REVIEW ARTICLE

Farming the Native Micro-biome: Engineering Rhizosphere Communities for Climate Resilient Agriculture

Ayaz Haider Khan

Department of Plant Breeding and Genetics, university of Agriculture Faisalabad, Pakistan
*Corresponding author: mrayazhaiderkhan@gmail.com

ABSTRACT

Rhizosphere microbiome is an important factor in determining the health of plants, and it affects nutrient cycling, plant resilience to the stress, and stability of the soil ecosystem. Native microbial community is a solution to climate-resilient agriculture, which is a sustainable way of ensuring the world can manage its food security as it endures the strain of climate change and land degradation. The review summarizes the information present in the literature on assembly of rhizo-sphere micro-biome specifically with regard to how interactions between plant genetics, root exudates, the properties of the soil (such as physicochemical processes that occur) and the interactions between the microbes in the assembly influence each other. We discuss the Biodiversity-Ecosystem Functioning (BEF) paradigm through which the focus is given to how the diversity of microorganisms implies that more functional redundancy, niche complementarity and positive interactions are achieved as to maximize the growth of plants, and the ability to resist stresses. It also speaks about the possibilities of novel microbiome engineering strategies including synthetic microbial consortia and systems of selection and management of microbial communities in agriculture as they may be used to optimize indigenous microbial communities. We also remark on the microbiome regarding one of the potential fixes in climate-imposed contrasted stresses (e.g., abiotic drought, tunneling salinity), soil pollution, and an impossibility of scalability, environmental predictability, regulation. Finally, we end up with some future directions, that involve some multi-omics introduction, machine learning to design microbiome as a possibility, and testing subsequent to the field which will render the asset a real world practice. The hope of transformation in seeking rhizosphere croplands through microbiome engineering is highlighted in this contribution that confronts the basic ecology and agricultural innovation amid a changing climatic pattern.

Key words: Rhizosphere microbiome, Climate resilient agriculture, Biodiversity ecosystem functioning, Microbiome engineering, Synthetic microbial consortia, Stress resilience, Sustainable agriculture.

INTRODUCTION

The growing demands of rapidly increasing population, coupled with pressure of climate change and land degradation is necessitating the shift towards more sustainable and resilient agricultural practices (Muñoz-Márquez et al., 2022; Zafar et al., 2025). The main theme for this is to optimize the plant health and productivity. In this view, the rhizo-sphere (the narrow zone of soil directly influenced by plant roots) is a critical factor. It is more then just a source of water and nutrients but rather a hotspot for biological organisms giving rise to a complex biological community hence called as the micro-biome.

The microbiome interacts with the host plant and gathers nutrients, tolerates stress, supresses pathogens, and structure soil formation, thereby influences plant fitness and yield (Zhang et al., 2023).

The microbiome assembly is influenced by a complex interplay of host plant genetics, root exudation, soil physicochemical properties, and microbe-microbe interactions, leading to larger changes (Duret et al., 2024). The diversity is enhanced by functional redundancy, niche complementarity, and synergistic interactions. The traditional approaches like single strain bio-inoculants showed promise, but they often failed due to poor persistence, competition with the native microbiome, and lack of functional diversity (Han et al.,

2021). Consequently, we need to develop more optimized strategies for microbiome engineering and management that accounts for ecological principles and moves toward manipulating the native community or designing synthetic associations.

This review aims to (1) synthesize current knowledge on the assembly processes and key drivers (plant, soil, biotic) shaping the rhizo-sphere microbiome and its temporal dynamics; (2) critically examine the conceptual framework linking micro-biome biodiversity to critical ecosystem functions (nutrient cycling, stress resilience, soil health) using Biodiversity-Ecosystem Functioning (BEF) principles; (3) evaluate the potential and limitations of emerging engineering strategies, including micro-biome breeding, agricultural management practices, synthetic communities, and holobiont engineering; (4) explore the micro-biome's role in enhancing plant resilience to global challenges, specifically climate change and soil contamination; and (5) identify major knowledge gaps and outline future research directions for translating rhizosphere micro-biome science into practical, sustainable agriculture.

Assembly and Dynamics of the Rhizosphere Micro-biome

a) Sources and Acquisition of Plant-Associated Microbes

The primary reservoir of Plant-Associated microbes is soil. It hosts the rhizosphere microbiota which is dynamically changed by factors such as pore structure, moisture, and nutrient availability. Microbes of many taxa but particularly Proteobacteria, Planctomycetes, Actinobacteria, Verrucomicrobia, Bacteroidetes, and Acidobacteria are selected by plants from bulk soil. 78.2% of the diazotrophs are mainly originated from soil, while the rhizosphere and airborne microbes influence the roots and leaves (Han et al., 2021).

The microbes which colonize inside internal plant tissues such as roots, stems, seeds are called endophytes. These endophytes are known not to produce any pathogenic responses in the plant. Such microbes are commonly derived from soil or by seeds. During seed dormancy, many seed-borne endophytes can be persisted in root tissues of perennial nature. These are then recolonized as the plant grows upward. In case of rice, vertical transmission of endophytes through contaminated seeds have been observed (Peng et al., 2025).

The early colonizers from bulk soil or from any old root/tissue segment exert strong priority effects which is the deriver of trajectory of next coming microbial community's assembly. Air transmitted microbial communities (such as leave colonizing) especially combined with dust, rainwater, and animal vectors are significant sources of acquisition of microbes. After which factors like motility, adhesion capacity, and growth rate determine the success of colonization. The extent of the role played by phyllo-sphere microbiomes has been demonstrated recently and it is encouraged

that such assemblies found on leaves impact the rhizosphere assemblies, by provoking plant systemic immune systems as a cross kingdom signaling mechanism. (Muller et al., 2013).

b) Key Drivers of Micro-biome Assembly

The genetics of a plant is a significant driver of how rhizosphere is shaped. Perennial woody plants support more microbial diversity in terms of functionality and assembly, provided if they have greater degree of heterozygosity. Domesticated plants are always more homozygous compared to their wild relatives and that is why crops such as wheat, rice, maize, barley etc. host similar microbes. Genetically modified varieties such as, M579 come in with a different microbiome profile. Disease resistant genotypes have more diverse microbial communities compared to the susceptible ones (Zhang et al., 2023).

Root exudate composition is also very important driver of microbiome assembly. Specific metabolites such maize benzoxazinoids affect taxonomic specificity (Hemelda & Noutoshi, 2025), whereas sugars like glucose, sucrose, and trehalose lure Proteobacteria and Actinobacteria. The exudate composition is affected by plant development stage and circadian rhythms. Barley under drought stress will produce more sucrose in exudates encouraging more fungal assembly. Plants transport proteins are responsible for regulation of exudates. Biosynthetic pathways can influence assembly of bio-control related communities. Deep metabolic profiling discloses that secondary products such as coumarins of the Arabidopsis roots are potentially selective, which favor the enrichment of Pseudomonas spp, which complement the iron mobilization and control of pathogens (Zhang et al., 2023).

Chemical and physical properties of soil such as moisture, pH, nutrient availability (N, P, K) and organic compounds significantly change the microbial communities. Galactose and arabinose can be increased by phosphorous insufficiency. Soil types can be a driver of assembly of microbiome, chernozem and other soil types effectively change the microbial composition in soybean microbiome. Antibiotic resistance genes tend to assemble in urban soils.

Agronomical practices such as conservation tillage and no-tillage activities are linked with increased microbial diversity. Fertilization practices continued for longer terms are also associated with increased microbial assembly. Concentrated localized nutrient hubs are sites of microbial stratification. Ectomy-corrhizal fungi are hardier and more sustained in deeper soils, and nutrient rich topsoil hosts copiotrophic bacteria (Duret et al., 2025).

Arbuscular (AMF) and ectomycorrhizae (EMF) like symbiotic fungi change the bacterial community structure. Laccaria bicolor (EMF) increased Pseudo-monas populations by increasing of the transport of carbon to the rhizosphere. Methylo-bacterium and

Azospirillum are keystone taxa that assist the stability of microbial community networks, while Bacillus subtilis EPS/TasA gene expression promotes the production of biofilms, increasing community complexity. Fusarium and other phyto-pathogens are suppressed by antagonistic interactions, which mostly involve biocontrol agents like Bacillus and Pseudomonas.

Pythium like pathogens due to their sequestration nature of plant-derived sugars can reduce carbon pools. On the contrary, Trichoderma spp. type beneficial microbes and plant growth-promoting rhizo-bacteria prompt exudation or increase nitrogen fixation (Han et al., 2021). Plant strategies like "cry for help" recruits stress-adapted microbial partners under adverse conditions. Archea is less studied but contributes to nutrient cycling including ammonia oxidation and sulphur reduction.
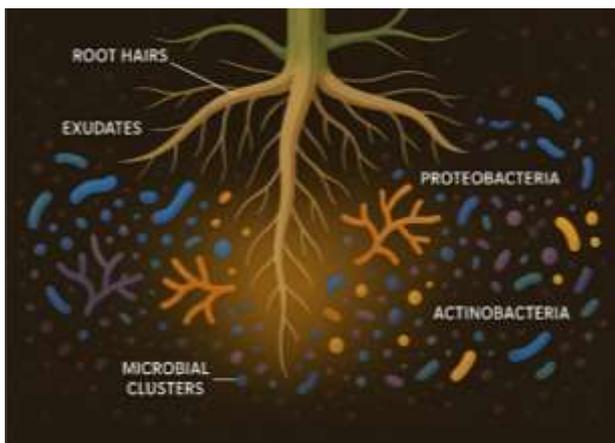
Fig 1: The assembly of rhizosphere microbiomes. Taxonomically heterogeneous microbes (e.g., Proteobacteria shown in blue, Actinobacteria in orange) attracted by the root exudates (yellow-orange gradients) depend upon plant genes and soil characteristics. Root hair-colonized microbial communities multiply on the root surface to produce a synergetic nutrient use recycling and withdrawal backbone under bombardment. Image generated using Sora.ChatGPT .com (OpenAI, 2025).

c) Temporal Dynamics and Feedback Loops (Plant–Soil Feedbacks)

As mentioned above, microbial community structure changes with plant's developmental stages. Younger plants with more exudation activity concentrate more sucrose and promote copiotrophic type microbes. Older plants with more nitrogen fixation promote nitrogen-cycling taxa's bacteria (Shi et al., 2011). More sensitive dynamics to developmental stages are to microbial communities in phyllosphere and in rhizosphere. In Panax notoginseng, advantageous biocontrol bacteria reach their highest levels in the third growth year, while pathogens generally build up over time. Seasonal cycles like growth and dormancy cycles influence microbial activity. Winter dormancy generally degrades microbial diversity and function (Esperschütz et al., 2009).

Biodiversity as the Engine of Rhizosphere Function
a) Biodiversity–Ecosystem Functioning (BEF) in the Rhizosphere

A plant's rhizosphere is constantly changing which involves the interaction of plant roots, microbial communities and soil particles to maintain the ecosystem functioning. Influence of root exudates on microbial community structure creates specie specific microbiomes. The biodiversity-ecosystem functioning framework states that with increase in bacterial diversity, there is increase of stability, productivity and resilience of ecosystem. This occurs through mechanisms such as functional redundancy, synergic interactions and niche complementary.

There is a significant contribution of both rare and common taxa in the rhizospheric processes. Within the common taxa, the proteobacteria and the action-bacteria are the main contributors to carbon dynamics and nutrient turnover. On the contrary, the rare taxa have a disproportional contribution under specific environmental conditions to ecosystem multi-functionality. The dominant taxa, rare organisms are the ones which fulfil the specialized roles to enhance stability, backed up by the mass-ratio hypothesis. The side-by-side delivery of multiple ecosystem services is the ecosystem multi-functionality (Shi et al., 2011). This multi-functionality is directly proportionated by the diversity of microbiome. Reduction in soil complexity is brought by activities such as sieving, which in turn reduces the biodiversity contributing to its critical roles.

b) Mechanistic Pathways Enhancing Rhizosphere Function via Microbial Biodiversity

Functional redundancy is when multiple taxa perform the same function and confer to the robustness to rhizosphere functioning under stress. For example, nitrogen fixation is sustained by a wide range of bacteria such as Azotobacter, Rhizobium and Azospirillum, maintaining nitrogen availability even under specie loss. Similarly, phosphate solubilization is sustained by multiple bacterial genera such as Pseudomonas, Penicillium, and Bacillus, ensuring consistent supply. The functional redundancy is seen in maize rhizosphere, where microbial diversity buffers functional loss under stress. The analysis of 150 field trials confirmed that the multi-strain microbial consortia, with the number of taxa, exceeding 20, can guarantee 30 additional functional redundancy against drought conditions in comparison to single inoculants performed by individual inoculants (Li et al., 2024).

Microbial taxa occupy different spatial and metabolic niches, this increases its overall nutrient use efficiency. Mycorrhizal fungi extend themselves far from the rhizosphere allowing access to immobile nutrient. Pseudomonas enhance the attaining of phosphorous in complement with plant uptake mechanisms. Rare taxa are often specialized in nitrogen cycling particularly under diversified planting systems. Bacteria and Rhizobacteria often live in

distant habitats, this reduces competitions and enhances complementarity.

The microbial communities show different properties which are more then ones for single strains by metabolic cooperation and signaling interactions. Plant growth- promoting rhizobacteria enhance the stress tolerance, while some modulate phytohormone levels to increase root plasticity and growth. The flavonoids act as communication medium to promote efficient symbiosis between the rhizobia and the mycorrhizae. Root exudates like sugars and organic acids, function to attract beneficial microbes and induce antimicrobial properties. Maize hybrids have abundant auxin-producing bacteria compared to inbred lines for superior root adaptability.

The diversity in soil microbiome also suppresses soil borne pathogens by multiple methods. Pseudomonas spp. removes Fusarium by fighting it for nutrients (Kumar & Jagadeesh, 2016). Bacillus spp. and Streptomyces are known to make Lipopeptides and antibiotics which remove pathogens. *Trichoderma* and arbuscular mycorrhizal fungi (AMF) host defenses against biotic. Combination of Trichoderma harzianum and Bacillus subtilis strain that genetically produced enzyme labeled chitinase enabled pathogens to be suppressed synergistically and also reduced the occurrence of the Fusarium wilt among tomatoes in the field by 65 percent when used in the field.

Fig 2: The BEF principles of ecosystem functioning in the rhizosphere. The ecosystem functions (bottom) are thus determined by the microbial diversity (top) in terms of functional redundancy (several tax clients exercise mutually overlapping functions), niche complementarity (use of various items), and synergistic interactions (e.g. exchange of metabolites). It is associated with improved multiple nutrient cycling, resilience to stress and healthy soil (adapted by Shi et al., 2011; De Vries et al., 2020). Image generated using Sora.ChatGPT.com (OpenAI, 2025).

c) Biodiversity-Driven Impacts on Core Rhizosphere Functions

There are symbiotic and free-living bacteria that perform biological nitrogen fixation. Owing to the inaccessibility of insoluble phosphates, the organic acid releasing microbes, such as Pseudomonas, Bacillus, and Penicillium, are able to mobilize phosphates (Babana &

Antoun, 2006). The plant hormones that were targeted and regulated as a result of PGR involvement are auxins, cytokinin's, as well as ACC deaminase, which influence the growth and the plant stress response (Glick, 2005).

Microbes also secrete exopolysaccharides that are vital in soil aggregation enhancing porosity, water retention and control of erosion. Fungi such as Cladosporium are also beneficial and supersede Fusarium (Chen et al., 2021). Bacillus and Pseudomonas are involved in bioproduction of antifungal chemicals. Vast microbial associations alleviate the prevalence of disease, such as Fusarium wilt.

The plant growth promoting rhizobacteria (PGPR) have been documented to promote the water uptake of plants and drought resistance (De Vries et al., 2020). In halotolerant bacteria, otherwise demonstrated paradigmatically by Bacillus subtilis and Azospirillum, salt-stress alleviation strategy is achieved by augmentation of the osmotic response. The soils that are polluted with metals are detoxified by the metal-resistant microbes (e.g., Burkholderia and Pseudomonas) through siderophore secretion and chelation (Soni et al., 2022).

Engineering Strategies for Rhizosphere Microbiome Management

Bioinoculants or in other words, plant growth-promoting microbes (PGPMs) are some of the promising agents of promoting healthy soils and boosting crop productivity. These inoculants are only effective when microbial diversity is present as well as between genotype of the host with local microbiome conditions (Burz et al., 2019).

Bacillus, Pseudomonas, Rhizobium, Azospirillum, Bradyrhizobium, are observed to aid nutrient-taking up and enhance vegetative performance, by enhancing phosphate solubilization, nitrogen fixation and also production of phytohormones like indole-3-acetic acid (IAA) and cytokinins. All these features provoke better root structure, and, therefore, an increase in stress tolerance (Arora, 2020). Pseudomonas fluorescens has been used within the genus Pseudomonas where the microbe modulated microbial communities in oilseed crops has promoted the resilience of the crops when subjected to both abiotic and biotic stress. In other experiments the co-inoculation of Pseudomonas oryzihabitans and Brady-rhizobium together have built an increase in yields in soybean of about 10 %. Some Plant Growth-Promoting Rhizobacteria (PGPR) including Paraburkholderia fungorum and Delftia spp. overcome the need to use inorganic fertilizers by increasing the available nutrient and their uptake. Pseudomonas chlororaphis PA6, is another identified virulence factor which protects the host plant against all kinds of diseases and at the same time modifies its root exudates to attract a variety of desirable microbial organisms as well (Burz et al., 2019). Production of phenazines is associated with further suppression of pathogenic taxa.

The plants are also cultivated with the help of Trichoderma spp. and arbuscular mycorrhizal fungi (AMF, e.g, Glomus, Rhizophagus irregularis) that help the plants in nutrient uptake (phosphorus), water retention and provide plant protection against pathogens. Inoculation of AMF improves the rice yield with 9.7 % and makes it drought resistant. MF has been created and is commercially exploited in farming (Burz et al., 2019).

The community of bacteria (e.g., Enterobacter, Burkholderia and Bacillus) and fungi (e.g., Acrocalymma vagum) inside plants can diminish the oxidative stress, construct the osmoprotectants and induce systemic. As another example, Halothiobacillus halophilus enhances drought/salinity tolerance of Plantago coronopus.

Synergistic combinations (for example: Bacillus-AMF, Rhodo-pseudomonas palustris + Bacillus subtilis), have a much bigger performance than single-strain inoculants whose activity to meet complementary metabolic functions, amounted to an increase in yield of up to 17.73 %. Example: Bacterial SynCom (Stenotrophomonas rhizophila, Xanthomonas retroflexus, Microbacterium oxydans, Paenibacillus amylolyticus) with 4 species improves drought tolerance in Arabidopsis via biofilm formation. The edited Azospirillum brasilense with a higher ACC deaminase made the maize production in salty soil to improve by 22 percent hence the repercussions of genome editing in micro-biome engineering industry.

SYNCOM ENGINEERING
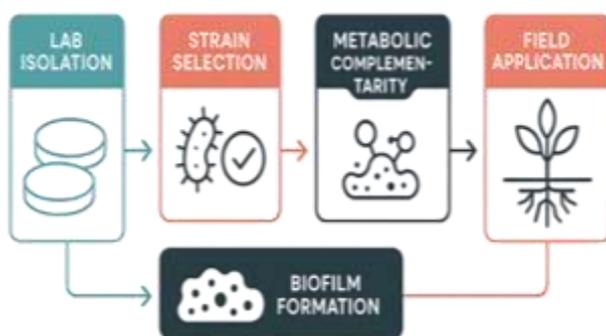
Fig 3: The pipeline of synthetic microbial consortium (SynCom) engineering. Image generated using Sora.Chat GPT.com (OpenAI, 2025).

The assembly of plant beneficial strains through metabolic screening, complementarity and colonization through biofilm are crucial steps between the lab isolation of plant-beneficial strains and use in the field. Modular design Strengthens the field persistence relative to inoculants of single strain.

It has been shown that single strain inoculants have a low tendency on competing with the native microbes. A niche competition is one of the reasons, as the presence of certain limiting factors present in the soil, Bacillus strain may acquire a monopoly, and consequently, this affects the scope of adaptive variety and the reduction of the functional resilience (del Carmen Orozco-Mosqueda et al., 2022). Antagonism of microbes adds another layer of complexity to efficacy of isolates. The competitors are used in microbial rivals to dominate ecological niches, through antimicrobial substances, which are lipo-peptides and proteins liberated by the type VI systems. Whether introduced strains survive will depend on the prioritizing influences of priority effects, i.e. on the competition on the specific substrates determining the bias in succession trajectories (Tkacz et al., 2018).

On the other hand, consortia escalate redundancy in functionality. The example of a synergetic mixture of populations of the Bacillus and Pseudomonas strains increases drought resistance of chickpea by exchanging various pathways of nutrient cycles (Kumar et al., 2016). By building the network of the hyphae in root cortices through MF, a habitat is provided to the bacteria that brings an improved exchange of nutrients together. Besides, the relationship between the cross-feeding and quorum-sensing allows microbiome networks to stabilise. Rhizobione transplantation in which the entire scene of the microbe community is in fact, mechanically moved over has shown different results. Although the concept of transplantation presents the keystone phyla that can inhibit pathogens, e.g., such as Actinobacteria and Proteobacteria, it can also disrupt the homeostasis of an ecosystem (Jiang et al., 2022). Such environmental disturbances (such as the establishment of non-native microbes) present a danger because they have a potential to destabilise native communities, and reduce ecosystem functionality (van Der Heijden et al., 2015).

Abiotic stressors (inappropriate pH, moisture regime etc.) normally worsen the efficacy of inoculants and the presence of resident microbiome in the rhizosphere will further degrade the inoculant performance. The mitigation measures encompass encapsulating live biocontrol agents even at nano level, seed coating and the use of prebiotics. The heterogeneity of agricultural fields exerts a major effect on the effectiveness of inoculants and soil heterogeneity occurs as a result of crop genotype (such as in japonica vs. indica rice microbiomes) and local climate role. Machine learning models thus have been posed as new formidable tools in predicting inoculant performance. Machine learning models that use soil metagenomics data combined with climate data would make predictions about inoculant success with 89 percent accuracy, showing proof of principle to create precision microbiome modulation with reduced cost, risk, and time to accomplish the objective (Patel et al., 2022).

Although soil microorganisms play a critical role in crop productivity, a mere 1 out of 100 microorganisms in soil can be cultivated and so the existing metabolic strategies are bound to be restricted. As such, it is

becoming common to design consortia using omic and AI-based approaches, such as the use of Chitinophaga spp. in organic degradation. There has been, however, a lack of a whole picture of the soil microbial metabolic networks. The microbiome of holophytes that is especially important in salt soils with regard to nutrient cycling and to managements of salt stress is Proteobacteria, Actinobacteria, halotolerant Acidobacteria, and Ascomycota (Tang et al., 2023). Other genera like Pseudomonas and Bacillus also have great effects on the health of plants (Xun et al., 2024). The transgressions of engineered strains can reach far; when someone fails to control them, they may spread some undesired ecological imbalances.

Enhancing Resilience to Global Challenges
a) Climate Change Adaptation

The effect of nanobiochar or biochar amendment is thus a rather large beneficial multiplier on microbial activity of soil, nutrient availabilities, drought tolerance and heat stress of plants. Vermicomposting is a significant and natural approach that helps to improve earth conditions and develop various microbial communities, hence water abiotic stress (Huang et al., 2024). At the same time, the resilience is enhanced by arbuscular mycorrhizal fungi (AMF) that contribute to an enlarged water and nutrient uptake under the influence of drought and salt stress. Above all, genome editing, or to be more specific, the modifications of the water-use-efficiency-related genes with the help of CRISPR/Cas9 methods enable the creation of the drought-resistant rice species (Rai et al., 2023). Climate change has altered the hydrological regimes and in the process made crop productivity and yield to be low. Agroecological systems have the potential to boost heterogeneity in microbes, and, thus, climate resilience, namely, through agroforestry or polyculture production (Glassmire et al., 2020).

Carbon sequestration through soil microbiomes provides the most important tool with which to sustain soil, and it is climate change that uproots the habitats of these microorganisms, enhancing the process of organic matter degradation and subsequent emission of CO_2. The presence of biochar adsorbed with microbes on biochar surface in a composite biochar-microbe can increase carbon storage in degraded soils by 40 percent and can increase nodulation of soybean crops by up to 80 percent in such soils as well (Palansooriya et al., 2025). The microbiomes (marine life) such as phytoplankton contribute a significant amount of carbon sequestration to the environment because of their highly effective atmospheric CO_2 uptake; however, due to the rise of sea temperatures and ocean acidity this potentiality is also dwindled (Hoegh-Guldberg et al., 2019). The microbial communities of cities, at the same time, are also altered under the influence of the changes in the way the land is used, and the shifts in the microbial diversity and functionality are significant. As a result, nanofertilizers

(NFs) have become one of the most technologically promising products that significantly increased the efficiency of the uptake of nutrients and also gave plants and crops a higher drought and salinity resistance parameter.

The ability of biochar to increase water-holding capability of a soil can supplement osmoprotection and tone down the level of stress hormones (Khan et al., 2021). The Arbuscular mycorrhizal fungi (AMF) can enhance drought tolerance by aiding the plants to stimulate their drought survival mechanisms, including osmotic adjustments, a higher level of antioxidants, and enhancement of phosphorus uptake (Wahab et al., 2023). The tools of genomic editing, most specifically CRISPR/Cas9, provide the opportunity to adjust the stress-response genes precisely, with an increased example of salt-tolerant tomatoes (Tran et al., 2023). The microbe symbiosis influences the metabolism of stress-hormones (e.g. ABA) and osmoprotective substances production (Diyaolu & Folarin, 2024). The assumption of the old friends is that the relationships of the microbes that have a long history promote the robustness of the hosts (Robinson & Jorgensen, 2020). Agro-forestry systems can help reduce the stress of drought and increase crop production by 150 percent or more in the dry spell in areas such as Faidherbia albida.
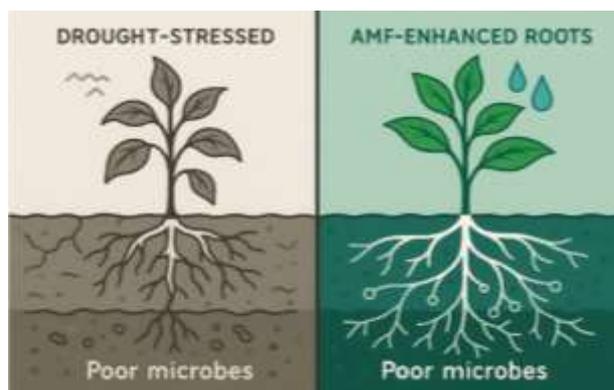
Fig 4: Change in drought resilience depended on microbial forcing in opposite ways. Left: Stressed plants having dysbiotic microbiome have bad roots and a low ability to hold water. Right: arbuscular mycorrhizal fungi (AMF): they improve their water/ nutrient uptake through their mycorrhizal networks and thereby plant vigor in drought. Image generated using Sora.ChatGPT.com (OpenAI, 2025).

They include soil probiotics which raises bioavailability of nutrients and water retention purposefully with Pseudomonas fluorescens that guarantees boosted nutrient cycling and water retention (Fahad et al., 2022). In its turn, nanobio-fertilizers (NBFs) which are a combination of nano-particles and useful microorganisms like Azotobacter and Rhizobium are also deemed to enhance plant stress tolerance. The inoculation of the plants with mycorrhizals also provides them with resistance to the infections in addition to the reduced dependence on

synthetics (Lahlali et al., 2021). A relatively new approach to genetic engineering, i.e. CRISPR/Cas9-mediated viral delivery, allows working out a fast solution by altering multiple genes related to stress. There is also the high-throughput sequencing method that has been employed to isolate stress tolerant strains of Arbuscular mycorrhizal fungi (Lahlali et al., 2021). It is also reported that beneficial microorganisms like Azotobacter vinelandii can reduce the dependence on the input of fertilizers. In addition, microbial consortia managed with AI-based approaches are progressively utilized to optimize species selection with respect to stress resistance. Lastly, probiotics, such as PaleoPower formulations, have the ability to restore damaged soils and to increase yield, in particular by +28.6% in agro-ecosystems severely affected during the periods of low rainfall (VijayKumar et al., 2024). At the same time, urban greening and other extensive rewilding projects have demonstrated that the microbial community is rejuvenated (Mills et al., 2017).

b) Contamination Resilience
When we look at what the recent researches are saying, we see that biochar is rather impressive. it also is able to stick the pollutants in the soil and speed up their degradation by microbes (Malik et al., 2024). Vermicompost, in its turn, speeds up the process of digestion of organic materials and minimizes the time of the introduction of pesticides to an environment. Sadly there is such a thing as disposing too many agrochemicals in fields, and the resultant upset of arbuscular mycorrhizal fungi (AMF) community is surely the wrong research paper topic (Powell & Rillig, 2018). One of the big criminals is glyphosate, It failed miserably on enriching the beneficial microbes such as Actinomycetota and gave a comfortable home to the pathogens (Zaller et al., 2014). To add to it, today the urban chemicals are beginning to transform the microbial ecology and reduce its diversity in the process (Wakefield-Rann et al., 2020).

Antimicrobial Abuse is inevitably bound to cause dysbiosis (Greenhough et al., 2018). Nanofertilizer, especially, zinc oxide (ZnO) and iron oxide (Fe_2O_3) nanoparticles have a prophylactic prospect against the toxicity of heavy metals towards plants (Almendros et al., 2022; Yusefi-Tanha et al., 2020). The consortia of microbes containing biochar-supported microbial consortia enhance phytoremediation of degraded soils. The Arbuscular mycorrhizal fungi (AMF) promotes the process of heavy metals phytoremediation by applying the two modes, namely chelation and phytoextraction (Wahab et al., 2023). Microbiomes degrade plastic materials in the soil with the help of plastic degrading-bacteria. Leguminous trees like Gliricidia sepium have the ability to stabilize the soil and on the same note degrade the pollutants.

Home gardens facilitate a good environment that facilitates good microorganism that is involved in detoxification and also ensures food security (Peyre et al., 2006). The nanobiochar application proves to contribute stability of microbial biomass to stressful situations imposed by pollutants (Rashid et al., 2023). There is also conservation of arbuscular mycorrhizal fungi diversity through the approach of sustainable land management such as organic farming or less tillage of the earth. A microbial consortium has been shown to degrade glyphosate residues to an extent of 36 % which is characterized by the presence of Pseudomonas putida. Both biochar and compost may be used in cleaning up of soils that are polluted (Coleman & Whitman, 2005). Indigenous knowledge teaches the necessary skills in management of microbes.

c) Weed Management Implications
The invasive weeds e.g. Prosopis juliflora change the soil microbiomes and substitute the indigenous vegetation (Kafle, 2009). Allelopathic bacteria are linked to weeds, which makes them more competitive (Tilman et al., 2011). Pathogenic microorganisms attacking the roots can also be included and the pathogens include the Phoma spp. The Trichoderma spp prevents pathogens that destroy weed.

Artificial intelligence approaches are now becoming prominent in the process of biological identification of bioherbicide strains (Bacillus subtilis), etc. (D'Urso & Broccolo, 2024). At the same time, it was revealed that the use of biochar and vermicompost had the capacity to promote ecosystems in which beneficial microbial communities succeed over communities with weed-related pathogens (Okebalama & Marschner, 2023). Various cropping modes, in particular, cover crops and rotation regimes have proven to enhance the structure of the arbuscular mycorrhizal fungus (AMF) in turn inhibiting weed growth indirectly. Additionally, not only transplantation of competitive crop microbiome can subvert weed establishment but also a competitive crop microbiome can act by excluding the niche of the weeds (Landis et al., 2000). In complementary, there is the incorporation of cover crops and microbial inoculants in cropping systems which enhances the health of the soil and therefore the ease of suppressing the weeds.

Current Challenges and Knowledge Gaps
a) Complexity and Context-Dependency of Micro-biome Interactions
Soil rhizosphere microbiome is one of the least understood microbial communities that consists of a diversity of thousands of operational taxonomic units (OTUs) where microbial interactions are highly diverse with context. The biotic factors, such as the genotype of the plant, the combination of root exudates, which is variable with plant development stage and the environment, the role of microbial interactions, and the ecological level of pathogen suppression should be considered as major factors (Berendsen et al., 2012; Bulgarelli et al., 2012).

Other abiotic factors that affect the composition and activity of the microbial community are the type of soil, weather conditions, past land-use, agricultural practices (including tilling and fertilization) and the variation of precipitation and temperature under changing climate (Bell et al., 2005). Moreover, the functional redundancy of microorganisms and dynamic interrelations between them, which are competitive, cooperative, and emerging community patterns, cannot be predicted precisely. This is because it is complicated to develop a universally effective microbial intervention considering the fact that what works out in the laboratory may not work out well in the field where competition and environmental stress have to be considered.

b) Predicting Outcomes of Microbiome Engineering Interventions

Although both successful advances in synthetic biology and microbial consortium engineering have been made, the long-term predictability of the manipulation of the microbiome is problematic due to a number of reasons.

- Ecological instability: genetically modified organisms (P. fluorescens to withstand drought) may never be stable or create stable in the fields as it was supposed (Timmis & Ramos, 2021).
- Connection with hosts: Rhizobia nitrogen-fixing, and phosphate-dissolving bacteria have effective activity and depend on compatibility with their host and the environment in the soil (Santos & Olivares, 2021).
- Trade off: The parasitic plants also interact with strigolactone, a plant growth regulator, and this causes the parasitic plants to interact with mutualistic mycorrhizae.
- The top down and bottom up engineering: In microbial engineering, such selected synthetic communities (SynComs) are not as fined-grained, at least with regard to emergent dynamics or unculturability such as reported by (Shong et al., 2012) and (Mee et al., 2014).
- Evolution of pathogens: Another aspect that diminishes resilience engineered microbial communities is the antibiotic resistance assessment by the pathogen and developing of strategies in response.
- The absence of standardization: Non-standardized approaches do not take into account the opportunity to reproduce the given research.

c) Scaling from Lab/Pot to Field: Persistence and Efficacy Challenges

The barrier to diffusing laboratory findings to the farm is limited by only some obstacles microbe longevity, transmission efficiency, soil variability, longevity of existence, adapting to the environment and pending the results of extended field tests.

- Microbial survival: In the case of the introduced strains, they are not able to colonize or successfully establish during niche competitions with the native microbiome or some environmental form such as drought or elevated temperatures (Ray et al., 2020).
- Delivery methods: Traditional inoculation of seed treatment or drenching the soil cannot help with accuracy due to irregular colonization.
- Soil heterogeneity: Such natural inconsistency creates a difficulty in the uniform application strategy.
- Long-term stability: Probably, synthetic microbiomes will not be the same when subjected to field conditions.
- Environmental adaptability: Although improved yields of maize were recorded as a result of the extensive maize yield increase with biochar-microbial amendments in Kenya, there has been a prevailing low adoption due to economic challenges (Njoroge et al., 2023).
- Long Field North Experiments Desireza: No-till farming represents conservation techniques that can be potentially helpful to microbial survival; nevertheless, it needs further confirmation.

d) Integrating Multi-Omics Data for Mechanistic Understanding

Despite the fact that, with the arrival of high-throughput sequencing, it has been possible to significantly reduce the barrier posed by metagenomics, transcriptomics, and metabolomics, there are still barriers. The reference databases currently available, and that have the potential to enable the functional annotation of the immature microbiome, is in its infancy.

Second, metatranscriptomics can be used to unveil microbial activities (e.g., nitrogen fixing activities of Azospirillum), although these studies are rather uncommon (Gómez-Godínez et al., 2019). Third, the integration of all kinds of data, e.g., transcriptomic and proteomic, are cumbersome. Lastly, there is no standardized protocol, which negatively affects reproducibility since the final results cannot be compared due to methodological differences.

e) Defining and Measuring Microbiome "Health" and "Function" Effectively

A healthy microbiome is yet to have a concise quantification because of the following reasons:

- Context specificity: microbe richness may not always have a positive influence on nutrient circulation and higher crop yields.
- Functional redundancy: This factor makes it more difficult to determine the resiliency and stability of the micro-biome.
- Categories of unknown and known functions: Functional measures are withdrawn at the expense of direct measures of taxonomic measure.
- Same expression in different crops: This is perhaps because of a fixed trait in plants and we cannot

eliminate the involvement of microbiome (Bakker et al., 2012).

- Lack of standardization: There is no standardization in the functional pathways that are used to define them.

f) Regulatory and Economic Hurdles for Microbiome-Based Products

The following are some of the issues which inhibit the commercialization and adoption of the bio-based technologies in the agro-food systems:

- Laws that are at their development: The existing laws in certain jurisdiction have failed in some jurisdiction to regulate the ecological risks involved in employing genetically modified microbes in ruining the existing ecosystem (del Carmen Orozco-Mosqueda et al., 2018).
- Potential obstacles: Horizontal gene transfer and environmental uncertainties will be replaced by the need to develop uniform regulation only on an international level.
- Extensive cost and elasticity: This process chain of the production constrains the rate at which it can be adopted in the low GNI countries (Belcher & Hughes, 2021).
- Farmer mistrust: Varying field results give rise to a factor that causes mistrust in bio-fertilizers and bio-pesticides by farmers.
- Intellectual and property and reproducibility: It does not have standard conventions to be implemented at large scale.

Future Directions and Conclusions

a) Mechanisms of host-microbe specificity and their uses

One of the numerous interactions awaiting elucidation is the molecular communication between host and microbe specificity, specifically the involvement of flavonoids, strigolactones, and root exudate completions (Sasse et al., 2018). Multilayered omic-based techniques like metabolomics and transcriptomics have enabled the mapping of principles of signaling networks, and quorum-sensing. The findings will enable the design of root exudate repertoires to specifically enrich with desirable microbial consortia. As an example, directed ecotropism of sucrose has been demonstrated to select drought-responsive microbe. Microfluidics and AI-aided phenotyping have even found multifaceted organisms such as Pseudomonas spp. as a biocontrol agent and Azospirillum spp. as nitrogen-fixing bacteria (Burz et al., 2019). A successful strain selection that is done should focus on niche complementarity, resistance against stress, and low antagonism so that the community remains stable. Nevertheless, a significant hurdle is the culturability of the soil microbes that can perhaps be overcome with the help of synthetic microbial communities (SynComs) based on recreating the native diversity. The integration of machine learning and ecological models on the assembly of microbe communities is very promising to enable more accurate predictions of microbe community assembly under environmental variation due to climate. One of the most important research objectives is the ability of predicting emergent properties, including pathogen suppression, of microbial interaction networks. However, these challenges are still reduced because data on soil heterogeneity and temporal variations in microbial activity are not available. After 10 years, 70% of microbiome transplants failed during field trial because the niche was dominated by native Actinobacteria, this makes preconditioning soils essential to this process.

b) Field Trials and the Long-Term Management of Microbiome

Biochar synergies with microbes, biochar with arbuscular mycorrhizal fungus (AMF) inoculates, and case-by-case crop rotating effects on the stability of micro-biomes should be assessed through field trials. Consortia that are based on Modular SynCom concepts (e.g. Pseudomonas AMF) will have 50 per cent higher field persistence of conventional inoculants. The most essential performance indicators are functional resilience, e.g. nutrient cycling efficiency over several growing seasons (Lehmann et al., 2020). Standardized protocols are necessary to guarantee experimental reproducibility and genotypes of the crops that enhance mutualistic microbes, such as plants with high root exudates should be favored. The recent improvements in the CRISPR/Cas9-mediated editing of root characteristics such as the density of root hairs are harbingers of improved microbial colonization (Rai et al., 2023). The potential of microbiome engineering in the resilience of crops is attested by case studies, one of which is on rice varieties with enhanced Bacillus populations on salinity tolerance.

Any kind of agricultural practices that ensure sustainability especially involving polyculture and use of cover crop helps in preserving the microbial niches, biochar and vermicompost also enhance water retention and increase microbial biomass. Agrochemicals, mainly glyphosate will be limited to sustain healthier communities of AMF. Regulatory regimes should develop international guidelines on the release of genetically modified microorganisms (GMOs) and any possible hazardous effect like horizontal gene transfer (Mukherjee, 2019). Financial and subsidies for bio-fertilizers production and farmer educational programs are required to overcome the adoption barriers. Lastly, synCom technologies and research to practice translation will rely on establishment of public private partnerships.

REFERENCES

Almendros, P., González, D., Fernández, M. D., García-Gomez, C., & Obrador, A. (2022). Both Zn biofortification and nutrient distribution pattern in cherry tomato plants are influenced by the application of ZnO nanofertilizer. *Heliyon, 8*(3).

Arora, S. (2020). Halotolerant microbes for amelioration of salt-affected soils for sustainable agriculture. In *Phyto-microbiome in stress regulation* (pp. 323-343). Springer.

Babana, A. H., & Antoun, H. (2006). Effect of Tilemsi phosphate rock-solubilizing microorganisms on phosphorus uptake and yield of field-grown wheat (Triticum aestivum L.) in Mali. *Plant and soil, 287*(1), 51-58.

Bakker, M. G., Manter, D. K., Sheflin, A. M., Weir, T. L., & Vivanco, J. M. (2012). Harnessing the rhizosphere micro-biome through plant breeding and agricultural management. *Plant and soil, 360*(1), 1-13.

Belcher, B. M., & Hughes, K. (2021). Understanding and evaluating the impact of integrated problem-oriented research programmes: Concepts and considerations. *Research Evaluation, 30*(2), 154-168.

Bell, T., Newman, J. A., Silverman, B. W., Turner, S. L., & Lilley, A. K. (2005). The contribution of species richness and composition to bacterial services. *Nature, 436*(7054), 1157-1160.

Berendsen, R. L., Pieterse, C. M., & Bakker, P. A. (2012). The rhizosphere microbiome and plant health. *Trends in Plant Science, 17*(8), 478-486.

Bulgarelli, D., Rott, M., Schlaeppi, K., Ver Loren van Themaat, E., 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.

Burz, S. D., Abraham, A.-L., Fonseca, F., David, O., Chapron, A., Béguet-Crespel, F., Cenard, S., Le Roux, K., Patrascu, O., & Levenez, F. (2019). A guide for ex vivo handling and storage of stool samples intended for fecal microbiota transplantation. *Scientific reports, 9*(1), 8897.

Chen, M., Shi, H., Gou, S., Wang, X., Li, L., Jin, Q., Wu, H., Zhang, H., Li, Y., & Wang, L. (2021). In vivo genome editing in mouse restores dystrophin expression in Duchenne muscular dystrophy patient muscle fibers. *Genome Medicine, 13*(1), 57.

Coleman, D. C., & Whitman, W. B. (2005). Linking species richness, biodiversity and ecosystem function in soil systems. *Pedobiologia, 49*(6), 479-497.

D'Urso, F., & Broccolo, F. (2024). Applications of artificial intelligence in microbiome analysis and probiotic interventions An overview and perspective based on the current state of the art. *Applied Sciences, 14*(19), 8627.

del Carmen Orozco-Mosqueda, M., del Carmen Rocha-Granados, M., Glick, B. R., & Santoyo, G. (2018). Microbiome engineering to improve biocontrol and plant growth-promoting mechanisms. *Microbiological Research, 208*, 25-31.

del Carmen Orozco-Mosqueda, M., Fadiji, A. E., Babalola, O. O., Glick, B. R., & Santoyo, G. (2022). Rhizobiome engineering: Unveiling complex rhizosphere interactions to enhance plant growth and health. *Microbiological Research, 263*, 127137.

Diyaolu, C. O., & Folarin, I. O. (2024). The role of biodiversity in agricultural resilience: Protecting ecosystem services for sustainable food production. *Int. J. Res. Publ. Rev, 5*(10), 1560-1573.

Duret, M., Wallner, A., Besaury, L., & Aziz, A. (2025). Diversity and functional features of the root-associated bacteriome are dependent on grapevine susceptibility to Plasmopara viticola. *Environmental Microbiome, 20*(1), 30.

Duret, M., Wallner, A., Buée, M., & Aziz, A. (2024). Rhizosphere microbiome assembly, drivers and functions in perennial ligneous plant health. *Microbiological Research, 287*, 127860.

Esperschütz, J., Buegger, F., Winkler, J., Munch, J., Schloter, M., & Gattinger, A. (2009). Microbial response to exudates in the rhizosphere of young beech trees (Fagus sylvatica L.) after dormancy. *Soil Biology and Biochemistry, 41*(9), 1976-1985.

Fahad, S., Chavan, S. B., Chichaghare, A. R., Uthappa, A. R., Kumar, M., Kakade, V., Pradhan, A., Jinger, D., Rawale, G., Yadav, D. K., Kumar, V., Farooq, T. H., Ali, B., Sawant, A. V., Saud, S., Chen, S., & Poczai, P. (2022). Agroforestry Systems for Soil Health Improvement and Maintenance. *Sustainability, 14*(22), 14877. https://www.mdpi.com/2071-1050/14/22/14877

Glassmire, A. E., Zehr, L. N., & Wetzel, W. C. (2020). Disentangling dimensions of phytochemical diversity: alpha and beta have contrasting effects on an insect herbivore. *Ecology, 101*(11), e03158.

Glick, B. R. (2005). Modulation of plant ethylene levels by the bacterial enzyme ACC deaminase. *FEMS microbiology letters, 251*(1), 1-7.

Gómez-Godínez, L. J., Fernandez-Valverde, S. L., Romero, J. C. M., & Martínez-Romero, E. (2019). Metatranscriptomics and nitrogen fixation from the rhizoplane of maize plantlets inoculated with a group of PGPRs. *Systematic and applied microbiology, 42*(4), 517-525.

Greenhough, B., Dwyer, A., Grenyer, R., Hodgetts, T., McLeod, C., & Lorimer, J. (2018). Unsettling antibiosis: how might interdisciplinary researchers generate a feeling for the microbiome and to what effect? *Palgrave Communications, 4*(1), 1-12.

Han, J., Dong, Y., & Zhang, M. (2021). Chemical fertilizer reduction with organic fertilizer effectively improve soil fertility and microbial community from newly cultivated land in the Loess Plateau of China. *Applied Soil Ecology, 165*, 103966.

Hemelda, N. M., & Noutoshi, Y. (2025). Root-exuded sugars as drivers of rhizosphere microbiome assembly. *Plant Biotechnology*, 25.0214 a.

Hoegh-Guldberg, O., Jacob, D., Taylor, M., Guillén Bolaños, T., Bindi, M., Brown, S., Camilloni, I. A., Diedhiou, A., Djalante, R., & Ebi, K. (2019). The human imperative of stabilizing global climate change at 1.5 C. *Science, 365*(6459), eaaw6974.

Huang, L., Meng, Y., Pan, B., Pan, B., Wei, J., Ding, J., Deng, Y., Su, X., Yuan, Z., & Zhang, M. (2024). Multidimensional effects of green waste vermicomposting on cadmium contaminated soil ecosystems: From physicochemical properties to microbial communities. *Journal of Hazardous Materials, 480*, 136429.

Jiang, G., Zhang, Y., Gan, G., Li, W., Wan, W., Jiang, Y., Yang, T., Zhang, Y., Xu, Y., & Wang, Y. (2022). Exploring rhizo-microbiome transplants as a tool for protective plant-microbiome manipulation. *ISME communications, 2*(1), 10.

Kafle, N. (2009). Land degradation issues in Nepal and its management through agroforestry. *Journal of Agriculture and Environment*.

Khan, H. A., Naqvi, S. R., Mehran, M. T., Khoja, A. H., Niazi, M. B. K., Juchelková, D., & Atabani, A. (2021). A performance evaluation study of nano-biochar as a potential slow-release nano-fertilizer from wheat straw residue for sustainable agriculture. *Chemosphere, 285*, 131382.

Kumar, K. H., & Jagadeesh, K. (2016). Microbial consortia-mediated plant defense against phytopathogens and growth benefits. *South Indian Journal of Biological Sciences, 2*(4), 395-403.

Kumar, M., Mishra, S., Dixit, V., Kumar, M., Agarwal, L., Chauhan, P. S., & Nautiyal, C. S. (2016). Synergistic effect

of Pseudomonas putida and Bacillus amyloliquefaciens ameliorates drought stress in chickpea (Cicer arietinum L.). *Plant signaling & behavior*, *11*(1), e1071004.

Lahlali, R., Ibrahim, D. S., Belabess, Z., Roni, M. Z. K., Radouane, N., Vicente, C. S., Menéndez, E., Mokrini, F., Ait Barka, E., & e Mota, M. G. d. M. (2021). High-throughput molecular technologies for unraveling the mystery of soil microbial community: challenges and future prospects. *Heliyon*, *7*(10).

Landis, D. A., Wratten, S. D., & Gurr, G. M. (2000). Habitat management to conserve natural enemies of arthropod pests in agriculture. *Annual review of entomology*, *45*(1), 175-201.

Lehmann, J., Bossio, D. A., Kögel-Knabner, I., & Rillig, M. C. (2020). The concept and future prospects of soil health. *Nature Reviews Earth & Environment*, *1*(10), 544-553.

Li, Q., Duncan, S., Li, Y., Huang, S., & Luo, M. (2024). Decoding plant specialized metabolism: new mechanistic insights. *Trends in Plant Science*, *29*(5), 535-545.

Malik, S., Laura, J. S., & Khyalia, P. (2024). Assessing the potential sustainability benefit of Agricultural residues: Biomass conversion to Biochar and its use for soil and crop improvement. *Egyptian Journal of Soil Science*, *64*(4), 1479-1493.

Mee, M. T., Collins, J. J., Church, G. M., & Wang, H. H. (2014). Syntrophic exchange in synthetic microbial communities. *Proceedings of the national academy of sciences*, *111*(20), E2149-E2156.

Mills, J. G., Weinstein, P., Gellie, N. J., Weyrich, L. S., Lowe, A. J., & Breed, M. F. (2017). Urban habitat restoration provides a human health benefit through microbiome rewilding: the Microbiome Rewilding Hypothesis. *Restoration ecology*, *25*(6), 866-872.

Mukherjee, D. (2019). Microbial interventions in soil and plant health for improving crop efficiency. In *Microbial Interventions in Agriculture and Environment: Volume 3: Soil and Crop Health Management* (pp. 17-47). Springer.

Muller, E. E., Glaab, E., May, P., Vlassis, N., & Wilmes, P. (2013). Condensing the omics fog of microbial communities. *Trends in microbiology*, *21*(7), 325-333.

Muñoz-Márquez, E., Soto-Parra, J. M., Noperi-Mosqueda, L. C., & Sánchez, E. (2022). Application of Molybdenum Nanofertilizer on the Nitrogen Use Efficiency, Growth and Yield in Green Beans. *Agronomy*, *12*(12), 3163. https://www.mdpi.com/2073-4395/12/12/3163

Njoroge, D. M., Dossa, G. G., Ye, L., Lin, X., Schaefer, D., Tomlinson, K., Zuo, J., & Cornelissen, J. H. (2023). Fauna access outweighs litter mixture effect during leaf litter decomposition. *Science of the Total Environment*, *860*, 160190.

Okebalama, C. B., & Marschner, B. (2023). Reapplication of biochar, sewage waste water, and NPK fertilizers affects soil fertility, aggregate stability, and carbon and nitrogen in dry-stable aggregates of semi-arid soil. *Science of the Total Environment*, *866*, 161203.

OpenAI. (2025). *AI-generated image*. Sora.ChatGPT.com, Digital image generated by AI.

Palansooriya, K. N., Dissanayake, P. D., El-Naggar, A., Gayesha, E., Wijesekara, H., Krishnamoorthy, N., Cai, Y., & Chang, S. X. (2025). Biochar-based controlled-release fertilizers for enhancing plant growth and environmental sustainability: a review. *Biology and Fertility of Soils*, *61*(4), 701-715.

Patel, C., Vyas, S., & Saikia, P. (2022). A futuristic survey on learning techniques for internet of things (IoT) security: developments, applications, and challenges. *Authorea Preprints*.

Peng, Q., Sun, S. e., Ma, J., Chen, S., Gao, L., Du, X., Liu, X., Zhu, F., Peng, W., & Liu, Y. (2025). The effect of developmental stages on microbiome assembly in the phyllosphere and rhizosphere of rice grown in urban area soil. *Environmental Microbiome*, *20*(1), 86.

Peyre, A., Guidal, A., Wiersum, K. F., & Bongers, F. (2006). Dynamics of homegarden structure and function in Kerala, India. *Agroforestry Systems*, *66*(2), 101-115.

Powell, J. R., & Rillig, M. C. (2018). Biodiversity of arbuscular mycorrhizal fungi and ecosystem function. *New phytologist*, *220*(4), 1059-1075.

Rai, G. K., Khanday, D. M., Kumar, P., Magotra, I., Choudhary, S. M., Kosser, R., Kalunke, R., Giordano, M., Corrado, G., & Rouphael, Y. (2023). Enhancing crop resilience to drought stress through CRISPR-Cas9 genome editing. *Plants*, *12*(12), 2306.

Rashid, M. I., Shah, G. A., Iqbal, Z., Shahzad, K., Ali, N., Rehan, M., Alhakamy, N. A. A., & Klemeš, J. J. (2023). Nanobiochar reduces ammonia emission, increases nutrient mineralization from vermicompost, and improves maize productivity. *Journal of cleaner Production*, *414*, 137694.

Ray, P., Lakshmanan, V., Labbé, J. L., & Craven, K. D. (2020). Microbe to microbiome: a paradigm shift in the application of microorganisms for sustainable agriculture. *Frontiers in Microbiology*, *11*, 622926.

Robinson, J. M., & Jorgensen, A. (2020). Rekindling old friendships in new landscapes: The environment–microbiome–health axis in the realms of landscape research. *People and Nature*, *2*(2), 339-349. https://doi.org/https://doi.org/10.1002/pan3.10082

Santos, L. F., & Olivares, F. L. (2021). Plant microbiome structure and benefits for sustainable agriculture. *Current Plant Biology*, *26*, 100198.

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.

Shi, S., Richardson, A. E., O'Callaghan, M., DeAngelis, K. M., Jones, E. E., Stewart, A., Firestone, M. K., & Condron, L. M. (2011). Effects of selected root exudate components on soil bacterial communities. *FEMS Microbiology Ecology*, *77*(3), 600-610.

Shong, J., Diaz, M. R. J., & Collins, C. H. (2012). Towards synthetic microbial consortia for bioprocessing. *Current opinion in biotechnology*, *23*(5), 798-802.

Soni, S., Vishwakarma, G., Singh, S., Kumar, S., Singh, R., Awasthi, P., & Gangwar, V. (2022). Commercial use of plant growth regulators in horticultural crops: An overview. *Pharma Innovation J*, *11*(6), 112-119.

Tang, L., Zhan, L., Han, Y., Wang, Z., Dong, L., & Zhang, Z. (2023). Microbial community assembly and functional profiles along the soil-root continuum of salt-tolerant Suaeda glauca and Suaeda salsa. *Frontiers in Plant Science*, *14*, 1301117.

Tilman, D., Balzer, C., Hill, J., & Befort, B. L. (2011). Global food demand and the sustainable intensification of agriculture. *Proceedings of the national academy of sciences*, *108*(50), 20260-20264.

Timmis, K., & Ramos, J. L. (2021). The soil crisis: the need to treat as a global health problem and the pivotal role of microbes in prophylaxis and therapy. In (Vol. 14, pp. 769-797): Wiley Online Library.

Tkacz, A., Hortala, M., & Poole, P. S. (2018). Absolute quantitation of microbiota abundance in environmental samples. *Microbiome*, *6*(1), 110.

Tran, M. T., Son, G. H., Song, Y. J., Nguyen, N. T., Park, S., Thach, T. V., Kim, J., Sung, Y. W., Das, S., & Pramanik, D. (2023). CRISPR-Cas9-based precise engineering of SlHyPRP1 protein towards multi-stress tolerance in tomato. *Frontiers in Plant Science*, *14*, 1186932.

van Der Heijden, M. G., Martin, F. M., Selosse, M. A., & Sanders, I. R. (2015). Mycorrhizal ecology and evolution: the past, the present, and the future. *New phytologist*, *205*(4), 1406-1423.

VijayKumar, R., Tiwari, P., Daniel, S., Kumar, K. R., Mishra, I., Ks, A., & Shah, D. (2024). Agroforestry Systems: A Pathway to Resilient and Productive Landscapes. *International Journal of Enviornment and Climate Change*, *14*(12), 177-193.

Wahab, A., Muhammad, M., Munir, A., Abdi, G., Zaman, W., Ayaz, A., Khizar, C., & Reddy, S. P. P. (2023). Role of arbuscular mycorrhizal fungi in regulating growth, enhancing productivity, and potentially influencing ecosystems under abiotic and biotic stresses. *Plants*, *12*(17), 3102.

Wakefield-Rann, R., Fam, D., & Stewart, S. (2020). Routine exposure: Social practices and environmental health risks in the home. *Social Theory & Health*, *18*(4), 299-316.

Xun, W., Liu, Y., Ma, A., Yan, H., Miao, Y., Shao, J., Zhang, N., Xu, Z., Shen, Q., & Zhang, R. (2024). Dissection of rhizosphere microbiome and exploiting strategies for sustainable agriculture. *New phytologist*, *242*(6), 2401-2410.

Yusefi-Tanha, E., Fallah, S., Rostamnejadi, A., & Pokhrel, L. R. (2020). Zinc oxide nanoparticles (ZnONPs) as a novel nanofertilizer: Influence on seed yield and antioxidant defense system in soil grown soybean (Glycine max cv. Kowsar). *Science of the Total Environment*, *738*, 140240.

Zafar, M. M., Razzaq, A., Anwar, Z., Ijaz, A., Zahid, M., Iqbal, M. M., Farid, G., Seleiman, M. F., Zaman, R., Rauf, A., & Xuefei, J. 2025. Enhancing salt tolerance and yield potential in cotton: Insights from physiological responses, genetic variability, and heterosis. Turkish Journal of Agriculture and Forestry, 49(1), 110–124. https://doi.org/10.55730/1300-011X.3252

Zaller, J. G., Heigl, F., Ruess, L., & Grabmaier, A. (2014). Glyphosate herbicide affects belowground interactions between earthworms and symbiotic mycorrhizal fungi in a model ecosystem. *Scientific reports*, *4*(1), 5634.

Zhang, L., Bao, L., Li, S., Liu, Y., & Liu, H. (2023). Substances derived from myxobacteria that prevent and control plant pathogenic diseases and their prevention and control principles. *Frontiers in Microbiology*, *14*.