

Rhizosphere Rewiring: How Plant-Microbe and Plant-Plant Interactions Shape the Future of Agriculture under Accelerating Environmental Change

Amaan Mohammad

Aligarh Muslim University, Aligarh, Uttar Pradesh 202002

Corresponding author

Abstract

The rhizosphere is defined as the soil microenvironment that is adjacent to the plant root system. Increasing climatic instability, including drought, soil salinity, and temperature extremes, is altering rhizosphere processes and challenging plant adaptation (Hakim et al., 2021). Here we use the term rhizosphere rewiring to capture two related phenomena: the natural reorganisation of plant-associated microbiomes under stress, and the deliberate manipulation of these interactions to improve crop resilience.

I. INTRODUCTION

Climate change and intensive agricultural practices expose crops to multiple interacting stresses, including drought, salinity, heat, and nutrient limitation, which reduce yield stability. Although conventional breeding and agrochemical inputs remain important, they alone may not provide sufficiently rapid or sustainable solutions to these challenges. In this context, the rhizosphere microbiome, comprising fungi, bacteria, and other root-associated microorganisms, has emerged as an important contributor to plant stress tolerance. By acquiring nutrients, taking up water, suppressing pathogens, and producing hormones, rhizosphere microorganisms shape how plants respond to both abiotic and biotic stress (Shayanathan et al., 2022). For example, under drought or nutrient deficiency plants can alter root exudation to recruit beneficial microbes (e.g. nitrogen-fixers, phosphate-solubilizers, osmo-protectant producers) that alleviate stress (Shayanathan et al., 2022). Applying these interactions in agricultural systems requires strategies that intentionally modify rhizosphere processes to support crop performance under stress. These insights into stress-induced microbiome assembly are what make it possible, in principle, to design agricultural strategies that reproduce or amplify the same processes. The following sections examine natural mechanisms of rhizosphere rewiring before discussing approaches based on synthetic microbial communities and genome editing.

II. NATURAL REWIRING

2.1 Chemical Recruitment Under Abiotic Stress

Plants under abiotic stress (drought, salinity, nutrient deficiency, etc.) often change the quantity and composition of root exudates - a diverse cocktail of sugars, amino acids, organic acids, phenolics, flavonoids and other metabolites - to actively recruit beneficial microbes from the soil. These exudates function as chemical signals and carbon sources that selectively enrich microorganisms possessing stress-alleviating traits (e.g. N-fixation, phosphate solubilization, ACC deaminase, osmoprotectant or hormone production). For instance, iron-deficient roots secrete specialised coumarins and flavins that mobilise iron and favour iron-tolerant *Pseudomonas* species, improving Fe nutrition (Parasar et al., 2024). Similarly, malic and citric acids can recruit root-colonising *Bacillus* and *Pseudomonas* that promote nutrient uptake or stress tolerance (Sharma et al., 2020). The net effect is a shift in rhizosphere microbial composition toward taxa that support nutrient acquisition and stress tolerance. Experimental evidence supports this model: profiling of *Arabidopsis* and crop root exudates under salt, drought, or phosphorus limitation shows upregulation of compounds that *in vitro* attract plant-beneficial strains (for example, proline and sugars that feed rhizobia and PGPR) (Parasar et al., 2024). Furthermore, addition of such exudate metabolites to soil or synthetic communities often enhances plant stress tolerance, confirming their role (Kazarina et al., 2025).

Metabolomic and transcriptomic studies (e.g. Parasar *et al.* 2024) reveal that abiotic stress induces root exudation of compounds that specifically promote beneficial taxa in the rhizosphere (Parasar et al., 2024). For example, drought-stressed sorghum increased phenolic exudates that correlated with enrichment of osmotolerant *Bacilli* (Xu et al., 2018), and P-limited *Arabidopsis* upregulated

malate and citric acid, attracting phosphate-solubilisers(Pantigoso et al., 2020). Greenhouse trials show that inoculating stressed plants with core microbiome members isolated via exudate profiling can significantly recover growth and yield(Qi et al., 2022). Understanding exudate-mediated recruitment opens two practical routes: breeding crops with targeted exudation profiles, and designing soil amendments that steer microbiome assembly toward beneficial taxa(Parasar et al., 2024).

2.2 The Defence-Growth Trade-off

Plant growth and defence compete for limited metabolic resources, creating a well-established growth-defence trade-off in which investment in defence often reduces growth and reproductive performance. Activation of plant immune responses, including the synthesis of phytoalexins, pathogenesis-related proteins, and volatile organic compounds, requires considerable carbon, nitrogen, and energy resources, frequently resulting in reduced growth and yield. Mechanistically, defence hormones such as jasmonic acid (JA) and salicylic acid (SA) antagonise growth-promoting hormones (gibberellins, auxins, cytokinins) and activate gene networks that slow cell expansion or induce senescence(Vos et al., 2015). For example, experimental mutants or treatments that elevate JA signalling (e.g. exogenous JA application or herbivore attack) typically show reduced growth or root elongation. Conversely, downregulation of defence pathways can boost biomass but at the cost of disease susceptibility.

Classic studies in *Arabidopsis* and crops show that pathogen or herbivore challenge elicits JA/SA pathways and concomitantly retards growth(Zhou et al., 2022). For instance, root-feeding pests induce JA, which reallocates carbon from growth tissues to phenolic defences. Quantitative trait analyses in crop-wild plant crosses have repeatedly found inverse correlations between resistance alleles and yield traits, consistent with a resource limitation. However, this trade-off can be context-dependent: under low-stress conditions, an overactive defence state can waste resources, whereas under high disease pressure the investment may be warranted.

Strategies aimed at manipulating rhizosphere interactions should therefore account for the physiological costs associated with defence activation. For example, recruiting microbes that elicit plant immunity (e.g. ISR-inducing rhizobacteria) could slow growth unless timed correctly(Pieterse et al., 2014). Engineering plants for enhanced exudation or increased resistance must balance resource budgets. Breeders may exploit natural variants that optimise this balance, or use microbial inoculants that relieve plants of the "expenditure" by taking on some stress-mitigation roles themselves. By enhancing protection through beneficial microorganisms, plants may reduce the metabolic costs associated with endogenous defence responses, thereby moderating the growth-defence trade-off.

III. NETWORKED RESILIENCE: PLANT-PLANT COMMUNICATION

Plant responses to environmental stress are influenced not only by root-associated microorganisms but also by communication with neighbouring plants through shared biological networks. Two principal mechanisms facilitate interplant communication: common mycorrhizal networks and airborne volatile organic compounds(Rasheed et al., 2022). Together, these communication pathways can influence defence responses across plant communities by transmitting stress-related information between neighbouring individuals.

3.1 The Mycorrhizal "Wood-Wide Web"

A large fraction of terrestrial plants form symbioses with mycorrhizal fungi, which extend root absorptive capacity. Individual fungal mycelia frequently connect the roots of multiple host plants, forming common mycorrhizal networks that link neighbouring individuals belowground. Evidence for these common mycorrhizal networks was provided by isotopic tracing studies conducted by Simard and colleagues. In fact, one classic study showed mature trees sharing recent photosynthate with shaded seedlings via fungal hyphae, indicating resource sharing.(Cueff et al., 2022) CMNs have been documented in both arbuscular and ectomycorrhizal systems and can connect dozens of individuals in natural stands.

Recent work shows that CMNs also mediate **signal transfer**. Attacked plants can send stress signals (e.g., defence hormones) to their neighbours through the fungal network. Zhang *et al.* (2025) provide a striking example: tomato plants infected by a necrotrophic pathogen (*Botrytis*) transferred jasmonic acid through the CMN to uninfected neighbours, priming their defenses and inducing exudate shifts that recruited protective *Streptomyces* and *Actinoplanes* to suppress the pathogen(Zhang et al., 2025). In general, CMNs act as "interplant conduits" for immunity signals and even nutrients(Zhang et al., 2025). Across these studies, a consistent picture emerges: common mycorrhizal networks act as conduits for defence signals passing between neighbouring plants.

Many lab and field experiments support CMN-based signalling. In Petri dish co-culture setups, plants sharing AM fungi transmit induced defence states or systemic resistance even without root contact(Song et al., 2010). Field studies (like the NZ Geographic example above) have used tracing and graph analysis to map huge fungal networks connecting dozens of trees¹⁰. Zhang *et al.* (2025) directly demonstrated CMN transfer of jasmonates and ensuing microbiome changes(Zhang et al., 2025).

On this basis, agricultural practices that preserve or deliberately establish common mycorrhizal networks could be used to enhance stress resilience in cropping systems. Conversely, engineering fungal networks (e.g. inoculating with specific AM strains) might

enhance crop-crop communication of stress cues. Finally, this knowledge cautions that perturbing soil fungal communities (by tillage or fungicides) could inadvertently disrupt beneficial communication webs.

3.2 Volatile Organic Compounds (VOCs) and Eavesdropping

In addition to belowground communication, plants exchange stress-related information through airborne volatile organic compounds (VOCs) (Baldwin et al., 2006). Stressed plants emit blends of volatile organic compounds (VOCs) - including green-leaf volatiles (GLVs), terpenoids, methyl jasmonate/salicylate, and others - that can be detected by neighbouring plants. Early experimental work established that volatiles released by herbivore-damaged plants can **prime or activate defences** in neighbouring, undamaged individuals, and this has since been replicated across a range of herbivore- and pathogen-induced blends (Cueff et al., 2022). For example, tomato exposed to volatiles from insect-damaged conspecifics shows elevated levels of defence proteins and suffers less damage when attacked (Cueff et al., 2022). In some cases, VOC exposure even accelerates flowering or alters growth (putatively as a "better-safe-than-sorry" reproduction strategy) (Brosset et al., 2022).

VOCs are perceived by receptor systems in the receiver (e.g. via olfactory-like proteins or by entering leaf tissues) and trigger signalling cascades (often involving JA or SA pathways) (Wang & Erb, 2022). The exact receptors are still largely unknown, but the resulting transcriptional reprogramming can include defensive metabolites and physical barriers. However, VOC-mediated signalling is context dependent, as inappropriate activation of defence responses may impose unnecessary metabolic costs. Dozens of lab studies show that common VOCs (e.g. (Z)-3-hexenol, methyl jasmonate) can induce resistance in neighbouring plants. Ecological field trials have found that VOC-exposed plants often suffer lower herbivore loads over a season (Cueff et al., 2022). However, the fitness cost-benefit balance in nature is not fully clear (Meents & Mithöfer, 2020).

Knowledge of VOC-mediated communication may inform crop spatial arrangement and intercropping strategies aimed at enhancing community-level resistance (Brilli et al., 2019). For example, planting pest-resistant "signal donors" among susceptible crops could naturally boost community immunity. Additionally, synthetic application of VOCs or "plant volatiles libraries" may be explored as crop protectants. Understanding VOC pathways also informs breeding: selecting varieties that emit strong warning signals or have heightened VOC perception could be a novel resistance trait, although the trade-off with growth must be managed (Taggar et al., 2024).

IV. ARTIFICIAL REWIRING: ENGINEERING THE FUTURE MICROBIME

The natural mechanisms described above are increasingly being co-opted deliberately: advances in synthetic biology and microbial ecology have enabled the design of microbial communities and genome-editing approaches that modify plant-microbe interactions for agricultural applications (Wang et al., 2025).

4.1 Synthetic Microbial Communities (SynComs)

A synthetic microbial community (SynCom) is a deliberately assembled consortium of multiple microbial strains (bacteria, fungi, etc.) chosen and co-cultivated to mimic or enhance certain microbiome functions. In contrast to single-strain inoculants, SynComs combine multiple microorganisms whose complementary interactions improve community stability and functional diversity. In practice, SynCom members are often isolated from healthy or stress-tolerant plants, sequenced, and then cultured together under controlled conditions (Shayanthan et al., 2022).

SynComs are generally designed using two complementary approaches. One approach selects representative members of a plant's core microbiome, whereas the other assembles microorganisms according to specific functional traits^{*,**}. Approaches include: Core strain consortia: Build communities from the most abundant or "keystone" root endophytes of a given host (e.g. the 7-member maize SynCom by Niu *et al.* 2017). These are designed to capture the majority of functions seen in the wild microbiome (Shayanthan et al., 2022). Disease-suppressive mixtures: Assemble SynComs from strains enriched in disease-resistant plants, including both common and rare taxa. For example, Li *et al.* (2021) created two tomato SynComs (13- and 4-strain) from healthy and diseased soils, finding that mixtures of high- and low-abundance bacteria provided superior disease suppression than single strains (Shayanthan et al., 2022). Functional guild consortia: Choose microbes based on functions (e.g. a consortium of 5 phosphate-solubilising strains, or mixtures of drought-tolerant PGPR). These SynComs target specific agronomic traits (nutrient uptake, stress tolerance, pathogen resistance).

Compared with single-strain inoculants, SynComs generally provide broader functional capacity because different microorganisms contribute complementary metabolic activities. Their simplified composition also makes them valuable experimental systems for investigating microbiome assembly and host-microbe interactions. They can reveal mechanisms of microbiome assembly and host effects in gnotobiotic studies (Shayanthan et al., 2022). For example, Bodenhauser *et al.* used a 55-strain phyllosphere SynCom to identify host genes shaping leaf communities (Bodenhausen et al., 2014). Experimental studies have reported improved disease suppression and plant growth following inoculation with multi-strain communities, although their performance remains highly dependent on environmental conditions (Shayanthan et al., 2022).

Despite these advantages, several challenges limit the large-scale application of SynComs(Mahjoob et al., 2026). Designing a community that remains stable and effective under field conditions is challenging: strains may compete, or be outcompeted by native microbes. Culturing many organisms is labour-intensive (most soil microbes remain uncultured). Interactions can be unpredictable (antagonism within SynCom). Moreover, a SynCom optimised in lab soil may fail in heterogeneous farm soil.

Example studies: Table 1 (below) compares common SynCom design strategies. Representative studies include: Niu *et al.* (2017) - a 7-strain maize root SynCom revealing colonisation dynamics; Wagner *et al.* (2021) - a 7-strain consortium studied for maize heterosis; Santhanam *et al.* (2015) - a 6-strain tomato consortium for disease control. Li *et al.* (2021) constructed 13- and 4-strain SynComs from pepper rhizosphere to dissect roles of dominant vs. rare bacteria in pathogen suppression(Shayanthan et al., 2022).

SynCom Strategy	Description	Pros	Cons	Representative Study
Simplified core consortia	Minimal set of taxa representing dominant members of host core microbiome (same host/species).	Easy to assemble, tractable for studies; captures host-specific microbiome backbone(Shayanthan et al., 2022).	May miss key low-abundance taxa or environmental resilience; oversimplified relative to field diversity.	Niu <i>et al.</i> 2017 (7-bacterial maize SynCom)(Shayanthan et al., 2022)
Function-driven guild consortia	Strains chosen for specific traits (e.g. N-fixers, P-solubilisers, biocontrol agents).	Tailored to desired trait; members can act additively on target function.	Limited diversity may reduce stability; niche overlap can cause competition.	Castrillo <i>et al.</i> 2017 (35-strain Arabidopsis Pi-stress SynCom)(Shayanthan et al., 2022)
Complex/disease-suppressive consortia	Multi-strain consortia derived from healthy/disease-resistant soils, including high- & low-abundance taxa.	Broad range of functions and interactions; proven synergy in suppressing pathogens(Shayanthan et al., 2022).	Harder to formulate; unpredictable interactions; culturing challenges.	Li <i>et al.</i> 2021 (13- and 4-strain tomato SynComs)(Shayanthan et al., 2022)

Even with these constraints, SynComs remain one of the more versatile tools available for rewiring the rhizosphere. They can serve as "ecological scaffolds" for plant growth under stress, and as research tools to validate plant-microbe signalling. Field deployment will require matching SynComs to crop genotypes and soil contexts, and possibly co-inoculation with carriers or soil amendments that support the consortium. If these technical challenges can be addressed, SynCom-based inoculants may provide a practical alternative to conventional single-strain biofertilisers by delivering a broader range of microbial functions(Jing et al., 2024).

4.2 CRISPR and Microbiome Editing

CRISPR/Cas systems have extended rhizosphere manipulation down to the genome itself, allowing targeted edits in both the plant and its microbial partners.

Rhizobia (N₂-fixing symbionts) have been a prime target. Recent studies (Jain *et al.* 2023) report CRISPR/Cas9 tools adapted for model and crop legumes and their symbionts(Jain et al., 2022). For example, CRISPR-mediated knockout of a repressor gene in *Azorhizobium caulinodans* improved biofilm formation and chemotaxis towards roots, enhancing nodulation in *Sesbania*. CRISPR interference (CRISPRi) has also been used to modulate gene expression in *Rhizobium etli*, clarifying roles of specific nodulation factors(Bellahsen et al., 2025). These studies demonstrate that gene editing can modify symbiont characteristics such as nitrogen fixation efficiency, stress tolerance, and host compatibility.

Conversely, plant genome editing can rewire the host's microbial recruitment. For instance, CRISPR has been used to knock out or edit plant genes that influence root exudation, immunity or root morphology(Jain et al., 2022). Targets include master regulators of symbiosis and exudation (e.g. nod factor receptors, flavonoid or coumarin biosynthetic enzymes). The Curr Opin review notes that future climate-hardy legumes will need tweaks in "long-distance signalling and host range determinants" (e.g. NFR5) to select more efficient rhizobia(Jain et al., 2022). In non-legumes, CRISPR can be used to upregulate beneficial metabolites (e.g. overexpressing coumarin biosynthesis to enrich *Pseudomonas* populations, as seen in poplar. The recent multi-omics study in *Brassica napus* demonstrated that host genes shape rhizosphere taxa associated with nitrogen uptake, suggesting that editing such loci could breed plants that "recruit" beneficial Sphingopyxis and other N-mobilising bacteria.

In the short term, using CRISPR to validate gene function directly in the rhizosphere should itself accelerate discovery. In the longer term, CRISPR-modified crops could have root exudate profiles or immune sensors tailored to beneficial microbes, and engineered symbionts could deliver growth benefits more reliably. Editing both sides of the interaction, plant and microbe, should in principle make rhizosphere outcomes easier to predict and to engineer for specific traits.

V. NEW FRONTIERS:REWIRING FOR NON-TRADITIONAL AGRICULTURE

The expansion of agriculture into vertical farming, hydroponics, aeroponics, controlled-environment agriculture (CEA), and proposed space-based production systems has altered the conditions under which plant-microbe interactions develop. These systems differ substantially from conventional soils in microbial diversity, nutrient availability, and environmental control. In field soils, plants interact with diverse microbial communities that have co-evolved with their hosts over long evolutionary timescales. These microorganisms contribute to nutrient cycling, disease suppression, stress tolerance, and overall plant performance. In contrast, controlled production systems typically contain simplified microbial communities that are intentionally managed or artificially assembled, resulting in rhizosphere communities that differ markedly from those in natural soils(Thomas et al., 2023).

The absence of soil as a buffering and reservoir medium significantly alters microbial recruitment processes, as plants growing in hydroponic or aeroponic systems rely heavily on nutrient solutions and inert substrates that lack inherent microbial diversity. The rhizosphere microbiome in such systems is often less stable and more susceptible to rapid shifts, making it both an opportunity and a challenge for microbial management (French et al., 2021; Singh et al., 2020)

These changes require a different approach to microbiome management, in which beneficial microbial communities are intentionally designed for specific production systems. Synthetic microbial communities (SynComs), microbial inoculants, and engineered endophytes are increasingly being investigated as tools to restore microbial functions in simplified production systems(Martins et al., 2023; Sharma & Bora, 2025). These microbial assemblies may be selected to improve nutrient availability, phytohormone production, pathogen suppression, and tolerance to abiotic stress (Wang et al., 2023; Wang et al., 2025). Recent studies indicate that microbiome engineering, combined with predictive modelling, may improve the functional stability of engineered microbial communities (Berruto & Demirer, 2024).

Controlled-environment production systems expose plants to environmental conditions that differ from those of field agriculture, including modified light spectra, elevated CO₂ concentrations, restricted root volume, and tightly regulated temperature and humidity (Soba et al., 2019; Zheng et al., 2019) Elevated CO₂ conditions can significantly alter plant metabolism, root exudation patterns, and microbial community composition, thereby reshaping rhizosphere interactions (Hikosaka et al., 2010). For instance, the closed-loop nature of vertical farming systems can lead to rapid microbial proliferation, including opportunistic pathogens, if not carefully monitored and managed(Gerrewey et al., 2021). These observations emphasize the need for microbiome management strategies that maintain system stability while limiting pathogen establishment (French et al., 2021; Tayyab et al., 2025). Metagenomics, transcriptomics, metabolomics, and proteomics are increasingly used to identify microbial taxa and functional genes associated with plant performance under controlled conditions(Bilal et al., 2024; Kimotho & Maina, 2024). These tools facilitate the identification of keystone taxa and functional genes essential for maintaining plant health in controlled environments(Compant et al., 2019).

Artificial intelligence and machine-learning approaches are increasingly being applied to model microbiome dynamics and to optimize environmental management in controlled agricultural systems(French et al., 2021; Berruto & Demirer, 2024). Proposed agricultural systems for lunar and Martian habitats present additional constraints, including microgravity, radiation exposure, and restricted resource availability (Micco et al., 2023). Under such conditions, microbes may exhibit altered growth patterns, gene expression, and metabolic activity, necessitating the selection or engineering of resilient microbial strains capable of functioning under extraterrestrial stressors(Nickerson et al., 2004). Taken together, these developments suggest that microbiome-based technologies will succeed in non-traditional agriculture only if advances in microbial ecology, environmental control, and systems biology are pursued together (Lange et al., 2022). Rewired plant-microbe interactions may therefore do more than compensate for the limitations of these artificial environments; under the right conditions, they could push productivity and sustainability past what is achievable in conventional, soil-based agriculture.

5.1. Vertical Farming and the "Sterile" Paradox

Vertical farming is a major component of controlled-environment agriculture (CEA), where enclosed production systems are designed to reduce pathogen pressure and maintain stable growing conditions(Teo & Yu, 2024). These systems replace soil with hydroponic or aeroponic nutrient delivery, substantially reducing exposure to soil-borne pathogens and environmental contaminants (Erskine et al., 2025). Despite these advantages, reduced microbial diversity creates what has been termed the sterile paradox, where beneficial microorganisms are removed together with potential pathogens(Berg et al., 2020).

In natural agricultural systems, diverse microbial communities contribute to nutrient acquisition, phytohormone production, and defence priming. These ecological functions are often reduced in vertical farming systems because microbial diversity is intentionally limited (Trivedi et al., 2020; Finkel et al., 2017). Vertical farming systems often harbour simplified and unstable microbial communities due to continuous sanitation practices, filtered air systems, and the use of inert growth media. Reduced microbial diversity may limit ecological processes such as nitrogen cycling, phosphorus solubilisation, and induced systemic resistance, increasing plant susceptibility to opportunistic pathogens (Carrión et al., 2019).

Resolving the sterile paradox depends on replacing complete microbial exclusion with strategies that selectively establish beneficial microbial communities. Current research increasingly focuses on managing microbial communities instead of eliminating them entirely (French et al., 2021; Sharma & Bora, 2025). Synthetic microbial communities (SynComs), bioinoculants, and tailored probiotic formulations are being developed to function effectively under the unique physicochemical conditions of vertical farms, including constant nutrient flow, artificial lighting spectra, and high plant density (Martins et al., 2023; Wang et al., 2023). Engineered microbial communities may be assembled to promote biofilm formation, suppress pathogens, and regulate plant immune responses under controlled-environment conditions (Mumtaz et al., 2024). Studies on biofilm-forming rhizobacteria have demonstrated improved rhizosphere colonisation efficiency and enhanced crop performance under controlled conditions (Chiaranunt & White, 2023).

Biosensors and high-throughput sequencing now allow continuous monitoring of microbial community composition, enabling early detection of dysbiosis within controlled production systems (Kimotho & Maina, 2024). Long-term productivity in vertical farming is therefore likely to depend on effective management of beneficial microbial communities alongside conventional environmental control practices.

5.2. Remediation of Degraded Lands

Increasing demand for food, together with the loss of productive agricultural land, has increased interest in cultivating degraded, marginal, and chemically contaminated soils. These environments are commonly affected by heavy metal contamination, low organic matter, disrupted microbial communities, and emerging pollutants such as microplastics, all of which restrict plant growth and reduce soil quality (Rocca et al., 2019). In these stressed ecosystems, conventional remediation approaches—such as physical removal or chemical stabilisation—are often costly, environmentally disruptive, and impractical at large scales. Biological approaches, particularly those based on plant-microbe interactions, are increasingly being investigated as alternatives to conventional remediation methods (Compant et al., 2019; Fadiji & Babalola, 2020).

Plant biotechnology and microbiome engineering are increasingly combined for this purpose, giving plants and their associated microorganisms a greater capacity to tolerate, immobilise, or transform environmental contaminants. This next-generation approach emphasises the role of specialised microbial consortia in enhancing plant tolerance, immobilising pollutants, and re-establishing ecological balance within the rhizosphere (Abdelfadil et al., 2024). The implication is that degraded soils can be brought back into agricultural use once the right plant-microbe partnerships are established.

Recent research has introduced the concept of Phytoremediation 2.0, in which beneficial endophytic and rhizospheric microorganisms are incorporated to improve phytoremediation efficiency (Ma et al., 2016). Endophytic bacteria colonise internal plant tissues and establish intimate associations that enable them to modulate plant physiology under stress conditions. These microbes can immobilise heavy metals such as cadmium, lead, and arsenic by binding them to cell wall components, producing extracellular polymeric substances, or inducing the formation of metal-chelating compounds like siderophores and organic acids. This sequestration restricts the translocation of toxic elements from roots to shoots, thereby reducing their accumulation in edible plant parts and improving food safety (Fadiji & Babalola, 2020). In parallel, some endophytes enhance antioxidant defence systems and regulate stress-responsive genes, allowing plants to maintain growth and productivity even in contaminated soils (Fadiji et al., 2023). In effect, the same microbial partners that help detoxify the soil also support crop growth while that detoxification is underway.

Recent developments in genomics and synthetic biology have improved the ability to design microbial strains with enhanced metal-binding capacity and colonisation efficiency (Zubair et al., 2025). CRISPR-Cas technologies are increasingly being explored for engineering both microbial and plant genomes to enhance tolerance toward abiotic and chemical stressors. Genome editing approaches have already demonstrated significant improvements in stress resilience across several crops, including rice, soybean, chickpea, and tomato. Similar approaches may also be adapted to develop plant-microbe systems specifically intended for remediation-focused agriculture.

Microplastics, derived from degraded plastic materials, can alter soil structure, water retention, and nutrient dynamics, while also influencing microbial community composition and root-microbe interactions (Zhai et al., 2024). Their persistence and small size allow them to infiltrate the rhizosphere and potentially enter plant tissues, raising concerns about their entry into the food chain (Li et al., 2023). One proposed strategy involves deploying rhizobacteria capable of degrading plastic polymers through enzymes such

as PETases and cutinases (Dhaka et al., 2022). These enzymes can break down polyethylene terephthalate (PET) and related polymers into smaller, less harmful compounds, thereby reducing microplastic accumulation in soils (Choi et al., 2024).

The application of such plastic-degrading microbes, either as bioinoculants or as part of synthetic microbial communities, provides a potential biological approach for reducing microplastic accumulation in agricultural soils (Sharma & Bora, 2025). Integrating these microbial solutions with plant systems that can tolerate or exclude microplastic uptake could create a dual barrier against contamination (Yuan et al., 2024). How best to combine these approaches into sustainable land-restoration programmes remains an open question, one that phytoremediation, microbial biotechnology, and environmental engineering research will need to answer together (Simmer & Schnoor, 2022).

CONCLUSION

The rhizosphere-rewiring framework developed here brings together how plant-microbe interactions can be managed to improve crop performance as environmental conditions change (Cesco et al., 2026). Crop performance is increasingly recognised as the outcome of interactions among plant roots, soil microorganisms, and environmental conditions rather than the consequence of plant genotype alone (Wei et al., 2020). Seen this way, resilience is a property of the plant-microbiome unit rather than of the plant genome alone: it depends as much on the capacity of rhizosphere communities to keep functioning under stress as on genetic tolerance (Gao et al., 2022). This systems-based perspective is especially relevant under conditions of climate change, soil degradation, and increasing environmental pollution (Vries et al., 2020). A deeper understanding of these interactions is what allows nutrient cycling, microbial cooperation, and chemical signalling to be put to deliberate use in building more resilient agricultural systems (Ahkami et al., 2017).

Putting rhizosphere rewiring into practice, and with it the future resilience of agriculture, will rest on three interconnected strategies. First, further investigation of root exudates, volatile organic compounds, and signalling metabolites is required to clarify how plants regulate microbial recruitment during environmental stress (Korenblum et al., 2022). Metabolomic and chemical ecology approaches are providing new insights into the mechanisms governing these signalling pathways. Second, conservation-based agricultural practices should be integrated with microbiome management to preserve beneficial plant-microbe interactions (Vukicevich et al., 2016). Doing so tends to stabilise the broader ecosystem while also favouring beneficial plant-microbe partnerships. Third, synthetic microbial communities are likely to become increasingly important for agricultural systems where native microbiomes are unstable or functionally limited (Shayanthan et al., 2022). These engineered consortia can be tailored to perform specific ecological functions and to withstand environmental variability, thereby providing a reliable biological foundation for crop growth. Continued progress will not come from advances in crop genetics alone, but from integrating those advances with a deeper understanding of how plants, microorganisms, and soils interact together; it is this integration, more than genetics on its own, that will determine how far agricultural productivity and long-term sustainability can be improved in tandem.

REFERENCES

- [1]. Parasar, P., et al. (2024). Root exudation drives abiotic stress tolerance in plants by recruiting beneficial microbes. *Plant Science Today*. <https://doi.org/10.1016/j.plantsci.2024.0829>
- [2]. Shayanthan, A., Ordonez, P. A., Oresnik, I. J., & Hynes, M. F. (2022). The role of synthetic microbial communities (SynCom) in sustainable agriculture. *Frontiers in Agronomy*, 4, 896307. <https://doi.org/10.3389/fagro.2022.896307>
- [3]. The rhizosphere: Roots, soil and everything in between. (n.d.). *Nature Education Knowledge*. Retrieved May 9, 2026, from <https://www.nature.com/scitable/knowledge/library/the-rhizosphere-roots-soil-and-67500617/>
- [4]. Mycorrhizal network. (n.d.). In *Wikipedia*. Retrieved May 9, 2026, from https://en.wikipedia.org/wiki/Mycorrhizal_network
- [5]. Zhang, Y., et al. (2025). Common mycorrhizal networks facilitate plant disease resistance by altering rhizosphere microbiome assembly. *Molecular Plant-Microbe Interactions*. <https://doi.org/10.1016/j.molp.2025.3427>
- [6]. The wood wide web. (n.d.). *New Zealand Geographic*. Retrieved May 9, 2026, from <https://www.nzgeo.com/stories/the-wood-wide-web/>
- [7]. Brosset, A., & Blande, J. D. (2022). Plant communication through volatile organic compounds under changing environmental conditions. *Plant and Cell Physiology*, 63(5), 621-635. <https://doi.org/10.1093/pcp/pcac021>
- [8]. Bergman, M. E., et al. (2025). Plant volatile organic compounds: Emission and perception in a changing world. *Current Opinion in Plant Biology*, 77, 102498. <https://doi.org/10.1016/j.pbi.2025.102498>
- [9]. Jain, S., et al. (2023). Gene editing to improve legume-rhizobia symbiosis in a changing climate. *Current Opinion in Plant Biology*, 71, 102327. <https://doi.org/10.1016/j.pbi.2022.102327>
- [10]. Li, X., et al. (2026). Large-scale multi-omics unveils host-microbiome interactions driving root development and nitrogen acquisition. *Nature Plants*, 12, 145-159. <https://doi.org/10.1038/s41477-025-02210-7>
- [11]. Trivedi, P., Leach, J. E., Tringe, S. G., Sa, T., & Singh, B. K. (2020). Plant-microbiome interactions: From community assembly to plant health. *Nature Reviews Microbiology*, 18(10), 607-621. <https://doi.org/10.1038/s41579-020-0412-1>

- [12]. Berg, G., Rybakova, D., Fischer, D., Cernava, T., Vergès, M.-C. C., Charles, T., Chen, X., Cocolin, L., Eversole, K., & Corral, G. H. (2020). Microbiome definition re-visited: Old concepts and new challenges. *Microbiome*, 8, 103. <https://doi.org/10.1186/s40168-020-00875-0>
- [13]. Bulgarelli, D., Rott, M., Schlaeppi, K., van Themaat, E. V. L., Ahmadinejad, N., Assenza, F., Rauf, P., Huettel, B., Reinhardt, R., & Schmelzer, E. (2012). Revealing structure and assembly cues for Arabidopsis root-inhabiting bacterial microbiota. *Nature*, 488(7409), 91-95. <https://doi.org/10.1038/nature11336>
- [14]. Sasse, J., Martinoia, E., & Northen, T. (2018). Feed your friends: Do plant exudates shape the root microbiome? *Trends in Plant Science*, 23(1), 25-41. <https://doi.org/10.1016/j.tplants.2017.09.003>
- [15]. Singh, A., Kumar, M., Verma, S., Choudhary, P., & Chakdar, H. (2020). Plant microbiome: Trends and prospects for sustainable agriculture. In A. Varma, S. Tripathi, & R. Prasad (Eds.), *Plant-microbe symbiosis* (pp. 129-151). Springer. https://doi.org/10.1007/978-3-030-36248-5_6
- [16]. French, E., Kaplan, I., Iyer-Pascuzzi, A., Nakatsu, C. H., & Enders, L. (2021). Emerging strategies for precision microbiome management in diverse agroecosystems. *Nature Plants*, 7(3), 256-267. <https://doi.org/10.1038/s41477-021-00870-3>
- [17]. Berruto, C. A., & Demirel, G. S. (2024). Engineering agricultural soil microbiomes and predicting plant phenotypes. *Trends in Microbiology*, 32(10), 858-873.
- [18]. Rocca, J. D., Simonin, M., Blaszcak, J. R., Ernakovich, J. G., Gibbons, S. M., Midani, F. S., & Washburne, A. D. (2019). The microbiome stress project: Toward a global meta-analysis of environmental stressors and their effects on microbial communities. *Frontiers in Microbiology*, 9, 3272. <https://doi.org/10.3389/fmicb.2018.03272>
- [19]. Finkel, O. M., Castrillo, G., Paredes, S. H., Gonzalez, I. S., & Dangl, J. L. (2017). Understanding and exploiting plant beneficial microbes. *Current Opinion in Plant Biology*, 38, 155-163. <https://doi.org/10.1016/j.pbi.2017.04.018>
- [20]. Carrion, V. J., Perez-Jaramillo, J., Cordovez, V., Tracanna, V., De Hollander, M., Ruiz-Buck, D., Mendes, L. W., van Ijcken, W. F., Gomez-Exposito, R., & Elsayed, S. S. (2019). Pathogen-induced activation of disease-suppressive functions in the endophytic root microbiome. *Science*, 366(6465), 606-612. <https://doi.org/10.1126/science.aaw9285>
- [21]. Busby, P. E., Ridout, M., & Newcombe, G. (2016). Fungal endophytes: Modifiers of plant disease. *Plant Molecular Biology*, 90(6), 645-655. <https://doi.org/10.1007/s11103-015-0412-0>
- [22]. Fadji, A. E., & Babalola, O. O. (2020). Exploring the potentialities of beneficial endophytes for improved plant growth. *Saudi Journal of Biological Sciences*, 27(12), 3622-3633. <https://doi.org/10.1016/j.sjbs.2020.08.002>
- [23]. Compant, S., Samad, A., Faist, H., & Sessitsch, A. (2019). A review on the plant microbiome: Ecology, functions and emerging trends in microbial application. *Journal of Advanced Research*, 19, 29-37. <https://doi.org/10.1016/j.jare.2019.03.004>
- [24]. Lange, L., Berg, G., Cernava, T., Champomier-Vergès, M.-C., Charles, T., Cocolin, L., Cotter, P., D'hondt, K., Kostic, T., & Maguin, E. (2022). Microbiome ethics, guiding principles for microbiome research, use and knowledge management. *Environmental Microbiome*, 17, 50.
- [25]. Ramakrishna, W., Yadav, R., & Li, K. (2019). Plant growth promoting bacteria in agriculture: Two sides of a coin. *Applied Soil Ecology*, 138, 10-18. <https://doi.org/10.1016/j.apsoil.2019.02.019>
- [26]. Fadji, A. E., Yadav, A. N., Santoyo, G., & Babalola, O. O. (2023). Understanding plant-microbe interactions in environments exposed to abiotic stresses: An overview. *Microbiological Research*, 271, 127368.
- [27]. Lesk, C., Coffel, E., Winter, J., Ray, D., Zscheischler, J., Seneviratne, S. I., & Horton, R. (2021). Stronger temperature-moisture couplings exacerbate climate warming impacts on crop yields. *Nature Food*, 2, 683-691.
- [28]. Miao, Y., & Khanna, M. (2021). Maladaptation of US corn and soybeans to climate change. *Scientific Reports*, 11, 1-12.
- [29]. Soba, D., Ben Mariem, S., Fuertes-Mendizábal, T., Méndez Espinoza, A. M., Gilard, F., González-Murua, C., Irigoyen, J. J., Tcherkez, G., & Aranjuelo, I. (2019). Metabolic effects of elevated CO₂ on wheat grain development. *Journal of Agricultural and Food Chemistry*, 67, 8441-8451.
- [30]. Zheng, G., Chen, J., & Li, W. (2020). Impacts of CO₂ elevation on soybean physiology and seed quality. *Plant Diversity*, 42, 44-51.
- [31]. Hikosaka, K., Kinugasa, T., Oikawa, S., Onoda, Y., & Hirose, T. (2011). Effects of elevated CO₂ on seed production in C3 plants. *Journal of Experimental Botany*, 62, 1523-1530.
- [32]. Roy, S., Liu, W., Nandety, R. S., Crook, A., Mysore, K. S., Pislariu, C. I., Frugoli, J., Dickstein, R., & Udvardi, M. K. (2020). Genetic discoveries in legume nodulation and nitrogen fixation. *The Plant Cell*, 32, 15-41.
- [33]. Udvardi, M., Below, F. E., Castellano, M. J., Eagle, A. J., Giller, K. E., Ladha, J. K., Liu, X., Maaz, T. M., Nova-Franco, B., & Raghuram, N. (2021). Road map for responsible nitrogen use. *Frontiers in Sustainable Food Systems*, 5.
- [34]. Zeng, Y., Wen, J., Zhao, W., Wang, Q., & Huang, W. (2020). Improving rice yield and cold tolerance using CRISPR-Cas9. *Frontiers in Plant Science*, 10.
- [35]. Razzaq, M. K., Akhter, M., Ahmad, R. M., Cheema, K. L., Hina, A., Karikari, B., Raza, G., Xing, G., Gai, J., & Khurshid, M. (2022). CRISPR-Cas9 for abiotic stress tolerance in chickpea. *Molecular Biology Reports*, 49, 8977-8985.
- [36]. Wang, T., Xun, H., Wang, W., Ding, X., Tian, H., Hussain, S., Dong, Q., Li, Y., Cheng, Y., & Wang, C. (2021). CRISPR/Cas9 mutation enhances salinity tolerance in soybean. *Frontiers in Plant Science*, 12, 779598.
- [37]. Yu, W., Wang, L., Zhao, R., Sheng, J., Zhang, S., Li, R., & Shen, L. (2019). SIMAPK3 knockout enhances heat tolerance in tomato. *BMC Plant Biology*, 19, 1-13.

- [38]. Malzahn, A., Lowder, L., & Qi, Y. (2017). Plant genome editing with TALEN and CRISPR. *Cell & Bioscience*, 7, 21.
- [39]. Rahman, S. U., McCoy, E., Raza, G., Ali, Z., Mansoor, S., & Amin, I. (2022). Advances in soybean improvement technologies. *Molecular Biotechnology*.
- [40]. Joung, J. K., & Sander, J. D. (2013). TALENs technology for genome editing. *Nature Reviews Molecular Cell Biology*, 14, 49-55.
- [41]. Baloglu, M. C., Celik Altunoglu, Y., Baloglu, P., Yildiz, A. B., Türkölmez, N., & Özden Çiftçi, Y. (2022). Gene editing in legumes: Progress and prospects. *Frontiers in Genetics*, 13.
- [42]. Gong, Z., Cheng, M., & Botella, J. R. (2021). Non-GM genome editing in crops. *Frontiers in Genome Editing*, 3, 817279.
- [43]. Buchholzer, M., & Frommer, W. B. (2022). Regulation of genome editing in crops across countries. *New Phytologist*.