](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/rna) interference (RNAi) technology and CRISPR/Cas 9 have been frequently preferred by the scientific community to improve the functioning of microbes ([Zamore et al., 2000](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib116)). The RNAi technology is the latest technique that has been used to inhibit the expression of particular genes via systematic procedures like the introduction of double standard RNA (dsRNA), which later activates [dicer](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/dicer) proteins which results in fragmentation of dsRNA called siRNA, further with the help of [argonaute proteins](https://www.sciencedirect.com/topics/immunology-and-microbiology/argonaute-protein%22%20%5Co%20%22Learn%20more%20about%20argonaute%20proteins%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages), antisense strand of siRNA led to the formation of RISC (RNA-induced silencing complex) which ultimately bind with the mRNA and stop the translation process or gene expression by degrading the RNA ([Filipowicz, 2005](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib31)).

Although the RNAi technology did not allow the [genetically modified microbes](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/transgenic-microorganism) (GM microbes) to kill the pathogen directly, it enabled the strain to carry the dsRNA that degrade or knock out the genes related to pathogenesis. Recently, various authors reported using RNAi technology to modify the functioning of microbes. For example, [Ganbaatar et al. (2017)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib32) reported about the genetically modified strain of *Escherichia coli* via RNAi technology, containing specific gene sequences that target specifically [Mythimna separata](https://www.sciencedirect.com/topics/immunology-and-microbiology/mythimna-separata%22%20%5Co%20%22Learn%20more%20about%20Mythimna%20separata%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages)*,* a corn pathogen. Similarly, [Leonard et al. (2020)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib53) improved the resistance power of honeybees against the mites using RNAi technology.

[CRISPR](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/crispr) and CRISPR/Cas 9 are powerful gene editing tools to improve the microbes' genetic architecture ([Qiu et al., 2019](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib78)). Although by the process of [CRISPR](https://www.sciencedirect.com/topics/immunology-and-microbiology/clustered-regularly-interspaced-short-palindromic-repeat) and CRISPR/Cas9 technologies, gene editing has been easily carried out. During the process, the Cas 9 protein acts as an RNA-guided [DNA](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/dna) [endonuclease](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/endonuclease%22%20%5Co%20%22Learn%20more%20about%20endonuclease%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) and helps insert or delete the target location of the gene into the cell via the help of [guide RNA](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/guide-rna) ([Cong et al., 2013](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib24)). In previous studies, various authors have used the CRISPER /Cas9 technology to modify the functioning of plants and microbes by silencing and editing the choice of gene ([Andersen et al., 2015](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib6), [Ali et al., 2015](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib5), [Goold et al., 2018](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib36)). [Kemal et al. (2016)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib44) reported about the genetically engineered [Pseudomonas](https://www.sciencedirect.com/topics/immunology-and-microbiology/pseudomonas) putida strain KT2440 that efficiently controls the pathogen [Fusarium oxysporum](https://www.sciencedirect.com/topics/immunology-and-microbiology/fusarium-oxysporum%22%20%5Co%20%22Learn%20more%20about%20Fusarium%20oxysporum%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) in banana. The genetically modified strain *P. putida* sensed the [fusaric acid](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/fusaric-acid%22%20%5Co%20%22Learn%20more%20about%20fusaric%20acid%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) released by the pathogen and produced inhibitors that check the growth of *F. oxysporum*. Similarly, [Ryu et al. (2020)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib83) reported about the genetically engineered microbial strains of cereal crops that express the N2 fixing genes in response to the chemical signal in the plant rhizospheric region and synchronize the plant-associated microbes.

Similarly, [Li et al. (2023)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib54) have used clustered regularly interspaced short palindromic repeats (CRISPR)-Cas9 to edit the pathogenesis-related gene of the phytopathogenic bacteria to enhance plant productivity. [Liang et al. (2020)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib55) reported about the strain *Rhodococcus* spp. having a wide range of metabolic activities, the ability to tolerate [organic solvents](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/organic-solvents), and the bioremediation process. The strain has been genetically modified using the CRISPER to enhance the catalytic property and reduce by-product formation by silencing the by-product-related gene and substituting the [nitrile hydratase](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/nitrile-hydratase%22%20%5Co%20%22Learn%20more%20about%20nitrile%20hydratase%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) gene.

Improving the reliability and predictability of farming systems by incorporating [transgenic](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/transgenics) or gene editing is a contentious issue. However, it [faces](https://www.sciencedirect.com/topics/immunology-and-microbiology/face) many challenges, including the limited survival of [genetically modified microbes](https://www.sciencedirect.com/topics/immunology-and-microbiology/transgenic-microorganism) and the risk of gene transfer between strains. In addition, efficacy, survivability, and environmental risks associated with newly introduced [genetically modified organisms](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/transgenic-organism) are the crucial issue ([Wang and Chang, 2011](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib102)). Moreover, introducing [genetically modified organisms](https://www.sciencedirect.com/topics/immunology-and-microbiology/transgenic-organism) necessitates constant monitoring of their behaviour and fate, a process hindered by high costs, specialized expertise requirements, and susceptibility to biosafety regulations. Coupled with legal restrictions in many nations, to address these challenges, well-informed policy decisions grounded in scientific understanding are essential ([Glandorf et al., 2019](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib34)).

Although [rhizospheric bacteria](https://www.sciencedirect.com/topics/immunology-and-microbiology/rhizosphere-bacterium%22%20%5Co%20%22Learn%20more%20about%20rhizospheric%20bacteria%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) are involved in traits like phytohormone modulations, phosphate [solubilization](https://www.sciencedirect.com/topics/immunology-and-microbiology/solubilization%22%20%5Co%20%22Learn%20more%20about%20solubilization%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages), [ammonia production](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/ammonia-formation), and nutrient acquisition, the microbial agent's engineering can lead to significant growth promotion activities and other microbiome services. Previously, authors reported enhancement in growth promotion attributes of microbial strains using genetic engineering. For example, through an engineering approach, [Singh et al. (2022)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib89) enhanced the D-glucose utilization pattern in [Azospirillum brasilense](https://www.sciencedirect.com/topics/immunology-and-microbiology/azospirillum-brasilense%22%20%5Co%20%22Learn%20more%20about%20Azospirillum%20brasilense%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages), enhancing the colonization rate and promoting [root growth](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/root-growth). [Raaijmakers et al. (1995)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib79) reported inoculation of gene-coding [siderophore](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/siderophore%22%20%5Co%20%22Learn%20more%20about%20siderophore%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) receptors into the strain of [*Pseudomonas*](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/pseudomonas)*fluorescent* for more competent in the soil. Similarly, [Suárez et al. (2008)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib91) reported overexpression of the trehalose-6-phosphate [synthase](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/synthase%22%20%5Co%20%22Learn%20more%20about%20synthase%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) gene in a genetically engineered [Rhizobium etli](https://www.sciencedirect.com/topics/immunology-and-microbiology/rhizobium-etli%22%20%5Co%20%22Learn%20more%20about%20Rhizobium%20etli%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages), which, after inoculation, enhanced nodule formation and [nitrogenase](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/nitrogenase%22%20%5Co%20%22Learn%20more%20about%20nitrogenase%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) activity in [Phaseolus](https://www.sciencedirect.com/topics/immunology-and-microbiology/phaseolus%22%20%5Co%20%22Learn%20more%20about%20Phaseolus%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages)*vulgaris*. [Zhang et al. (2012)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib117) reported enhancement in the biocontrol potential of *Burkholderia vietnamiensis* by integrating the [chitinase](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/chitinase%22%20%5Co%20%22Learn%20more%20about%20chitinase%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) gene of *Bacillus subtilis*.

However, for the engineering of microbial strains, generally, two methodologies have been followed; the first one is the bottom-up approach- through which the microbial strains are isolated from the plant and soil and, after characterization ([Compant et al., 2019](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib23)). Genetically engineered to contain the desired traits and further the genetically engineered microbes inoculated into the plants ([Dubey and Sharma, 2021](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib30)). Top-down is another in-situ approach, the choice of character or gene introduced into many hosts via horizontal gene transfer (HGT). In addition, the other top-down approach has been used to transfer exogenous genes into the random microbial populations to modulate the plant growth-promoting traits ([Compant et al., 2019](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib23)).

**9. Soil amendment**

To successfully control soil-borne pathogens, using suppressive composts is one of the emerging and sustainable aspects. Although the extent, reliability, and expected outcomes differ after applying suppressive composts. Nevertheless, the research community thinks of a possible mechanism to shape the rhizospheric microbiome and uses it for growth promotion and phytopathogen management. In previous studies, various authors used microbial compost to suppress plant pathogen growth and growth promotion. The application of the compost not only inhibits the growth of pathogens but also manipulate the rhizospheric microbiome through different assembly pattern. Previously, [Antoniou et al. (2017)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib7) reported the impact of soil compost application on tomato disease suppressiveness and growth promotion. The author observed enhancement in the morphological yields and control of phytopathogen growth, possibly due to the microorganisms present in the compost. The compost application also modulates the assembly pattern of the rhizospheric microbiome. Previously, authors reported that soil or disease-suppressive soil amendment significantly shapes the rhizospheric microbiome. For example, [Chapelle et al. (2016)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib19) reported about sugar beet seedlings growing in disease-suppressive soils, which was used to inhibit the growth of the pathogen [Rhizoctonia solani](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/rhizoctonia-solani%22%20%5Co%20%22Learn%20more%20about%20Rhizoctonia%20solani%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages), which also modulates the abundance of some specific bacterial genera. Further, [Siegel-Hertz et al. (2018)](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib88) reported that disease-suppressive soils significantly lower the disease severity of [Fusarium](https://www.sciencedirect.com/topics/immunology-and-microbiology/fusarium%22%20%5Co%20%22Learn%20more%20about%20Fusarium%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages) wilt. Additionally, these soils support the growth of different microbial communities, especially the higher abundance of bacterial communities than the non-amendment soil. However, using plants as selective agents to enhance beneficial microbial functions in soil implies considering additional factors, For instance, the presence of different soil can affect the plant physiology, which results in changes in the interaction patterns of soil and microbes ([Hakim et al., 2021](https://www.sciencedirect.com/science/article/pii/S0944501323002550%22%20%5Cl%20%22bib38)). However, functional attributes of plants may be modified through amending soil quality, as the improved quality can manipulate and attract some novel microbial communities in the rhizosphere.

**10. Conclusion**

Recently, rhizospheric microbiomes have gained widespread usage as biofertilizers or biopesticides, effectively boosting agricultural productivity and safeguarding crops against pathogenic threats. These microbiomes exert influence on plant functional nutrient acquisition and phosphate [solubilization](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/solubilization%22%20%5Co%20%22Learn%20more%20about%20solubilization%20from%20ScienceDirect%27s%20AI-generated%20Topic%20Pages), as well as regulating phytohormones under both normal and stressful conditions. The rhizosphere serves as a dynamic hub for symbiotic and [pathogenic microbes](https://www.sciencedirect.com/topics/immunology-and-microbiology/pathogenic-microbes) alike. Recruitment of beneficial microbiomes into the rhizosphere holds significant promise for enhancing plant performance. Rhizosphere engineering provides a unique opportunity to improve the functioning by altering root exudate characteristics, shaping beneficial microbiomes in the rhizosphere, changing the plant genotypes or microbiome engineering, and soil amendment. Previous studies have indicated that modifying the exudation pattern of the rhizosphere can effectively shape the rhizospheric microbiome's composition. Furthermore, identifying genes responsible for root exudate specificity, coupled with their targeted inoculation, presents a viable strategy for recruiting beneficial microbial communities in the plant rhizosphere. Similarly, the microbiome, being the other integral component of the rhizosphere, can have its growth-promoting attributes or antagonistic potential adjusted by manipulating the metabolic functions of microbes. This can be achieved through alterations in metabolic pathways or the introduction of specific genes. However, for effective modulation of microbiomes or rhizospheric microbiomes, to harness microbiome services, a comprehensive understanding of biochemical and molecular factors is imperative. Future research endeavors should focus on unraveling these intricate factors, laying the groundwork for unlocking the full potential of rhizospheric microbiomes. This exploration promises to revolutionize agriculture by harnessing the services of microbiomes, thereby contributing to sustainable and resilient agricultural systems.